

Protein View: gi|367460260

Chain A, Crystal Structure Of Bovine Serum Albumin

Database: NCBIInr
Score: 161
Expect: 2.5e-09
Nominal mass (M_r): 68416
Calculated pI: 5.60
Taxonomy: **Bos taurus**

This protein sequence matches the following other entries:

- [gi|367460261](#) from **Bos taurus**
- [gi|407943891](#) from **Bos taurus**
- [gi|407943892](#) from **Bos taurus**
- [gi|529482051](#) from **Bos taurus**
- [gi|529482052](#) from **Bos taurus**

Sequence similarity is available as [an NCBI BLAST search of gi|367460260 against nr.](#)

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: **Carbamidomethyl (C)**
Variable modifications: **Oxidation (M), Acetyl (Protein N-term), Methyl (C-term)**
Mass values searched: 31
Mass values matched: 20

Protein sequence coverage: 31%

Matched peptides shown in **bold red**.

1	DTHK SEIAHR	FKDLGEEHFK	GLVLIAFSQY	LQQCPFDEHV	KLVNELTEFA
51	KTCVADESHA	GCEK SLHTLF	GDELCK VASL	RETYGDMADC	CEKQEPERNE
101	CFLSHKDDSP	DLPKLPDPN	TLCDEFKADE	KKFWGK YLYE	IARR HPYFYA
151	PELLYYANKY	NGVFQECQA	EDKGACLLPK	IETMREKVLV	SSARQRLRCA
201	SIQKFGERAL	KAWSVARLSQ	KFPKAEFVEV	TKLVTDLTKV	HKECCHGDL
251	ECADDRADLA	KYICDNQDTI	SSKLKECCDK	PLLEKSHCIA	EVEKDAIPEN
301	LPPLTADFAE	DKDVCK NYQE	AKDAFLGSFL	YEYSRRHPEY	AVSVLLRLAK
351	EYEATLEECC	AKDDPHACYS	TVFDK LKHLV	DEPQNLIKQN	CDQFEKLG EY
401	GFQNALIVRY	TR KVPQVSTP	TLVEVSR SLG	KVGTRCCTKP	ESER MPCTED
451	YLSLILNRLC	VLHEKTPVSE	KVTKCCTESL	VNR RPCFSAL	TPDETYVPKA
501	FDEKLETFHA	DICTLPDTEK	QIKKQ TALVE	LLKHK PKATE	EQLKTMENF
551	VAFVDK CCAA	DDKEACFAVE	GPKLVVSTQT	ALA	

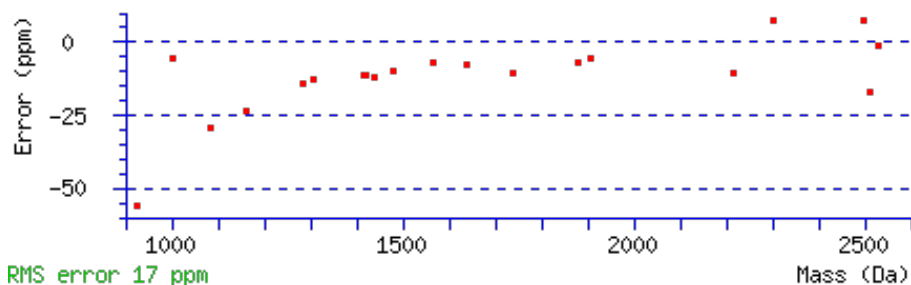
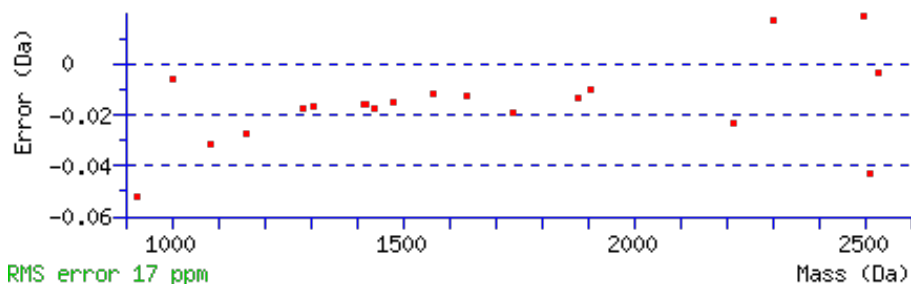
Unformatted sequence string: **583 residues** (for pasting into other applications).

Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	M	Peptide
5 - 12	1001.5470	1000.5397	1000.5454	-0.0057	1	K.SEIAHRFK.D + Methyl (C-term)
42 - 51	1163.6036	1162.5963	1162.6234	-0.0270	0	K.LVNELTEFAK.T
65 - 76	1419.6778	1418.6705	1418.6864	-0.0159	0	K.SLHTLFGDELCK.V
137 - 143	927.4413	926.4340	926.4861	-0.0521	0	K.YLYEIAR.R
137 - 144	1083.5626	1082.5553	1082.5872	-0.0319	1	K.YLYEIARR.H
317 - 335	2301.0991	2300.0918	2300.0749	0.0169	1	K.NYQEAKDAFLGSLYVEYSR.R
323 - 335	1567.7313	1566.7240	1566.7354	-0.0114	0	K.DAFLGSLYVEYSR.R
336 - 347	1439.7941	1438.7869	1438.8045	-0.0176	1	R.RHPEYAVSVLLR.L
337 - 347	1283.6929	1282.6856	1282.7034	-0.0177	0	R.HPEYAVSVLLR.L
378 - 388	1305.6996	1304.6923	1304.7088	-0.0165	0	K.HLVDEPQNLIK.Q
389 - 409	2529.2159	2528.2086	2528.2118	-0.0032	1	K.QNCDQFEKLGEYGFQNALIVR.Y
397 - 409	1479.7808	1478.7735	1478.7881	-0.0147	0	K.LGEYGFQNALIVR.Y
413 - 427	1639.9255	1638.9182	1638.9305	-0.0123	1	R.KVPQVSTPTLVEVSR.S
445 - 458	1740.8105	1739.8032	1739.8222	-0.0190	0	R.MPCTEDYLSLILNR.L + Oxidation (M)
484 - 499	1880.9076	1879.9003	1879.9138	-0.0135	0	R.RPCFSALTPDETYVPK.A
500 - 520	2498.2094	2497.2021	2497.1835	0.0186	1	K.AFDEKLFTFHADICTLPDTEK.Q
500 - 520	2512.1636	2511.1563	2511.1992	-0.0428	1	K.AFDEKLFTFHADICTLPDTEK.Q + Methyl (C-term)
505 - 520	1907.9108	1906.9035	1906.9135	-0.0100	0	K.LFTFHADICTLPDTEK.Q
538 - 556	2215.0719	2214.0646	2214.0878	-0.0232	1	K.ATEEQLKTVMENFVAFVDK.C + Oxidation (M)
545 - 556	1415.6719	1414.6646	1414.6803	-0.0157	0	K.TVMENFVAFVDK.C + Oxidation (M)

No match to: 825.0184, 840.9929, 860.9885, 870.4753, 876.9688, 1202.5995, 1386.6935, 1789.9010, 2211.1038, 2284.1515, 2438.1873



LOCUS 3V03_A 583 aa linear MAM 10-OCT-2012
DEFINITION Chain A, Crystal Structure Of Bovine Serum Albumin.
ACCESSION 3V03_A

VERSION 3V03_A GI:367460260
 DBSOURCE pdb:molecule 3V03, chain 65, release Oct 10, 2012;
 deposition: Dec 7, 2011;
 class: Transport Protein;
 source: Mmdb_id: 96253, Pdb_id 1: 3V03;
 Exp. method: X-Ray Diffraction.

KEYWORDS .

SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (residues 1 to 583)
 AUTHORS Majorek,K.A., Porebski,P.J., Dayal,A., Zimmerman,M.D.,
 Jablonska,K., Stewart,A.J., Chruszcz,M. and Minor,W.
 TITLE Structural and immunologic characterization of bovine, horse, and
 rabbit serum albumins
 JOURNAL Mol. Immunol. 52 (3-4), 174-182 (2012)
 PUBMED 22677715

REFERENCE 2 (residues 1 to 583)
 AUTHORS Majorek,K.A., Porebski,P.J., Chruszcz,M., Almo,S.C., Minor,W., New
 Yor and Structural Genomics Research Consortium (Nysgrc).
 TITLE Direct Submission
 JOURNAL Submitted (07-DEC-2011)

COMMENT 1 Serum Albumin.

FEATURES Location/Qualifiers

source	1..583 /organism="Bos taurus" /db_xref="taxon:9913"
Region	1..172 /region_name="Domain 1" /note="NCBI Domains"
Region	5..184 /region_name="ALBUMIN" /note="Albumin domain, contains five or six internal disulphide bonds; albuminoid superfamily includes alpha-fetoprotein which binds various cations, fatty acids and bilirubin; vitamin D-binding protein which binds to vitamin D, its metabolites, and fatty acids; cd00015" /db_xref="CDD:28899"
Het	join(bond(6),bond(248),bond(251)) /heterogen="(CA,1000)"
SecStr	6..14 /sec_str_type="helix" /note="helix 1"
Het	join(bond(13),bond(254),bond(258),bond(258),bond(254), bond(258)) /heterogen="(CA,1002)"
SecStr	17..31 /sec_str_type="helix" /note="helix 2"
Site	order(27,31,46,67,71,74,99,102..103) /site_type="binding" /db_xref="CDD:28899"
SecStr	36..55 /sec_str_type="helix" /note="helix 3"
Bond	bond(53,62) /bond_type="disulfide"
SecStr	66..76 /sec_str_type="helix" /note="helix 4"
Bond	bond(75,91) /bond_type="disulfide"
Bond	bond(90,101) /bond_type="disulfide"
SecStr	95..105 /sec_str_type="helix" /note="helix 5"
Het	join(bond(109),bond(109),bond(111),bond(111)) /heterogen="(CA,1001)"

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Bond        bond(123,168)
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            /note="helix 7"
Site        order(134,137..138,141,157,160)
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Bond        bond(167,176)
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Region      173..372
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            /note="NCBI Domains"
SecStr      178..204
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            /note="helix 9"
Region      196..376
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            /note="Albumin domain, contains five or six internal
            disulphide bonds; albuminoid superfamily includes
            alpha-fetoprotein which binds various cations, fatty acids
            and bilirubin; vitamin D-binding protein which binds to
            vitamin D, its metabolites, and fatty acids; cd00015"
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Bond        bond(199,245)
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            /note="helix 10"
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            /db_xref="CDD:28899"
SecStr      227..246
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Bond        bond(244,252)
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SecStr      249..266
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Bond        bond(277,288)
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SecStr      282..291
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SecStr      314..321
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            /note="helix 14"
Bond        bond(315,360)
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SecStr      322..336
            /sec_str_type="helix"
            /note="helix 15"
Site        order(326,329..330,333,349,352)
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            /db_xref="CDD:28899"
SecStr      342..359
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            /note="helix 16"
Bond        bond(359,368)
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Region      373..537
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Region     /note="helix 17"
            388..574
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            disulphide bonds; albuminoid superfamily includes
            alpha-fetoprotein which binds various cations, fatty acids
            and bilirubin; vitamin D-binding protein which binds to
            vitamin D, its metabolites, and fatty acids; cd00015"
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Bond       bond(391,437)
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Site       order(410,414,429,452,456,459,484,487..488)
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SecStr     419..431
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            /note="helix 19"
Bond       bond(436,447)
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SecStr     444..463
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            /note="helix 20"
Bond       bond(460,476)
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SecStr     470..477
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            /note="helix 21"
Bond       bond(475,486)
            /bond_type="disulfide"
SecStr     482..490
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            /note="helix 22"
Bond       bond(513,558)
            /bond_type="disulfide"
SecStr     517..534
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            /note="helix 23"
Site       order(524,527..528,531,547,550)
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            /db_xref="CDD:28899"
SecStr     540..559
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            /note="helix 24"
Bond       bond(557,566)
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SecStr     564..582
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            /note="helix 25"

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