

All Projects

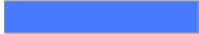
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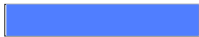




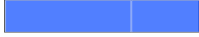


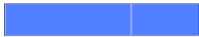




















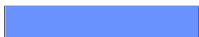





Created: today at 12:57

Summary Templates 49 Models 1 Project Data ▼






























































Template Results ⓘ

Templates							
Quaternary Structure Sequence Similarity Alignment More ▼							
↕Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/> ✓	4mf3.1.A Glutamate receptor ionotropic, kainate 1 <i>Crystal Structure of Human GRIK1 complexed with a 6-(tetrazolyl)aryl decahydroisoquinoline antagonist</i>						
▼	<div></div>	0.90	0.65	99.61	X-ray, 3.0Å	homo-dimer ✓	2 x SXI ⓘ
<input type="checkbox"/>	8r36.1.A Glutamate receptor ionotropic, kainate 1 <i>Crystal structure of the Gluk1 ligand-binding domain in complex with kainate and BPAM538 at 1.90 A resolution</i>						
▼	<div></div>	0.89	0.65	98.44	X-ray, 1.9Å	homo-dimer ✓	2 x KAI ⓘ, 1 x 9TE ⓘ
<input type="checkbox"/>	5cmk.1.A Glutamate receptor ionotropic, kainate 2 <i>Crystal structure of the GluK2EM LBD dimer assembly complex with glutamate and LY466195</i>						
▼	<div></div>	0.89	0.59	87.89	X-ray, 1.8Å	homo-dimer ✓	1 x GLU ⓘ, 2 x LI ⓘ, 1 x LY5 ⓘ
<input type="checkbox"/>	5cmk.1.B Glutamate receptor ionotropic, kainate 2 <i>Crystal structure of the GluK2EM LBD dimer assembly complex with glutamate and LY466195</i>						
▼	<div></div>	0.88	0.60	87.89	X-ray, 1.8Å	homo-dimer ✓	1 x GLU ⓘ, 2 x LI ⓘ, 1 x LY5 ⓘ
<input type="checkbox"/>	3g3f.1.A Glutamate receptor, ionotropic kainate 2 <i>Crystal structure of the GluR6 ligand binding domain dimer with glutamate and NaCl at 1.38 Angstrom resolution</i>						
▼	<div></div>	0.88	0.59	86.33	X-ray, 1.4Å	homo-dimer ✓	2 x GLU ⓘ
<input type="checkbox"/>	2wky.1.A GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 1 <i>Crystal structure of the ligand-binding core of GluR5 in complex with the agonist 4-AHCP</i>						
▼	<div></div>	0.88	0.59	98.44	X-ray, 2.2Å	homo-dimer ✓	2 x IBC ⓘ
<input type="checkbox"/>	3u92.1.B Glutamate receptor, ionotropic kainate 3 <i>Crystal structure of the GluK3 ligand binding domain complex with kainate and zinc: P2221 form</i>						
▼	<div></div>	0.87	0.54	84.65	X-ray, 1.9Å	homo-tetramer ✓	4 x KAI ⓘ, 16 x ZN ⓘ
<input type="checkbox"/>	3u92.1.A Glutamate receptor, ionotropic kainate 3 <i>Crystal structure of the GluK3 ligand binding domain complex with kainate and zinc: P2221 form</i>						
▼	<div></div>	0.87	0.54	84.65	X-ray, 1.9Å	homo-tetramer ✓	4 x KAI ⓘ, 16 x ZN ⓘ

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	3u94.1.B Glutamate receptor, ionotropic kainate 3 <i>Crystal structure of the GluK3 ligand binding domain complex with glutamate and zinc: P21212 form</i>						
▼		0.87	0.52	84.65	X-ray, 2.0Å	homo-tetramer ✓	4 x GLU  , 13 x ZN 
<input type="checkbox"/>	1s9t.1.A Glutamate receptor, ionotropic kainate 2 <i>Crystal structure of the GLUR6 ligand binding core in complex with quisqualate at 1.8Å resolution</i>						
▼		0.87	0.49	86.33	X-ray, 1.8Å	homo-tetramer ✓	4 x QUS 
<input type="checkbox"/>	5kuh.1.A Glutamate receptor ionotropic, kainate 2 <i>GluK2EM with LY466195</i>						
▼		0.88	0.28	87.89	EM	homo-tetramer ✓	4 x LY5 
<input type="checkbox"/>	5kuh.1.B Glutamate receptor ionotropic, kainate 2 <i>GluK2EM with LY466195</i>						
▼		0.88	0.28	87.89	EM	homo-tetramer ✓	4 x LY5 
<input type="checkbox"/>	A0A2J8MQ35.1.A Glutamate receptor <i>AlphaFold DB model of A0A2J8MQ35_PANTR (gene: A0A2J8MQ35_PANTR, organism: Pan troglodytes (Chimpanzee))</i>						
▼		0.91	-	99.61	AlphaFold v2	monomer ✓	None
<input type="checkbox"/>	2zns.1.A Glutamate receptor, ionotropic kainate 1 <i>Crystal structure of the ligand-binding core of the human ionotropic glutamate receptor, GluR5, in complex with glutamate</i>						
▼		0.89	-	99.61	X-ray, 2.0Å	monomer ✓	1 x GLU 
<input type="checkbox"/>	3fvo.2.A Glutamate receptor, ionotropic kainate 1 <i>Crystal structure of the human glutamate receptor, GluR5, ligand-binding core in complex with 8-epi-neodysiherbaine A in space group P1</i>						
▼		0.89	-	99.61	X-ray, 1.5Å	monomer ✓	1 x 8EP 
<input type="checkbox"/>	2znu.1.A Glutamate receptor, ionotropic kainate 1 <i>Crystal structure of the ligand-binding core of the human ionotropic glutamate receptor, GluR5, in complex with a novel selective agonist, neodysiherbaine A</i>						
▼		0.89	-	99.61	X-ray, 1.8Å	monomer ✓	1 x NDZ 
<input type="checkbox"/>	2znt.1.A Glutamate receptor, ionotropic kainate 1 <i>Crystal structure of the ligand-binding core of the human ionotropic glutamate receptor, GluR5, in complex with a novel selective agonist, dysiherbaine</i>						
▼		0.89	-	99.61	X-ray, 1.6Å	monomer ✓	1 x DYH 
<input type="checkbox"/>	5cmm.1.A Glutamate receptor ionotropic, kainate 2 <i>Crystal structure of the GluK2EM LBD dimer assembly complex with 2S,4R-4-methylglutamate</i>						
▼		0.88	-	87.89	X-ray, 1.3Å	monomer ✓	1 x SYM 
<input type="checkbox"/>	5neb.2.A Glutamate receptor ionotropic, kainate 1 <i>Structure of GluK1 ligand-binding domain (S1S2) in complex with LM-12b at 2.05 Å resolution</i>						
▼		0.88	-	98.44	X-ray, 2.0Å	monomer ✓	1 x 8VE 
<input type="checkbox"/>	3qxm.1.A Glutamate receptor ionotropic, kainate 2 <i>Crystal Structure of Human GluK2 Ligand-Binding Core in Complex with Novel Marine-Derived Toxins, Neodysiherbaine A</i>						

↓Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
▼		0.88	-	86.33	X-ray, 1.6Å	monomer ✓	1 x NDZ 
<input type="checkbox"/>				3u94.4.A Glutamate receptor, ionotropic kainate 3 <i>Crystal structure of the GluK3 ligand binding domain complex with glutamate and zinc: P21212 form</i>			
▼		0.88	-	84.65	X-ray, 2.0Å	monomer ✓	1 x GLU  , 4 x ZN 
<input type="checkbox"/>				3u94.2.A Glutamate receptor, ionotropic kainate 3 <i>Crystal structure of the GluK3 ligand binding domain complex with glutamate and zinc: P21212 form</i>			
▼		0.87	-	84.65	X-ray, 2.0Å	monomer ✓	1 x GLU  , 3 x ZN 
<input type="checkbox"/>				3u94.5.A Glutamate receptor, ionotropic kainate 3 <i>Crystal structure of the GluK3 ligand binding domain complex with glutamate and zinc: P21212 form</i>			
▼		0.87	-	84.65	X-ray, 2.0Å	monomer ✓	1 x GLU  , 4 x ZN 
<input type="checkbox"/>				6jmv.1.A Glutamate receptor ionotropic, kainate 3 <i>Crystal structure of the GluK3 ligand binding domain complex with SYM and zinc</i>			
▼		0.87	-	84.65	X-ray, 1.8Å	monomer ✓	1 x SYM  , 2 x ZN 
<input type="checkbox"/>				6jmv.2.A Glutamate receptor ionotropic, kainate 3 <i>Crystal structure of the GluK3 ligand binding domain complex with SYM and zinc</i>			
▼		0.87	-	84.65	X-ray, 1.8Å	monomer ✓	2 x ZN  , 1 x SYM 
<input type="checkbox"/>				4iy6.1.B Glutamate receptor 2 <i>Crystal structure of the GLUA2 ligand-binding domain (S1S2J-L483Y-N754S) in complex with glutamate and ME-CX516 at 1.72 Å resolution</i>			
▼		0.80	0.60	52.94	X-ray, 1.7Å	homo-dimer ✓	2 x MQR  , 4 x MQS  , 2 x GLU 
<input type="checkbox"/>				5ns9.1.A Glutamate receptor 2, Glutamate receptor 2 <i>Crystal structure of the GluA2 LBD (L483Y-N754S-L758V) in complex with glutamate</i>			
▼		0.80	0.58	53.33	X-ray, 1.4Å	homo-dimer ✓	2 x GLU 
<input type="checkbox"/>				3tkd.1.B GLUTAMATE RECEPTOR 2 <i>Crystal structure of the GluA2 ligand-binding domain (S1S2J-L483Y-N754S) in complex with glutamate and cyclothiazide at 1.45 Å resolution</i>			
▼		0.80	0.55	52.94	X-ray, 1.4Å	homo-dimer ✓	2 x GLU  , 2 x CYZ 
<input type="checkbox"/>				5fth.1.A GLUTAMATE RECEPTOR 2 <i>Crystal structure of the GluA2 K738M-T744K LBD in complex with glutamate (zinc form)</i>			
▼		0.79	0.48	52.94	X-ray, 2.9Å	homo-dimer ✓	2 x GLU  , 4 x ZN 
<input type="checkbox"/>				2gfe.1.A Glutamate receptor 2 <i>Crystal structure of the GluR2 A476E S673D Ligand Binding Core Mutant at 1.54 Angstroms Resolution</i>			
▼		0.79	0.47	52.94	X-ray, 1.5Å	homo-dimer ✓	3 x ZN  , 2 x GLU 
<input type="checkbox"/>				5fth.1.A GLUTAMATE RECEPTOR 2 <i>Crystal structure of the GluA2 K738M-T744K LBD in complex with glutamate (zinc form)</i>			
▼		0.79	0.47	53.54	X-ray, 2.9Å	homo-dimer ✓	2 x GLU  , 4 x ZN 

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	4yu0.1.A Glutamate receptor 2, Glutamate receptor 2 <i>Crystal structure of a tetramer of GluA2 TR mutant ligand binding domains bound with glutamate at 1.26 Angstrom resolution</i>						
▼		0.80	-	53.33	X-ray, 1.3Å	monomer ✓	1 x GLU
<input type="checkbox"/>	2gfe.2.A Glutamate receptor 2 <i>Crystal structure of the GluR2 A476E S673D Ligand Binding Core Mutant at 1.54 Angstroms Resolution</i>						
▼		0.79	-	52.94	X-ray, 1.5Å	monomer ✓	2 x ZN , 1 x GLU
<input type="checkbox"/>	4pe5.1.A Glutamate receptor ionotropic, NMDA 1 <i>Crystal Structure of GluN1a/GluN2B NMDA Receptor Ion Channel</i>						
▼		0.68	-	32.13	X-ray, 4.0Å	hetero-tetramer ⚠	3 x NAG-NAG-BMA-MAN, 2 x NAG-NAG-BMA-MAN-MAN-MAN, 1 x NAG-NAG, 1 x W , 2 x GLY , 8 x NAG , 2 x QEL , 2 x GLU
<input type="checkbox"/>	9d37.1.C Glutamate receptor ionotropic, NMDA 1 <i>Nonactive state of Gly-, Glu- bound GluN1a-2B-2D NMDAR</i>						
▼		0.67	-	32.13	EM	hetero-tetramer ⚠	1 x NAG-NAG, 2 x GLY , 4 x NAG , 2 x GLU
<input type="checkbox"/>	9d37.1.A Glutamate receptor ionotropic, NMDA 1 <i>Nonactive state of Gly-, Glu- bound GluN1a-2B-2D NMDAR</i>						
▼		0.67	-	32.13	EM	hetero-tetramer ⚠	1 x NAG-NAG, 2 x GLY , 4 x NAG , 2 x GLU
<input type="checkbox"/>	8usw.1.C Glutamate receptor ionotropic, NMDA 1 <i>CNQX-bound GluN1a-3A NMDA receptor</i>						
▼		0.63	-	32.13	EM	hetero-tetramer ⚠	2 x DQC
<input type="checkbox"/>	8vur.1.C Glutamate receptor ionotropic, NMDA 1 <i>Human GluN1-2A with IgG 003-102 WT conformation</i>						
▼		0.63	-	32.13	EM	hetero-hexamer ⚠	None
<input type="checkbox"/>	8usw.1.A Glutamate receptor ionotropic, NMDA 1 <i>CNQX-bound GluN1a-3A NMDA receptor</i>						
▼		0.62	-	32.13	EM	hetero-tetramer ⚠	2 x DQC
<input type="checkbox"/>	8jf7.1.C Glutamate receptor ionotropic, NMDA 1 <i>Triheteromeric NMDA receptor GluN1-GluN2A-GluN3A in complex with glycine, glutamate, a GluN1-specific Fab, and a GluN2A-specific Fab</i>						
▼		0.61	-	32.13	EM	hetero-10-mer ⚠	None
<input type="checkbox"/>	8jf7.1.A Glutamate receptor ionotropic, NMDA 1 <i>Triheteromeric NMDA receptor GluN1-GluN2A-GluN3A in complex with glycine, glutamate, a GluN1-specific Fab, and a GluN2A-specific Fab</i>						
▼		0.55	-	32.13	EM	hetero-10-mer ⚠	None
<input type="checkbox"/>	8p3s.1.B Glutamate receptor 2 <i>Homomeric GluA2 flip R/G-unedited Q/R-edited F231A mutant in tandem with TARP gamma-2, desensitized conformation 2</i>						

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
▼		0.39	0.00	47.52	EM	hetero-octamer 	7 x PLM  , 4 x OLC  , 5 x POV 
<input type="checkbox"/>	8p3q.1.B Glutamate receptor 2 <i>Homomeric GluA2 flip R/G-unedited Q/R-edited F231A mutant in tandem with TARP gamma-2, desensitized conformation 3</i>						
▼		0.37	0.10	47.52	EM, 3.0Å	hetero-octamer 	7 x PLM  , 4 x OLC  , 5 x POV 
<input type="checkbox"/>	8p3q.1.D Glutamate receptor 2 <i>Homomeric GluA2 flip R/G-unedited Q/R-edited F231A mutant in tandem with TARP gamma-2, desensitized conformation 3</i>						
▼		0.37	0.10	47.52	EM, 3.0Å	hetero-octamer 	7 x PLM  , 4 x OLC  , 5 x POV 
<input type="checkbox"/>	7ldd.1.D Glutamate receptor <i>native AMPA receptor</i>						
▼		0.37	-	47.52	EM	hetero-14-mer 	6 x NAG-NAG, 4 x ZK1  , 2 x R16  , 4 x OCT  , 4 x HP6  , 3 x D10  , 6 x NAG  , 4 x D12  , 4 x C14  , 4 x DD9  , 2 x XVD 
<input type="checkbox"/>	7lde.1.B Glutamate receptor <i>native AMPA receptor</i>						
▼		0.37	-	47.52	EM	hetero-14-mer 	5 x NAG-NAG, 4 x ZK1  , 2 x R16  , 4 x OCT  , 4 x HP6  , 3 x D10  , 7 x NAG  , 4 x D12  , 4 x C14  , 4 x DD9  , 2 x XVD 
<input type="checkbox"/>	7lde.1.D Glutamate receptor <i>native AMPA receptor</i>						
▼		0.36	-	47.52	EM	hetero-14-mer 	5 x NAG-NAG, 4 x ZK1  , 2 x R16  , 4 x OCT  , 4 x HP6  , 3 x D10  , 7 x NAG  , 4 x D12  , 4 x C14  , 4 x DD9  , 2 x XVD 
<input type="checkbox"/>	8p3q.1.C Glutamate receptor 2 <i>Homomeric GluA2 flip R/G-unedited Q/R-edited F231A mutant in tandem with TARP gamma-2, desensitized conformation 3</i>						
▼		0.36	0.10	47.52	EM, 3.0Å	hetero-octamer 	7 x PLM  , 4 x OLC  , 5 x POV 
<input type="checkbox"/>	8p3q.1.A Glutamate receptor 2 <i>Homomeric GluA2 flip R/G-unedited Q/R-edited F231A mutant in tandem with TARP gamma-2, desensitized conformation 3</i>						
▼		0.35	0.10	47.52	EM, 3.0Å	hetero-octamer 	7 x PLM  , 4 x OLC  , 5 x POV 

The full list of templates matching your target sequence includes the following templates which are not in the list above. The full template list is available in text or html format.

1a55.1.A, 1ggg.1.A, 1ggg.1.B, 1gr2.1.A, 1hsl.1.A, 1hsl.1.B, 1i69.1.A, 1i69.1.B, 1i6a.1.A, 1ii5.1.A, 1iit.1.A, 1ixc.1.C, 1ixc.1.D, 1ixi.1.A, 1iz1.1.A, 1iz1.1.B, 1iz1.1.C, 1iz1.1.D, 1lb8.1.A, 1lb9.1.A, 1lbb.1.A, 1lbc.2.A, 1lst.1.A, 1m5c.1.B, 1m5d.1.A, 1m5e.2.A, 1m5f.1.A, 1m5f.3.C, 1mqd.3.B, 1mqh.1.A, 1my0.1.B, 1p10.1.B, 1p1q.2.B, 1p1u.1.B, 1p1w.1.A, 1pb9.1.A, 1pbq.2.A, 1quk.1.A, 1qul.1.A, 1s9t.1.A, 1tt1.1.A, 1twy.1.A, 1twy.2.A, 1twy.3.A, 1twy.5.A, 1twy.6.A, 1txf.1.A, 1us5.1.A, 1vso.1.A, 1wdn.1.A, 1wvj.1.B, 1xhy.1.A, 1xs5.1.A, 1xt8.1.A, 1y1m.2.A, 1y1z.1.A, 1yae.1.A, 1yae.3.A, 1yae.5.A, 1yae.6.A, 1zbn.1.A, 2a5s.2.A, 2a5t.1.B, 2abh.1.A, 2aix.1.B, 2anj.1.A, 2cex.1.A, 2cex.2.A, 2cex.3.A, 2de2.1.A, 2de3.1.A, 2dvz.1.A, 2esn.1.A, 2esn.1.B, 2esn.1.C, 2esn.1.D, 2f34.2.A, 2f36.1.A, 2f36.1.C, 2f36.1.D, 2f5x.1.A, 2f6g.1.A, 2f6g.1.B, 2f6p.1.A, 2f6p.1.B, 2f78.1.A, 2f78.1.B, 2f7a.1.A, 2f7a.1.B, 2f7b.1.A, 2f7c.1.A, 2f8d.1.A, 2f97.1.B, 2fyi.1.A, 2fyi.1.B, 2fyi.2.A, 2gfe.1.A, 2gfe.2.A, 2h98.1.A, 2h98.1.B,

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