

NP276

Protein	Mutation Type	Sequence	Molecular Weight (with Met removed)
NP276 WT	None (Double Met M21 M61)	MGSSHHHHHHSSGLVPRGSHMDVEKLRQLYAAGERDF SIVDLRGAVLENINLSGAILHGAMLDEANLQQANLSR ADLSGATLNGADLRGANLSKADLSDAILDNAILEGAI LDEAVLNQANLKAANLEQAILSHANIREADLSEANLE AADLSGADLAIADLHQANLHQAAALERANLTGANLEDA NLEGTILEGGNNLAT	20928.00
NP276 M211	Single Met Mutant	MGSSHHHHHHSSGLVPRGSHIDVEKLRQLYAAGERDF SIVDLRGAVLENINLSGAILHGAMLDEANLQQANLSR ADLSGATLNGADLRGANLSKADLSDAILDNAILEGAI LDEAVLNQANLKAANLEQAILSHANIREADLSEANLE AADLSGADLAIADLHQANLHQAAALERANLTGANLEDA NLEGTILEGGNNLAT	20909.97
NP276 M211 I101C	Single Met Cys Mutant	MGSSHHHHHHSSGLVPRGSHIDVEKLRQLYAAGERDF SIVDLRGAVLENINLSGAILHGAMLDEANLQQANLSR ADLSGATLNGADLRGANLSKADLSDACLDAILEGAI LDEAVLNQANLKAANLEQAILSHANIREADLSEANLE AADLSGADLAIADLHQANLHQAAALERANLTGANLEDA NLEGTILEGGNNLAT	20899.95
NP276 M211 I101C M611	Single Cys Mutant	MGSSHHHHHHSSGLVPRGSHIDVEKLRQLYAAGERDF SIVDLRGAVLENINLSGAILHGAILDEANLQQANLSR ADLSGATLNGADLRGANLSKADLSDACLDAILEGAI LDEAVLNQANLKAANLEQAILSHANIREADLSEANLE AADLSGADLAIADLHQANLHQAAALERANLTGANLEDA NLEGTILEGGNNLAT	20881.92
NP276 M211 I101C K25A	Single Met Cys Mutant 2 Lys	MGSSHHHHHHSSGLVPRGSHIDVEALRQLYAAGERDF SIVDLRGAVLENINLSGAILHGAMLDEANLQQANLSR ADLSGATLNGADLRGANLSKADLSDACLDAILEGAI LDEAVLNQANLKAANLEQAILSHANIREADLSEANLE AADLSGADLAIADLHQANLHQAAALERANLTGANLEDA NLEGTILEGGNNLAT	20842.85
NP276 M211 I101C K25A K94A	Single Met Cys Lys Mutant	MGSSHHHHHHSSGLVPRGSHIDVEALRQLYAAGERDF SIVDLRGAVLENINLSGAILHGAMLDEANLQQANLSR ADLSGATLNGADLRGANLSAADLSDACLDAILEGAI LDEAVLNQANLKAANLEQAILSHANIREADLSEANLE AADLSGADLAIADLHQANLHQAAALERANLTGANLEDA NLEGTILEGGNNLAT	20785.76
NP276 M211 I101C K25A K94A K123A	Single Met Cys Mutant No Lys	MGSSHHHHHHSSGLVPRGSHIDVEALRQLYAAGERDF SIVDLRGAVLENINLSGAILHGAMLDEANLQQANLSR ADLSGATLNGADLRGANLSAADLSDACLDAILEGAI LDEAVLNQANLAAAANLEQAILSHANIREADLSEANLE AADLSGADLAIADLHQANLHQAAALERANLTGANLEDA NLEGTILEGGNNLAT	20728.66
NP276 M211 I101C K25A K94A K123A	Single Met Cys Lys (C- term)Mutant	MGSSHHHHHHSSGLVPRGSHIDVEALRQLYAAGERDF SIVDLRGAVLENINLSGAILHGAMLDEANLQQANLSR ADLSGATLNGADLRGANLSAADLSDACLDAILEGAI LDEAVLNQANLAAAANLEQAILSHANIREADLSEANLE	20755.73

T201K		AADLSGADLAIADLHQANLHQAAALERANLTGANLEDA NLEGTILEGGNNLAK	
NP276 M211 K25A K94A K123A T201K I101M	Double Met, Single Lys (C- term)Mutant	MGSSHHHHHSSGLVPRGSHIDVEALRQLYAAGERDF SIVDLRGAVLENINLSGAILHGAMLDEANLQQANLSR ADLSGATLNGADLRGANLSAADLSDAILDNAILEGAI LDEAVLNQANLAAANLEQAILSHANIREADLSEANLE AADLSGADLAIADLHQANLHQAAALERANLTGANLEDA NLEGTILEGGNNLAK	20783.79
NP276 M211 M61Hag	Single Met with Hag replacement	MGSSHHHHHSSGLVPRGSHIDVEKLRQLYAAGERDF SIVDLRGAVLENINLSGAILHGA{Hag}LDEANLQQA NLSRADLSGATLNGADLRGANLSKADLSDAILDNAIL EGAILDEAVLNQANLKAANLEQAILSHANIREADLSE ANLEAADLSGADLAIADLHQANLHQAAALERANLTGAN LEDANLEGTILEGGNNLAT	20818 [AND with N-term. Gluconoylation 20996]

SBL

SBL-S156C

AQSVPWGISRVOAPAAHNRGLTGSGVKVAVLDTGISTHPDLNIRGGASFVPGEPTQDGNGHGTH
VAGTIAALNNSIGVLGVAPSAELYAVKVLGASGSGSVSSIAQGLEWAGNNGMHVANLSLGSPSPS
ATLEQAVNSATSRGVLVVAASGNCGAGSISYPARYANAMAVGATDQNNNRASFQYAGLDIVAP
GVNVQSTYPGSTYASLNGTSMATPHVAGAAALVKQKNPSWSNVQIRNHLKNTATSLGSTNLYGSG
LVNAEAATR

Calculated average isotopic mass = 26714.5

SSβG

β-Glycosidase from *Sulfolobus solfataricus* (SsβG) (PDB code 1GOW)

WT

M/GHHHHHHHSFPNSFRFGWSQAGFQSEMGTPGSEDPNTDWYKWVHDPENMAAGLVSGDLPENGP
 GYWGNKYKTFHDNAQKMGLKIARLNVEWSRIFPNPLPRPQNFDESKQDVTEVEINENELKRLDEYA
 NKDALNHYREIFKDLKSRGLYFILNMYHWPLPLWLHDP IRVRRGDF TGPSGWLSTRTVYEFARFS
 AYIAWKFDLVDVEYSTMNEPNVVGGLGYVGKSGFPPGYLSFELSRRAMYNI IQAHARAYDGIKS
 VSKKPVGIIYANSSFQPLTDKDMEAVEAENDNRWWFFDAI IRGEITRGNEKIVRDDLKGRLDWI
 GVNYYTRTVVKRTEKGYVSLGGYGHCERNVSVSLAGLPTSDFGWEFFPEGLYDVLTKYWNRYHLY
 MYVTENGIADDADYQRPYYLVSHVYQVHRAINSADVRGYLHWLADNYEWASGF SMRFGLLKVD
 YNTKRLYWRPSALVYREIATNGAITDEIEHLNSVPPVKPLRH

Calculated mass; 57414 (N-terminal methionine cleaved)

SsβG 9xIle 439Cys 43Met

M/GHHHHHHHSFPNSFRFGWSQAGFQSEIGTPGSEDPNTDWYKWVHDPENMAAGLVSGDLPENGP
 GYWGNKYKTFHDNAQKIGLKIARLNVEWSRIFPNPLPRPQNFDESKQDVTEVEINENELKRLDEYA
 NKDALNHYREIFKDLKSRGLYFILNIYHWPLPLWLHDP IRVRRGDF TGPSGWLSTRTVYEFARFS
 AYIAWKFDLVDVEYSTINEPNVVGGLGYVGKSGFPPGYLSFELSRRAIYNI IQAHARAYDGIKS
 VSKKPVGIIYANSSFQPLTDKIEAVEIAENDNRWWFFDAI IRGEITRGNEKIVRDDLKGRLDWI
 GVNYYTRTVVKRTEKGYVSLGGYGHSERNVSVSLAGLPTSDFGWEFFPEGLYDVLTKYWNRYHLY
 IYVTENGIADDADYQRPYYLVSHVYQVHRAINSADVRGYLHWLADNYEWASGF CIRFGLLKVD
 YNTKRLYWRPSALVYREIATNGAITDEIEHLNSVPPVKPLRH

Calculated mass; 57252 (N-terminal methionine cleaved)

SsβG 9xIle 439Cys 43Haa

M/GHHHHHHHSFPNSFRFGWSQAGFQSEIGTPGSEDPNTDWYKWVHDPEN{Haa}AAGLVSGDLP
 ENGPYWGNYKTFHDNAQKIGLKIARLNVEWSRIFPNPLPRPQNFDESKQDVTEVEINENELKRL
 DEYANKDALNHYREIFKDLKSRGLYFILNIYHWPLPLWLHDP IRVRRGDF TGPSGWLSTRTVYEF
 ARFSAYIAWKFDLVDVEYSTINEPNVVGGLGYVGKSGFPPGYLSFELSRRAIYNI IQAHARAYD
 GIKSVSKKPVGIIYANSSFQPLTDKIEAVEIAENDNRWWFFDAI IRGEITRGNEKIVRDDLKGR
 LDWIGVNYYTRTVVKRTEKGYVSLGGYGHSERNVSVSLAGLPTSDFGWEFFPEGLYDVLTKYWN
 YHLYIYVTENGIADDADYQRPYYLVSHVYQVHRAINSADVRGYLHWLADNYEWASGF CIRFGL
 LKVDYNTKRLYWRPSALVYREIATNGAITDEIEHLNSVPPVKPLRH

Calculated mass; 57247 (N-terminal methionine cleaved)

SsβG M43Hag P152A C344S 9Ile

M/GHHHHHHHSFPNSFRFGWSQAGFQSEIGTPGSEDPNTDWYKWVHDPEN[Hag]AAGLVSGDLP
 ENGPYWGNYKTFHDNAQKIGLKIARLNVEWSRIFPNPLPRPQNFDESKQDVTEVEINENELKRL
 DEYANKDALNHYREIFKDLKSRGLYFILNIYHWA LPLWLHDP IRVRRGDF TGPSGWLSTRTVYEF
 ARFSAYIAWKFDLVDVEYSTINEPNVVGGLGYVGKSGFPPGYLSFELSRRAIYNI IQAHARAYD
 GIKSVSKKPVGIIYANSSFQPLTDKIEAVEIAENDNRWWFFDAI IRGEITRGNEKIVRDDLKGR
 LDWIGVNYYTRTVVKRTEKGYVSLGGYGHSERNVSVSLAGLPTSDFGWEFFPEGLYDVLTKYWN
 YHLYIYVTENGIADDADYQRPYYLVSHVYQVHRAINSADVRGYLHWLADNYEWASGFSIRFGL
 LKVDYNTKRLYWRPSALVYREIATNGAITDEIEHLNSVPPVKPLRH

Calculated mass; 57189 (N-terminal methionine cleaved)

Table: all S β G mutants

Mutant	calculated mass (N-terminal methionine cleaved)
S β G C344S 9Ile	57235
S β G M43Hag C344S 9Ile	57215
S β G E387A	57356
S β G W151A C344S 9Ile	57120
S β G W151F C344S 9Ile	57267
S β G H150A C344S 9Ile	57169
S β G H150F C344S 9Ile	57245
S β G W151A	57299
S β G W151F	57446
S β G H150A	57348
S β G H150F	57424
S β G P152A	57388
S β G S432P	57424
S β G E206A	57356
S β G M43Hag P152A C344S 9Ile	57189

Qbeta

Protein	Mutation Type	Sequence	Molecular Weight (with Met removed)
Q β WT	None (Single Met)	M/AKLETVTLGNIGKDG M QTLV LNPRGVNPTNGVSL SQAGAVPALEKRVTVSVSQPSRNRKNYKVQVKIQNPT ACTANGSCDPSVTRQAYADVTF SFTQYSTDEERAFVR TELAALLASPLLIDAIDQLNPAY	14125
Q β M16Hag	Single Met with Hag replacement	M/AKLETVTLGNIGKDG {Hag} QTLV LNPRGVNPTNG VASLSQAGAVPALEKRVTVSVSQPSRNRKNYKVQVKI QNPTACTANGSCDPSVTRQAYADVTF SFTQYSTDEER AFVRTELAALLASPLLIDAIDQLNPAY	14105

Miscellaneous

Arylsulfatase from *Pseudomonas aeruginosa* (PDB code 1HDH)

M/SKRPNFLVIVADDLGFSDIGAFGGEIATPNLDALAIAGLRLTDFHTASTGSPTRSMLLT
GTDHIIAGIGTMAEALTPELEGKPGYEGHLNERVVALPELLREAGYQTLMAGKWHLGL
KPEQTPHARGFERSFLLPGAANHYGFEPPYDESTPRILKGTALYVEDERYLDTLPEG
FYSSDAFGDKLLQYLKERDQSRPFFAYLPFSAPHWPLQAPREIVEKYRGRYDAGPEAL
RQERLARLKEGLVEADVEAHPVLALTREWEALEDEERAKSARAMEVYAAMVERMDW
NIGRVVDYLRRQGELDNTFVLFMSDNGAEGALLEAFPKFGPDLLGFLDRHYDNSLENIG
RANSYVWYGPRWAQAATAPSRLYKAFTTQGGIRVPALVRYPRLSRQGAISHAFATVMD
VTPTLLDLAGVRHPGKRWGRGREAEPGRSWLWLSGETEAAHDENTVTGWELFGMR
AIRQGDWKAVYLPAPVGPATWQLYDLARDPGEIHDLDLADSQPGKLAELIEHWKRYVSET
GVVEGASPFLVR

Calculated mass (N-terminal methionine cleaved) = 59768

Chalcone Reductase (PDB code 1ZGD)

M/GSVEIPTKVL TNTSSQLKMPVVGMSAPDFTCKKDTKDAIIEAIKQGYRHFDTAAAYG
SEQALGEALKEAIELGLVTRDDL FVTSKLWVTENHPHLVIPALQKSLKTLQLDYLDLYLIH
WPLSSQPGKFSFPIDVADLLPFDVKGWESMEESLKLGLTKAIGVSNFSVKLENLLSV
ATVLPVAVNQVEMNLAWQQKLRFCNAHGIVLTA FSPVRK GASRGPNEVMENDMLKEI
ADAHGKSVAQISLRWLYEQGVTFVPKSYDKERMNQNLRIFDWSLTKEDHEKIAQIKQNR
LIPGPTKPLNDLYDD

β -Glycosidase from *Thermosphaera aggregans* (TabG) (PDB code 1ZGD)

KFPKDFMIGYSSSPFQFEAGIPGSEDPNSDWWVWVHDPENTAAGLVSGDLPENGPY
WNLYKNDHDLAEKLG VNTIRVGVEWSRIFPKPTFNVKVPVERDENGSIHVVDVDDKAVE
RLDELANKEAVNHVYVEMYKDWVERGRKLILNLYHWPLPLWLHNPIMVRRMGPDRAPS
GWLNEESVVEFAKYAAYIAWKMGELPVMWSTMNEPNVVEYEQGYMFVKGGFPPGYLS
FEADKARRNMIQAHARAYDNIKRFSSKPVGLIYAFQWFELLEGPAEVDFKFKSSKLYY
FTDIVSKGSSIIAEYRRDLANRLDWLG VNYYSRLVYKIVDDKPIILHGYGFLCTPGGISPA
ENPCSDFGWEVYPEGLYLLLKELYNRYGVDLIVTENGVS DSRDALRPAYLVSHVYSVW
KAVNEGIPVKGYLHWSLTDNYEWAQGFQKFGFLVMVDFKTKKRYLRPSALVFREIATH
NGIPDELQHLTLIQ