Relationship of sequence and structure to specificity in the alpha-amylase family of enzymes

The hydrolases and transferases that constitute the alpha-amylase family are multidomain proteins, but each has a catalytic domain in the form of a (beta/alpha)(8)-barrel, with the active site being at the C-terminal end of the barrel beta-strands. Although the enzymes are believed to share the same catalytic acids and a common mechanism of action, they have been assigned to three separate families - 13, 70 and 77 - in the classification scheme for glycosidase hydrolases and transferases that is based on amino acid sequence similarities. Each enzyme has one glutamic acid and two aspartic acid residues necessary for activity, while most enzymes of the family also contain two histidine residues critical for transition state stabilisation. These five residues occur in four short sequences conserved throughout the family, and within such sequences some key amino acid residues are related to enzyme specificity. A table is given showing motifs distinctive for each specificity as extracted from 316 sequences, which should aid in identifying the enzyme from primary structure information. Where appropriate, existing problems with identification of some enzymes of the family are pointed out. For enzymes of known three-dimensional structure, action is discussed in terms of molecular architecture. The sequence-specificity and structure-specificity relationships described may provide useful pointers for rational protein engineering.

General information
State: Published
Organisations: Carlsberg Research Center
Contributors: MacGregor, E. A., Janecek, S., Svensson, B.
Pages: 1-20
Publication date: 2001
Peer-reviewed: Yes

Publication information
Journal: BBA General Subjects
Volume: 1546
ISSN (Print): 0304-4165
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.35
Web of Science (2017): Impact factor 3.679
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.97 SJR 2.122 SNIP 1.486
Web of Science (2016): Impact factor 4.702
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.97 SJR 2.122 SNIP 1.486
Web of Science (2015): Impact factor 5.083
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.1 SJR 1.78 SNIP 1.303
Web of Science (2014): Impact factor 4.381
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.05 SJR 1.672 SNIP 1.233
Web of Science (2013): Impact factor 3.829
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.78 SJR 2.084 SNIP 1.514
Web of Science (2012): Impact factor 3.848
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.73 SJR 2.066 SNIP 1.515
Web of Science (2011): Impact factor 5
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.83 SNIP 1.27
Web of Science (2010): Impact factor 4.663
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.219 SNIP 1.087
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.079 SNIP 0.953
Scopus rating (2007): SJR 1.071 SNIP 0.931
Scopus rating (2006): SJR 0.951 SNIP 0.847
Scopus rating (2005): SJR 1.247 SNIP 1.148
Scopus rating (2004): SJR 1.363 SNIP 1.097
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.061 SNIP 1.05
Scopus rating (2002): SJR 1.052 SNIP 1.147
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.01 SNIP 1.013
Scopus rating (2000): SJR 0.916 SNIP 0.824
Scopus rating (1999): SJR 0.823 SNIP 0.848
Original language: English
URLs:
Source: orbit
Source-ID: 189518
Research output: Research - peer-review › Journal article – Annual report year: 2001