

**Genomic analysis of the immune-related genes of amphioxus reveals extraordinary
innate complexity and diversity**

Supplementary Information

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1 Gene models containing TIR domains

TIR domain-containing genes	
model ID	annotation and structure
57373	Toll-like receptor
61417	Toll-like receptor
66945	Toll-like receptor
68489	Toll-like receptor
73275	Toll-like receptor
74077	Toll-like receptor
76085	Toll-like receptor
78080	Toll-like receptor
82252	Toll-like receptor
82677	Toll-like receptor
85671	Toll-like receptor
88143	Toll-like receptor
88412	Toll-like receptor
88496	Toll-like receptor
88657	Toll-like receptor
89467	Toll-like receptor
89468	Toll-like receptor
89511	Toll-like receptor
89513	Toll-like receptor
89514	Toll-like receptor
91751	Toll-like receptor
92915	Toll-like receptor
94576	Toll-like receptor
96585	Toll-like receptor
97448	Toll-like receptor
99056	Toll-like receptor
100709	Toll-like receptor
105256	Toll-like receptor
107910	Toll-like receptor
112715	Toll-like receptor
121913	Toll-like receptor
126412	Toll-like receptor
141796	Toll-like receptor
141800	Toll-like receptor
142289	Toll-like receptor
142546	Toll-like receptor
151391	Toll-like receptor
151614	Toll-like receptor
151633	Toll-like receptor
151645	Toll-like receptor
151818	Toll-like receptor
176159	Toll-like receptor
189045	Toll-like receptor
199122	Toll-like receptor
209440	Toll-like receptor

TIR domain-containing genes	
model ID	annotation and structure
210161	Toll-like receptor
210181	Toll-like receptor
212115	Toll-like receptor
213606	Toll-like receptor
213613	Toll-like receptor
214025	Toll-like receptor
214070	Toll-like receptor
218598	Toll-like receptor
218638	Toll-like receptor
218677	Toll-like receptor
218685	Toll-like receptor
218730	Toll-like receptor
218741	Toll-like receptor
218776	Toll-like receptor
218790	Toll-like receptor
224551	Toll-like receptor
225202	Toll-like receptor
227113	Toll-like receptor
230014	Toll-like receptor
231890	Toll-like receptor
236291	Toll-like receptor
236303	Toll-like receptor
247177	Toll-like receptor
253137	Toll-like receptor
BfTLR1a	Toll-like receptor
BfTLR1b	Toll-like receptor
65511	IL-1 receptor-like, IG-TM-TIR
100499	IL-1 receptor-like, IG-TM-TIR
123976	IL-1 receptor-like, IG-TM-TIR
102466	IL-1 receptor-like, IG-TM-TIR
91330	Apaf1-L, TIR-NBARC-WD40
66949	CARD-TIR1, Bacterial-TIR
67068	CARD-TIR1, Bacterial-TIR
67074	CARD-TIR1, Bacterial-TIR
78651	CARD-TIR2, Bacterial-TIR
123059	CARD-TIR2, Bacterial-TIR
63875	CARD-TIR3, Bacterial-TIR
86311	CARD-TIR3, Bacterial-TIR
89591	CARD-TIR3, Bacterial-TIR
91235	CARD-TIR3, Bacterial-TIR
101263	CARD-TIR3, Bacterial-TIR
105723	CARD-TIR3, Bacterial-TIR
71397	CARD-TIR-LRR, Bacterial-TIR
94911	CARD-TIR-LRR, Bacterial-TIR
108131	CARD-TIR-LRR, Bacterial-TIR
152579	DD-TIR,

TIR domain-containing genes	
model ID	annotation and structure
172209	DD-TIR,
239641	DD-TIR,
91369	DD-TIR-TIR, Plant-TIR
91370	DD-TIR-TIR, Plant-TIR
95419	DD-TIR-TIR, Plant-TIR
126252	DD-TIR-TIR, Plant-TIR
126253	DD-TIR-TIR, Plant-TIR
127607	DD-TIR-TIR, Plant-TIR
127608	DD-TIR-TIR, Plant-TIR
127609	DD-TIR-TIR, Plant-TIR
89399	DED-CARD-TIR1, Plant-TIR
96757	TIR-F, Plant-TIR
96758	TIR-F, Plant-TIR
84739	LRR-CCP-TM-TIR,
99565	LRR-CCP-TM-TIR,
151632	LRR-CCP-TM-TIR,
161828	LRR-CCP-TM-TIR,
226732	LRR-CCP-TM-TIR,
237289	LRR-CCP-TM-TIR,
237294	LRR-CCP-TM-TIR,
241695	LRR-CCP-TM-TIR,
77814	LRR-DD-TIR, Plant-TIR
77815	LRR-DD-TIR, Plant-TIR
77822	LRR-DD-TIR, Plant-TIR
125503	MAL-like,
84994	MyD88,
246353	MyD88,
92083	MyD88-L,
102703	RIG-I-helicase-like, Bacterial-TIR
102704	RIG-I-helicase-like, Bacterial-TIR
106572	RIG-I-helicase-like, Bacterial-TIR
84448	SARM,
95677	SARM,
67462	SARM-like,
67580	SARM-like,
75614	SARM-like,
75615	SARM-like,
75616	SARM-like,
88079	SARM-like,
88090	SARM-like,
93247	SARM-like,
93376	SARM-like,
93377	SARM-like,
130981	SARM-like,
131196	SARM-like,
66570	TIR-25OS, Bacterial-TIR

TIR domain-containing genes	
model ID	annotation and structure
66838	TIR-25OS, Bacterial-TIR
69107	TIR-A,
69110	TIR-A,
69123	TIR-A,
83956	TIR-B,
73641	TIR-C,
83590	TIR-C,
109027	TIR-C,
87577	TIR-D,
87578	TIR-D,
87584	TIR-D,
87595	TIR-D,
89683	TIR-D,
91177	TIR-D,
126176	TIR-D,
142406	TIR-D,
244314	TIR-D,
244348	TIR-D,
258945	TIR-D,
63431	TIR-E,
102150	TIR-E,
78250	TIR-NTRK,
79955	TIR-NTRK,
63858	TPR-TIR1,
68269	TPR-TIR1,
68270	TPR-TIR1,
68271	TPR-TIR1,
89568	TPR-TIR1,
142220	TPR-TIR1,
151769	TPR-TIR1,
163085	TPR-TIR1,
224538	TPR-TIR1,
224604	TPR-TIR1,
89231	TPR-TIR2,
120893	TPR-TIR2,
83599	TPR-TIR3,
83606	TPR-TIR3,
255990	TRAM-like,

2 NOD/NALP-like receptor (NLR) gene models

NLR. Unpredicted= the domain is not captured by the gene model but detected manually; weak=the e-value is weak for the domain;
NACHTonly=only NACHT domain are found in the model, no DFD or LRR domain are found; 2X=2 gene in 1 model.

model ID	type	curated structure and notes
97355	DLR	2 DLRs in 1 model , DEATH+DEATH+DEATH+LRR, noNACHT
97356	DLR	2 DLRs in 1 model , DEATH+DEATH+DEATH+LRR, noNACHT
121797	DLR	CARD+DEATH+LRR, noNACHT
77771	DLR	2 DLRs in 1 model, CARD+DEATH+DEATH+LRR+DEATH+DEATH+LRR, noNACHT
132252	DLR	CARD+LRR, NACHT missing
123610	DLR	CARD+LRR, NACHT missing
84707	DLR	CARD+LRR, noNACHT
93547	DLR	CARD+LRR, noNACHT
67373	DLR	CARD+LRR, noNACHT
71410	DLR	CARD+LRR, noNACHT
97354	DLR	DEATH+DEATH+DEATH+LRR, noNACHT
77788	DLR	DEATH+DEATH+DEATH+LRR, noNACHT
97353	DLR	DEATH+DEATH+DEATH+LRR, noNACHT
97360	DLR	DEATH+DEATH+DEATH+LRR, noNACHT
97359	DLR	DEATH+DEATH+DEATH+LRR, noNACHT
87869	DLR	DEATH+DEATH+LRR, noNACHT
90340	DLR	DEATH+DEATH+LRR, noNACHT
99488	DLR	2X, LRR+DED+DEATH+LRR, NACHT missing
77774	DLR	DED+DEATH+LRR, NACHT missing
77772	DLR	DED+DEATH+long distance+DEATH+LRR, NACHT missing
97358	DLR	DED+DEATH+long distance+DEATH+LRR, NACHT missing
80239	DLR	DED+LRR, noNACHT
82622	NLR-without LRR	2 NLRs in 1 model , CARD+NACHT
67075	NLR-without LRR	*CARD+NACHT, similar to IPAF-IAP
67069	NLR-without LRR	*CARD+NACHT, similar to IPAF-IAP
76844	NLR-without LRR	*CARD+NACHT, similar to IPAF-IAP
118033	NLR-without LRR	CARD+NACHT
82623	NLR-without LRR	CARD+NACHT
94471	NLR-without LRR	CARD+NACHT
94467	NLR-without LRR	CARD+NACHT
98235	NLR-without LRR	Death+NACHT
68649	NLR-without LRR	Death+NACHT
65486	NLR-without LRR	Death+NACHT
90562	NLR-without LRR	Death+NACHT
86966	NLR-without LRR	DED+NACHT
82625	NLR-without LRR	NACHTonly
99539	NLR-without LRR	NACHTonly
68903	NLR-without LRR	NACHTonly
92858	NLR-without LRR	NACHTonly
94466	NLR-without LRR	NACHTonly
89728	NLR-without LRR	NACHTonly
89729	NLR-without LRR	NACHTonly
95569	NLR-without LRR	NACHTonly
111653	NLR-without LRR	NACHTonly

NLR. Unpredicted= the domain is not captured by the gene model but detected manually; weak=the e-value is weak for the domain;
NACHTonly=only NACHT domain are found in the model, no DFD or LRR domain are found; 2X=2 gene in 1 model.

model ID	type	curated structure and notes
99537	NLR-without LRR	NACHTonly
87011	NLR-without LRR	NACHTonly
89726	NLR-without LRR	NACHTonly
69065	NLR-without LRR	NACHTonly
103519	NLR-without LRR	NACHTonly
69066	NLR-without LRR	NACHTonly
96741	NLR-without LRR	NACHTonly
78182	NLR-without LRR	NACHTonly
78183	NLR-without LRR	NACHTonly
120153	NLR-without LRR	NACHTonly
101177	NLR-without LRR	NACHTonly
111243	NLR-without LRR	NACHTonly
126540	NLR-without LRR	DEATH+NACHT
92164	NLR	Death+NACHT+weakLRR
100912	NLR	Death+NACHT+weakLRR
94470	NLR	CARD+NACHT+unpredictedLRR
92153	NLR	CARD+NACHT+unpredictedLRR
97362	NLR	DEATH+DEATH+NACHT+LRR
82460	NLR	DEATH+NACHT+LRR
69426	NLR	DEATH+NACHT+LRR
89453	NLR	DEATH+NACHT+LRR
82459	NLR	DEATH+NACHT+LRR
89473	NLR	DEATH+NACHT+LRR
82461	NLR	DEATH+NACHT+LRR
89477	NLR	DEATH+NACHT+LRR
89442	NLR	DEATH+NACHT+LRR
125541	NLR	DEATH+NACHT+LRR
86714	NLR	DEATH+NACHT+LRR
89467	NLR	DEATH+NACHT+LRR
81065	NLR	DEATH+NACHT+LRR
89451	NLR	DEATH+NACHT+LRR
94396	NLR	DEATH+NACHT+LRR
89479	NLR	DEATH+NACHT+LRR
72607	NLR	DEATH+NACHT+LRR
76840	NLR	DEATH+NACHT+LRR
67322	NLR	DEATH+NACHT+LRR
97974	NLR	DEATH+NACHT+LRR
100913	NLR	CARD+NACHT+unpredictedLRR
92163	NLR	CARD+NACHT+unpredictedLRR
129511	NLR	CARD+NACHT+unpredictedLRR
89475	NLR	DED+NACHT+LRR
86759	NLR	DED+NACHT+LRR
98233	NLR	CARD+NACHT+unpredictedLRR
77770	NLR	DED+NACHT+NACHT+LRR
94468	NLR	NACHT+LRR

NLR. Unpredicted= the domain is not captured by the gene model but detected manually; weak=the e-value is weak for the domain;
NACHTonly=only NACHT domain are found in the model, no DFD or LRR domain are found; 2X=2 gene in 1 model.

model ID	type	curated structure and notes
84232	NLR	NACHT+LRR
96740	NLR	NACHT+LRR
81619	NLR	NACHT+LRR
84231	NLR	NACHT+LRR
82055	NLR	NACHT+LRR
101176	NLR	NACHT+LRR
82054	NLR	NACHT+LRR
76141	NLR	NACHT+LRR
121225	NLR	NACHT+LRR
88344	NLR	NACHT+LRR
91835	NLR	NACHT+LRR
91836	NLR	NACHT+LRR
82280	NLR	NACHT+LRR
89472	NLR	NACHT+LRR
86076	NLR	NACHT+LRR
68962	NLR	NACHT+LRR
103818	NLR	NACHT+LRR
86771	NLR	NACHT+LRR
89448	NLR	NACHT+LRR
89444	NLR	NACHT+LRR
130082	NLR	NACHT+LRR
131068	NLR	NACHT+LRR
94464	NLR	NACHT+unpredictedLRR
89727	NLR	NACHT+unpredictedLRR
99538	NLR	NACHT+unpredictedLRR
94465	NLR	NACHT+unpredictedLRR
99540	NLR	NACHT+unpredictedLRR
74646	NLR	NACHT+unpredictedLRR
84915	NLR	NACHT+unpredictedLRR

3 LRRIG gene models in amphioxus

LRRIG. Abbreviations: 2X=2 gene in 1 model; Igweak=e-value for Ig domains is weak; TM=transmembrane region.		
Model ID	type	Curated structure
63604	LRRIG	LRR+IG+TM
63844	LRRIG	LRR+IG
64092	LRRIG	LRR+IG+TM
64321	LRRIG	LRR+IG+TM
64705	LRRIG	LRR+IG+TM
66968	LRRIG	LRR+IG+TM, new
67709	LRRIG	LRR+IG
68275	LRRIG	LRR+IG+TM
68350	LRRIG	LRR+IG
68351	LRRIG	LRR+IG
68352	LRRIG	LRR+IG
68353	LRRIG	LRR+IG
68354	LRRIG	LRR+IG
69034	LRRIG	LRR+IG+TM
69392	LRRIG	LRR+IG+TM
69475	LRRIG	LRR+IG+EGFn
69988	LRRIG	LRR+IG+TM
71245	LRRIG	LRR+IG
72086	LRRIG	LRR+IG
72087	LRRIG	LRR+IG
72597	LRRIG	LRR+IG+TM
72601	LRRIG	LRR+IG+TM
73312	LRRIG	LRR+IG+TM
74018	LRRIG	LRR+IG+TM, new
75313	LRRIG	LRR+IG+TM
75603	LRRIG	LRR+IG, new
75952	LRRIG	LRR+IG+FB3
76119	LRRIG	LRR+IG
76367	LRRIG	LRR+IGn
77660	LRRIG	LRR+IG+TM
78015	LRRIG	LRR+IG+TM, new
81060	LRRIG	LRR+IG, Igweak, similar to amigo
82421	LRRIG	LRR+IG+TM
82639	LRRIG	LRR+IG
82650	LRRIG	LRR+IG+TM
83558	LRRIG	LRR+IG
83765	LRRIG	LRR+IG+TM
83768	LRRIG	LRR+IG+TM
84268	LRRIG	LRR+IG+TM
84420	LRRIG	LRR+IG
84652	LRRIG	LRR+IG+TM
85332	LRRIG	LRR+IG
85492	LRRIG	LRR+IG+TM
85646	LRRIG	LRR+IG+TM
86938	LRRIG	LRR+IG+TM

LRRIG. Abbreviations: 2X=2 gene in 1 model; Igweak=e-value for Ig domains is weak; TM=transmembrane region.

Model ID	type	Curated structure
86942	LRRIG	LRR+IGn+TM
86943	LRRIG	LRR+IG+TM
87048	LRRIG	LRR+IG+TM, Igweak
87685	LRRIG	LRR+IG+TM
88487	LRRIG	LRR+IG+TM
88586	LRRIG	LRR+IG+TM, new
88681	LRRIG	LRR+IG, new
89096	LRRIG	LRR+IG+FB3
89403	LRRIG	LRR+IG+TM
89550	LRRIG	LRR+IG+TM
89830	LRRIG	LRR+IG
89831	LRRIG	LRR+IG
90600	LRRIG	LRR+IG+TM
90790	LRRIG	LRR+IG+TM
91739	LRRIG	LRR+IG+TM
91740	LRRIG	LRR+IG+TM
91741	LRRIG	LRR+IG+TM
91744	LRRIG	LRR+IG+TM, 2 gene in 1 model
92427	LRRIG	LRR+IG
92567	LRRIG	LRR+IG
92652	LRRIG	LRR+IG
92654	LRRIG	LRR+IG+TM
92655	LRRIG	LRR+IG+TM
92656	LRRIG	LRR+IG+TM
94442	LRRIG	LRR+IG+TM
95660	LRRIG	LRR+IG+TM
95739	LRRIG	LRR+IG+TM
98299	LRRIG	LRR+IG+TM, new
98712	LRRIG	LRR+IG
100983	LRRIG	LRR+IG
101892	LRRIG	LRR+IG+TM
101954	LRRIG	LRR+IG
102207	LRRIG	LRR+IG
102211	LRRIG	LRR+IG
104744	LRRIG	LRR+IG+TM, new
105231	LRRIG	LRR+IG+TM
106293	LRRIG	LRR+IG
109260	LRRIG	LRR+IG+TM
109525	LRRIG	LRR+IG+TM, new
110797	LRRIG	LRR+IG+TM
110892	LRRIG	LRR+IGn+TM
113454	LRRIG	LRR+IG+TM
117183	LRRIG	LRR+IG+TM
119123	LRRIG	LRR+IG+TM
119130	LRRIG	LRR+IG, 2 gene in 1 models
123849	LRRIG	LRR+IG

LRRIG. Abbreviations: 2X=2 gene in 1 model; Igweak=e-value for Ig domains is weak; TM=transmembrane region.

Model ID	type	Curated structure
124171	LRRIG	LRR+IG
124667	LRRIG	LRR+IG+TM
124849	LRRIG	LRR+IG+TM,new, in 1exon, there is another gene behind
124965	LRRIG	LRR+IGn+TM
126389	LRRIG	LRR+IGn+TM
129752	LRRIG	LRR+IG+TM, new, 2 gene in 1 models
129898	LRRIG	LRR+IG
130937	LRRIG	LRR+IG+FB3+TM
132257	LRRIG	LRR+IG+TM
132383	LRRIG	LRR+IG+TM
132440	LRRIG	LRR+IG+TM
132541	LRRIG	LRR+IGn+TM
136908	LRRIG	LRR+IG
136978	LRRIG	LRR+IG
137049	LRRIG	LRR+IG
145620	LRRIG	LRR+IG
146221	LRRIG	LRR+IG
146234	LRRIG	LRR+IG
146236	LRRIG	LRR+IG
147038	LRRIG	LRR+IG
147315	LRRIG	LRR+IG
147752	LRRIG	LRR+IG
156210	LRRIG	LRR+IG
156493	LRRIG	LRR+IG
156516	LRRIG	LRR+IG
156755	LRRIG	LRR+IG
166688	LRRIG	LRR+IG
166782	LRRIG	LRR+IG
175295	LRRIG	LRR+IG
175425	LRRIG	LRR+IG
175525	LRRIG	LRR+IG
175526	LRRIG	LRR+IG
176488	LRRIG	LRR+IG
184320	LRRIG	LRR+IG
185044	LRRIG	LRR+IG
185168	LRRIG	LRR+IG
185680	LRRIG	LRR+IG
185683	LRRIG	LRR+IG
185693	LRRIG	LRR+IG
185713	LRRIG	LRR+IG
185731	LRRIG	LRR+IG
185982	LRRIG	LRR+IG
185990	LRRIG	LRR+IG
186408	LRRIG	LRR+IG
186429	LRRIG	LRR+IG
186453	LRRIG	LRR+IG

LRRIG. Abbreviations: 2X=2 gene in 1 model; Igweak=e-value for Ig domains is weak; TM=transmembrane region.

Model ID	type	Curated structure
186468	LRRIG	LRR+IG
194955	LRRIG	LRR+IG+TM
195629	LRRIG	LRR+IG
196097	LRRIG	LRR+IG
196123	LRRIG	LRR+IG
204034	LRRIG	LRR+IG
205209	LRRIG	LRR+IG
205693	LRRIG	LRR+IG
205768	LRRIG	LRR+IG
207667	LRRIG	LRR+IG
209256	LRRIG	LRR+IG
209594	LRRIG	LRR+IG
209679	LRRIG	LRR+IG
210745	LRRIG	LRR+IG
210822	LRRIG	LRR+IG
214255	LRRIG	LRR+IG
214727	LRRIG	LRR+IG
215536	LRRIG	LRR+IG
220416	LRRIG	LRR+IG
220652	LRRIG	LRR+IG
224613	LRRIG	LRR+IG
224653	LRRIG	LRR+IG
224669	LRRIG	LRR+IG
224740	LRRIG	LRR+IG
225523	LRRIG	LRR+IG
225607	LRRIG	LRR+IG
225992	LRRIG	LRR+IG
226247	LRRIG	LRR+IG
226256	LRRIG	LRR+IG
231446	LRRIG	LRR+IG
235077	LRRIG	LRR+IG+FB3
236952	LRRIG	LRR+IG
237001	LRRIG	LRR+IG
239897	LRRIG	LRR+IG
242086	LRRIG	LRR+IG
246545	LRRIG	LRR+IG
247032	LRRIG	LRR+IG
248817	LRRIG	LRR+IG
255088	LRRIG	LRR+IG
255889	LRRIG	LRR+IG
258306	LRRIG	LRR+IG
259267	LRRIG	LRR+IG
267931	LRRIG	LRR+IG
284887	LRRIG	LRR+IG
67707	LRRIG	LRR+IG
94160	LRRIG	LRR+IG

LRRIG. Abbreviations: 2X=2 gene in 1 model; Igweak=e-value for Ig domains is weak; TM=transmembrane region.

Model ID	type	Curated structure
124849	LRRIG	LRR+IG
68886	LRRIG	LRR+IG
91793	LRRIG	LRR+IG
67374	LRRIG	LRR+IG
75603	LRRIG	LRR+IG
122775	LRRIG	LRR+IG
270856	LRRIG	LRR+IG
87050	LRRIG	LRR+IG, Igweak
256721	LRRIG	LRR+IG, Igweak
109788	LRRIG	LRR+IG, Igweak
84352	LRRIG	LRR+IG, Igweak
224612	LRRIG	LRR+IG, Igweak
73442	LRRIG	LRR+IG+TM
67708	LRRIG	LRR+IG+TM
91745	LRRIG	LRR+IG+TM
109525	LRRIG	LRR+IG+TM
66968	LRRIG	LRR+IG+TM
78015	LRRIG	LRR+IG+TM
105604	LRRIG	LRR+IG+TM
104744	LRRIG	LRR+IG+TM
87047	LRRIG	LRR+IG+TM, Igweak
87046	LRRIG	LRR+IG+TM, Igweak
89502	LRRIG	LRR+IG+TM, Igweak
78115	LRRIG	LRR+IG+TM, Igweak
88296	LRRIG	LRR+IG+TM, Igweak
89503	LRRIG	LRR+IG+TM, Igweak
67136	LRRIG	LRR+IG+TM, Igweak
88586	LRRIG	LRR+IG+TM, Igweak
110432	LRRIG	LRR+IG+TM, Igweak
67601	LRRIG	LRR+IG+TM, Igweak
105807	LRRIG	LRR+IG+TM, Igweak
107517	LRRIG	LRR+IG+TM, Igweak
110523	LRRIG	LRR+IG+TM, Igweak
89253	LRRIG	LRR+IG+TM, Igweak
63448	LRRIG	LRR+IG+TM, Igweak
79849	LRRIG	LRR+IGn+TM
113421	LRRIG	IG+TM
110796	LRRIG	IG+TM
96599	LRRIG	IG+TM
88166	LRRIG	IG+TM
66561	LRRIG	IG+TM
86937	LRRIG	IG+TM
72599	LRRIG	IG+TM
76620	LRRIG	IG+TM
63877	LRRIG	IG+TM
67602	LRRIG	IG+TM

LRRIG. Abbreviations: 2X=2 gene in 1 model; Igweak=e-value for Ig domains is weak; TM=transmembrane region.

Model ID	type	Curated structure
105125	LRRIG	IG+TM
102169	LRRIG	IG+TM
132309	LRRIG	IGn+TM
86941	LRRIG	IGn+TM
89007	LRRIG	IGn+TM
188006	LRRIG	IGonly
197849	LRRIG	IGonly
207770	LRRIG	IGonly
259419	LRRIG	IGonly
259078	LRRIG	IGonly
78116	LRRIG	IGonly, weak

4 Other LRR-containing gene models, including LRR-only gene models.

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
64425	#DLR	LRRonly, but >65% identity to DLR
68701	#DLR	LRRonly, but >65% identity to DLR
71837	#DLR	LRRonly, but >65% identity to DLR
71866	#DLR	LRRonly, but >65% identity to DLR
74759	#DLR	LRRonly, but >65% identity to DLR
77182	#DLR	LRRonly, but >65% identity to DLR
80680	#DLR	LRRonly, but >65% identity to DLR
82199	#DLR	LRRonly, but >65% identity to DLR
82202	#DLR	LRRonly, but >65% identity to DLR
82694	#DLR	LRRonly, but >65% identity to DLR
87500	#DLR	LRRonly, but >65% identity to DLR
87556	#DLR	LRRonly, but >65% identity to DLR
87564	#DLR	LRRonly, but >65% identity to DLR
92604	#DLR	LRRonly, but >65% identity to DLR
97537	#DLR	LRRonly, but >65% identity to DLR
100136	#DLR	LRRonly, but >65% identity to DLR
100163	#DLR	LRRonly, but >65% identity to DLR
100170	#DLR	LRRonly, but >65% identity to DLR
103435	#DLR	LRRonly, but >65% identity to DLR
107593	#DLR	LRRonly, but >65% identity to DLR
147457	#DLR	LRRonly, but >65% identity to DLR
151599	#DLR	LRRonly, but >65% identity to DLR
176829	#DLR	LRRonly, but >65% identity to DLR
177262	#DLR	LRRonly, but >65% identity to DLR
178007	#DLR	LRRonly, but >65% identity to DLR
207843	#DLR	LRRonly, but >65% identity to DLR
208060	#DLR	LRRonly, but >65% identity to DLR
232319	#DLR	LRRonly, but >65% identity to DLR
244008	#DLR	LRRonly, but >65% identity to DLR
60670	#FB-LRR	LRRonly, but >65% identity to FB-LRR
231009	#LDL-LRR-GPCR	LRRonly, but >65% identity to LDL-LRR-GPCR
107166	#LRR-CCP	LRRonly, but >65% identity to LRR-CCP
205486	#LRR-CCP-CLECT	LRRonly, but >65% identity to LRR-CCP-CLECT
218184	#LRR-CCP-CLECT	LRRonly, but >65% identity to LRR-CCP-CLECT
81939	#LRR-CLECT	LRRonly, but >65% identity to LRR-CLECT
140130	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
140184	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
150403	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
159041	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
169312	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
170090	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
186263	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
196245	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
217855	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
217879	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
217926	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
217978	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
218103	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
218112	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
218151	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
218164	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
218165	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
218172	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
222247	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
222347	#LRR-DD-PK	LRRonly, but >65% identity to LRR-DD-PK
150406	#LRR-DD-TIR	LRRonly, but >65% identity to LRR-DD-TIR
218147	#LRR-DD-TIR	LRRonly, but >65% identity to LRR-DD-TIR
218230	#LRR-DD-TIR	LRRonly, but >65% identity to LRR-DD-TIR
252651	#LRR-EGF	LRRonly, but >65% identity to LRR-EGF
142233	#LRR-FN	LRRonly, but >65% identity to LRR-FN
213241	#LRR-FN	LRRonly, but >65% identity to LRR-FN
231199	#LRR-FN	LRRonly, but >65% identity to LRR-FN
231593	#LRR-FN	LRRonly, but >65% identity to LRR-FN
231607	#LRR-FN	LRRonly, but >65% identity to LRR-FN
231619	#LRR-FN	LRRonly, but >65% identity to LRR-FN
234983	#LRR-FN	LRRonly, but >65% identity to LRR-FN
143066	#LRR-FTP-CCP	LRRonly, but >65% identity to LRR-FTP-CCP
152080	#LRR-FTP-CCP	LRRonly, but >65% identity to LRR-FTP-CCP
152678	#LRR-FTP-CCP	LRRonly, but >65% identity to LRR-FTP-CCP
206093	#LRR-FTP-CCP	LRRonly, but >65% identity to LRR-FTP-CCP
227739	#LRR-FTP-CCP	LRRonly, but >65% identity to LRR-FTP-CCP
66879	#LRR-GPS	LRRonly, but >65% identity to LRR-GPS
66880	#LRR-GPS	LRRonly, but >65% identity to LRR-GPS
66881	#LRR-GPS	LRRonly, but >65% identity to LRR-GPS
68740	#LRR-GPS	LRRonly, but >65% identity to LRR-GPS
80871	#LRR-GPS	LRRonly, but >65% identity to LRR-GPS
83019	#LRR-GPS	LRRonly, but >65% identity to LRR-GPS
84124	#LRR-GPS	LRRonly, but >65% identity to LRR-GPS
113016	#LRR-GPS	LRRonly, but >65% identity to LRR-GPS
132735	#LRR-GPS	LRRonly, but >65% identity to LRR-GPS
241975	#LRR-GPS	LRRonly, but >65% identity to LRR-GPS
63448	#LRRIG	LRRonly, but >65% identity to NLRR
67136	#LRRIG	LRRonly, but >65% identity to NLRR
67374	#LRRIG	LRRonly, but >65% identity to NLRR
67601	#LRRIG	LRRonly, but >65% identity to NLRR
67707	#LRRIG	LRRonly, but >65% identity to NLRR
67708	#LRRIG	LRRonly, but >65% identity to NLRR
68514	#LRRIG	LRRonly, but >65% identity to NLRR
73214	#LRRIG	LRRonly, but >65% identity to NLRR

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
78115	#LRRIG	LRRonly, but >65% identity to NLRR
82422	#LRRIG	LRRonly, but >65% identity to NLRR
84352	#LRRIG	LRRonly, but >65% identity to NLRR
87046	#LRRIG	LRRonly, but >65% identity to NLRR
87047	#LRRIG	LRRonly, but >65% identity to NLRR
87050	#LRRIG	LRRonly, but >65% identity to NLRR
88296	#LRRIG	LRRonly, but >65% identity to NLRR
88425	#LRRIG	LRRonly, but >65% identity to NLRR
88485	#LRRIG	LRRonly, but >65% identity to NLRR
89253	#LRRIG	LRRonly, but >65% identity to NLRR
89502	#LRRIG	LRRonly, but >65% identity to NLRR
89503	#LRRIG	LRRonly, but >65% identity to NLRR
91793	#LRRIG	LRRonly, but >65% identity to NLRR
94160	#LRRIG	LRRonly, but >65% identity to NLRR
101126	#LRRIG	LRRonly, but >65% identity to NLRR
105604	#LRRIG	LRRonly, but >65% identity to NLRR
105807	#LRRIG	LRRonly, but >65% identity to NLRR
106636	#LRRIG	LRRonly, but >65% identity to NLRR
107517	#LRRIG	LRRonly, but >65% identity to NLRR
109788	#LRRIG	LRRonly, but >65% identity to NLRR
110432	#LRRIG	LRRonly, but >65% identity to NLRR
110523	#LRRIG	LRRonly, but >65% identity to NLRR
112135	#LRRIG	LRRonly, but >65% identity to NLRR
112701	#LRRIG	LRRonly, but >65% identity to NLRR
113004	#LRRIG	LRRonly, but >65% identity to NLRR
113428	#LRRIG	LRRonly, but >65% identity to NLRR
125642	#LRRIG	LRRonly, but >65% identity to NLRR
137599	#LRRIG	LRRonly, but >65% identity to NLRR
137640	#LRRIG	LRRonly, but >65% identity to NLRR
140346	#LRRIG	LRRonly, but >65% identity to NLRR
141278	#LRRIG	LRRonly, but >65% identity to NLRR
147543	#LRRIG	LRRonly, but >65% identity to NLRR
148882	#LRRIG	LRRonly, but >65% identity to NLRR
148928	#LRRIG	LRRonly, but >65% identity to NLRR
150608	#LRRIG	LRRonly, but >65% identity to NLRR
150664	#LRRIG	LRRonly, but >65% identity to NLRR
151619	#LRRIG	LRRonly, but >65% identity to NLRR
156015	#LRRIG	LRRonly, but >65% identity to NLRR
158326	#LRRIG	LRRonly, but >65% identity to NLRR
160911	#LRRIG	LRRonly, but >65% identity to NLRR
161858	#LRRIG	LRRonly, but >65% identity to NLRR
162163	#LRRIG	LRRonly, but >65% identity to NLRR
162872	#LRRIG	LRRonly, but >65% identity to NLRR
171183	#LRRIG	LRRonly, but >65% identity to NLRR
172156	#LRRIG	LRRonly, but >65% identity to NLRR

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
175060	#LRRIG	LRRonly, but >65% identity to NLRR
176304	#LRRIG	LRRonly, but >65% identity to NLRR
177127	#LRRIG	LRRonly, but >65% identity to NLRR
177177	#LRRIG	LRRonly, but >65% identity to NLRR
177788	#LRRIG	LRRonly, but >65% identity to NLRR
177892	#LRRIG	LRRonly, but >65% identity to NLRR
177931	#LRRIG	LRRonly, but >65% identity to NLRR
185503	#LRRIG	LRRonly, but >65% identity to NLRR
187668	#LRRIG	LRRonly, but >65% identity to NLRR
188125	#LRRIG	LRRonly, but >65% identity to NLRR
188174	#LRRIG	LRRonly, but >65% identity to NLRR
205194	#LRRIG	LRRonly, but >65% identity to NLRR
205317	#LRRIG	LRRonly, but >65% identity to NLRR
205500	#LRRIG	LRRonly, but >65% identity to NLRR
206376	#LRRIG	LRRonly, but >65% identity to NLRR
209621	#LRRIG	LRRonly, but >65% identity to NLRR
209854	#LRRIG	LRRonly, but >65% identity to NLRR
210754	#LRRIG	LRRonly, but >65% identity to NLRR
210820	#LRRIG	LRRonly, but >65% identity to NLRR
211647	#LRRIG	LRRonly, but >65% identity to NLRR
213446	#LRRIG	LRRonly, but >65% identity to NLRR
215675	#LRRIG	LRRonly, but >65% identity to NLRR
221137	#LRRIG	LRRonly, but >65% identity to NLRR
224612	#LRRIG	LRRonly, but >65% identity to NLRR
224745	#LRRIG	LRRonly, but >65% identity to NLRR
226216	#LRRIG	LRRonly, but >65% identity to NLRR
227131	#LRRIG	LRRonly, but >65% identity to NLRR
227729	#LRRIG	LRRonly, but >65% identity to NLRR
228295	#LRRIG	LRRonly, but >65% identity to NLRR
231595	#LRRIG	LRRonly, but >65% identity to NLRR
233656	#LRRIG	LRRonly, but >65% identity to NLRR
233932	#LRRIG	LRRonly, but >65% identity to NLRR
235005	#LRRIG	LRRonly, but >65% identity to NLRR
236944	#LRRIG	LRRonly, but >65% identity to NLRR
238475	#LRRIG	LRRonly, but >65% identity to NLRR
238680	#LRRIG	LRRonly, but >65% identity to NLRR
240722	#LRRIG	LRRonly, but >65% identity to NLRR
241423	#LRRIG	LRRonly, but >65% identity to NLRR
241914	#LRRIG	LRRonly, but >65% identity to NLRR
242451	#LRRIG	LRRonly, but >65% identity to NLRR
242468	#LRRIG	LRRonly, but >65% identity to NLRR
243537	#LRRIG	LRRonly, but >65% identity to NLRR
248397	#LRRIG	LRRonly, but >65% identity to NLRR
249634	#LRRIG	LRRonly, but >65% identity to NLRR
253305	#LRRIG	LRRonly, but >65% identity to NLRR

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
254633	#LRRIG	LRRonly, but >65% identity to NLRR
255786	#LRRIG	LRRonly, but >65% identity to NLRR
256118	#LRRIG	LRRonly, but >65% identity to NLRR
256721	#LRRIG	LRRonly, but >65% identity to NLRR
256728	#LRRIG	LRRonly, but >65% identity to NLRR
258226	#LRRIG	LRRonly, but >65% identity to NLRR
259332	#LRRIG	LRRonly, but >65% identity to NLRR
284390	#LRRIG	LRRonly, but >65% identity to NLRR
79749	#LRR-PK	LRRonly, but >65% identity to LRR-PK
102102	#LRR-PK	LRRonly, but >65% identity to LRR-PK
142223	#LRR-PK	LRRonly, but >65% identity to LRR-PK
187254	#LRR-PK	LRRonly, but >65% identity to LRR-PK
118979	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
125096	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
137530	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
155757	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
169824	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
201916	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
201991	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
207102	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
214464	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
214559	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
214686	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
214697	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
222043	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
226277	#LRR-RAS	LRRonly, but >65% identity to LRR-RAS
86717	#NLR	LRRonly, but >65% identity to NLR
138268	#NLR	LRRonly, but >65% identity to NLR
138301	#NLR	LRRonly, but >65% identity to NLR
141883	#NLR	LRRonly, but >65% identity to NLR
167681	#NLR	LRRonly, but >65% identity to NLR
218712	#NLR	LRRonly, but >65% identity to NLR
218748	#NLR	LRRonly, but >65% identity to NLR
226285	#NLR	LRRonly, but >65% identity to NLR
257779	#NLR	LRRonly, but >65% identity to NLR
77824	#PIDD-L	LRRonly, but >65% identity to PIDD-L
218429	#PIDD-L	LRRonly, but >65% identity to PIDD-L
260758	#PIDD-L	LRRonly, but >65% identity to PIDD-L
88727	#TLR	LRRonly, but >65% identity to TLR
136852	#TLR	LRRonly, but >65% identity to TLR
138055	#TLR	LRRonly, but >65% identity to TLR
174268	#TLR	LRRonly, but >65% identity to TLR
185811	#TLR	LRRonly, but >65% identity to TLR
186255	#TLR	LRRonly, but >65% identity to TLR
218687	#TLR	LRRonly, but >65% identity to TLR

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
218688	#TLR	LRRonly, but >65% identity to TLR
218715	#TLR	LRRonly, but >65% identity to TLR
218774	#TLR	LRRonly, but >65% identity to TLR
243974	#TLR	LRRonly, but >65% identity to TLR
247178	#TLR	LRRonly, but >65% identity to TLR
254197	#TLR	LRRonly, but >65% identity to TLR
58172	FB-LRR	FB-LRR
59461	FB-LRR	FB-LRR
61520	FB-LRR	FB-LRR
67760	FB-LRR	FB-LRR
71258	FB-LRR	FB-LRR
73295	FB-LRR	FB-LRR
76210	FB-LRR	FB-LRR
83341	FB-LRR	FB-LRR
83436	FB-LRR	FB-LRR
84015	FB-LRR	FB-LRR
93403	FB-LRR	FB-LRR
102461	FB-LRR	FB-LRR
109395	FB-LRR	FB-LRR
121756	FB-LRR	FB-LRR
123439	FB-LRR	FB-LRR
126380	FB-LRR	FB-LRR
127069	FB-LRR	FB-LRR
128800	FB-LRR	FB-LRR
132622	FB-LRR	FB-LRR
260896	FB-LRR	FB-LRR
281835	FB-LRR	FB-LRR
281976	FB-LRR	FB-LRR
284186	FB-LRR	FB-LRR
286331	FB-LRR	FB-LRR
63627	LDL-LRR-GPCR	LDL-LRR-GPCR, similar to relaxin receptor
63628	LDL-LRR-GPCR	LDL-LRR-GPCR, similar to relaxin receptor
69654	LDL-LRR-GPCR	LDL-LRR-GPCR, similar to relaxin receptor
91421	LDL-LRR-GPCR	LDL-LRR-GPCR, similar to relaxin receptor
91429	LDL-LRR-GPCR	LDL-LRR-GPCR, similar to relaxin receptor
98820	LDL-LRR-GPCR	LDL-LRR-GPCR, similar to relaxin receptor
111564	LDL-LRR-GPCR	LDL-LRR-GPCR, similar to relaxin receptor
134702	LDL-LRR-GPCR	LDL-LRR-GPCR, similar to relaxin receptor
68886	LRR-BTB	LRR-BTB
87098	LRR-BTB	LRR-BTB
67388	LRR-CAS	LRR+CAS, LRR similar to MASL1
75631	LRR-CAS	LRR+CAS, LRR similar to MASL1
80701	LRR-CAS	LRR+CAS, LRR similar to MASL1
63272	LRR-CCP	LRR+CCP
81788	LRR-CCP	LRR+CCP

Other LRR-containing gene models, including LRR-only. Unkown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
80710	LRR-CCP-CLECT	*2X, LRR+CCP+CLECT
88353	LRR-CLECT	LRR+CLECT
74989	LRR-DD-STK	LRR+DEATH+S_TKc
77802	LRR-DD-STK	LRR+DEATH+S_TKc
77807	LRR-DD-STK	LRR+DEATH+S_TKc
77808	LRR-DD-STK	LRR+DEATH+S_TKc
77821	LRR-DD-STK	LRR+DEATH+S_TKc
77823	LRR-DD-STK	LRR+DEATH+S_TKc
77826	LRR-DD-STK	LRR+DEATH+S_TKc
77827	LRR-DD-STK	LRR+DEATH+S_TKc
80222	LRR-DD-STK	LRR+DEATH+S_TKc
80223	LRR-DD-STK	LRR+DEATH+S_TKc
80224	LRR-DD-STK	LRR+DEATH+S_TKc
80225	LRR-DD-STK	LRR+DEATH+S_TKc
80227	LRR-DD-STK	LRR+DEATH+S_TKc
77813	LRR-DD-TIR	LRR+DEATH+absentTIR
77814	LRR-DD-TIR	LRR-death-TIR
77815	LRR-DD-TIR	LRR-death-TIR
77822	LRR-DD-TIR	LRR-death-TIR
87451	LRR-EF	LRR+EF, similar to Caspase recruitment domain protein 4 [Danio rerio].
124980	LRR-EF	LRR+EF, similar to Caspase recruitment domain protein 4 [Danio rerio].
124994	LRR-EF	LRR+EF, similar to Caspase recruitment domain protein 4 [Danio rerio].
72506	LRR-EGF	LRR-EGF
120234	LRR-EGF	LRR-EGF
79821	LRR-FN	LRR+FN3+TM
80653	LRR-FN	LRR+FN3+TM
89353	LRR-FN	LRR+FN3+TM
91298	LRR-FN	LRR+FN3+TM
89746	LRR-FTP-CCP	LRR-FTP-CCP
99565	LRR-FTP-CCP	LRR-FTP-CCP
124143	LRR-GEL	LRR-GEL
126653	LRR-GEL	LRR-GEL
66878	LRR-GPS	LRR-GPS
70546	LRR-GPS	LRR-GPS
90437	LRR-GPS	LRR-GPS
90965	LRR-GuK	LRR+GuK
203463	LRR-GuK	LRR+GuK
245190	LRR-IG-PTK	LRR+Ign+TM+PTK, similar to rat neuronal tyrosine kinase receptor
94014	LRR-PDZ	LRR-PDZ, +DEATH
98247	LRR-PDZ	LRR-PDZ
198676	LRR-PDZ	LRR-PDZ
65300	LRR-PK	LRR+PK, PK is distant
67613	LRR-PK	LRR+TM+PK
89744	LRR-PK	LRR+TM+PK, receptor tyrosine kinase
124153	LRR-PK	LRR+PK

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
143685	LRR-PP3C	LRR-PP3C
214316	LRR-PP3C	LRR-PP3C
69050	LRR-RAS	LRR+weakRAS
74993	LRR-RAS	LRR+weakRAS, To MASL1
75175	LRR-RAS	LRR+weakRAS, To MASL1
75632	LRR-RAS	LRR+RAS, similar to MASL1
76134	LRR-RAS	LRR+RAS, similar to MASL1
77887	LRR-RAS	LRR+RAS ,similar to human MFHAS1, encodin 2 exon, involved in B-cell
82061	LRR-RAS	LRR+RAS, similar to MASL1
83804	LRR-RAS	LRR+RAS+PK
86475	LRR-RAS	LRR+RAS, similar to MASL1
89276	LRR-RAS	LRR+RAS, similar to MASL1
89737	LRR-RAS	LRR+RAS ,similar to human MFHAS1, encodin 1 exon, involved in B-cell
106240	LRR-RAS	LRR+RAS+PK
119973	LRR-RAS	LRR+RAS+PK
126447	LRR-RAS	LRR-RAS, 2 gene inside
130711	LRR-RAS	LRR+RAS+PK
164586	LRR-RAS	LRR+RAS, similar to MASL1
200524	LRR-RAS	LRR+RAS ,similar to human MFHAS1, encodin 3 exon, involved in B-cell
214496	LRR-RAS	LRR+RAS, similar to MASL1
214669	LRR-RAS	LRR+RAS, similar to MASL1
214682	LRR-RAS	LRR+weakRAS, To MASL1
218979	LRR-RAS	LRR+RAS, similar to MASL1
219295	LRR-RAS	LRR+RAS, similar to MASL1
221883	LRR-RAS	LRR+RAS, similar to MASL1
223431	LRR-RAS	LRR+RAS, similar to MASL1
223487	LRR-RAS	LRR+RAS, similar to MASL1
243711	LRR-RAS	LRR+RAS, similar to MASL1
288807	LRR-RAS	LRR+weakRAS
65562	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
68259	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 2 exon, involved in B-cell, DD is distant from LRR
74291	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
74292	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
80159	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
89740	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
90625	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
90914	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR

Other LRR-containing gene models, including LRR-only. Unkown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
118978	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
118982	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
88773	LRR-SAM	LRR-SAM
106032	LRR-SAM	LRR-SAM
82780	LRR-STK	LRR+S_TKc
66953	LRR-TM-DD	LRR+TM+DEATH, receptor in 1 exon
84125	LRR-TM-DD	LRR+TM+DEATH, receptor
107976	LRR-TM-DD	LRR+TM+DEATH, receptor
108708	PAN-LRR	PAN-LRR
109614	PAN-LRR	PAN-LRR
67596	PERO	peroxidase, LRR+IGn+peroxidase, extra
91948	PERO	peroxidase, LRR+IGn+peroxidase, extra
93124	PIDD-L	LRR+DEATH, similar rat PIDD at 7% identity
107130	PIDD-L	LRR+DEATH, similar rat PIDD
121822	PIDD-L	LRR+DEATH
133361	PIDD-L	LRR+DEATH
92645	PX-LRR	PX-LRR
208888	PX-LRR	PX-LRR
245569	PX-LRR	PX-LRR
94832	TPR-ANK-LRR	similar to human Ikb related protein
99825	TPR-ANK-LRR	similar to human Ikb related protein
63488	unknown	LRR+
64810	unknown	LRR+
67148	unknown	LRR+FBG
67180	unknown	LRR+
67847	unknown	LRR+EGF+finger..
67849	unknown	LRR+
68184	unknown	LRR+
68569	unknown	unknown
71581	unknown	LRR and kringle
72961	unknown	LRR+ANK, ANK is distant
73442	unknown	multiple IG+LRR
78389	unknown	LRR+Tryp
78542	unknown	unknown
78548	unknown	unknown
82482	unknown	LRR+cNMP, cNMP is distant
82767	unknown	LRR+AMP
82834	unknown	LRR and WD40
83058	unknown	*similar to titin,notNLRR, LRR+IG+FB3
83245	unknown	LRR+
83478	unknown	unknown
85228	unknown	LRR+ZU5+
86312	unknown	LRR+CUB+CLECT+PK

Other LRR-containing gene models, including LRR-only. Unkown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
86604	unknown	unknown
87510	unknown	Cap Gly+LRR
88108	unknown	LRR and kringle
88715	unknown	LRR+IQ
90181	unknown	LRR+
90183	unknown	LRR+
92709	unknown	unknown
93431	unknown	unknown
99571	unknown	LRR+
100134	unknown	LRR-ZnF
109449	unknown	LRR+EF
110575	unknown	LRR and WD40
112280	unknown	Kelch+LRR
117415	unknown	LRR+TPR
118655	unknown	LRR+cNMP, cNMP is distant
119045	unknown	LRR+TPR
119689	unknown	LRR-ZnF
119795	unknown	LRR+EF
120446	unknown	LRR+
122031	unknown	LRR and WD40
123340	unknown	LRR+, DEATH
126076	unknown	similar to titin,notNLRR weakLRR+IG+FB3+FB3
126438	unknown	LRR and kringle
126584	unknown	multiple IG+LRR
126654	unknown	LRR+ZU5+
127177	unknown	LRR+
127227	unknown	LRR and PAN
273639	unknown	LRR+EGF+LamG
283559	unknown	Cap Gly+LRR
63368	LRRonly	
65356	LRRonly	
66743	LRRonly	
67182	LRRonly	
67558	LRRonly	
70616	LRRonly	
71121	LRRonly	
71123	LRRonly	
71127	LRRonly	
71129	LRRonly	
71157	LRRonly	
74570	LRRonly	
75851	LRRonly	
76946	LRRonly	
76947	LRRonly	
78094	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
78099	LRRonly	
78101	LRRonly	
78102	LRRonly	
78124	LRRonly	
78541	LRRonly	
81918	LRRonly	
82151	LRRonly	
82906	LRRonly	
84068	LRRonly	
86709	LRRonly	
86979	LRRonly	
86992	LRRonly	
88418	LRRonly	
88419	LRRonly	
88420	LRRonly	
88421	LRRonly	
88426	LRRonly	
88427	LRRonly	
88460	LRRonly	
88461	LRRonly	
88462	LRRonly	
88465	LRRonly	
88470	LRRonly	
88471	LRRonly	
88472	LRRonly	
88473	LRRonly	
88474	LRRonly	
89454	LRRonly	
89478	LRRonly	
89480	LRRonly	
89481	LRRonly	
89483	LRRonly	
89485	LRRonly	
89516	LRRonly	
89518	LRRonly	
91398	LRRonly	
92001	LRRonly	
92734	LRRonly	
96335	LRRonly	
97219	LRRonly	
103967	LRRonly	
104538	LRRonly	
105930	LRRonly	
105931	LRRonly	
108139	LRRonly	

Other LRR-containing gene models, including LRR-only. Unkown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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108255	LRRonly	
109672	LRRonly	
111794	LRRonly	
111808	LRRonly	
112317	LRRonly	
112563	LRRonly	
112564	LRRonly	
112602	LRRonly	
133161	LRRonly	
137659	LRRonly	
139027	LRRonly	
139047	LRRonly	
139050	LRRonly	
139098	LRRonly	
141619	LRRonly	
149222	LRRonly	
149651	LRRonly	
150194	LRRonly	
151408	LRRonly	
151410	LRRonly	
158323	LRRonly	
160088	LRRonly	
162914	LRRonly	
176692	LRRonly	
177176	LRRonly	
187660	LRRonly	
201950	LRRonly	
207538	LRRonly	
208162	LRRonly	
209571	LRRonly	
210364	LRRonly	
218595	LRRonly	
218596	LRRonly	
218807	LRRonly	
221138	LRRonly	
224879	LRRonly	
226257	LRRonly	
230668	LRRonly	
238253	LRRonly	
247337	LRRonly	
248452	LRRonly	
251340	LRRonly	
251365	LRRonly	
251458	LRRonly	
258322	LRRonly	

Other LRR-containing gene models, including LRR-only. Unkown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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258331	LRRonly	
259214	LRRonly	
70076	LRRonly	
77865	LRRonly	
77866	LRRonly	
77868	LRRonly	
77870	LRRonly	
77871	LRRonly	
77873	LRRonly	
77874	LRRonly	
80107	LRRonly	
80172	LRRonly	
80173	LRRonly	
80174	LRRonly	
80175	LRRonly	
80176	LRRonly	
80177	LRRonly	
80178	LRRonly	
80179	LRRonly	
86877	LRRonly	
86885	LRRonly	
111890	LRRonly	
113414	LRRonly	
139479	LRRonly	
148371	LRRonly	
151539	LRRonly	
151556	LRRonly	
152890	LRRonly	
157749	LRRonly	
172154	LRRonly	
172168	LRRonly	
186798	LRRonly	
194097	LRRonly	
205378	LRRonly	
213495	LRRonly	
218003	LRRonly	
218084	LRRonly	
218212	LRRonly	
222055	LRRonly	
222056	LRRonly	
224198	LRRonly	
227098	LRRonly	
227404	LRRonly	
227405	LRRonly	
238486	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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249789	LRRonly	
256706	LRRonly	
79291	LRRonly	
85413	LRRonly	
87518	LRRonly	
94415	LRRonly	
96294	LRRonly	
176618	LRRonly	
256071	LRRonly	
256763	LRRonly	
265150	LRRonly	
65021	LRRonly	
68796	LRRonly	
71541	LRRonly	
76418	LRRonly	
78158	LRRonly	
78510	LRRonly	
87582	LRRonly	
137589	LRRonly	
142210	LRRonly	
142264	LRRonly	
142267	LRRonly	
158333	LRRonly	
158338	LRRonly	
159240	LRRonly	
162850	LRRonly	
177105	LRRonly	
187622	LRRonly	
199068	LRRonly	
210765	LRRonly	
216110	LRRonly	
218779	LRRonly	
229509	LRRonly	
230145	LRRonly	
230179	LRRonly	
230749	LRRonly	
235233	LRRonly	
240415	LRRonly	
240489	LRRonly	
241798	LRRonly	
244698	LRRonly	
249425	LRRonly	
250160	LRRonly	
255824	LRRonly	
263107	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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278477	LRRonly	
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67972	LRRonly	
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68065	LRRonly	
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69301	LRRonly	
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69832	LRRonly	
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72911	LRRonly	
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72972	LRRonly	
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74905	LRRonly	
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75271	LRRonly	
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76488	LRRonly	
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77396	LRRonly	
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80445	LRRonly	
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81930	LRRonly	
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81933	LRRonly	
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82493	LRRonly	
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82684	LRRonly	
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82740	LRRonly	
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83045	LRRonly	
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83812	LRRonly	
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83850	LRRonly	
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85369	LRRonly	
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87247	LRRonly	
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87481	LRRonly	
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87526	LRRonly	
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88182	LRRonly	
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88579	LRRonly	
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92668	LRRonly	
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92670	LRRonly	
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92671	LRRonly	
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92868	LRRonly	
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92914	LRRonly	
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94800	LRRonly	
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95153	LRRonly	
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97538	LRRonly	
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103434	LRRonly	
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103436	LRRonly	
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108010	LRRonly	
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122597	LRRonly	
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140998	LRRonly	
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142317	LRRonly	
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151577	LRRonly	
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151578	LRRonly	
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151600	LRRonly	
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151602	LRRonly	
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151605	LRRonly	
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Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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151608	LRRonly	
151635	LRRonly	
152922	LRRonly	
195375	LRRonly	
210386	LRRonly	
213447	LRRonly	
214940	LRRonly	
219023	LRRonly	
221145	LRRonly	
224704	LRRonly	
227114	LRRonly	
243633	LRRonly	
243736	LRRonly	
66934	LRRonly	
66972	LRRonly	
66973	LRRonly	
67184	LRRonly	
68328	LRRonly	
68338	LRRonly	
76944	LRRonly	
79907	LRRonly	
83090	LRRonly	
85326	LRRonly	
86975	LRRonly	
92703	LRRonly	
92704	LRRonly	
92706	LRRonly	
99572	LRRonly	
99573	LRRonly	
99910	LRRonly	
99911	LRRonly	
104563	LRRonly	
107933	LRRonly	
107934	LRRonly	
107935	LRRonly	
111234	LRRonly	
119916	LRRonly	
63619	LRRonly	
63621	LRRonly	
63625	LRRonly	
66634	LRRonly	
67144	LRRonly	
75502	LRRonly	
88312	LRRonly	
95307	LRRonly	

Other LRR-containing gene models, including LRR-only. Unkown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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141364	LRRonly	
170226	LRRonly	
170280	LRRonly	
177186	LRRonly	
188196	LRRonly	
214542	LRRonly	
221439	LRRonly	
234135	LRRonly	
242411	LRRonly	
252772	LRRonly	
66010	LRRonly	
67095	LRRonly	
67701	LRRonly	
67762	LRRonly	
67763	LRRonly	
67797	LRRonly	
68634	LRRonly	
69743	LRRonly	
71083	LRRonly	
71839	LRRonly	
71868	LRRonly	
75134	LRRonly	
76374	LRRonly	
76381	LRRonly	
76973	LRRonly	
76982	LRRonly	
81224	LRRonly	
83068	LRRonly	
83438	LRRonly	
83439	LRRonly	
87130	LRRonly	
90180	LRRonly	
96209	LRRonly	
98216	LRRonly	
102420	LRRonly	
103229	LRRonly	
103740	LRRonly	
105038	LRRonly	
106020	LRRonly	
106558	LRRonly	
108199	LRRonly	
110326	LRRonly	
112462	LRRonly	
112463	LRRonly	
113019	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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130131	LRRonly	
144638	LRRonly	
150685	LRRonly	
152220	LRRonly	
177919	LRRonly	
254107	LRRonly	
67684	LRRonly	
68051	LRRonly	
68584	LRRonly	
68585	LRRonly	
70310	LRRonly	
71372	LRRonly	
71376	LRRonly	
71378	LRRonly	
72039	LRRonly	
72578	LRRonly	
75586	LRRonly	
77214	LRRonly	
77369	LRRonly	
80333	LRRonly	
82681	LRRonly	
82693	LRRonly	
86155	LRRonly	
86156	LRRonly	
86168	LRRonly	
86285	LRRonly	
86296	LRRonly	
88728	LRRonly	
88729	LRRonly	
93134	LRRonly	
96308	LRRonly	
96309	LRRonly	
96462	LRRonly	
97608	LRRonly	
98066	LRRonly	
102518	LRRonly	
103692	LRRonly	
103694	LRRonly	
105003	LRRonly	
105526	LRRonly	
107058	LRRonly	
112067	LRRonly	
119623	LRRonly	
194191	LRRonly	
255925	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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215030	LRRonly	
226512	LRRonly	
186588	LRRonly	
212273	LRRonly	
218604	LRRonly	
218613	LRRonly	
230024	LRRonly	
66772	LRRonly	
99657	LRRonly	
99665	LRRonly	
99667	LRRonly	
99688	LRRonly	
99698	LRRonly	
99699	LRRonly	
99700	LRRonly	
137032	LRRonly	
141719	LRRonly	
73444	LRRonly	
75945	LRRonly	
84897	LRRonly	
88374	LRRonly	
88378	LRRonly	
96131	LRRonly	
98413	LRRonly	
104303	LRRonly	
104306	LRRonly	
109258	LRRonly	
110694	LRRonly	
75515	LRRonly	
83208	LRRonly	
101410	LRRonly	
111426	LRRonly	
143269	LRRonly	
151565	LRRonly	
152920	LRRonly	
152923	LRRonly	
152924	LRRonly	
187251	LRRonly	
220253	LRRonly	
91930	LRRonly	
134756	LRRonly	
148974	LRRonly	
158057	LRRonly	
166389	LRRonly	
205695	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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221275	LRRonly	
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221597	LRRonly	
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59583	LRRonly	
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60354	LRRonly	
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61163	LRRonly	
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63338	LRRonly	
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63470	LRRonly	
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64062	LRRonly	
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64161	LRRonly	
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64164	LRRonly	
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64167	LRRonly	
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64248	LRRonly	
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64379	LRRonly	
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64797	LRRonly	
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65276	LRRonly	
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65322	LRRonly	
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65346	LRRonly	
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65721	LRRonly	
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65797	LRRonly	
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65991	LRRonly	
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66304	LRRonly	
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66658	LRRonly	
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66944	LRRonly	
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66946	LRRonly	
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66947	LRRonly	
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66951	LRRonly	
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67213	LRRonly	
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67214	LRRonly	
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67215	LRRonly	
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67234	LRRonly	
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67387	LRRonly	
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67566	LRRonly	
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67664	LRRonly	
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67703	LRRonly	
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67777	LRRonly	
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67778	LRRonly	
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67779	LRRonly	
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67780	LRRonly	
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67781	LRRonly	
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67867	LRRonly	
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68458	LRRonly	
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68460	LRRonly	
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68656	LRRonly	
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68799	LRRonly	
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68832	LRRonly	
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Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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69048	LRRonly	
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69264	LRRonly	
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69549	LRRonly	
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69561	LRRonly	
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70062	LRRonly	
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70478	LRRonly	
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70490	LRRonly	
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70761	LRRonly	
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71073	LRRonly	
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71448	LRRonly	
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71584	LRRonly	
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72033	LRRonly	
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72385	LRRonly	
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73521	LRRonly	
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73523	LRRonly	
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74056	LRRonly	
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74180	LRRonly	
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74810	LRRonly	
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74861	LRRonly	
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74961	LRRonly	
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75215	LRRonly	
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75318	LRRonly	
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75418	LRRonly	
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75531	LRRonly	
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75542	LRRonly	
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76271	LRRonly	
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76289	LRRonly	
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76625	LRRonly	
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76811	LRRonly	
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77007	LRRonly	
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77288	LRRonly	
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78770	LRRonly	
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79785	LRRonly	
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80851	LRRonly	
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80919	LRRonly	
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81648	LRRonly	
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81975	LRRonly	
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82609	LRRonly	
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82651	LRRonly	
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82652	LRRonly	
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82757	LRRonly	
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82778	LRRonly	
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82882	LRRonly	
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82905	LRRonly	
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83363	LRRonly	
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Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
83370	LRRonly	
83457	LRRonly	
83458	LRRonly	
83459	LRRonly	
83469	LRRonly	
83838	LRRonly	
83930	LRRonly	
84121	LRRonly	
84180	LRRonly	
84294	LRRonly	
84317	LRRonly	
84638	LRRonly	
84916	LRRonly	
85044	LRRonly	
85165	LRRonly	
85677	LRRonly	
85884	LRRonly	
86281	LRRonly	
86634	LRRonly	
86934	LRRonly	
87382	LRRonly	
87442	LRRonly	
87695	LRRonly	
87828	LRRonly	
88052	LRRonly	
88186	LRRonly	
88275	LRRonly	
88277	LRRonly	
88317	LRRonly	
88449	LRRonly	
88634	LRRonly	
88649	LRRonly	
88701	LRRonly	
88799	LRRonly	
89115	LRRonly	
89375	LRRonly	
90198	LRRonly	
90259	LRRonly	
90337	LRRonly	
90455	LRRonly	
90461	LRRonly	
90584	LRRonly	
90851	LRRonly	
91453	LRRonly	
91648	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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91731	LRRonly	
91732	LRRonly	
91733	LRRonly	
91737	LRRonly	
91828	LRRonly	
91983	LRRonly	
92046	LRRonly	
92291	LRRonly	
92322	LRRonly	
92674	LRRonly	
92705	LRRonly	
93083	LRRonly	
93091	LRRonly	
93336	LRRonly	
93382	LRRonly	
93565	LRRonly	
93621	LRRonly	
93884	LRRonly	
94020	LRRonly	
94117	LRRonly	
94265	LRRonly	
94439	LRRonly	
94441	LRRonly	
95224	LRRonly	
95376	LRRonly	
95757	LRRonly	
97344	LRRonly	
97373	LRRonly	
97486	LRRonly	
97498	LRRonly	
97615	LRRonly	
98157	LRRonly	
99661	LRRonly	
99772	LRRonly	
100245	LRRonly	
100468	LRRonly	
100721	LRRonly	
101034	LRRonly	
101215	LRRonly	
101300	LRRonly	
101301	LRRonly	
102021	LRRonly	
102024	LRRonly	
102617	LRRonly	
103548	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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103673	LRRonly	
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103705	LRRonly	
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103706	LRRonly	
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104522	LRRonly	
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104756	LRRonly	
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104848	LRRonly	
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104933	LRRonly	
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105173	LRRonly	
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105270	LRRonly	
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105980	LRRonly	
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105984	LRRonly	
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106234	LRRonly	
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106756	LRRonly	
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107691	LRRonly	
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107881	LRRonly	
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107911	LRRonly	
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108134	LRRonly	
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108556	LRRonly	
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108716	LRRonly	
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108980	LRRonly	
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108986	LRRonly	
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109122	LRRonly	
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109348	LRRonly	
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109415	LRRonly	
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109527	LRRonly	
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109618	LRRonly	
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109944	LRRonly	
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110498	LRRonly	
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110607	LRRonly	
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112281	LRRonly	
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112754	LRRonly	
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113569	LRRonly	
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114839	LRRonly	
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115127	LRRonly	
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115247	LRRonly	
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115963	LRRonly	
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116022	LRRonly	
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117061	LRRonly	
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117207	LRRonly	
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117747	LRRonly	
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117866	LRRonly	
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118129	LRRonly	
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118155	LRRonly	
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118480	LRRonly	
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118496	LRRonly	
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Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
118586	LRRonly	
118592	LRRonly	
119726	LRRonly	
119759	LRRonly	
119761	LRRonly	
121438	LRRonly	
121505	LRRonly	
121775	LRRonly	
122399	LRRonly	
122523	LRRonly	
122525	LRRonly	
123080	LRRonly	
123111	LRRonly	
123291	LRRonly	
123640	LRRonly	
123682	LRRonly	
123770	LRRonly	
123859	LRRonly	
123898	LRRonly	
123979	LRRonly	
123981	LRRonly	
124131	LRRonly	
124150	LRRonly	
124159	LRRonly	
124305	LRRonly	
124308	LRRonly	
124389	LRRonly	
124501	LRRonly	
124759	LRRonly	
125137	LRRonly	
125210	LRRonly	
125356	LRRonly	
125409	LRRonly	
125539	LRRonly	
125576	LRRonly	
125776	LRRonly	
125784	LRRonly	
125785	LRRonly	
125970	LRRonly	
126028	LRRonly	
126504	LRRonly	
126507	LRRonly	
126534	LRRonly	
126569	LRRonly	
126802	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
126829	LRRonly	
127100	LRRonly	
127301	LRRonly	
127889	LRRonly	
128309	LRRonly	
128316	LRRonly	
128348	LRRonly	
128422	LRRonly	
128705	LRRonly	
128780	LRRonly	
129456	LRRonly	
129743	LRRonly	
130144	LRRonly	
130226	LRRonly	
130472	LRRonly	
130644	LRRonly	
130981	LRRonly	
131013	LRRonly	
131169	LRRonly	
131747	LRRonly	
131829	LRRonly	
132485	LRRonly	
132519	LRRonly	
133274	LRRonly	
133370	LRRonly	
135144	LRRonly	
136091	LRRonly	
136613	LRRonly	
136801	LRRonly	
136843	LRRonly	
136845	LRRonly	
137525	LRRonly	
137613	LRRonly	
137623	LRRonly	
137690	LRRonly	
137713	LRRonly	
137818	LRRonly	
138079	LRRonly	
138137	LRRonly	
138235	LRRonly	
138495	LRRonly	
139658	LRRonly	
140169	LRRonly	
140459	LRRonly	
140695	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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141333	LRRonly	
141908	LRRonly	
142262	LRRonly	
142291	LRRonly	
143587	LRRonly	
145968	LRRonly	
146434	LRRonly	
147222	LRRonly	
148100	LRRonly	
148475	LRRonly	
148546	LRRonly	
148550	LRRonly	
148843	LRRonly	
149712	LRRonly	
149730	LRRonly	
149734	LRRonly	
150273	LRRonly	
150281	LRRonly	
150286	LRRonly	
150324	LRRonly	
150575	LRRonly	
150706	LRRonly	
150725	LRRonly	
150726	LRRonly	
151361	LRRonly	
151377	LRRonly	
152748	LRRonly	
153558	LRRonly	
154456	LRRonly	
155872	LRRonly	
158315	LRRonly	
158371	LRRonly	
158398	LRRonly	
159380	LRRonly	
160523	LRRonly	
160524	LRRonly	
160564	LRRonly	
160620	LRRonly	
160638	LRRonly	
160881	LRRonly	
161784	LRRonly	
161787	LRRonly	
163002	LRRonly	
164390	LRRonly	
165792	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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166441	LRRonly	
167278	LRRonly	
168674	LRRonly	
170291	LRRonly	
170779	LRRonly	
176183	LRRonly	
176756	LRRonly	
177061	LRRonly	
177167	LRRonly	
177215	LRRonly	
177381	LRRonly	
177720	LRRonly	
177782	LRRonly	
177816	LRRonly	
177844	LRRonly	
177850	LRRonly	
177860	LRRonly	
177921	LRRonly	
179778	LRRonly	
185851	LRRonly	
186516	LRRonly	
186766	LRRonly	
187123	LRRonly	
195868	LRRonly	
196068	LRRonly	
196343	LRRonly	
196347	LRRonly	
196521	LRRonly	
196980	LRRonly	
197524	LRRonly	
197751	LRRonly	
198747	LRRonly	
199264	LRRonly	
201520	LRRonly	
201812	LRRonly	
203691	LRRonly	
204729	LRRonly	
205037	LRRonly	
205113	LRRonly	
206003	LRRonly	
206491	LRRonly	
206558	LRRonly	
206808	LRRonly	
207368	LRRonly	
207825	LRRonly	

Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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208714	LRRonly	
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208979	LRRonly	
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210256	LRRonly	
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210302	LRRonly	
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211073	LRRonly	
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211146	LRRonly	
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212033	LRRonly	
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212176	LRRonly	
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212235	LRRonly	
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212402	LRRonly	
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212444	LRRonly	
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212652	LRRonly	
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212896	LRRonly	
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213228	LRRonly	
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213854	LRRonly	
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214218	LRRonly	
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214691	LRRonly	
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215332	LRRonly	
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215395	LRRonly	
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216381	LRRonly	
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216772	LRRonly	
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217684	LRRonly	
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220064	LRRonly	
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222466	LRRonly	
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222483	LRRonly	
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223269	LRRonly	
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223476	LRRonly	
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223683	LRRonly	
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223806	LRRonly	
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224546	LRRonly	
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224565	LRRonly	
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224602	LRRonly	
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225174	LRRonly	
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225198	LRRonly	
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225249	LRRonly	
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225256	LRRonly	
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225413	LRRonly	
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225473	LRRonly	
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227746	LRRonly	
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227943	LRRonly	
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227946	LRRonly	
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228029	LRRonly	
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228289	LRRonly	
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229101	LRRonly	
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230008	LRRonly	
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Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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230034	LRRonly	
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230123	LRRonly	
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230199	LRRonly	
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230724	LRRonly	
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231020	LRRonly	
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231498	LRRonly	
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231882	LRRonly	
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231916	LRRonly	
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231987	LRRonly	
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232037	LRRonly	
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232577	LRRonly	
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233421	LRRonly	
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233611	LRRonly	
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235470	LRRonly	
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235861	LRRonly	
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236185	LRRonly	
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236476	LRRonly	
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236544	LRRonly	
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238182	LRRonly	
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239104	LRRonly	
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239771	LRRonly	
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240452	LRRonly	
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241287	LRRonly	
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241289	LRRonly	
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241295	LRRonly	
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241327	LRRonly	
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241921	LRRonly	
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242036	LRRonly	
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245026	LRRonly	
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246124	LRRonly	
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246152	LRRonly	
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246565	LRRonly	
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246657	LRRonly	
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247145	LRRonly	
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247157	LRRonly	
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247512	LRRonly	
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248292	LRRonly	
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248570	LRRonly	
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248726	LRRonly	
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248734	LRRonly	
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248758	LRRonly	
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249144	LRRonly	
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249382	LRRonly	
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249741	LRRonly	
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251131	LRRonly	
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Other LRR-containing gene models, including LRR-only. Unknown=the protein structure is difficult to determine;

#=indicates models containing LRR only but actually fragment of other LRR genes

model ID	type	structure and notes
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251517	LRRonly	
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252288	LRRonly	
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252703	LRRonly	
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252713	LRRonly	
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253249	LRRonly	
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255627	LRRonly	
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255628	LRRonly	
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255918	LRRonly	
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256183	LRRonly	
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256188	LRRonly	
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256833	LRRonly	
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257874	LRRonly	
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260309	LRRonly	
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260421	LRRonly	
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264182	LRRonly	
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270453	LRRonly	
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274073	LRRonly	
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274884	LRRonly	
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275098	LRRonly	
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275303	LRRonly	
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276668	LRRonly	
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277336	LRRonly	
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277364	LRRonly	
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277514	LRRonly	
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280379	LRRonly	
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281171	LRRonly	
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284994	LRRonly	
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287459	LRRonly	
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289081	LRRonly	
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289275	LRRonly	
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289666	LRRonly	
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289668	LRRonly	
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5 C-type lectin (CTL) gene models

CTL models. Family A01-G05 represent different subfamilies; family A-G represent less reliable subfamilies; family X represent the unclassified gene models; family marked unknown represent genes with multiple CTLD, complex structures and problematic gene models.

model ID	family	sugar Binding motif	Gene model structure (not curated)
87574	A	exist	Kringle+EGF+CTLD
87576	A	exist	EGF+CTLD
87006	A	exist	CTLD
90935	A	exist	CTLD
90951	A	exist	CTLD
205239	A	exist	CTLD
205303	A	exist	CTLD
170434	A	exist	CTLD
205962	A	exist	CTLD
233931	A	exist	CTLD
234454	A	exist	CTLD
98100	A	exist	(Collagen triple helix repeat)+CTLD
98101	A	exist	(Collagen triple helix repeat)+CTLD
71528	A	exist	CTLD
100514	A	exist	CTLD
241743	A	exist	CTLD
73484	A	exist	CTLD
216618	A	exist	CTLD
65526	A	exist	CTLD
178460	A	exist	CTLD
233976	A	exist	CTLD
239555	A	exist	CTLD
133335	A	exist	(Animal haem peroxidase)
125849	A	exist	(Animal haem peroxidase)
238727	A	exist	CTLD
208968	A	exist	CTLD
241245	A	exist	CTLD
251740	A	exist	CTLD
256645	A	exist	CTLD
198699	A	not exist	CTLD
198863	A	not exist	CTLD
199118	A	not exist	CTLD
199187	A	not exist	CTLD
180738	A	not exist	CTLD
81963	A	not exist	CTLD
82209	A	not exist	(Collagen triple helix repeat)+CTLD
83002	A	not exist	(DNA binding RFX)+CTLD
84962	A	not exist	CTLD
89184	A	not exist	CTLD
91224	A	not exist	(Collagen triple helix repeat)+CTLD+(Organic anion transporter polypeptide (OATP), C-terminal)
93206	A	not exist	CTLD
141691	A	not exist	CTLD
234469	A	not exist	CTLD

CTL models. Family A01-G05 represent different subfamilies; family A-G represent less reliable subfamilies; family X represent the unclassified gene models; family marked unknown represent genes with multiple CTLD, complex structures and problematic gene models.

model ID	family	sugar Binding motif	Gene model structure (not curated)
234485	A	not exist	CTLD
234523	A	not exist	CTLD
178436	A	not exist	CTLD
238534	A	not exist	CTLD
72279	A	not exist	CTLD
245849	A	not exist	CTLD
74124	A	not exist	CTLD
74132	A	not exist	CTLD
249188	A	not exist	col+CTLD
213726	A	not exist	CTLD
253808	A	not exist	CTLD
255513	A	not exist	CTLD
178412	A	not exist	CTLD
178552	A	not exist	CTLD
122248	A	not exist	CTLD
94107	A	not exist	CTLD
234483	A	not exist	CTLD
107697	A	not exist	CTLD
90409	A	not exist	MAM+(Frizzled CRD region)+CTLD+(Frizzled CRD region)+Krigle+(Suchi/SCR/CCP)+(Neurotransmitter-gated ion-channel ligand-binding)+(Neurotransmitter-gated ion-channel transmembrane region)
69302	A	not exist	MAM+(Frizzled CRD region)+CTLD+(Krigle)
178345	A	not exist	CTLD
98293	A	not exist	CTLD
254456	A	not exist	CTLD
68373	A	not exist	(Thrombospondin,type)+(Suchi/SCR/CCP)2+CTLD+(Suchi/SCR/CCP)4
68381	A	not exist	(Thrombospondin,type)+(Suchi/SCR/CCP)+CTLD+(Suchi/SCR/CCP)7
72281	A	not exist	CTLD
92818	A01	exist	(Collagen triple helix repeat)+CTLD
92827	A01	exist	(Collagen triple helix repeat)+CTLD
81457	A01	exist	CTLD
259208	A01	exist	CTLD
83492	A01	exist	CTLD
83493	A01	exist	CTLD
83496	A01	exist	CTLD
67145	A01	exist	CTLD
67156	A01	exist	CTLD
112476	A01	exist	CTLD
112477	A01	exist	CTLD
86994	A01	exist	CTLD
67824	A01	exist	CTLD
67826	A01	exist	CTLD
87387	A01	exist	CTLD
87395	A01	exist	CTLD
68070	A01	exist	CTLD

CTL models. Family A01-G05 represent different subfamilies; family A-G represent less reliable subfamilies; family X represent the unclassified gene models; family marked unknown represent genes with multiple CTLD, complex structures and problematic gene models.

model ID	family	sugar Binding motif	Gene model structure (not curated)
88323	A01	exist	CTLD
88353	A01	exist	CTLD+(Leucine-rich repeat)
89100	A01	exist	CTLD
89117	A01	exist	CTLD
89119	A01	exist	CTLD
89144	A01	exist	CTLD
89147	A01	exist	(Zn-finger, C2H2 type)+CTLD
89157	A01	exist	CTLD
89161	A01	exist	(Proprotein convertase,P)+Cadherin+CTLD
89167	A01	exist	CTLD
89175	A01	exist	CTLD+(Zn-finger, C2H2 type)
63837	A01	exist	CTLD
63950	A01	exist	CTLD
68911	A01	exist	CTLD+(Suchi/SCR/CCP)12
92792	A01	exist	(Zn-finger, C2H2 type)+CTLD
259297	A01	exist	CTLD
228589	A01	exist	CTLD
231411	A01	exist	CTLD
178505	A01	exist	CTLD
233984	A01	exist	CTLD
234034	A01	exist	CTLD
234043	A01	exist	CTLD
206846	A01	exist	CTLD
206964	A01	exist	CTLD
161402	A01	exist	CTLD
178404	A01	exist	CTLD
178423	A01	exist	CTLD
178508	A01	exist	CTLD
178520	A01	exist	CTLD
178533	A01	exist	CTLD
178542	A01	exist	CTLD
178546	A01	exist	CTLD
178683	A01	exist	CTLD
234543	A01	exist	CTLD
234548	A01	exist	CTLD
234556	A01	exist	CTLD
234580	A01	exist	CTLD
234598	A01	exist	CTLD
234638	A01	exist	CTLD
234639	A01	exist	CTLD
234642	A01	exist	CTLD
234644	A01	exist	CTLD
234645	A01	exist	CTLD
234663	A01	exist	CTLD
234692	A01	exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
234733	A01	exist	CTLD
98181	A01	exist	CTLD
237925	A01	exist	CTLD
178656	A01	exist	CTLD
178657	A01	exist	CTLD
178568	A01	exist	CTLD
239426	A01	exist	CTLD
239435	A01	exist	CTLD
200104	A01	exist	CTLD
178590	A01	exist	CTLD
178658	A01	exist	CTLD
242960	A01	exist	CTLD
243353	A01	exist	CTLD
244404	A01	exist	CTLD
178563	A01	exist	CTLD
178595	A01	exist	CTLD
247755	A01	exist	CTLD
247763	A01	exist	CTLD
247766	A01	exist	CTLD
247779	A01	exist	CTLD
247789	A01	exist	CTLD
247826	A01	exist	CTLD
178439	A01	exist	CTLD
212851	A01	exist	CTLD
212919	A01	exist	CTLD
213009	A01	exist	CTLD
178449	A01	exist	CTLD
178539	A01	exist	CTLD
178613	A01	exist	CTLD
178639	A01	exist	CTLD
178640	A01	exist	CTLD
248820	A01	exist	CTLD
248827	A01	exist	CTLD
248862	A01	exist	CTLD
178621	A01	exist	CTLD
178747	A01	exist	CTLD
249293	A01	exist	CTLD
249525	A01	exist	CTLD
213768	A01	exist	CTLD
249981	A01	exist	CTLD
251043	A01	exist	CTLD
178609	A01	exist	CTLD
251134	A01	exist	CTLD
152066	A01	exist	CTLD
201105	A01	exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
201116	A01	exist	CTLD
201215	A01	exist	CTLD
201217	A01	exist	CTLD
201424	A01	exist	CTLD
141675	A01	exist	CTLD
215121	A01	exist	CTLD
178482	A01	exist	CTLD
252358	A01	exist	CTLD
253467	A01	exist	CTLD
189341	A01	exist	CTLD
171473	A01	exist	CTLD
217268	A01	exist	CTLD
189332	A01	exist	CTLD
202042	A01	exist	CTLD
217378	A01	exist	CTLD
254837	A01	exist	CTLD
255528	A01	exist	CTLD
202449	A01	exist	CTLD
219853	A01	exist	CTLD
220260	A01	exist	CTLD
189082	A01	exist	CTLD
189079	A01	exist	CTLD
178405	A01	exist	CTLD
257566	A01	exist	CTLD
223066	A01	exist	CTLD
236680	A01	not exist	CTLD
240413	A01	not exist	CTLD
189268	A01	not exist	CTLD
67154	A01	not exist	CTLD
112475	A01	not exist	CTLD
112743	A01	not exist	CTLD
125435	A01	not exist	CTLD
89118	A01	not exist	CTLD
89145	A01	not exist	(Zn-finger, C2H2 type)6+CTLD+(Zn-finger, C2H2 type)3
89151	A01	not exist	CTLD+(Zn-finger, C2H2 type)
89176	A01	not exist	(Zn-finger, C2H2 type)3+CTLD
89180	A01	not exist	CTLD
89182	A01	not exist	CTLD
90069	A01	not exist	CTLD
189084	A01	not exist	CTLD
189132	A01	not exist	CTLD
141655	A01	not exist	CTLD
234016	A01	not exist	CTLD
141836	A01	not exist	CTLD
160071	A01	not exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
178524	A01	not exist	CTLD
178534	A01	not exist	CTLD
178550	A01	not exist	CTLD
178557	A01	not exist	CTLD
178684	A01	not exist	CTLD
197409	A01	not exist	CTLD
234527	A01	not exist	CTLD
234601	A01	not exist	CTLD
234604	A01	not exist	CTLD
234700	A01	not exist	CTLD
234711	A01	not exist	CTLD
234714	A01	not exist	CTLD
234728	A01	not exist	CTLD
98190	A01	not exist	CTLD
129473	A01	not exist	(Zn-finger, C2H2 type)+CTLD+(Zn-finger, C2H2 type)
239424	A01	not exist	CTLD
239446	A01	not exist	CTLD
189193	A01	not exist	CTLD
209286	A01	not exist	CTLD
245993	A01	not exist	CTLD
247810	A01	not exist	CTLD
247832	A01	not exist	CTLD
247833	A01	not exist	CTLD
213034	A01	not exist	CTLD
178541	A01	not exist	CTLD
178642	A01	not exist	CTLD
248838	A01	not exist	CTLD
248840	A01	not exist	CTLD
106537	A01	not exist	CTLD
75207	A01	not exist	(Pancreatitis-associated protein)+CTLD
251564	A01	not exist	CTLD
108089	A01	not exist	CTLD+(Fibrinogen,beta/gamma chain,C-terminal)
108090	A01	not exist	CTLD
189333	A01	not exist	CTLD
255370	A01	not exist	CTLD
257795	A01	not exist	CTLD
89079	A01X	not exist	CTLD
178781	A02	exist	CTLD
235261	A02	exist	CTLD
76465	A02	not exist	CTLD
94612	A02	not exist	CTLD
141634	A02	not exist	CTLD
178815	A02	not exist	CTLD
235202	A02	not exist	CTLD
138245	A02	not exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
141736	A02	not exist	CTLD
189089	A02	not exist	CTLD
189136	A02	not exist	CTLD
189195	A02	not exist	CTLD
216006	A02	not exist	CTLD
216064	A02	not exist	CTLD
216073	A02	not exist	CTLD
76454	A02	not exist	CTLD
76456	A02	not exist	CTLD
76468	A02	not exist	CTLD
235161	A02X	not exist	CTLD
234399	A03	exist	CTLD
234431	A03	exist	CTLD
208601	A03	exist	CTLD
208611	A03	exist	CTLD
189156	A03	exist	CTLD
224022	A03	exist	CTLD
224039	A03	exist	CTLD
111946	A04	exist	CTLD
244717	A04	not exist	CTLD
255687	A04	not exist	CTLD
255697	A04	not exist	CTLD
129955	A05	exist	(Collagen triple helix repeat)+CTLD+Orange
188711	A05	exist	CTLD
254297	A05	exist	CTLD
254348	A05	exist	CTLD
189815	A05	not exist	(Collagen triple helix repeat)+CTLD
83844	A06	exist	CTLD
88463	A06	exist	(Collagen triple helix repeat)+CTLD
88464	A06	exist	(Collagen triple helix repeat)+CTLD+(Collagen triple helix repeat)
172107	A06	exist	CTLD
205353	A06	exist	CTLD
205421	A06	exist	CTLD
205489	A06	exist	CTLD
189210	A06	exist	CTLD
229566	A06	exist	CTLD
229609	A06	exist	CTLD
229611	A06	exist	CTLD
229634	A06	exist	CTLD
206563	A06	exist	CTLD
207562	A06	exist	CTLD
236999	A07	exist	CTLD
220851	A07	exist	CTLD
66616	A07	not exist	CTLD
66617	A07	not exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
66618	A07	not exist	CTLD
105901	A07	not exist	CTLD
189167	A08	exist	CTLD
189362	A08	exist	CTLD
204262	A08	exist	CTLD
66587	A08	exist	(Sushi/SCR/CCP)9+CTLD
89745	A08	exist	(Sushi/SCR/CCP)7+VWF+CTLD
89747	A08	exist	CTLD
208160	A08	exist	CTLD
99520	A08	exist	CTLD
99524	A08	exist	(Sushi/SCR/CCP)7+CTLD
252948	A08	exist	CTLD
189086	A08	not exist	CTLD
66579	A08	not exist	(Sushi/SCR/CCP)6+CTLD
234086	A08X	not exist	CTLD
189469	A09	exist	CTLD
230570	A09	exist	CTLD
235791	A09	exist	CTLD
189435	A09	exist	CTLD
178904	A09	exist	CTLD
224206	A10	exist	CTLD
189377	A10	exist	CTLD
232682	A10	exist	CTLD
178518	A10	exist	CTLD
248246	A10	exist	CTLD
221224	A10	exist	CTLD
259157	A11	exist	CTLD
88068	A11	exist	(Carbohydrate-binding WSC)+CTLD
88072	A11	exist	(D-galactoside/L-rhamnose binding SUEL lectin)+(Chitin-binding, type 1)+CTLD+(Chitin-binding, type 1)
204627	A11	exist	CTLD
204686	A11	exist	CTLD
189380	A11	exist	CTLD
220740	A11	exist	CTLD
178900	A11	not exist	CTLD
161762	A12	not exist	CTLD
113249	A12	not exist	CTLD
111836	A12	not exist	CTLD
258396	A12	not exist	CTLD
178646	A13	not exist	CTLD
126306	A13	not exist	(Collagen triple helix repeat)+CTLD
91545	A13	not exist	CTLD
228635	A13	not exist	CTLD
228752	A13	not exist	CTLD
216726	A13	not exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
224982	A14	exist	CTLD
225064	A14	exist	CTLD
178538	A14	exist	CTLD
242890	A14	exist	CTLD
205238	A15	exist	CTLD
205272	A15	exist	CTLD
205418	A15	exist	CTLD
229615	A15	exist	CTLD
125323	B	exist	(Sushi/SCR/CCP)+CTLD+(N/apple PAN)+(Sushi/SCR/CCP)2+(Proteinase inhibitor I1,Kazal)+(Sushi/SCR/CCP)2+VWF+(Peptidase S1,chymotrypsin)
83177	B01	exist	CTLD+(Myb,DNA-binding)+(Inorganic pyrophosphatase)
83178	B01	exist	CTLD
112447	B01	exist	(Rhodopsin-like GPCR superfamily)+FA58C+CTLD
86706	B01	exist	CTLD
109631	B01	exist	CTLD
67059	B01	not exist	CTLD
83985	B01	not exist	(Kringle)+CTLD
67466	B01	not exist	CTLD
68034	B01	not exist	FA58C+Kringle+CTLD
68932	B01	not exist	(Kringle)+CTLD
92290	B01	not exist	(Sushi/SCR/CCP)+CTLD
92778	B01	not exist	Kringle+CTLD
69661	B01	not exist	(Kringle)+CTLD
79127	B01	not exist	FA58C+(Fucoselectin tachylectin-4 pentraxin-1)+CTLD
79129	B01	not exist	FA58C+(N/apple PAN)+CTLD
225828	B02	exist	CTLD
189383	B02	exist	CTLD
230630	B02	exist	CTLD
189212	B02	exist	CTLD
178611	B02	exist	CTLD
178771	B02	exist	CTLD
189227	B02	exist	CTLD
85528	B02	not exist	(sulfoltransferase)+FA58C+CTLD+(Fibronectin)
85535	B02	not exist	FA58C+CTLD+(Fibronectin+PKD/REJ-like protein)
259171	B03	not exist	CTLD
178753	B03	not exist	CTLD
179081	B03	not exist	CTLD
178708	B03	not exist	CTLD
178763	B03	not exist	CTLD
232345	B03	not exist	CTLD
255354	B03	not exist	CTLD
110103	B03	not exist	CTLD
85013	B04	exist	CTLD
68957	B04	exist	CTLD
68958	B04	exist	(D-galactoside/L-rhamnose binding SUEL

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model ID	family	sugar Binding motif	Gene model structure (not curated)
			lectin)+CUB+(Suchi/SCR/CCP)+CTLD+(D-galactoside/L-rhamnose binding SUEL lectin)+CUB+(Suchi/SCR/CCP)3
246347	B04	exist	CTLD
141845	B04	exist	CTLD
198156	B04	exist	CTLD
212378	B04	exist	CTLD
178960	B04	exist	CTLD
67800	B04X	not exist	CTLD
107715	B05	exist	(Peptidase inhibitor I9,subtilisin propeptide)+CTLD+(Peptidase S8 and S53, subtilisin, kexin, sedolisin)
178118	B05	exist	CTLD
150470	B05	exist	CTLD
198988	C01	exist	CTLD
225395	C01	exist	CTLD
225716	C01	exist	CTLD
85725	C01	exist	FA58C+CTLD+(Kringle)+(Neurotransmitter-gated ion-channel ligand-binding)
90034	C01	exist	LDL+Kringle+CTLD+LDL+Kringle+(Cytochrome P450)
229456	C01	exist	CTLD
189172	C01	exist	CTLD
232601	C01	exist	CTLD
178448	C01	exist	CTLD
233904	C01	exist	CTLD
71622	C01	exist	(LDL)2+CTLD+(Kringle)+LDL+(Suchi/SCR/CCP)+(Neurotransmitter-gated ion-channel ligand-binding)+(Neurotransmitter-gated ion-channel transmembrane region)
237180	C01	exist	CTLD
178637	C01	exist	CTLD
240742	C01	exist	CTLD
241152	C01	exist	CTLD
241450	C01	exist	CTLD
210040	C01	exist	CTLD
241727	C01	exist	CTLD
241754	C01	exist	CTLD
210242	C01	exist	CTLD
245847	C01	exist	CTLD
245868	C01	exist	CTLD
245875	C01	exist	CTLD
247247	C01	exist	CTLD
248201	C01	exist	CTLD
178738	C01	exist	CTLD
189093	C01	exist	CTLD
214042	C01	exist	CTLD
256129	C01	exist	CTLD
256753	C01	exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
84939	C01	not exist	CTLD+Kringle
68883	C01	not exist	CTLD+LDL+(Kringle)+(Suchi/SCR/CCP)+(Neurotransmitter-gated ion-channel transmembrane region)
249478	C01	not exist	CTLD
215896	C01	not exist	CTLD
120203	C01X	not exist	(Reeler region)+CTLD
68724	C01X	not exist	(Thrombospondin,type)+CTLD+(Kringle)2+FA58C+ (Kringle) 2
152110	C02	exist	CTLD
205862	C02	exist	CTLD
142661	C02	exist	CTLD
220745	C02	exist	CTLD
97643	C02	exist	(EGF)2+CTLD
109391	C02	exist	(Sushi/SCR/CCP)+(EGF)2+CTLD+(Sushi/SCR/CCP)+EGF+(Lipoxygenase,L H2)+(Ion transport protein)
141074	C02	exist	CTLD
189281	C02	exist	CTLD
224782	C02	exist	CTLD
224799	C02	exist	CTLD
224876	C02	exist	CTLD
224909	C02	exist	CTLD
67351	C02	exist	FA58C+(N/apple PAN)+CTLD
85352	C02	exist	(Thrombospondin,type)+CTLD+VWF
85571	C02	exist	CTLD
87084	C02	exist	CTLD+(Neurotransmitter-gated ion-channel transmembrane region)
87086	C02	exist	(Fibrinogen,beta/gamma chain,C-terminal globular)+CTLD+FA58C+(Sushi/SCR/CCP)2
89771	C02	exist	(Cell surface antigen)+CTLD
118915	C02	exist	CTLD+Lipase
126746	C02	exist	CTLD+(Carboxylesterase,type B)
93173	C02	exist	(N/apple PAN)+CTLD
170736	C02	exist	CTLD
189288	C02	exist	CTLD
204946	C02	exist	CTLD
205051	C02	exist	CTLD
205103	C02	exist	CTLD
141690	C02	exist	CTLD
150859	C02	exist	CTLD
197387	C02	exist	CTLD
197446	C02	exist	CTLD
233173	C02	exist	CTLD
233174	C02	exist	CTLD
233286	C02	exist	CTLD
233777	C02	exist	CTLD
206902	C02	exist	CTLD
178856	C02	exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
209193	C02	exist	CTLD
209272	C02	exist	CTLD
242119	C02	exist	CTLD
141297	C02	exist	CTLD
141344	C02	exist	CTLD
242657	C02	exist	CTLD
211083	C02	exist	CTLD
212070	C02	exist	CTLD
247615	C02	exist	CTLD
247875	C02	exist	CTLD
248156	C02	exist	CTLD
248185	C02	exist	CTLD
248953	C02	exist	CTLD
213265	C02	exist	CTLD
213443	C02	exist	CTLD
251651	C02	exist	CTLD
251662	C02	exist	CTLD
141768	C02	exist	CTLD
189214	C02	exist	CTLD
189318	C02	exist	CTLD
217720	C02	exist	CTLD
217752	C02	exist	CTLD
217815	C02	exist	CTLD
217838	C02	exist	CTLD
255465	C02	exist	CTLD
171742	C02	exist	CTLD
220116	C02	exist	CTLD
256886	C02	exist	CTLD
178768	C02	exist	CTLD
189443	C02	exist	CTLD
222750	C02	exist	CTLD
175600	C02	exist	CTLD
222847	C02	exist	CTLD
223230	C02	exist	CTLD
141335	C02	exist	CTLD
224043	C02	exist	CTLD
124580	C02	not exist	(Membrane attack complex component/perforin/complement C9)+EGF+(Furin-like repeat)+FA58C+(N/apple PAN)+CTLD+EGF+(Speract/scavenger receptor)+(Sushi/SCR/CCP)
63812	C02	not exist	FA58C+EGF+(Speract/scavenger receptor)+EGF+CTLD +(Speract/scavenger receptor)+EGF+(Fibronectin, type)+(Endoglin/CD105 antigen)
225911	C02	not exist	CTLD
67449	C02	not exist	(TNFR/CD207/30/40/95 cysteine-rich region)2+CTLD+(TNFR/CD207/30/40/95 cysteine-rich region)
189280	C02	not exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
227667	C02	not exist	CTLD
227676	C02	not exist	CTLD
152100	C02	not exist	CTLD
152078	C02	not exist	CTLD
231328	C02	not exist	CTLD
206333	C02	not exist	CTLD
207131	C02	not exist	CTLD
236081	C02	not exist	CTLD
105925	C02	not exist	CTLD
142637	C02	not exist	CTLD
248416	C02	not exist	CTLD
213437	C02	not exist	CTLD
213500	C02	not exist	CTLD
214247	C02	not exist	CTLD
178686	C02	not exist	CTLD
214762	C02	not exist	CTLD
197433	C02	not exist	CTLD
252594	C02	not exist	CTLD
152071	C02	not exist	CTLD
219740	C02	not exist	CTLD
219916	C02	not exist	CTLD
220024	C02	not exist	CTLD
224064	C02	not exist	CTLD
198861	C02	not exist	CTLD
90527	C02	not exist	CTLD+(Thrombospondin,typeI)+(Neurotransmitter-gated ion-channel transmembrane region)
178831	C02	not exist	CTLD
231168	C02	not exist	CTLD
248155	C02	not exist	CTLD
141721	C02	not exist	CTLD
222816	C02	not exist	CTLD
222970	C02	not exist	CTLD
106412	D	exist	CTLD+(EGF)2
67980	D	exist	(Carbohydrate-binding WSC)+CTLD+VWF+(Cysteine-rich TIL region)+(Beta-proneller repeat TECPR)5+VWF+(Cysteine-rich TIL region)+(Beta-proneller repeat TECPR)4+VWF
205618	D	exist	CTLD
123387	D	not exist	CTLD+(EGF)2
83191	D	not exist	CTLD+(EGF)2+(Endoplasmic reticulum targeting sequence)
88361	D	not exist	CTLD+EGF+(Thrombospondin type 3 repeat)2+(Thrombospondin, C-terminal)
81527	D01	not exist	(Protein of unknown function DUF6)+CTLD
84680	D01	not exist	(Nidogen,extracellular region)+CTLD
84760	D01	not exist	NIDO+VWF+(Sushi/SCR/CCP)+CTLD
125402	D01	not exist	NIDO+CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
98424	D01	not exist	CTLD
71516	D01	not exist	(Nidogen,extracellular region)+CTLD
90417	D02	not exist	(Cysteine-rich TIL region)+CTLD
90418	D02	not exist	CTLD
90419	D02	not exist	(Protease inhibitor I2, Kunitz metazoa)+CTLD
111820	D02	not exist	(Cysteine-rich TIL region)2+CTLD
90394	D03	not exist	VWF+(EGF)2+CTLD
90411	D03	not exist	VWF+(EGF)2+CTLD
88713	D03	not exist	CTLD
68568	D03	not exist	(Beta-ketoacyl synthase)+CTLD
96397	D03	not exist	VWF+(Sushi/SCR/CCP)3+CTLD
97334	D03	not exist	VWF+(Sushi/SCR/CCP)3+CTLD
97887	D03	not exist	LDL+(Frizzled CRD region)+LDL+(Frizzled CRD region)2+CTLD
112029	D04	exist	CTLD
82101	D04	exist	CTLD
118433	D04	exist	CTLD+(N/apple PAN)
67349	D04	exist	CTLD+(N/apple PAN)
103487	D04	exist	CTLD
84619	D04	not exist	CTLD
110671	D04	not exist	CTLD
83172	D04X	not exist	(Patatin)+CTLD
112400	D05	exist	FA58C+CTLD+(Fibronectin,type III)+(Ion transport protein)
92551	D05	exist	(Pentaxin)+FA58C+CTLD+(Fibronectin,type III)
244180	D05	exist	CTLD
244218	D05	exist	CTLD
178313	D05	exist	CTLD
178341	D05	exist	CTLD
216499	D05	exist	CTLD
255542	D05	exist	CTLD
85195	D06	exist	CTLD+(Fibronectin,type3+Lipoxygenase,LH2)+(Cation channel+Zn-finger-like,PHD finger)
67064	D06	exist	LDL+(Kringle)+LDL+CTLD+(Fucolectin tachylectin-4 pentraxin-1)+LDL+Kringle+GPCR+(Kringle)+GPCR
87121	D06	exist	CTLD+LDL+Kringle+(Sushi/SCR/CCP)+(Neurotransmitter-gated ion-channel transmembrane region)
119148	D06	not exist	Kringle+CTLD
142511	D06	not exist	CTLD
213566	D06X	not exist	CTLD
119076	D07	not exist	Kringle+CTLD
101110	D07	not exist	(FA58C)2+(Beta-propeller repeat TECPR)5+(FA58C)2+CTLD
129574	D07	not exist	Kringle+FA58C+(Beta-propeller repeat TECPR)6+CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
107994	D07	not exist	Kringle+CTLD
66531	D08	exist	CTLD
125972	D08	exist	CTLD+EGF+(Kringle)2
69093	D08	exist	(G-protein beta WD-40 repeat)6+CTLD+VWF
101111	D08	exist	CTLD+(FA58C)2
176590	D08	exist	CTLD
106943	D08	exist	CTLD+FA58C
241083	D08X	not exist	CTLD
257504	D09	exist	CTLD
67420	D09	not exist	(Sushi/SCR/CCP)2+(CUB)2+(Beta-proneller repeat TECPR)4+(LDL)3+CTLD+CUB
80692	D09	not exist	CTLD
100688	D09X	not exist	CTLD
224792	D10	exist	CTLD
205605	D10	exist	CTLD
205740	D10	exist	CTLD
205825	D10	exist	CTLD
69307	D11	exist	EGF+CTLD+uDENN+DENN+dDENN
231717	D11	exist	(EGF)2+CTLD
231773	D11	exist	(EGF)2+CTLD
238265	D11	exist	(EGF)2+CTLD
239249	D11	exist	(EGF)2+CTLD
246571	D11	exist	EGF+CTLD
224211	D11	exist	CTLD
177451	D11	exist	CTLD
227738	D11	exist	CTLD
94170	D11	exist	CTLD
208182	D11	exist	CTLD
208392	D11	exist	CTLD
240469	D11	exist	CTLD
246593	D11	exist	CTLD
257955	D11	exist	CTLD
223290	D11	exist	CTLD
223434	D11	exist	CTLD
176800	D11	exist	(EGF)2+CTLD
177991	D11	exist	CTLD
177442	D11	exist	CTLD
208665	D11	exist	CTLD
239316	D11	exist	CTLD
251700	D11	exist	CTLD
223426	D11	exist	CTLD
233815	D11	exist	(EGF)2+CTLD
210423	D11	exist	CTLD
233812	D11	exist	CTLD
233835	D11	exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
233880	D11	exist	CTLD
177822	D11	exist	CTLD
243926	D11	exist	CTLD
243967	D11	exist	CTLD
244065	D11	exist	CTLD
250837	D11	exist	CTLD
87757	D11	exist	(EGF)4+CTLD
239367	D11	exist	(EGF)2+CTLD
241125	D11	exist	(EGF)2+CTLD
246074	D11	exist	(EGF)2+CTLD
201924	D11	exist	(EGF)2+CTLD
220055	D11	exist	(EGF)2+CTLD
186967	D11	exist	EGF+CTLD
203219	D11	exist	CTLD
67080	D11	exist	(Kringle)+CTLD
83855	D11	exist	C2+(Ras GTPase-activating protein)+(Pleckstrin-like)+CTLD
93193	D11	exist	(Collagen triple helix repeat)+CTLD
204756	D11	exist	CTLD
204841	D11	exist	CTLD
230945	D11	exist	CTLD
206727	D11	exist	CTLD
70915	D11	exist	CTLD+(Rhodopsin-like GPCR superfamily)
234412	D11	exist	CTLD
234953	D11	exist	CTLD
208334	D11	exist	CTLD
208530	D11	exist	CTLD
208613	D11	exist	CTLD
208724	D11	exist	CTLD
135764	D11	exist	CTLD
142451	D11	exist	CTLD
239277	D11	exist	CTLD
239294	D11	exist	CTLD
151710	D11	exist	CTLD
200057	D11	exist	CTLD
188120	D11	exist	CTLD
177928	D11	exist	CTLD
142762	D11	exist	CTLD
189446	D11	exist	CTLD
215823	D11	exist	CTLD
187995	D11	exist	CTLD
223467	D11	exist	CTLD
180253	D11	not exist	CTLD
232097	D11	not exist	CTLD
178068	D11	not exist	CTLD
178245	D11	not exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
178116	D11	not exist	CTLD
220074	D11	not exist	CTLD
100107	D11	not exist	(EGF)2+CTLD
238147	D11	not exist	CTLD
254523	D11	not exist	CTLD
245649	D11	not exist	CTLD
71663	D11	not exist	EGF+CTLD
250477	D11	not exist	(EGF)2+CTLD
187333	D11	not exist	EGF+CTLD
87407	D11	not exist	CTLD+BRICHOS
151236	D11	not exist	CTLD
151312	D11	not exist	CTLD
171293	D11	not exist	CTLD
234430	D11	not exist	CTLD
208738	D11	not exist	CTLD
178070	D11	not exist	CTLD
240595	D11	not exist	CTLD
212143	D11	not exist	CTLD
249680	D11	not exist	CTLD
142308	D11	not exist	CTLD
79074	D11	not exist	CTLD
256692	D11	not exist	CTLD
150756	D11	not exist	CTLD
151639	D11	not exist	CTLD
67477	D11X	not exist	EGF+(Kringle)+CTLD
85340	D11X	not exist	(TYPE 2 antifreeze protein)+CTLD
100142	D11X	not exist	CTLD
124483	D12	exist	CTLD+VWF+(Cysteine-rich TIL region)2+(VWF)2+(Protease inhibitor 12,Kunitz metazoa)
187367	D12	exist	CTLD
175982	D12	exist	CTLD
87573	D13	not exist	(Zn-finger,MYNO type)+CTLD+(PKD/REJ-like protein)
70115	D13	not exist	GPS+(Lipoxygenase,LH2)+(Myb,DNA-binding)+(Ion transport protein)
95235	D13	not exist	CTLD+(PKD/REJ-like protein)+GPS+(Lipoxygenase,LH2)+(Polycystic kidney disease typeI protein)2+(Polycystic kidney disease type 2 protein)+(Ion transport protein)
92894	D14	exist	(Fucoselectin tachylelectin-4 pentraxin-1)+CTLD+Kringle+(FA58C)2+(Speract/scavenger receptor)
92895	D14	not exist	(FA58C)2+(N/apple PAN)+CTLD+Kringle
74138	D14	not exist	(Fucoselectin tachylelectin-4 pentraxin-1)+CTLD+(Kringle)
86707	D15	not exist	LDLa+CUB+CTLD
92683	D15	not exist	(CUB)2+(Beta-propeller repeat TECPR)3+(LDL)3+CUB+CTLD
64068	D15	not exist	CTLD+CTLD
84714	D15X	not exist	CUB+(Beta-propeller repeat TECPR)2+(LDL)3+CUB+CTLD
91463	D16	exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
91464	D16	exist	CTLD
229099	D16	exist	CTLD
91906	E	exist	(Membrane attack complex component/perforin/complement C9)+(EGF)3+CTLD
259182	E	exist	CTLD
123411	E	exist	(Glycosyl transferase, family 29)+FA58C+CTLD
230826	E	exist	CTLD
258165	E	exist	CTLD
89470	E	not exist	(Membrane attack complex component/perforin/complement C9)+(Furin-like repeat)+(EGF)2+CTLD
124444	E01	exist	(Cysteine-rich TIL region)+VWF+CTLD+(Core region in kinesin and myosin motor)+(Band 4.1)
253544	E01	exist	CTLD
219989	E01	exist	CTLD
220069	E01	exist	CTLD
222648	E01	exist	CTLD
222597	E01X	not exist	CTLD
226848	E02	exist	CTLD
226860	E02	exist	CTLD
207827	E02	exist	CTLD
207847	E02	exist	CTLD
207869	E02	exist	CTLD
207933	E02	exist	CTLD
207962	E02	exist	CTLD
208006	E02	exist	CTLD
208012	E02	exist	CTLD
222515	E02	exist	CTLD
222692	E02	exist	CTLD
86739	E03	exist	CTLD
125768	E03	exist	CTLD
94348	E03	exist	CTLD
113445	E03	exist	(Collagen helix repeat)+CTLD
160273	E03	exist	CTLD
208572	E03	exist	CTLD
214672	E03	exist	CTLD
75618	E03	exist	CTLD
223334	E03	exist	CTLD
223335	E03	exist	CTLD
223353	E03	exist	CTLD
223401	E03	exist	CTLD
223488	E03	exist	CTLD
223516	E03	exist	CTLD
223573	E03	exist	CTLD
80757	E03	exist	CTLD
80760	E03	exist	CTLD

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model ID	family	sugar Binding motif	Gene model structure (not curated)
223358	E03	not exist	CTLD
92776	F	not exist	(Speract/scavenger receptor)+CTLD+EGF+(Tumour necrosis factor subfamily)
152060	F	not exist	CTLD
213412	F01	exist	CTLD
223202	F01	exist	CTLD
223257	F01	exist	CTLD
241489	F01	not exist	CTLD
89418	F02	exist	(N/apple PAN)2+CTLD
89421	F02	exist	(N/apple PAN)2+CTLD
90551	F02	exist	(Collagen triple helix repeat)+CTLD
69438	F02	exist	(Collagen triple helix repeat)+CTLD
220113	F02	exist	CTLD
78982	F02	exist	CTLD
222643	F02	exist	CTLD
152054	F02	exist	CTLD
150729	F02	exist	CTLD
122198	F02	not exist	(Ricin B lectin)2+(Doublecortin)2+CTLD+(Sushi/SCR/CCP)+EGF+(Thrombospondin, type I)+(Neurotransmitter-gated ion-channel transmembrane region)
189295	F03	exist	CTLD
229794	F03	exist	CTLD
216192	F03	exist	CTLD
248244	F04	exist	CTLD
255438	F04	exist	CTLD
255453	F04	exist	CTLD
88050	F05	exist	CTLD+VWF+(Cysteine-rich TIL region)+VWF+(Cysteine-rich TIL region)+(EGF)3
88051	F05	exist	CTLD+VWF+(Cysteine-rich TIL region)+VWF+(Cysteine-rich TIL region)+EGF
103750	F05	exist	CTLD+VWF+(Cysteine-rich TIL region)+VWF+(Cysteine-rich TIL region)2+(Sushi/SCR/CCP)+VWF+(Cysteine-rich TIL region)
105411	G	not exist	(LDL)2+CTLD
106440	G	not exist	(LDL)3+CTLD
63398	G01	exist	(protein kinase)+(Sushi/SCR/CCP)+EGF+CTLD
118754	G01	exist	(Sushi/SCR/CCP)3+EGF+CTLD
72979	G01	exist	(Thrombospondin,type)+EGF+(Suchi/SCR/CCP)+EGF+CTLD
77076	G01	exist	(Thrombospondin,type)+Suchi/SCR/CCP+EGF+CTLD
125405	G01	exist	(Sushi/SCR/CCP)2+EGF+CTLD
215006	G01	exist	EGF+CTLD
77075	G01	exist	EGF+(Suchi/SCR/CCP)2+CTLD
121550	G01	exist	(Sushi/SCR/CCP)4+CTLD
68379	G01	exist	(Thrombospondin,type)+(Suchi/SCR/CCP)2+EGF+CTLD
103181	G01	exist	CTLD
68372	G01	exist	(Thrombospondin,type

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model ID	family	sugar Binding motif	Gene model structure (not curated)
			) +EGF+(Suchi/SCR/CCP)+CTLD+(Suchi/SCR/CCP)2+EGF+CTLD
133202	G01	not exist	(Suchi/SCR/CCP)10+EGF+CTLD
83969	G02	not exist	VWF+(EGF)2+CTLD
83970	G02	not exist	(EGF)4+(Thrombospondin,type)2+CTLD
67520	G02	not exist	(Somatomedin B)+VWF+EGF+CTLD
67521	G02	not exist	(EGF)4+(Thrombospondin,type)+CTLD
88348	G02	not exist	EGF+CTLD
88354	G02	not exist	(Ankyrin)2+(EGF)2+CTLD
133116	G02	not exist	(Suchi/SCR/CCP)+CTLD
66671	G02	not exist	CTLD
83968	G02	not exist	(Thrombospondin,type)+CTLD
112652	G02	not exist	VWF+(Suchi/SCR/CCP)4+(Thrombospondin,type I)+CTLD
67517	G02	not exist	(Somatomedin B)+(Animal haem peroxidase)+(Suchi/SCR/CCP)2+CTLD
87531	G02	not exist	(Suchi/SCR/CCP)2+(EGF)4+CTLD
290149	G03	not exist	(EGF)2+CTLD
83028	G03	not exist	EGF+CTLD+EGF
83101	G03	not exist	(EGF)2+CTLD
83102	G03	not exist	(Thrombospondin,type)2+(EGF)2+CTLD
112326	G04	exist	CTLD+EGF
68722	G04	exist	EGF+(Suchi/SCR/CCP)2+VWF+CTLD
118258	G04	exist	CTLD+VWF
123688	G04	exist	CTLD
118493	G04	exist	(TatD deoxyribonuclease)+CTLD
68709	G04	exist	(Suchi/SCR/CCP)3+VWF+CTLD
64431	G04	exist	(Suchi/SCR/CCP)3+CTLD +CTLD
243853	G04	exist	CTLD
202884	G04	exist	CTLD
119074	G05	exist	(EGF)3+CTLD+(EGF)2
82264	G05	not exist	CTLD+EGF
82907	G05	not exist	EGF+CTLD+(EGF)2
82908	G05	not exist	EGF+CTLD+(EGF)2
82909	G05	not exist	EGF+CTLD+(EGF)2
85294	G05	not exist	VWF+(Chitin binding peritrophin-A)+CTLD+EGF
85297	G05	not exist	VWF+Cache+EGF+CTLD
86078	G05	not exist	CTLD+EGF
87114	G05	not exist	(Speract/scavenger receptor)+EGF+CTLD+(EGF)2+Phosphofructokinase
68133	G05	not exist	(Allergen V5/Tpx-1 related)+EGF+CTLD+EGF
113094	G05	not exist	CTLD+EGF
125935	G05	not exist	(EGF)2+CTLD+(EGF)2
90588	G05	not exist	(Laminin,N-terminal)+(Lamin-type,EGF-like)+(EGF)3+CTLD+EGF
90593	G05	not exist	(EGF)2+CTLD+(EGF)2
90594	G05	not exist	(EGF)3+CTLD
90596	G05	not exist	EGF+CTLD+EGF
63814	G05	not exist	(EGF)4+CTLD
68964	G05	not exist	CTLD+(EGF)3

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model ID	family	sugar Binding motif	Gene model structure (not curated)
119075	G05	not exist	(EGF)3
119097	G05	not exist	(EGF)2+CTLD+(EGF)2
69397	G05	not exist	(EGF)2+CTLD+(EGF)3
69403	G05	not exist	(Laminin, N-terminal)+(EGF)3+CTLD+EGF
69465	G05	not exist	EGF+CTLD+(EGF)2
69474	G05	not exist	CTLD+(EGF)2
69476	G05	not exist	(EGF)3
69478	G05	not exist	(EGF)2+CTLD+EGF
69479	G05	not exist	EGF+CTLD+(EGF)2
69480	G05	not exist	EGF+CTLD+EGF
69482	G05	not exist	EGF+CTLD+(EGF)2
69486	G05	not exist	(Speract/scavenger receptor)+CTLD+EGF
69489	G05	not exist	(EGF)2+CTLD
69494	G05	not exist	(Laminin, N-terminal)+(EGF)2+CTLD+EGF
93669	G05	not exist	(Chitin binding Peritrophin-A)+CTLD+EGF
127871	G05	not exist	(EGF)2+CTLD+EGF
96151	G05	not exist	EGF+CTLD+EGF
106950	G05	not exist	(Laminin,N-terminal)+(Lamin-type,EGF-like)+EGF+CTLD+EGF
119095	G05X	not exist	CTLD+EGF
82263	G05X	not exist	(EGF)2+CTLD
85579	G05X	not exist	EGF+CTLD
93668	G05X	not exist	CUB+EGF+CTLD+EGF
87354	X00	exist	CTLD+VWF
93177	X00	exist	VWF+(Hyalin)+CTLD
93178	X00	exist	CTLD
230594	X00	exist	CTLD
209652	X00	exist	CTLD
142632	X00	exist	CTLD
118386	X00	exist	LDL+(Laminin-type,EGF-like)+LDL+CTLD+(Laminin-type,EGF-like)+(Peptidase M1,membrane alanine aminopeptidase)
118391	X00	exist	LDL+(N/apple PAN)+CTLD+(Laminin-type,EGF-like)
129979	X00	exist	LDL+CTLD
110586	X00	exist	LDL+CTLD
112726	X00	not exist	LDL+(Speract/scavenger receptor)+(CTLD)2+LDL
98676	X00	not exist	CTLD+Krigle+(Somatomedin B)+(GPCR,family2,secretin-like)
98689	X00	not exist	CTLD+Krigle+(Somatomedin B)+(GPCR,family2,secretin-like)
99375	X00	not exist	CTLD+(EGF)5
79634	X00	not exist	CTLD+(EGF)4
133341	X00	not exist	CTLD
118622	X00	not exist	CTLD
68243	X00	not exist	CTLD+GPS+(CPCR,family2,secretin-like)+(EGF)2+(Hormone receptor,extracellular)
68193	X00	not exist	(Suchi/SCR/CCP)6+EGF+CTLD
68240	X00	not exist	(CPCR,family2,secretin-like)+CTLD
105827	X00	not exist	CTLD+(TypeII fibronectin,collagen+binding)5

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model ID	family	sugar Binding motif	Gene model structure (not curated)
76012	X00	not exist	CTLD
76013	X00	not exist	CTLD
208697	X00X	not exist	CTLD
88190	X00X	not exist	CTLD+EGF
96306	X00X	not exist	CTLD+LDL+CUB+(Sushi/SCR/CCP)4+EGF+(Sushi/SCR/CCP)2
86953	X00X	not exist	CUB+(Frizzled CRD region)+Kringle+(Sushi/SCR/CCP)+(Neurotransmitter-gated ion-channel ligand-binding)+(Neurotransmitter-gated ion-channel transmembrane region)+(Parallel beta-helix repeat)3+(Speract/scavenger receptor)+(Parallel beta-helix repeat)+CUB+(Parallel beta-helix repeat)4+(EGF)2+Cadherin
112262	X00X	not exist	(Cysteine-rich TIL region)
127226	X00X	not exist	(Cystine-rich TIL region)+VWF+CTLD
126292	X00X	not exist	(GMP-PDE,delta subunit)+FA58C+CTLD+(Thrombospondin,type1)+(Plasmodium falciparum CPW-WPC)+CUB+(Thrombospondin,type1)+GPS+(GPCR,family 2,secretin-like)
75156	X00X	not exist	(Beta-ketoacyl synthase)2+(Acy1 transferase region)+SAM+(Zinc-containing alcohol dehydrogenase superfamily)+FA58C+CTLD
107968	X00X	not exist	CTLD
219540	X00X	not exist	CTLD
81633	X00X	not exist	VWF+EGF+(Suchi/SCR/CCP)5+EGF+CTLD
98202	X00X	not exist	LDL+CTLD
105530	X00X	not exist	CTLD+(EGF)3
67706	X00X	not exist	CTLD
90919	X00X	not exist	CTLD+(Nerve growth factor)
94044	X00X	not exist	CTLD
99376	X00X	not exist	CTLD
78440	X00X	not exist	(Beta-Ig-H3/fasciclin)+CTLD
80471	X00X	not exist	CTLD
69468	X00X	not exist	EGF+CTLD+EGF
103902	X00X	not exist	CTLD+EGF
126948	X00X	not exist	CTLD+VWF
84875	X00X	not exist	(Rhodopsin-like GPCR superfamily)+CTLD
88151	X00X	not exist	CTLD+(Neurotransmitter-gated ion-channel ligand-binding)+(Neurotransmitter-gated ion-channel transmembrane region)
89803	X00X	not exist	CTLD+(Neurotransmitter-gated ion-channel ligand-binding)+(Gamma-aminobutyric acid A receptor)
103131	X00X	not exist	NIDO
76059	X00X	not exist	CTLD
118457	unknown	not test	VWF+(Sushi/SCR/CCP)+Hyalin+EGF+CTLD+Pentaxin+EGF+(Sushi/SCR/CP)
88018	unknown	not test	CTLD+EGF+FA58C+CTLD+EGF+PKD+(PKD/REJ-like protein)+GPS+(Lipoxygenase,LH2)+(Polycystic kidney disease type 1 protein)2+(Polycystic kidney disease type 2 protein)+(Ion transport protein)
92136	unknown	not test	CTLD+EGF+FA58C+CTLD+EGF+PKD+(PKD/REJ-like

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model ID	family	sugar Binding motif	Gene model structure (not curated)
			protein)+GPS+(Lipoxygenase,LH2)
63481	unknown	not test	(Collagen triple helix repeat)+CTLD +CTLD
84919	unknown	not test	CTLD+(Rhodopsin-like GPCR superfamily)
118443	unknown	not test	(CTLD)2
87009	unknown	not test	CTLD+(Collagen triple helix repeat)+CTLD
87487	unknown	not test	(Collagen triple helix repeat)+CTLD+(Collagen triple helix repeat)+CTLD
88322	unknown	not test	(CTLD)2
89085	unknown	not test	(CTLD)2
89101	unknown	not test	(CTLD)2
89170	unknown	not test	(CTLD)2+(Zn-finger, C2H2 type)
125701	unknown	not test	(Metridin-like ShK toxin)+EGF+(Metridin-like ShK toxin)+CTLD+(Metridin-like ShK toxin)+EGF+(Metridin-like ShK toxin)+CTLD+(Metridin-like ShK toxin)+EGF+(Metridin-like ShK toxin)
92698	unknown	not test	CTLD+(Sushi/SCR/CCP)+CTLD
72026	unknown	not test	FA58C+CTLD+CTLD
100843	unknown	not test	(CTLD)2
130739	unknown	not test	(Proteinase inhibitor I9,subtilisin propeptide)+CTLD+(Carbohydrate-binding WSC)+CTLD+(Peptidase S8 and S53,subtilisin,kexin,sedolisin)
105900	unknown	not test	(CTLD)2
74841	unknown	not test	(GTP1/0BG)2+(Fucoselectin tachylectin-4 pentraxin-1)+CTLD+CTLD
67478	unknown	not test	EGF+CTLD+(Kringel)+CTLD
87758	unknown	not test	CTLD+EGF+CTLD
89027	unknown	not test	EGF+CTLD+LDL+FA58C+CTLD+FA58C+(LDL)3
125961	unknown	not test	Sulfotransferase+(NHL repeat)+(EGF)2+CTLD
86312	unknown	not test	CUB+CTLD+(Rhodopsin-like GPCR superfamily)
113017	unknown	not test	CTLD+CUB+CTLD
119094	unknown	not test	CTLD+EGF+CTLD+(EGF)2
79635	unknown	not test	CTLD+(EGF)3+CTLD
118208	unknown	not test	(CTLD)2+LDL
107966	unknown	not test	(CTLD)2
108198	unknown	not test	(CTLD)2
67509	unknown	not test	EGF+CTLD+EGF+CTLD+EGF+(Fibronectin, type I)+(Endoglin/CD105 antigen)
68380	unknown	not test	(Suchi/SCR/CCP)+CTLD(Suchi/SCR/CCP)+EGF
67400	unknown	not test	CTLD+CTLD
67406	unknown	not test	CTLD+CTLD+FA58C
85664	unknown	not test	(Speract/scavenger receptor)+CTLD+CUB+(Thrombospondin,type I)
88284	unknown	not test	(CTLD)2+(Fibronectin,typeIII)
90506	unknown	not test	CTLD+(Sushi/SCR/CCP)+(Thrombospondin,typeI)+CTLD+(Sushi/SCR/CCP)+(Neurotransmitter-gated ion-channel transmembrane region)+(Endoglin/CD105 antigen)
93222	unknown	not test	(CTLD)2+LDL+Kringel+(Sushi/SCR/CCP)+(Neurotransmitter-gated ion-channel ligand-binding)+(Neurotransmitter-gated ion-channel transmembrane region)
97333	unknown	not test	CTLD+(Thrombospondin,typeI)+CTLD+(Fibronectin,typeIII)+(Endoglin/CD

CTL models. Family A01-G05 represent different subfamilies; family A-G represent less reliable subfamilies; family X represent the unclassified gene models; family marked unknown represent genes with multiple CTLD, complex structures and problematic gene models.

model ID	family	sugar Binding motif	Gene model structure (not curated)
			105 antigen)
70991	unknown	not test	(N/apple PAN)+LCCL+CTLD+(P-type trefoil)+FA58C+CTLD+(Fibronectin,type)3
92699	unknown	not test	(LDL)2+CTLD+CUB+CTLD
75597	unknown	not test	FA58C+CTLD+CTLD
107967	unknown	not test	(CTLD)2
108196	unknown	not test	(CTLD)2
108197	unknown	not test	(CTLD)2
110148	unknown	not test	FA58C+(CTLD)2+CUB
79948	unknown	not test	CTLD+CTLD
67190	unknown	not test	CTLD+(FA58C)3+CTLD+FA58C+VWF+(Cysteine-rich TIL region)+(Endoglin/CD105 antigen)
67292	unknown	not test	EGF+CTLD
67297	unknown	not test	(EGF)2+CTLD
68621	unknown	not test	LDL+EGF+CTLD+EGF
90415	unknown	not test	VWF+EGF+CTLD+VWF+EGF+CTLD
92276	unknown	not test	(Immunoglobulin subtype)2+CTLD+EGF+CTLD
69398	unknown	not test	EGF+CTLD+(EGF)2+CTLD+EGF
69459	unknown	not test	EGF+CTLD+EGF+CTLD
69462	unknown	not test	(P-type trefoil)+EGF+CTLD+(EGF)2+CTLD+EGF
69463	unknown	not test	EGF+CTLD+(EGF)2+CTLD+EGF
69473	unknown	not test	EGF+CTLD+EGF+CTLD+EGF
101343	unknown	not test	LDL+EGF+CTLD+EGF+CTLD
129759	unknown	not test	EGF+VWF+(Cysteine-rich TIL region)+VWF+(Cysteine-rich TIL region)+VWF+(Cysteine-rich TIL region)+(CTLD)2+VWF+(Cysteine-rich TIL region)+VWF
67519	unknown	not test	(Thrombospondin,type)+CTLD+(Thrombospondin,type)+CTLD
67985	unknown	not test	(TonB box, N-terminal)+CTLD+CTLD+VWF+(Beta-proneller repeat TECPR)5+VWF
91679	unknown	not test	CTLD
92892	unknown	not test	FA58C+Krigle+FA58C+(Fucoselectin tachylectin-4 pentraxin-1)2+Krigle+(Speract/scavenger receptor)+CTLD
127286	unknown	not test	(Frizzled CRD region)+CTLD
129542	unknown	not test	MAM+(Frizzled CRD region)+MAM+CTLD
129573	unknown	not test	CTLD+(FA58C)2+CTLD
130115	unknown	not test	CTLD+FA58C+CTLD
106125	unknown	not test	(Membrane attack complex component/perforin/complement C9)+CTLD+FA58C+CTLD
109700	unknown	not test	(CTLD)2
70176	unknown	not test	(Aldo/keto reductase)+CTLD+EGF+CTLD+EGF+(G-protein beta WD-40 repeat)2
83478	unknown	not test	(Leucine-rich repeat)2+CTLD+(Peptidase M12A,astacin)+(Pentaxin)+ CTLD
98614	unknown	not test	(CTLD)2+LDL
118375	unknown	not test	(Apple-like)3+(Sushi/SCR/CCP)+(CTLD)2
125304	unknown	not test	(Thrombospondin,type1)+Krigle+CTLD+MAM+(CTLD)3+EGF+(PKD/REJ

CTL models. Family A01-G05 represent different subfamilies; family A-G represent less reliable subfamilies; family X represent the unclassified gene models; family marked unknown represent genes with multiple CTLD, complex structures and problematic gene models.

model ID	family	sugar Binding motif	Gene model structure (not curated)
68569	unknown	not test	-like protein)+GPS+(Lipoxygenase,LH2)+(Ion transport protein) (Thrombospondin,type)+(Kringle)+CTLD+EGF+MAM+CTLD+SEA+EGF+(PKD/REJ-like calcium-binding)+GPS+(Lipoxygenase,LH2)+(Cation (non K+) channel, TM region)+(IQ calmodulin-binding region)+(Leucine-rich repeat)+(Cation (non K+) channel, TM region)
82587	unknown	not test	CTLD+CTLD+CTLD
67129	unknown	not test	CTLD+CTLD+CTLD+CUB
87486	unknown	not test	(Collagen triple helix repeat)+(CTLD)2+(Collagen triple helix repeat)+CTLD+(Collagen triple helix repeat)+CTLD+(Collagen triple helix repeat)+CTLD
125166	unknown	not test	(CTLD)2+CUB+(Protease-associated PA)+(Peptidase M28)+(Transferrin receptor-like dimerisation region)
88291	unknown	not test	(CTLD)2+CUB+Sulfatase
89102	unknown	not test	(CTLD)3
89120	unknown	not test	(CTLD)2
97544	unknown	not test	(Collagen triple helix repeat)2+CTLD+(Collagen triple helix repeat)+CTLD+(Collagen triple helix repeat)+CTLD
80710	unknown	not test	(Leucine-rich repeat)+(Cysteine-rich flanking region, C-terminal)+(Suchi/SCR/CCP)+CTLD+(Leucine-rich repeat)2+(Cysteine-rich flanking region, C-terminal)+(Suchi/SCR/CCP)+CTLD
85621	unknown	not test	CTLD+CUB+(Kringle)
132727	unknown	not test	CTLD+FA58C+(CTLD)2+FA58C+CTLD+(D-galactoside/L-rhamnose binding SUEL lectin)+FA58C+LCCL+(CTLD)3
66146	unknown	not test	CTLD +(D-galactoside/L-rhamnose binding SUEL lectin)+FA58C+LCCL+CTLD +CTLD +CTLD +CTLD +CTLD +CTLD+CTLD
80311	unknown	not test	CTLD+CTLD+FA58C+CTLD+CTLD+(D-galactoside/L-rhamnose binding SUEL lectin)+FA58C+CTLD+CTLD+CTLD+CTLD+CTLD+CTLD+CTLD+CTLD
80319	unknown	not test	CTLD+CTLD+FA58C+CTLD+CTLD+(D-galactoside/L-rhamnose binding SUEL lectin)+CTLD+CTLD+CTLD+(Pentaxin)+CTLD
90412	unknown	not test	CTLD+VWF+EGF+CTLD
69088	unknown	not test	(Beta-propeller repeat TECPR)+FA58C+CTLD+VWF+CTLD+CTLD+VWF
83982	unknown	not test	CTLD+EGF+CTLD+EGF+CTLD+EGF+(Fibronectin,type) +(Endoglin/CD105 antigen)
83984	unknown	not test	FA58C+EGF+CTLD+EGF+CTLD+EGF+CTLD+EGF+CTLD+EGF+CTLD+ (EGF)3+(Fibronectin,type) +(Endoglin/CD105 antigen)
67468	unknown	not test	CTLD+CTLD+CTLD+CTLD
90416	unknown	not test	EGF+VWF+(Cysteine-rich TIL region)+CTLD+VWF+(Cysteine-rich TIL region)+(CTLD)2+VWF+CTLD+EGF+VWF+(Cysteine-rich TIL region)+CTLD+EGF+VWF+EGF+CTLD+VWF+(Cysteine-rich TIL region)+CTLD+(Cysteine-rich TIL region)+CTLD
69469	unknown	not test	EGF+CTLD+EGF+CTLD+EGF+CTLD+EGF
101341	unknown	not test	LDL+(EGF)3+CTLD+LDL+EGF+(CTLD)2

CTL models. Family A01-G05 represent different subfamilies; family A-G represent less reliable subfamilies; family X represent the unclassified gene models; family marked unknown represent genes with multiple CTLD, complex structures and problematic gene models.

model ID	family	sugar Binding motif	Gene model structure (not curated)
83031	unknown	not test	FA58C+CTLD+CTLD+FA58C+Kringe+CTLD+(Immunoglobulin-like)
68195	unknown	not test	CTLD+CTLD+SEA+(Suchi/SCR/CCP)6
69086	unknown	not test	CTLD+CTLD+CTLD+(Carbohydrate-binding WSC)+FA58C+CTLD+(Carbohydrate-binding WSC)+(Beta-propeller repeat TECPR)3+FA58C+CTLD
100740	unknown	not test	EGF+CTLD+(EGF)2+CTLD+EGF+CTLD+EGF
92896	unknown	not test	CTLD+Kringe+(FA58C)3+(N/apple PAN)+CTLD+(Fucoselectin tachylectin-4 pentraxin-1)+CTLD
67104	unknown	not test	LDL+CTLD+LDL
67305	unknown	not test	CTLD
79417	unknown	not test	/
80809	unknown	not test	(Type antifreeze protein)
93172	unknown	not test	CTLD
106427	unknown	not test	CTLD
106523	unknown	not test	CTLD
112742	unknown	not test	
112971	unknown	not test	(Collagen triple helix repeat)+CTLD
112998	unknown	not test	Kringe+CTLD
161421	unknown	not test	CTLD
171522	unknown	not test	CTLD
216155	unknown	not test	CTLD
216240	unknown	not test	CTLD
228966	unknown	not test	CTLD
246577	unknown	not test	CTLD
65280	unknown	not test	
70487	unknown	not test	CTLD
82498	unknown	not test	
88385	unknown	not test	CTLD
88387	unknown	not test	CTLD
91544	unknown	not test	(Collagen triple helix repeat)
91678	unknown	not test	CTLD+(D-galactoside/L-rhamnose binding SUEL lectin)
109335	unknown	not test	CTLD
204647	unknown	not test	CTLD
205253	unknown	not test	CTLD
234547	unknown	not test	CTLD
251545	unknown	not test	CTLD
103428	unknown	not test	
151120	unknown	not test	
68774	unknown	not test	CTLD+(Suchi/SCR/CCP)12
69300	unknown	not test	EGF
70628	unknown	not test	CTLD
75530	unknown	not test	(Proprotein convertase,P)+(Peptidase S8 and S53,subtilisin,kexin,sedolisin)+(Proprotein convertase,P)
76426	unknown	not test	CTLD
79558	unknown	not test	CTLD

CTL models. Family A01-G05 represent different subfamilies; family A-G represent less reliable subfamilies; family X represent the unclassified gene models; family marked unknown represent genes with multiple CTLD, complex structures and problematic gene models.

model ID	family	sugar Binding motif	Gene model structure (not curated)
80587	unknown	not test	EGF
83869	unknown	not test	CTLD
92274	unknown	not test	CTLD+(ABC transporter)+(ABC transporter, transmembrane region)+(ABC transporter)
92780	unknown	not test	(Pentaxin)+CTLD
96590	unknown	not test	(Peptidase S1,chymotrypsin)
96592	unknown	not test	
100171	unknown	not test	CTLD
100988	unknown	not test	EGF
107722	unknown	not test	CTLD
108819	unknown	not test	
110805	unknown	not test	
142469	unknown	not test	CTLD
151872	unknown	not test	CTLD
205231	unknown	not test	CTLD
85544	unknown	not test	
85545	unknown	not test	
86703	unknown	not test	CTLD
89369	unknown	not test	CTLD
109763	unknown	not test	FA58C+CTLD
112834	unknown	not test	(EGF)6
124245	unknown	not test	
66602	unknown	not test	CTLD
81941	unknown	not test	CTLD
97331	unknown	not test	(D-galactoside/L-rhamnose binding SUEL lectin)+(Thrombospondin,type2)4+CTLD
100367	unknown	not test	
178185	unknown	not test	
189415	unknown	not test	CTLD
66624	unknown	not test	(Glutaredoxin)+(Glutathione S-transferase, C-terminal)
93640	unknown	not test	
95998	unknown	not test	FA58C+Kringle+CTLD
97819	unknown	not test	
121102	unknown	not test	FA58C+(N/apple PAN)+CTLD
96235	unknown	not test	CUB
96574	unknown	not test	(Zinc transporter ZIP)
95237	unknown	not test	
86697	unknown	not test	(Thrombospondin,type)
117181	unknown	not test	
108241	unknown	not test	
64428	unknown	not test	CTLD
64900	unknown	not test	(Plexin)+EGF+(Cadherin)3
65264	unknown	not test	LDL+CUB
68317	unknown	not test	CTLD+(EGF)2+(Thrombospondin type3 repeat)6+(Thrombospondin terminal)
68706	unknown	not test	EGF+CTLD

CTL models. Family A01-G05 represent different subfamilies; family A-G represent less reliable subfamilies; family X represent the unclassified gene models; family marked unknown represent genes with multiple CTLD, complex structures and problematic gene models.

model ID	family	sugar Binding motif	Gene model structure (not curated)
68707	unknown	not test	(EGF)2+CTLD
80821	unknown	not test	(EGF)5+CTLD
81157	unknown	not test	CTLD
85314	unknown	not test	FA58C+(kringle)
97687	unknown	not test	(EGF)2+(TypeII antifreeze protein)
101415	unknown	not test	EGF+CTLD
123130	unknown	not test	(Ricin B lectin)+(Doublecortin)2+FA58C+CTLD+(Sushi/SCR/CCP)+EGF+(Thrombos pondin,type I)+(Neurotransmitter-gated ion+channel transmembrane region)
234637	unknown	not test	CTLD
246131	unknown	not test	(EGF)2+CTLD
88397	unknown	not test	FA58C
67600	unknown	not test	(Membrane attack complex component/perforin/complement C9)+EGF+(Speract/scavenger receptor)+CTLD
68309	unknown	not test	CTLD+(EGF)2+(Thrombospondin type3 repeat)8+(Thrombospondin terminal)
71652	unknown	not test	EGF+CTLD
85329	unknown	not test	EGF+CTLD
90586	unknown	not test	(Membrane attack complex component/perforin/complement C9)+FA58C+(Speract/scavenger receptor)2+Kringlet+CTLD
101114	unknown	not test	Kringlet+CTLD
109991	unknown	not test	CTLD+(Neurotransmitter-gated ion-channel)
111615	unknown	not test	FA58C
125198	unknown	not test	LCCL+FA58C+EGF
129474	unknown	not test	
129834	unknown	not test	(Carbonic anhydrase, eukaryotic)+CTLD
131810	unknown	not test	CTLD+(Peptidase S8 and S53,subtilisin,kexin,sedolisin)
71152	unknown	not test	(TPR repeat)+CUB+(Beta-propeller repeat TECPR)2+(LDL)2+CTLD+CUB+CTLD
81921	unknown	not test	(EGF)3+CTLD
88195	unknown	not test	(Carbohydrate-binding WSC)+CTLD+(Beta-propeller repeat TECPR)3+VWF+(Cysteine-rich TIL region)+(Beta-propeller repeat TECPR)4+VWF
88364	unknown	not test	(CUB)2+(Beta-propeller repeat TECPR)2+(LDL)5+FA58C+CTLD+(CUB)2
88408	unknown	not test	(TPR repeat)5+CUB+(Beta-propeller repeat TECPR)+(LDL)2+CTLD+CUB+CTLD
67060	unknown	not test	(TonB box, N-terminal)+CTLD
67120	unknown	not test	(FA58C)2+CTLD
67454	unknown	not test	EGF+CTLD
68036	unknown	not test	FA58C+(Kringlet)+CTLD
68394	unknown	not test	CTLD+(Suchi/SCR/CCP)12
68395	unknown	not test	(Suchi/SCR/CCP)7+EGF
68804	unknown	not test	(Cadherin)+(Nidogen,extracellular region)+AMOP+VWF+CTLD
68926	unknown	not test	(Pentaxin)+CTLD
69402	unknown	not test	(EGF)4
69464	unknown	not test	EGF+CTLD+EGF

CTL models. Family A01-G05 represent different subfamilies; family A-G represent less reliable subfamilies; family X represent the unclassified gene models; family marked unknown represent genes with multiple CTLD, complex structures and problematic gene models.

model ID	family	sugar Binding motif	Gene model structure (not curated)
70527	unknown	not test	(Ribosomal protein)
75553	unknown	not test	CTLD+FA58C
81788	unknown	not test	(Leucine-rich repeat)+(Suchi/SCR/CCP)2
85071	unknown	not test	(Peptidase M12B,ADAM/reprolysin+Disintegrin)+(Kringle)+(Carbohydrate-binding WSC)+CTLD
87344	unknown	not test	VWF+CTLD+(VWF)2
87876	unknown	not test	(EGF)2
87886	unknown	not test	(EGF)3
90595	unknown	not test	(EGF)3+CTLD+EGF
96115	unknown	not test	(EGF)2+CTLD+EGF
98740	unknown	not test	CTLD+EGF
99249	unknown	not test	
100559	unknown	not test	(N/apple PAN)+EGF+CTLD
105130	unknown	not test	NIDO
107165	unknown	not test	(Sushi/SCR/CCP)2
118576	unknown	not test	EGF+CTLD
122977	unknown	not test	(Sushi/SCR/CCP)
125245	unknown	not test	MAM+(Speract/scavenger receptor)+(MAM)2+(Thrombospondin,subtype1)+(Immunoglobulin-like)+(G TP-binding protein SAR1)
125377	unknown	not test	(Eukaryotic translation initiation factor 4E)+(Speract/scavenger receptor)+EGF+CTLD+EGF+(Pyridoxal-5'-phosphate-dependent enzyme, beta subunit)
125867	unknown	not test	(Importin-beta, N-terminal)+EGF+CTLD
126258	unknown	not test	EGF+CTLD+EGF
131641	unknown	not test	(Sushi/SCR/CCP)
133444	unknown	not test	(Sushi/SCR/CCP)2+EGF+CTLD
189520	unknown	not test	CTLD
258173	unknown	not test	CTLD
63486	unknown	not test	(Myb,DNA-binding)+(phospholipase A2)
76950	unknown	not test	EGF+CUB
84589	unknown	not test	(Speract/scavenger receptor)+(Parallel beta-helix repeat)4+(Speract/scavenger receptor)+(Parallel beta-helix repeat)4+(Speract/scavenger receptor)+(Parallel beta-helix repeat)+MAM+(Parallel beta-helix repeat)2+CTLD+EGF+Plenxin+EGF+VWF+EGF+(Cadherin)
86521	unknown	not test	(Animal haem peroxidase)+EGF
88285	unknown	not test	(FA58C)2+CTLD
94043	unknown	not test	
99251	unknown	not test	EGF
100742	unknown	not test	(EGF)2+CTLD
109987	unknown	not test	FA58C+EGF
111362	unknown	not test	
124134	unknown	not test	(Pleckstrin-like)+(RepA/Rep+ protein KID)5
129334	unknown	not test	(Carbonic anhydrase, eukaryotic)

CTL models. Family A01-G05 represent different subfamilies; family A-G represent less reliable subfamilies; family X represent the unclassified gene models; family marked unknown represent genes with multiple CTLD, complex structures and problematic gene models.

model ID	family	sugar Binding motif	Gene model structure (not curated)
72968	unknown	not test	VWF+(Cysteine-rich TIL region)+EGF+(VWC out)+EGF+(VWF)2+CTLD
81597	unknown	not test	CTLD+(EGF)2
84342	unknown	not test	(Fibrinogen, beta/gamma chain, C-terminal globular)+EGF+GPS+(Lipoxygenase,LH2)+(Polycystic kidney disease type 1 protein)2+(Polycystic kidney disease type 2 protein)+(Ion transport protein)
93534	unknown	not test	EGF
107054	unknown	not test	LCCL+FA58C+Link+(P-type trefoil)+(Fucoselectin tachylectin-4 pentraxin-1)+(Fibronectin,typeIII)
88566	unknown	not test	(Thrombospondin,typeI)+CTLD+(VWF)2
90526	unknown	not test	CTLD+(Sushi/SCR/CCP)+(Thrombospondin,typeI)+(Gamma-aminobutyric acid A receptor)
112840	unknown	not test	(Sushi/SCR/CCP)4
120397	unknown	not test	(Amine oxidase)
219852	unknown	not test	CTLD
110163	unknown	not test	(Calcium-translocating P-type ATPase,PMCA-type)
110188	unknown	not test	
86168	unknown	not test	(Leucine-rich repeat)
68703	unknown	not test	
70116	unknown	not test	CTLD+GPS+(Lipoxygenase,LH2)+(Ion transport protein)+(PKD/REJ-like protein)+GPS+(Lipoxygenase,LH2)+(Ion transport protein)
83186	unknown	not test	LDL+EGF
95238	unknown	not test	(PKD/REJ-like protein)+GPS+(Lipoxygenase,LH2)+(Polycystic kidney disease type 2 protein)+(Ion transport protein)
111088	unknown	not test	(Zn-finger,MYNO type)
80820	unknown	not test	
69475	unknown	not test	(Leucine-rich repeat)2+(Cysteine-rich flanking region, C-terminal)+(Immunoglobulin-like)+(EGF)2
90592	unknown	not test	(EGF)4
72090	unknown	not test	
102074	unknown	not test	
87375	unknown	not test	CTLD+EGF+CTLD
92210	unknown	not test	CTLD+(Collagen triple helix repeat)+CTLD
70648	unknown	not test	CTLD
88258	unknown	not test	EGF
67996	unknown	not test	(EGF)4+CTLD+EGF+(Follistatin-like,N-terminal)
92278	unknown	not test	CTLD+(FA48C)2+CTLD
118467	unknown	not test	(Peptidase M10A and M12B, matrixin and adamalysin)+(Peptidase, metallopeptidases)+(Hemopexin)+(Major facilitator superfamily)+CTLD
92287	unknown	not test	(Sushi/SCR/CCP)3+CTLD+(Sushi/SCR/CCP)4+CTLD
80237	unknown	not test	CTLD
105894	unknown	not test	CTLD

6 Scavenger receptor Gene models (CD36 and receptor containing SRCR domain)

CD36 and Receptor containing SRCR domains		
Model ID	Type	Transmembrane Topology (i=cytoplasmic, o=extracellular)
126670	CD36	
125946	CD36	
125924	CD36	
119088	CD36	
69447	CD36	
69445	CD36	
85274	SRCR	Topology=o739-761i
84297	SRCR	Topology=o2552-2574i2613-2631o2651-2673i2716-2738o2758-2780i2862-2884o3048-3070i3091-3113o3142-3161i3182-3204o3244-3266i
124580	SRCR	
82606	SRCR	
86431	SRCR	Topology=i24-46o
113170	SRCR	
92892	SRCR	
111228	SRCR	
90586	SRCR	
86433	SRCR	Topology=i29-51o
112943	SRCR	
68925	SRCR	
87114	SRCR	
91305	SRCR	
63812	SRCR	Topology=o1259-1281i
87220	SRCR	Topology=o512-534i
86426	SRCR	Topology=i29-51o1089-1111i
217630	SRCR	
85664	SRCR	
125377	SRCR	
92788	SRCR	
257492	SRCR	
62947	SRCR	
219663	SRCR	
111230	SRCR	
251656	SRCR	
224545	SRCR	
172661	SRCR	
152015	SRCR	
231213	SRCR	
162804	SRCR	
151101	SRCR	
126230	SRCR	
213459	SRCR	
113105	SRCR	
230072	SRCR	
215815	SRCR	
124846	SRCR	Topology=o1098-1120i

CD36 and Receptor containing SRCR domains		
Model ID	Type	Transmembrane Topology (i=cytoplasmic, o=extracellular)
86397	SRCR	
234302	SRCR	
230523	SRCR	
86428	SRCR	Topology=i29-51o
201095	SRCR	
68917	SRCR	
68915	SRCR	
228377	SRCR	
157554	SRCR	
120140	SRCR	
258288	SRCR	
74849	SRCR	
228339	SRCR	
121741	SRCR	Topology=o2229-2251i
68921	SRCR	
162766	SRCR	
125180	SRCR	Topology=o614-636i
240866	SRCR	
88804	SRCR	
209249	SRCR	
235225	SRCR	
235212	SRCR	
228446	SRCR	
152914	SRCR	
236530	SRCR	
140421	SRCR	
130619	SRCR	Topology=i7-29o1858-1880i
125512	SRCR	
124847	SRCR	Topology=i9-31o
113270	SRCR	Topology=o596-618i
94923	SRCR	Topology=o247-269i
92784	SRCR	
69406	SRCR	
243719	SRCR	
209271	SRCR	
215951	SRCR	
124606	SRCR	
205893	SRCR	
77850	SRCR	
77841	SRCR	
205587	SRCR	
251434	SRCR	
228337	SRCR	
212352	SRCR	
212283	SRCR	
124845	SRCR	

CD36 and Receptor containing SRCR domains		
Model ID	Type	Transmembrane Topology (i=cytoplasmic, o=extracellular)
92794	SRCR	
90049	SRCR	Topology=i329-351o366-388i401-418o448-470i475-497o2014-2036i2057-2079o2094-2116i2177-2194o2418-2440i2453-2475o2500-2522i2543-2565o2575-2594i2601-2623o
65355	SRCR	
240732	SRCR	
236048	SRCR	
228316	SRCR	
258286	SRCR	
241480	SRCR	
236008	SRCR	
120139	SRCR	Topology=o908-930i
157226	SRCR	
77852	SRCR	
92782	SRCR	
92363	SRCR	
67600	SRCR	
222222	SRCR	
190827	SRCR	
180201	SRCR	
92536	SRCR	
92361	SRCR	
290203	SRCR	
162753	SRCR	
67122	SRCR	Topology=o672-694i
66950	SRCR	Topology=i13-35o
124605	SRCR	
80207	SRCR	
233525	SRCR	
88806	SRCR	
222346	SRCR	
222111	SRCR	
259361	SRCR	
244335	SRCR	
240740	SRCR	
231739	SRCR	
222143	SRCR	
222135	SRCR	
72389	SRCR	
258018	SRCR	
244336	SRCR	
236208	SRCR	
229164	SRCR	
213732	SRCR	
161365	SRCR	
155318	SRCR	
222064	SRCR	

CD36 and Receptor containing SRCR domains		
Model ID	Type	Transmembrane Topology (i=cytoplasmic, o=extracellular)
215966	SRCR	
221693	SRCR	
112429	SRCR	
259060	SRCR	
229025	SRCR	
222206	SRCR	
241741	SRCR	
213688	SRCR	
199915	SRCR	
244328	SRCR	
259056	SRCR	
229189	SRCR	
162243	SRCR	
153045	SRCR	
87192	SRCR	
160842	SRCR	
240741	SRCR	
215830	SRCR	
155098	SRCR	
245835	SRCR	
242958	SRCR	
218205	SRCR	
145966	SRCR	
222178	SRCR	
258021	SRCR	
241102	SRCR	
84589	SRCR	Topology=o4661-4683i
243348	SRCR	
153041	SRCR	
233056	SRCR	
220336	SRCR	
112726	SRCR	
85354	SRCR	Topology=o622-644i
251944	SRCR	
251270	SRCR	
218007	SRCR	
92776	SRCR	
86444	SRCR	
228931	SRCR	
249635	SRCR	
257879	SRCR	
88807	SRCR	
209911	SRCR	
222136	SRCR	
157797	SRCR	
249625	SRCR	

CD36 and Receptor containing SRCR domains		
Model ID	Type	Transmembrane Topology (i=cytoplasmic, o=extracellular)
225847	SRCR	
242035	SRCR	
222060	SRCR	
218145	SRCR	
212061	SRCR	
172473	SRCR	
159063	SRCR	
209265	SRCR	
217976	SRCR	
160810	SRCR	
107492	SRCR	
162577	SRCR	
258024	SRCR	
259049	SRCR	
218428	SRCR	
152446	SRCR	
251316	SRCR	
212331	SRCR	
138861	SRCR	
153126	SRCR	
208393	SRCR	
190876	SRCR	
125245	SRCR	
94530	SRCR	
86446	SRCR	
221774	SRCR	
218082	SRCR	
161692	SRCR	
235436	SRCR	
87043	SRCR	Topology=o731-753i923-940o
244386	SRCR	
229159	SRCR	
117208	SRCR	
89612	SRCR	
118449	SRCR	
190848	SRCR	
190849	SRCR	
99338	SRCR	Topology=o671-693i
162286	SRCR	
85063	SRCR	Topology=o356-378i
258350	SRCR	
227745	SRCR	
104581	SRCR	Topology=o356-378i
228987	SRCR	
86953	SRCR	Topology=o672-694i701-723o733-755i768-787o3911-3933i
124090	SRCR	Topology=o394-416i

CD36 and Receptor containing SRCR domains		
Model ID	Type	Transmembrane Topology (i=cytoplasmic, o=extracellular)
233250	SRCR	
180233	SRCR	
228964	SRCR	
88356	SRCR	
112799	SRCR	
219135	SRCR	
99337	SRCR	
218480	SRCR	
89541	SRCR	Topology=o650-672i
271527	SRCR	
85621	SRCR	Topology=i52-74o568-590i597-614o2413-2432i
66952	SRCR	Topology=i32-54o
86956	SRCR	Topology=o4-23i264-286o301-323i344-366o
215906	SRCR	
235236	SRCR	
83012	SRCR	
255517	SRCR	
128313	SRCR	
112525	SRCR	
83541	SRCR	Topology=i66-88o328-350i479-501o
83542	SRCR	Topology=o192-214i617-639o1269-1291i
88357	SRCR	Topology=i7-29o580-602i
112524	SRCR	
112523	SRCR	
109937	SRCR	Topology=o40-62i261-283o1120-1142i
92894	SRCR	
68750	SRCR	Topology=i5-24o
64474	SRCR	Topology=i5-24o
79362	SRCR	Topology=o525-547i
68749	SRCR	Topology=i7-29o
79413	SRCR	Topology=o564-586i
64471	SRCR	
68748	SRCR	
79370	SRCR	Topology=o629-651i
68751	SRCR	Topology=i5-27o
79411	SRCR	Topology=o526-548i
64475	SRCR	Topology=i5-27o
103884	SRCR	Topology=o1003-1025i
79412	SRCR	Topology=o646-668i
79051	SRCR	Topology=o1087-1109i
79425	SRCR	Topology=o507-529i
79052	SRCR	
79191	SRCR	Topology=o564-586i
87352	SRCR	Topology=o570-592i
79395	SRCR	Topology=o1008-1030i
79394	SRCR	Topology=o603-625i

CD36 and Receptor containing SRCR domains

Model ID	Type	Transmembrane Topology (i=cytoplasmic, o=extracellular)
69486	SRCR	
102977	SRCR	Topology=i40-62o
79371	SRCR	Topology=o470-492i

7 Gene models of RIG-I-like helicases (RLH), GNBP and PGRP.

Model ID	Type	Curated structure
76000	RLH	DED+DEAD+HELLc
93013	RLH	DEATH+DEAD+HELLc
93024	RLH	unpredictedDEATH+DEAD+HELLc
102701	RLH	unpredictedCARD+TIR+DEAD+HELLc
102703	RLH	unpredictedCARD+TIR+DEAD+HELLc
102704	RLH	unpredictedCARD+TIR+DEAD+HELLc
106572	RLH	unpredictedCARD+TIR+DEAD+HELLc
108575	RLH	DED+DEAD+HELLc
110298	RLH	weakCARD+DEAD+HELLc, card similar to card of MDA5
145021	RLH	unpredictedCARD+TIR+DEAD+HELLc
235564	RLH	weakCARD+DEAD+HELLc, card similar to card of MDA5
249506	RLH	unpredictedCARD+TIR+DEAD+HELLc
249510	RLH	unpredictedCARD+TIR+DEAD+HELLc
73944	GNBP	
91243	GNBP	
131449	GNBP	
105027	GNBP	
65842	GNBP	
101548	GNBP	
121315	GNBP	
130991	GNBP	
121314	GNBP	
118718	PGRP	
170705	PGRP	
255561	PGRP	
170081	PGRP	
93285	PGRP	
255551	PGRP	
234035	PGRP	
208603	PGRP	
76871	PGRP	
84404	PGRP	
218247	PGRP	
98442	PGRP	
289080	PGRP	
92716	PGRP	
170930	PGRP	
151022	PGRP	
286842	PGRP	
92775	PGRP	
285125	PGRP	
216728	PGRP	
76882	PGRP	
76866	PGRP	
76867	PGRP	
76868	PGRP	

8 Gene models encoding the genes of the complement system.

The complement system		
Model ID	Type	Annotation and curated structure
Complement related serine protease gene models		
125322	Bf1	CCP+CCP+VWA+Tryp_SPc
76225	Bf3	CCP+CCP+VWA+Tryp_SPc+Tryp_SPc
125323	Bf2	CTLD+Apple+CCP+FIMAC+CCP+CCP+VWA+Tryp_SPc
103299	Bf-like?	
91518	MASP3	MASP1/3,CUB+EGF+CUB+CCP+CCP+Tryp_SPc
109713	MASP3	MASP1/3,CUB+EGF+CUB+CCP+CCP+Tryp_SPc
126297	MASP1	MASP1/3,CUB+EGF+CUB+CCP+CCP+Tryp_SPc
132458	MASP1	MASP1/3,CUB+EGF+CUB+CCP+CCP+Tryp_SPc
288621	MASP-A	EGF+(CCP)5+Tryp_SPc, similar to coagulation factor
75995	MASP-A	EGF+(CCP)6+Tryp_SPc, similar to coagulation factor
118458		EGF+CCP+IG+Tryp_SPc+SR
84099		CUB+Kringle+Tryp_SPc
84108		_CUB_
84107		_CUB_
123416		CUB+CUB+LDLa+Tryp_SPc
123741		_CUB_
123417		_CUB_
123740		_CUB_
123742		_CUB_
119701		_CUB_
261914		_CUB_
84096		_CUB_
84097		CUB+Tryp_SPc
263105		_CUB_
267281		_CUB_
84106		_CUB_
125352		Chitin+CCP+Tryp_SPc
120051		Chitin+CCP+Tryp_SPc
118633		_CUB_
83281		_CUB_
132269		_CUB_

The complement system

Model ID	Type	Annotation and curated structure
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Thioester containing, including C3/C4/C5-like,CD109,A2M

132771		amphiC3
129974		amphiC3
127891		between C3/C4/C5 and A2M/CD109
96214		between C3/C4/C5 and A2M/CD109
120995		CD109
101769		between CD109 and A2M
129822		between CD109 and A2M
122130		alpha-2-macroglobulin, A2M
219323		alpha-2-macroglobulin, A2M
108991		alpha-2-macroglobulin, A2M
108989		partial
108989		partial
122003		partial
62661		partial

C6/C7/C8/C9-like

134616	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
105963	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
102289	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
81773	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
110173	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
81766	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
65208	_C6L	LDLa+MACPF+EGF
76018	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1

other gene models containing FIMAC domains

133398		Apple+CCP+FIMAC
88767		IG+CCP+FIMAC
118439		(FIMAC) _n +EGF+(TSP1) ₃
125323		

The complement system

Model ID	Type	Annotation and curated structure
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C1q-like gene models

68090		COL__,in one exon
68456		COL__,in one exon
69113		COL__,in one exon
69125		COL__,in one exon
69126		COL__,
69127		COL__,in one exon
69129		COL__,in one exon
69134		COL__,in one exon
69135		COL__,in one exon
69136		COL__,in one exon
69137		COL__,in one exon
69138		COL__,in one exon
69139		COL__,in one exon
69140		COL__,in one exon
69141		COL__,
69142		COL__,in one exon
69143		COL__,in one exon
69147		COL__,in one exon
69148		COL__,in one exon
69149		COL__,in one exon
69150		COL__,in one exon
69151		COL__,in one exon
69152		COL__,in one exon
69153		COL__,in one exon
69154		COL__,in one exon
69155		COL__,in one exon
69156		COL__,in one exon
72886		,
79363		,
79372		COL__,
79375		COL__,
79378		COL__,
81688		COL__,in one exon
84170		COL__,in one exon
84276		COL__,in one exon
86729		COL__,in one exon
89395		COL__,in one exon
89759		COL__,in one exon
89760		COL__,in one exon
89761		COL__,in one exon
91625		COL__,in one exon
93307		COL__,in one exon
95714		,
101063		COL__,in one exon
102732		COL__,in one exon

The complement system

Model ID	Type	Annotation and curated structure
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C1q-like gene models

104278		COL_ ₁ in one exon
104351		,
104352		,
107144		COL_ ₁ ,
118898		COL_ ₁ in one exon
118972		COL_ ₁ in one exon
121448		,
121453		COL_ ₁ ,
122828		,
122833		,
124212		COL_ ₁ in one exon
125147		,
170045		,
206566		,
206639		,
210338		,
211311		COL_ ₁ in one exon
227079		COL_ ₁ unpredictedCOL
230795		COL_ ₁ unpredictedCOL
236777		COL_ ₁ ,
237147		COL_ ₁ in one exon
242807		COL_ ₁ ,
243622		COL_ ₁ in one exon
249796		COL_ ₁ in one exon
252103		COL_ ₁ ,
252230		,
255268		COL_ ₁ in one exon
255281		COL_ ₁ in one exon
255306		COL_ ₁ ,
275395		COL_ ₁ in one exon

The complement system

Model ID	Type	Annotation and curated structure
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Fibrinogen-containing gene models, including Ficolin-like

104277		family_FCN-A,unpredictedCOL_
148190		family_FCN-A,unpredictedCOL_
209224		family_FCN-A,unpredictedCOL_
228338		family_FCN-A,unpredictedCOL_
228378		family_FCN-A,unpredictedCOL_
228425		family_FCN-A,unpredictedCOL_
228454		family_FCN-A,unpredictedCOL_
228471		family_FCN-A,unpredictedCOL_
243239		family_FCN-A,unpredictedCOL_
254661		family_FCN-A,unpredictedCOL_
86425		family_FCN-A,COL_
86426		family_FCN-A,COL_
86431		family_FCN-A,COL_
86433		family_FCN-A,COL_
224984		family_FCN-A,COL_
57693		family_FCN-A,
62198		family_FCN-A,
77841		family_FCN-A,
77850		family_FCN-A,
77852		family_FCN-A,
77854		family_FCN-A,
80212		family_FCN-A,
83845		family_FCN-A,
86428		family_FCN-A,
86430		family_FCN-A,
89086		family_FCN-A,
94499		family_FCN-A,
96239		family_FCN-A,
167976		family_FCN-A,
217989		family_FCN-A,
218135		family_FCN-A,
218195		family_FCN-A,
218208		family_FCN-A,
221767		family_FCN-A,
222098		family_FCN-A,
222114		family_FCN-A,
222116		family_FCN-A,
222151		family_FCN-A,
222155		family_FCN-A,
222217		family_FCN-A,
222221		family_FCN-A,
222229		family_FCN-A,
222257		family_FCN-A,
222276		family_FCN-A,
222322		family_FCN-A,

The complement system

Model ID	Type	Annotation and curated structure
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Fibrinogen-containing gene models, including Ficolin-like

222343	family_FCN-A,
222351	family_FCN-A,
228347	family_FCN-A,
228373	family_FCN-A,
228416	family_FCN-A,
228421	family_FCN-A,
228426	family_FCN-A,
228436	family_FCN-A,
228479	family_FCN-A,
228481	family_FCN-A,
231341	family_FCN-A,
231428	family_FCN-A,
231434	family_FCN-A,
231703	family_FCN-A,
233139	family_FCN-A,
241745	family_FCN-A,
242967	family_FCN-A,
245662	family_FCN-A,
59778	family_FCN-B,unpredictedCOL_
83487	family_FCN-B,unpredictedCOL_
107377	family_FCN-B,unpredictedCOL_
199730	family_FCN-B,unpredictedCOL_
199923	family_FCN-B,unpredictedCOL_
233138	family_FCN-B,unpredictedCOL_
233969	family_FCN-B,unpredictedCOL_
234037	family_FCN-B,unpredictedCOL_
234065	family_FCN-B,unpredictedCOL_
234077	family_FCN-B,unpredictedCOL_
239520	family_FCN-B,unpredictedCOL_
257844	family_FCN-B,unpredictedCOL_
257848	family_FCN-B,unpredictedCOL_
67810	family_FCN-B,COL_
67811	family_FCN-B,COL_
67813	family_FCN-B,COL_
67814	family_FCN-B,COL_
67816	family_FCN-B,COL_
67819	family_FCN-B,COL_
67820	family_FCN-B,COL_
67822	family_FCN-B,COL_
83490	family_FCN-B,COL_
97821	family_FCN-B,COL_
112632	family_FCN-B,COL_
112633	family_FCN-B,COL_
123506	family_FCN-B,COL_
67719	family_FCN-B,

The complement system

Model ID	Type	Annotation and curated structure
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Fibrinogen-containing gene models, including Ficolin-like

67812		family_FCN-B,
67818		family_FCN-B,
97805		family_FCN-B,
113232		family_FCN-B,
234008		family_FCN-B,
239462		family_FCN-B,
239556		family_FCN-B,
242434		family_FCN-B,
237286		,weakCOL_
237311		,weakCOL_
86504		,distantCOL_
57244		
58006		
58106		
58349		
58350		
58353		
59120		
59174		
59294		
59340		
59661		
59663		
60409		
62447		
62610		
62930		
64969		
65207		
67148		
67196		
67220		
67516		
68408		
68409		
68411		
68412		
68413		
69324		
69325		
69330		
71948		
77690		
77847		
78620		

The complement system

Model ID	Type	Annotation and curated structure
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Fibrinogen-containing gene models, including Ficolin-like

80207

80875

80903

81173

82708

82714

82743

82745

83369

83376

83573

83656

84134

84135

84136

84137

84161

84342

85386

85388

85395

85397

86061

86147

86148

86305

86306

86502

86503

86506

86801

87086

87589

87598

87852

88316

88429

88596

88599

88602

89668

89888

91052

91190

91270

The complement system

Model ID	Type	Annotation and curated structure
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Fibrinogen-containing gene models, including Ficolin-like

91522		
91708		
91759		
92948		
92969		
92970		
93027		
93437		
94425		
94501		
95365		
95895		
96224		
96225		
96226		
97299		
99252		
102053		
102722		
102723		
102728		
103345		
104091		
105468		
107889		
108084		
108085		
108089		
108533		
108703		
108711		
109331		
109609		
109616		
110403		
110827		
111454		
111456		
111458		
111954		
112661		
112675		
112676		
112865		
113998		

The complement system

Model ID	Type	Annotation and curated structure
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Fibrinogen-containing gene models, including Ficolin-like

119082		
123510		
124492		
124560		
124714		
124749		
125263		
125446		
125930		
126820		
127383		
129698		
135447		
139039		
148657		
149356		
149947		
149983		
150155		
150221		
151856		
158328		
158533		
168051		
168279		
168939		
169102		
176246		
187528		
187914		
200241		
201395		
201526		
201726		
203157		
203248		
203749		
203922		
203952		
204935		
205632		
205913		
206036		
206913		
206924		

The complement system

Model ID	Type	Annotation and curated structure
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Fibrinogen-containing gene models, including Ficolin-like

207164		
209344		
209438		
209555		
210003		
210323		
212802		
215774		
217757		
218233		
219630		
220763		
220899		
221048		
222082		
222102		
223439		
223471		
223563		
223660		
223677		
223686		
223713		
224083		
224864		
227092		
227168		
229861		
233199		
233209		
233831		
234918		
234927		
239343		
240565		
241969		
242798		
243282		
244837		
245361		
246430		
247629		
247635		
247643		
248340		

The complement system

Model ID	Type	Annotation and curated structure
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Fibrinogen-containing gene models, including Ficolin-like

248658		
248685		
249788		
250527		
252156		
252163		
252169		
252175		
252196		
253182		
253185		
253186		
253219		
253483		
254708		
254709		
254768		
254777		
255337		
255420		
255928		
255934		
256405		
256907		
257588		
257786		
257790		
257791		
257793		
258375		
272750		
273618		

The complement system

Model ID

Collectin-like gene models

see the C-type lectin section.

CCP-containing gene models

92290	64144	214761	68883
130689	96122	213302	67421
201126	95320	207101	67241
97334	92621	206425	84839
70467	85740	201271	73581
68195	74801	186571	68978
90333	66706	153580	63797
125288	216625	126932	107080
112314	213239	118754	67243
87789	210659	112915	129967
99521	112418	109713	122977
90332	91397	103182	113038
69075	68673	94762	110937
92698	254782	93176	92765
80710	223272	91518	84760
103529	124695	89744	214507
88273	103549	89642	99315
211430	99565	85300	93716
104686	97339	83481	67925
88270	85773	67803	67422
224944	124580	66592	64431
112840	85301	257502	68166
112416	69303	239170	133281
96397	259222	235842	130441
92287	226711	233277	128120
90526	68073	232376	112831
125322	248483	224807	96116
125152	68671	223205	130446
113083	179291	214926	126591
74134	124606	204663	118602
125323	108141	200491	118458
88271	96306	194004	108616
288621	93180	184362	99313
232069	88161	176064	94765
123987	85471	135646	88227
75995	124504	125352	68722
82719	118449	124605	122198
76225	94766	90506	96564
246401	88196	88159	88198
125197	64392	82713	131641
82707	206895	77076	127408
112787	110933	72979	110939

The complement system

Model ID

CCP-containing gene models

63398	71622	68653	103554
106430	178371	68379	84841
95076	108066	236177	101310
254617	88313	217719	94778
237111	80634	206236	92843
214746	68393	200428	92771
112652	103347	178912	70751
110136	85725	118068	123130
89746	109581	113208	81153
223188	82501	112819	126772
208581	86274	103750	112573
204802	125175	68372	110908
103544	199938	241070	252134
76481	133282	235843	103563
68381	126704	232377	100333
68373	104909	232050	88260
67209	94775	171596	84091
279632	84840	148972	72827
258916	201166	120051	91888
241697	88239	89745	68804
206936	79598	213687	67419
204699	67517	200877	67073
176545	66626	199472	124626
146724	66599	189517	123314
134770	63272	99524	123306
186390	112727	92077	85352
134938	68710	237327	83283
70575	67523	196397	86959
68380	67515	88162	81991
249894	126438	63926	67067
221052	94278	135058	90827
204816	86467	97609	135164
180200	124780	235822	122528
149855	112690	83988	102856
133202	90409	241484	82105
77075	87121	231419	81990
68394	86953	214800	90824
239173	99522	199608	129395
204651	92623	187059	125860
186667	104786	136198	126037
185458	100771	135954	97998
134821	93222	133444	91889
121550	92840	133398	90952
235546	86708	118457	90936
223176	83483	105944	85621

The complement system

Model ID

CCP-containing gene models

118375	73689	103525	82705
97306	68958	92076	67956
68395	67254	91924	88566
66587	63795	87531	87086
241085	109391	77088	85742
235568	107165	69073	67085
224933	98991	68193	124862
146389	98870	67440	118609
133116	90821	67225	90034
124153	90383	66579	81154
81631	88751	195200	80380
233160	86715	194677	128980
224954	84251	136893	71334
135151	81788	125405	113235
88767	68709	110812	90357
81633	67806	103527	63530
247717	67420	92090	99125
240313	67255	69071	88262
235833	67239	69025	63538
221441	94295	69004	

9 Gene models encoding the genes of TNFs and TNFRs

Model ID	Type	annotations
Gene models of TNF		
68700		
100450		
65431		
79180		
201658		
238834		
238790		
238811		
68699		
200149		
201657		
248118		
65492		
100482		
104530		
65354		
65331		
238756		
201749		
199711		
65330		
92776		
66950		
100484		
98680		
65494		
74190		
65495		
100485		
100483		
66952		
65496		
65493		
212591		
64528		
69253		
66948		
100486		
Gene models of TNF receptors		
106349	DR	
122203	DR	
123136	DR	
124709	DR	NGFR
128913	DR	

Model ID	Type	annotations
Gene models of TNF receptors		
64947	DR	
78890	DR	
82338	DR	
90916	DR	
91614	DR	
91616	DR	
91618	DR	
94929	DR	
94933	DR	
99118	DR	
69672	DR	EDAR
106346	DR	
100729	TNFR	
110235	TNFR	
118322	TNFR	
124491	TNFR	
125959	TNFR	
125960	TNFR	
126334	TNFR	
142700	TNFR	
189967	TNFR	
208621	TNFR	
210269	TNFR	
228950	TNFR	
228986	TNFR	
229325	TNFR	ortholog of BjTNFR1
229334	TNFR	
245590	TNFR	same to 82667
245642	TNFR	
255594	TNFR	
65754	TNFR	
65780	TNFR	
70529	TNFR	
70536	TNFR	
80795	TNFR	
82667	TNFR	TNFR+caspase????
86310	TNFR	
90654	TNFR	
91617	TNFR	
99119	TNFR	
99120	TNFR	
99124	TNFR	
99125	TNFR	ortholog of BjTNFR2

10 Gene models containing Death-fold domains, except NLR and DR.

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
71628	ANK-CARD1	*ANK+CARD+ANK+CARD,2X, ANK to ankyrin/DAPK, CARD 50% identity to NLRR_82622_94471
87517	ANK-CARD1	CARDonly, similar to ANK-CARD_71628
106650	ANK-CARD1	CARDonly, similar to ANK-CARD_71628
89399	DED-CARD-TIR	DED+CARD+(TIR?X), problematic prediction
70282	ANK-CARD2	ANK+CARD, in 1 exon
90989	ANK-CARD2	ANK+CARD, in 1 exon
82450	ANK-CARD3	ANK+CARD, similar to DAPK/ankyrin?
99404	ANK-CARD3	ANK+CARD+CARD, similar to DAPK/ankyrin
82347	ANK-CARD3	ANK+CARD+CARD, similar to DAPK/ankyrin!
129004	ANK-CARD3	ANK+X1region+(DEATH?), problematic prediction
91807	ANK-CARD3	CARDonly, similar to ANK-CARD_99404
72518	ANK-CARD3	X1region+CARD+CARD, similar to DAPK, in 1 exon, X1region 18% similar to DAPK1
81181	ANK-CARD3	X1region+CARD+CARD, similar to DAPK, in 1 exon, X1region 18% similar to DAPK1
67342	ANK-DD1	ANK+X1region+DEATH+DEATH, similar to DAPK!
81081	ANK-DD1	ANK+X1region+DEATH+DEATH, similar to DAPK!
71643	ANK-DD2	ANK+X1+DEATH+X2, similar to DAPK, B
71650	ANK-DD2	weakANK+X1+DEATH+X2, similar to DAPK, B
82806	ANK-DD2	X1+DEATHonly+X2, similar to DAPK, B
110170	ANK-DD3	ANK+DEATH, similar to ankyrin
110172	ANK-DD3	ANK+DEATH+(RAS+DEATH+GLY), similar to ankyrin, problematic prediction
81759	ANK-DD3	unpredictedANK+DEATH+(RAS+DEATH+Gly), similar to ankyrin, problematic prediction
248019	ANK-DD4	ANK+DEATH, similar to ankyrin
276588	Apaf1	CARD+NBARC+WD40
94122	Apaf1-L1	DEATH+NBARC+TPR
124795	Apaf1-L1	DEATH+NBARC+TPR
106573	Apaf1-L2	(CARD?)+DED+NBARC, problematic prediction, similar to Apaf1-L_75564
75564	Apaf1-L2	DED+NBARC+TPR
111726	Apaf1-L2	DED+NBARC+TPR
101242	Apaf1-L2	NBARC, problematic prediction
111350	Apaf1-L3A	DED+NBARC+TPR+(DEATH+DEATH)?
104344	Apaf1-L3A	NBARC+TPR+DEATH+DEATH+(unpredictedDED+NBARC+TPR+DEATH+DEATH)?
104344	Apaf1-L3B	(NBARC+TPR+DEATH+DEATH)?+unpredicted(DED+NBARC)+TPR+DEATH+DEATH
111352	Apaf1-L3B	(NHL-DED!)+weakNBARC+TPR
111351	Apaf1-L3B	NBARC+TPR+(DEATH+DEATH)?
127718	Apaf1-L4	CARD+CARD+weakNBARC
127724	Apaf1-L4	CARD+CARD+weakNBARC
131365	Apaf1-L4	CARD+CARD+weakNBARC
96518	Apaf1-L4	CARD+weakNBARC
118997	Apaf1-L4	CARD+weakNBARC
84718	Apaf1-L5	DEATH+CARD+weakNBARC
93758	Apaf1-L5	DED+weakNBARC+TPR

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
132138	Apaf1-L5	DED+weakNBARC+TPR
112047	CARD	CARDonly
93411	CARD	CARDonly
80000	CARD	CARDonly
81331	CARD	CARDonly
84479	CARD	CARDonly
96127	CARD	CARDonly
98935	CARD	CARDonly
102458	CARD	CARDonly
107709	CARD	CARDonly
108172	CARD	CARDonly
123369	CARD	CARDonly
272268	CARD	CARDonly
120869	CARD	CARDonly, 46 to Apaf1-L4_131365
88966	CARD	CARDonly+other
69505	CARD1	CARDonly
69697	CARD1	CARDonly
82976	CARD1	CARDonly
95978	CARD1	CARDonly
69699	CARD1	CARDonly, 3
95977	CARD1	CARDonly, 3
81332	CARD2	CARDonly
84459	CARD2	CARDonly
101787	CARD3	CARDonly
97183	CARD3	CARDonly
89215	CARD-3DD	CARD+DEATH+DEATH+DEATH, similar to DD-DD_63494
82839	CARD-3DD	CARD+DEATH+DEATH+DEATH+(S_TKc)
213810	CARD-3DD	CARD+unpredicted(DEATH+DEATH)+DEATH
94052	CARD-3DD	DEATH+DEATH, similar to CRADD-DEATH
63494	CARD-3DD	DEATH+DEATH+DEATH, similar to CRADD-DEATH
126780	CARD4	CARD+CARD
127415	CARD4	CARD+CARD, 2
126781	CARD4	CARDonly, 2
102561	CARD5	CARDonly, 1
67423	CARD5	CARDonly, 42% similar to DLR_9354
99574	CARD6	CARDonly, 44% to DED-CARD2_8685, 45% to NLR_92153
99575	CARD6	CARDonly, similar to DED-CARD2
99912	CARD6	CARDonly, similar to DED-CARD2
99913	CARD6	CARDonly, similar to DED-CARD2
99914	CARD6	CARDonly, similar to DED-CARD2
126035	CARD7	CARDonly
131932	CARD7	CARDonly
123340	CARD-DD-NRF	(ANK+LRR+DEATH?)+CARD+DEATH+NRF, problematic prediction
74014	CARD-DD-NRF	CARD+DEATH+NRF, similar to ANK-CARD1_86694

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
105877	CARD-FB3A	CARD+FB3+weakNACHT
105878	CARD-FB3A	CARD+FB3+weakNACHT
73230	CARD-FB3A	CARD+FB3+weakNACHT
74261	CARD-FB3B	CARD+FB3+(TPR?), TPR similar to RAS-C_73989
86694	CARD-TIR1	CARD?+CARD+weakTIR, card 55% similar to ANK-CARD_71628, problematic prediction
67068	CARD-TIR1	CARD+weakTIR, card 55% similar to ANK-CARD_71628
67074	CARD-TIR1	CARD+weakTIR, card 55% similar to ANK-CARD_71628
66949	CARD-TIR1	CARD+weakTIR, card 55% similar to ANK-CARD_71628
71397	CARD-TIR2A	CARD+weakTIR
91235	CARD-TIR2A	CARD+weakTIR
94911	CARD-TIR2A	CARD+weakTIR
105723	CARD-TIR2A	CARD+weakTIR
86311	CARD-TIR2A	CARD+weakTIR+(DEATH?)
101263	CARD-TIR2A	CARD+weakTIR+(S_TKc?)
108131	CARD-TIR2A	CARD+weakTIR+(X3)?
71410	CARD-TIR2A	CARD+weakTIR+LRR, noNACHT
82394	CARD-TIR2A	CARDonly,similar to CARD+weakTIR
82402	CARD-TIR2A	CARDonly,similar to CARD+weakTIR
67885	CARD-TIR2A	CARDonly+(S_TKc?), similar to CARD-TIR_105723
63875	CARD-TIR2A	partialCARD+TIR, similar to CARD-TIR_94911
121797	CARD-TIR2B	(CARD-weakTIR)?X+DEATH+LRR, noNACHT
77771	CARD-TIR2B	2X, (CARD-weakTIR)?X+DEATH+DEATH+LRR+DEATH+DEATH+LRR, noNACHT
78891	CARD-X2	weakCARD+X2
82339	CARD-X2	weakCARD+X2
109587	CARD-ZnF1	(CARD+ZnF)+CARD+ZnF, 2X, in 1exon
109587	CARD-ZnF1	CARD+ZnF+(CARD+ZnF), 2X, in 1exon
66131	CARD-ZnF1	CARD-ZnF
64255	CARD-ZnF2	*CARD-ZnF, 2X
98002	CARD-ZnF2	CARD+ZnF
64262	CARD-ZnF2	CARD+ZnF+NHL
79862	CARD-ZnF2	CARD+ZnF+NHL
64260	CARD-ZnF2	CARD-ZnF
64261	CARD-ZnF2	CARD-ZnF
65966	CARD-ZnF2	CARD-ZnF
85162	CARD-ZnF2	CARD-ZnF
91143	CASP2L1	(DED+OTUB)+CASP+(CASP+DEATH?)
91143	CASP2L1	(DED+OTUB+CASP)+CASP+(DEATH?)
81923	CASP2L1	casp2, CASP+(DEATH?X)
105738	CASP2L1	casp2, DEATH+CASP
105741	CASP2L1	casp2, DEATH+CASP
89710	CASP2L1	DEATH+CASP, GLY,bbtFADD1
89710	CASP2L1	DEATH+CASP, GLY,bbtFADD1
89710	CASP2L1	DEATH+CASP, GLY,bbtFADD1

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
244359	CASP2L2A	partialCARD+CASP
124779	CASP2L2B	(CASP?X)+CARD+CASP
73465	CASP2L3	CASP2+(DEATH?X)
93797	CASP7L	DEATH+CASP
103363	CASP7L	DEATH+CASP
111974	CASP7L	DEATH+CASP
81881	CASP7L	DEATH+CASP
84192	CASP8	cas8, DED+DED+CASP
194931	CASP8	cas8, DED+DED+CASP
215159	CRADD	CARD+unpredict(DEATH+DED+DEATH+CARD)+DEATH
170157	CRADD-L1	CARD+DEATH
82436	CRADD-L2	CARD+DEATH
82441	CRADD-L3	CARD+unpredictedDEATH
155734	DAPK	DEATHonly, DAPK1, A, unpredictedSTK in front
232198	DAPK	DEATHonly, DAPK1, A, unpredictedSTK in front
82641	DD-CARD1	(CARD)?+DEATH, similar to DD-CARD_74750
80688	DD-CARD1	(CARD)?+DEATH+CARD, similar to DD-CARD_74751
100206	DD-CARD1	CARDonly
74751	DD-CARD1	DEATH+CARD
80689	DD-CARD1	DEATH+CARD
74750	DD-CARD1	DEATH+CARD+(DEATH?)
69233	DD-CARD2	DEATH+CARD+(IG?Xvcbp)
117443	DD-CARD2	DEATH+CARD+(IG?Xvcbp)
121802	DD-DD	DEATH+DEATH
122538	DD-DD	DEATH+DEATH
66255	DD-FB3A	DEATH+FB3
102082	DD-FB3B	DEATH+FB3
107725	DD-FB3B	DEATH+FB3
86773	DD-ZnF	DEATH+ZnF, DD 50% similar toApaf1-L3B_111351
130541	DD-ZnF	DEATH+ZnF, DD 50% similar toApaf1-L3B_111351
94014	DEATH	(LRR)+DEATHonly, 64% similar to NLR
105686	DEATH	DEATH+DEATH
79761	DEATH	DEATHonly
82637	DEATH	DEATHonly
63414	DEATH	DEATHonly
68001	DEATH	DEATHonly
78868	DEATH	DEATHonly
79455	DEATH	DEATHonly
82861	DEATH	DEATHonly
86474	DEATH	DEATHonly
87378	DEATH	DEATHonly
112309	DEATH	DEATHonly
124482	DEATH	DEATHonly
107097	DEATH	DEATHonly

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
68600	DEATH	DEATHonly
98244	DEATH	DEATHonly
105178	DEATH	DEATHonly
105185	DEATH	DEATHonly
71566	DEATH	DEATHonly
71567	DEATH	DEATHonly
63467	DEATH	DEATHonly
94017	DEATH	DEATHonly
102149	DEATH	DEATHonly
102160	DEATH	DEATHonly
121154	DEATH	DEATHonly
109429	DEATH	DEATHonly
91512	DEATH	DEATHonly
132056	DEATH	DEATHonly
73050	DEATH	DEATHonly
82395	DEATH	DEATHonly
82400	DEATH	DEATHonly
63550	DEATH	DEATHonly, 10
98009	DEATH	DEATHonly, 10
170987	DEATH	DEATHonly, 100% similar to CARD-3DD_82839
64544	DEATH	DEATHonly, 11
69237	DEATH	DEATHonly, 11
68940	DEATH	DEATHonly, 12
86090	DEATH	DEATHonly, 12
74755	DEATH	DEATHonly, 13
80684	DEATH	DEATHonly, 13
78865	DEATH	DEATHonly, 14
82310	DEATH	DEATHonly, 14
67766	DEATH	DEATHonly, 15
83441	DEATH	DEATHonly, 15
103968	DEATH	DEATHonly, 16
119651	DEATH	DEATHonly, 16
86464	DEATH	DEATHonly, 17
92143	DEATH	DEATHonly, 17
92144	DEATH	DEATHonly, 17
96200	DEATH	DEATHonly, 17
100932	DEATH	DEATHonly, 17
100933	DEATH	DEATHonly, 17
100934	DEATH	DEATHonly, 17
100935	DEATH	DEATHonly, 17
100936	DEATH	DEATHonly, 17
100937	DEATH	DEATHonly, 17
100931	DEATH	DEATHonly, 17
132814	DEATH	DEATHonly, 17

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
82837	DEATH	DEATHonly, 2
82838	DEATH	DEATHonly, 2
92768	DEATH	DEATHonly, 3
105187	DEATH	DEATHonly, 3
74105	DEATH	DEATHonly, 4
111442	DEATH	DEATHonly, 4
63484	DEATH	DEATHonly, 43% similar to DD-FB3B_107725
94035	DEATH	DEATHonly, 43% similar to DD-FB3B_107725
120536	DEATH	DEATHonly, 5
121587	DEATH	DEATHonly, 5
212621	DEATH	DEATHonly, 50% similar to CRADD_215159
101243	DEATH	DEATHonly, 51% similar to Apaf1-L5_84718
78700	DEATH	DEATHonly, 56% similar to NLR
90118	DEATH	DEATHonly, 58% similar to FADD-L2_75746
122725	DEATH	DEATHonly, 6
123768	DEATH	DEATHonly, 6
75745	DEATH	DEATHonly, 60% similar to FADD-L2_72890
100412	DEATH	DEATHonly, 63% similar to DLR
102705	DEATH	DEATHonly, 63% similar to NLAA_98235
231848	DEATH	DEATHonly, 65% similar to CRADD_170157
113100	DEATH	DEATHonly, 66% similar to CARD-DD-NRF_123340
63401	DEATH	DEATHonly, 7
69803	DEATH	DEATHonly, 7
69806	DEATH	DEATHonly, 7
97361	DEATH	DEATHonly, 80% similar to DLR
63511	DEATH	DEATHonly, 9
94069	DEATH	DEATHonly, 9
63430	DEATH	DEATHonly, similar to Apaf1-L1
63432	DEATH	DEATHonly, similar to GLY1A
77825	DEATH	DEATHonly, similar to LRR-DD-STK_80225
79206	DEATH	DEATHonly, similar to NHL-DD1_85628
87091	DEATH	DEATHonly, similar to NLAA
65479	DEATH	DEATHonly, similar to NLR
69811	DEATH	DEATHonly, similar to NLR
74430	DEATH	DEATHonly, similar to NLR
79758	DEATH	DEATHonly, similar to NLR
91149	DEATH	DEATHonly, similar to NLR
98008	DEATH	DEATHonly, similar to NLR
69804	DEATH	DEATHonly, similar to RIPK
118521	DEATH	DEATHonly, similar to UNC5, B
83464	DEATH	DEATHonly, similar to UNC5, B
67629	DEATH	DEATHonly, similar to UNC5-L_90864
88240	DEATH	DEATHonly, similar to UNC5-L_90864
100684	DEATH	DEATHonly, similar to UNC5-L_90864

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
104289	DEATH	DEATHonly, similar to UNC5-L_90864
122411	DEATH	DEATHonly, similar to UNC6, A
65551	DEATH	DEATHonly, similar(47%) to LRR-RAS-DD_74292
81924	DEATH	DED+DEATH+DEATH, similar to NHL-DED-DD_87290
72927	DED	DED+distantPK, 60% similar to DED-CARD2_86852
87096	DED	DEDonly
106098	DED	DEDonly
110001	DED	DEDonly
72323	DED	DEDonly, 1
103717	DED	DEDonly, 1
117890	DED	DEDonly, 2
131447	DED	DEDonly, 2
66876	DED	DEDonly, 3
95966	DED	DEDonly, 3
76446	DED	DEDonly, 4
98404	DED	DEDonly, 4
75688	DED	DEDonly, 65% similar to DED-GBP_75690
105683	DED	DEDonly, 65% similar to NLAA_86966
84272	DED	DEDonly, similar to DED-CARD_89399
105685	DED	DEDonly, similar to DED-TPR
64268	DED	DEDonly, similar to FADD-L_64269
85156	DED	DEDonly, similar to NHL-DD1_85155
64269	DED	DEDonly, similar to NHL-DD1_85155
101305	DED	DEDonly, similar to NLAA_86966
111453	DED	DEDonly, similar to NLR
78018	DED-CARD1	DED+CARD
123816	DED-CARD1	DED+CARD+PRY
86852	DED-CARD2	DED+CARD
86851	DED-CARD2	DED+CARD, similar to CASP8
202645	DEDD	DEDonly
255178	DEDD	DEDonly
75677	DED-GBP	(GBP)+DED+GBP
75690	DED-GBP	(LRR-DD-STK-S_TKc)X+DED+GBP
106843	DED-GBP	(NLR-DEATH)+FB3+DED+DED+GBP+(NLR-DEATH), problematic prediction
75715	DED-GBP	DED+GBP
84337	DED-SPRY	SPRY+DED+SPRY, SPRY 40% similar to DED-CARD1_123816
72209	DED-TPR	DED+TPR, in close exons
89753	DED-TPR	DED+TPR, in close exons
89754	DED-TPR	DED+TPR, in close exons
89757	DED-TPR	DED+TPR, in close exons
243662	FADD	DED+DEATH
255736	FADD	DED+DEATH
76036	FADD-L1	DED+DEATH, A
105349	FADD-L1	DED+DEATH, A

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
75746	FADD-L2	DED+DED+DEATH+X3
72890	FADD-L2	DED+DED+DEATH+X3+(DEATH?)
79767	FADD-L3	DED+DEATH
133183	FB3-CARD	(FB3+CARD)n
122507	FB3-CARD	(FB3+CARD)n
91148	GLY1A	DED()+OTUB
91144	GLY1A	DED+DEATH+OTUB+X3+Gly
89707	GLY1A	DED+DED()+OTUB+Gly+(NLR-DEATH)
105739	GLY1A	DED+Gly
91147	GLY1A	DEDonly
129004	GLY1B	(ANK?)+X3+weakTIR+DEATHonly, problematic prediction
91425	GLY1B	SAM+weakTIR+DEATH+DEATH
124825	GLY1B	TPR+X3+weakTIR+DEATH+DEATH+Gly
73982	GLY1B	TPR+X3+weakTIR+DEATH+Gly
73989	GLY1B	TPR+X3+weakTIR+DEATH+Gly
97971	GLY1B	X3+weakTIR+DEATH+Gly
77596	GLY1C	DEATH+Gly, DEATH not similar to other
77601	GLY1C	DEATH+Gly, DEATH not similar to other
72365	GLY2A	()+Gly+CARD()+DEATH
94542	GLY2A	(CARD+RAS+DEATH+Gly)+CARD+RAS+DEATH+(NLR-DEATH)
86413	GLY2A	(CARD+RAS+DEATH+Gly)+CARD+RAS+DEATH+CARD
72363	GLY2A	(RAS+DEATH+Gly)+CARD+RAS+DEATH+Gly
86417	GLY2A	(RAS+DEATH+Gly)+CARD+RAS+DEATH+Gly+(CARD+DEATH)
94487	GLY2A	CARD+RAS+CARD+RAS+DEATH
94488	GLY2A	CARD+RAS+DEATH
94539	GLY2A	CARD+RAS+DEATH+Gly
86416	GLY2A	CARD+RAS+DEATH+Gly
94542	GLY2A	CARD+RAS+DEATH+Gly+(CARD+RAS+DEATH)+(NLR-DEATH)
86413	GLY2A	CARD+RAS+DEATH+Gly+(CARD+RAS+DEATH)+CARD
86415	GLY2A	DEATH+Gly
86453	GLY2A	RAS+DEATH+Gly
72363	GLY2A	RAS+DEATH+Gly+(CARD+RAS+DEATH+Gly)
86417	GLY2A	RAS+DEATH+Gly+(CARD+RAS+DEATH+Gly+CARD+DEATH)
94541	GLY2A	shortCARD+DEATH
72353	GLY2A	weakTIR+CARD+RAS+DEATH+Gly, in close exons
72379	GLY2A	weakTIR+CARD+RAS+DEATH+Gly, in close exons
72355	GLY2A	weakTIR+CARD+RAS+DEATH+Gly, in close exons
88830	GLY2B	shortCARD+RAS+DEATH+Gly
110172	GLY3	(ANK+DEATH)+RAS+DEATH+Gly
81759	GLY3	(unpredictedANK+DEATH)+RAS+DEATH+Gly
110169	GLY3	DEATH+(Gly), 66% similar to GLY3
77498	GLY4	()+Gly+DEATH
87083	GLY5	DEATH+OTUB
123581	IGFN-TM-CARD	(ANK)+IGFN+TM+CARD+CARD, questionable prediction

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
83070	IGFN-TM-CARD	CARD+CARD+(IG)
83058	IGFN-TM-CARD	IGFN+TM+CARD+CARD
102503	IGFN-TM-CARD	IGFN+TM+CARD+CARD+(IGFN)
83683	IGFN-TM-CARD	IGFN+TM+CARD+CARD+(IGFN)
83685	IGFN-TM-CARD	IGFN+TM+CARD+CARD+(IGFN)
83691	IGFN-TM-CARD	IGFN+TM+CARD+CARD+(IGFN)
83746	IGFN-TM-CARD	IGFN+TM+CARD+CARD+(IGFN+TM+CARD+CARD)
83746	IGFN-TM-CARD	IGFN+TM+CARD+CARD+(IGFN+TM+CARD+CARD)
123608	IGFN-TM-CARD	IGFN+TM+CARD+CARD+CARD
83693	IGFN-TM-CARD	IGFN+TM+partialCARD+CARD
215403	IRAK	DEATH+S_TKc, similar to IRAK4
107434	IRAK-L1	DEATH+distantS_TKc, uncertain
81532	IRAK-L2	DEATH+S_TKc
81535	IRAK-L2	DEATH+S_TKc, similar to IRAK-L_81532
82839	IRAK-L3	CARD+DEATH+DEATH+DEATH+S_TKc, uncertain
77823	LRR-DD-STK	(LRR+unpredictedDEATH+S_TKc)+LRR+DEATH+S_TKc
82834	LRR-DD-STK	(WD40)?+LRR+DEATH
77813	LRR-DD-STK	LRR+DEATH
74989	LRR-DD-STK	LRR+DEATH+S_TKc
77802	LRR-DD-STK	LRR+DEATH+S_TKc
77807	LRR-DD-STK	LRR+DEATH+S_TKc
77821	LRR-DD-STK	LRR+DEATH+S_TKc
77826	LRR-DD-STK	LRR+DEATH+S_TKc
77827	LRR-DD-STK	LRR+DEATH+S_TKc
80224	LRR-DD-STK	LRR+DEATH+S_TKc
80225	LRR-DD-STK	LRR+DEATH+S_TKc
77808	LRR-DD-STK	LRR+DEATH+S_TKc, in close exons, perfect
80223	LRR-DD-STK	LRR+DEATH+S_TKc+(LRR+DEATH+S_TKc)
80223	LRR-DD-STK	LRR+DEATH+S_TKc+LRR+DEATH+S_TKc
80227	LRR-DD-STK	LRR+unpredictedDEATH+S_TKc
77823	LRR-DD-STK	LRR+unpredictedDEATH+S_TKc+(LRR+DEATH+S_TKc)
77811	LRR-DD-STK	unpredictedLRR+partialDEATH+S_TKc
77822	LRR-DD-TIR	LRR+DEATH+partialTIR
77815	LRR-DD-TIR	LRR+DEATH+TIR
68259	LRR-RAS-CARD	LRR+RAS+CARD+CARD,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
80159	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 0 exon, involved in B-cell, DD is distant from LRR
89740	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
90914	LRR-RAS-DD	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
90625	LRR-RAS-DD	LRR+RAS+FB3+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
74291	LRR-RAS-DD1	LRR+RAS+DEATH, in 2 close exons, LRR-RAS 15% similar to MASL1
74292	LRR-RAS-DD1	LRR+RAS+DEATH, in 2 close exons, LRR-RAS 15% similar to MASL1
65562	LRR-RAS-DD1	LRR+RAS+DEATH, in 2 close exons, LRR-RAS 15% similar to MASL1
118978	LRR-RAS-DD2	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
118982	LRR-RAS-DD2	LRR+RAS+DEATH,similar to human MFHAS1, encodin 1 exon, involved in B-cell, DD is distant from LRR
107976	LRR-TM-DD1	LRR+TM+DEATH, receptor
84125	LRR-TM-DD1	LRR+TM+DEATH, receptor in 1 exon
66953	LRR-TM-DD2	LRR+TM+DEATH, receptor
67956	multiDD	multiple DEATH
113048	multiDD	multiple DEATH
113306	multiDD	multiple DEATH
113307	multiDD	multiple DEATH
118609	multiDD	multiple DEATH
92079	multiDED	(GLY4-gly)+4DED
84994	MyD88	MyD88
246353	MyD88	MyD88
91369	MyD88-L1	*Death+weakTIR+weakTIR, true tir with homolog from sea urchin
91370	MyD88-L1	*Death+weakTIR+weakTIR, true tir with homolog from sea urchin
95419	MyD88-L1	*Death+weakTIR+weakTIR, true tir with homolog from sea urchin
126252	MyD88-L1	*Death+weakTIR+weakTIR, true tir with homolog from sea urchin
126253	MyD88-L1	*Death+weakTIR+weakTIR, true tir with homolog from sea urchin
127607	MyD88-L1	*Death+weakTIR+weakTIR, true tir with homolog from sea urchin
127608	MyD88-L1	*Death+weakTIR+weakTIR, true tir with homolog from sea urchin
127609	MyD88-L1	*Death+weakTIR+weakTIR, true tir with homolog from sea urchin
117008	MyD88-LX	(X3)?X+DEATHonly, similar to MyD88-L_63433
63433	MyD88-LX	DEATH+TIR, nonTLR-TIR
84667	NHL-DD1	A, (Gly)+DEATH+NHL+(DEATH+DEATH+DEATH+ZnF)
84670	NHL-DD1	A, DEATH+NHL
84671	NHL-DD1	A, DEATH+NHL
85631	NHL-DD1	A, DEATH+NHL+(DEATH+ZnF)
85628	NHL-DD1	A, DEATH+NHL+(Gly+NHL)
85155	NHL-DD1	DEATHonly, similar to FADD-L_64269
90230	NHL-DD2	DEATH+ZnF+NHL
67900	NHL-DD2	DEATHonly, similar to NHL-DD_90230
87296	NHL-DED	(DED)+DED+NHL
87290	NHL-DED	(DED+DEATH+NHL)+DED+NHL
87330	NHL-DED	DED+()
87341	NHL-DED	DED+()+DED+(), 2X
87316	NHL-DED	DED+()+DED+NHL, 2X
84318	NHL-DED	DED+DED
83452	NHL-DED	DED+NHL
87276	NHL-DED	DED+NHL

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
87278	NHL-DED	DED+NHL
87279	NHL-DED	DED+NHL
87280	NHL-DED	DED+NHL
87282	NHL-DED	DED+NHL
87283	NHL-DED	DED+NHL
87285	NHL-DED	DED+NHL
87286	NHL-DED	DED+NHL
87287	NHL-DED	DED+NHL
87288	NHL-DED	DED+NHL
87289	NHL-DED	DED+NHL
87291	NHL-DED	DED+NHL
87292	NHL-DED	DED+NHL
87294	NHL-DED	DED+NHL
87297	NHL-DED	DED+NHL
87298	NHL-DED	DED+NHL
87300	NHL-DED	DED+NHL
87302	NHL-DED	DED+NHL
87303	NHL-DED	DED+NHL
87306	NHL-DED	DED+NHL
87307	NHL-DED	DED+NHL
87308	NHL-DED	DED+NHL
87309	NHL-DED	DED+NHL
87312	NHL-DED	DED+NHL
87314	NHL-DED	DED+NHL
87315	NHL-DED	DED+NHL
87317	NHL-DED	DED+NHL
87319	NHL-DED	DED+NHL
87320	NHL-DED	DED+NHL
87321	NHL-DED	DED+NHL
87322	NHL-DED	DED+NHL
87323	NHL-DED	DED+NHL
87324	NHL-DED	DED+NHL
87325	NHL-DED	DED+NHL
87326	NHL-DED	DED+NHL
87327	NHL-DED	DED+NHL
87328	NHL-DED	DED+NHL
87332	NHL-DED	DED+NHL
87334	NHL-DED	DED+NHL
87336	NHL-DED	DED+NHL
87338	NHL-DED	DED+NHL
93221	NHL-DED	DED+NHL
109861	NHL-DED	DED+NHL
87284	NHL-DED	DED+NHL+(DED+DEATH+NHL)
87293	NHL-DED	DED+NHL+(DED+DEATH+NHL)

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
87310	NHL-DED	DED+NHL+(DED+DEATH+NHL)
87301	NHL-DED	DEDonly, similar to NHL-DED_87278
124881	NHL-DED	DEDonly, similar to NHL-DED_87285
87284	NHL-DED-DD	(DED+NHL)+DED+DEATH+NHL
87293	NHL-DED-DD	(DED+NHL)+DED+DEATH+NHL
87310	NHL-DED-DD	(DED+NHL)+DED+DEATH+NHL
87299	NHL-DED-DD	DEATH+NHL
87305	NHL-DED-DD	DED+DEATH+(VCBP-IG)
87295	NHL-DED-DD	DED+DEATH+NHL
87311	NHL-DED-DD	DED+DEATH+NHL
87313	NHL-DED-DD	DED+DEATH+NHL
87329	NHL-DED-DD	DED+DEATH+NHL
87331	NHL-DED-DD	DED+DEATH+NHL
87335	NHL-DED-DD	DED+DEATH+NHL
87290	NHL-DED-DD	DED+DEATH+NHL+(DED+NHL)
276184	PEA15	DEDonly
279265	PEA15	DEDonly
93124	PIDD	LRR+DEATH, no ortholog to PIDD
107130	PIDD	LRR+DEATH, no ortholog to PIDD
121822	PIDD-L1	LRR+DEATH, DEATH 40% similar to LRR-DD-STK
133361	PIDD-L2	LRR+DEATH, no ortholog to PIDD
93013	RIGI1	DEATH+DEAD+HELLc
76000	RIGI2	DED+DEAD+HELLc
108575	RIGI2	DED+DEAD+HELLc
102703	RIGI-L	*CARD+weakTIR+DEAD, member of RIGI, with weak TIR
102704	RIGI-L	*CARD+weakTIR+DEAD, member of RIGI, with weak TIR
106572	RIGI-L	*CARD+weakTIR+DEAD, member of RIGI, with weak TIR
80064	RIPK	S_TKc+DEATH
108561	RIPK	TPK+DD,RIPK1, RIP
80066	RIPK-L1	S_TKc+DEATH
108559	RIPK-L1	S_TKc+DEATH
66228	RIPK-L2	CARDonly
66229	RIPK-L2	S_TKc+CARD, uncertain
121176	SPRY-DD	SPRY+DEATH
132101	SPRY-DD	SPRY+DEATH
126003	THOC1	THO+DEATH
126015	THOC1	THO+DEATH
111653	tripleCARD	(NACHT)+CARD+CARD+CARD
126782	tripleCARD	CARD+CARD+CARD
133737	UNC5	Igcam+TSP1+TM+ZU5+DEATH
209377	UNC5	Igcam+TSP1+TM+ZU5+DEATH
67582	UNC5-L1	DEATH+DEATH, similar to UNC5-L_91964
90864	UNC5-L1	DEATHonly
91964	UNC5-L1	DEATHonly

DFD gene model. 2X=2 genes in 1 model; X1/X2/X3=3 unknown conserved domains; weak=the e-value for the domain is weak; unpredicted=the domain is not captured by gene prediction program but identified by manual inspection; ?=possible computational domain fusion.

Model ID	group	curated structures
76983	UNC5-L2	IG?+ZU5+DEATH, similar to UNC5-L_90216
67887	UNC5-L2	IG+ZU5+DEATH, similar to UNC5-L_90216
90217	UNC5-L2	IG+ZU5+DEATH, similar to UNC5-L_90216
67886	UNC5-L2	TM+ZU5+DEATH, A
90216	UNC5-L2	TM+ZU5+DEATH, A
78837	UNC5-L2	ZU5+DEATH
82284	UNC5-L2	ZU5-DEATH
136671	UNC5-L3	ZU5+DEATH
231042	UNC5-L3	ZU5+DEATH
67784	UNC5-L4	TSP1+TM+DEATH
71638	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
71640	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
71645	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
71647	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
71649	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
87764	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
95147	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
99486	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
101917	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
106660	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
106662	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
71642	X1-CARD	X1region+CARDonly, similar to DAPK/ankyrin
67622	X1-CARD-STK	X1region+CARD+S_TKc, similar to DAPK/ankyrin

11 TRAF gene models.

Model ID	Type
237984	
238009	
99999	
237951	
68986	
68989	
68992	
107021	
250202	
68995	
68997	
107017	
68994	
250186	
250196	
250205	
250208	
250213	
68993	
250201	
68990	
115711	
170776	
85024	
88126	
68985	
107005	
84269	
89402	
69354	
68988	
107010	
109339	
68991	
107013	
259400	

12 Caspase gene models.

Caspase. 2X/3X=2 or 3 genes in 1 model.

Model ID	type	notes
124779	CASP2L	2X, CARD+CASP
89710	CASP2L	3X, DEATH+CASP,(DEATH)2+DED+CASP+CASP+DED+DEATH+DED+DEATH+CASP
67496	CASP2L	unpredictedCARD+casp2
79454	CASP2L	unpredictedDEATH+casp2
244359	CASP2L	unpredictedCARD+casp2
81923	CASP2L	CASP2+distantDEATH
105738	CASP2L	casp2, DEATH+CASP2
105741	CASP2L	casp2, DEATH+CASP2
91143	CASP2L	2X,otubain+CASP+otubain+CASP+guanylate+DEATH
73465	CASP2L	CASP2+5k+DEATH
88809	CASP3L	
209226	CASP3L	
221096	CASP3L	
221118	CASP3L	
221225	CASP3L	
56658	CASP6	casp6
120993	CASP6	casp6
72366	CASP7	casp7
277718	CASP7	casp7
84192	CASP8	casp8, DED+DED+CASP
194931	CASP8	casp8, DED+DED+CASP
82667	CASP8L	TNFR+CASP
82986	CASP8L	
94722	CASP8L	
159062	CASP8L	
160750	CASP8L	
169348	CASP8L	
187671	CASP8L	unpredictedDEATH+10k+CASP
210336	CASP8L	
232179	CASP8L	
234792	CASP8L	
245601	CASP8L	
250204	CASP8L	
252571	CASP8L	
255730	CASP8L	
235423	CASP8L	
103623	CASP8L	
87544	CASP8L	
178970	CASP8L	unpredictedDED+8k+CASP+unpredicted(DED+DEATH)
188950	CASP8L	unpredictedCARD+8k+CASP
231349	CASP8L	
68000	CASP8L	RNAbinding+CASP10
219551	CASP8L	
92562	CASP2/9L	
138180	CASP2/9L	

Caspase. 2X/3X=2 or 3 genes in 1 model.

Model ID	type	notes
158006	CASP2/9L	
214667	CASP2/9L	unpredictedRAB+CASP
66918	CASP9L	
214500	CASP2/9L	
287672	CASP2/9L	unpredictedCRAD+CASP
67388	CASP2/9L	LRR+CASP, LRR similar to MASL1
75631	CASP2/9L	LRR+CASP, LRR similar to MASL1
80701	CASP2/9L	LRR+CASP, LRR similar to MASL1
284570	MALT1	IG+CASP, ortholog to MALT1
237417	MALT1	IG+IG+CASP, ortholog to MALT1
81881	unknown	unpredictedDEATH+CASP
111974	unknown	unpredictedDEATH+CASP
75104	unknown	
75105	unknown	
101604	unknown	
93797	unknown	DEATH+CASP
103363	unknown	DEATH+CASP
66705	unknown	DED+CASP
95321	unknown	DED+CASP

13 Other gene models, including MIF,IL-17,effectors, transcriptional factors,kinases.

Other gene models, including MIF,IL-17,effectors, transcriptional factors,kinases

Model ID	type	notes
migration inhibitory factor (MIF) gene models		
126427		
126425		
124795		
127246		
133022		
111370		
IL-17 gene models		
230778		
127768		
67593		
127767		
91950		
132638		
117645		
92872		
94805		
94821		
94820		
112862		
66165		
Gene models of other kinases and transcriptional factors		
133442	NFKB	
210462	NFKB	
217215	NFAT	
217146	NFAT	
209309	NFKB	
79830	ikaros	
111710	ikaros	
112005	ikaros	
172091	ikaros	
195683	ikaros	
87945	PU/spi	
231930	PU/spi	
229939	PU/spi	
80298	IKK	
80298	IKK	
199352	TBK	
212708	TBK	
123253	TBK	
74350	TBK	
60037	MAPK	
218574	MAPK	

Other gene models, including MIF,IL-17,effectors, transcriptional factors,kinases

Model ID	type	notes
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Gene models of other kinases and transcriptional factors

68429	STAT	
73552	STAT	
233038	STAT	
257705	STAT	
86371	JNK	
251426	JNK	
86372	JNK	
85282	p38MAPK	
93656	p38MAPK	
90761	JAK	

transcriptional factor IRF gene models

201596		amphiIRF1, similar to humanIRF3/7/5/6
212808		amphiIRF1, similar to humanIRF3/7/5/6
152487		amphiIRF11, similar to humanIRF3/7/5/6
229218		amphiIRF2, similar to humanIRF3/7/5/6
178789		amphiIRF2, similar to humanIRF3/7/5/6
118813		amphiIRF3, similar to humanIRF4/8/9
125300		amphiIRF3, similar to humanIRF4/8/9
251372		amphiIRF4, similar to humanIRF1/2
209310		amphiIRF4, similar to humanIRF1/2
232921		amphiIRF5, similar to humanIRF4/8/9
204422		amphiIRF6, similar to humanIRF4/8/9
68559		amphiIRF7
88706		amphiIRF8
68560		amphiIRF8
88707		amphiIRF9
89979		amphiIRF10
97839		amphiIRF10
204482		unknown

MACPF-containing gene models, C6-like/perforins

134616	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
105963	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
102289	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
81773	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
110173	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
81766	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
65208	_C6L	LDLa+MACPF+EGF
76018	_C6L	TSP1+TSP1+LDLa+MACPF+EGF+TSP1
67061		MACPF
86688		MACPF+distantFurin_Kringle
102093		MACPF
86686		MACPF+distantFurin_Kringle
63809		MACPF+distantFurin_Kringle

Other gene models, including MIF,IL-17,effectors, transcriptional factors,kinases

Model ID	type	notes
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MACPF-containing gene models, C6-like/perforins

105134		MACPF+chitin
88402		MACPF+distantFurin_Kringle+PK
97589		MACPF+Furin+F58AC
106125		MACPF+CTLD+F58C
88988		MACPF+F58C
125400		MACPF+F58C
111559		MACPF
112179		MACPF
101213		MACPF+Furin
89006		MACPF+F58C
63382		MACPF
82668		MACPF+F58C
71536		MACPF
106127		MACPF
90586		MACPF+F58C
73492		MACPF
124580		MACPF+furin+F58C+CTLD+EGF+SR+CCP
69406		MACPF+furin+F58C+SR
130518		MACPF
124451		MACPF
92260		MACPF
89470		MACPF+Furin
111252		MACPF+Furin
67600		MACPF?+?
105135		MACPF+chitin
113132		MACPF
123900		MACPF
93114		MACPF
91906		MACPF+?EGF+CTLD
102810		MACPF+F58C
88232		MACPF+Furin
78467		MACPF
88782		MACPF??
105473		MACPF+Furin
81553		MACPF??
122359		MACPF+Furin
106022		MACPF??

nitric oxide synthase gene models

84311
116914
120590
126200
90855
116894

Other gene models, including MIF,IL-17,effectors, transcriptional factors,kinases

Model ID	type	notes
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peroxidase gene models

231450

258982

111866

77428

275043

131284

114533

107039

94318

131657

14 amphioxus VCBP and VCP gene models.

Model ID	name
63474	VCBP
79169	VCBP
87305	VCBP
94024	VCBP
96959	VCBP
96984	VCBP
122264	VCBP
128158	VCBP
128165	VCBP
76818	VCP
76819	VCP
94090	VCP
106767	VCP
106769	VCP
121473	VCP

15 Other apoptosis related gene models.

Model ID	name	notes
68590	Apaf1-L	Apaf1-L,
75564	Apaf1-L	Apaf1-L,DFD,
94122	Apaf1-L	Apaf1-L,DFD,
104330	Apaf1-L	Apaf1-L,
104344	Apaf1-L	Apaf1-L,DFD,DFD,
107712	Apaf1-L	Apaf1-L,
111350	Apaf1-L	Apaf1-L,DFD,
111351	Apaf1-L	Apaf1-L,DFD,
111726	Apaf1-L	Apaf1-L,DFD,
276588	Apaf1-L	Apaf1-L,DFD,
67376	BIR	
90287	BIR	
104523	BIR	
105373	BIR	
179588	BIR	
201532	BIR	
202860	BIR	
202918	BIR	
203045	BIR	
203058	BIR	
203077	BIR	
203130	BIR	
203142	BIR	
203179	BIR	
223993	BIR	
224120	BIR	
224204	BIR	
247510	BIR	
247521	BIR	
272301	BIR	
78689	Bcl	
77884	Bcl	
67809	Bcl	
80164	Bcl	
113229	Bcl	
241318	Bcl	
247509	Bcl	
206502	Bcl	
126027	Bcl	

16 Classification of LRRonly gene models, by BLASTCLUST program.

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR63368_1000174	A65	A60	A50
LRR65356_7000062	A65	A60	A50
LRR67182_13000094	A65	A60	A50
LRR70616_29000066	A65	A60	A50
LRR71129_32000032	A65	A60	A50
LRR71127_32000030	A65	A60	A50
LRR71123_32000026	A65	A60	A50
LRR71121_32000024	A65	A60	A50
LRR207538_32.183.1	A65	A60	A50
LRR149222_32.106.1	A65	A60	A50
LRR75851_60000081	A65	A60	A50
LRR76947_67000111	A65	A60	A50
LRR78124_75000047	A65	A60	A50
LRR78102_75000025	A65	A60	A50
LRR218596_75.45.1	A65	A60	A50
LRR78541_78000019	A65	A60	A50
LRR224198_100.95.1	A65	A60	A50
LRR82906_116000012	A65	A60	A50
LRR84068_127000036	A65	A60	A50
LRR86709_154000043	A65	A60	A50
LRR86992_157000044	A65	A60	A50
LRR86979_157000031	A65	A60	A50
LRR88473_174000076	A65	A60	A50
LRR88472_174000075	A65	A60	A50
LRR88471_174000074	A65	A60	A50
LRR88470_174000073	A65	A60	A50
LRR88465_174000068	A65	A60	A50
LRR88462_174000065	A65	A60	A50
LRR88461_174000064	A65	A60	A50
LRR88460_174000063	A65	A60	A50
LRR88427_174000030	A65	A60	A50
LRR88426_174000029	A65	A60	A50
LRR88421_174000024	A65	A60	A50
LRR88420_174000023	A65	A60	A50
LRR88418_174000021	A65	A60	A50
LRR89518_187000083	A65	A60	A50
LRR89485_187000050	A65	A60	A50
LRR89481_187000046	A65	A60	A50
LRR230668_274.35.1	A65	A60	A50
LRR162914_274.34.1	A65	A60	A50
LRR97219_300000002	A65	A60	A50
LRR103967_449000020	A65	A60	A50
LRR104538_466000021	A65	A60	A50
LRR248452_512.66.1	A65	A60	A50
LRR105931_512000024	A65	A60	A50

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR105930_512000023	A65	A60	A50
LRR108255_616000003	A65	A60	A50
LRR109672_702000014	A65	A60	A50
LRR258331_959.11.1	A65	A60	A50
LRR133161_9590007	A65	A60	A50
LRR111808_959000006	A65	A60	A50
LRR139027_1078.1.1	A65	A60	A50
LRR112317_1146000001	A65	A60	A50
LRR112564_1366000002	A65	A60	A50
LRR112563_1366000001	A65	A60	A50
LRR259214_2353.2.1	A65	A60	A50
LRR199068_1.493.1		A60	A50
LRR67558_15000050		A60	A50
LRR71157_32000060		A60	A50
LRR71541_34000022		A60	A50
LRR209571_39.251.1		A60	A50
LRR210765_43.234.1		A60	A50
LRR158338_64.80.1		A60	A50
LRR76946_67000110		A60	A50
LRR78101_75000024		A60	A50
LRR78099_75000022		A60	A50
LRR78094_75000017		A60	A50
LRR218807_75.171.1		A60	A50
LRR218595_75.53.1		A60	A50
LRR79291_83000102		A60	A50
LRR265150_830060		A60	A50
LRR221138_87.146.1		A60	A50
LRR224879_104.91.1		A60	A50
LRR160088_104.90.1		A60	A50
LRR82151_109000009		A60	A50
LRR187660_109.121.1		A60	A50
LRR85413_141000062		A60	A50
LRR87518_162000058		A60	A50
LRR87582_163000052		A60	A50
LRR88474_174000077		A60	A50
LRR88425_174000028		A60	A50
LRR88419_174000022		A60	A50
LRR89516_187000081		A60	A50
LRR89483_187000048		A60	A50
LRR89480_187000045		A60	A50
LRR89478_187000043		A60	A50
LRR89454_187000019		A60	A50
LRR91398_209000025		A60	A50
LRR92001_216000054		A60	A50
LRR226257_235.17.1		A60	A50
LRR94415_252000064		A60	A50

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR177931_257.104.1		A60	A50
LRR229509_264.81.1		A60	A50
LRR230145_269.35.1		A60	A50
LRR96294_282000008		A60	A50
LRR176618_282.50.1		A60	A50
LRR96335_283000005		A60	A50
LRR158323_306.32.1		A60	A50
LRR235233_321.87.1		A60	A50
LRR137659_338.10.1		A60	A50
LRR241798_401.64.1		A60	A50
LRR246124_466.39.1		A60	A50
LRR176692_467.36.1		A60	A50
LRR139050_467.8.1		A60	A50
LRR248397_511.20.1		A60	A50
LRR249425_536.34.1		A60	A50
LRR151410_580.19.1		A60	A50
LRR108139_610000009		A60	A50
LRR151408_710.14.1		A60	A50
LRR256071_773.1.1		A60	A50
LRR258322_956.3.1		A60	A50
LRR111794_956000002		A60	A50
LRR70076_26000116	B65	B60	A50
LRR205486_26.214.1	B65	B60	A50
LRR205378_26.78.1	B65	B60	A50
LRR172168_26.220.1	B65	B60	A50
LRR77874_73000145	B65	B60	A50
LRR77873_73000144	B65	B60	A50
LRR77871_73000142	B65	B60	A50
LRR77870_73000141	B65	B60	A50
LRR77868_73000139	B65	B60	A50
LRR77866_73000137	B65	B60	A50
LRR77865_73000136	B65	B60	A50
LRR218212_73.215.1	B65	B60	A50
LRR218184_73.150.1	B65	B60	A50
LRR218084_73.74.1	B65	B60	A50
LRR218003_73.78.1	B65	B60	A50
LRR194097_73.369.1	B65	B60	A50
LRR157749_73.92.1	B65	B60	A50
LRR80179_91000076	B65	B60	A50
LRR80178_91000075	B65	B60	A50
LRR80177_91000074	B65	B60	A50
LRR80176_91000073	B65	B60	A50
LRR80174_91000071	B65	B60	A50
LRR80172_91000069	B65	B60	A50
LRR80107_91000004	B65	B60	A50
LRR222056_91.101.1	B65	B60	A50

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR222055_91.35.1	B65	B60	A50
LRR151556_91.46.1	B65	B60	A50
LRR148371_91.34.1	B65	B60	A50
LRR86885_156000036	B65	B60	A50
LRR86877_156000028	B65	B60	A50
LRR227405_245.32.1	B65	B60	A50
LRR227404_245.182.1	B65	B60	A50
LRR151539_245.31.1	B65	B60	A50
LRR256706_811.5.1	B65	B60	A50
LRR139479_981.1.1	B65	B60	A50
LRR111890_981000003	B65	B60	A50
LRR113414_2819000001	B65	B60	A50
LRR65021_6000016		B60	A50
LRR187123_26.265.1		B60	A50
LRR152890_26.77.1		B60	A50
LRR120446_450105		B60	A50
LRR213495_54.161.1		B60	A50
LRR137589_56.14.1		B60	A50
LRR76418_64000029		B60	A50
LRR186798_73.293.1		B60	A50
LRR78158_75000081		B60	A50
LRR80173_91000070		B60	A50
LRR250160_557.25.1		B60	A50
LRR142264_557.10.1		B60	A50
LRR152924_31.61.1	C65		B50
LRR152923_31.60.1	C65		B50
LRR187254_32.364.1	C65		B50
LRR75515_58000028	C65		B50
LRR220253_82.88.1	C65		B50
LRR79749_88000013	C65		B50
LRR152920_109.39.1	C65		B50
LRR83245_119000072	C65		B50
LRR83208_119000035	C65		B50
LRR151565_247.12.1	C65		B50
LRR143269_560.9.1	C65		B50
LRR142223_1002.1.1	C65		B50
LRR67797_16000097	D65		
LRR67763_16000063	D65		
LRR67762_16000062	D65		
LRR67701_16000001	D65		
LRR68634_19000214	D65		
LRR83439_121000022	D65		
LRR83438_121000021	D65		
LRR90180_195000057	D65		
LRR98216_317000026	D65		
LRR102420_409000001	D65		

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR63625_2000054			
LRR63621_2000050			
LRR63619_2000048			
LRR117207_20318			
LRR117061_20003			
LRR177782_1.416.1			A50
LRR199264_1.145.1			
LRR63338_1000144			
LRR274884_10209			
LRR198747_1.48.1			
LRR170291_1.313.1			
LRR64062_3000092			A50
LRR64167_3000197			
LRR64164_3000194			
LRR64161_3000191			
LRR275098_30249			
LRR275303_50057			
LRR197751_5.831.1			
LRR185851_5.641.1			
LRR168674_5.385.1			
LRR138079_5.32.1			
LRR113569_50003			
LRR65276_6000271			
LRR201950_7.100.1			A50
LRR150194_7.121.1			A50
LRR151635_7.134.1			B50
LRR151605_7.133.1			B50
LRR260309_70419			
LRR201520_7.219.1			
LRR150575_7.127.1			
LRR65346_7000052			
LRR65322_7000028			
LRR201991_7.29.1			
LRR201812_7.205.1			
LRR196347_7.691.1			
LRR117747_70179			
LRR65797_8000183			
LRR65721_8000107			
LRR260421_80102			
LRR117866_80156			
LRR65991_9000035			
LRR164390_10.167.1			B50
LRR66304_10000058			
LRR118155_100161			
LRR118129_100106			
LRR66743_11000204			A50

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR203691_11.474.1			A50
LRR66772_11000233			
LRR66658_11000119			
LRR66968_12000123			
LRR66951_12000106			
LRR66946_12000101			
LRR66944_12000099			
LRR66973_12000128			
LRR66972_12000127			
LRR66947_12000102			
LRR66934_12000089			
LRR66881_12000036			
LRR66880_12000035			
LRR66879_12000034			
LRR67234_13000146			
LRR67215_13000127			
LRR67214_13000126			
LRR67213_13000125			
LRR67184_13000096			
LRR67144_13000056			
LRR67387_14000080			
LRR118480_140196			
LRR67684_15000176			C50
LRR67664_15000156			
LRR67566_15000058			
LRR118496_150034			
LRR67703_16000003			B50
LRR67781_16000081			
LRR67780_16000080			
LRR67779_16000079			
LRR67778_16000078			
LRR67777_16000077			
LRR118592_160194			
LRR67867_16000167			
LRR67760_16000060			
LRR118586_160173			
LRR68065_17000097			B50
LRR68051_17000083			C50
LRR68338_18000150			
LRR68328_18000140			
LRR68585_19000165			C50
LRR68584_19000164			C50
LRR68460_19000040			
LRR68458_19000038			
LRR68514_19000094			
LRR68796_20000144			A50

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR68832_20000180			
LRR68799_20000147			
LRR68740_20000088			
LRR69050_21000183			
LRR69048_21000181			
LRR69264_22000202			
LRR119045_220214			
LRR69301_23000008			B50
LRR69561_24000066			A50
LRR69549_24000054			A50
LRR204729_24.48.1			
LRR165792_24.141.1			
LRR205113_25.23.1			B50
LRR205037_25.72.1			B50
LRR276668_250218			
LRR70062_26000102			
LRR70310_27000130			C50
LRR205695_27.7.1			
LRR206093_28.294.1			
LRR70490_28000094			
LRR70478_28000082			
LRR206003_28.3.1			
LRR151578_29.47.1	LRR151578_29.47.1		B50
LRR151577_29.46.1			B50
LRR70761_30000049			B50
LRR151608_30.92.1	LRR151608_30.92.1		B50
LRR206808_30.309.1			
LRR206558_30.217.1			
LRR206491_30.51.1			
LRR119623_310032			C50
LRR71073_31000120			
LRR207368_32.229.1			A50
LRR188174_32.373.1			A50
LRR71378_33000063			C50
LRR71376_33000061			C50
LRR71372_33000057			C50
LRR71448_33000133			
LRR277336_330252			
LRR119726_330130			
LRR208162_34.42.1			A50
LRR71584_34000065			
LRR277364_350018			
LRR119795_350009			
LRR72033_36000088			A50
LRR160881_36.87.1			A50
LRR208714_36.218.1			B50

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR72039_36000094			C50
LRR167278_36.117.1			
LRR277514_360104			
LRR119916_360143			
LRR208979_37.50.1			
LRR155872_38.55.1			
LRR136091_38.5.1			
LRR72385_38000042			
LRR72578_39000089			C50
LRR136852_39.10.1			
LRR186766_39.232.1			
LRR166441_39.141.1			
LRR210364_41.197.1			A50
LRR210256_41.166.1			A50
LRR72911_41000036			B50
LRR210386_41.155.1			B50
LRR210302_41.188.1			
LRR176756_42.201.1			
LRR211146_44.8.1			B50
LRR73444_44000102			
LRR211073_44.47.1			
LRR73523_45000029			
LRR73521_45000027			
LRR150273_45.47.1			
LRR212033_47.57.1			
LRR278477_480159			A50
LRR263107_480161			A50
LRR74018_48000012			
LRR212273_48.84.1			
LRR147543_48.55.1			
LRR212235_48.265.1			
LRR212176_48.267.1			
LRR74180_49000036			
LRR212652_49.27.1			
LRR212402_49.102.1			
LRR140695_49.28.1			
LRR74570_51000147			A50
LRR212896_51.3.1			
LRR58172_52000011			
LRR74810_53000131			A50
LRR177860_53.191.1			A50
LRR213241_53.121.1			
LRR213228_53.84.1			
LRR213447_54.88.1			B50
LRR161784_54.170.1			
LRR74993_54000161			

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR74961_54000129			
LRR74861_54000029			
LRR149734_54.75.1			
LRR213854_55.55.1			A50
LRR151602_56.73.1			B50
LRR214218_56.16.1			
LRR75318_56000176			
LRR75215_56000073			
LRR75175_56000033			
LRR75418_57000092			
LRR75586_58000099			C50
LRR75603_58000116			
LRR75542_58000055			
LRR75531_58000044			
LRR214697_58.278.1			
LRR214691_58.184.1			
LRR214686_58.189.1			
LRR214682_58.206.1			
LRR214559_58.262.1			
LRR214464_58.12.1			
LRR215030_60.57.1			
LRR215332_61.258.1			
LRR75945_61000039			
LRR215395_61.9.1			
LRR76210_62000112			
LRR76271_63000026			B50
LRR76289_63000044			
LRR215675_63.177.1			
LRR150664_63.55.1			
LRR159240_64.86.1			A50
LRR76488_64000099			B50
LRR187251_64.194.1			B50
LRR151361_64.61.1			
LRR216110_65.52.1			A50
LRR76625_65000112			
LRR76811_66000136			C50
LRR216381_66.190.1			
LRR150286_66.48.1			
LRR150281_66.47.1			
LRR121438_660067			
LRR76944_67000108			
LRR216772_67.15.1			
LRR77007_68000021			
LRR264182_680049			
LRR121505_680022			
LRR77214_69000053			C50

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR77288_69000127			
LRR77396_70000092			B50
LRR77369_70000065			C50
LRR152678_70.57.1			
LRR217684_71.224.1			
LRR121756_710148			
LRR121775_720032			
LRR78015_74000123			
LRR218779_75.128.1			A50
LRR218613_75.77.1			
LRR218604_75.166.1			
LRR186588_75.174.1			
LRR185811_75.170.1			
LRR174268_75.138.1			
LRR219023_76.61.1			B50
LRR78510_77000135			A50
LRR78548_78000026			
LRR78542_78000020			
LRR280379_780264			
LRR78770_79000078			
LRR220064_81.27.1			
LRR158371_81.85.1			
LRR150324_81.32.1			
LRR122399_860108			
LRR221145_87.58.1			B50
LRR152922_87.61.1			B50
LRR195868_88.370.1			
LRR79785_88000049			
LRR221597_88.360.1			
LRR221439_88.52.1			
LRR221275_88.55.1			
LRR166389_88.277.1			
LRR158057_88.169.1			
LRR148974_88.54.1			
LRR134756_88.4.1			
LRR79907_89000070			
LRR222043_90.215.1			
LRR122525_900142			
LRR122523_900136			
LRR80175_91000072			A50
LRR186516_91.261.1			A50
LRR222247_91.316.1			
LRR222483_92.69.1			
LRR222466_92.98.1			
LRR80445_93000120			B50
LRR122597_930120			B50

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR80333_93000008			C50
LRR137525_93.10.1			
LRR195375_94.356.1			B50
LRR151600_94.66.1			B50
LRR223269_95.17.1			
LRR223476_96.93.1			
LRR80851_97000022			B50
LRR223806_97.55.1			
LRR177816_97.180.1			
LRR160620_97.123.1			
LRR80919_97000090			
LRR80871_97000042			
LRR281171_970209			
LRR223683_97.43.1			
LRR136845_101.3.1			
LRR224565_102.48.1			
LRR224546_102.85.1			
LRR224602_102.38.1			
LRR224704_103.35.1			B50
LRR81648_104000053			
LRR225256_106.14.1			
LRR225249_106.75.1			
LRR225198_106.53.1			
LRR225174_106.178.1			
LRR81975_107000030			
LRR225473_107.3.1			
LRR225413_107.2.1			
LRR150725_107.27.1			
LRR123080_1080090			
LRR123111_1100021			
LRR82652_113000085			
LRR82651_113000084			
LRR82609_113000042			
LRR82693_114000033			C50
LRR82681_114000021			C50
LRR82778_114000118			
LRR82767_114000107			
LRR82757_114000097			
LRR82882_115000104			
LRR82905_116000011			
LRR123291_1160036			
LRR83045_117000045			B50
LRR83019_117000019			
LRR83090_118000006			
LRR83370_120000090			
LRR83363_120000083			

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR83459_121000042			
LRR83458_121000041			
LRR83457_121000040			
LRR83469_121000052			
LRR83436_121000019			
LRR83850_125000046			B50
LRR83812_125000008			B50
LRR83930_125000126			
LRR83838_125000034			
LRR123640_1250035			
LRR123682_1260005			
LRR84180_128000065			
LRR84124_128000009			
LRR84121_128000006			
LRR123770_1280109			
LRR84317_129000087			
LRR84294_129000064			
LRR84352_130000022			
LRR123859_1300100			
LRR123898_1310076			
LRR84638_133000024			
LRR114839_1330008			
LRR123981_1340043			
LRR123979_1340038			
LRR84916_136000032			
LRR84897_136000013			
LRR59461_136000005			
LRR85044_137000086			
LRR85165_139000012			
LRR124131_1390014			
LRR124150_1400007			
LRR85326_140000078			
LRR124159_1400036			
LRR85369_141000018			B50
LRR85677_144000050			A50
LRR124308_1450016			
LRR124305_1450010			
LRR85884_146000032			
LRR59583_146000015			
LRR124389_1460072			
LRR86168_149000032			C50
LRR86156_149000020			C50
LRR86155_149000019			C50
LRR124501_1490034			
LRR86296_150000055			C50
LRR86285_150000044			C50

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR86281_150000040			
LRR86634_153000061			C50
LRR124759_1550099			
LRR86934_156000085			
LRR86975_157000027			
LRR87247_159000106			B50
LRR87442_161000070			
LRR87382_161000010			
LRR87695_165000040			
LRR87828_166000069			
LRR125096_1670117			
LRR88052_169000001			
LRR125137_1690058			
LRR88182_170000056			B50
LRR88186_170000060			
LRR88277_172000014			B50
LRR88275_172000012			B50
LRR88317_172000054			
LRR88312_172000049			
LRR88378_173000043			
LRR88374_173000039			
LRR125210_1730058			
LRR88449_174000052			
LRR88634_176000087			B50
LRR88579_176000032			B50
LRR88586_176000039			
LRR88649_176000102			
LRR88729_177000080			C50
LRR88728_177000079			C50
LRR88727_177000078			C50
LRR88701_177000052			
LRR88681_177000032			
LRR115127_1780001			
LRR88799_179000004			
LRR125356_1790059			
LRR125409_1820038			
LRR89115_183000039			
LRR89375_186000014			
LRR125539_1860071			
LRR125576_1880067			
LRR125785_1950101			
LRR125784_1950100			
LRR90198_195000075			
LRR125776_1950080			
LRR90259_196000028			
LRR115247_1960017			

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR90337_197000004			
LRR90461_198000023			
LRR90455_198000017			
LRR90584_199000049			
LRR125970_2000058			
LRR126028_2010095			
LRR90851_202000055			
LRR91453_209000080			B50
LRR91648_212000027			
LRR91737_213000019			
LRR91733_213000015			
LRR91732_213000014			
LRR91731_213000013			
LRR91828_214000021			A50
LRR91930_215000040			
LRR60354_215000001			
LRR91983_216000036			
LRR92046_217000036			
LRR126507_2170054			
LRR126504_2170048			
LRR126569_2190054			
LRR126534_2190003			
LRR92322_221000052			B50
LRR92291_221000021			
LRR92671_226000038			B50
LRR92670_226000037			B50
LRR92668_226000035			B50
LRR92674_226000041			
LRR92734_227000035			A50
LRR92705_227000006			
LRR92706_227000007			
LRR92704_227000005			
LRR92703_227000004			
LRR92868_229000071			B50
LRR92914_230000023			B50
LRR126802_2300028			
LRR126829_2310032			
LRR93091_232000050			
LRR93083_232000042			
LRR93134_233000011			C50
LRR226277_235.16.1			
LRR93336_236000048			
LRR93382_237000027			
LRR226512_237.27.1			
LRR127100_2410027			
LRR227098_242.37.1			A50

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR227114_242.60.1			B50
LRR93884_244000090			
LRR149730_244.21.1			
LRR94117_247000044			
LRR227746_248.6.1			A50
LRR227739_248.22.1			
LRR148475_249.16.1			A50
LRR94265_250000033			
LRR60670_250000004			
LRR228029_250.116.1			
LRR227946_250.9.1			
LRR227943_250.10.1			
LRR127301_2500045			
LRR94441_253000025			
LRR94439_253000023			
LRR228289_253.3.1			
LRR94800_258000029			B50
LRR148100_262.9.1			
LRR95153_263000051			B50
LRR137818_264.10.1			
LRR95224_265000008			
LRR150706_266.62.1			A50
LRR95376_266000087			
LRR230008_267.100.1			
LRR230024_268.113.1			
LRR230123_268.118.1			
LRR230034_268.117.1			
LRR196343_268.119.1			
LRR230179_269.44.1			A50
LRR162850_269.36.1			A50
LRR160524_270.49.1			
LRR230199_270.92.1			
LRR187622_274.63.1			A50
LRR230749_275.95.1			A50
LRR230724_275.23.1			A50
LRR161787_277.68.1			A50
LRR231020_277.50.1			
LRR231009_277.1.1			
LRR137613_277.6.1			
LRR158398_278.40.1			
LRR231199_279.21.1			
LRR96131_279000036			
LRR127889_2800043			
LRR96309_282000023			C50
LRR96308_282000022			C50
LRR231498_282.1.1			

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR231619_284.60.1			
LRR231607_284.20.1			
LRR231593_284.21.1			
LRR150726_284.19.1			
LRR231595_284.13.1			
LRR96462_285000022			C50
LRR231987_287.61.1			
LRR231916_287.94.1			
LRR160564_288.36.1			
LRR160523_288.34.1			
LRR232037_288.62.1			
LRR196521_288.75.1			
LRR232577_295.59.1			
LRR177176_300.50.1			A50
LRR97344_301000049			
LRR97373_302000028			
LRR233421_303.87.1			
LRR97498_304000031			
LRR97486_304000019			
LRR128316_3040030			
LRR128309_3040018			
LRR233611_305.21.1			
LRR97608_306000021			C50
LRR177919_306.54.1			
LRR150685_306.17.1			
LRR97615_306000028			
LRR128348_3060042			
LRR177844_308.80.1			A50
LRR234135_311.11.1			
LRR177186_311.88.1			
LRR141908_311.22.1			
LRR128422_3110007			
LRR196980_314.50.1			B50
LRR98066_314000025			C50
LRR98157_316000037			
LRR234983_319.1.1			
LRR98299_319000018			
LRR61163_320000009			
LRR152748_320.48.1			
LRR98413_321000031			
LRR235470_324.2.1			
LRR197524_326.83.1			
LRR128705_3260014			
LRR235861_328.58.1			
LRR128780_3290011			
LRR236185_333.11.1			

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR159380_333.54.1			
LRR154456_333.39.1			
LRR155757_333.43.1			
LRR177850_334.121.1			
LRR236476_335.5.1			
LRR284390_3360045			
LRR236544_337.41.1			
LRR194191_341.86.1			C50
LRR99573_345000003			
LRR99572_345000002			
LRR99700_346000067			
LRR99699_346000066			
LRR99698_346000065			
LRR99688_346000055			
LRR99667_346000034			
LRR99665_346000032			
LRR99661_346000028			
LRR99657_346000024			
LRR141719_346.19.1			
LRR137032_346.6.1			
LRR99772_347000072			
LRR99911_350000009			
LRR99910_350000008			
LRR238253_354.43.1			A50
LRR238182_354.9.1			
LRR238486_356.41.1			A50
LRR100245_356000010			B50
LRR149712_356.47.1			
LRR137530_356.10.1			
LRR284994_3600057			
LRR100468_361000001			
LRR160638_363.32.1			B50
LRR239104_365.13.1			
LRR100721_366000034			
LRR129456_3670028			
LRR115963_3710008			
LRR239771_373.51.1			
LRR101034_374000011			
LRR101215_378000001			
LRR101301_379000036			B50
LRR101300_379000035			B50
LRR158333_380.36.1			A50
LRR240415_381.51.1			A50
LRR240489_382.32.1			A50
LRR240452_382.41.1			A50
LRR129743_3840028			

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR116022_3840003			
LRR240722_385.11.1			
LRR196068_390.58.1			
LRR241295_393.18.1			
LRR241289_393.16.1			
LRR241287_393.24.1			
LRR176183_393.25.1			
LRR241327_394.58.1			
LRR139658_395.5.1			
LRR102024_398000021			
LRR102021_398000018			
LRR102102_400000008			
LRR241921_403.71.1			
LRR241975_404.26.1			
LRR270453_4050050			
LRR242036_405.4.1			
LRR177215_409.41.1			B50
LRR102518_411000013			C50
LRR102617_413000023			
LRR130144_4160024			
LRR151377_420.21.1			B50
LRR130226_4220032			
LRR177105_428.46.1			A50
LRR243974_435.17.1			
LRR103548_438000009			
LRR130472_4400021			
LRR103673_441000026			
LRR103694_442000006			C50
LRR103692_442000004			C50
LRR103706_442000018			
LRR103705_442000017			
LRR177167_444.62.1			
LRR167681_444.45.1			
LRR244698_445.28.1			A50
LRR142267_445.6.1			A50
LRR245026_449.136.1			A50
LRR130644_4510011			
LRR147222_457.20.1			
LRR104306_459000021			
LRR104303_459000018			
LRR146434_466.27.1			
LRR104522_466000005			
LRR246152_467.1.1			
LRR104563_467000006			
LRR175060_474.35.1			
LRR104756_474000015			

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR104744_474000003			
LRR246565_476.5.1			A50
LRR170779_476.28.1			A50
LRR246657_477.8.1			A50
LRR104848_477000022			A50
LRR142210_478.10.1			A50
LRR104933_479000028			
LRR105003_481000013			C50
LRR131013_4830028			
LRR247157_485.23.1			A50
LRR247145_485.10.1			
LRR105173_486000032			
LRR247337_489.65.1			A50
LRR139098_489.10.1			A50
LRR139047_489.9.1			A50
LRR105270_489000037			
LRR247512_493.9.1			B50
LRR143066_496.14.1			
LRR105526_497000018			C50
LRR131169_5020023			
LRR142317_507.4.1			B50
LRR287459_5100015			A50
LRR248292_510.37.1			A50
LRR248570_514.45.1			
LRR105984_514000008			
LRR105980_514000004			
LRR248734_518.46.1			
LRR248726_518.34.1			
LRR179778_518.43.1			
LRR248758_518.29.1			
LRR163002_518.35.1			
LRR158315_518.27.1			
LRR138495_518.4.1			
LRR138137_518.3.1			
LRR106234_524000010			
LRR177921_525.12.1			
LRR249144_530.16.1			
LRR249382_534.10.1			B50
LRR135144_536.1.1			
LRR249741_545.54.1			A50
LRR249789_546.16.1			A50
LRR106756_547000009			
LRR107058_560000013			C50
LRR107166_565000029			
LRR251131_577.8.1			
LRR131747_5780013			

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR251365_580.9.1			A50
LRR251340_580.17.1			A50
LRR141619_580.8.1			A50
LRR251458_584.17.1			A50
LRR251517_587.25.1			B50
LRR107691_588000004			
LRR131829_5930006			
LRR177061_599.33.1			
LRR107935_599000032			
LRR107934_599000031			
LRR107933_599000030			
LRR107911_599000008			
LRR108010_603000018			B50
LRR142262_608.12.1			B50
LRR108134_610000004			
LRR252288_611.3.1			
LRR252651_627.7.1			
LRR136613_627.6.1			
LRR252703_628.40.1			
LRR108556_632000014			B50
LRR138055_639.2.1			
LRR108716_641000018			
LRR253249_643.11.1			
LRR177720_656.37.1			
LRR288807_6570017			
LRR136801_657.2.1			
LRR108980_658000006			A50
LRR108986_658000012			
LRR109122_666000011			
LRR254197_675.8.1			
LRR109258_676000002			
LRR141364_680.11.1			
LRR109348_681000011			
LRR109415_685000002			
LRR109449_686000018			
LRR140169_688.8.1			
LRR137713_688.4.1			
LRR254633_692.16.1			
LRR109527_692000010			
LRR109525_692000008			
LRR109618_699000011			
LRR289081_7060031			
LRR149651_710.13.1			A50
LRR132485_7100015			
LRR132519_7150003			
LRR109944_721000002			

Classification of LRRonly models			
LRR+model ID+scaffold ID	65% identity	60% identity	50% identity
LRR137623_731.2.1			
LRR140459_735.4.1			
LRR289275_7390019			
LRR132622_7400011			
LRR255628_741.23.1			
LRR255627_741.14.1			
LRR177381_741.22.1			
LRR255824_759.14.1			A50
LRR148550_759.13.1			
LRR142291_764.3.1			A50
LRR255925_764.8.1			C50
LRR255918_764.10.1			
LRR132735_7710014			
LRR110498_773000010			A50
LRR256188_778.4.1			
LRR256183_778.10.1			
LRR110607_782000011			
LRR274073_7840002			
LRR142233_792.5.1			
LRR110694_792000007			
LRR256763_815.10.1			A50
LRR289668_8170017			
LRR289666_8170015			
LRR256833_819.14.1			
LRR148843_819.10.1			
LRR111234_861000001			
LRR141333_864.1.1			
LRR111426_889000003			B50
LRR257779_894.3.1			
LRR257874_903.11.1			
LRR143587_910.1.1			A50
LRR136843_911.1.1			
LRR112067_1028000001			C50
LRR133274_10570003			
LRR112281_1122000002			
LRR133370_13490001			
LRR112602_1385000004			A50
LRR112701_1456000003			
LRR112754_1514000001			
LRR113016_1854000001			