

☰ All Projects

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

Created: today at 12:57

Summary

Templates 49

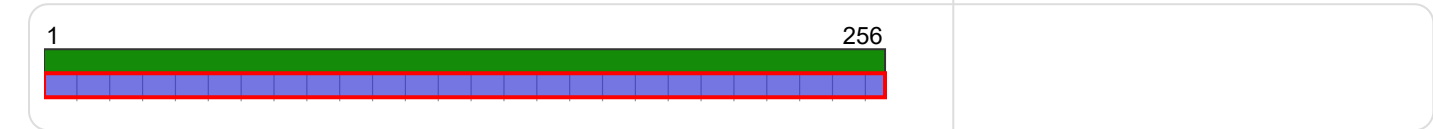
Models 1

Project Data ▾

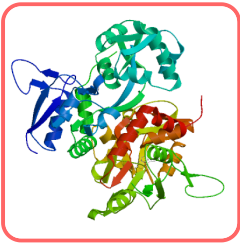
## Model Results ⓘ

Order by:

GMQE ▾



### Model 01



Structure Assessment

Compare ☐

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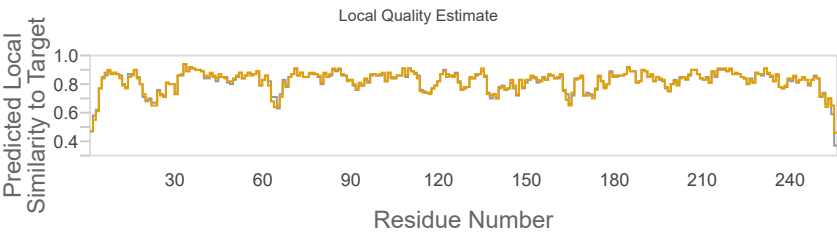
**Oligo-State**  
Homo-dimer  
(matching prediction)

**GMQE**  
0.88

**QMEANDisCo Global:**  
0.82 ± 0.05

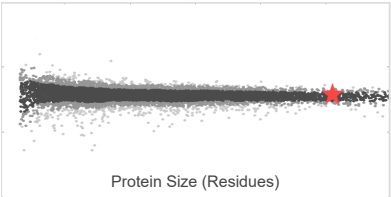
**Ligands**  
2 x SXI ⓘ ▾

#### 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%

## Model-Template Alignment

|            |                                      |     |
|------------|--------------------------------------|-----|
| Model_01:A | ANRTLIVTILFEPYVMYRKSDKPLYGNDREFGYC   | 35  |
| Model_01:B | ANRTLIVTILFEPYVMYRKSDKPLYGNDREFGYC   | 35  |
| 4mf3.1.A   | ANRTLIVTILFEPYVMYRKSDKPLYGNDREFGYC   | 37  |
| Model_01:A | LLLLKELSNILGFIYDVKLVPDGKYGAQNDKGEWN  | 70  |
| Model_01:B | LLLLKELSNILGFIYDVKLVPDGKYGAQNDKGEWN  | 70  |
| 4mf3.1.A   | LDLLKELSNILGFIYDVKLVPDGKYGAQNDKGEWN  | 72  |
| Model_01:A | GMVKELIDHRADLAVAPLTITYVREKVIDFSKPFM  | 105 |
| Model_01:B | GMVKELIDHRADLAVAPLTITYVREKVIDFSKPFM  | 105 |
| 4mf3.1.A   | GMVKELIDHRADLAVAPLTITYVREKVIDFSKPFM  | 107 |
| Model_01:A | TLGISILYRKGTPIIDSADDLAKQTKIEYGAVRDGS | 140 |
| Model_01:B | TLGISILYRKGTPIIDSADDLAKQTKIEYGAVRDGS | 140 |
| 4mf3.1.A   | TLGISILYRKGTPIIDSADDLAKQTKIEYGAVRDGS | 142 |
| Model_01:A | TMTFFKKSKISTYEKMWAFMSSRQQTALVRNSDEG  | 175 |
| Model_01:B | TMTFFKKSKISTYEKMWAFMSSRQQTALVRNSDEG  | 175 |
| 4mf3.1.A   | TMTFFKKSKISTYEKMWAFMSSRQQTALVRNSDEG  | 177 |
| Model_01:A | IQRVLTIDYALLMESTSIEYVTQRNCNLTQIGGLI  | 210 |
| Model_01:B | IQRVLTIDYALLMESTSIEYVTQRNCNLTQIGGLI  | 210 |
| 4mf3.1.A   | IQRVLTIDYALLMESTSIEYVTQRNCNLTQIGGLI  | 212 |
| Model_01:A | DSKGYGVGTPIGSPYRDKITIAILQLQEEGKLHMM  | 245 |
| Model_01:B | DSKGYGVGTPIGSPYRDKITIAILQLQEEGKLHMM  | 245 |
| 4mf3.1.A   | DSKGYGVGTPIGSPYRDKITIAILQLQEEGKLHMM  | 247 |
| Model_01:A | KEKWWRGNGCP                          | 256 |
| Model_01:B | KEKWWRGNGCP                          | 256 |
| 4mf3.1.A   | KEKWWRGNGCP                          | 258 |