

A biochemical characterization of the selenoproteome in *Gallus gallus* via bioinformatics analysis: structure-function relationships and interactions of binding molecules

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The accession number and amino acid sequences of chicken

GPx1

GPx1 [Gallus gallus]

LOCUS NP_001264782 195 aa linear
VRT 31-JUL-2016

DEFINITION glutathione peroxidase 1 [Gallus gallus].

ACCESSION NP_001264782 XP_003642043

VERSION NP_001264782.2

DBSOURCE REFSEQ: accession NM_001277853.2

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

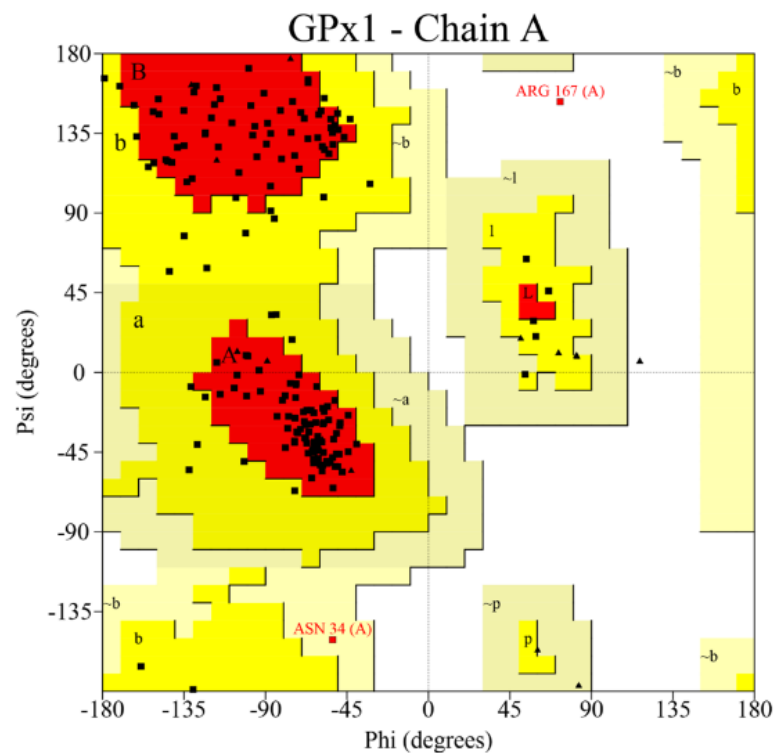
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001264782.2 glutathione peroxidase 1 [Gallus gallus]
MAATGLAGILARPLGAAEPLALSSLRGKVLLVVNVASLU
GTTTRDFLQLNELQQRYGPRGLRVLGFPNCNQFGHQEN
ATNEEILRSLEYVRPGNGFKPNFTMFEKCEVNGKGAHP
LFAFLREALPFPHDDPSALMTNPQYIIWSPVCRNDVSW
NFEKFLVGPDGVPFRRYSRHFETIKLQDDIELLLQKVPKE
ALQ

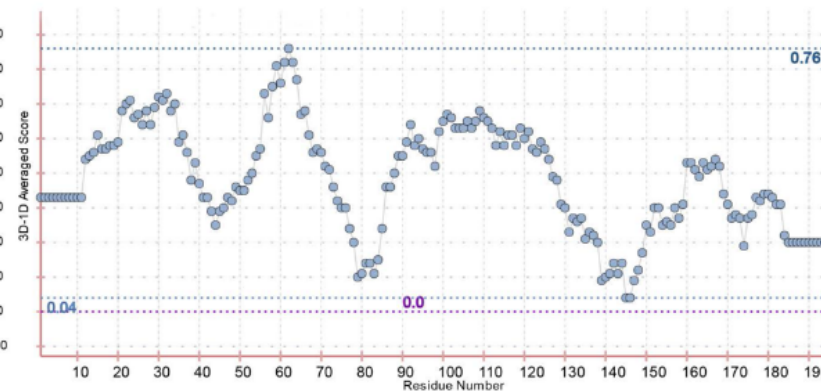
Analysis of the GPx1

The structural modeling of chicken GPx1



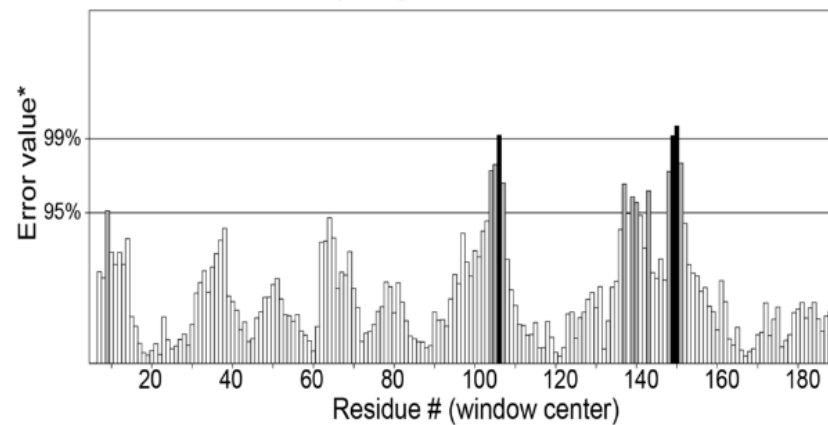
Verify 3D

90.77% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 92.973



The predictions of ligand binding sites in chicken GPx1

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
GPx1	POP	0.12	150, 151, 155, 168, 169, 170, 171
	PER	0.08	39, 40, 41, 42, 155
	CA	0.05	69, 70, 106
	3GKNB00	0.04	62, 99, 100
	AMP	0.03	34, 35, 36, 66, 67, 68, 150, 171

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

GPx2

GPx2 [Gallus gallus]

LOCUS NP_001264783 191 aa linear
VRT 26-JUL-2016

DEFINITION glutathione peroxidase 2 [Gallus gallus].

ACCESSION NP_001264783 XP_003641324

VERSION NP_001264783.1

DBSOURCE REFSEQ: accession NM_001277854.1

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

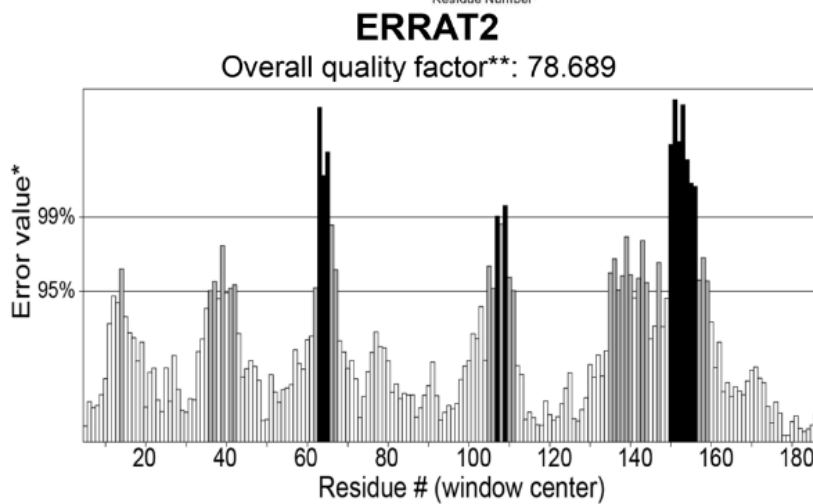
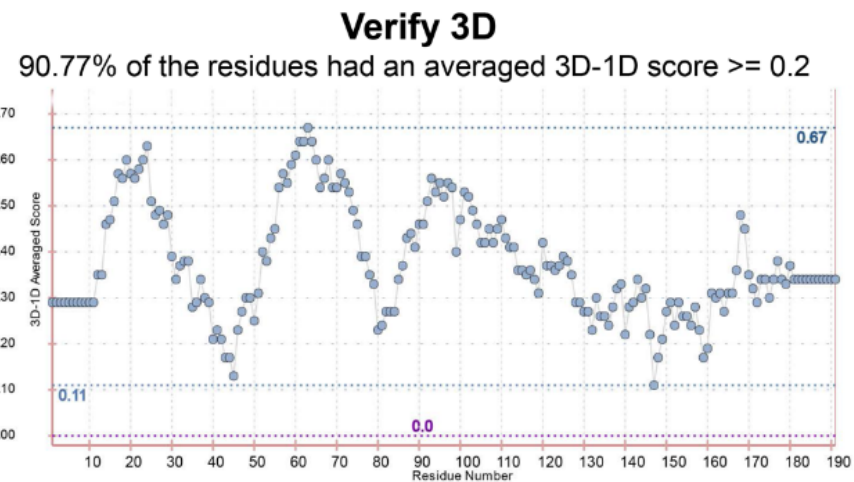
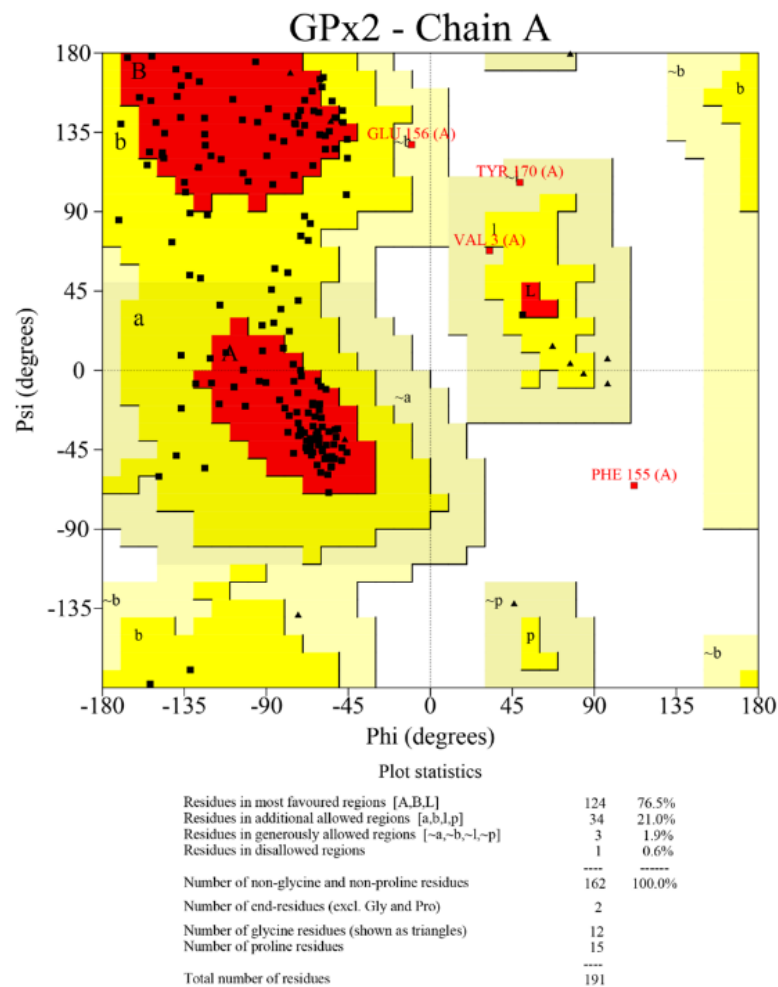
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001264783.1 glutathione peroxidase 2 [Gallus gallus]
MSVPIAKSFYDLSATSLQGEKVDFNVFRGRVVLIENTVAS
LUGTTVRDYTQLNQLQARYPRRLVVLGFPCNQFGYQEN
GTNEEILNCLKHVRPGGGFEPNFTLFQKCQVNGKDTHP
VFAYLKAHLPAVPDEADHLMAEPRFLVWSPVRRSDISW
NFEKFLVGPEGEPPRRYSPRLPTTQIEPDIQRLLKLAK

Analysis of the GPx2

The structural modeling of chicken GPx2



The predictions of ligand binding sites in chicken GPx2

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
GPx2	POP	0.15	126, 151, 152, 156, 169, 170, 171,172
	C6W	0.04	40, 69, 109
	BIH	0.04	17, 18, 63, 99, 100, 101
	BEZ	0.04	36, 41
	CA	0.03	10, 11, 23, 25

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

GPx3

GPx3 [Gallus gallus]

LOCUS NP_001156704 219 aa linear
VRT 03-AUG-2016

DEFINITION glutathione peroxidase 3 precursor
[Gallus gallus].

ACCESSION NP_001156704

VERSION NP_001156704.1

DBSOURCE REFSEQ: accession NM_001163232.2

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

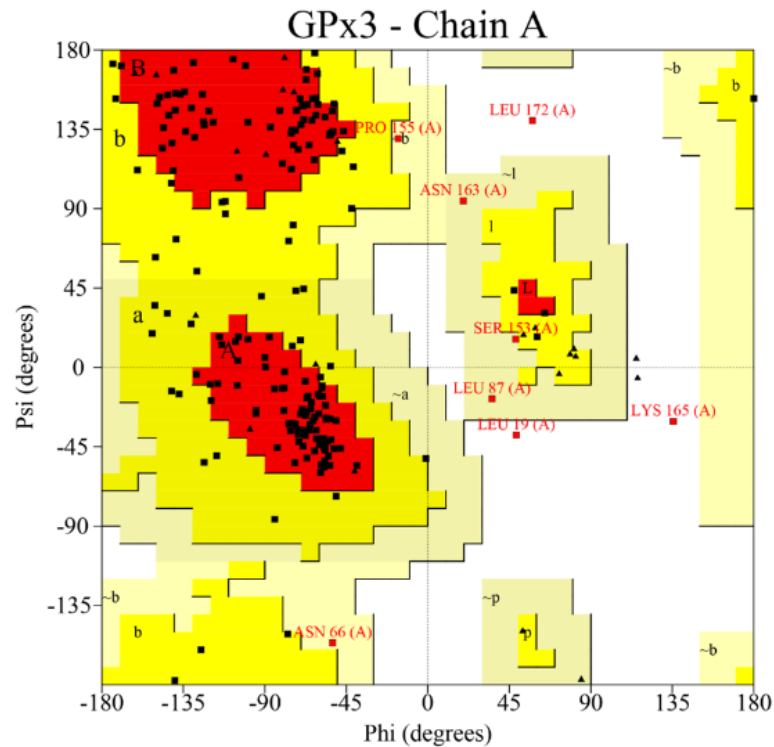
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001156704.1 glutathione peroxidase 3 precursor
[Gallus gallus]

MGCRAACVLAVLLAGLVPLGQGQEREKVKCYDSVRGTI
YDYGALTIDGDEYIPFRKYAGKMVLFVNVATYUGLTLQYL
ELNALQNELGPYGLVVLGFPSNQFGKQEPGQNSEILPAL
KYVRPGGGFVVPNFQLFQKGDVNGAKEQKVYSFLKNSC
PPVAEEFGNPKNLFWEPLRNHDIKWNFEKFLVGTGVP
VMRWYHRANIATVKNDIIAYMRQQRGQ

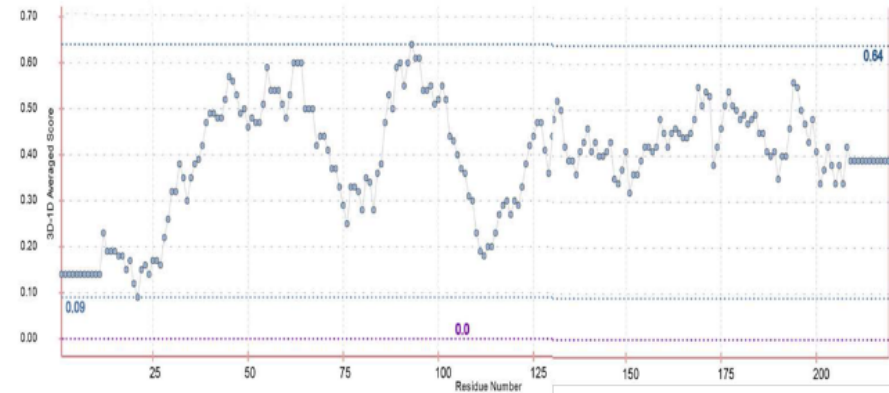
Analysis of the GPx3

The structural modeling of chicken GPx3



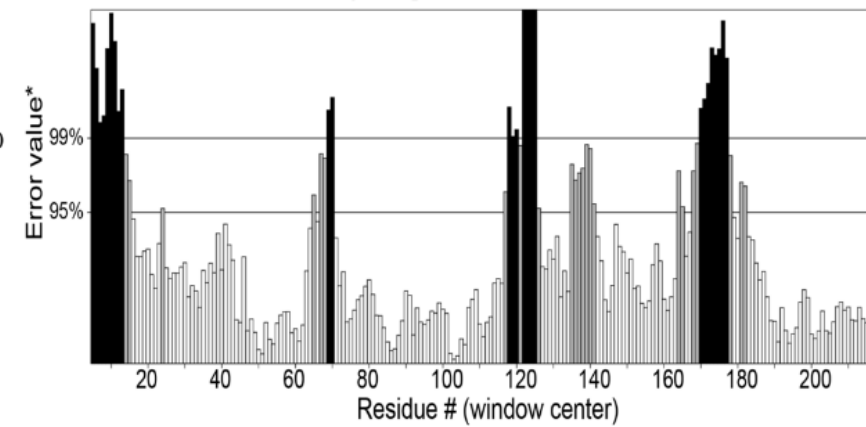
Verify 3D

87.21% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 76.777



The predictions of ligand binding sites in chicken GPx3

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
GPx3	POP	0.11	156, 157, 177, 178, 182, 195, 196, 197, 198
	GSH	0.05	68, 71, 73, 178, 179, 180, 181, 198, 199
	CU	0.05	68, 71, 74, 179
	CA	0.04	45, 46, 52, 131, 132
	CA	0.02	100, 101, 137

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

GPx4

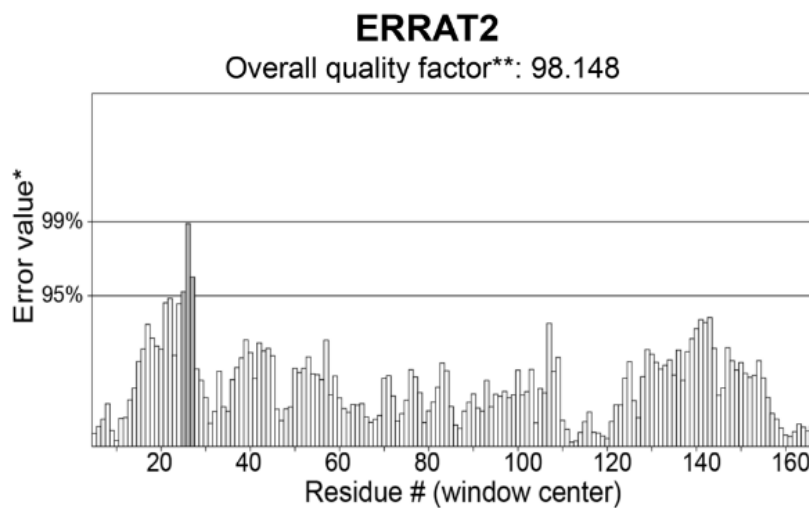
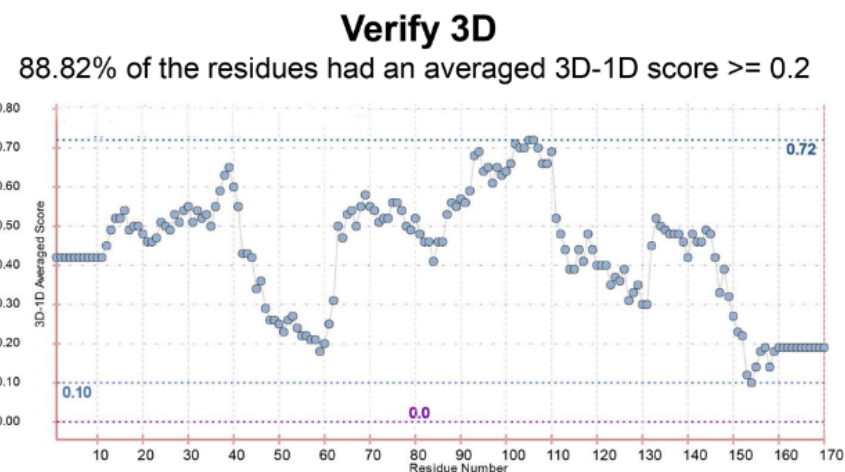
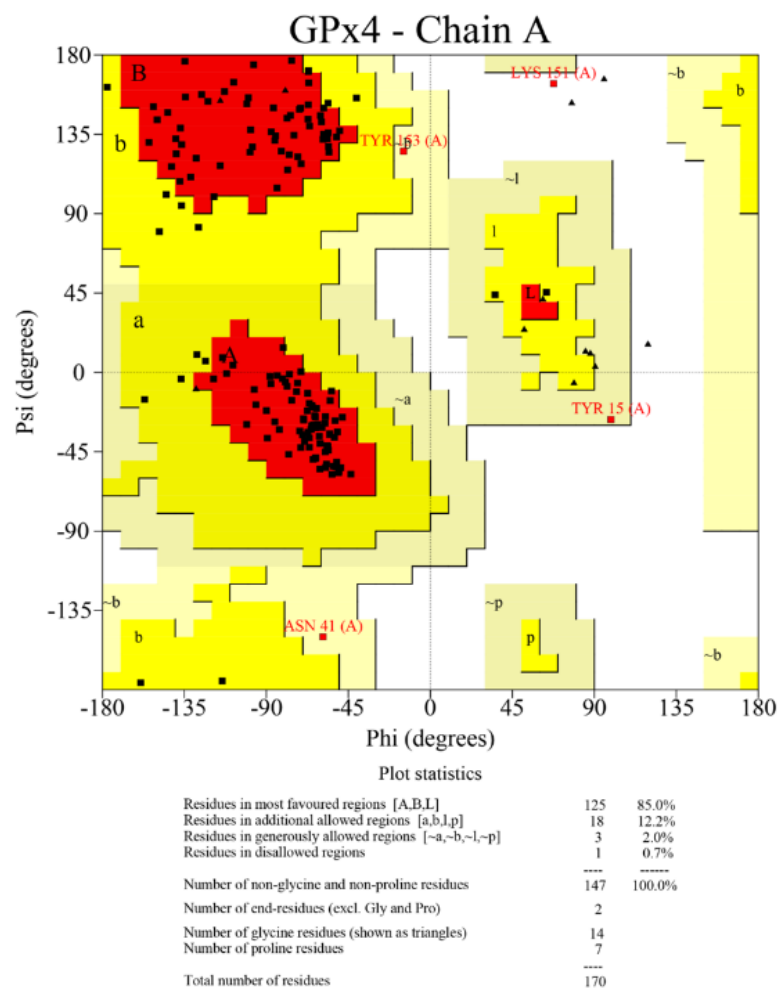
GPx4 [Gallus gallus]

LOCUS AF498316_1 170 aa linear
VRT 27-APR-2004
DEFINITION phospholipid hydroperoxide glutathione
peroxidase [Gallus gallus].
ACCESSION AAM18080
VERSION AAM18080.2
DBSOURCE accession AF498316.2
KEYWORDS .
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>AAM18080.2 phospholipid hydroperoxide glutathione
peroxidase [Gallus gallus]
MCAQADEWRSATSIYDFHARDIDGRDVSLEQYRGFVCII
TNVASKUGKTAVNYTQLVDLHARYAEKGLRILAFPCNQF
GKQEPGDDAQIKAFAEGYGVKFD MF SKIEVNGDGAHPL
WKWLKEQPKGRGTLGNAIKWNFTKFLINREGQVVKRYS
PMEDPYVIEKDLPAYL

Analysis of the GPx4

The structural modeling in chicken GPx4



The predictions of ligand binding sites in chicken GPx4

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
GPx4	POP	0.29	128, 129, 134, 135, 139, 152, 153, 154, 155
	PER	0.11	49, 50, 51, 52, 140
	BIH	0.07	21, 22, 69, 99, 100, 101
	SO4	0.06	105, 107, 109, 136
	CA	0.06	16, 17, 29, 30

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

DIO1

DIO1 [Gallus gallus]

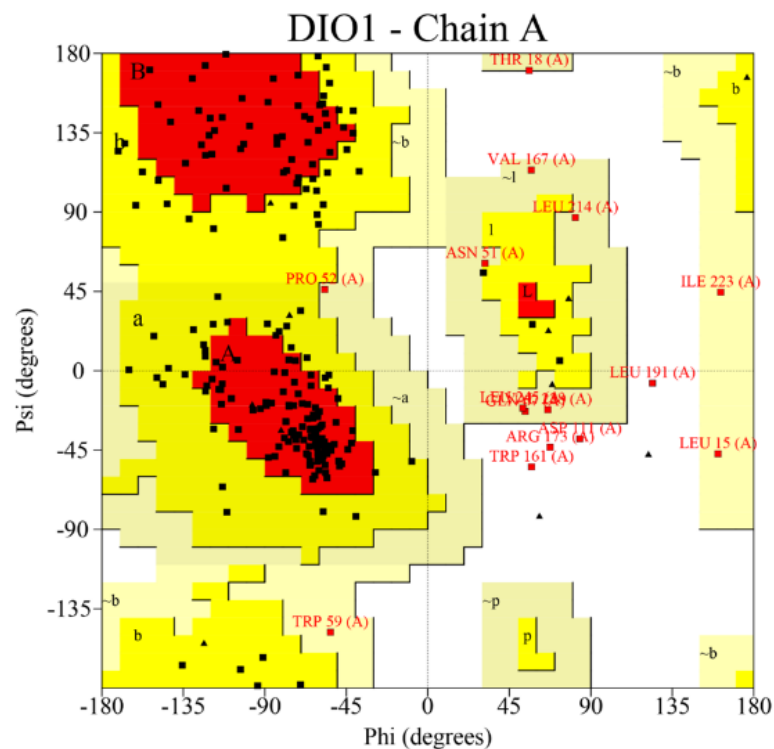
LOCUS NP_001091083 246 aa linear
VRT 29-APR-2016
DEFINITION type I iodothyronine deiodinase [Gallus gallus].
ACCESSION NP_001091083 XP_422487
VERSION NP_001091083.1
DBSOURCE REFSEQ: accession NM_001097614.1
KEYWORDS RefSeq.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001091083.1 type I iodothyronine deiodinase [Gallus gallus]

MLSIRVLLHKLLILLQVTL SVVVGKTMMILFPD TTKRYILKL
GEKSRMNQNP KFSYENWGPTFFSFQYLLFVLKVKWRR
LEDEAHEGRPAPNTPVVALNGEMQHLSFMRDNRPLIL
NFGSCTUPSFMLKFDEFNKLVKDFSSIADFLIIYIEEAHAV
DGWAFRNNVVIKNHRSLED RKTA AQFLQQKNPLCPVVL
DTMENLSSSKYAALPERLYILQAGNVIYKGGVGPWNYH
PQEIRAVLEKLK

Analysis of the DIO1

The structural modeling of chicken DIO1

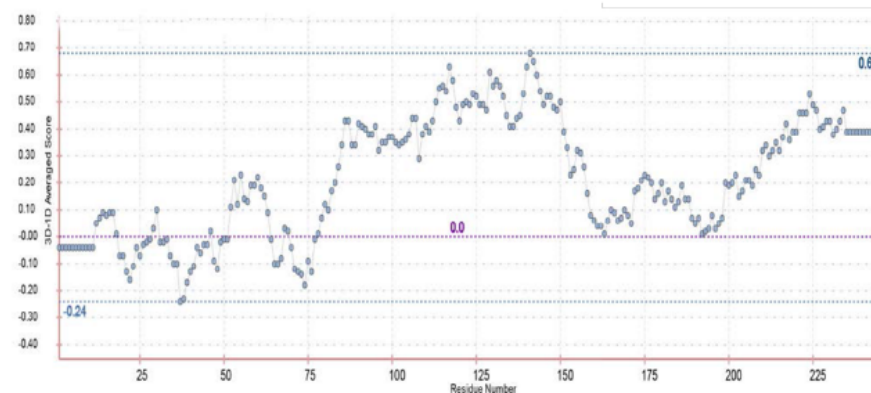


Plot statistics

Residues in most favoured regions [A,B,L]	143	65.0%
Residues in additional allowed regions [a,b,l,p]	63	28.6%
Residues in generously allowed regions [-a,-b,-l,-p]	10	4.5%
Residues in disallowed regions	4	1.8%
Number of non-glycine and non-proline residues	220	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	11	
Number of proline residues	13	
Total number of residues	246	

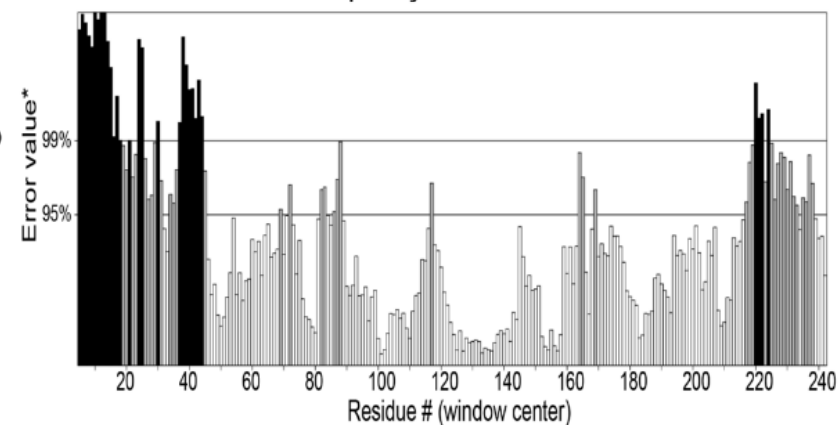
Verify 3D

84.82% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 70.168

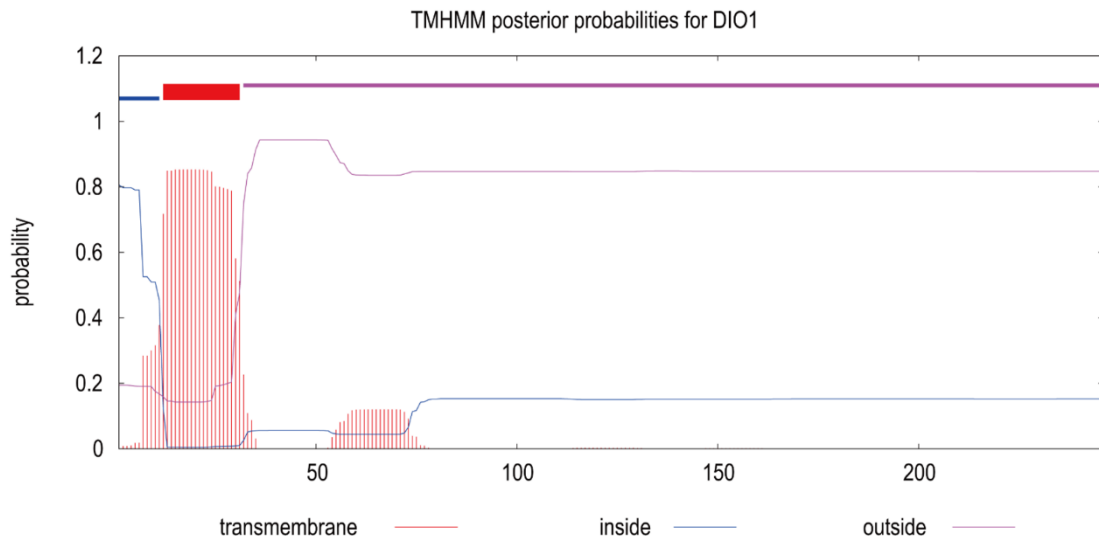


The predictions of ligand binding sites in chicken DIO1

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
DIO1	PER	0.10	123, 125, 126, 127, 212
	GSH	0.06	84, 85, 208, 225
	8H8	0.04	98, 183, 186, 194
	3GKNA00	0.03	124, 125, 126, 154, 155, 156, 157, 165
	BIH	0.03	97, 98, 146, 191, 192, 193

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The predictions of transmembrane helices in chicken DIO1



DIO1 Number of predicted TMHs: 1
 # DIO1 Exp number of AAs in TMHs: 20.41455
 # DIO1 Exp number, first 60 AAs: 18.69271
 # DIO1 Total prob of N-in: 0.80572
 # DIO1 POSSIBLE N-term signal sequence

DIO1	TMHMM2.0	inside	1	11
DIO1	TMHMM2.0	TMhelix	12	31
DIO1	TMHMM2.0	outside	32	246

The accession number and amino acid sequences of chicken

DIO2

DIO2 [Gallus gallus]

LOCUS NP_989445 279 aa linear

VRT 22-MAY-2016

DEFINITION type II iodothyronine deiodinase
isoform a [Gallus gallus].

ACCESSION NP_989445

VERSION NP_989445.2

DBSOURCE REFSEQ: accession NM_204114.3

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

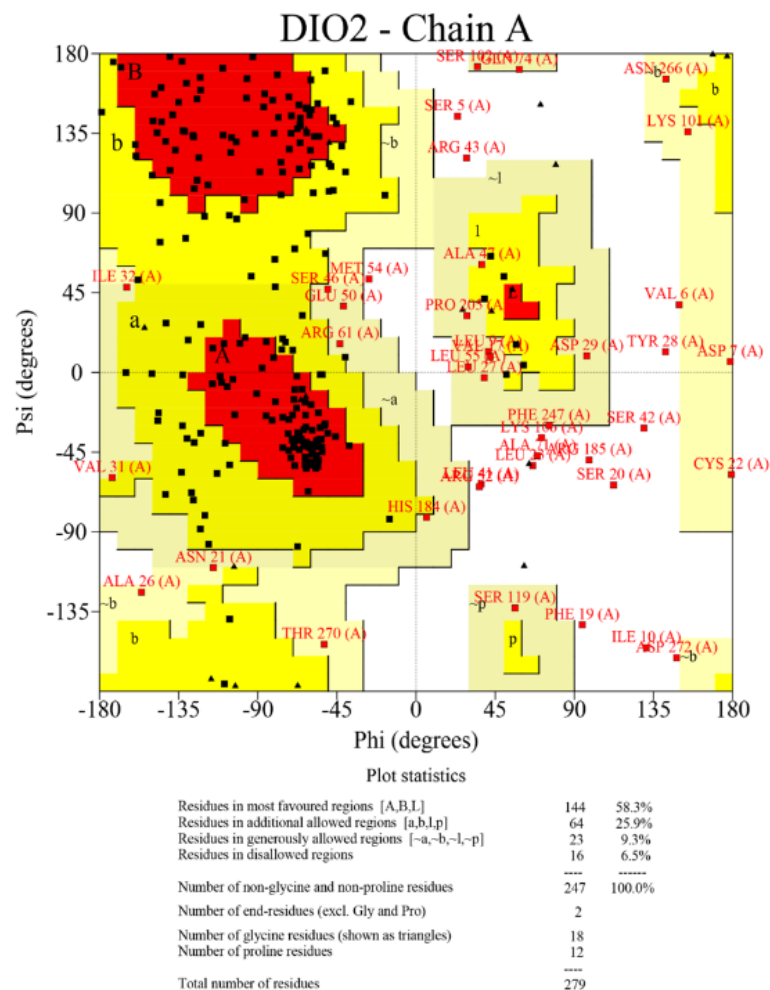
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_989445.2 type II iodothyronine deiodinase isoform a
[Gallus gallus]

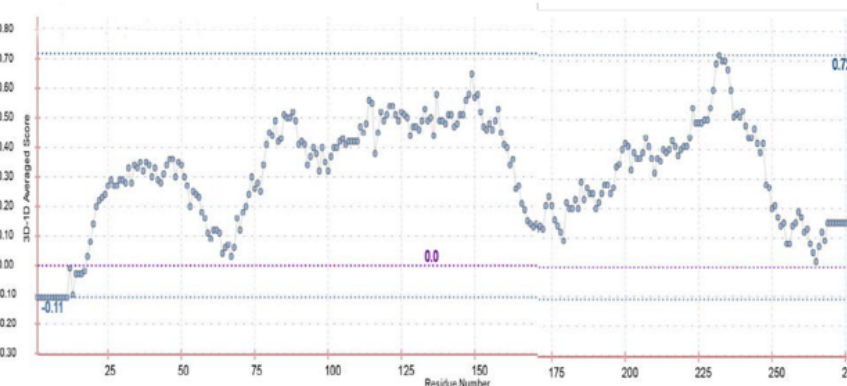
MGLLSVDLLITLQILPVFFSNCLFLALYDSVILLKHMVLFSL
RSKSARGEWRRMLTSEGLRCVWNSFLLDAYKQVKLGG
EAPNSSVIHIAKGNDGSNSSWKS VGGKCGTKCHLLDFA
NSERPLVVNFGSATUPPFTSQLSAFSKLVEEFSGVADFL
LVYIDEAHPSDGWAAPGISPSSFVKKHRNQEDRCAAA
HQLLERFSLPPQCQVADCMDNNANVAYGVSFERVCI
VRQKIAYLGGKGPFFYNLQEVRLWLEQNFSKRUNPLST
EDLSTDVSL

Analysis of the DIO2

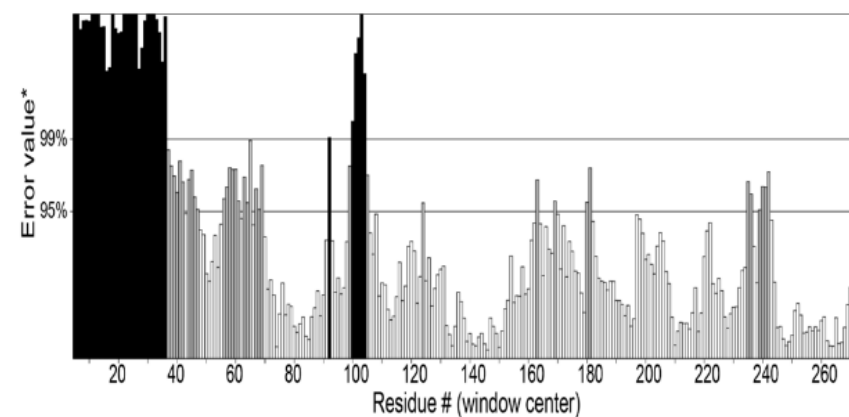
The structural modeling of chicken DIO2



Verify 3D
83.84% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2
Overall quality factor**: 73.063



The predictions of ligand binding sites in chicken DIO2

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
DIO2	3DRNA	0.14	131, 132, 133, 134, 163, 164, 226
	AKG	0.04	255, 258
	700	0.03	126, 128, 138, 142, 249, 250
	TS5	0.03	131, 132, 134, 225, 226, 227, 250
	THJ	0.03	254, 257

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

DIO3

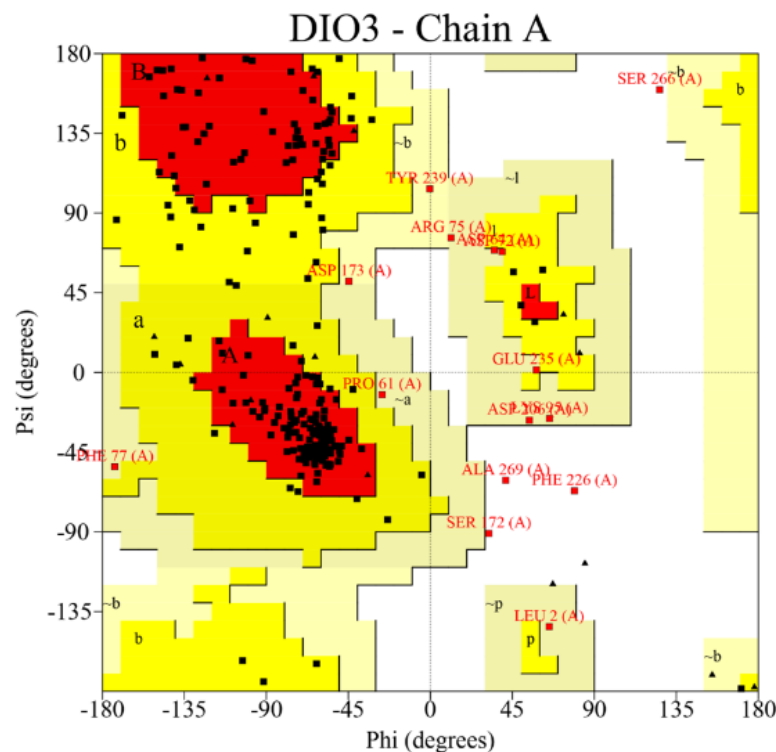
DIO3 [*Gallus gallus*]

LOCUS NP_001116120 274 aa linear
VRT 28-JUN-2016
DEFINITION thyroxine 5-deiodinase [*Gallus gallus*].
ACCESSION NP_001116120 XP_426465
VERSION NP_001116120.1
DBSOURCE REFSEQ: accession NM_001122648.2
KEYWORDS RefSeq.
SOURCE *Gallus gallus* (chicken)
ORGANISM *Gallus gallus*
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001116120.1 thyroxine 5-deiodinase [*Gallus gallus*]
MLHSLGAHTLQLLTQAAACILLFPRFLLTAVMLWLLDFLCI
RKKMLTMPTAEEAAGAGEGPPPDDPPVCVSDSNRMFT
LESLKAVWHGQKLDFFKSAHVGSPAPNPEVIQLDGQKR
LRILDFARGKRPLILNFGSCTUPPFMARLRSFRRLAAHF
VDIADFLLVYIEEAHPDSDGWVSSDAAYSIPKHQCLQDRL
RAAQLMREGAPDCPLAVDTMDNASSAAYGAYFERLYVI
QEEKVMYQGGRGPEGYKISELRSWLDQYKTRLQSPGA
VVIQV

Analysis of the DIO3

The structural modeling of chicken DIO3

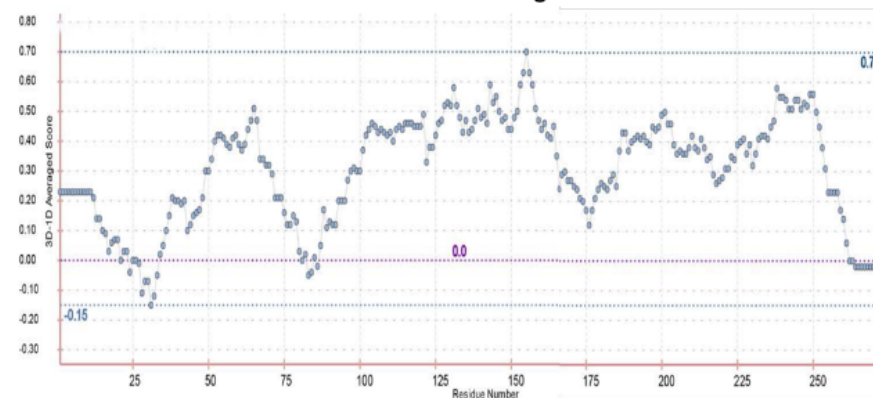


Plot statistics

Residues in most favoured regions [A,B,L]	180	76.3%
Residues in additional allowed regions [a,b,l,p]	42	17.8%
Residues in generously allowed regions [-a,-b,-l,-p]	10	4.2%
Residues in disallowed regions	4	1.7%
Number of non-glycine and non-proline residues	236	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	17	
Number of proline residues	19	
Total number of residues	274	

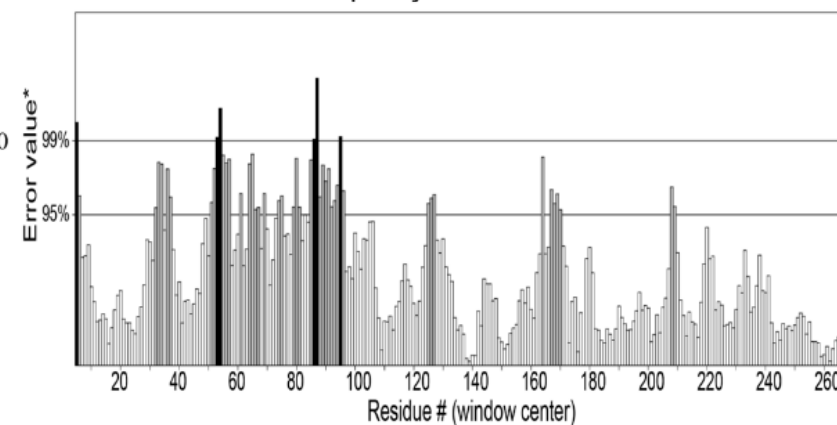
Verify 3D

85.18% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 81.509

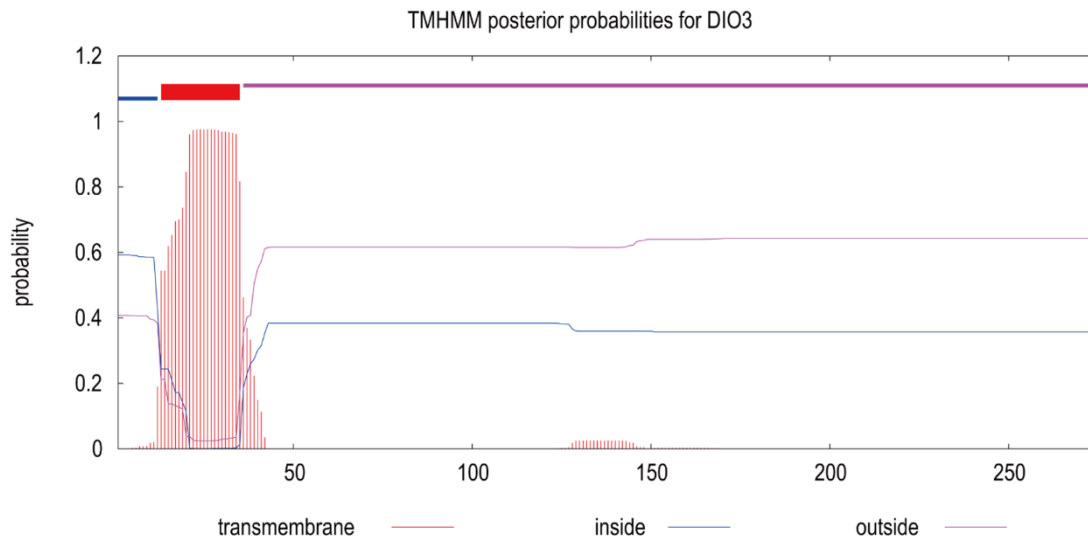


The predictions of ligand binding sites in chicken DIO3

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
DIO3	GSH	0.16	137, 138, 140, 227
	GSH	0.06	97, 98, 223, 240
	BIH	0.03	111, 160, 206, 207, 208
	TS5	0.03	137, 138, 140, 225, 226, 227, 249
	COM	0.03	119, 221, 222, 230, 232

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The predictions of transmembrane helices in chicken DIO3



DIO3 Number of predicted TMHs: 1
 # DIO3 Exp number of AAs in TMHs: 22.21104
 # DIO3 Exp number, first 60 AAs: 21.69484
 # DIO3 Total prob of N-in: 0.59249
 # DIO3 POSSIBLE N-term signal sequence

DIO3	TMHMM2.0	inside	1	12
DIO3	TMHMM2.0	TMhelix	13	35
DIO3	TMHMM2.0	outside	36	274

The accession number and amino acid sequences of chicken

TrxR1

TrxR1 [Gallus gallus]

LOCUS NP_001025933 499 aa linear

VRT 10-FEB-2016

DEFINITION thioredoxin reductase 1, cytoplasmic
[Gallus gallus].

ACCESSION NP_001025933 XP_416317

VERSION NP_001025933.2

DBSOURCE REFSEQ: accession NM_001030762.2

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

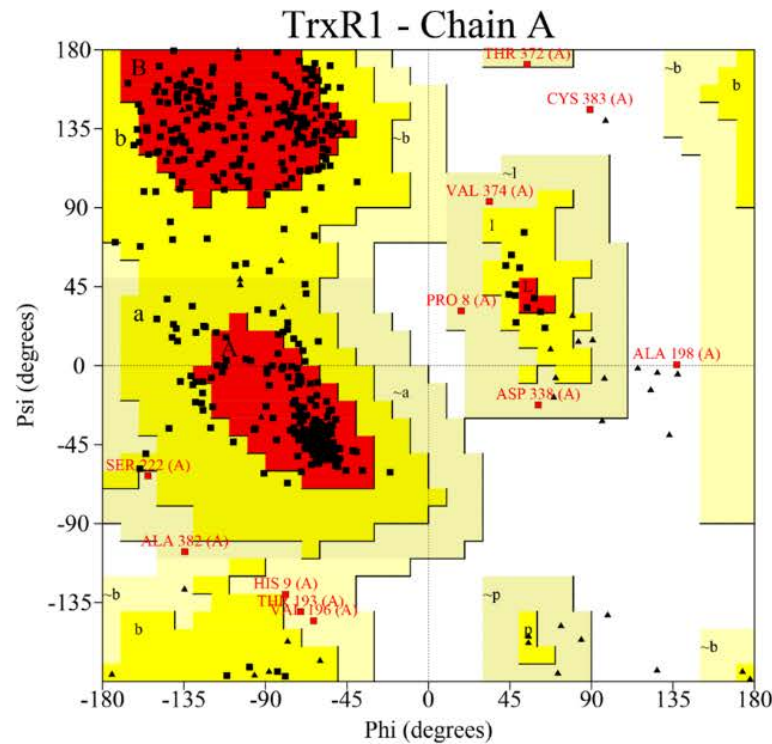
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001025933.2 thioredoxin reductase 1, cytoplasmic [Gallus gallus]
MNGHTAVPHSYDYDLIVIGGGSGGLAAAKEAAKYEEKVMVLDFVTPTPL
GNSWGLGGTCVNVGCIPKKLMHQAALLGQALQDSRKFGWQFTEEVK
HNWMTMTESVQNYIGSLNWGYRVALREKKVTYENAYGEFVGPHTVKA
TNKRGVEKLYTAERFLIATGERPRYLGI PGDKEYCISDDLFSLPYCPGK
TLVVGASYVALECAGFLAGLGLDVTVMVRSILLRGFDQDMANKIGEYME
EHGIKFIREFVPIKVEQIEEGTPGRLKVTA KSTKDDQVIEEEYNTVLLAIG
RDACTRKIGLDKVGKINEKTGKIPVDDMEQTNVPYIYAIGDILQDRLELT
PVAIQAGRLLVQRLYAGSTLKC DYVNVPTTVFTPLEYGACGYSEENAIQ
KFGEENIEVYHSHFWPLEWTVPSRDNNKCYAKIICNIQDNQRVIGFHV
LGP NAGEVTQGFAAAMKCGLT KDQLDSTIGIHPVCAEVFTTLSITKRS
GENTLQSGCUG

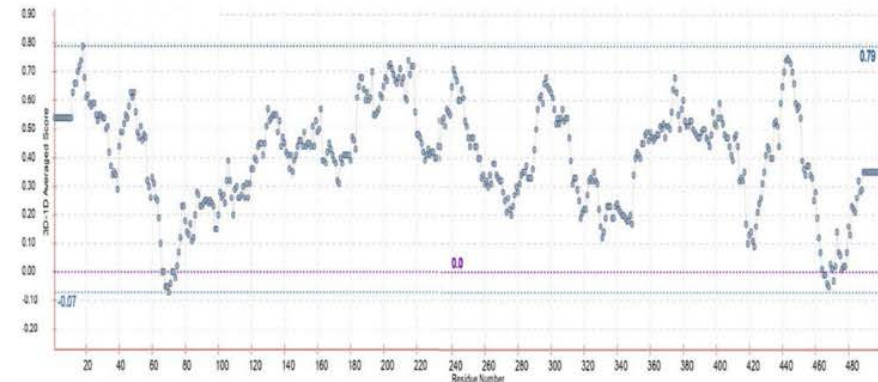
Analysis of the TrxR1

The structural modeling of chicken TrxR1



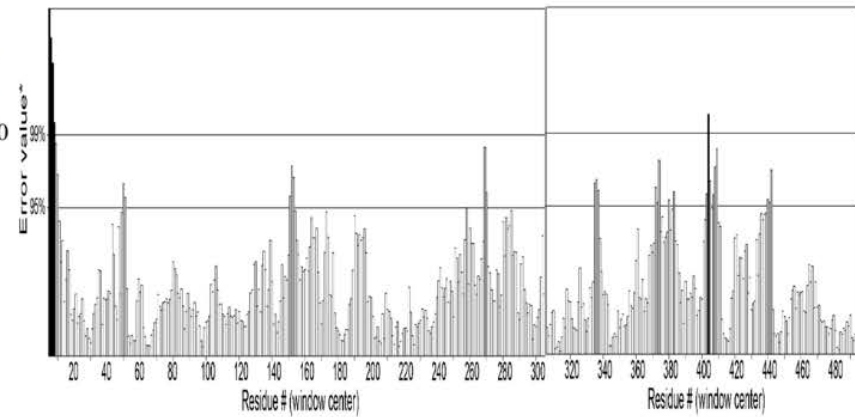
Verify 3D

87.78% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor^{**}: 93.673



The predictions of ligand binding sites in chicken TrxR1

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
TrxR1	FAD	0.98	18, 19, 21, 22, 23, 41, 42, 43, 44, 57, 58, 59, 61, 62, 63, 64, 68, 130, 131, 132, 160, 161, 162, 180, 201, 293, 296, 333, 334, 341, 342, 343, 344, 346, 375
	NAP	0.43	67, 168, 196, 197, 198, 199, 200, 204, 221, 222, 226, 252, 290, 291, 292, 293, 341, 342, 373
	CA6	0.07	21, 22, 25, 26, 29, 30, 33, 56, 60, 63, 64, 65, 112, 113, 123, 343, 347
	NAP	0.06	166, 168, 197, 198, 199, 221, 222, 223, 226, 252, 291, 292, 293, 315, 341
	WPF	0.06	22, 25, 26, 29, 56, 116, 119, 120, 125, 347

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

TrxR2

TrxR2 [Gallus gallus]

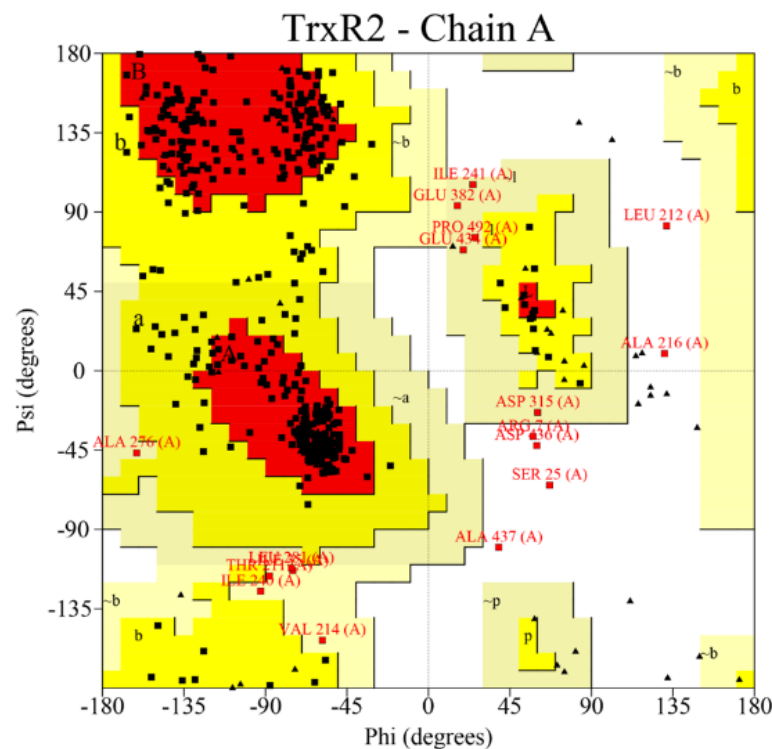
LOCUS NP_001116163 518 aa linear
VRT 05-MAY-2012
DEFINITION thioredoxin reductase 2, mitochondrial
[Gallus gallus].
ACCESSION NP_001116163 XP_415076
VERSION NP_001116163.1
DBSOURCE REFSEQ: accession NM_001122691.1
KEYWORDS RefSeq.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001116163.1 thioredoxin reductase 2, mitochondrial [Gallus gallus]

MAALWRRGERFLGVPGLCRTARALSGKKEYDLLVIGGGSGGL
ACAKEAAQFGKNVAVLDYVEPSPRGTKWGLGGTCVNVGCIPK
KLMHQAALLGGALKDAQHYGWSVAHPVHHNWSVMAQAVQN
YVKSLNWDGHRVQLQDKKVKYFNMKGSFSDSHTVCGIAKGGK
ETTLTAEKIVATGGRPKYPHTITGALEYGITSDDLFWLKDSPGK
TLVVGASYVSLECAFLTIGLDTTVIMRIIMRSIPLRGFDQQMA
SLVTEHMESYGTKFLKKCVPAKVEKLESSRLQVTWKNTLGT
ETDSFDTVMWAVGRVPDIKTLNLDSVGKTNSETGKIIVDASEA
TSVPHIYAIGDITEGRPELTPTAIAAGKLLARRLFGHSSELMDDYD
NVPTTVFTPLEYGCVGLSEEKAVQCYGSDNVEVFHAYYKPLEF
TVAERDAAQCYIKMVCLREREQRILGLHFIGPNAGEVIQGFALG
IKCGATYPQLMKTIGIHPTCAEEITKLHITKRSGLDATVTGCUG

Analysis of the TrxR2

The structural modeling of chicken TrxR2

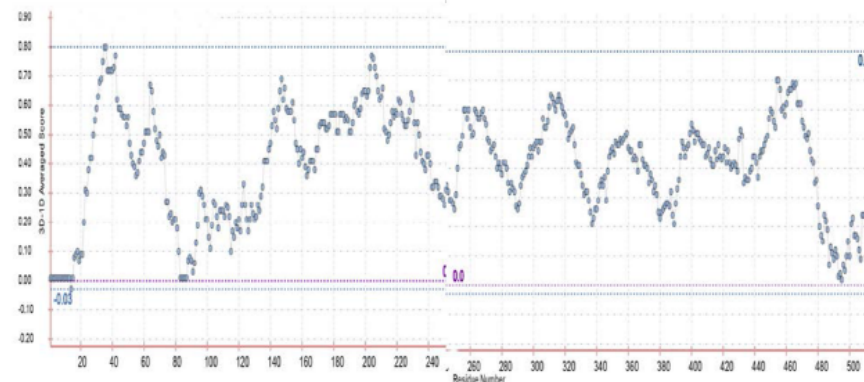


Plot statistics

Residues in most favoured regions [A,B,L]	352	79.6%
Residues in additional allowed regions [a,b,l,p]	74	16.7%
Residues in generously allowed regions [-a,-b,-l,-p]	10	2.3%
Residues in disallowed regions	6	1.4%
Number of non-glycine and non-proline residues	442	100.0%
Number of end-residues (excl. Gly and Pro)	1	
Number of glycine residues (shown as triangles)	55	
Number of proline residues	20	
Total number of residues	518	

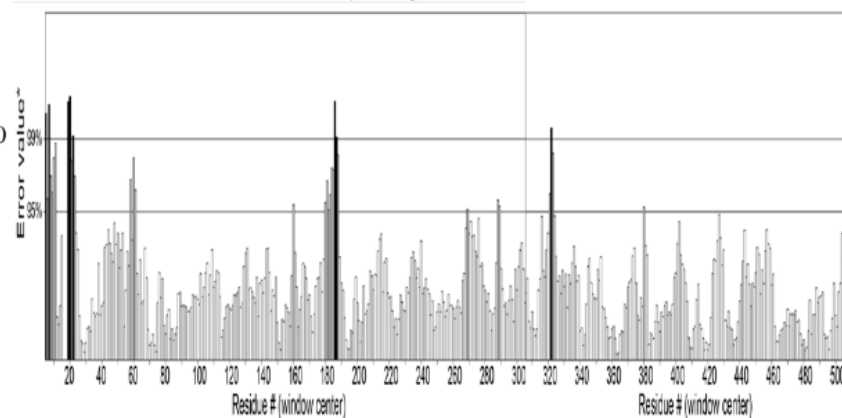
Verify 3D

87.07% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor^{**}: 93.651



The predictions of ligand binding sites in chicken TrxR2

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
TrxR2	FAD	0.99	35, 36, 38, 39, 40, 58, 59, 60, 61, 74, 75, 76, 78, 79, 80, 81, 85, 147, 148, 149, 177, 178, 179, 198, 219, 312, 315, 352, 353, 360, 361, 362, 363, 365, 394
	NAP	0.23	84, 185, 214, 215, 216, 217, 218, 219, 222, 239, 244, 248, 274, 309, 310, 312, 360, 361, 392
	CA6	0.05	38, 39, 42, 43, 46, 47, 50, 73, 77, 80, 81, 82, 129, 130, 140, 362, 366
	NDP	0.04	84, 185, 214, 215, 216, 217, 218, 219, 222, 238, 239, 248, 274, 309, 310, 311, 312, 360, 361, 392, 394
	WPF	0.03	39, 42, 43, 46, 73, 133, 137, 142, 366

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

TrxR3

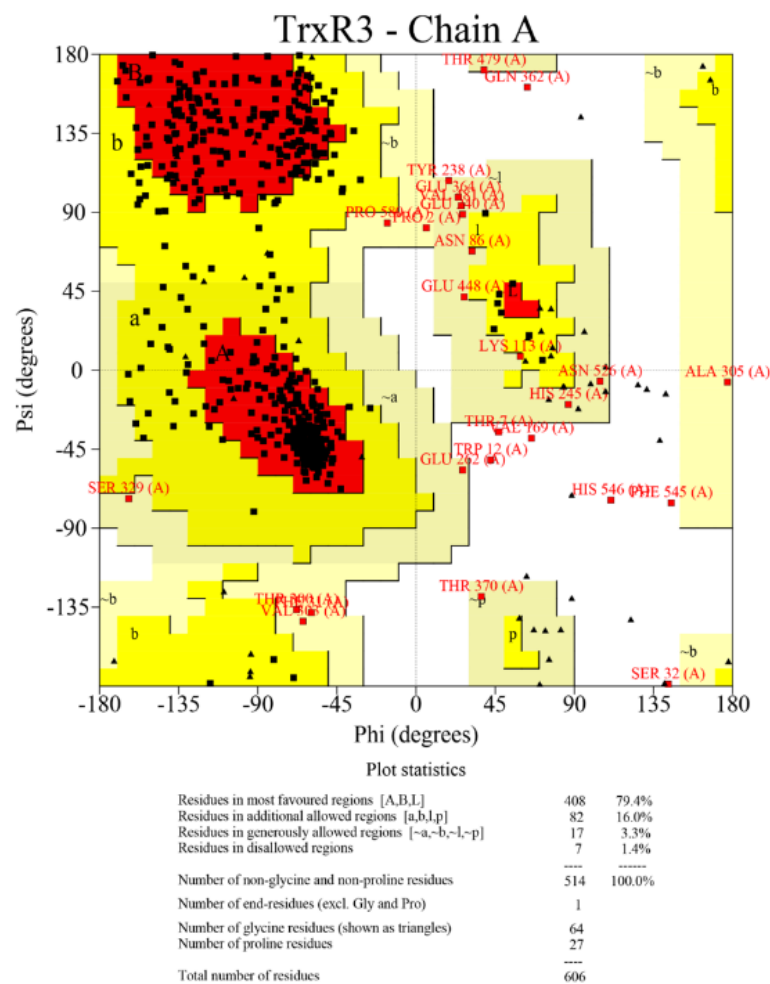
TrxR3 [Gallus gallus]

LOCUS NP_001116249 606 aa linear
VRT 10-FEB-2016
DEFINITION thioredoxin reductase 3 [Gallus gallus].
ACCESSION NP_001116249 XP_414371
VERSION NP_001116249.1
DBSOURCE REFSEQ: accession NM_001122777.1
KEYWORDS RefSeq.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001116249.1 thioredoxin reductase 3 [Gallus gallus]
MPPPGQTQLPDWDGLKLRVRTLIATHRVMIFSKSYCPYCHRVKELFSSL
GVQYYALELDVTDDGPSIQQVLAELTNQRTVPNVFINGKHIGGCATYK
AYENGTQLRILGDVKDAETYDYDLIVIGGGSGGLACSKEAATLGKKVMV
LDYVVPTPLGTSWGLGGTCVNVGCIPKKLMHQAALLGQALKDSRAYG
WQYDEQVKHNWEIMVEAVQNYIGSLNWGYRLSLREKSVTYQNSYGEF
VEPHKIKATNRKGQVITYHTAETFLATGERPRYLGIPGDKEYCITSDDL
SLPYCPGKTLVVGASYVALECAGFLAGLGLDVTVMVRSILLRGFDQEMA
EKIGAHMETHGVTFIRKVVPTQVERLEDGTPGRLKVTAKSTEGPEFFEG
EYNTVLIAIGRDACTRNIGLQTIGVKINEKNGKVPVNDERTNPVYVYAIG
DILDGKLELTPVAIQAGKLLARRLYGGSSSTKCDYINVPTTVFTPLEYGSC
GLAEEKAIEEYGKQNLVYHSLFWPLEWTVPGRDNNTCYAKIICNKLDG
NRVVG FHVLPNAGEVTQGFAAAIKCGLTKELLDETIGIHPTCAEVFTTM
DITKSSGQDITQRCUG

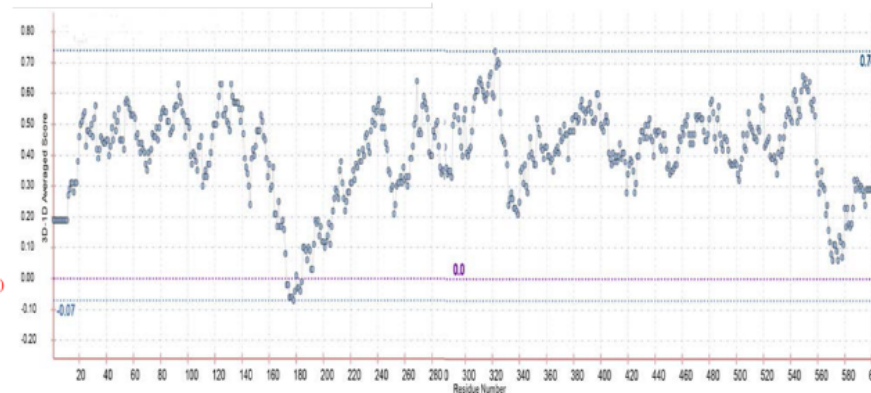
Analysis of the TrxR3

The structural modeling of chicken TrxR3



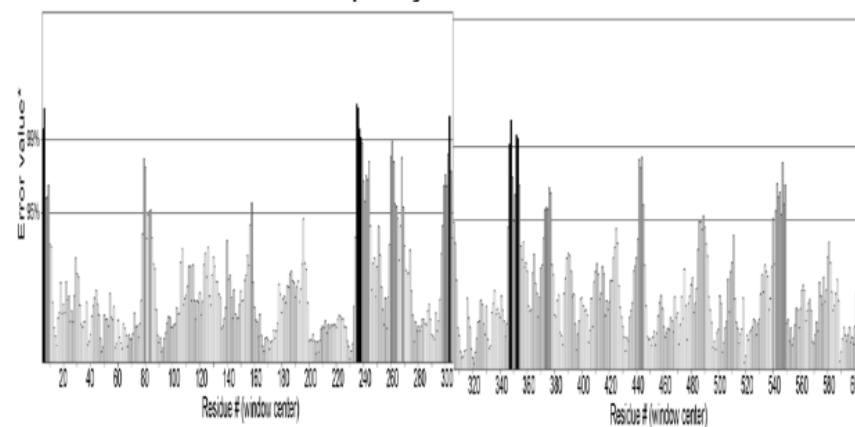
Verify 3D

88.94% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor^{**}: 90.117



The predictions of ligand binding sites in chicken TrxR3

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
TrxR3	FAD	0.96	125, 126, 128, 129, 130, 148, 149, 150, 151, 164, 165, 166, 168, 169, 170, 171, 175, 237, 238, 239, 267, 268, 269, 287, 308, 400, 403, 440, 441, 448, 449, 450, 451, 453, 482
	NAP	0.14	273, 275, 304, 305, 328, 329, 330, 333, 359, 398, 399, 400, 422, 448
	NDP	0.04	174, 305, 306, 307, 308, 311, 327, 328, 329, 333, 359, 397, 398, 399, 400, 448, 449, 480, 482
	CA6	0.04	128, 129, 132, 133, 136, 137, 140, 163, 167, 170, 171, 172, 219, 220, 230, 450, 454
	WPF	0.03	129, 132, 133, 136, 163, 167, 223, 226, 227, 454

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

Sell

Sell [Gallus gallus]

LOCUS NP_001026699 400 aa linear

VRT 08-JUL-2016

DEFINITION ethanolaminephosphotransferase 1

[Gallus gallus].

ACCESSION NP_001026699 XP_426219

VERSION NP_001026699.2

DBSOURCE REFSEQ: accession NM_001031528.3

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

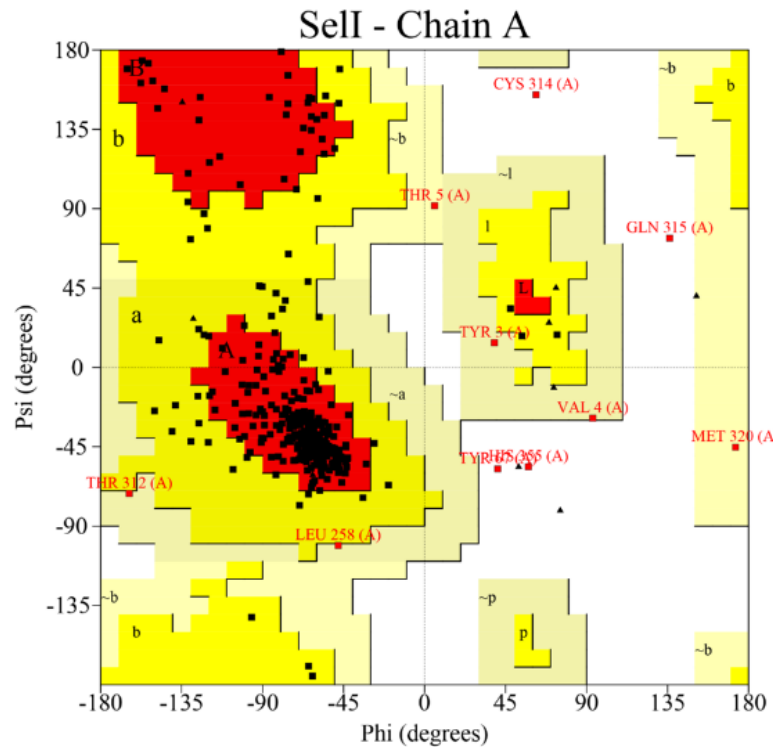
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001026699.2 ethanolaminephosphotransferase 1 [Gallus gallus]
MEYVTAEQLAGFSKYKYSAVDSNPLSLYVMHPFWNTIVKIFPTWLPAPNLI
TFSGFLLLWFNFFLMAYFDPDFYASAPDHQHPNGVWVWVGLLNFIAYT
LDGVDGKQARRTNSSTPLGELFDHGLDSWACVYFVTVYSTFGRGST
GVSFVFLYLLLWVFLFSFILSHWEKYNTGILFLPWGYDISQVTISIVYIVTA
IVGVEAWYAPFLFNFLYRDLFTTMIIACALTVTLPMSLYNFYKAYKNNTLK
HHSVYEIMLPLVSPVLLFALCTTWIFVSPMDILEVHPRLFYFMVGTAFAFI
SCQLIVCQMSSTRCQPLNWMLLPIALVLFMVMSGFAPSSETLLLYLLTAF
LTLAHIHYGVVVVSQLSRHFNIRPFSLKKPTPDULGMEEEEKISLRSAEVL

Analysis of the Sell

The structural modeling of chicken Sell

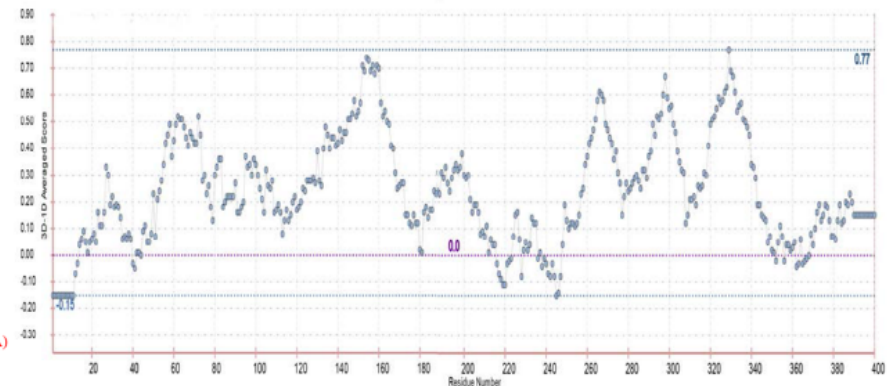


Plot statistics

Residues in most favoured regions [A,B,L]	306	85.2%
Residues in additional allowed regions [a,b,l,p]	43	12.0%
Residues in generously allowed regions [-a,-b,-l,-p]	6	1.7%
Residues in disallowed regions	4	1.1%
Number of non-glycine and non-proline residues	359	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	18	
Number of proline residues	21	
Total number of residues	400	

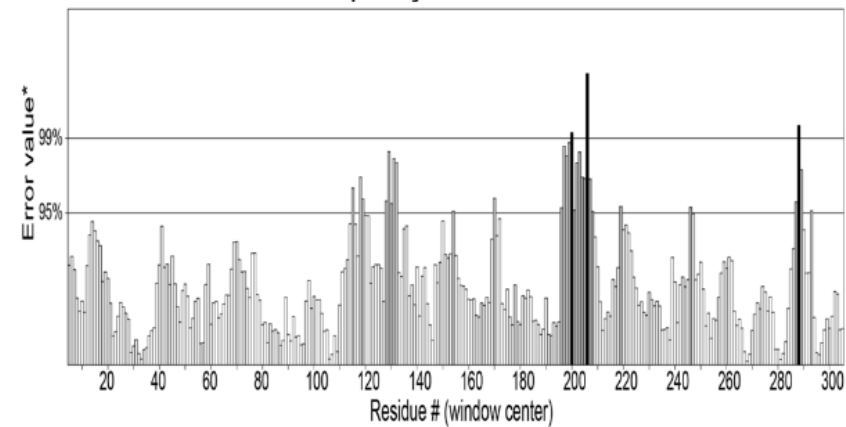
Verify 3D

82.25% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 88.520

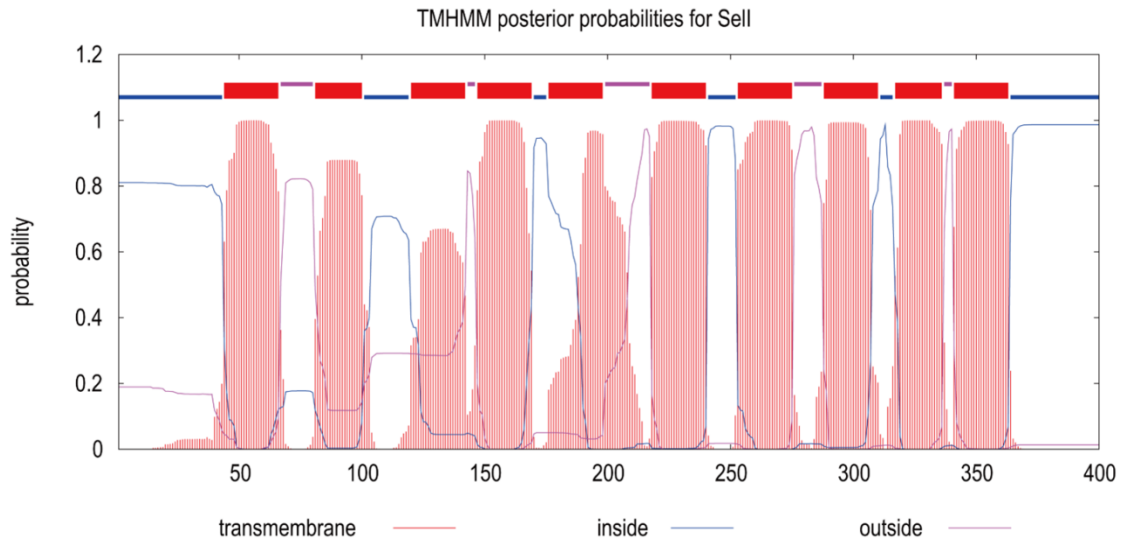


The predictions of ligand binding sites in chicken Sell

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
Sell	MN	0.05	48, 51
	8PH	0.05	26, 61, 65
	CL	0.05	120, 123, 261, 262
	BCL	0.05	62, 65
	MG	0.05	294, 295

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The predictions of transmembrane helices in chicken Sell



Sell Number of predicted TMHs: 10
 # Sell Exp number of AAs in TMHs: 206.19139
 # Sell Exp number, first 60 AAs: 17.19627
 # Sell Total prob of N-in: 0.81044
 # Sell POSSIBLE N-term signal sequence

Sell	TMHMM2.0	inside	1	43
Sell	TMHMM2.0	TMhelix	44	66
Sell	TMHMM2.0	outside	67	80
Sell	TMHMM2.0	TMhelix	81	100
Sell	TMHMM2.0	inside	101	119
Sell	TMHMM2.0	TMhelix	120	142
Sell	TMHMM2.0	outside	143	146
Sell	TMHMM2.0	TMhelix	147	169
Sell	TMHMM2.0	inside	170	175
Sell	TMHMM2.0	TMhelix	176	198
Sell	TMHMM2.0	outside	199	217
Sell	TMHMM2.0	TMhelix	218	240
Sell	TMHMM2.0	inside	241	252
Sell	TMHMM2.0	TMhelix	253	275
Sell	TMHMM2.0	outside	276	287
Sell	TMHMM2.0	TMhelix	288	310
Sell	TMHMM2.0	inside	311	316
Sell	TMHMM2.0	TMhelix	317	336
Sell	TMHMM2.0	outside	337	340
Sell	TMHMM2.0	TMhelix	341	363
Sell	TMHMM2.0	inside	364	400

The accession number and amino acid sequences of chicken

SelS

SelS [Gallus gallus]

LOCUS NP_001019905 194 aa linear

VRT 25-AUG-2016

DEFINITION selenoprotein S [Gallus gallus].

ACCESSION NP_001019905 XP_413890

VERSION NP_001019905.1

DBSOURCE REFSEQ: accession NM_001024734.2

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

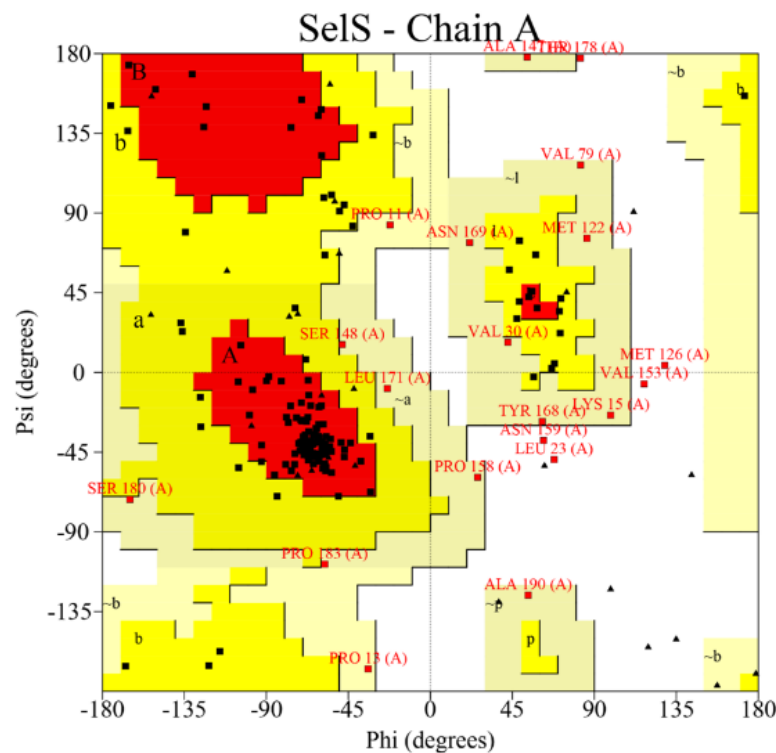
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001019905.1 selenoprotein S [Gallus gallus]

MELGDRGGAGPGPGKPALEREGLELLQHTVGALLSSY
GWYILLACVAIYLIVQKISPYLRMRPSSQQGATGAAVEPD
MVVRRQEALLASRLRMQEELNAQAERYKEKQRQLEEQ
KRRQKIEMWESMQEGKSYKGNLKLSSQQAESGASTSS
AVPKSKPNKKPLRGGGYNPLSGEGGGTCSWRPGRRG
PSAGGUG

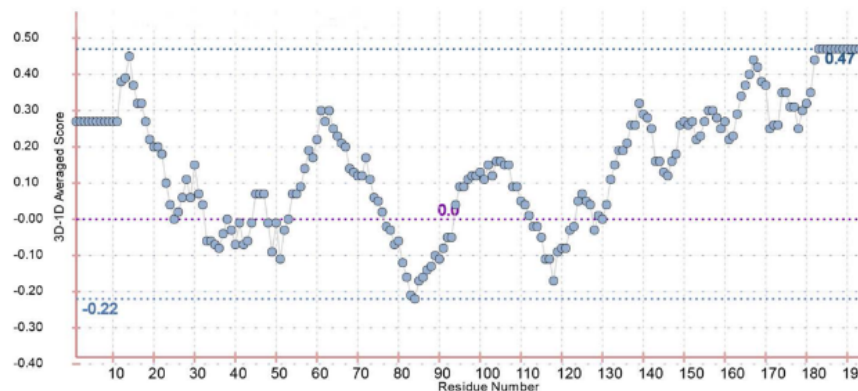
Analysis of the Sels

The structural modeling of chicken Sels



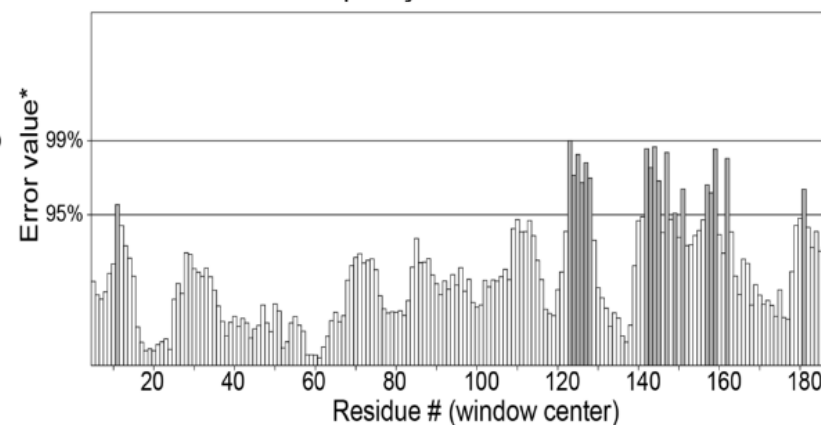
Verify 3D

82.27% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 89.247

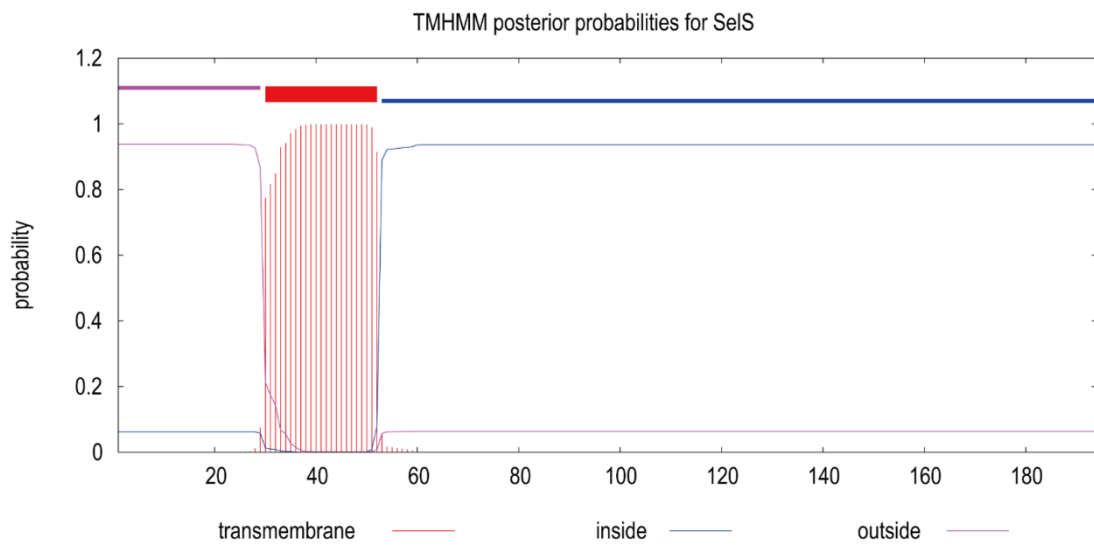


The predictions of ligand binding sites in chicken SelS

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SelS	Nuc.AcId	0.06	19, 20, 23, 24, 27, 31, 35
	CA	0.06	62, 63, 65, 69, 90
	FE	0.05	30, 33, 121
	Nuc.AcId	0.04	25, 26, 29, 30, 32, 33, 34, 36
	CPL	0.04	52, 54, 103, 104, 106

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The predictions of transmembrane helices in chicken SelS



SelS Number of predicted TMHs: 1
 # SelS Exp number of AAs in TMHs: 22.35942
 # SelS Exp number, first 60 AAs: 22.35882
 # SelS Total prob of N-in: 0.06185
 # SelS POSSIBLE N-term signal sequence

SelS	TMHMM2.0	outside	1	29
SelS	TMHMM2.0	TMhelix	30	52
SelS	TMHMM2.0	inside	53	194

The accession number and amino acid sequences of chicken

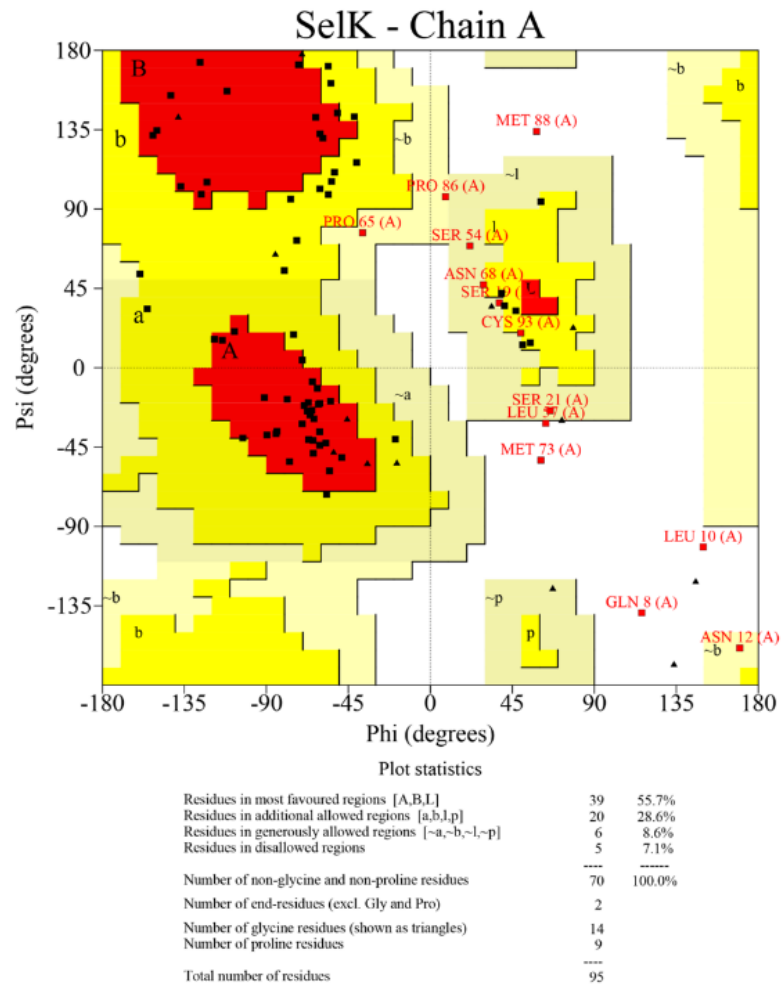
SelK

SelK [Gallus gallus]

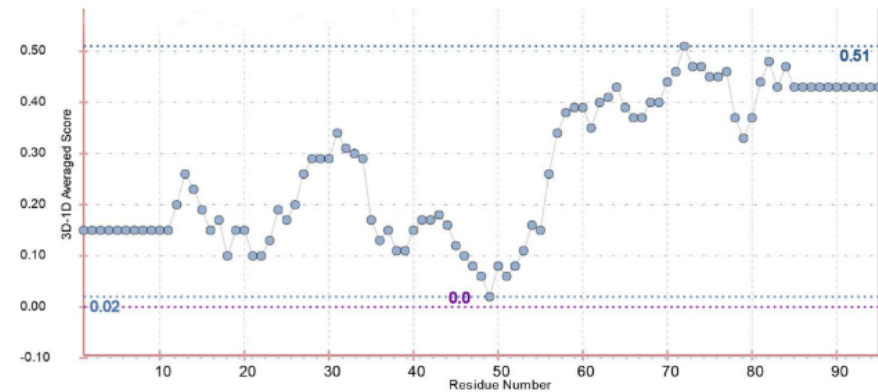
LOCUS NP_001020612 95 aa linear
VRT 24-APR-2016
DEFINITION selenoprotein K [Gallus gallus].
ACCESSION NP_001020612 XP_414337
VERSION NP_001020612.1
DBSOURCE REFSEQ: accession NM_001025441.2
KEYWORDS RefSeq.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.
>NP_001020612.1 selenoprotein K [Gallus gallus]
MVYISNGQVLDNRSRAPWSLSAITDFFWSIADFVVMFFQ
SIIQPDLRRRGYTSSSYLGQSDGRGPPGNPRRRMGRIN
HWGGGPPPPMAGGGUGR

Analysis of the SelK

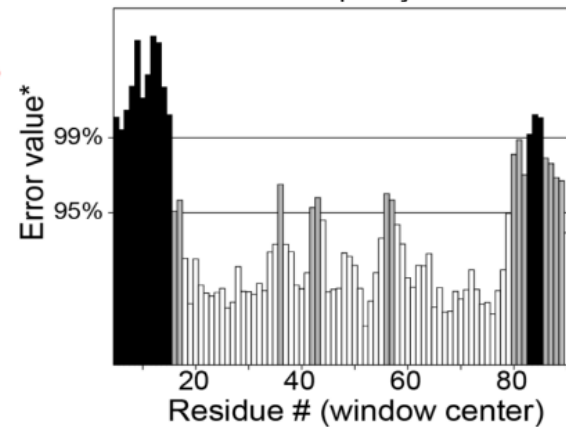
The structural modeling of chicken SelK



Verify 3D
84.74% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2
Overall quality factor**: 76.667



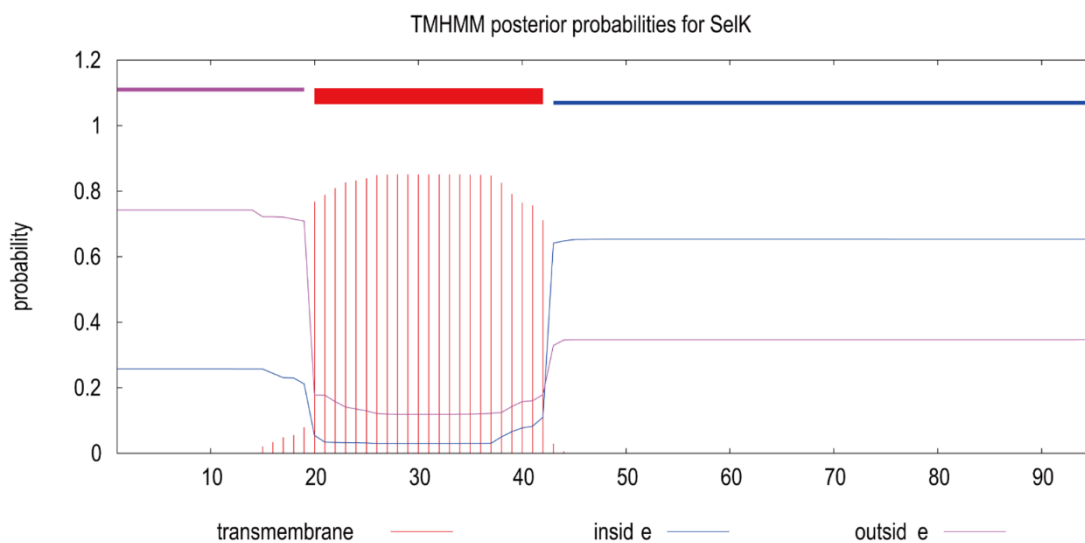
The predictions of ligand binding sites in chicken SelK

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SelK	32M	0.09	30, 34
	CLA	0.08	37, 38
	BCL	0.04	33, 37
	EDO	0.04	20, 38
	IMD	0.04	1, 9, 11, 50

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction

2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The predictions of transmembrane helices in chicken SelK



SelK Number of predicted TMHs: 1
 # SelK Exp number of AAs in TMHs: 19.19388
 # SelK Exp number, first 60 AAs: 19.19131
 # SelK Total prob of N-in: 0.25750
 # SelK POSSIBLE N-term signal sequence

SelK	TMHMM2.0	outside	1	19
SelK	TMHMM2.0	TMhelix	20	42
SelK	TMHMM2.0	inside	43	95

The accession number and amino acid sequences of chicken

SeIT

SeIT [Gallus gallus]

LOCUS NP_001006557 199 aa linear

VRT 24-APR-2016

DEFINITION selenoprotein T precursor [Gallus gallus].

ACCESSION NP_001006557 XP_422843

VERSION NP_001006557.3

DBSOURCE REFSEQ: accession NM_001006557.3

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

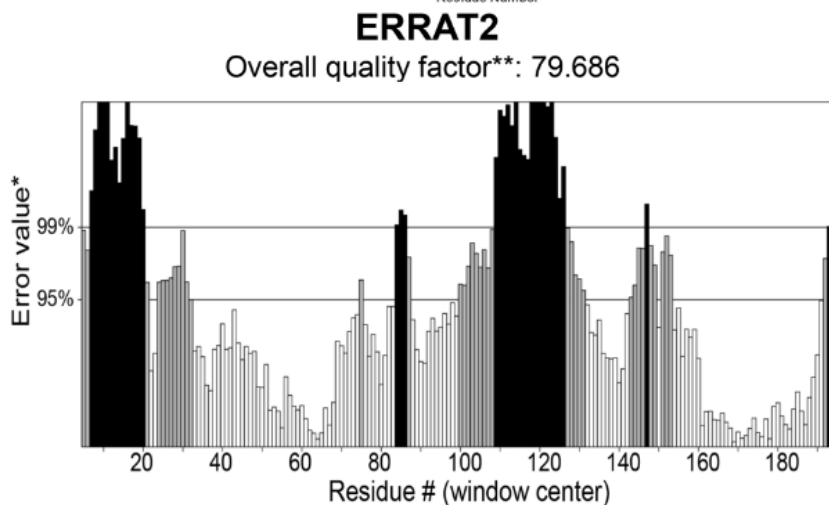
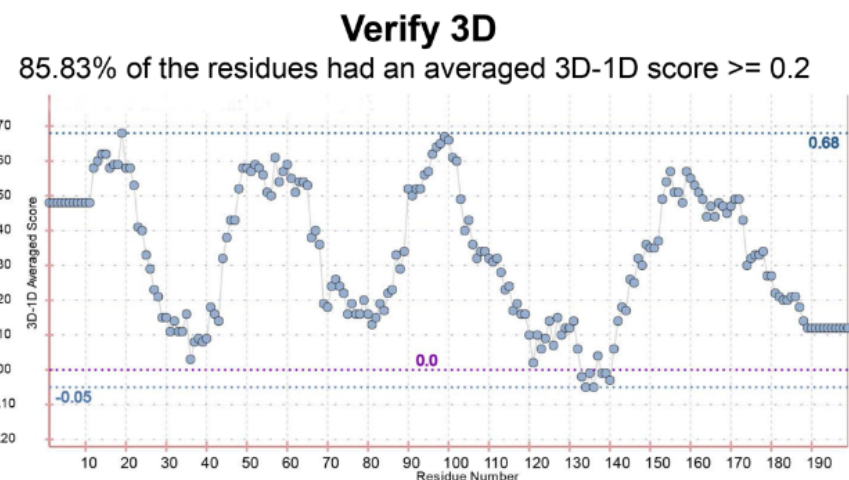
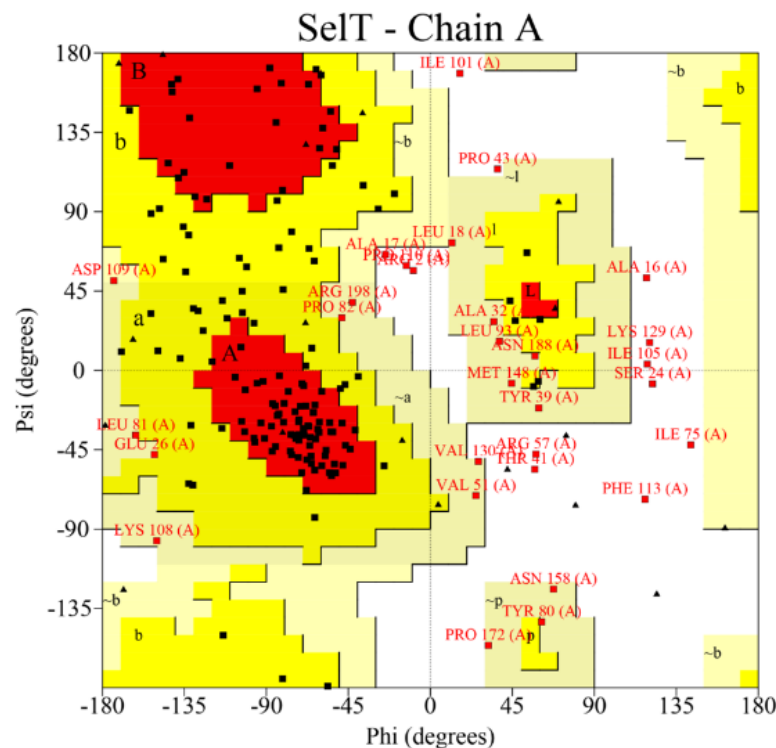
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001006557.3 selenoprotein T precursor [Gallus gallus]

MRAAGLGLGIGLLLLAALAGPGGSAEQGGVPAKKLRMA
YATGPLLKFQICVSUGYRRVFEEYMRVISQRYPPDIRIEGE
NYLPQPIYRHIASFLSVFKLVLIIGLIIVGKDPFAFFGMQAP
SIWQWGQENKVYACMMVFFLSNMIENQCMSTGAFEITL
NDVPVWSKLESGHLPSMQQLVQILDNEMKLVHMHESM
PHHRS

Analysis of the SeIT

The structural modeling of chicken SeIT

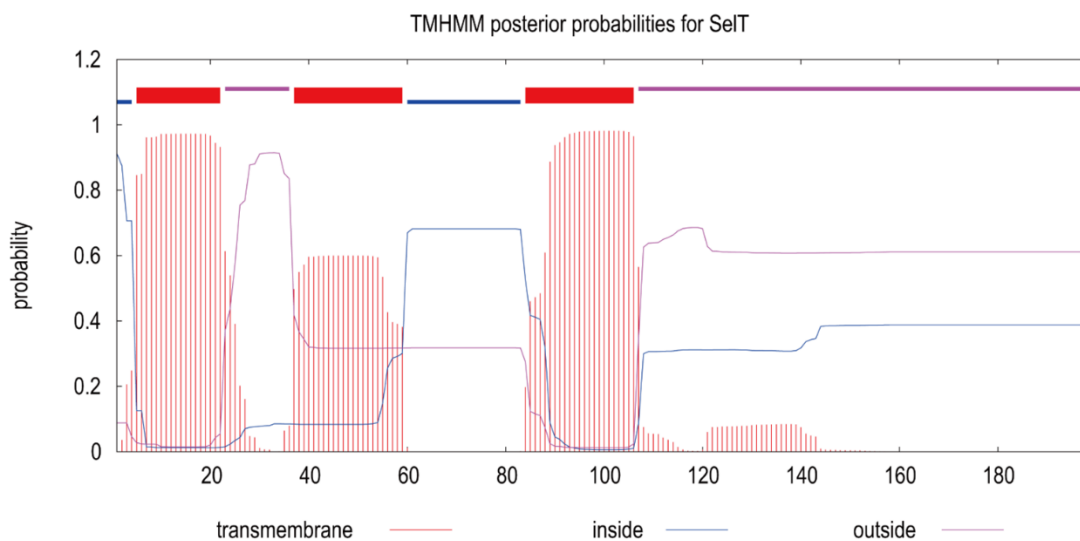


The predictions of ligand binding sites in chicken SeIT

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SeIT	TFA	0.14	153, 163
	A46	0.04	97, 98, 132, 136
	MG	0.03	141, 144
	MG	0.03	172, 176
	1U3AA00	0.03	47, 58, 59, 62, 153, 165, 171, 172, 173, 177

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The predictions of transmembrane helices in chicken SelT



SelT Number of predicted TMHs: 3
 # SelT Exp number of AAs in TMHs: 54.95809
 # SelT Exp number, first 60 AAs: 32.55588
 # SelT Total prob of N-in: 0.91209
 # SelT POSSIBLE N-term signal sequence

SelT	TMHMM2.0	inside	1	4
SelT	TMHMM2.0	TMhelix	5	22
SelT	TMHMM2.0	outside	23	36
SelT	TMHMM2.0	TMhelix	37	59
SelT	TMHMM2.0	inside	60	83
SelT	TMHMM2.0	TMhelix	84	106
SelT	TMHMM2.0	outside	107	199

The accession number and amino acid sequences of chicken

SeIN

SeIN [Gallus gallus]

LOCUS NP_001108444 530 aa linear

VRT 10-FEB-2016

DEFINITION selenoprotein N precursor [Gallus gallus].

ACCESSION NP_001108444 XP_417734

VERSION NP_001108444.1

DBSOURCE REFSEQ: accession NM_001114972.1

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

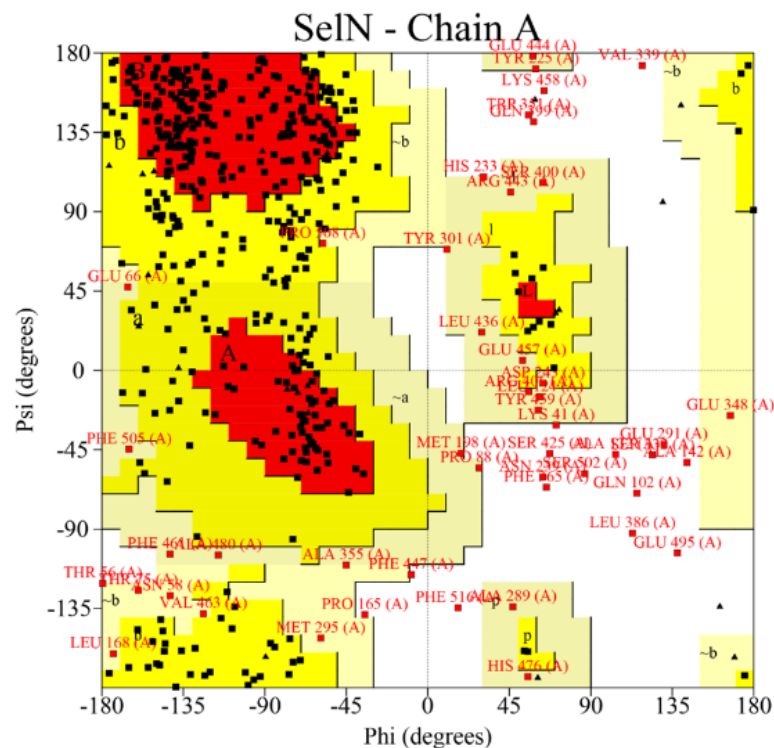
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001108444.1 selenoprotein N precursor [Gallus gallus]
MAVPGAAPSRLALALAALAALAAVKYYRDAEAARQQELALKSLGSEGLF
LFSSLDTNNDLYLSPEEFKPIAEKLTGVTPVSDFEEDAPDPNGETLSIVA
KFQPLVMETMTKSKDGFLGISHVALSGLRNWTAPVSPKSVMLARQFKA
FLPPKNKLDLGDPWWIIPSELNIFTGYLSNNRFYPPPPKGKEIIHRLLSM
FHPRPFVKTRFAPQGGSVACIQAISTYYYYTIAFRIHAEFQLNEPPDFPFWF
SPGQFTGYIVLSKDSSHVREFKLFVPNKRSLNVDMEWLYGASEGSNME
VDIGYLPQMELESTGPSVPSVIYDENGVIDSRDPSGEPIQFVFEEITW
QQEIPWEEAAQKLEVAMYPFKKVSYPFTEAFERAKAEKKLVHSILLWG
ALDDQSCUGSGRTLRETVLESSPILALLNESFISSWSLVKELEELQTNRE
NEFYSKLADLHLEKYNFPVEMIICLPNGTVIHHINANYFLDITSMKPEDVE
SSIFSFSANFDDPSTATYLQFLKEGLQRAKAYLQN

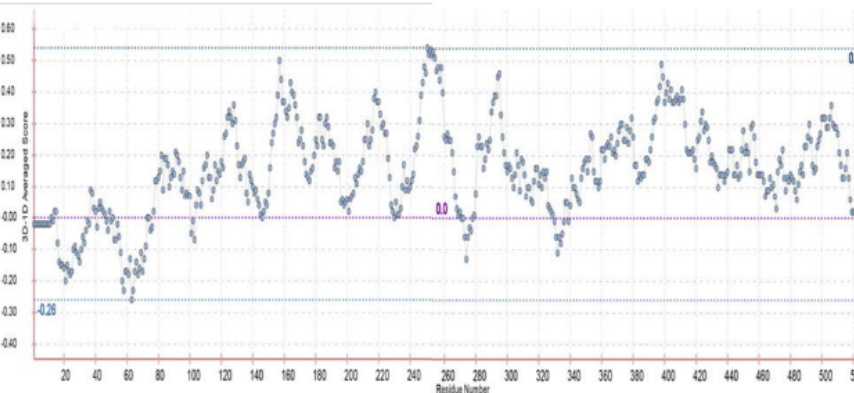
Analysis of the SeIN

The structural modeling of chicken SeIN



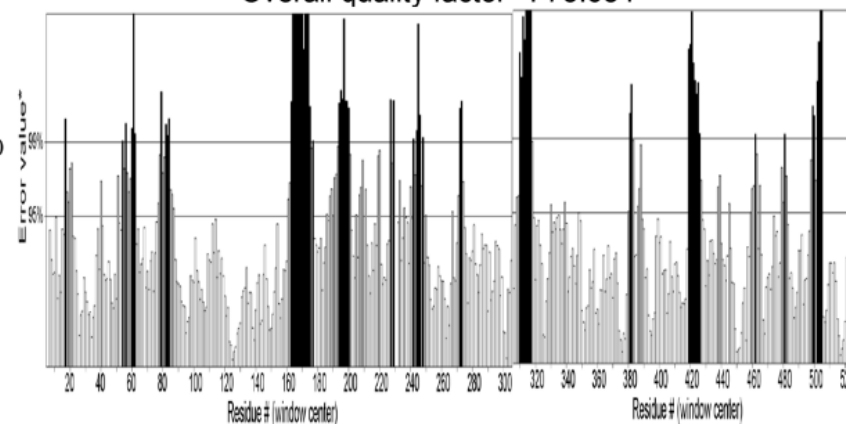
Verify 3D

76.63% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 73.684



The predictions of ligand binding sites in chicken SeIN

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SeIN	FE	0.07	451, 455
	ADP	0.05	207, 256, 257, 270, 284, 285
	ADP	0.05	177, 206, 255, 256, 257, 258, 271, 284, 285
	CA	0.02	250, 388
	N/A	0.02	308, 313, 329, 358, 373, 380, 394

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

SelH

SelH [Gallus gallus]

LOCUS NP_001264794 129 aa linear

VRT 03-MAY-2016

DEFINITION selenoprotein H [Gallus gallus].

ACCESSION NP_001264794 XP_003641378

VERSION NP_001264794.1

DBSOURCE REFSEQ: accession NM_001277865.1

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

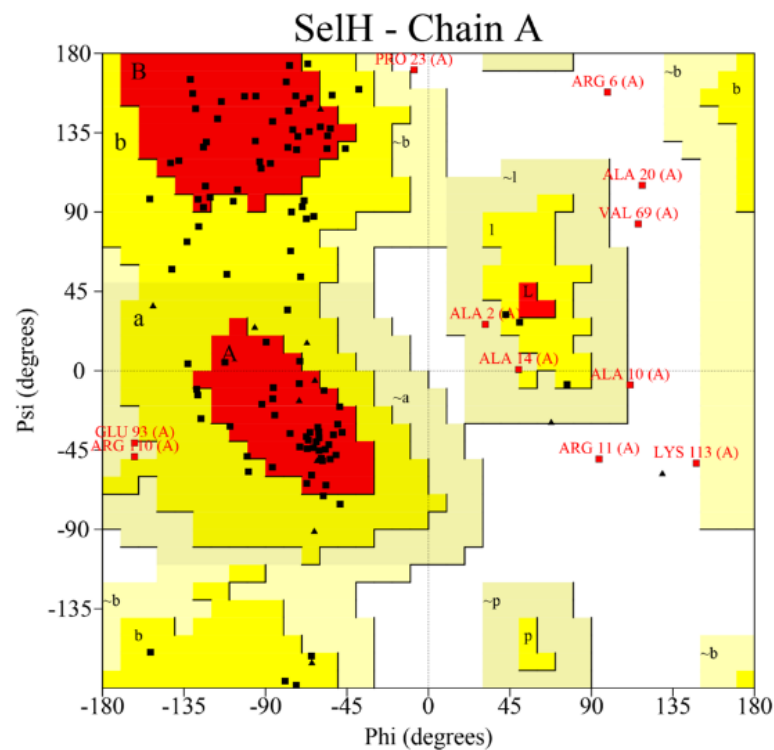
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001264794.1 selenoprotein H [Gallus gallus]

MAPRGRKRAARRPAEPEARADPPEKRPRDEAEGSPGD
AGGPRVVIEHCRSURVYGRNAAALSEALRGAVAALAVEI
NPRQPRRNSFEVSLVKEDGSTVQLWSGIGKGPPRKLKF
PEPAAVVEALRSSLA

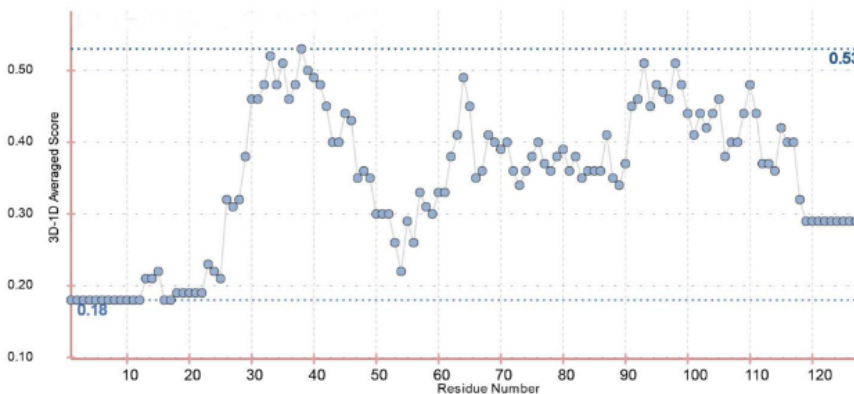
Analysis of the SelH

The structural modeling of chicken SelH



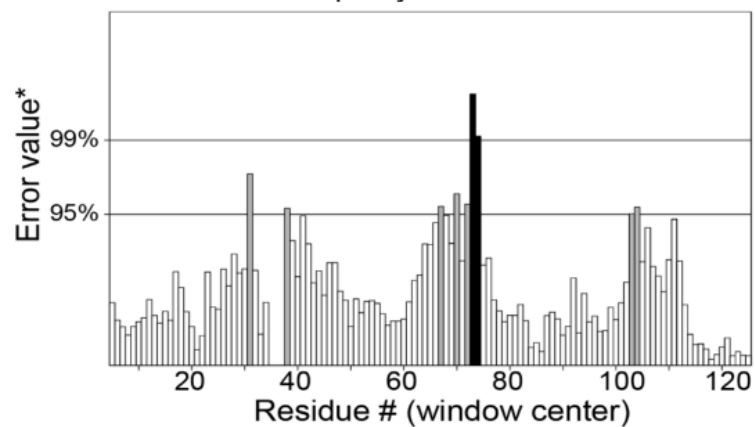
Verify 3D

85.27% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 92.373



The predictions of ligand binding sites in chicken SelH

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SelH	CLA	0.07	61, 72
	1R64A00	0.06	47, 51, 52, 53, 54 ,55, 57, 81, 82, 83, 84, 85, 103, 104, 106, 107, 108, 110, 111, 112, 113, 114
	PHO	0.06	60, 61, 64, 65
	MG	0.03	82, 85
	PO4	0.03	50, 51, 52, 53, 86

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

SelW

SelW [Gallus gallus]

LOCUS ACX47065 85 aa linear VRT
17-AUG-2011

DEFINITION selenoprotein W [Gallus gallus].

ACCESSION ACX47065

VERSION ACX47065.1

DBSOURCE accession GQ919055.1

KEYWORDS .

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

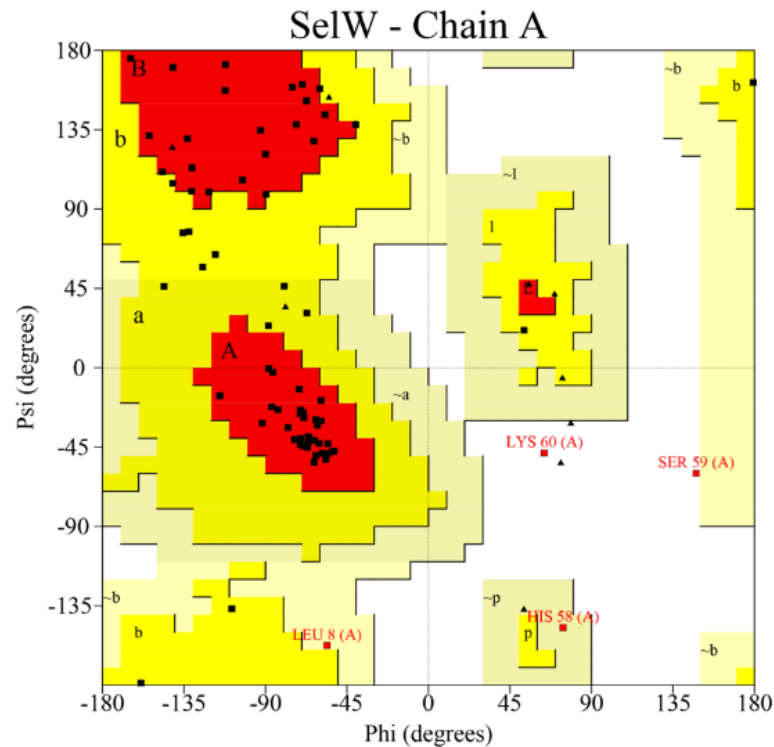
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>ACX47065.1 selenoprotein W [Gallus gallus]

MPLRVTVLYCGAUGYKPKYERLRAELEKRFPGALEMRG
QGTQEVTGWFEVTVGSRLVHSSKKNMGDFVDTDAKLQRI
VAAIQAAALP

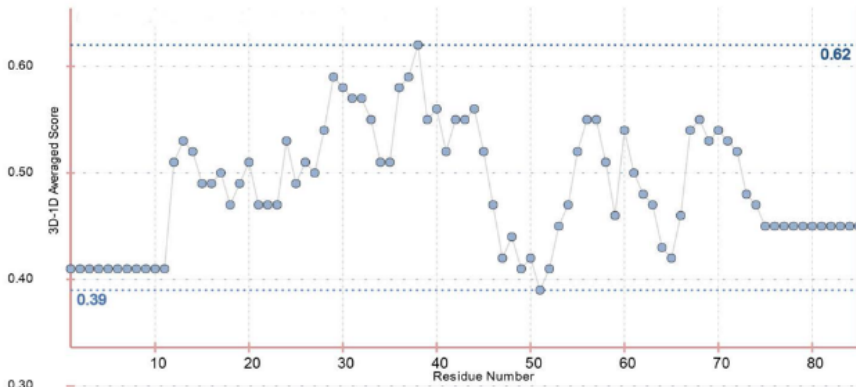
Analysis of the SelW

The structural modeling of chicken SelW



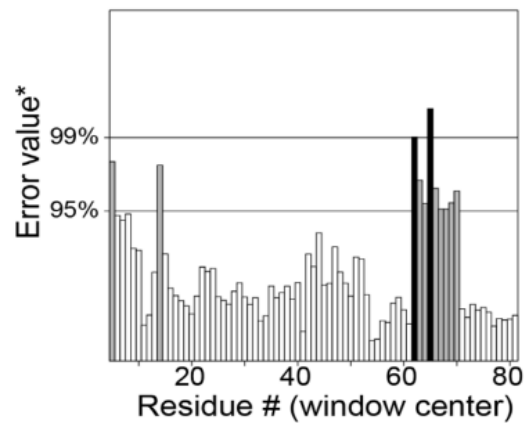
Verify 3D

100.00% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 85.714



The predictions of ligand binding sites in chicken SelW

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SelW	ZN	0.12	10, 13
	MG	0.06	25, 28
	2REMC00	0.05	13, 18, 44, 45, 46, 47, 60, 61, 65, 66, 68
	MG	0.04	29, 30, 77
	SO4	0.04	72, 75, 76

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

Sep15

Sep15 [Gallus gallus]

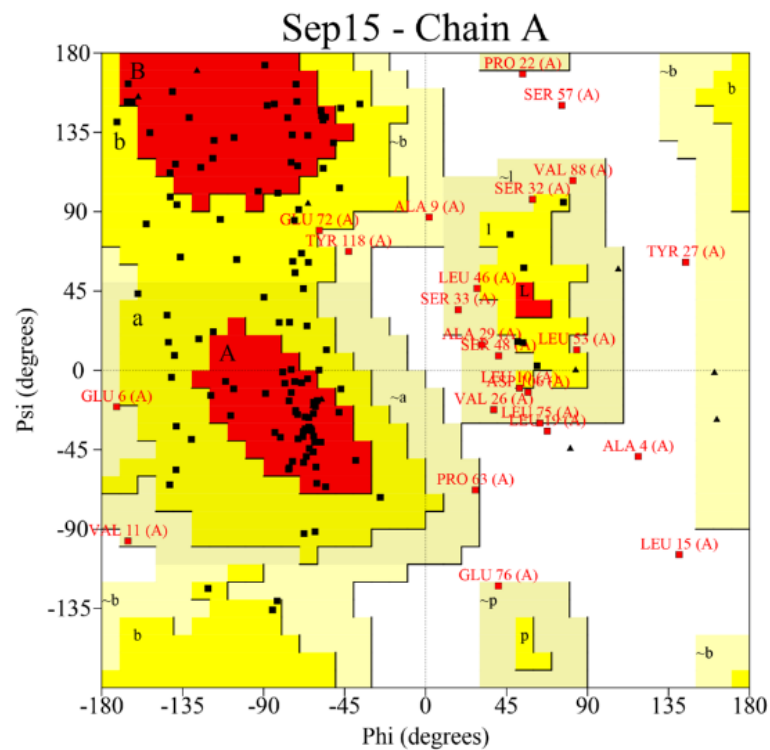
LOCUS NP_001012944 160 aa linear
VRT 24-APR-2016
DEFINITION 15 kDa selenoprotein precursor [Gallus gallus].
ACCESSION NP_001012944 XP_422358
VERSION NP_001012944.2
DBSOURCE REFSEQ: accession NM_001012926.2
KEYWORDS RefSeq.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001012944.2 15 kDa selenoprotein precursor
[Gallus gallus]

MAAAAELAALVRCWLCLLLGLPAINVYGAQLSSEACREL
GFSSNLLCSSCNLLGQFSLNQLDPFCRQCCQEEAQLT
RKLYAGAVLEVCGUKLGRFPQVQAFVRSDKPKLFRGLQI
KYVRGSDPVLKLLDDSGNIAEELSILKWNTDSVEEFLSE
KLERL

Analysis of the Sep15

The structural modeling of chicken Sep15

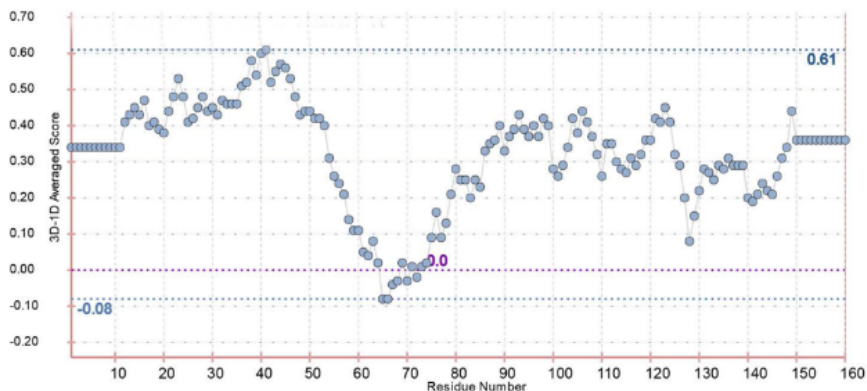


Plot statistics

Residues in most favoured regions [A,B,L]	74	51.7%
Residues in additional allowed regions [a,b,l,p]	47	32.9%
Residues in generously allowed regions [~a,~b,~l,~p]	17	11.9%
Residues in disallowed regions	5	3.5%
Number of non-glycine and non-proline residues	143	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	10	
Number of proline residues	5	
Total number of residues	160	

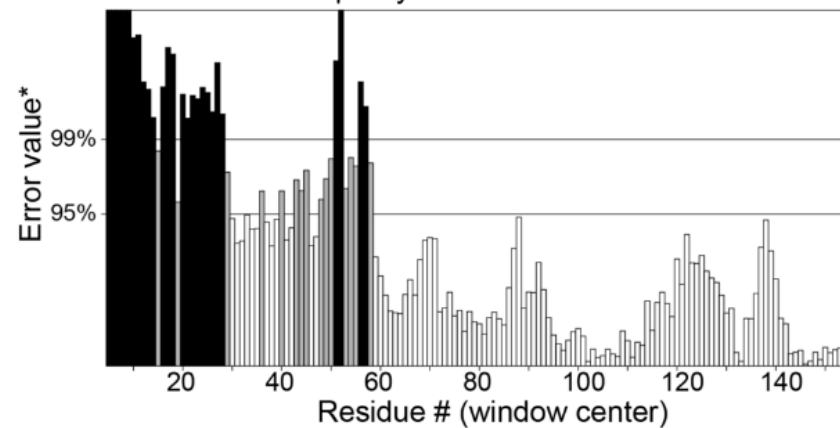
Verify 3D

85.00% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 73.026



The predictions of ligand binding sites in chicken Sep15

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
Sep15	ZN	0.15	47, 50, 65, 68
	NAP	0.04	102, 103
	IMD	0.04	126, 128, 139
	BEF	0.04	87, 88, 89, 124, 142
	CA	0.03	147, 150

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

SeIM

SeIM [Gallus gallus]

LOCUS NP_001264788 152 aa linear

VRT 24-APR-2016

DEFINITION selenoprotein M precursor [Gallus gallus].

ACCESSION NP_001264788

VERSION NP_001264788.1

DBSOURCE REFSEQ: accession NM_001277859.1

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

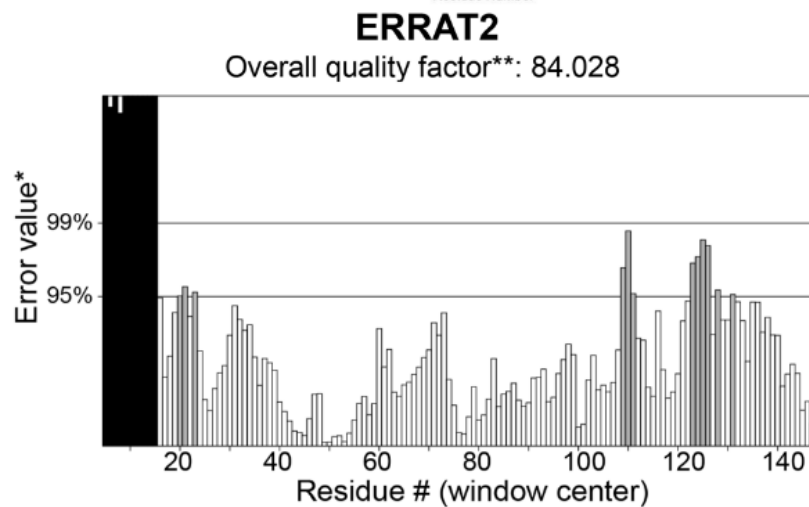
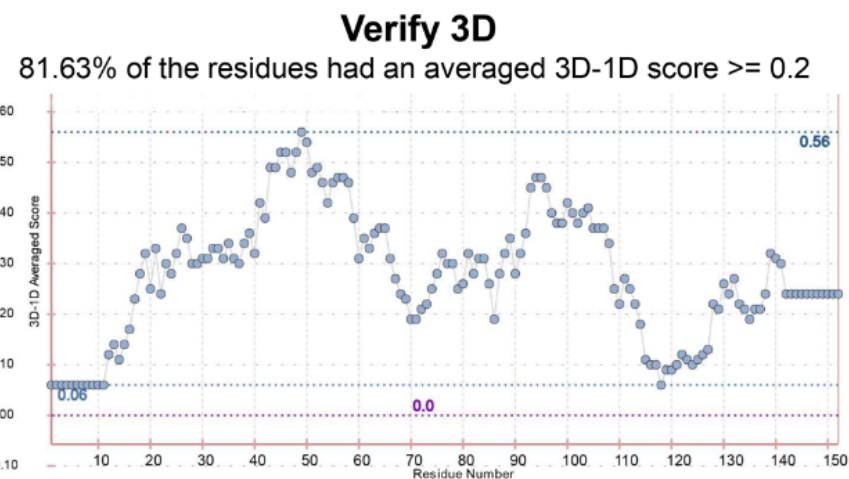
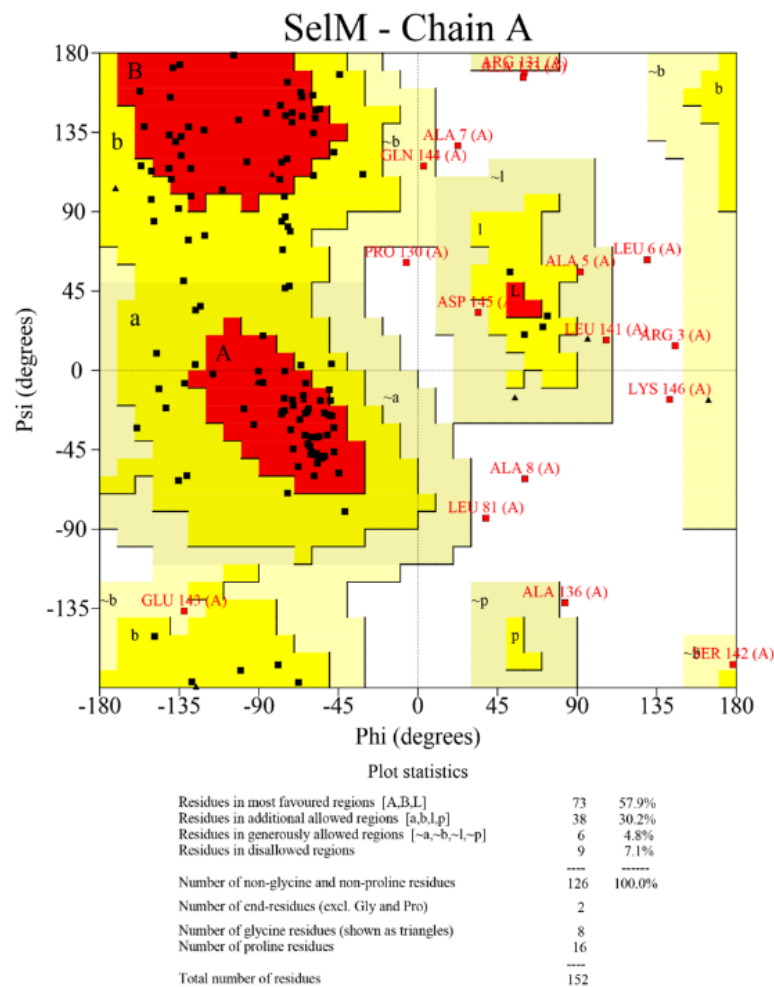
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001264788.1 selenoprotein M precursor [Gallus gallus]

MRRAALAALLLLAAAAGIERRPPRGLARGKVETCGGUR
LSRLPEVKAFVSQDIPLYHNLEMKHLPGADPELVLLSFR
YEELERIPLSDMTREEINQLVQELGFYRKETPEAPVPEE
FQFAPAKPLPTLTPTRRAPAADGKTLSEQDKKDHPDL

Analysis of the SelM

The structural modeling of chicken SelM



The predictions of ligand binding sites in chicken SelM

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SelM	ZN	0.11	34, 37
	UNK	0.06	98, 101
	MG	0.04	55, 56, 95
	S45	0.04	59, 86, 94, 97, 98, 101
	SE	0.04	84, 89

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

SepP1

SepP1 [Gallus gallus]

LOCUS NP_001026780 393 aa linear

VRT 24-APR-2016

DEFINITION selenoprotein P precursor [Gallus gallus].

ACCESSION NP_001026780 XP_429142

VERSION NP_001026780.2

DBSOURCE REFSEQ: accession NM_001031609.2

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

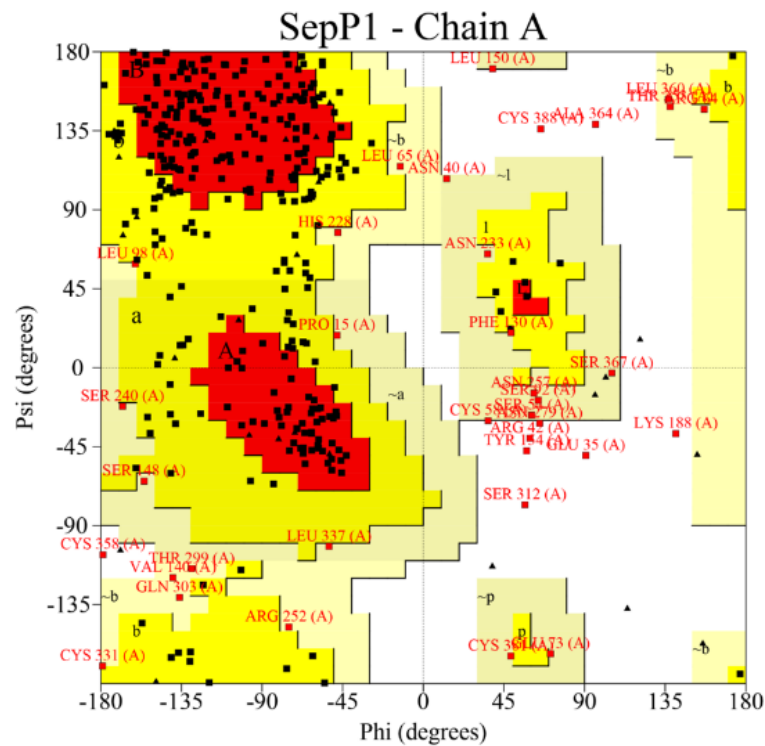
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001026780.2 selenoprotein P precursor [Gallus gallus]

MWAGLGLALVLCLLPGGGTESQRCQEPPEWHIGEESPMLNARGSVAV
VALLQASUYLCLLQASRLEDLRVKLENEGLVNI SYVVVNHQSPHSQKKF
HLLQESVSDHITVYQQDDHQADVWTTLNGNKDDFLIYDRCGRLVYHLG
LPYSFLSFQYVEEAIKIAYCENNCGNCSYTEPDIDNICENITKKEDENLAG
IEPEPEPSGQHSHHHHQLHRHRHHHHHREGGRHSKTQNHQAPSESQ
RRHPHNGRRHRVFNHNRHDQIGSHEQVETLPPGEGVENLPRVTKLUK
KGKTICKNQLTUNWQTASDSTTSSUCCHCRHLLFEELGNSITUQCRGA
LPNSCRUHGQLLAEDITESUQURLLTAAUESAAGGGSETSDTUQUQUER
AGNUAUKTN

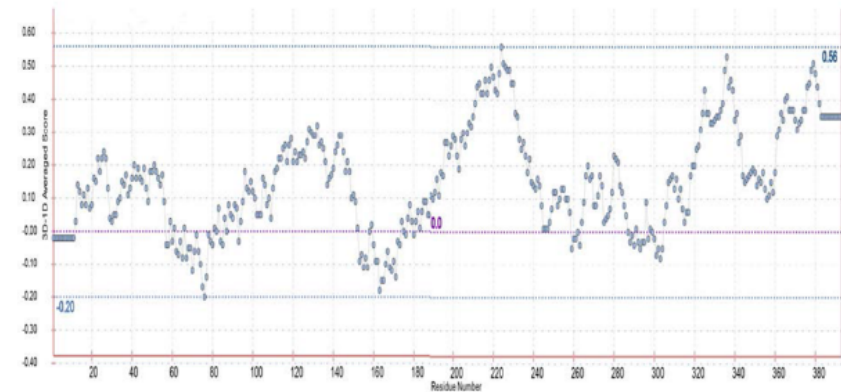
Analysis of the SepP1

The structural modeling of chicken SepP1



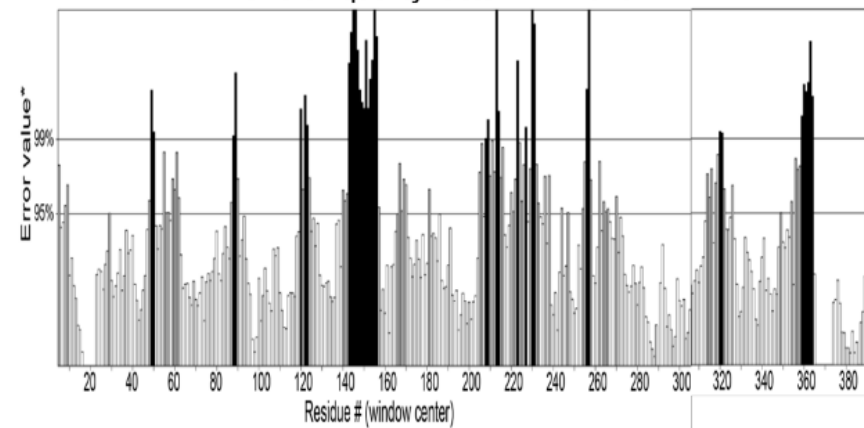
Verify 3D

85.37% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 71.545



The predictions of ligand binding sites in chicken SepP1

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SepP1	MG	0.06	32, 47, 48, 67, 135
	GLC	0.03	66, 129
	CA	0.03	67, 69, 79, 81, 122
	CA	0.03	40, 41, 139, 140
	ZN	0.03	134, 142

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction

2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

SepP2

SepP2 [*Gallus gallus*]

LOCUS XP_003641735 263 aa linear

VRT 04-JAN-2016

DEFINITION PREDICTED: selenoprotein Pb [*Gallus gallus*].

ACCESSION XP_003641735

VERSION XP_003641735.3

DBLINK BioProject: PRJNA10808

DBSOURCE REFSEQ: accession XM_003641687.3

KEYWORDS RefSeq.

SOURCE *Gallus gallus* (chicken)

ORGANISM *Gallus gallus*

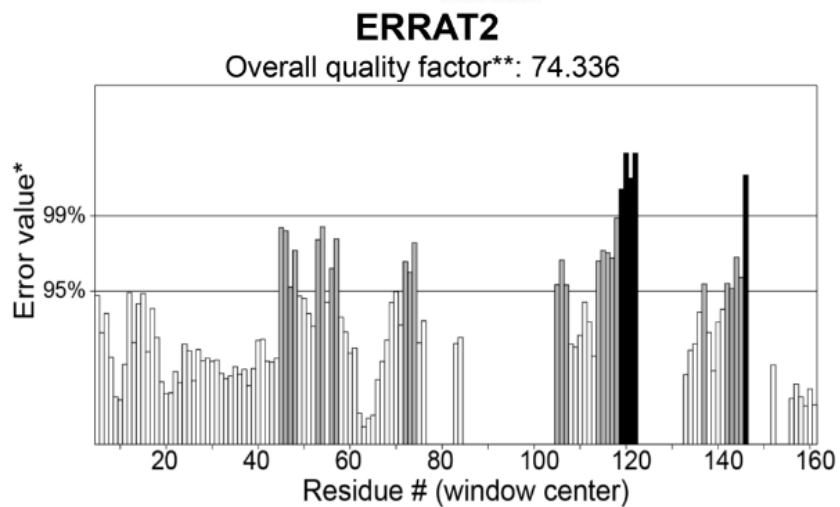
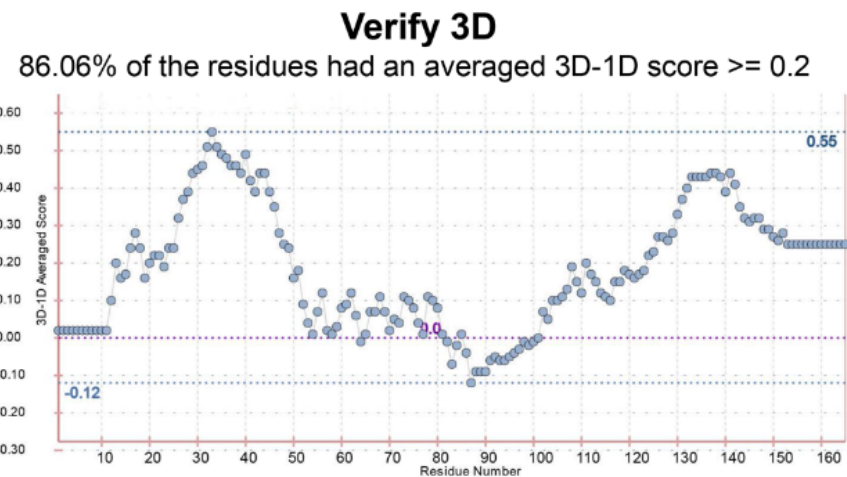
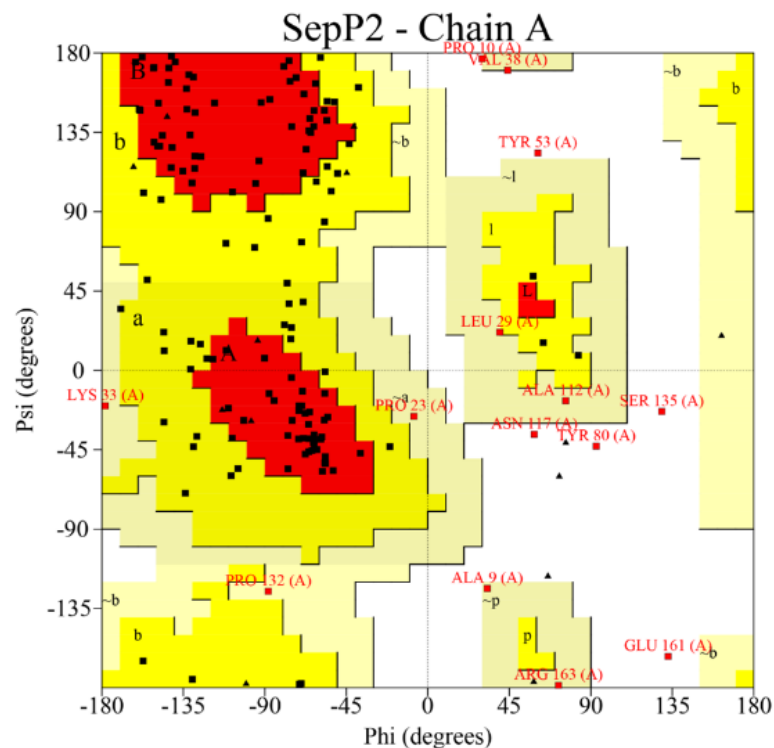
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>XP_003641735.3 PREDICTED: selenoprotein Pb [*Gallus gallus*]

MGPLLLALASCLGLAVASEGATNGSRLCHEAPAWRINGS
SPMEGAAGQVTVVALLKASUHFCLLQARSLGALRERLG
QQGVSDVRYVIVNEQAPLSRAMFGELQRHAPPGVVPV
QQQPHEPDVWQLLGGDKDDFLVYDRCGRLAFHIQLPY
SFLHLPYVESAIRFTHRKDFCGNCSLYPNSTQEANSTME
VPATLTPLPKQEEKESETPAHHQPNHLHPHHRAVGNGT
APEPSGDHRPAHAHHHHGAHGKLHPKGQTPEGRDP

Analysis of the SepP2

The structural modeling of chicken SepP2



The predictions of ligand binding sites in chicken SepP2

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SepP2	MG	0.07	32, 47, 48, 67, 135
	GLC	0.05	66, 129
	CA	0.03	67, 69, 79, 81, 122
	CA	0.02	40, 41, 139, 140
	ZN	0.02	134, 142

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

SelO

SelO [Gallus gallus]

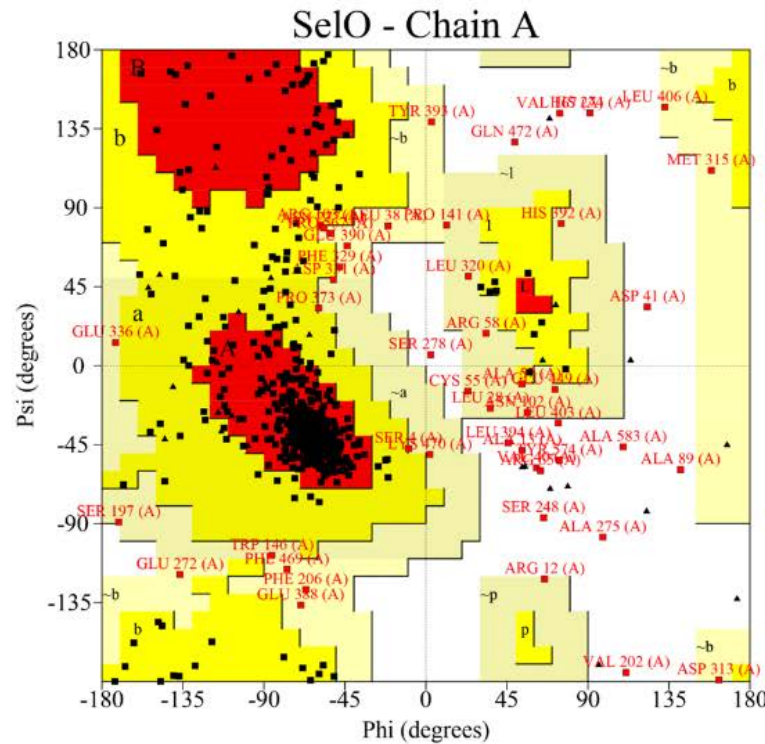
LOCUS NP_001108489 650 aa linear
VRT 29-SEP-2016

DEFINITION selenoprotein O [Gallus gallus].
ACCESSION NP_001108489 XP_415989
VERSION NP_001108489.2
DBSOURCE REFSEQ: accession NM_001115017.2
KEYWORDS RefSeq.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001108489.2 selenoprotein O [Gallus gallus]
MQRSAGPPSRPGSPERADGGGWLSALRFDNLALRSLPVDPSSEDCAP
RAVPGACFARVRPTPLRNPRLVAMSAPALALLGLEAGGPEAEREAEAL
YFSGNRLLPGSEPAAHCYCGHQFGSFAGQLGDGAAIYLGEVRGPRGA
RWELQLKGAGITPFSRQADGRKVLRSSIREFLCSEAMFHLGIPTTRAGT
CVTSDSEVVRDIFYDGNPKKERCTVVLRIASTFIRFGSFEIFKPPDEYTG
RKGPSVNRNDIRIQMLDYVIGTFYPEIQEAHADNSIQRNAAFFKEITKRT
ARLVAEWQCVGFCHGVLNTDNMSIVGLTIDYGPFMFMDRYDPEHICNG
SDNTGRYAYNKQPEICKWNLGKLAELVPELPLEISELILEEEYDAEFEK
HYLQKMRKKLGLIQLELEEDSKLVSELLETMHILTGGDFTNIFYLLSSFSV
DTPSPRLEDLFLEKLISQCASVEELRVAFKPQMDPRQLSMMLMLAQSNP
QLFALIGTKANINKELERIEQFSKLQQLTAADLLSRNKRHWTEWLEKYRV
RLHKEVESISDVDAWNTERVKVMNSNNPKYILRNYIAQNAIEAAENGDF
SEVRNVLKLLNPFQETEDSTEMETKEEEATATAACAQATRSRLSYCS
KPPLWASELCVTUSS

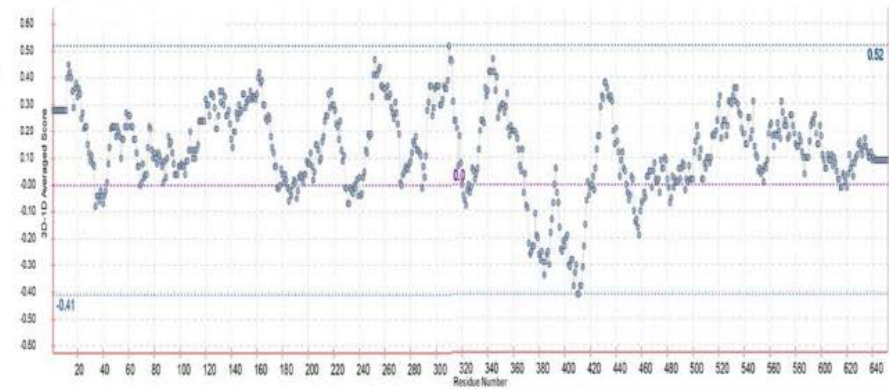
Analysis of the SeIO

The structural modeling of chicken SeIO



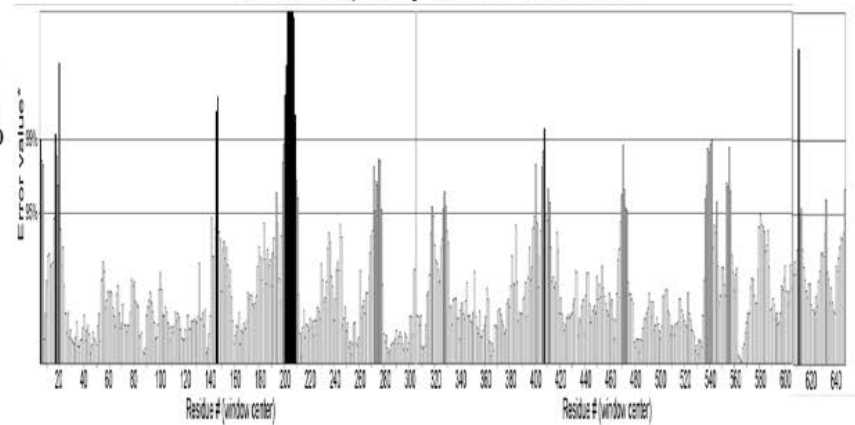
Verify 3D

85.89% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 90.528



The predictions of ligand binding sites in chicken SelO

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SelO	MG	0.12	314, 323
	FES	0.05	320, 321, 322, 324, 326, 327, 329, 331
	Nuc.Acid	0.04	288, 291
	FES	0.04	152, 153, 154, 202, 203
	Nuc.Acid	0.04	314, 315, 316, 317, 318, 319, 321

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

SelU

SelU [Gallus gallus]

LOCUS NP_001180447 224 aa linear
VRT 28-AUG-2016

DEFINITION redox-regulatory protein FAM213A
[Gallus gallus].

ACCESSION NP_001180447

VERSION NP_001180447.1

DBSOURCE REFSEQ: accession NM_001193518.1

KEYWORDS RefSeq.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

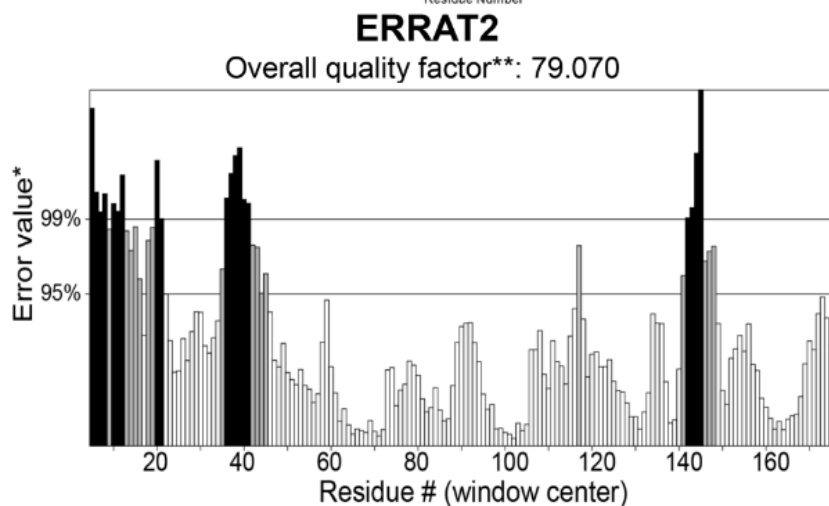
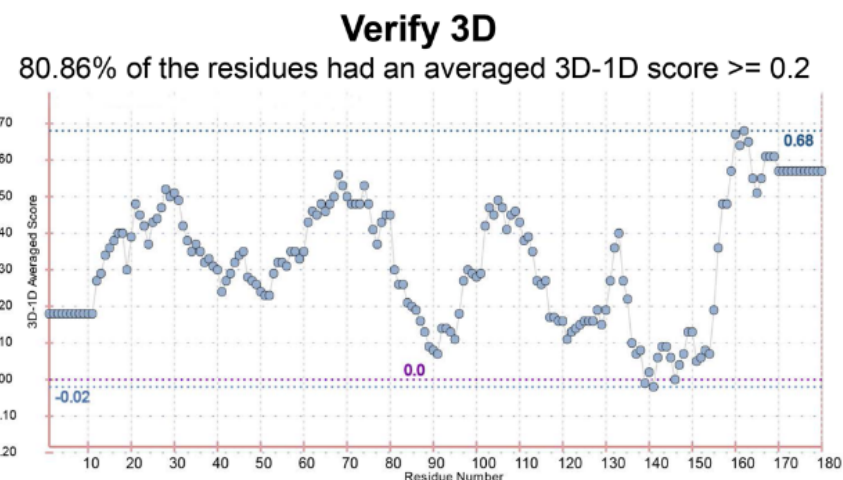
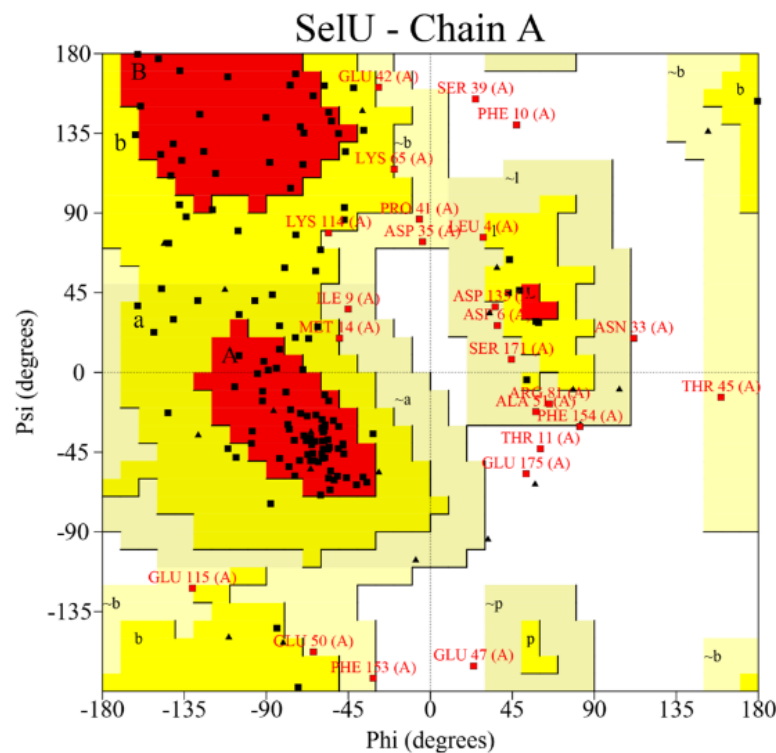
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.

>NP_001180447.1 redox-regulatory protein FAM213A
[Gallus gallus]

MSFLPDFGIFTMGMWSVGLGAVGAAITGIVLANTDLFLS
KPEKATLEFLEAIELKTLGSEPRTFKASELWKKNGAVIMA
VRRPGUFLCREEASELSSLKPQLSKLGVPLYAVVKEKIG
TEVEDFQHYFQGEIFLDEKRSFYGPRKRKMMLSGFFRI
GVWQNFFRAWKNGYSGNLEGEFTLGGVYVIGAGRQ
GVLLEHREKEFGDKVSLPSVLEAAEKIKPQAS

Analysis of the SelU

The structural modeling of chicken SelU



The predictions of ligand binding sites in chicken SelU

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
SelU	ACT	0.37	81, 85, 86, 87, 88
	2V2GC02	0.04	15, 19, 23, 35, 36, 37, 38, 39, 144
	MG	0.03	79, 80, 112, 113, 114, 141, 151
	CA	0.03	57, 58, 59, 64, 131, 132
	HOS	0.02	88, 91, 110, 112

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB

The accession number and amino acid sequences of chicken

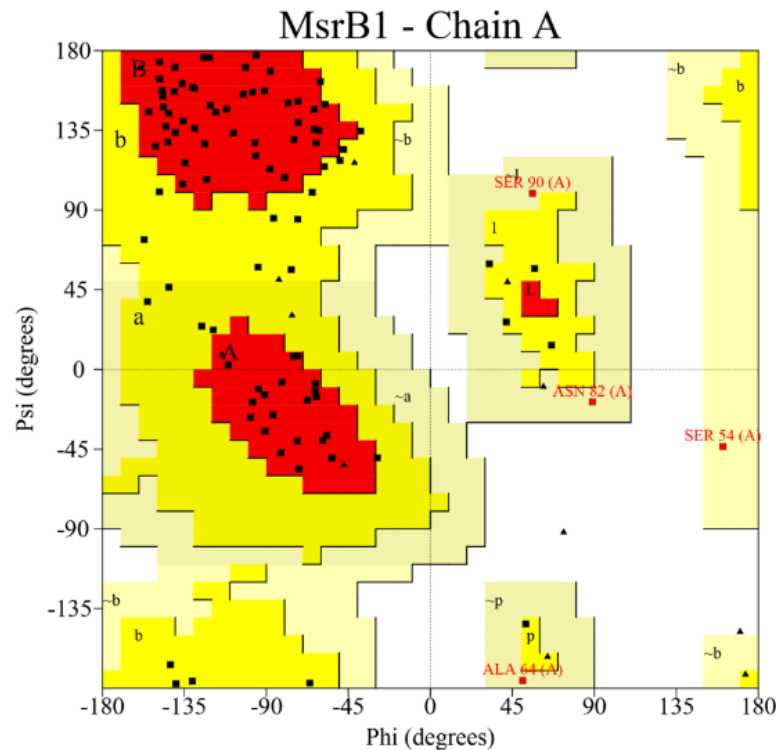
MsrB1

MsrB1 [Gallus gallus]

LOCUS NP_001129030 111 aa linear
VRT 24-APR-2016
DEFINITION methionine-R-sulfoxide reductase B1
[Gallus gallus].
ACCESSION NP_001129030 XP_414841
VERSION NP_001129030.1
DBSOURCE REFSEQ: accession NM_001135558.2
KEYWORDS RefSeq.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata;
Craniata; Vertebrata; Euteleostomi;
Archelosauria; Archosauria; Dinosauria;
Saurischia; Theropoda; Coelurosauria;
Aves; Neognathae; Galloanserae;
Galliformes; Phasianidae; Phasianinae;
Gallus.
>NP_001129030.1 methionine-R-sulfoxide reductase B1
[Gallus gallus]
MSFCSFFGGGEVFKDHFEPGVYVCARCGYELFSSRAKY
EHSSPWPAFTETIHEDSVAKRKERPGALKVSCGKCGNG
LGHEFLNDGPKRGQSRFUIFSSSLKFIPKGKSPQEN

Analysis of the MsrB1

The structural modeling of chicken MsrB1

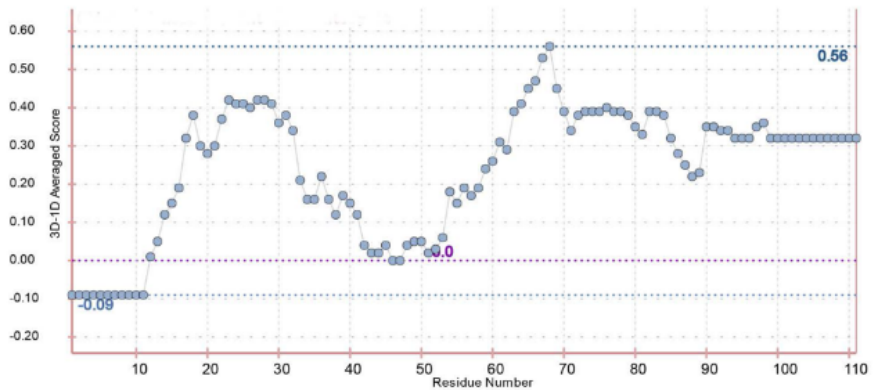


Plot statistics

Residues in most favoured regions [A,B,L]	64	71.1%
Residues in additional allowed regions [a,b,l,p]	22	24.4%
Residues in generously allowed regions [-a,-b,-l,-p]	4	4.4%
Residues in disallowed regions	0	0.0%
Number of non-glycine and non-proline residues	90	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	12	
Number of proline residues	7	
Total number of residues	111	

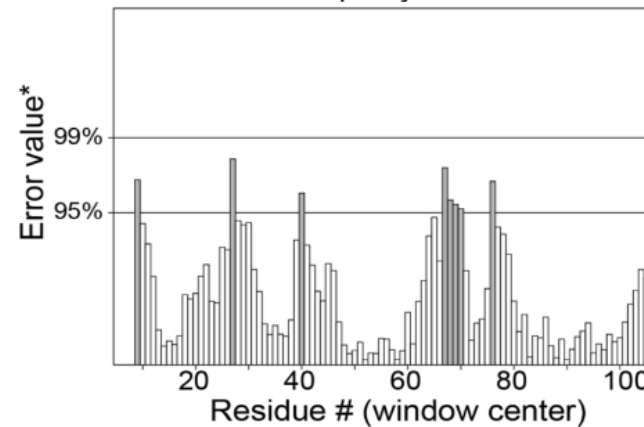
Verify 3D

83.96% of the residues had an averaged 3D-1D score ≥ 0.2



ERRAT2

Overall quality factor**: 91.919



The predictions of ligand binding sites in chicken MsrB1

Protein	Lig Name	C-score ^{EC}	Ligand Binding Site Residues
MsrB1	ZN	0.55	23, 26, 69, 72
	RSM	0.11	64, 77, 78, 80, 91, 93, 94
	PEPTIDE	0.02	64, 78, 80, 91, 93
	3HCHB02	0.01	24, 27, 100
	3HCHA02	0.01	36, 37, 38, 39

1. C-score is the confidence score of the prediction. C-score ranges (0-1), where a higher score indicates a more reliable prediction
2. Lig Name is name of possible binding ligand. The information of binding ligands is shown in PDB