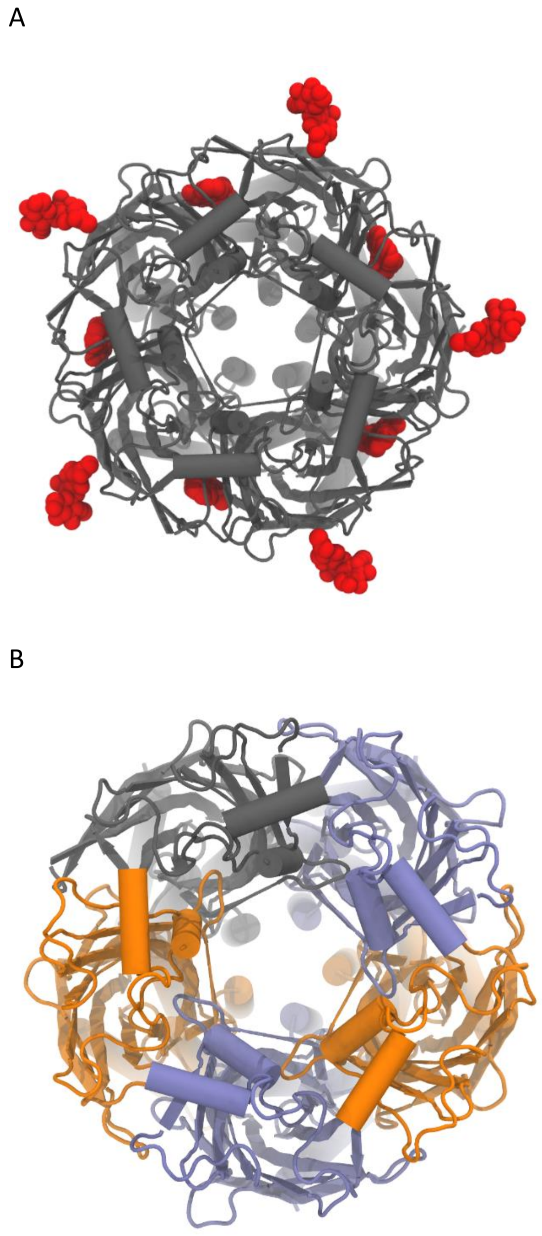
	GBRA4_HUMAN	GBRA6_HUMAN	GBRA3_HUMAN	GBRA5_HUMAN	GBRA1_HUMAN	GBRA2_HUMAN	GBRE_HUMAN	GBRG3_HUMAN	GBRG2_HUMAN	GBRG1_HUMAN	GBRR3_HUMAN	GBRR1_HUMAN	GBRR2_HUMAN	GBRD_HUMAN	GBRP_HUMAN	GBRT_HUMAN	GBRB1_HUMAN	GBRB2_HUMAN	GBRB3_HUMAN	4COF_GABA	GLRB_HUMAN	GLRA4_HUMAN	GLRA2_HUMAN	GLRA3_HUMAN	5CFB_GlyR	GLRA1_HUMAN	GLRA1_DANRE	3JAD_GlyR	GLUCB_CAEEL	GLUCL_CAEEL	3RIF_GluCl	4TNV_GluCl	GABR2_HUMAN	GABR1_HUMAN
GBRA4_HUMAN	100.00	69.98	56.44	56.83	58.07	56.82	37.84	43.08	43.21	44.59	31.97	32.46	32.07	33.91	33.59	28.24	34.45	32.06	34.37	42.17	29.33	33.25	34.97	33.64	42.86	34.57	34.12	41.92	29.10	31.19	35.03	35.35	11.75	12.39
GBRA6_HUMAN	69.98	100.00	61.11	62.04	60.77	60.49	38.90	48.35	48.98	51.27	33.75	33.76	33.83	35.03	33.78	32.33	37.33	36.50	37.57	41.87	33.42	36.21	37.19	37.25	43.75	37.28	37.08	41.92	31.12	32.20	35.93	36.56	14.53	12.83
GBRA3_HUMAN	56.44	61.11	100.00	69.70	69.30	69.84	36.38	43.59	41.86	43.88	29.76	31.25	31.00	33.16	33.16	29.23	35.46	35.21	36.90	41.57	28.71	32.62	34.79	32.85	40.48	33.99	34.66	40.42	28.20	29.02	35.03	35.65	14.05	14.55
GBRA5_HUMAN	56.83	62.04	69.70	100.00	70.51	72.77	36.73	46.21	45.37	45.76	31.07	30.24	31.26	34.20	33.60	29.79	37.11	37.03	37.70	41.87	28.36	34.06	35.31	33.82	40.77	35.48	36.02	40.72	30.71	29.59	34.43	35.05	13.43	11.84
GBRA1_HUMAN	58.07	60.77	69.30	70.51	100.00	76.63	36.34	43.10	45.43	45.34	31.71	30.77	30.86	32.99	32.98	30.23	37.43	35.93	38.38	41.87	28.57	34.97	36.48	36.30	41.96	35.73	36.02	41.92	31.07	30.46	34.43	34.74	13.87	12.04
GBRA2_HUMAN	56.82	60.49	69.84	72.77	76.63	100.00	36.28	43.73	43.38	44.01	30.71	30.02	31.31	34.29	32.17	30.84	36.68	36.29	38.42	41.87	31.58	35.62	35.98	36.88	41.96	36.16	35.95	41.32	30.69	31.19	35.33	35.65	14.29	12.42
GBRE_HUMAN	37.84	38.90	36.38	36.73	36.34	36.28	100.00	44.86	43.41	43.34	28.09	30.75	30.79	33.92	28.83	28.30	31.66	30.60	30.67	36.75	27.63	30.18	31.22	31.22	36.61	31.62	32.09	37.43	29.01	27.34	33.33	33.33	11.49	11.40
GBRG3_HUMAN	43.08	48.35	43.59	46.21	43.10	43.73	44.86	100.00	69.21	68.30	32.25	32.84	32.75	38.06	33.77	31.95	35.26	35.98	37.19	41.57	30.95	33.86	36.79	35.98	40.77	35.40	35.09	39.82	30.34	28.08	32.73	33.03	15.08	10.69
GBRG2_HUMAN	43.21	48.98	41.86	45.37	45.43	43.38	43.41	69.21	100.00	71.21	33.75	32.51	32.17	39.90	34.56	32.50	38.83	37.75	38.99	43.98	31.71	35.37	36.14	37.47	41.37	37.16	36.11	39.82	30.87	27.30	32.73	33.03	13.03	11.99
GBRG1_HUMAN	44.59	51.27	43.88	45.76	45.34	44.01	43.34	68.30	71.21	100.00	33.75	33.99	33.42	37.53	34.83	30.02	36.02	36.48	36.68	43.67	31.72	34.30	37.10	36.21	41.07	36.63	35.59	39.82	30.08	27.83	32.73	33.03	12.57	11.75
GBRR3_HUMAN	31.97	33.75	29.76	31.07	31.71	30.71	28.09	32.25	33.75	33.75	100.00	59.18	59.78	36.99	38.01	30.11	40.61	39.32	41.31	46.53	32.78	33.24	33.25	34.18	38.21	33.76	34.88	38.86	28.30	30.20	34.53	34.85	12.94	13.21
GBRR1_HUMAN	32.46	33.76	31.25	30.24	30.77	30.02	30.75	32.84	32.51	33.99	59.18	100.00	71.68	37.03	35.93	32.25	41.22	40.24	42.42	47.73	32.46	33.33	34.76	36.11	40.30	35.95	35.05	38.86	31.12	31.76	36.34	36.97	12.89	13.41
GBRR2_HUMAN	32.07	33.83	31.00	31.26	30.86	31.31	30.79	32.75	32.17	33.42	59.78	71.68	100.00	37.24	37.66	30.36	41.01	38.44	41.99	47.43	34.86	35.58	35.70	36.13	41.19	35.53	35.82	40.66	32.70	31.73	36.34	36.97	12.09	13.18
GBRD_HUMAN	33.91	35.03	33.16	34.20	32.99	34.29	33.92	38.06	39.90	37.53	36.99	37.03	37.24	100.00	40.14	34.94	40.23	39.86	39.21	47.29	33.74	38.48	38.08	36.68	42.26	37.76	38.64	43.24	31.71	32.04	36.34	36.67	12.68	12.54
GBRP_HUMAN	33.59	33.78	33.16	33.60	32.98	32.17	28.83	33.77	34.56	34.83	38.01	35.93	37.66	40.14	100.00	35.13	40.81	38.86	40.28	49.24	32.04	36.44	36.62	37.50	41.79	36.46	36.58	40.84	28.68	31.17	34.04	34.35	12.68	9.82
GBRT_HUMAN	28.24	32.33	29.23	29.79	30.23	30.84	28.30	31.95	32.50	30.02	30.11	32.25	30.36	34.94	35.13	100.00	40.64	38.98	41.79	51.51	30.75	34.00	34.73	34.17	41.19	34.10	34.20	40.06	30.30	28.20	32.73	33.03	13.29	11.89
GBRB1_HUMAN	34.45	37.33	35.46	37.11	37.43	36.68	31.66	35.26	38.83	36.02	40.61	41.22	41.01	40.23	40.81	40.64	100.00	76.32	76.33	88.55	33.18	37.07	37.53	36.69	43.15	36.89	37.47	43.84	31.57	33.75	38.74	39.09	13.29	11.31
GBRB2_HUMAN	32.06	36.50	35.21	37.03	35.93	36.29	30.60	35.98	37.75	36.48	39.32	40.24	38.44	39.86	38.86	38.98	76.32	100.00	79.45	89.46	33.41	36.97	37.68	36.12	43.45	36.32	37.38	44.44	33.00	34.65	39.64	40.00	13.30	11.82
GBRB3_HUMAN	34.37	37.57	36.90	37.70	38.38	38.42	30.67	37.19	38.99	36.68	41.31	42.42	41.99	39.21	40.28	41.79	76.33	79.45	100.00	97.89	33.57	37.23	38.42	37.56	44.35	37.05	37.87	44.74	32.75	33.17	38.14	38.48	14.29	11.66
4COF_GABA	42.17	41.87	41.57	41.87	41.87	41.87	36.75	41.57	43.98	43.67	46.53	47.73	47.43	47.29	49.24	51.51	88.55	89.46	97.89	100.00	40.73	43.85	46.36	45.76	45.90	45.15	45.76	46.04	38.07	38.91	38.72	39.08	17.32	12.02
GLRB_HUMAN	29.33	33.42	28.71	28.36	28.57	31.58	27.63	30.95	31.71	31.72	32.78	32.46	34.86	33.74	32.04	30.75	33.18	33.41	33.57	40.73	100.00	43.60	46.99	45.35	56.85	44.83	45.63	54.05	35.06	30.42	36.53	36.86	10.68	12.82
GLRA4_HUMAN	33.25	36.21	32.62	34.06	34.97	35.62	30.18	33.86	35.37	34.30	33.24	33.33	35.58	38.48	36.44	34.00	37.07	36.97	37.23	43.85	43.60	100.00	78.10	76.23	89.97	74.39	74.69	87.25	35.05	35.04	43.61	44.37	11.68	11.64
GLRA2_HUMAN	34.97	37.19	34.79	35.31	36.48	35.98	31.22	36.79	36.14	37.10	33.25	34.76	35.70	38.08	36.62	34.73	37.53	37.68	38.42	46.36	46.99	78.10	100.00	79.06	92.33	76.91	77.22	89.61	35.71	35.95	44.01	44.71	13.24	12.71
GLRA3_HUMAN	33.64	37.25	32.85	33.82	36.30	36.88	31.22	35.98	37.47	36.21	34.18	36.11	36.13	36.68	37.50	34.17	36.69	36.12	37.56	45.76	45.35	76.23	79.06	100.00	99.12	81.82	82.42	90.50	35.78	36.45	44.01	44.71	12.18	12.41
5CFB_GlyR	42.86	43.75	40.48	40.77	41.96	41.96	36.61	40.77	41.37	41.07	38.21	40.30	41.19	42.26	41.79	41.19	43.15	43.45	44.35	45.90	56.85	89.97	92.33	99.12	100.00	91.45	90.56	90.77	42.77	43.75	44.91	45.62	13.79	14.89
GLRA1_HUMAN	34.57	37.28	33.99	35.48	35.73	36.16	31.62	35.40	37.16	36.63	33.76	35.95	35.53	37.76	36.46	34.10	36.89	36.32	37.05	45.15	44.83	74.39	76.91	81.82	91.45	100.00	86.49	91.69	35.87	35.46	43.41	43.81	12.04	12.41
GLRA1_DANRE	34.12	37.08	34.66	36.02	36.02	35.95	32.09	35.09	36.11	35.59	34.88	35.05	35.82	38.64	36.58	34.20	37.47	37.38	37.87	45.76	45.63	74.69	77.22	82.42	90.56	86.49	100.00	98.52	35.64	35.95	43.71	44.41	11.61	13.64
3JAD_GlyR	41.92	41.92	40.42	40.72	41.92	41.32	37.43	39.82	39.82	39.82	38.86	38.86	40.66	43.24	40.84	40.06	43.84	44.44	44.74	46.04	54.05	87.25	89.61	90.50	90.77	91.69	98.52	100.00	41.54	44.01	44.11	44.82	14.73	16.24
GLUCB_CAEEL	29.10	31.12	28.20	30.71	31.07	30.69	29.01	30.34	30.87	30.08	28.30	31.12	32.70	31.71	28.68	30.30	31.57	33.00	32.75	38.07	35.06	35.05	35.71	35.78	42.77	35.87	35.64	41.54	100.00	44.07	50.88	50.74	10.27	10.66
GLUCL_CAEEL	31.19	32.20	29.02	29.59	30.46	31.19	27.34	28.08	27.30	27.83	30.20	31.76	31.73	32.04	31.17	28.20	33.75	34.65	33.17	38.91	30.42	35.04	35.95	36.45	43.75	35.46	35.95	44.01	44.07	100.00	98.82	98.52	11.96	11.11
3RIF_GluCl	35.03	35.93	35.03	34.43	34.43	35.33	33.33	32.73	32.73	32.73	34.53	36.34	36.34	36.34	34.04	32.73	38.74	39.64	38.14	38.72	36.53	43.61	44.01	44.01	44.91	43.41	43.71	44.11	50.88	98.82	100.00	99.70	14.29	12.02
4TNV_GluCl	35.35	36.56	35.65	35.05	34.74	35.65	33.33	33.03	33.03	33.03	34.85	36.97	36.97	36.67	34.35	33.03	39.09	40.00	38.48	39.08	36.86	44.37	44.71	44.71	45.62	43.81	44.41	44.82	50.74	98.52	99.70	100.00	14.40	12.17
GABR2_HUMAN	11.75	14.53	14.05	13.43	13.87	14.29	11.49	15.08	13.03	12.57	12.94	12.89	12.09	12.68	12.68	13.29	13.29	13.30	14.29	17.32	10.68	11.68	13.24	12.18	13.79	12.04	11.61	14.73	10.27	11.96	14.29	14.40	100.00	32.34
GABR1_HUMAN	12.39	12.83	14.55	11.84	12.04	12.42	11.40	10.69	11.99	11.75	13.21	13.41	13.18	12.54	9.82	11.89	11.31	11.82	11.66	12.02	12.82	11.64	12.71	12.41	14.89	12.41	13.64	16.24	10.66	11.11	12.02	12.17	32.34	100.00

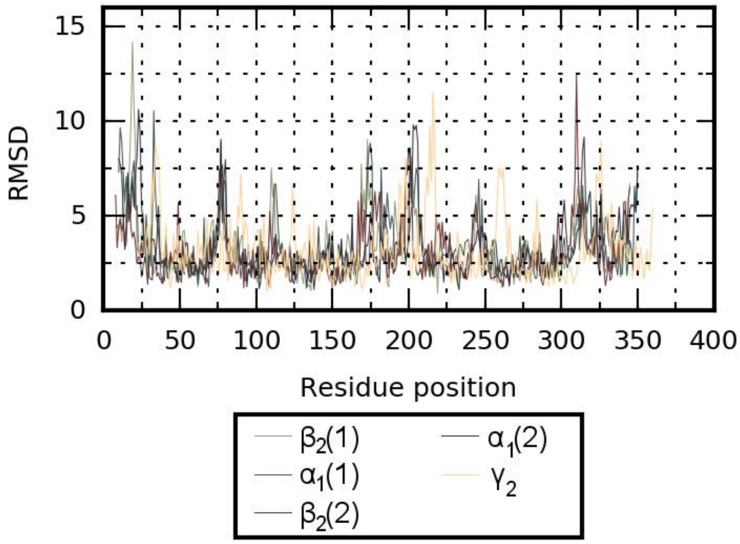
Supplementary Figure 1. Sequence identity of cys-loop receptor family subunits [in %].



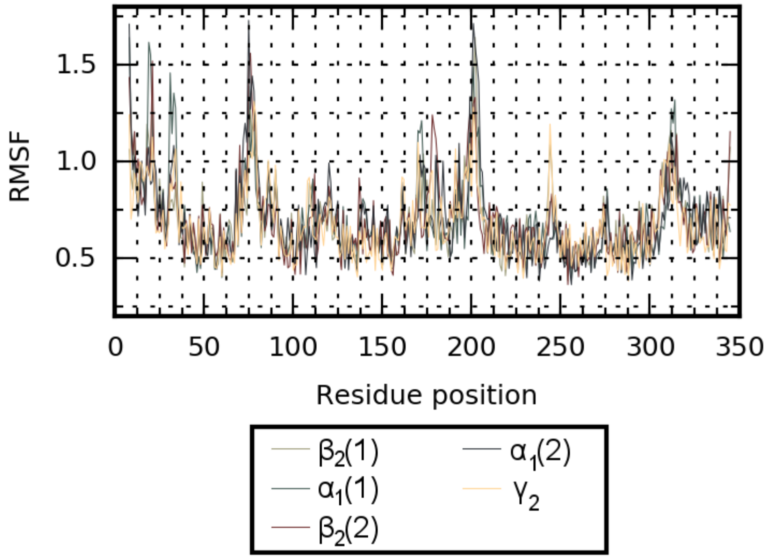
Supplementary Figure 2. A: Top view of GlyR (grey) with bound strychnine (red) structure used as a template. All subunits have same sequence. B: Same view of $\alpha_1\beta_2\gamma_2$ $GABA_A$R homology model. α_1 subunits in orange, β_2 in blue and γ_2 in grey.

Supplementary Figure 3. Sequence alignment of subunits comprised in the presented model and selected close homologs with recently obtained crystal structures. Residues colour code: hydrophobic - blue, polar uncharged - green, positive charge - red, negative charge - violet, glycine - orange, proline - yellow, cysteine - pink, others - no colour. Secondary structure prediction presented with red lines (α-helices) and green lines (β-strands).

A



B



Supplementary Figure 4. Mean values of RMSD and RMSF [Å] of respective subunits' residues over.