Supplemental data files

Figure S1. Sequence alignments (Clustal Omega) and structural predictions (PsiPred) of the human nAChR subunits and other representative Cys-loop receptor subunits (Cys-loop indicated in blue). An AChBP (pdb1I9B) is included for the crystal structural reference comparison with the PsiPred predictions for the extracellular domain. The intracellular portions are indicated with a light blue bar, and the highly variable central section is center-justified below. Intron-exon borders are also indicated in red.

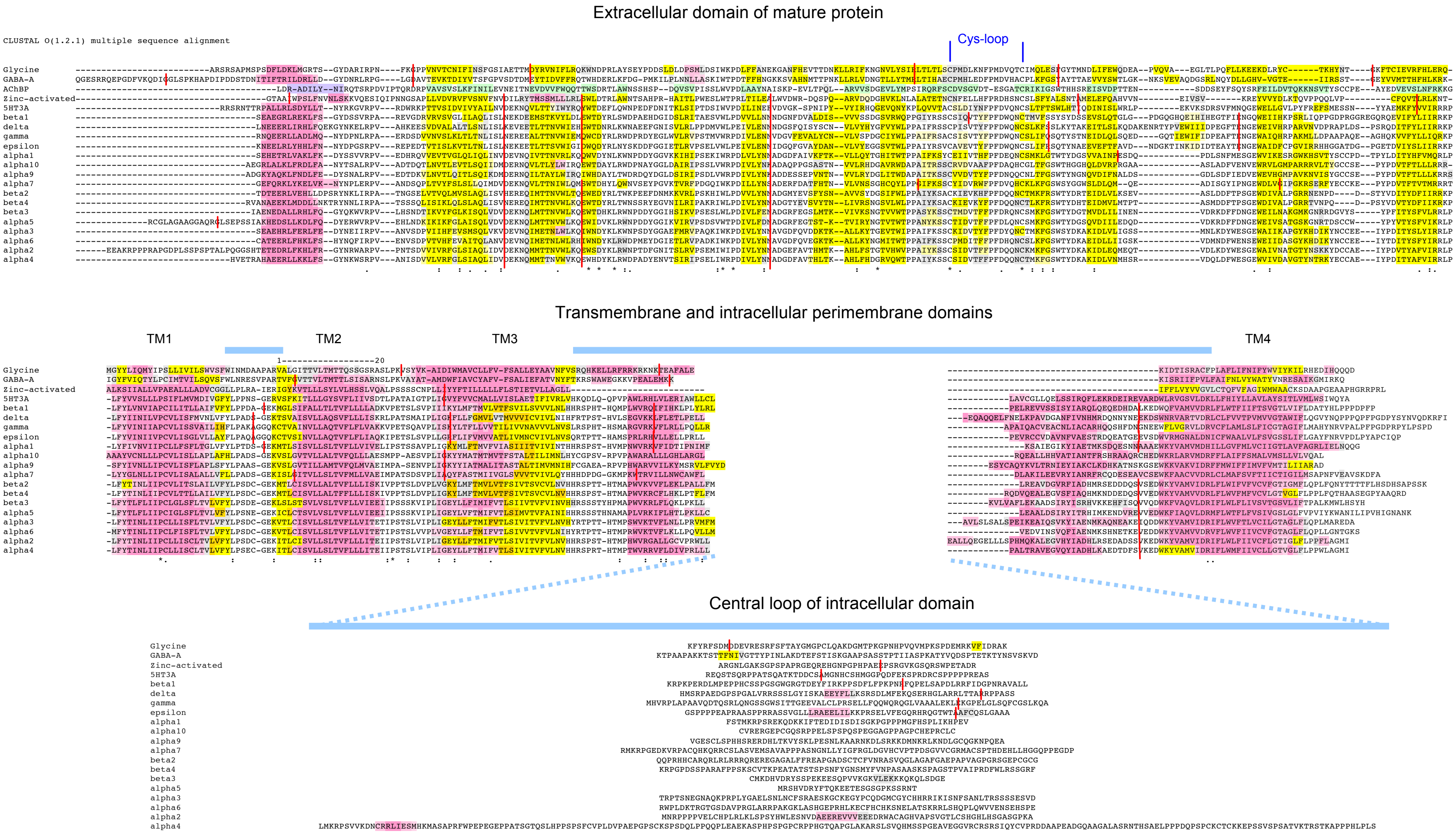
Table S1. Percent sequence identity among human intracellular domains.

Table S2. Accession numbers of sequences studied.

Table S3. Human gene locations.

Table S4. ELM analysis of $\alpha7$ sequences of multiple species and of all human nAChR subunits.

Multiple sequence alignment of pentameric ligand-gated Cys-loop ion-channel proteins



COLOR CODE

AChBP helix
AChBP strand
helix---
helix 50-75% confidence
helix <50% confidence
strand---
strand less confidence next to helix
strand less confidence next to coil
coil---
coil predicted with less confidence

Intracellular domain

* : . Clustal sequence conservation marks

| Intron-Exon border

Figure S1

	Glycine	**GABA-A**	**Zinc-act.**	**5HT3A**	**beta1**	**delta**	**epsilon**	**gamma**	**alpha1**	**alpha10**	**alpha9**	**alpha7**	**beta2**	**beta4**	**beta3**	**alpha5**	**alpha3**	**alpha6**	**alpha2**	**alpha4**
Glycine	100.00																			
GABA-A	10.53	100.00																		
Zinc-activated	12.50	50.00	100.00																	
5HT3A	9.62	8.57	40.00	100.00																
beta1	11.86	15.28	20.00	14.94	100.00															
delta	16.33	17.57	16.67	12.50	23.81	100.00														
epsilon	13.64	12.68	0.00	15.49	29.87	35.90	100.00													
gamma	12.24	10.81	6.25	12.00	26.14	26.40	37.93	100.00												
alpha1	13.33	13.04	0.00	16.30	33.33	27.78	21.13	25.33	100.00											
alpha10	13.04	5.00	41.67	25.71	18.92	18.46	20.97	13.85	14.93	100.00										
alpha9	13.33	14.93	14.29	16.05	13.83	8.70	12.64	8.70	16.87	29.73	100.00									
alpha7	21.05	12.99	11.76	23.81	20.62	18.45	17.53	17.76	23.53	25.00	12.62	100.00								
beta2	16.33	20.00	23.53	14.46	29.67	27.72	27.66	23.81	25.00	23.08	13.64	23.81	100.00							
beta4	18.87	16.22	20.00	16.87	28.00	24.75	23.66	23.36	33.72	24.62	10.75	23.42	44.54	100.00						
beta3	16.95	16.95	14.29	20.00	23.26	28.36	19.35	21.92	24.29	20.31	14.12	16.28	37.33	30.23	100.00					
alpha5	13.79	17.24	0.00	21.21	28.95	31.82	22.58	26.47	23.08	18.75	10.13	19.74	39.13	34.72	53.09	100.00				
alpha3	19.61	14.67	4.76	13.58	28.00	25.00	26.00	20.91	37.97	21.31	17.98	21.59	28.57	29.70	24.66	22.73	100.00			
alpha6	18.37	11.11	9.52	16.88	23.40	25.00	29.17	22.43	31.25	23.81	16.48	21.11	28.12	28.00	25.33	23.88	45.16	100.00		
alpha2	15.00	20.29	13.79	18.75	29.41	23.16	25.00	19.80	29.87	30.59	14.14	26.47	36.17	35.92	32.56	28.57	30.53	25.53	100.00	
alpha4	27.03	25.84	28.26	21.30	34.13	22.05	23.08	23.88	37.50	26.09	18.33	28.47	42.19	36.92	33.33	32.47	28.99	25.20	40.29	100.00

	human	**bovine**	**rat**	**chick**	**frog**	**zebrafish**
	Homo sapiens	*Bos taurus*	*Rattus norvegicus*	*Gallus gallus*	*Xenopus spp.*	*Danio rerio*
alpha1	Q53SH4	P02709	P25108	P09479	P22456	BC081554*
alpha2	Q15822	F1N4T3	P12389	P09480	F6YPK2	Q7ZZP7
alpha3	P32297	Q07263	P04757	P09481		F8W5I4
alpha4	P43681	E1BHK0	P09483	P09482	A9JRM3	Q0PJT8
alpha5	P30532	Q8SPU7	P20420	P26152	F7ELS1	Q567Y7
alpha6	Q15825	F1MQ06	P43143	P49581	F6SXF6	Q0PJT9
alpha7	P36544	P54131	Q05941	P22770	F6Q7N3	Q800C7
alpha9	Q9UGM1	F1MDD1	P43144	Q9PTS8	F6VVP3	F1Q7M1
alpha10	Q9GZZ6	F1MF20	Q9JLB5	Q9I8C7	F6ZMM6	R4GF05
beta1	P11230	P04758	P25109		P49579	G1FMP7
beta2	P17787	F1MUN1	P12390	P09484	A4IIS6	
beta3	Q05901	F1MF30	P12391	P43679	Q7SY88	Q7ZZP6
beta4	P30926	Q8SPU6	P12392	P26153	F7ERN7	
gamma	P07510	P13536	P18916	P02713	P05376	G1FMP9
delta	Q07001	P04759	P25110	F1NJ26	P09628	Q5BLJ3
epsilon	Q04844	P02715	P09660	------	P49580	G1FMQ0
5HT3A	P46098	F1N4Y2	P35563	F1NGS5	F6YC54	F1QQX3

Genbank accession	gene	subunit	chromosome map
NM_006529	GLRA3	Glycine	4q34.1
NM_000808	GABRA3	GABA-A	Xq28
AF364899	AChBP	AChBP	
NM_180990	ZACN	Zinc-activated	17q25.3
NM_000869	HTR3A	5HT3A	11q23.1
NM_000747	CHRNB	beta1	17p13.1
NM_000751	CHRND	delta	2q37.1
NM_005199	CHRNG	gamma	2q37.1
NM_000080	CHRNE	epsilon	17p13.2
NM_000079	CHRNA	alpha1	2q31.1
NM_020402	CHRNA10	alpha10	11p15.5
NM_017581	CHRNA9	alpha9	4p14
NM_000746	CHRNA7	alpha7	15q14
NM_000748	CHRNB2	beta2	1q21.3
NM_000750	CHRNB4	beta4	15q24
NM_000749	CHRNB3	beta3	8p11.2
NM_000745	CHRNB5	alpha5	15q24
NM_000743	CHRNA3	alpha3	15q24
NM_004198	CHRNA6	alpha6	8p11.21
NM_000742	CHRNA2	alpha2	8p21
NM_000744	CHRNA4	alpha4	20q13.33

	α7	α7	α7	α7	α7	α7	α10	α9	α1	γ	ε	δ	β1	β3	α5	α3	α6	α2	α4	β2	β4
ELM	human	bovine	rat	chick	frog	fish															
CLV_C14_Caspase3-7						1						1				1	1	2		1	
DEG_APCC_DBOX_1	1	1	1	1		1		1			1			1					1		1
DEG_APCC_KENBOX_2															1						
DEG_Nend_UBRbox_1			1	1																	
DEG_Nend_UBRbox_3		1			1	1															
DEG_SCF_TRCP1_1						1															
DOC_ANK_TNKS_1																				1	
DOC_CKS1_1	1										1	1				1	1				
DOC_CYCLIN_1							2	1		2		1	1	3	1	1	1	1	3		
DOC_MAPK_1	1	1	1	1		1				3	4	1					1		1		
DOC_MAPK_2													1								
DOC_PP1_RVXF_1								1								1				1	
DOC_PP2B_2										1			1						3		
DOC_WW_Pin1_4	2	2	2	2	3	2	3	1	2	1	4	2	2	1		2	2	3	9	1	5
LIG_14-3-3-1																			1		
LIG_14-3-3-2		1				1					1	1					1		1		
LIG_14-3-3-3											2	1				1		1	5		
LIG_Actin_WH2_2								1													
LIG_BIR_II_1										1	1										
LIG_BIR_III_2																	1		1		
LIG_CtBP_PxDLS_1							1														
LIG_EF_ALG2_ABM_2									1												
LIG_eIF4E_1								1													
LIG_EVH1_2									1				1								
LIG_LIR_Gen_1								1				3				1	1	2			
LIG_PTB_Apo_2									1												1
LIG_PTB_Phospho_1																					1
LIG_SH2_GRB2																					1
LIG_SH2_STAT3								1							1	1					
LIG_SH2_STAT5	2	2	2	2	2	2	1	2	1			2	3	1	2	2		1	2		1
LIG_SH3_3	2	1				1	2		1	1	2		1	1				1	7	1	2
LIG_TRAF2_1				2		1			1	1	1	1									
LIG_TRAF6																		1	1		
LIG_WW_3											1										
MOD_CDK_1											1			1					1		1
MOD_CK1_1	1	1	1	1	1	5	1	1	2	4	1		3	1	2	4	1	4	4	1	4
MOD_CK2_1	1	1	1	3	1	1			2	2	1	2		2	1	3	2	1	2	1	2
MOD_GSK3_1	1	1	1	2	2	4	1	2	1	1	1	1	1		3	6	1		5		3
MOD_LATS_1									1			1		1	1	1	1	1		1	1
MOD_NEK2_1				1					3	2	1	3			1	3	2		1		1
MOD_NEK2_2		1				1								1	1	2	1	1	3		1
MOD_PK_1											1								3		
MOD_PKA_1	1	1	1	1	1				1		1	2					1		1		
MOD_PKA_2	1	1	1	2	2	1			1		1	3	1	2	2	2	2		3	1	1
MOD_PKB_1																			1		
MOD_PLK	1	1	1		1	1							1					1	1	1	2
MOD_ProDKin_1	2	2	2	2	3	2	3	1	2	1	4	2	2	1		2	2	3	9	1	5
TRG_ENDOCYTIC_2	1	1	1	1	1	1		2				1	1	1				1			
TRG_ER_diArg_1			1								2	3	2			1	2		4	7	
TRG_LysEnd_APsAcLL_1				1	1	1	1			2	1	1	1					2			
TRG_PEX_1	1	1	1	1	1	1					1										
http://elm.eu.org/elms/browse_elms.html																					