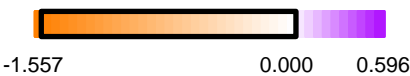
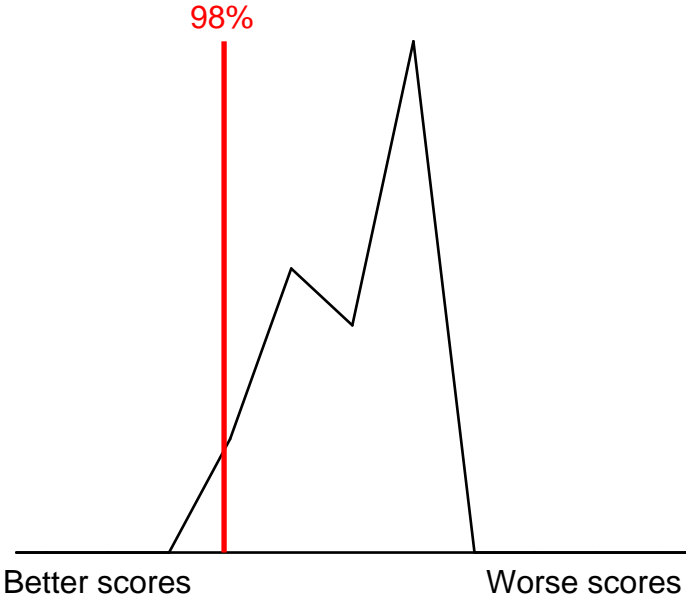
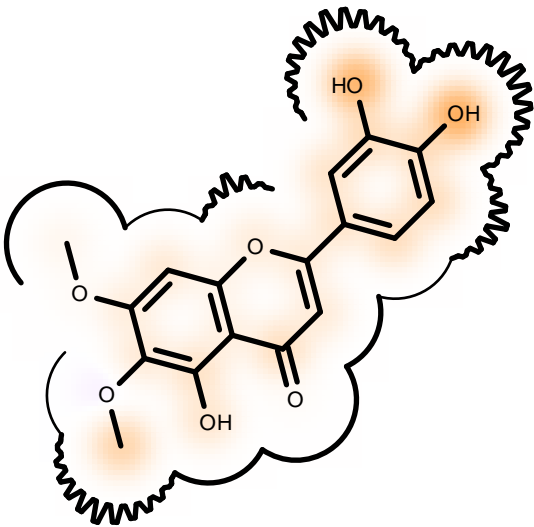


Molecule Name omega_1_16
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 1

Total Score -11.29

Score compared to other molecules



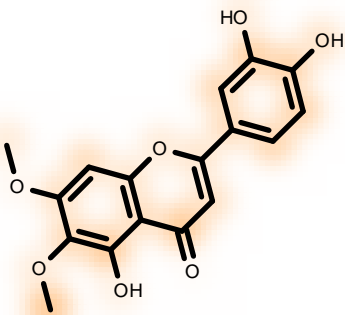
Protein Contact

Protein Cavity

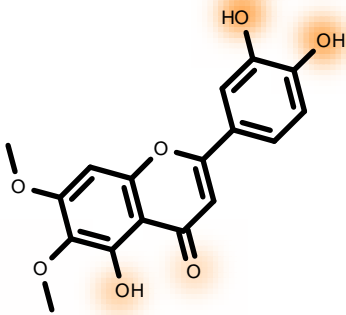
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

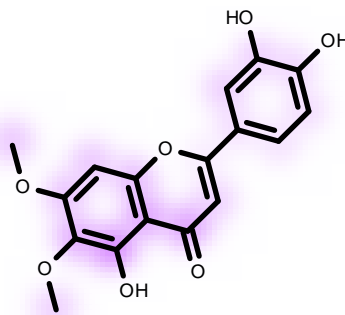
Shape -12.36



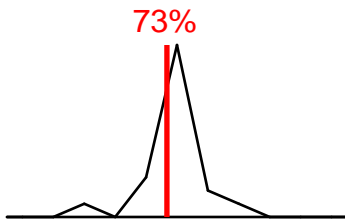
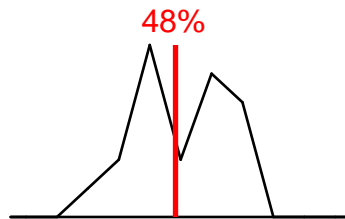
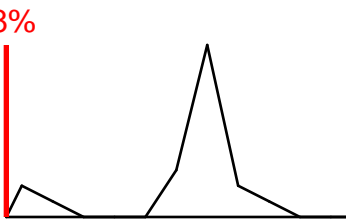
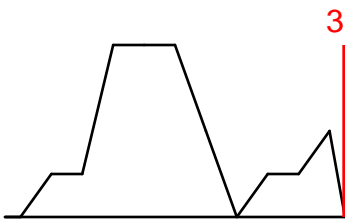
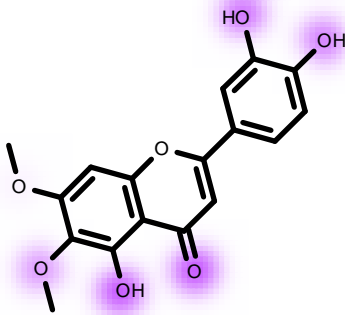
Hydrogen Bond -4.51



Protein Desolvation 3.09



Ligand Desolvation 2.49



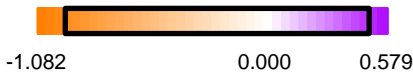
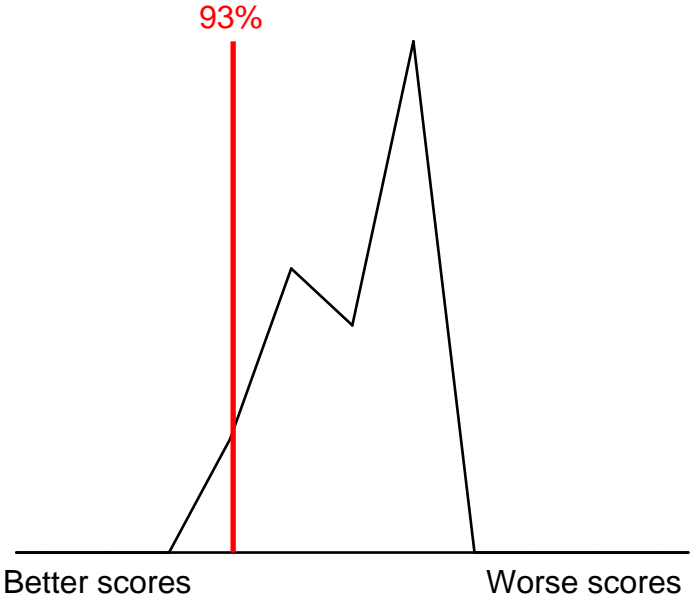
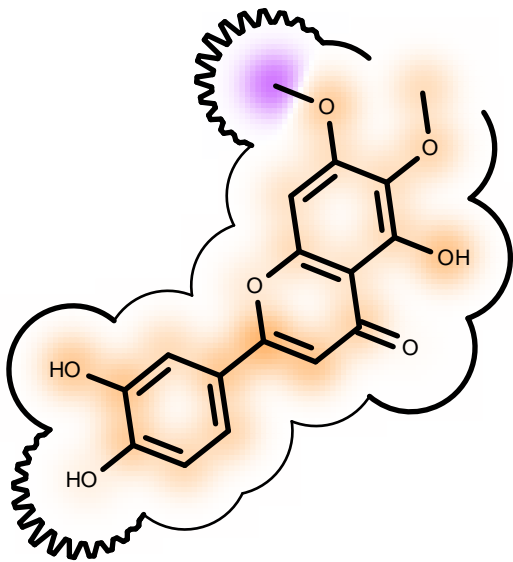
Acceptor
Metal

Donor
Contact

Molecule Name omega_1_10
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 2

Total Score -11.24

Score compared to other molecules



Protein Contact

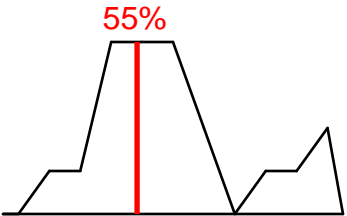
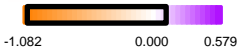
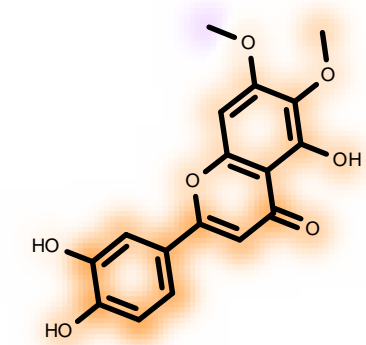


Protein Cavity

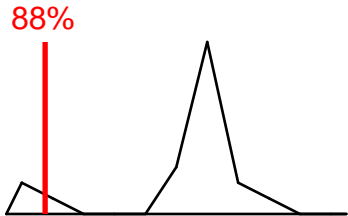
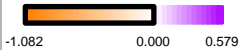
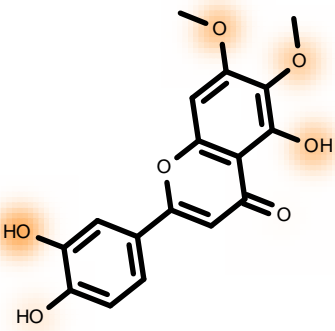
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

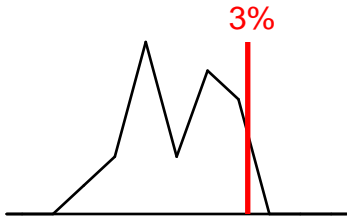
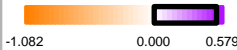
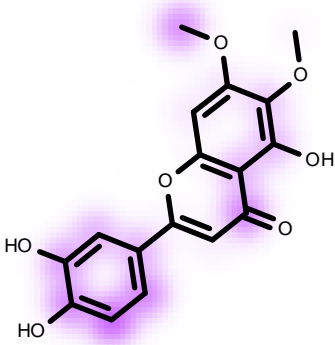
Shape -14.64



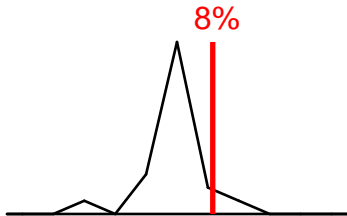
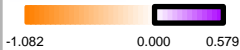
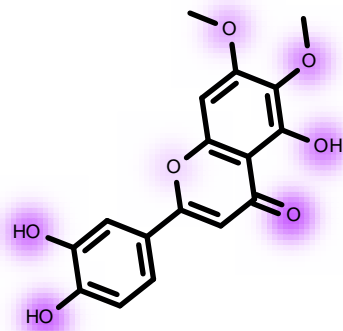
Hydrogen Bond -3.50



Protein Desolvation 3.91



Ligand Desolvation 2.99



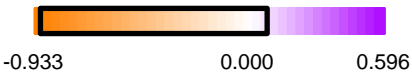
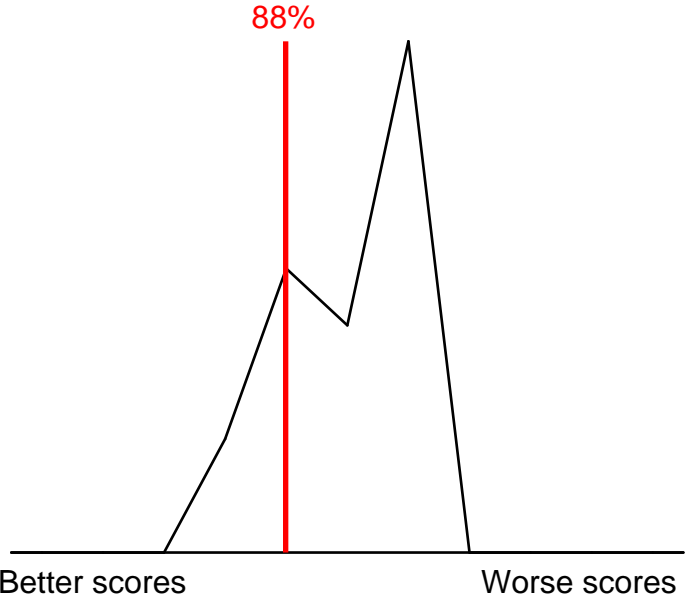
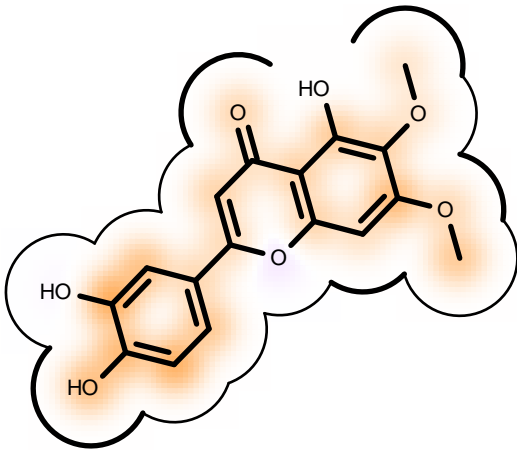
Acceptor
Metal

Donor
Contact

Molecule Name omega_1_4
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 3

Total Score -10.92

Score compared to other molecules



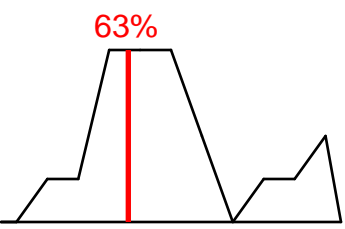
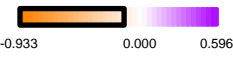
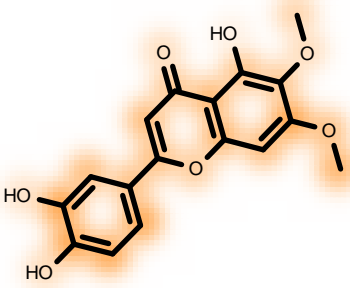
Protein Contact

Protein Cavity

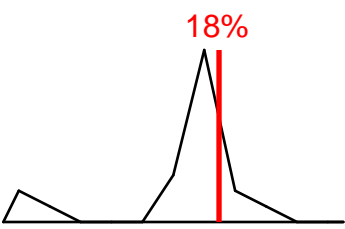
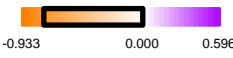
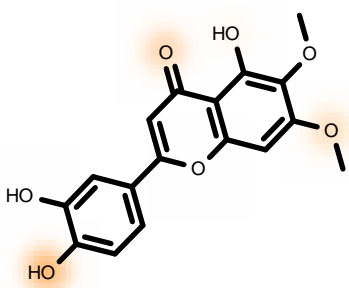
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

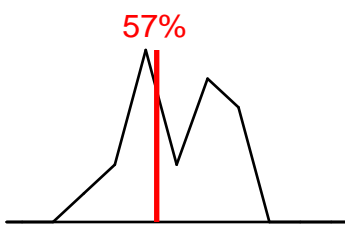
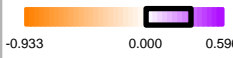
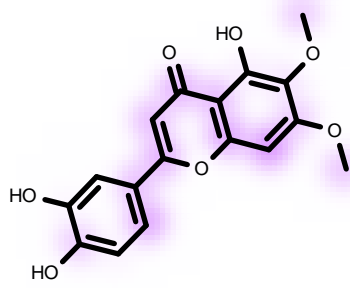
Shape -14.71



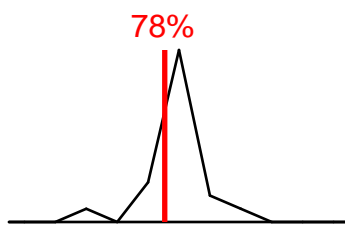
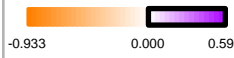
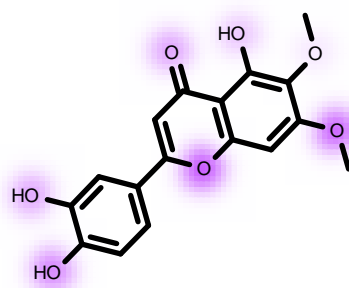
Hydrogen Bond -1.59



Protein Desolvation 2.93



Ligand Desolvation 2.45



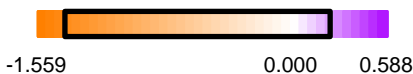
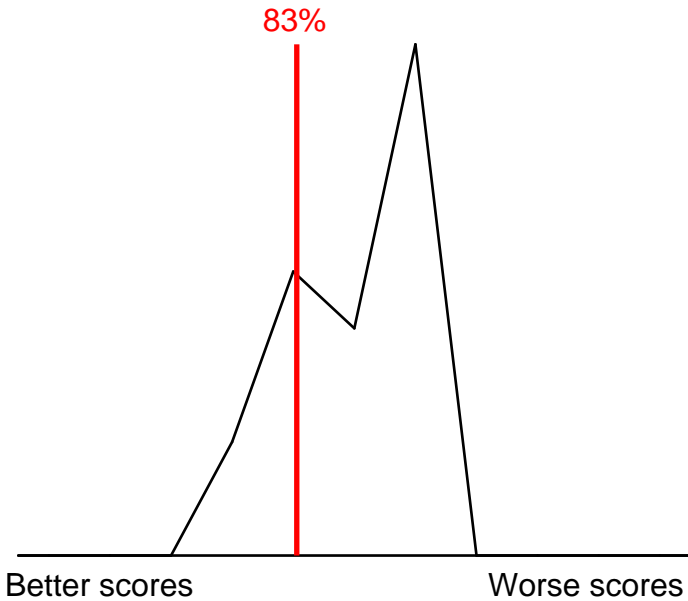
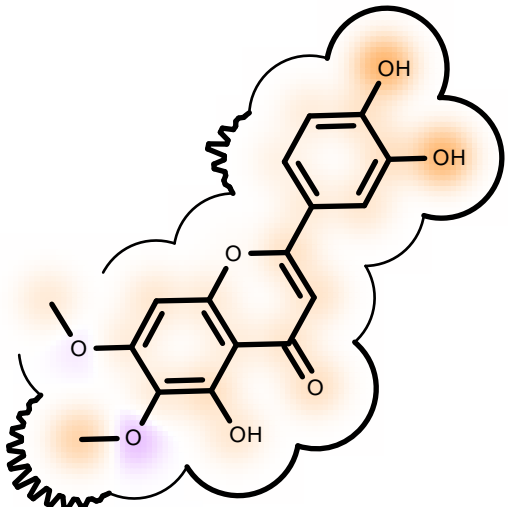
Acceptor
Metal

Donor
Contact

Molecule Name omega_1_13
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 4

Total Score -10.90

Score compared to other molecules



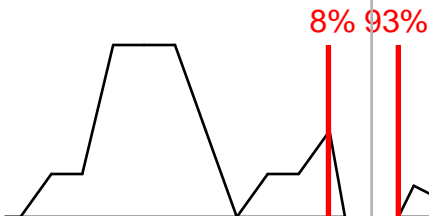
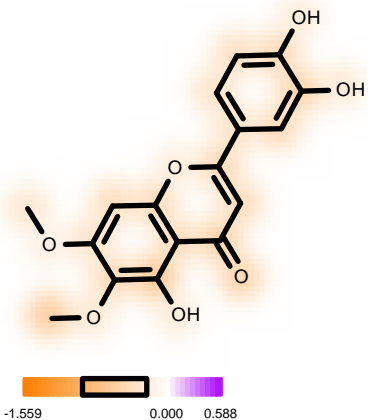
Protein Contact

Protein Cavity

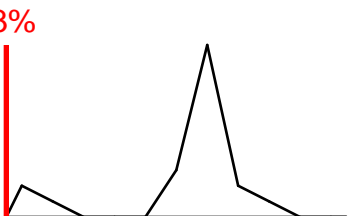
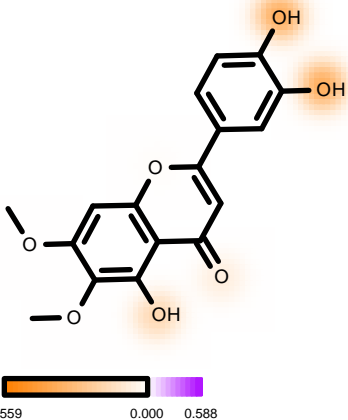
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

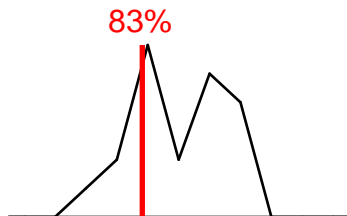
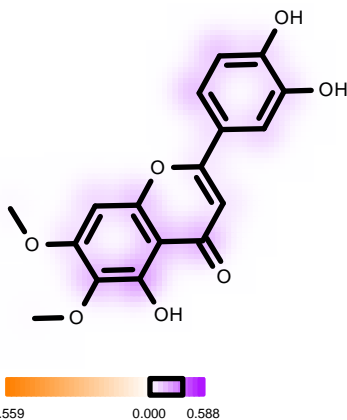
Shape -12.59



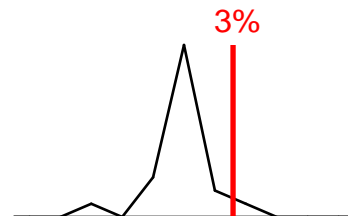
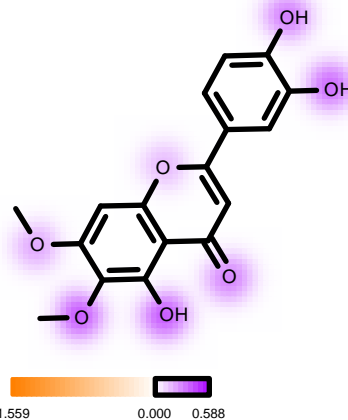
Hydrogen Bond -4.19



Protein Desolvation 2.75



Ligand Desolvation 3.13



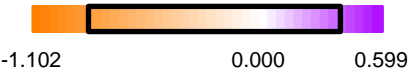
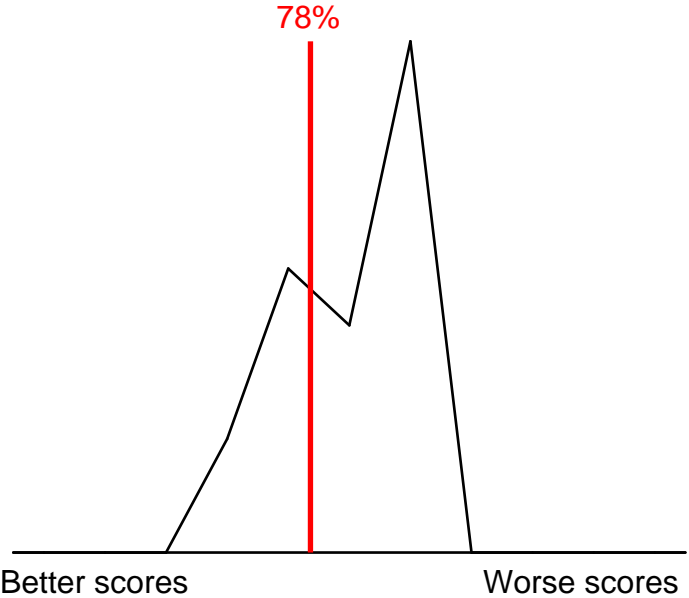
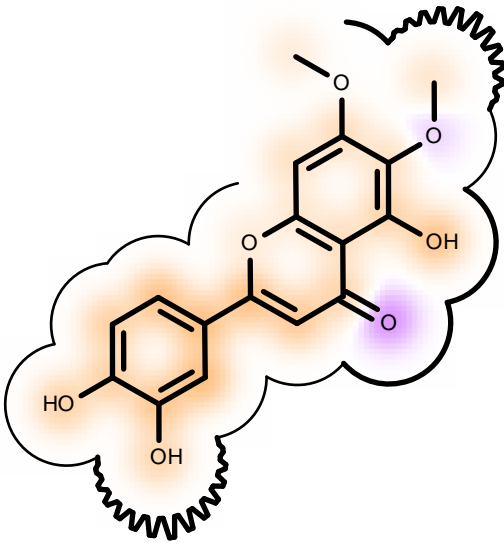
Acceptor
Metal

Donor
Contact

Molecule Name omega_1_14
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 5

Total Score -10.80

Score compared to other molecules



Protein Contact

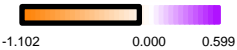
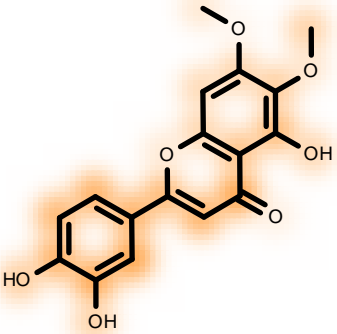


Protein Cavity

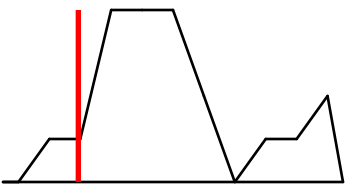
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

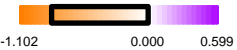
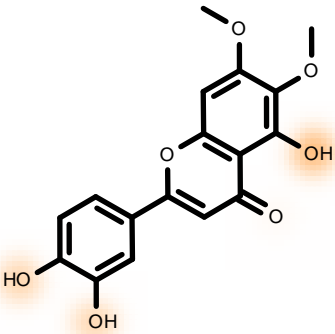
Shape -15.27



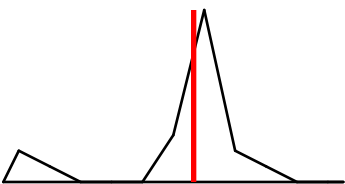
93%



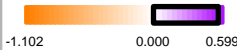
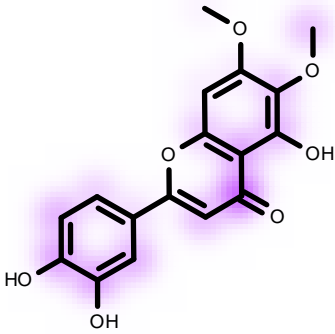
Hydrogen Bond -1.86



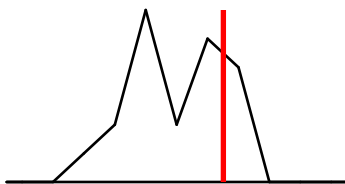
57%



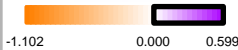
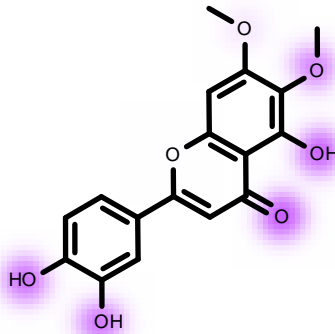
Protein Desolvation 3.65



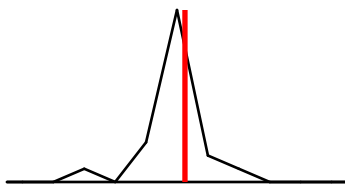
18%



Ligand Desolvation 2.69



38%



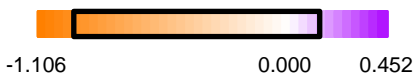
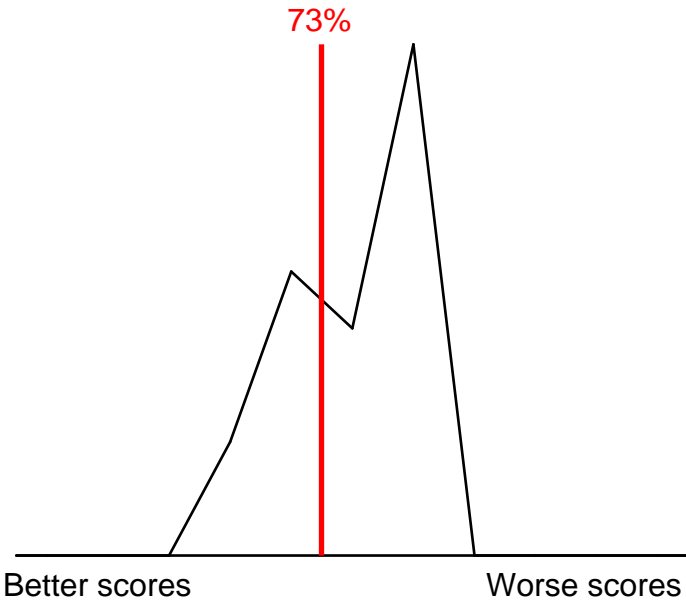
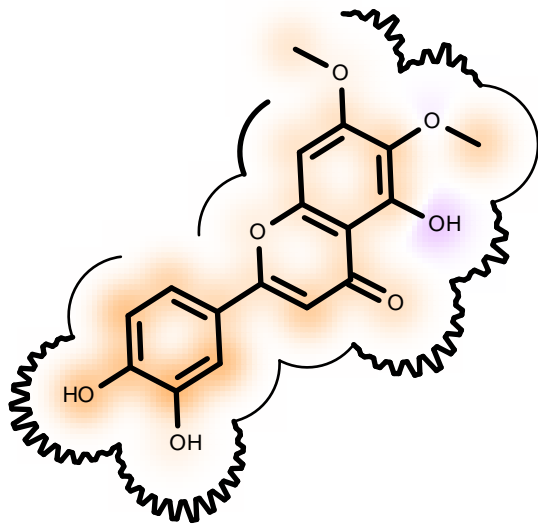
Acceptor
Metal

Donor
Contact

Molecule Name omega_1_12
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 6

Total Score -10.75

Score compared to other molecules

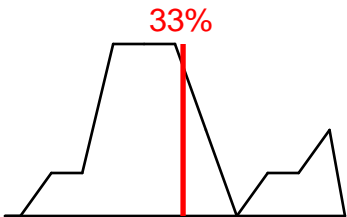
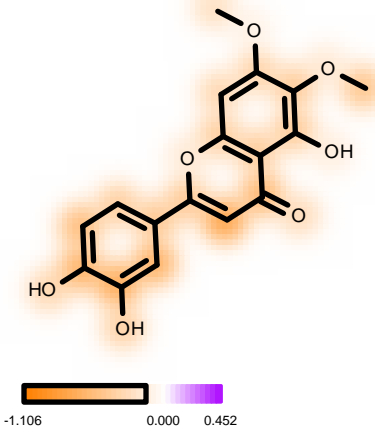


Protein Contact Protein Cavity

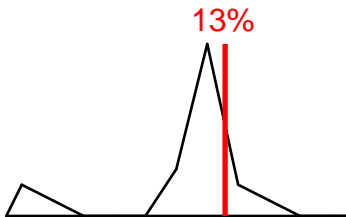
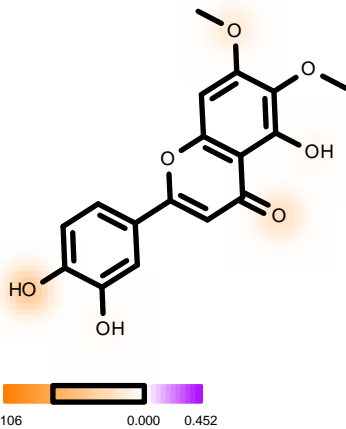
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

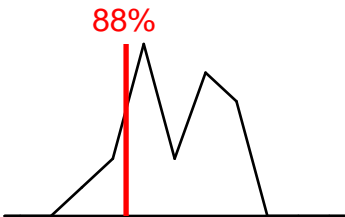
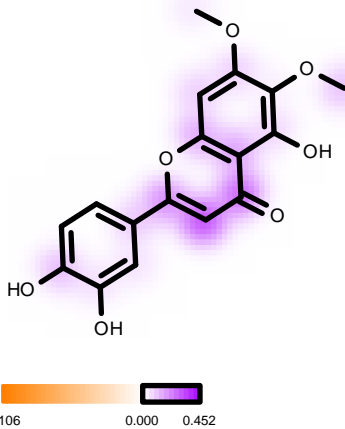
Shape -14.16



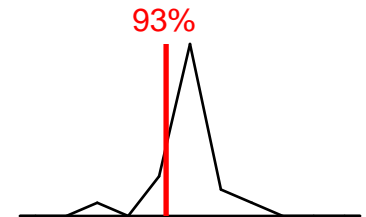
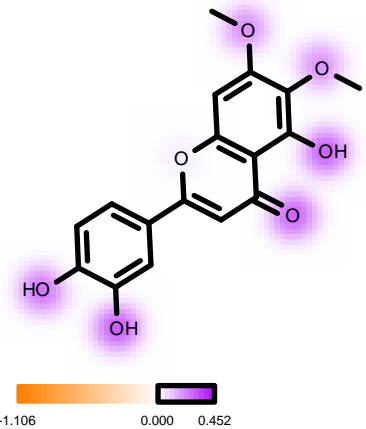
Hydrogen Bond -1.56



Protein Desolvation 2.62



Ligand Desolvation 2.34

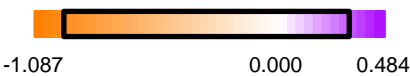
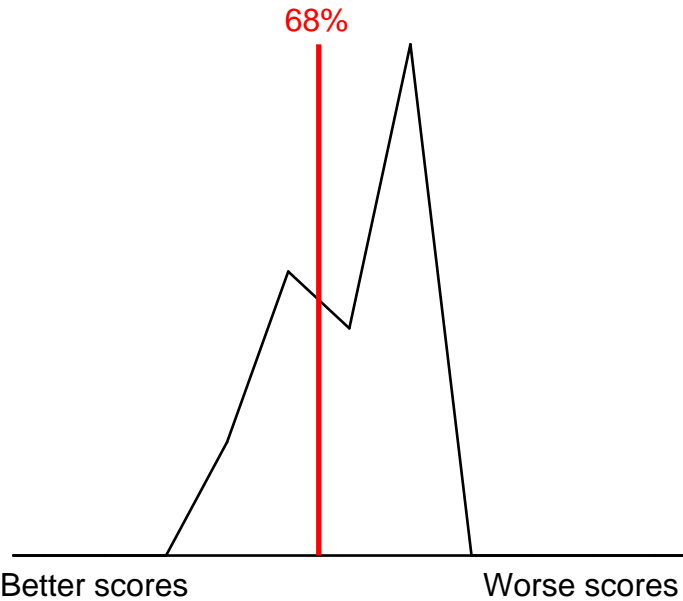
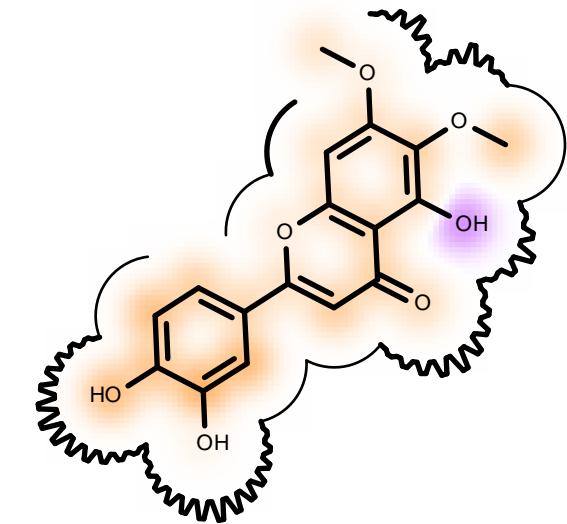


Acceptor Donor
Metal Contact

Molecule Name omega_1_12
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 7

Total Score -10.75

Score compared to other molecules

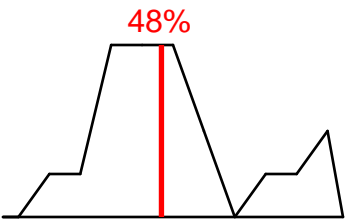
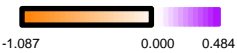
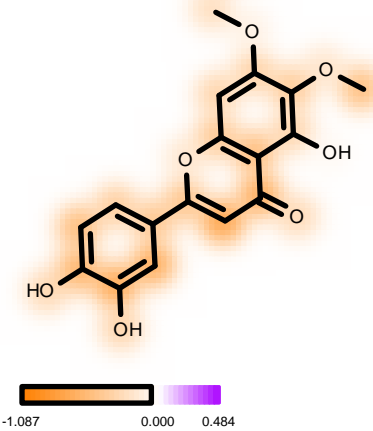


Protein Contact Protein Cavity

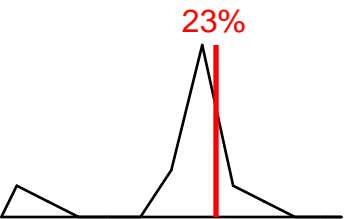
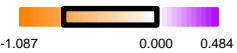
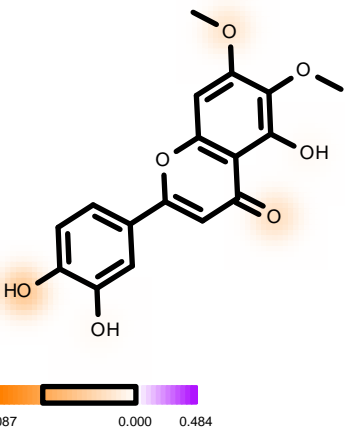
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

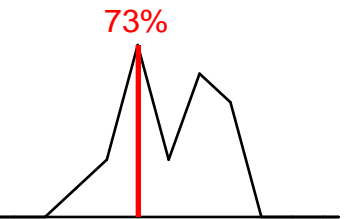
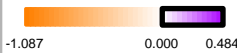
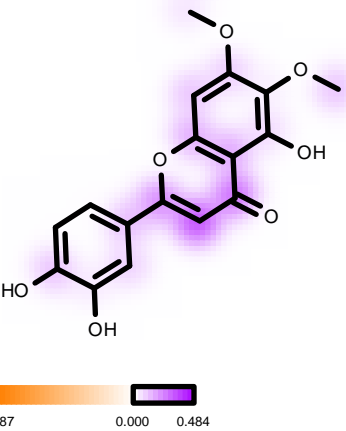
Shape -14.38



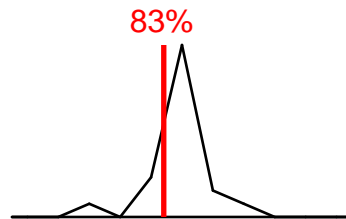
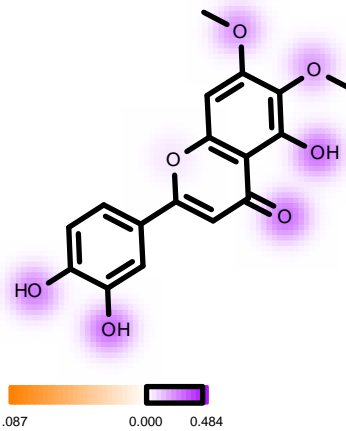
Hydrogen Bond -1.60



Protein Desolvation 2.82



Ligand Desolvation 2.41

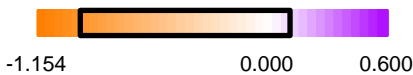
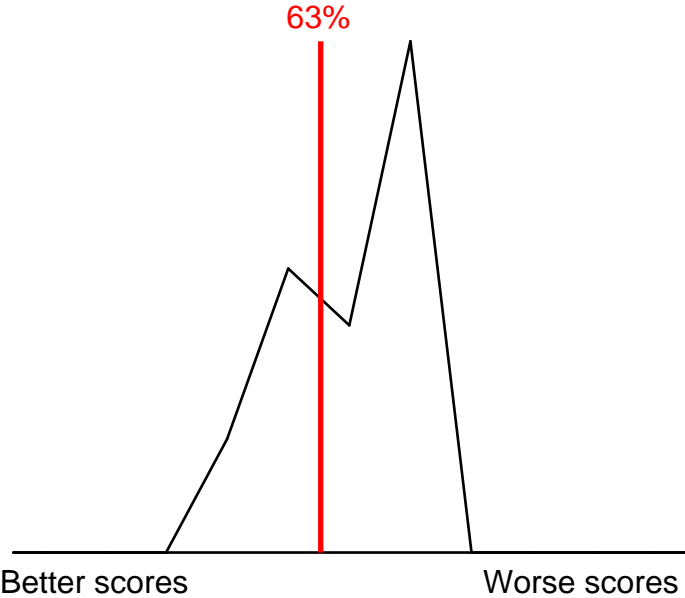
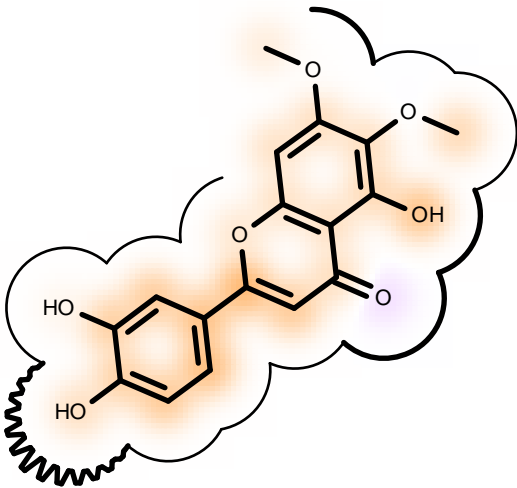


Acceptor Donor
Metal Contact

Molecule Name omega_1_16
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 8

Total Score -10.74

Score compared to other molecules



Protein Contact

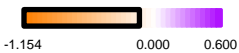
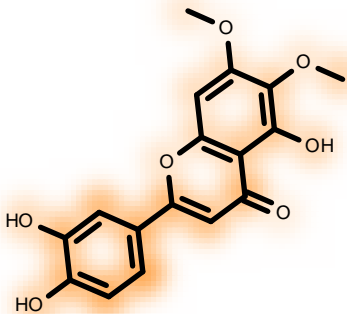


Protein Cavity

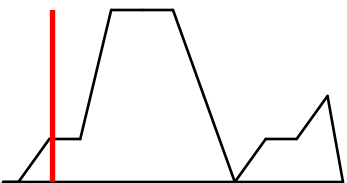
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

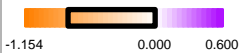
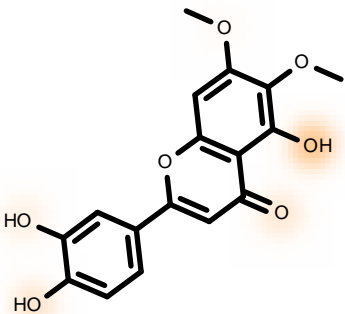
Shape -15.55



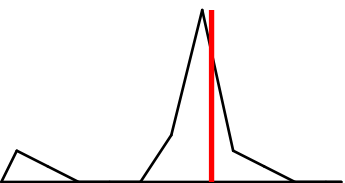
95%



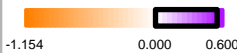
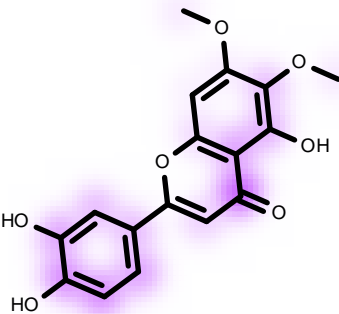
Hydrogen Bond -1.65



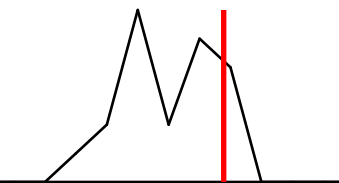
33%



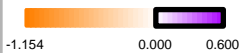
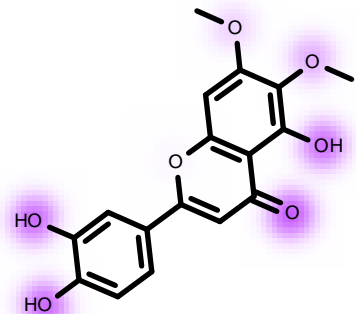
Protein Desolvation 3.74



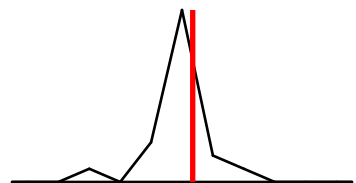
13%



Ligand Desolvation 2.72



33%



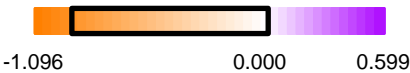
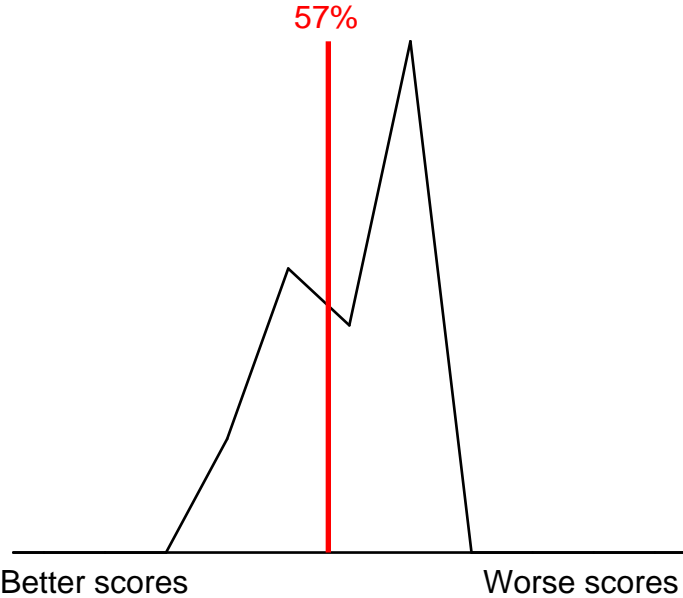
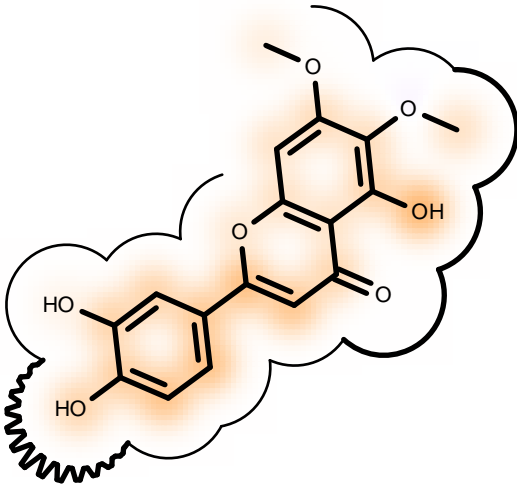
Acceptor
Metal

Donor
Contact

Molecule Name omega_1_16
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 9

Total Score -10.70

Score compared to other molecules

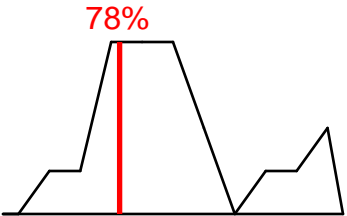
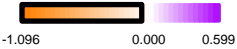
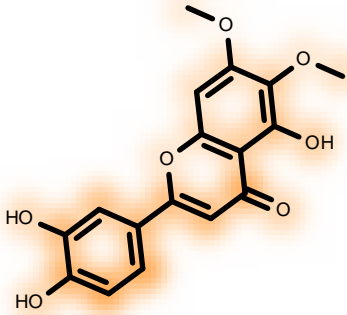


Protein Contact Protein Cavity

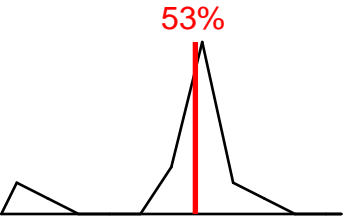
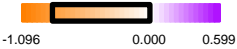
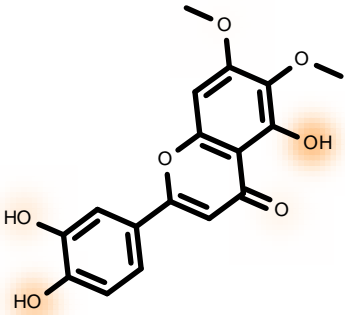
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

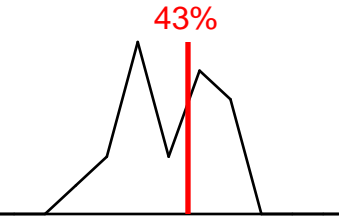
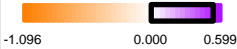
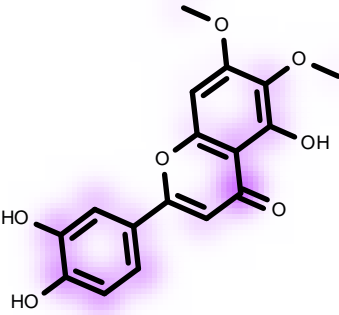
Shape -14.83



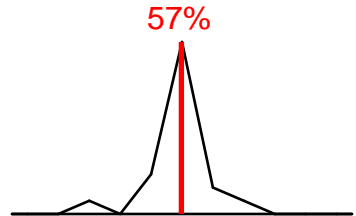
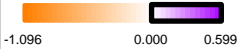
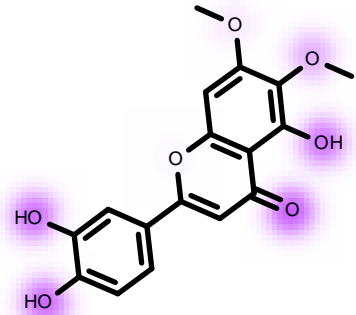
Hydrogen Bond -1.82



Protein Desolvation 3.35



Ligand Desolvation 2.60

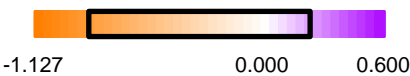
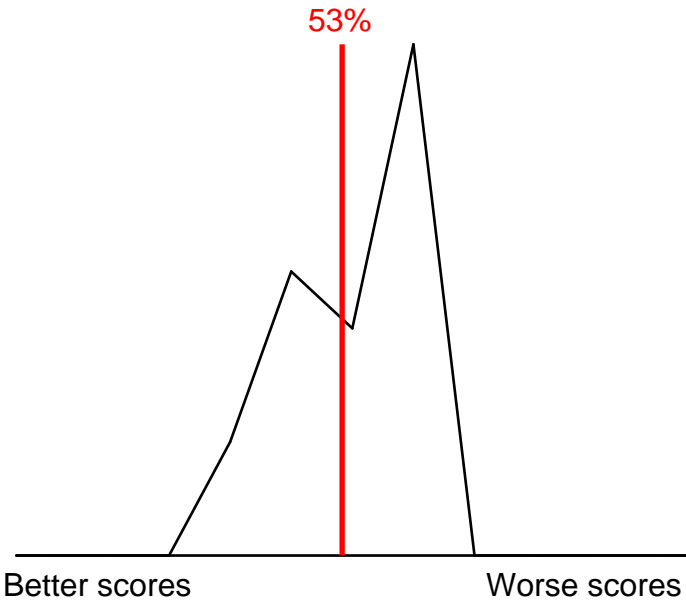
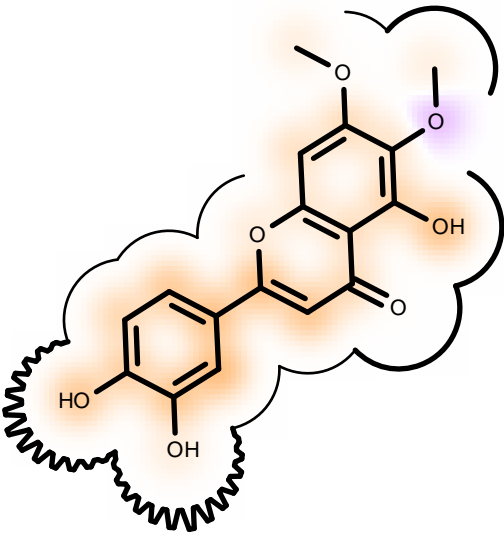


Acceptor Metal Donor Contact

Molecule Name omega_1_14
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 10

Total Score -10.64

Score compared to other molecules



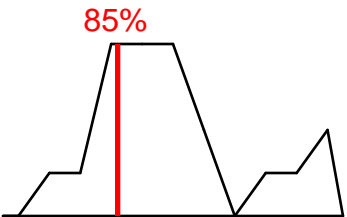
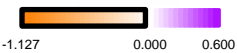
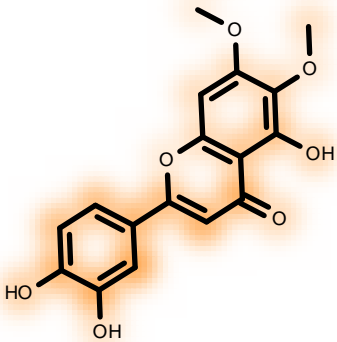
Protein Contact

Protein Cavity

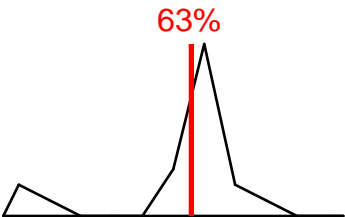
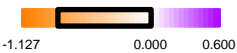
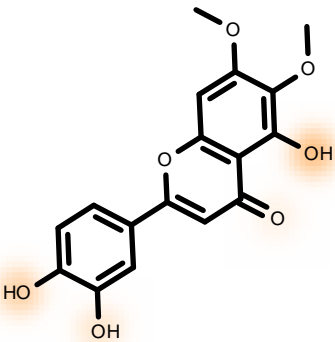
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

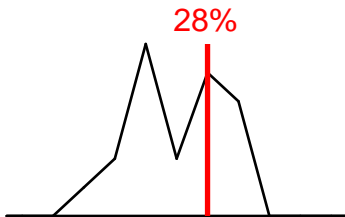
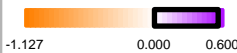
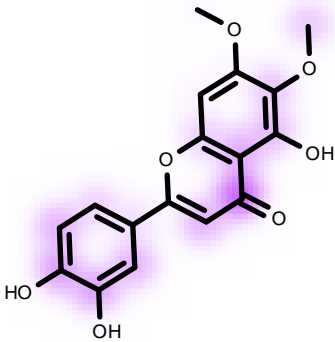
Shape -14.85



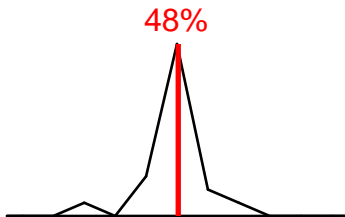
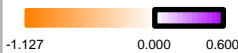
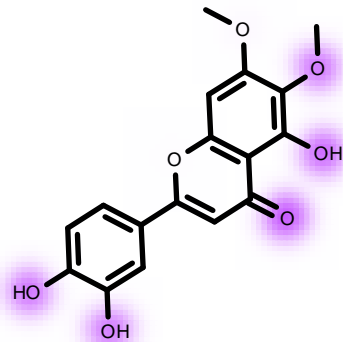
Hydrogen Bond -1.89



Protein Desolvation 3.48



Ligand Desolvation 2.62

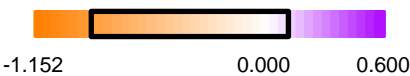
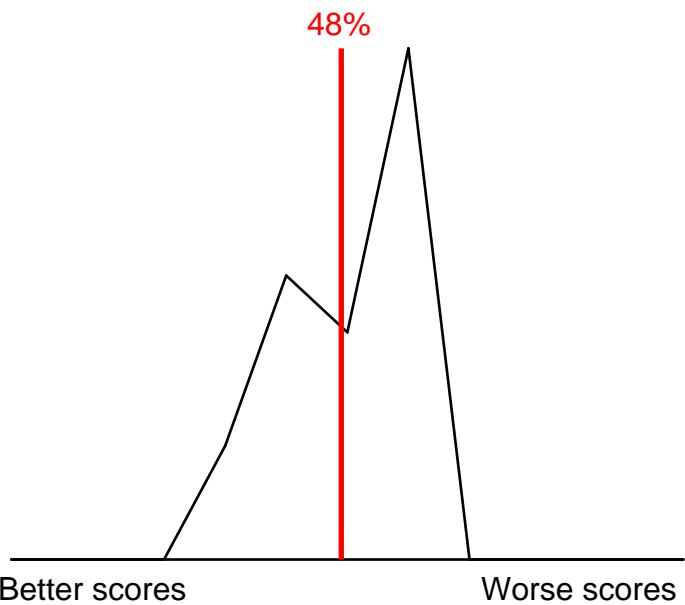
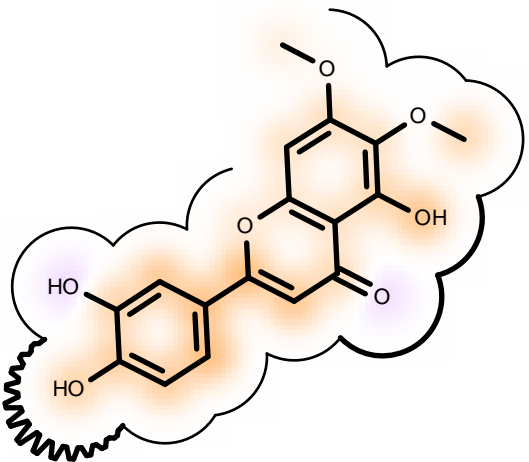


Acceptor Donor
Metal Contact

Molecule Name omega_1_16
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 11

Total Score -10.62

Score compared to other molecules

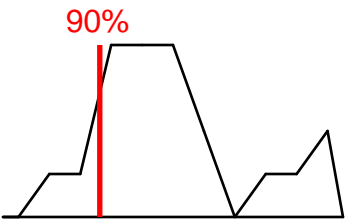
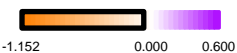
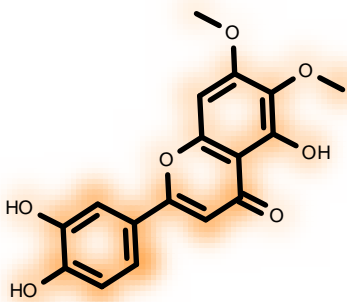


 Protein Contact  Protein Cavity

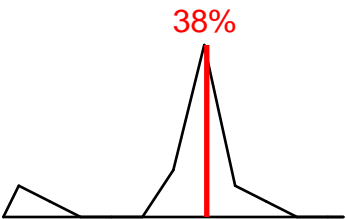
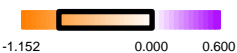
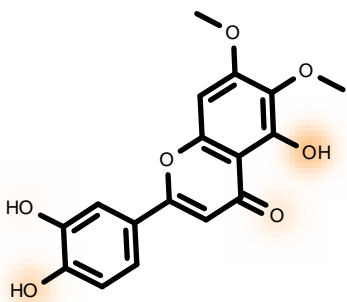
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

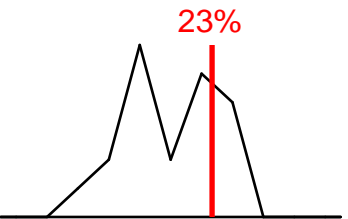
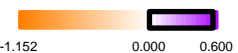
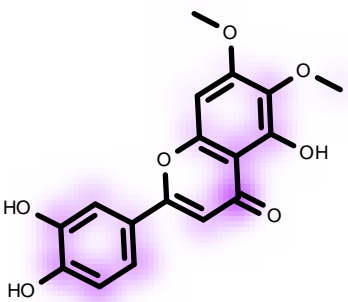
Shape -15.04



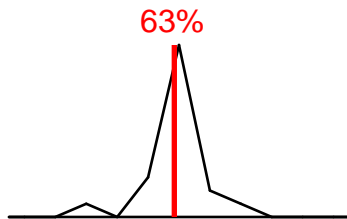
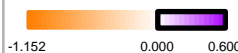
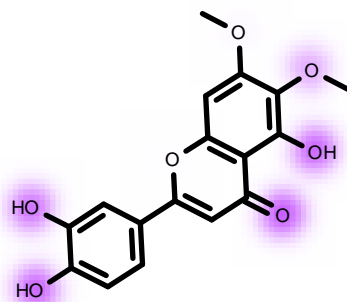
Hydrogen Bond -1.72



Protein Desolvation 3.59



Ligand Desolvation 2.55

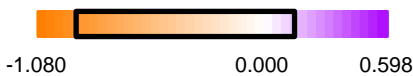
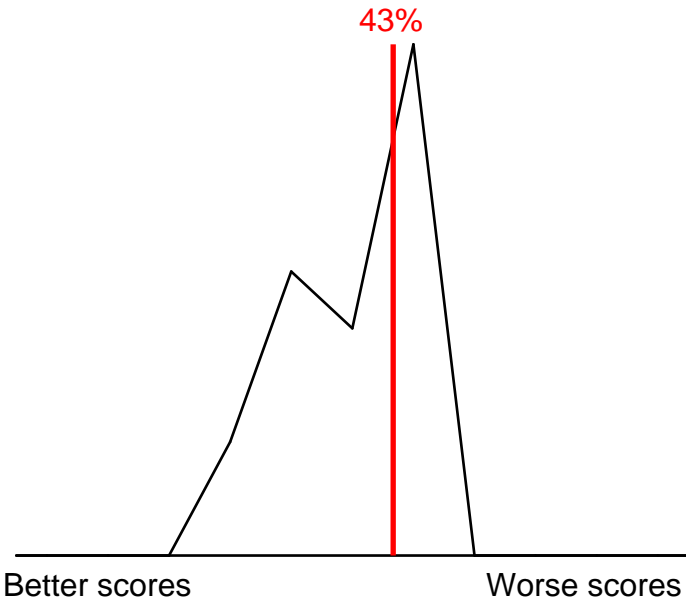
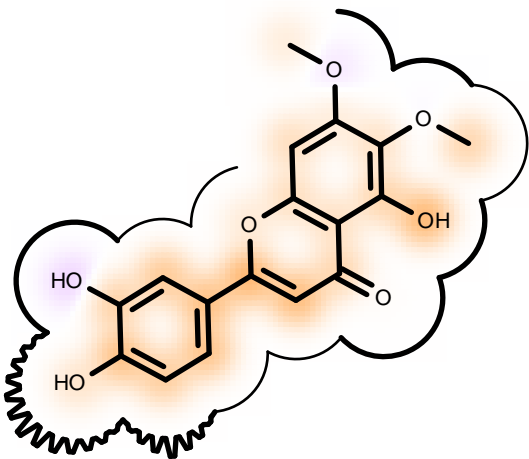


Acceptor **Donor**
Metal Contact

Molecule Name omega_1_16
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 12

Total Score -10.36

Score compared to other molecules

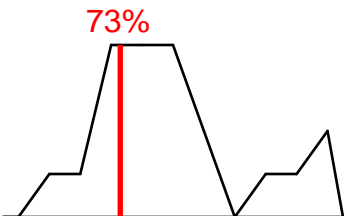
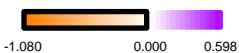
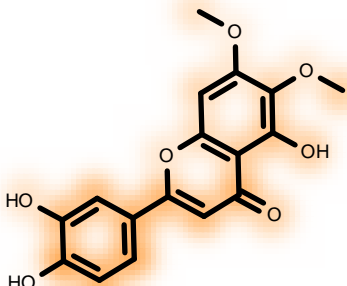


 Protein Contact  Protein Cavity

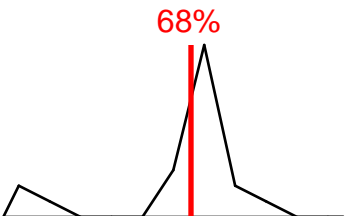
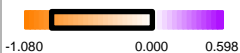
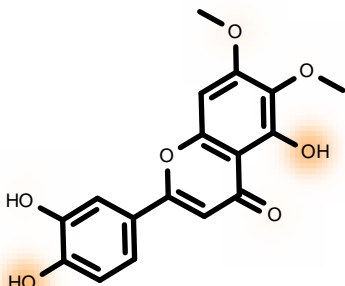
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

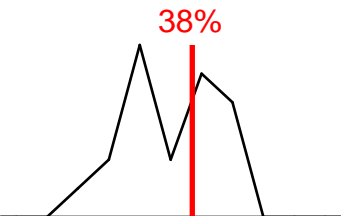
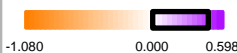
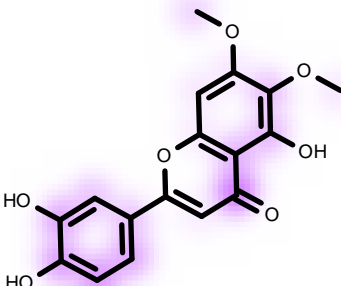
Shape -14.82



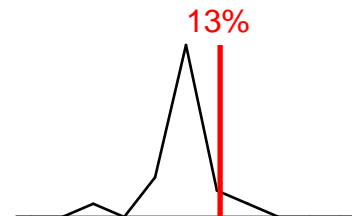
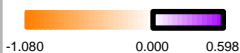
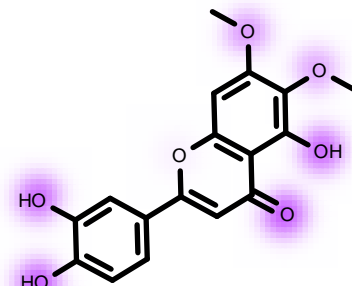
Hydrogen Bond -1.89



Protein Desolvation 3.38



Ligand Desolvation 2.97

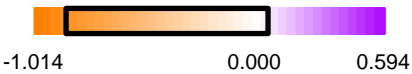
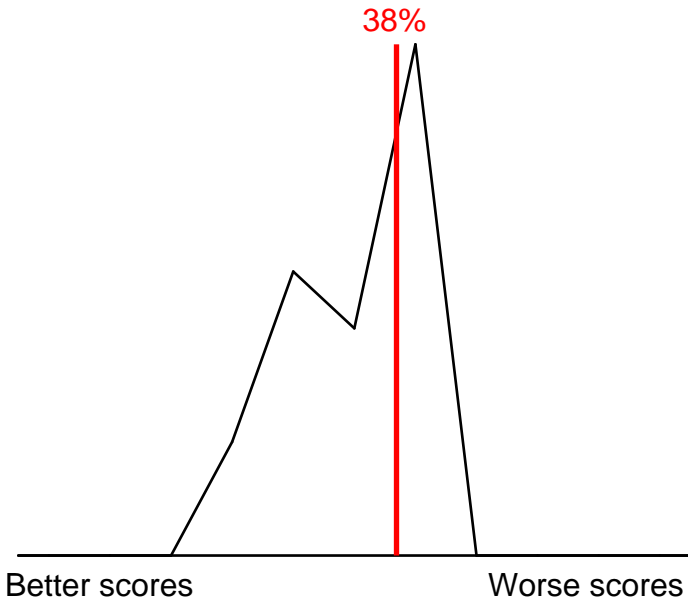
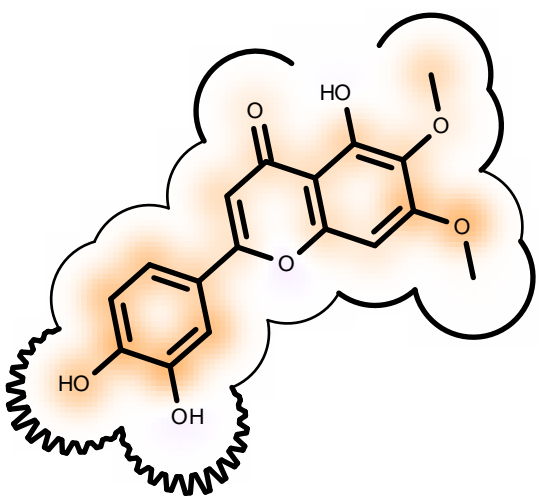


Acceptor **Donor**
Metal Contact

Molecule Name omega_1_2
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 13

Total Score -10.35

Score compared to other molecules

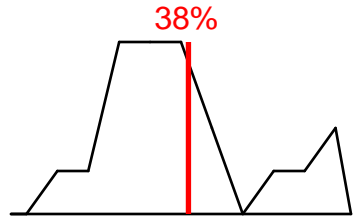
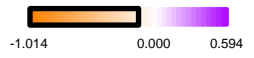
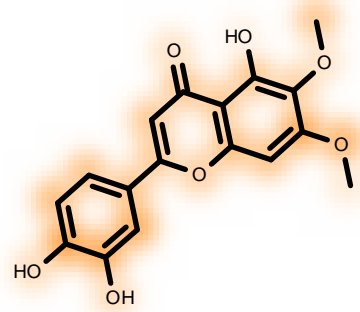


Protein Contact Protein Cavity

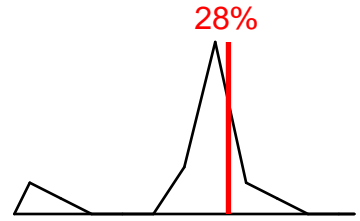
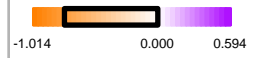
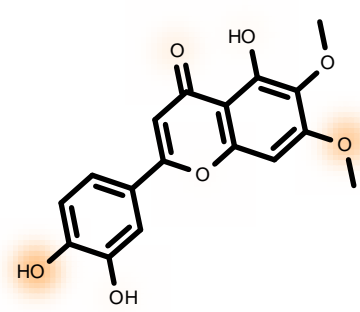
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

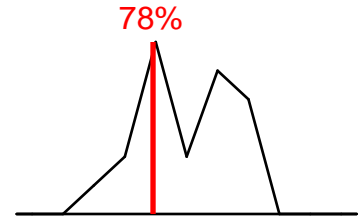
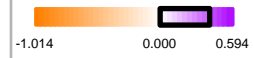
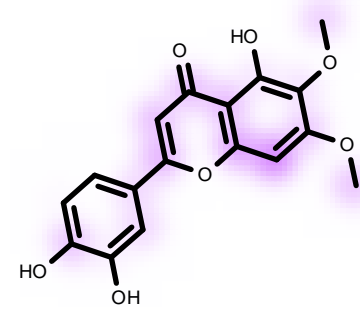
Shape -14.17



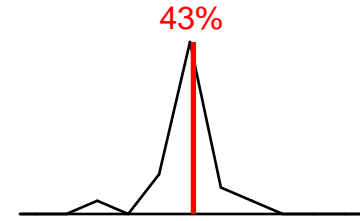
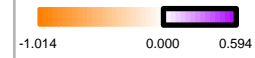
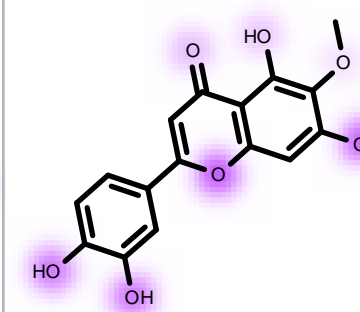
Hydrogen Bond -1.61



Protein Desolvation 2.78



Ligand Desolvation 2.64

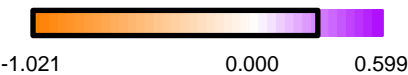
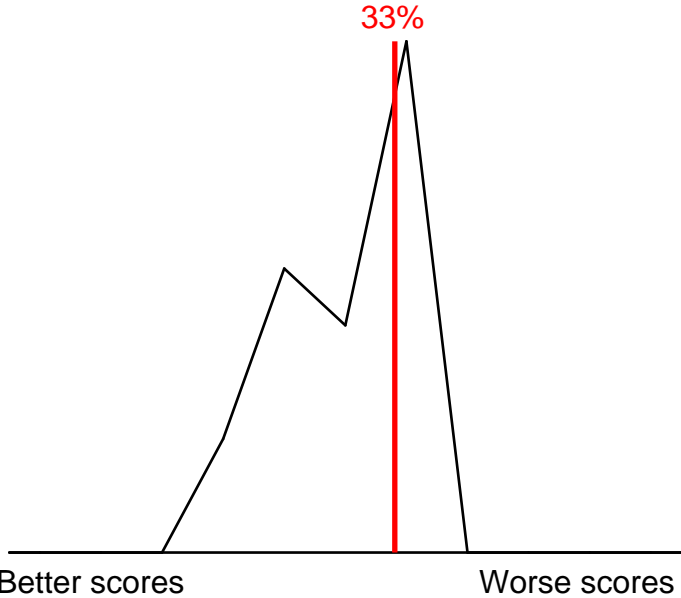
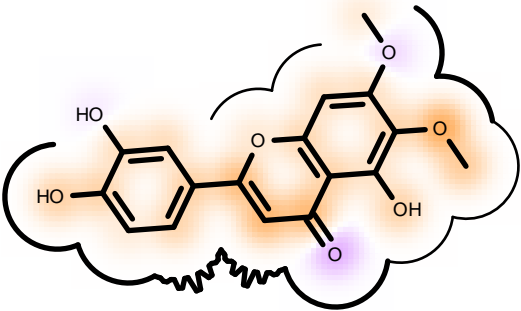


Acceptor Donor
Metal Contact

Molecule Name omega_1_16
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 14

Total Score -10.32

Score compared to other molecules

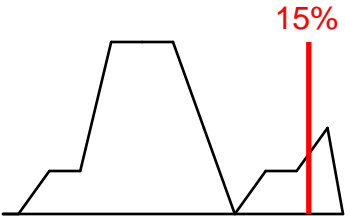
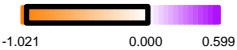
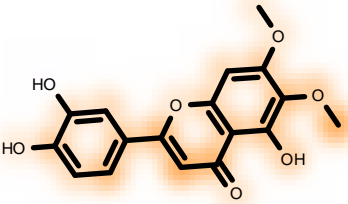


 Protein Contact  Protein Cavity

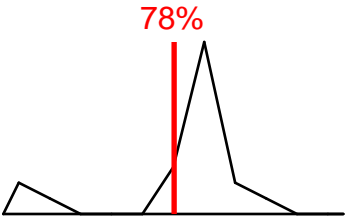
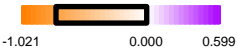
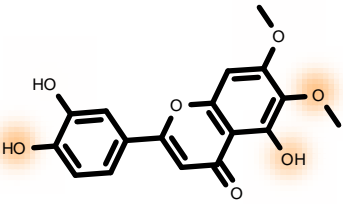
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

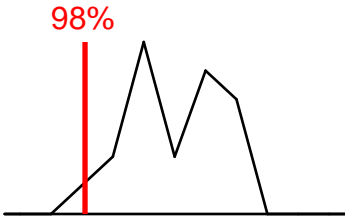
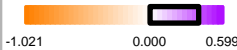
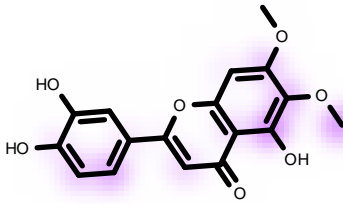
Shape -12.78



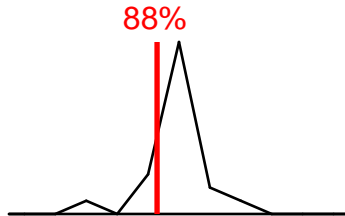
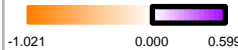
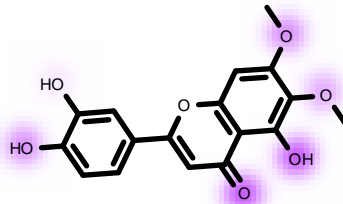
Hydrogen Bond -2.07



Protein Desolvation 2.18



Ligand Desolvation 2.37

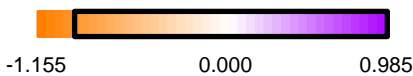
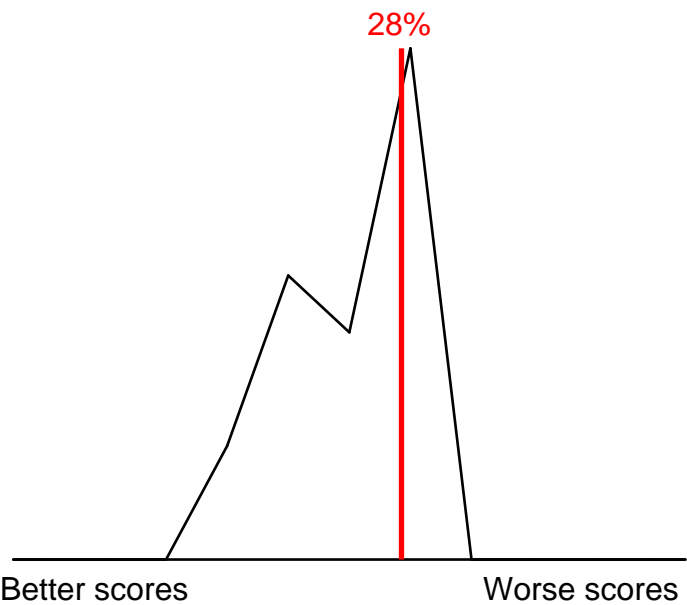
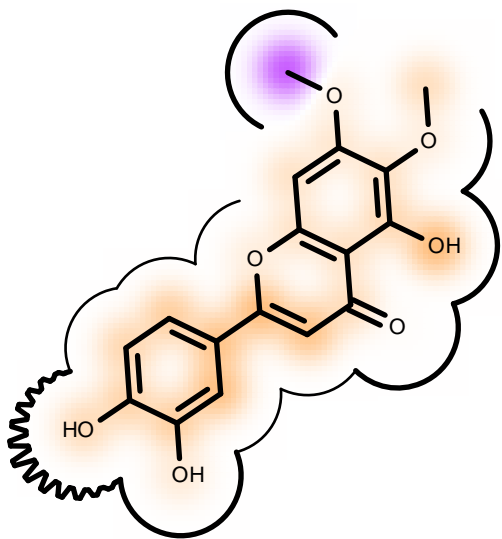


Acceptor **Donor**
Metal Contact

Molecule Name omega_1_13
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 15

Total Score -10.30

Score compared to other molecules



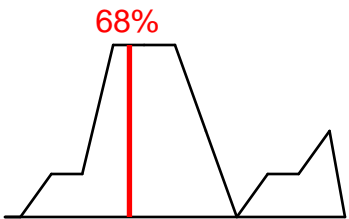
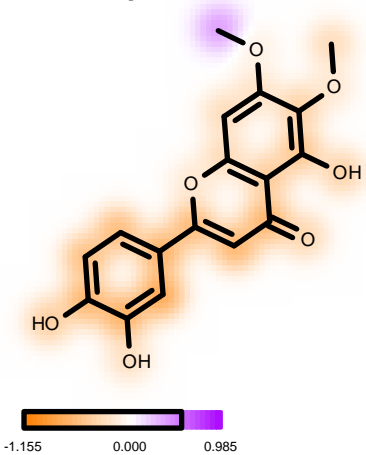
Protein Contact

Protein Cavity

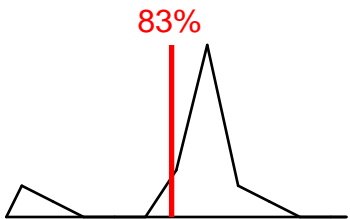
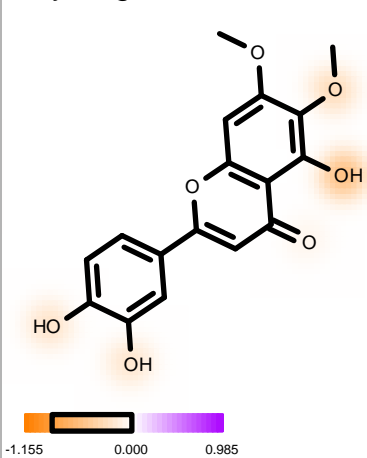
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

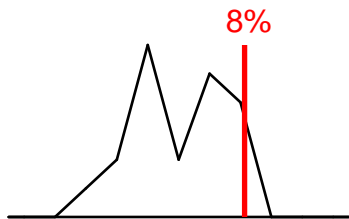
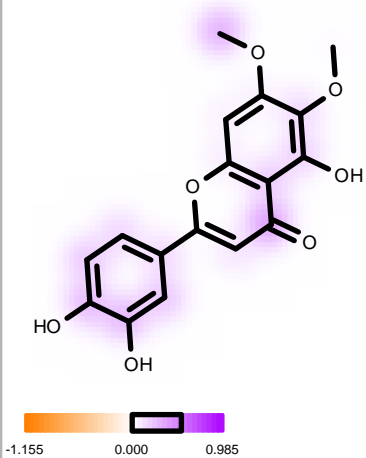
Shape -14.74



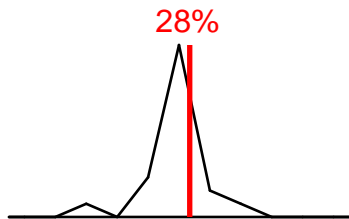
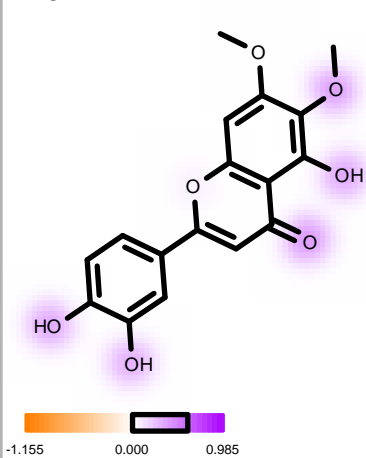
Hydrogen Bond -2.13



Protein Desolvation 3.86



Ligand Desolvation 2.72



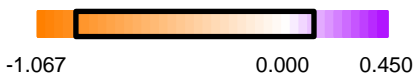
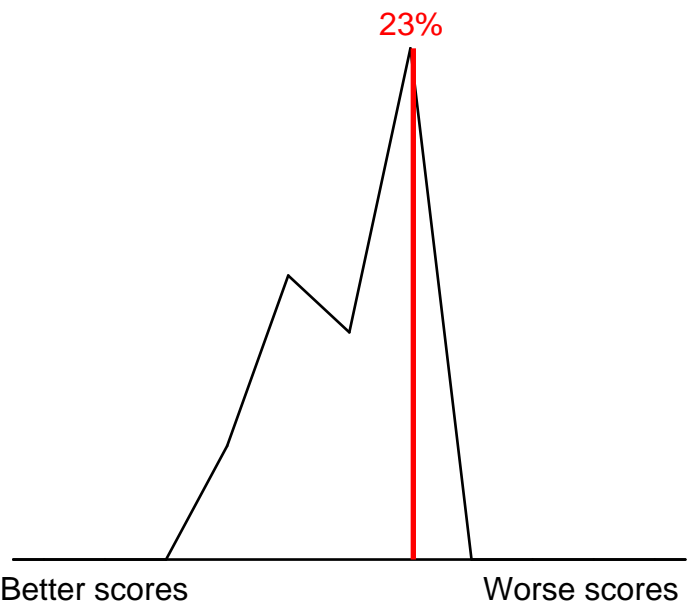
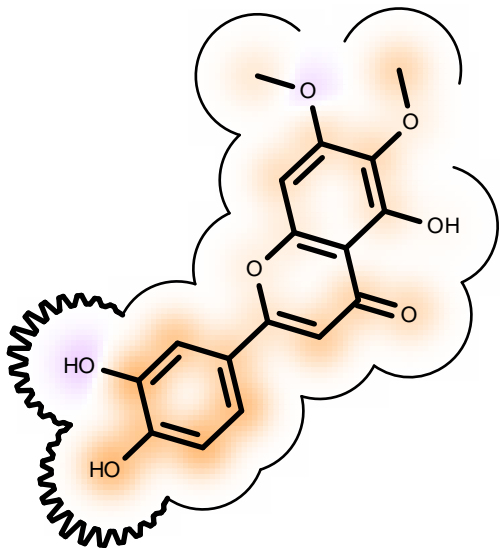
Acceptor
Metal

Donor
Contact

Molecule Name omega_1_10
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 16

Total Score -10.24

Score compared to other molecules

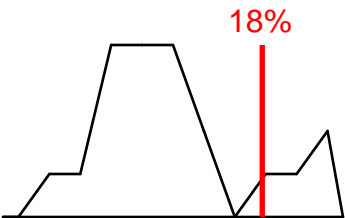
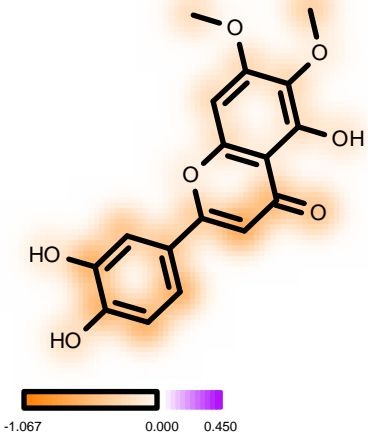


Protein Contact Protein Cavity

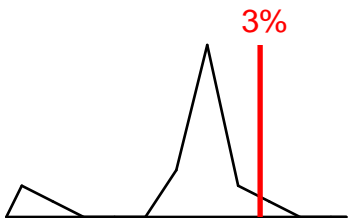
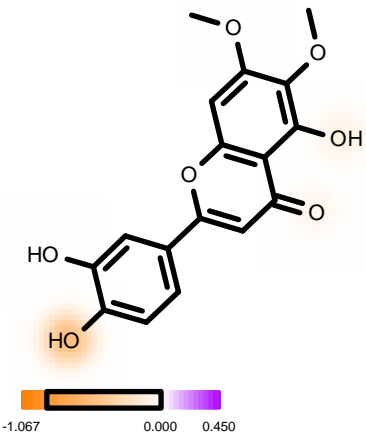
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

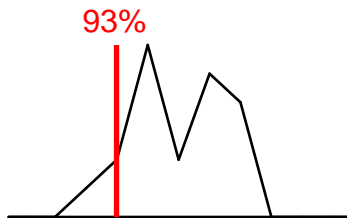
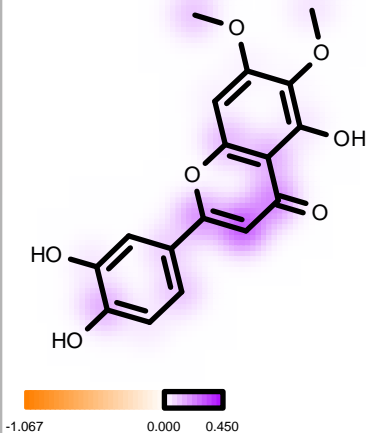
Shape -13.29



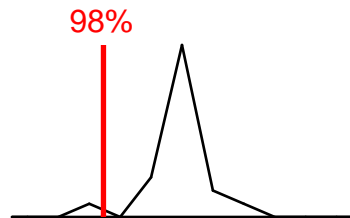
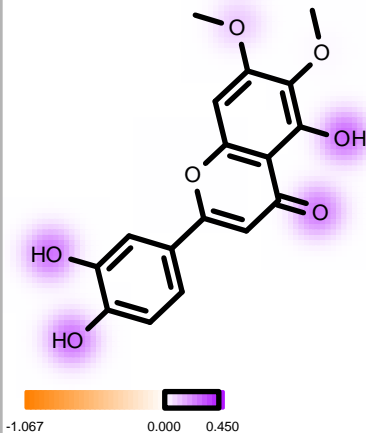
Hydrogen Bond -1.18



Protein Desolvation 2.47



Ligand Desolvation 1.75

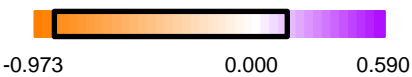
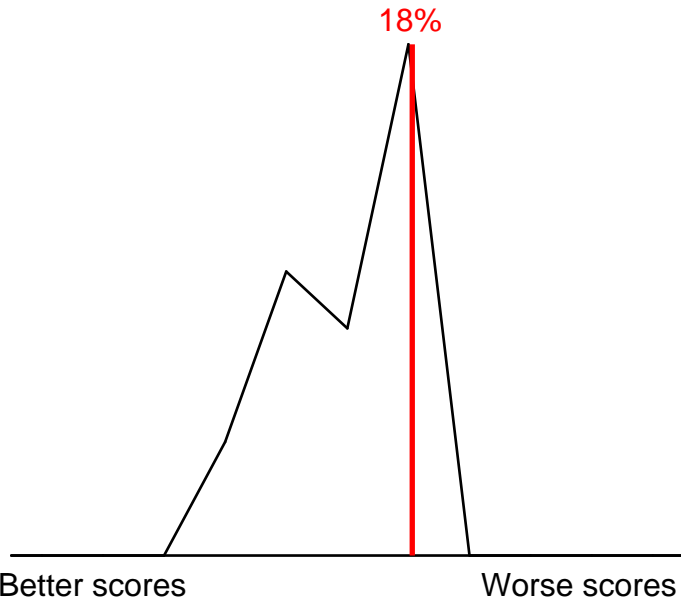
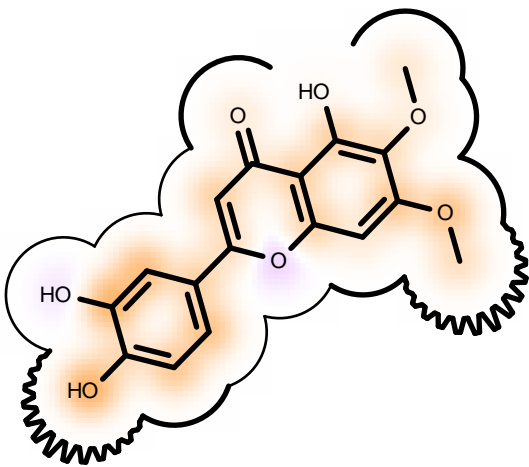


Acceptor Donor
Metal Contact

Molecule Name omega_1_4
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 17

Total Score -10.23

Score compared to other molecules

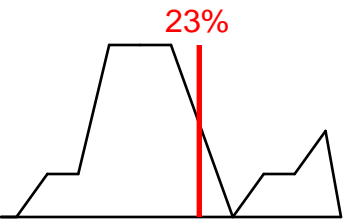
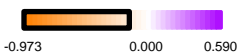
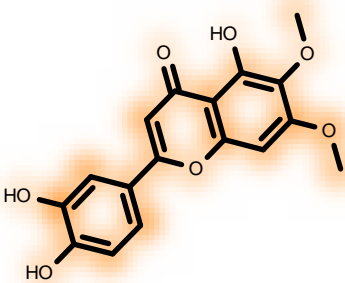


Protein Contact Protein Cavity

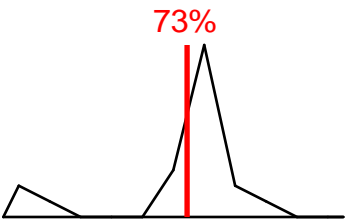
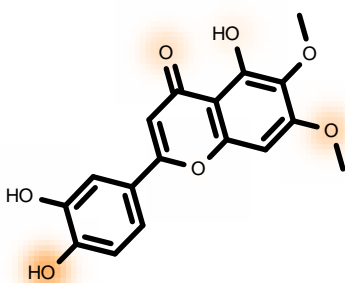
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

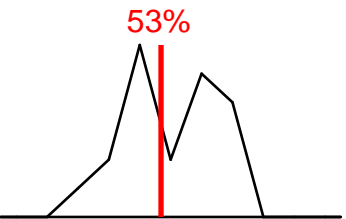
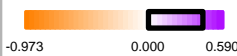
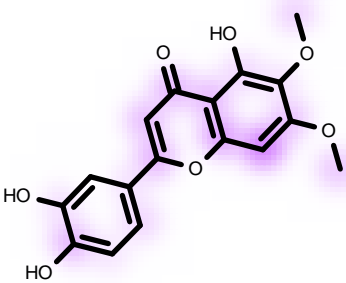
Shape -13.95



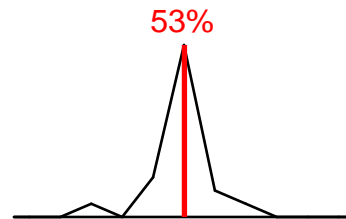
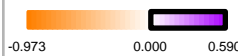
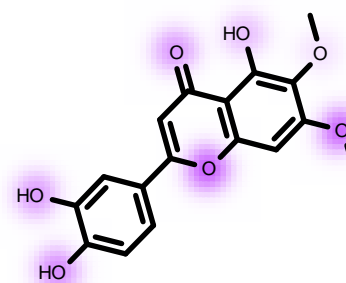
Hydrogen Bond -1.93



Protein Desolvation 3.04



Ligand Desolvation 2.61

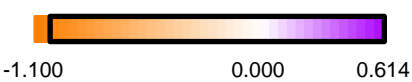
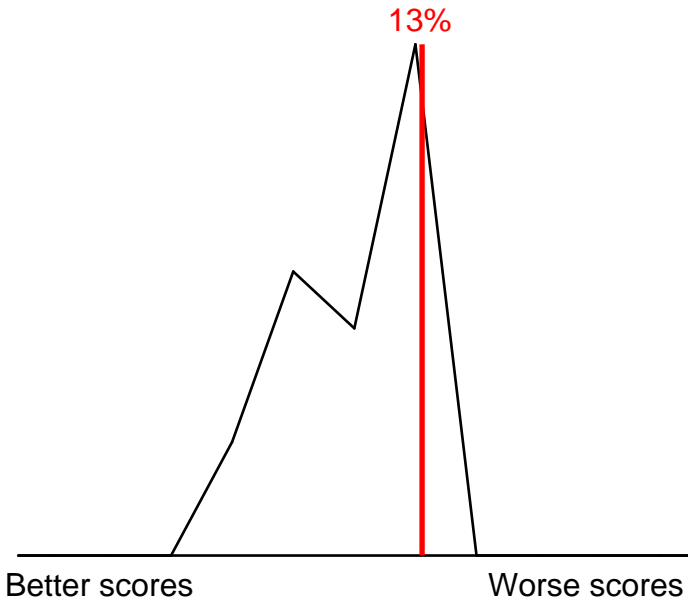
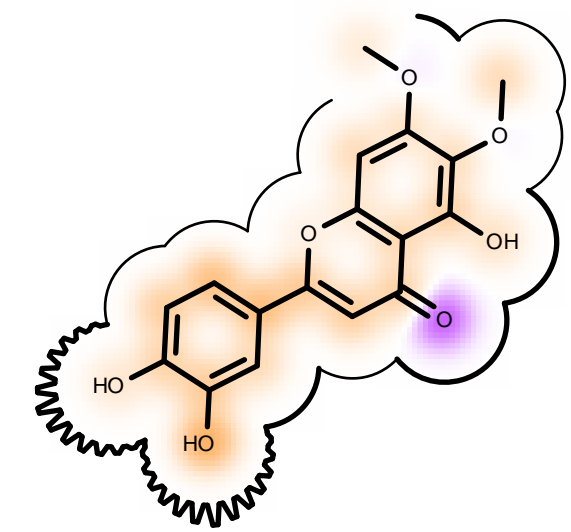


Acceptor Donor
Metal Contact

Molecule Name omega_1_14
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 18

Total Score -10.22

Score compared to other molecules

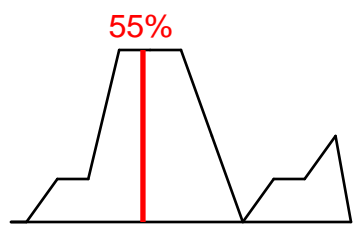
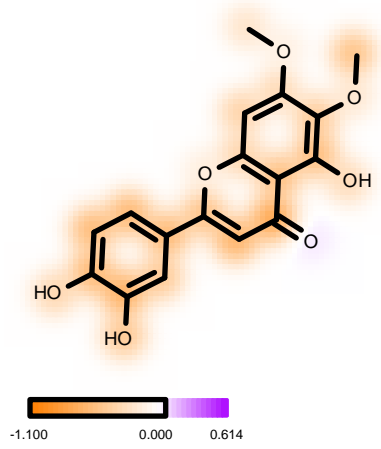


Protein Contact Protein Cavity

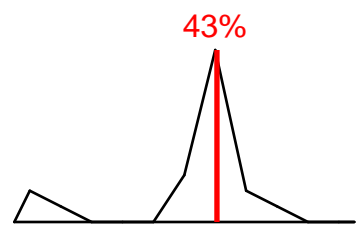
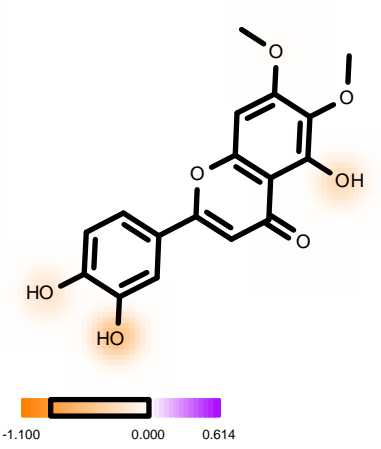
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

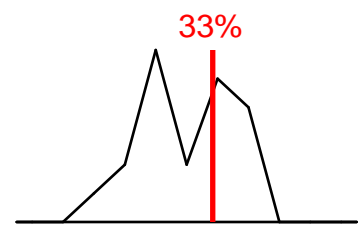
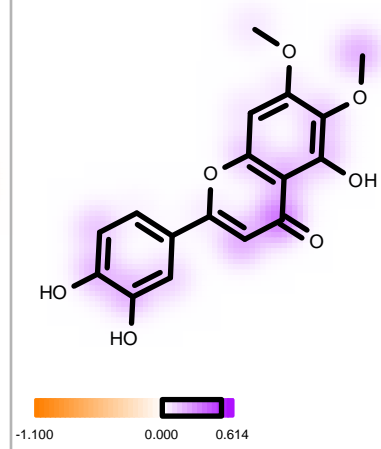
Shape -14.66



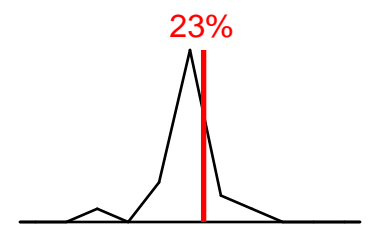
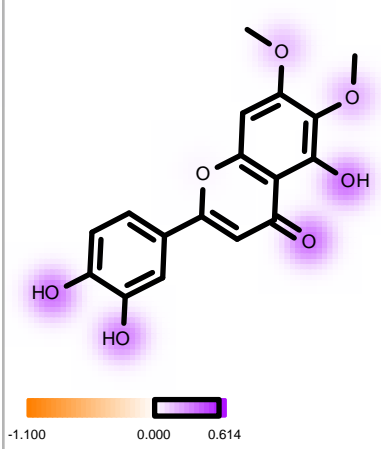
Hydrogen Bond -1.73



Protein Desolvation 3.43



Ligand Desolvation 2.75

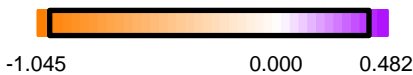
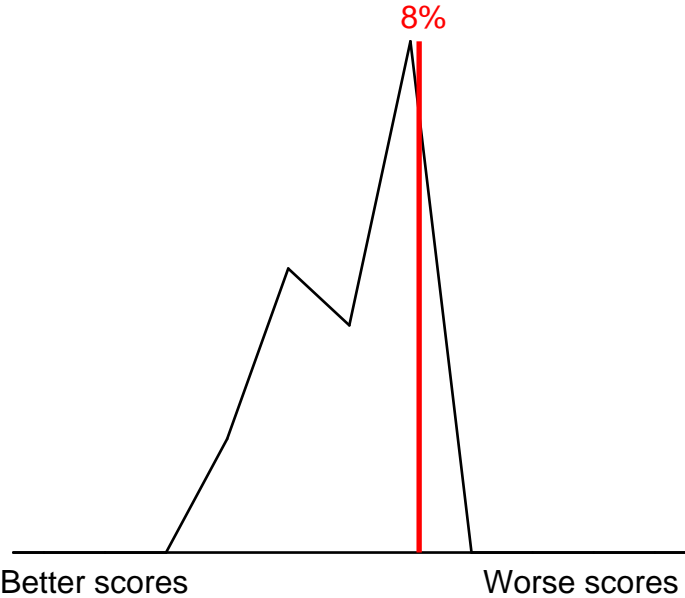
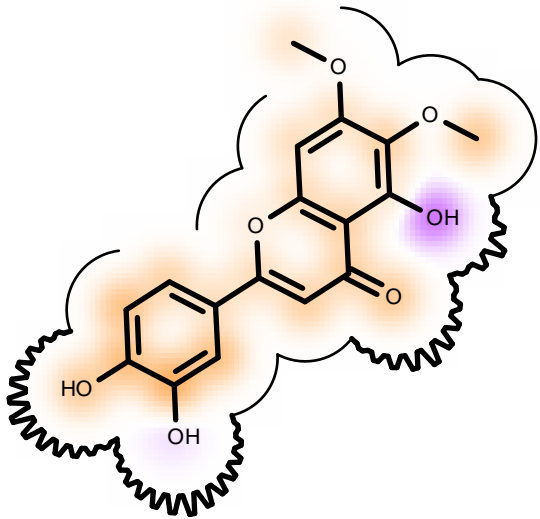


Acceptor Donor
Metal Contact

Molecule Name omega_1_12
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 19

Total Score -10.20

Score compared to other molecules

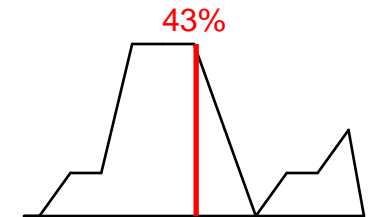
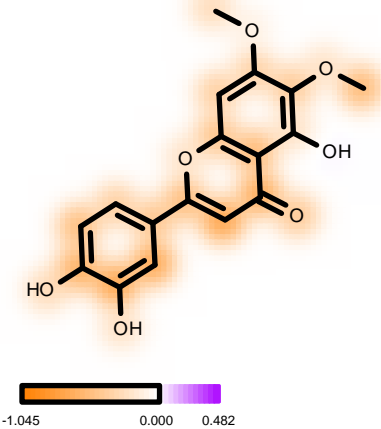


Protein Contact Protein Cavity

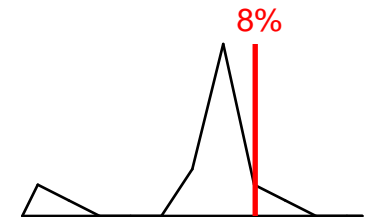
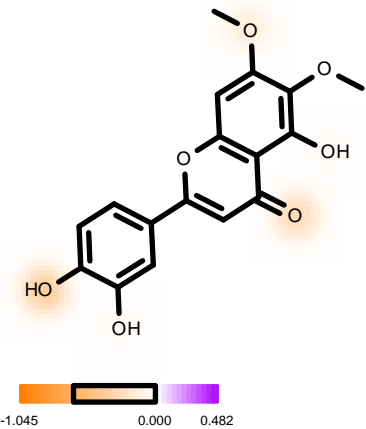
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

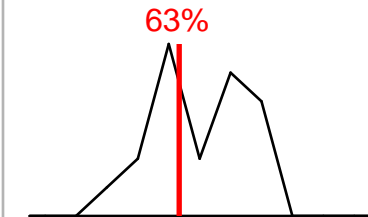
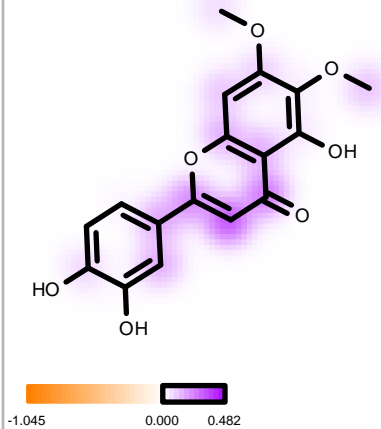
Shape -14.23



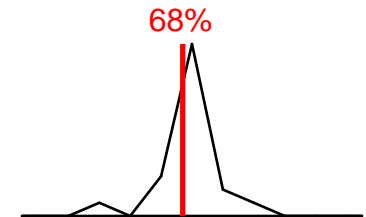
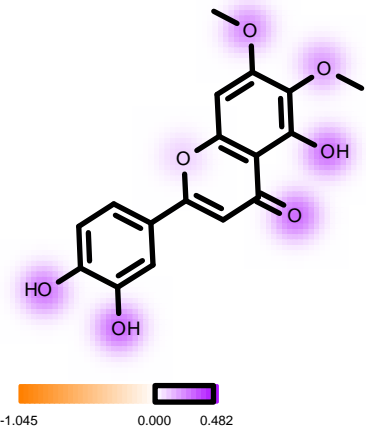
Hydrogen Bond -1.40



Protein Desolvation 2.92



Ligand Desolvation 2.50

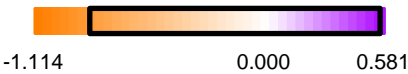
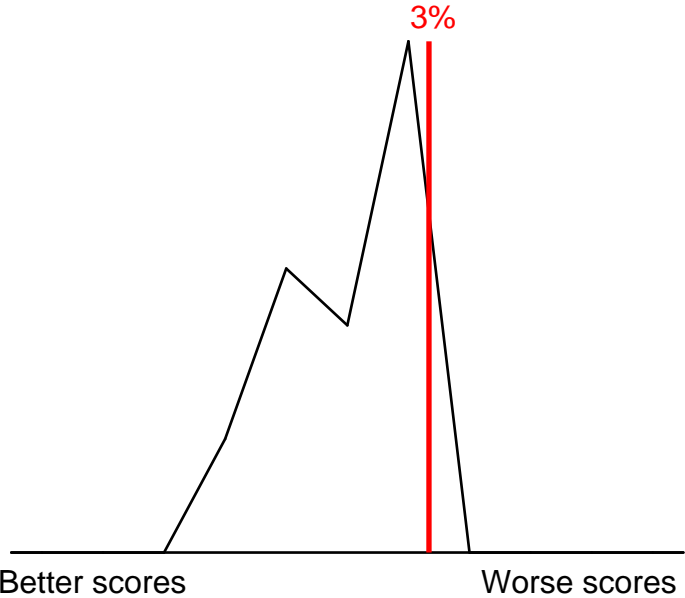
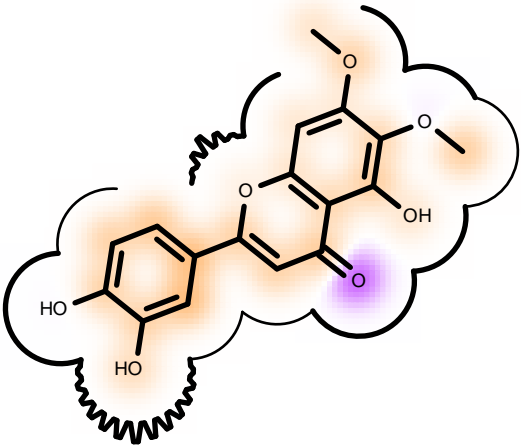


Acceptor Metal Donor Contact

Molecule Name omega_1_12
Molecular Weight 330.3
XLogP 1.2
PSA 109.4
Heavy Atoms 24
Acceptor Count 7
Donor Count 3
Chelator Count 3
Pose Index 20

Total Score -10.14

Score compared to other molecules



Protein Contact

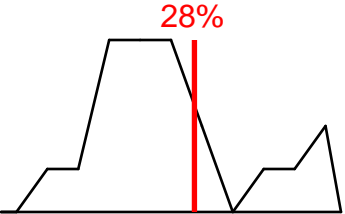
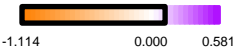
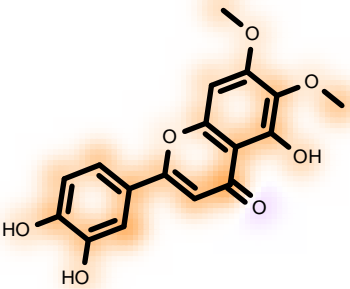


Protein Cavity

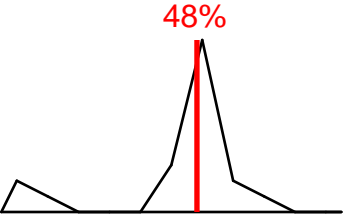
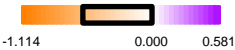
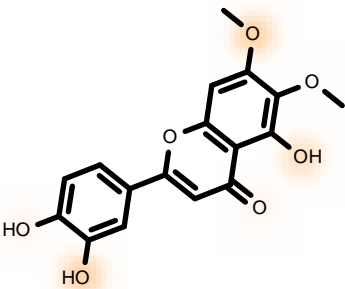
Residue Fingerprint

ALA256G	ALA278E
ALA278F	ALA293B
ALA293C	ALA336B
ARG252G	ARG291B
ASP316F	ASP333B
GLN255G	GLU264G
GLU292B	GLU292C
GLY290B	ILE263G
LYS260G	THR259G
VAL279E	VAL279F

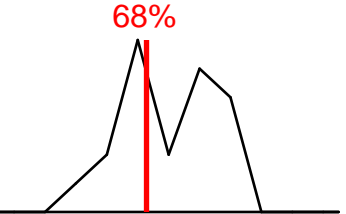
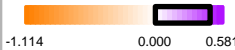
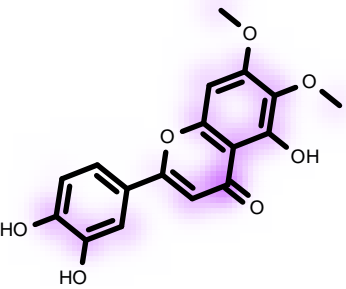
Shape -14.00



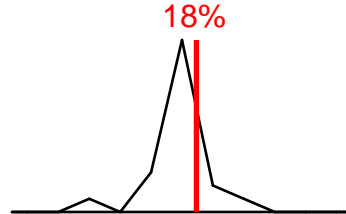
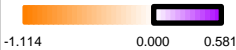
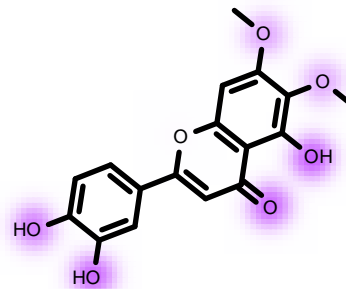
Hydrogen Bond -1.81



Protein Desolvation 2.91



Ligand Desolvation 2.76



Acceptor
Metal

Donor
Contact