# Figure 1

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                                                                                  ▽▼
HvSR    -MGSRDDDGHSTEGQGYAADINSIREARARIAPYVHKTPILSSTSIDAIAGKQLFFKCECFQKAGAFKIRGA   71
OsSR    MGSRGGSGGDGAESHGYAADIHSIREAQARIAPYVHKTPVLSSTSIDAIVGKQLFFKCECFQKAGAFKIRGA   72
AtSR    ---------MEANREKYAADILSIKEAHDRIKPYIHRTPVLTSESLNSISGRSLFFKCECLQKGGAFKFRGA   63
hSR     ------------MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA   60
mSR     ------------MCAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGA   60
EcTD    ------MADSQPLSGAPEGAEYLRAVLRAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGA   66

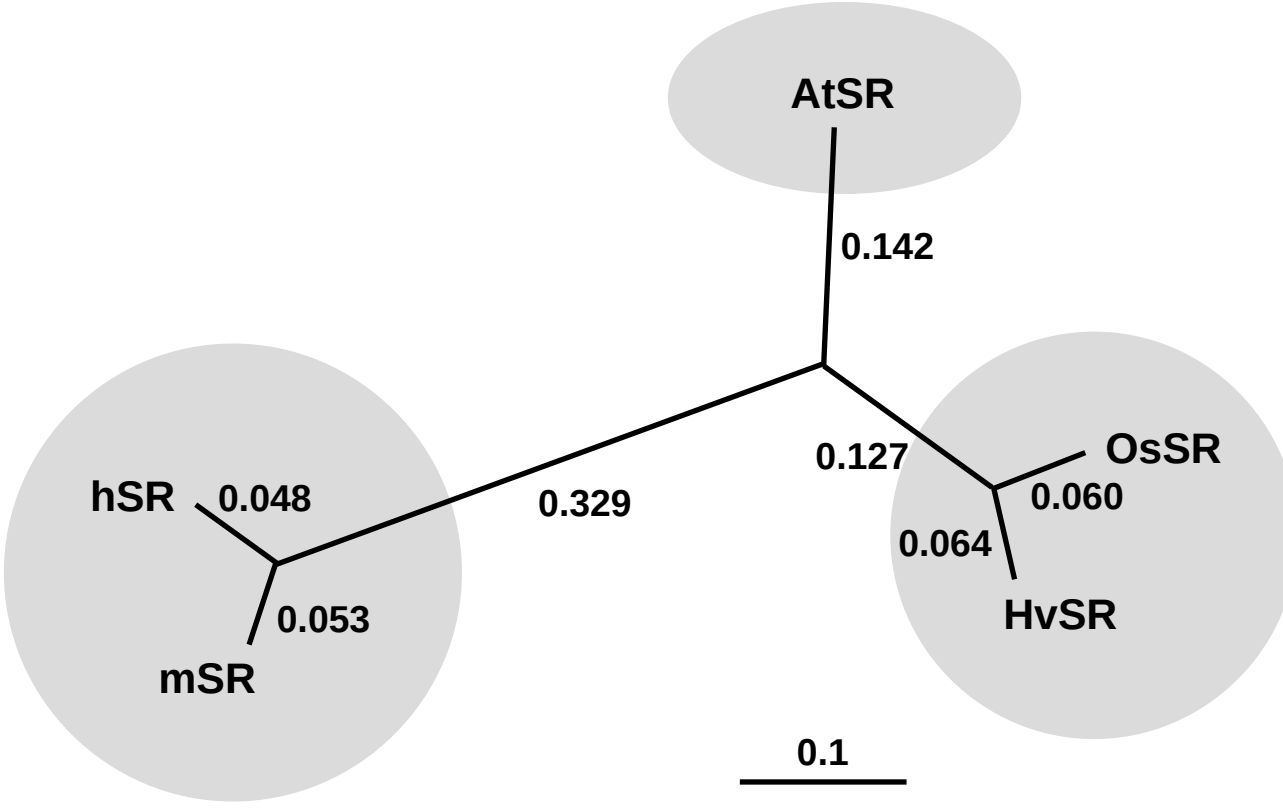
                                  ▽
HvSR    SNSIFALD---DSQAAKGVVTHSSGNHAAAVALAAKLRGIPAYIVIPKNAPACKVENVRRYGGQVIWSDVTM  140
OsSR    SNSIFALD---DDEASKGVVTHSSGNHAAAVALAAKLRGIPAYIVIPRNAPACKVDNVKRYGGHIIWSDVSI  141
AtSR    CNAVLSLD---AEQAAKGVVTHSSGNHAAALSLAAKIQGIPAYIVVPKGAPKCKVDNVIRYGGKVIWSEATM  132
hSR     LNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSD  132
mSR     LNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPSD  132
EcTD    YAMMAGLTE---EQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVLLHGANF  135

                                                                ****
HvSR    ESRESIAKKVQEETGAILIHPFNDKYTISGQGTVCLELLEQVPEIDTIIVPISGGGLISGVTLAAKAINPSI  212
OsSR    ESRESVAKRVQEETGAILVHPFNNKNTISGQGTVSLELLEEVPEIDTIIVPISGGGLISGVALAAKAINPSI  213
AtSR    SSREEIASKVLQETGSVLIHPYNDGRIISGQGTIALELLEQIQEIDAIVVPISGGGLISGVALAAKSIKPSI  204
hSR     ESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMLAGIAITVKALKPSV  204
mSR     ESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMVAGIAITIKALKPSV  204
EcTD    DEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLDRVFVPVGGGGLAAGVAVLIKQLMPQI  207

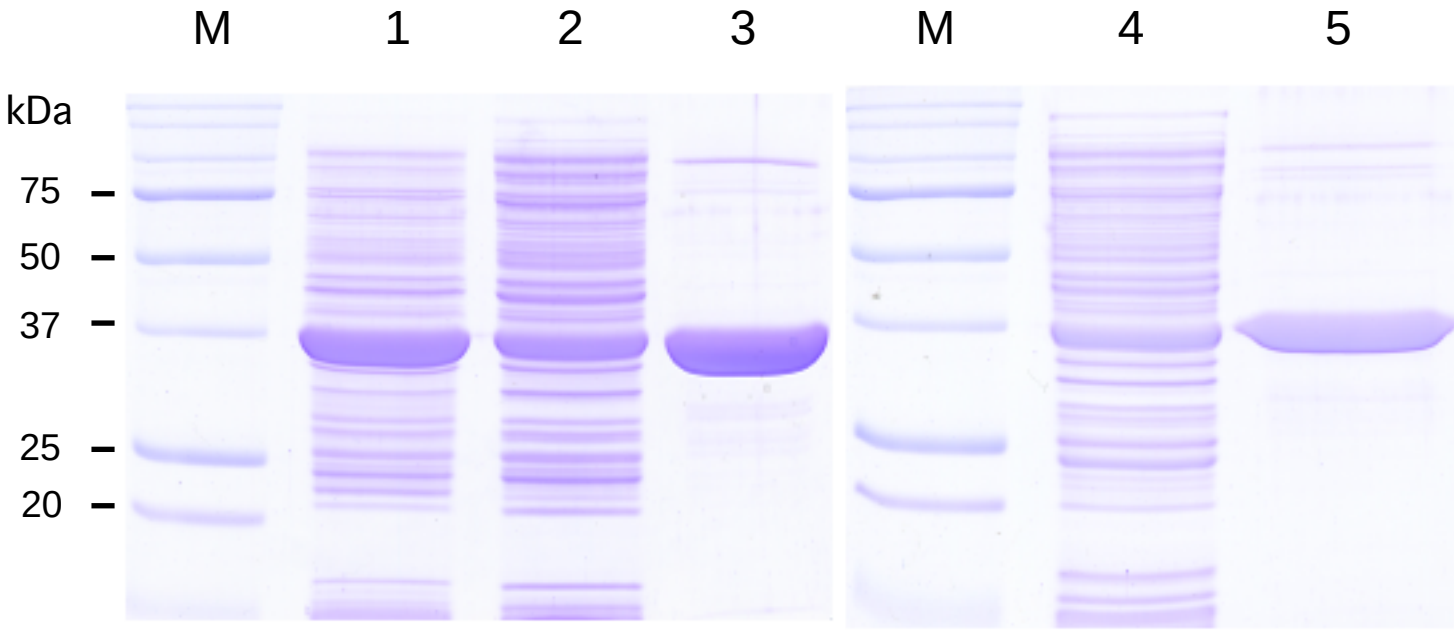
                                          ▽
HvSR    RILAAEPKGADDSAQSKAAGRIIK-LPATSTIADGLRAF-LGDLTWPVVRDLVDDVIVVDDNAIVDAMKMCY  236
OsSR    RILAAEPKGADDSAQSKAAGKIIT-LPSTNTIADGLRAF-LGDLTWPVVRDLVDDIIVVDDNAIVDAMKMCY  283
AtSR    RIIAAEPKGADDAAQSKVAGKIIT-LPVTNTIADGLRAS-LGDLTWPVVRDLVDDVVTLEECEIIEAMKMCY  274
hSR     KVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSS-IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVW  275
mSR     KVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSS-IGLNTWPIIRDLVDDVFTVTEDEIKYATQLVW  275
EcTD    KVIAVEAEDS-ACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQEYLDDIITVDSDAICAAMKDLF  278

                                                  ▽
HvSR    ETLKVAVEPSGAIGLAAALSDEFKQSSAWHESSKIGIIVSGGNVDLRVLWDSLYK------------      337
OsSR    EMLKVAVEPSGAIGLAAALSDEFKQSSAWHESSKIGIIVSGGNVDLGVLWESLYKR-----------      339
AtSR    EILKVSVEPSGAIGLAAVLSNSFRNNPSCRDCKNIGIVLSGGNVDLGSLWDSFKSSK----------      331
hSR     ERMKLLIEPTAGVGVAAVLSQHFQTVS--PEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV      340
mSR     GRMKLLIEPTAGVALAAVLSQHFQTVS--PEVKNVCIVLSGGNVDLTS-LNWVGQAERPAPYQTVSV      339
EcTD    EDVRAVAEPSGALALAG-MKKYIALHN--IRGERLAHILSGANVN----------------------      320
```

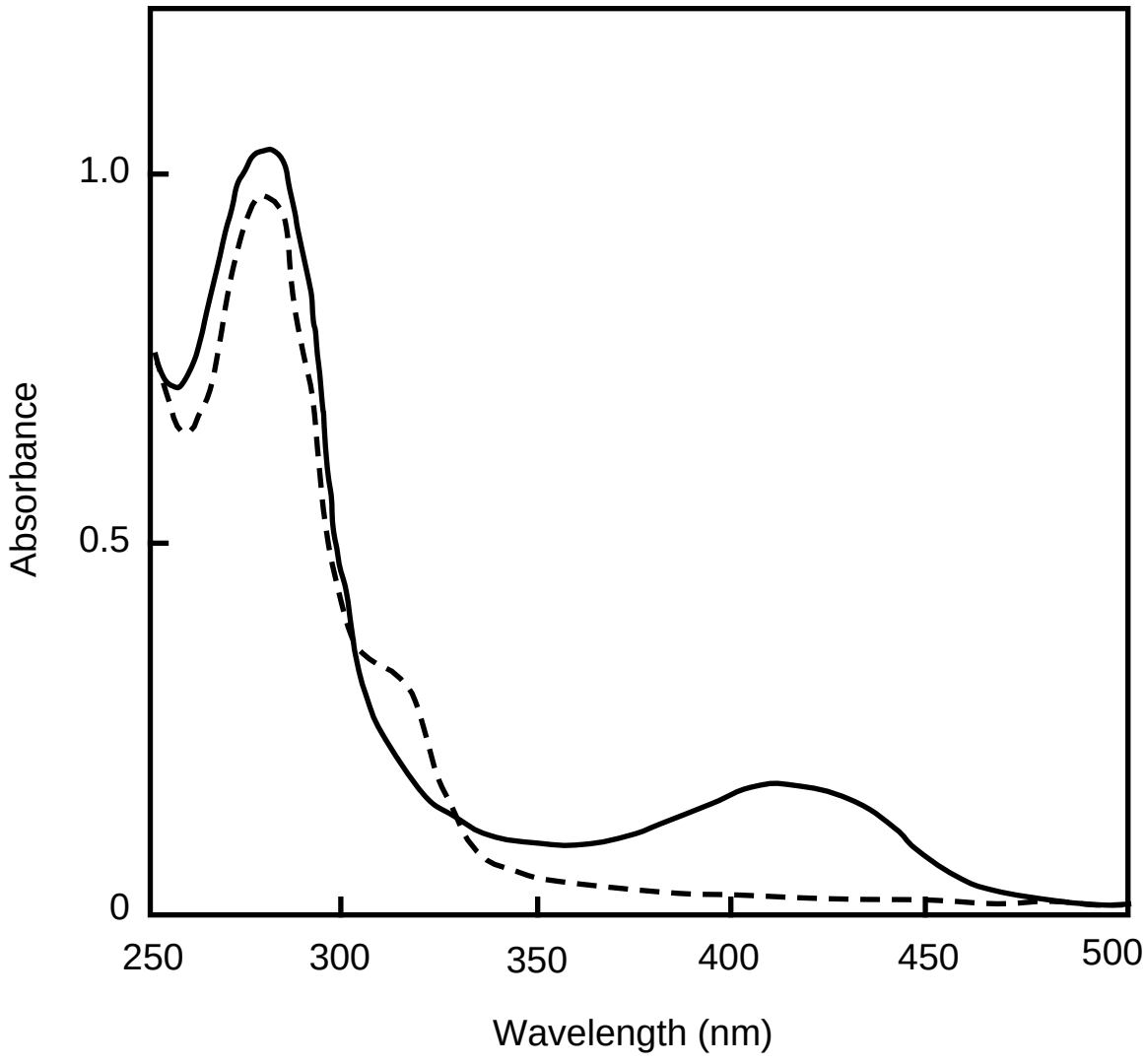
# Figure 2



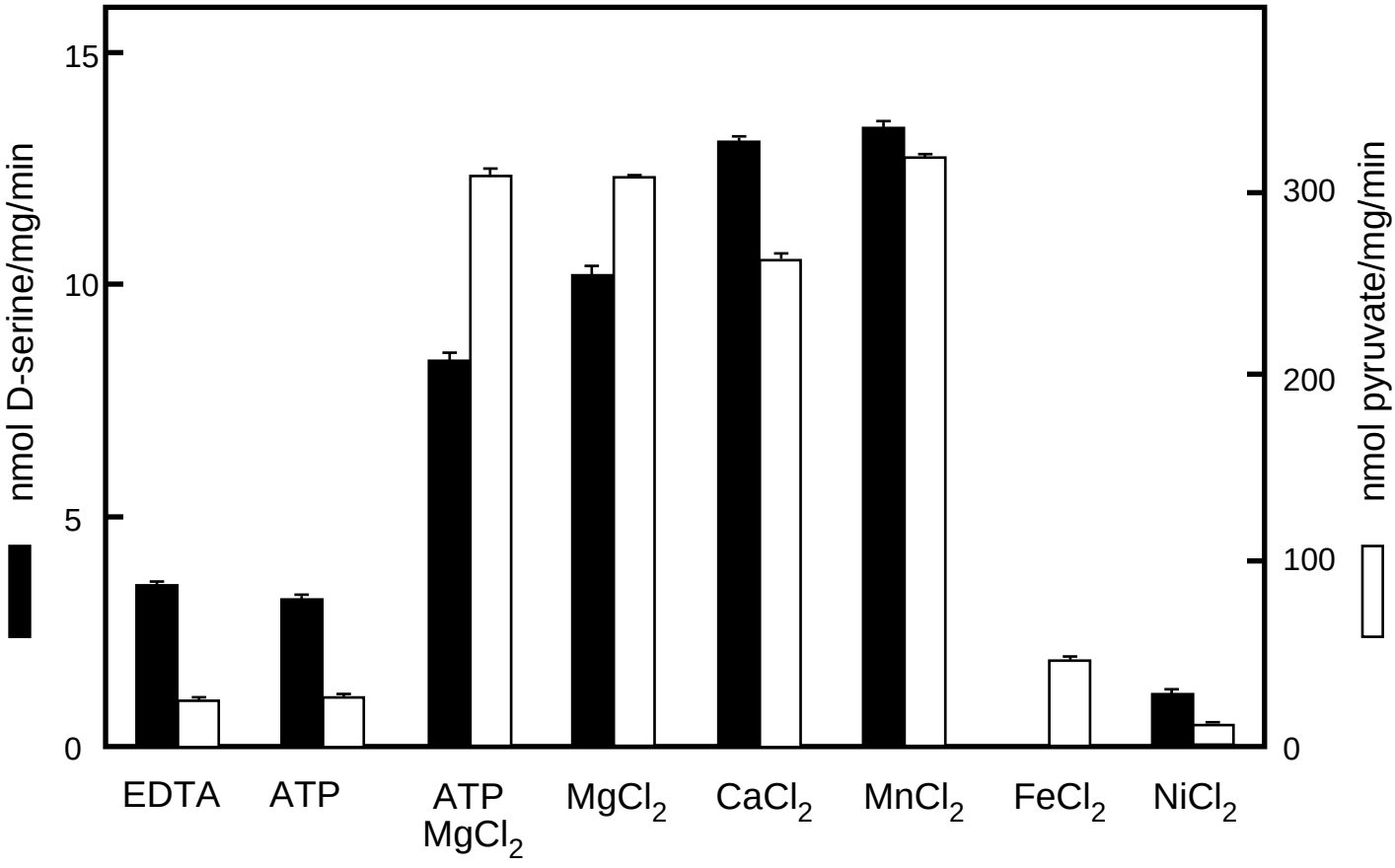
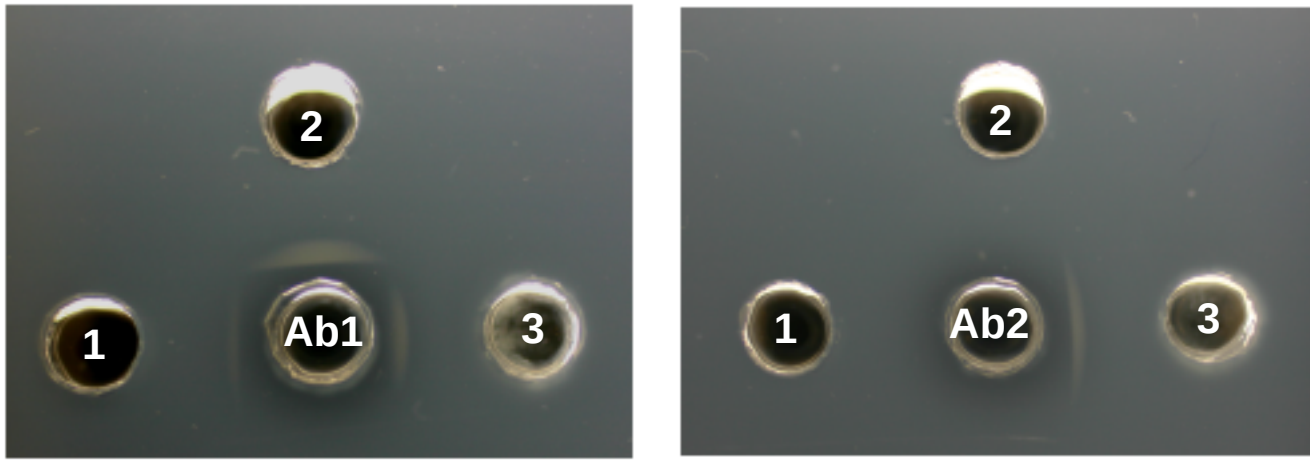
# Figure 3



# Figure 4



# Figure 5


15
10
5
0
nmol D-serine/mg/min
300
200
100
0
nmol pyruvate/mg/min
EDTA
ATP
ATP MgCl2
MgCl2
CaCl2
MnCl2
FeCl2
NiCl2

# Figure 6