

All Projects

# >2ZNS\_1|Chain A|Glutamate receptor, ionotropic kainate 1|Homo sapiens (9606) mutated.fasta

Created: today at 12:57

Summary    Templates 49    Models 1

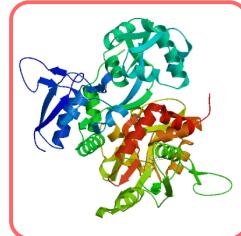
Project Data ▾

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## Model Results ⓘ



### Model 01



Structure Assessment

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Oligo-State  
Homo-dimer  
(matching prediction)

GMQE  
0.88

QMEANDisCo Global:  
0.82 ± 0.05

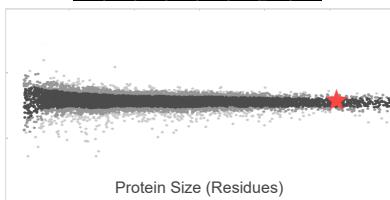
Ligands  
2 x SXI ⚙️ ▾

#### QMEANDisCo Local



#### QMEAN Z-Scores

QMEAN		0.89
Cβ		2.07
All Atom		1.26
solvation		1.08
torsion		0.14



#### Template

4mf3.1.A Glutamate receptor ionotropic, kainate 1

Crystal Structure of Human GRIK1 complexed with a 6-(tetrazolyl)aryl decahydroisoquinoline antagonist

Seq Identity

99.61%

**Coverage****Model-Template Alignment**

Model_01:A	AANRTLIVTPILEPEPYVMYRKSDKPLYGNDRFFEGYC	35
Model_01:B	AANRTLIVTPILEPEPYVMYRKSDKPLYGNDRFFEGYC	35
4mf3.1.A	AANRTLIVTPILEPEPYVMYRKSDKPLYGNDRFFEGYC	37
Model_01:A	LLLLKELSNIIGFIYDVKLVPDGKYGAQNDKGEWN	70
Model_01:B	LLLLKELSNIIGFIYDVKLVPDGKYGAQNDKGEWN	70
4mf3.1.A	LDLLKELSNIIGFIYDVKLVPDGKYGAQNDKGEWN	72
Model_01:A	GMVKELTDHRADLAVAPLTITYVREKVIDFSKPFM	105
Model_01:B	GMVKELTDHRADLAVAPLTITYVREKVIDFSKPFM	105
4mf3.1.A	GMVKELTDHRADLAVAPLTITYVREKVIDFSKPFM	107
Model_01:A	T1G1S1LYRKGTPIDSADDIAKQTKEFYGAVRDGS	140
Model_01:B	T1G1S1LYRKGTPIDSADDIAKQTKEFYGAVRDGS	140
4mf3.1.A	T1G1S1LYRKGTPIDSADDIAKQTKEFYGAVRDGS	142
Model_01:A	TMTFFFKKSKISTYEKMWAFMSSRQQTALVRNSDEG	175
Model_01:B	TMTFFFKKSKISTYEKMWAFMSSRQQTALVRNSDEG	175
4mf3.1.A	TMTFFFKKSKISTYEKMWAFMSSRQQTALVRNSDEG	177
Model_01:A	IQRVLTTDYALLMESTSIEYVTQRNCNLTQIGGLI	210
Model_01:B	IQRVLTTDYALLMESTSIEYVTQRNCNLTQIGGLI	210
4mf3.1.A	IQRVLTTDYALLMESTSIEYVTQRNCNLTQIGGLI	212
Model_01:A	DSKGYGVGTRIGSPYRDKITIAILQLQEEGKLHMM	245
Model_01:B	DSKGYGVGTRIGSPYRDKITIAILQLQEEGKLHMM	245
4mf3.1.A	DSKGYGVGTPIGSPYRDKITIAILQLQEEGKLHMM	247
Model_01:A	KEKWWRGNGCP	256
Model_01:B	KEKWWRGNGCP	256
4mf3.1.A	KEKWWRGNGCP	258