

SUPPLEMENTARY METHOD

Shotgun method:

TCA precipitation and tryptic digestion: Volumes of lysates containing 100 µg of total proteins from lens were adjusted to 60 µL and treated with 0.7 µL of 1 M DTT and 9.3 µL of 7.5% SDS at 95°C for 5 min before reduction. After the reaction, lysates were further treated with 8 µL of 50 mM IAM at room temperature for 30-min alkylation in the dark; subsequently proteins were precipitated by adding 52 µL of 50% TCA and incubated on ice for 15 min. After removing the supernatant by centrifugation at 13,000 x g for 10 min, the collected proteins were washed with 150 µL of 10% TCA, vortexed and centrifuged at 13,000 x g for 5 min. The precipitated proteins were washed again with 250 µL dd H₂O, vortexed and centrifuged three times under the same conditions. The resultant pellets were resuspended with 50 mM NH₄HCO₃ (pH 8.5), then digested with 4 µg of trypsin for 18 h at 37°C and further dried in a vacuum centrifuge to remove NH₄HCO₃. The resultant liquids were acidified by 10% TFA/ H₂O to pH 2.0~3.0 and applied onto the reverse phase C18 column pre-equilibrated with 200 µL of 0.1% TFA/ H₂O (pH 2.0~3.0). The column was also washed with 200 µL of 0.1% TFA/ H₂O (pH 3.0) and then eluted with a stepwise ACN gradient from 50% to 100% in 0.1% TFA at room temperature. Eluted solutions were dried in a vacuum centrifuge to remove organic solvent.

Nano LC-MS/MS analysis: The lyophilized powders were reconstituted in 12 µL of 0.1% FA in H₂O and analyzed by LTQ Orbitrap XL (Thermo Fisher Scientific, San Jose, CA). Reverse-phase nano LC separation was performed on an Agilent 1200 series nanoflow system (Agilent Technologies, Santa Clara, CA). A total of 10 µL sample from collected fractions was loaded onto an Agilent Zorbax XDB C18 precolumn (0.35 mm, 5 µm), followed by separation using a in-house handmade C18 column (i.d. 75 µm x 15-cm, 3 µm). The mobile phases used were (A) 0.1% FA and (B) 0.1% FA in 100% ACN. A linear gradient from 5% to 95% of (B) over a 70 min period at a flow rate of 300 nL/min was applied. The peptides were analyzed in the positive ion mode by applying a voltage of 1.8 kV to the injection needle. The MS was operated in a data-dependent mode, in which one full scan with m/z 400-1600 in the Orbitrap using a scan rate of 30 ms/scan. The fragmentation was performed using the CID mode with a normalized collision energy of 35 V. A repeat duration of 30 s was applied to exclude the same

m/z ions from the reselection for fragmentation. An in-house Xcalibur software (version 2.0.7, Thermo-Finnigan Inc., San Jose, CA) was used for the management of instrument control, data acquisition, and data processing.

Protein database search and characterization: Peptides were identified by peak lists converted from the nano LC-MS/MS spectra by bioinformatics searching against zebrafish (*Danio rerio*) taxonomy in the NCBI databases for exact matches using the Mascot search program (<http://www.matrixscience.com>). Parameters were set as follows: a mass tolerance of 10 ppm for precursor ions and 0.8 Da for fragment ions; no missed cleavage site allowed for trypsin; carbamidomethyl cysteine as fixed modification; oxidized methionine and amidated asparagine/glutamine as optional modification. Peptides were considered positively identified if their Mascot individual ion score was higher than 20 ($p < 0.05$).

Table S1. The ratio of $\alpha A / \alpha B$ (percent proportion) in three piscine lenses.

	Zebrafish	rice eel	catfish
αA^*	7.4	n.d.	6.2
αB^*	2.0	n.d.	n.d.
ratio($\alpha A / \alpha B$)*	3.7		

*Ratios of αA , αB and $\alpha A / \alpha B$ were determined from protein spots in 2-D gel by densitometry using *ImagineMaster* program. n.d., not detected

Table S2. Comparison of methionine content from protein sequences of various crystallins from zebrafish (*Danio rerio*).

Methionine	zebrafish(<i>Danio rerio</i>)	
	Amount	percentage
alphaA	1	0.6%
alphaB	4	2.4%
beta A1a	10	5.1%
beta A1-2	10	5.1%
beta A2a	11	5.3%
beta A2-2	7	3.6%
beta A4	6	3.1%
crystallin B1	13	5.6%
beta B1	16	7.2%
beta B2	2	1.0%
beta B3	4	1.5%
gamma M2(predicted)	23	13.2%
gamma M2c	23	13.1%
gamma M3	14	8.0%
gamma M5	13	7.3%
gamma M7	17	9.8%

Table S3. Comparison of crystallin numbers in zebrafish, rice eel and catfish lenses identified by 1-D/2-D gel and shotgun proteomic strategies

I. Zebrafish

	1D	2D	shotgun(zebrafish)
alpha-crystallin A chain [Danio rerio]	1	1	1
alpha-crystallin B chain [Danio rerio]	1	1	1
crystallin, alpha B, b [Danio rerio]	1		1
crystallin, beta A1a [Danio rerio]	1	1	1
crystallin, beta A1b [Danio rerio]	1		1
beta A1-2-crystallin [Danio rerio]	1		1
betaA1c-crystallin [Danio rerio]	1		1
beta A2 crystallin [Dissostichus mawsoni]			
beta A2-2 crystallin	1	1	1
crystallin, beta A2a [Danio rerio]	1	1	1
crystallin, beta A2b [Danio rerio]	1		
beta-crystallin A4 [Danio rerio]	1	1	1
crystallin B1 protein [Danio rerio]	1	1	1
crystallin, beta B1, like 2 [Danio rerio]	1	1	1
crystallin, beta B2 [Danio rerio]	1	1	1
crystallin, beta B3 [Danio rerio]	1	1	1
g-crystallin [Clarias fuscus]			
crystallin, gammaB [Danio rerio]	1	1	
crystallin, gammaD [Danio rerio]	1		1
crystallin, gamma M1 [Danio rerio]	1		1
gamma-crystallin M2-like [Oreochromis niloticus]			
crystallin, gamma M2a [Danio rerio]	1		1
crystallin, gamma M2b [Danio rerio]	1		
crystallin, gamma M2c [Danio rerio]	1	1	1
crystallin, gamma M2d11 [Danio rerio]	1		
crystallin, gamma M2f [Danio rerio]			1
crystallin, gamma M3 [Danio rerio]	1	1	1
crystallin, gamma M4 [Danio rerio]	1		1
crystallin, gamma M5 [Danio rerio]	1		1
crystallin, gamma M6 [Danio rerio]	1		1
crystallin, gamma M7 [Danio rerio]	1	1	1
crystallin, gamma Mx [Danio rerio]	1		1
gamma-crystallin N-A [Danio rerio]	1	1	1
gamma-crystallin N-B [Danio rerio]	1	1	1

crystallin, gamma S [Danio rerio]	1		
crystallin, gamma S1 [Danio rerio]	1	1	1
crystallin, gamma S2 [Danio rerio]	1	1	
crystallin, gamma S4 [Danio rerio]	1		1
PREDICTED: novel protein similar to crystallin, gamma family [Danio rerio]	1		
total count	35	18	29

II. Rice eel

Identified crystallins in rice eel	1D	2D	shotgun(zebrafish)
beta-crystallin a4 [Ictalurus punctatus]			
crystallin, beta A1a [Danio rerio]			
crystallin, beta A1b [Danio rerio]			1
PREDICTED: beta-crystallin A1-like [Oreochromis niloticus]			
PREDICTED: beta-crystallin A1-1-like [Oreochromis niloticus]			
beta A1-2-crystallin [Danio rerio]	1		
beta A2 crystallin [Dissostichus mawsoni]			
crystallin, beta A2a [Danio rerio]	1	1	1
beta-crystallin A4 [Danio rerio]	1	1	1
crystallin B1 protein [Danio rerio]	1	1	1
crystallin, beta B1, like 2 [Danio rerio]	1	1	
crystallin, beta B2 [Danio rerio]			1
crystallin, beta B3 [Danio rerio]			
gamma-crystallin A [Danio rerio]	1		1
crystallin, gammaB [Danio rerio]	1	1	1
crystallin, gammaD [Danio rerio]	1		
crystallin, gamma M1 [Danio rerio]			
gamma-crystallin M2-like [Oreochromis niloticus]			
crystallin, gamma M2b [Danio rerio]			
crystallin, gamma M2c [Danio rerio]	1		1
crystallin, gamma M2d7 [Danio rerio]	1		
crystallin, gamma M2d12 [Danio rerio]	1		
crystallin, gamma M2f [Danio rerio]	1		
crystallin, gamma M3 [Danio rerio]	1	1	
crystallin, gamma M5 [Danio rerio]		1	
crystallin, gamma M7 [Danio rerio]	1		
crystallin, gamma S [Danio rerio]			
crystallin, gamma S1 [Danio rerio]	1		
Total number of identified crystallins	15	7	8

III. Catfish

Identified crystallins in catfish*	1D	2D	shotgun(zebrafish)
alpha A crystallin*, Zebrafish	1*	1	
beta-crystallin a2 [Ictalurus punctatus]			
beta-crystallin a4 [Ictalurus punctatus]			
crystallin, beta A1a [Danio rerio]	1	1	1
crystallin, beta A1b [Danio rerio]	1		
beta A1-2-crystallin [Danio rerio]	1	1	
betaA1c-crystallin [Danio rerio]	1		
crystallin, beta A2a [Danio rerio]	1		
beta-crystallin A4 [Danio rerio]	1		1
crystallin B1 protein [Danio rerio]	1	1	1
crystallin, beta B1, like 2 [Danio rerio]	1	1	
crystallin, beta B2 [Danio rerio]	1	1	1
g-crystallin [Clarias fuscus]			
crystallin, gammaB [Danio rerio]			1
crystallin, gammaD [Danio rerio]		1	
crystallin, gamma M1 [Danio rerio]	1		
gamma-crystallin M2-like [Oreochromis niloticus]			
crystallin, gamma M2b [Danio rerio]	1	1	
crystallin, gamma M2c [Danio rerio]	1		
crystallin, gamma M2d2 [Danio rerio]	1		
Crystallin, gamma M2d4 [Danio rerio]	1		
crystallin, gamma M2d5 [Danio rerio]	1		
crystallin, gamma M2d6 [Danio rerio]	1		
crystallin, gamma M2d12 [Danio rerio]	1		
crystallin, gamma M2f [Danio rerio]	1		
crystallin, gamma M3 [Danio rerio]	1	1	
crystallin, gamma M5 [Danio rerio]	1		1
crystallin, gamma M7 [Danio rerio]	1		
gamma-crystallin N-B [Danio rerio]	1		
crystallin, gamma S1 [Danio rerio]	1	1	
crystallin, gamma S2 [Danio rerio]			
gamma crystallin-like [Danio rerio]	1		
PREDICTED: novel protein similar to crystallin, gamma family [Danio rerio]	1		
Total number of identified crystallins	26	10	6

* Peptides were identified by nano-LC-MS/MS by bioinformatics search in NCBI databases with Mascot program (<http://www.matrixscience.com>).

* "1" denotes positive identification.

Table S4-I. Results obtained from shotgun proteomic analyses on zebrafish

Identified Protein No.	Accession No.	Score	Matches	Sequences	Description
1	gi 23308655	159	24 (9)	8 (4)	alpha-crystallin A chain [Danio rerio]
2	gi 18858475	88	18 (7)	8 (3)	alpha-crystallin B chain [Danio rerio]
3	gi 62902024	43	17 (3)	6 (3)	beta A1-2-crystallin [Danio rerio]
4	gi 325296915	68	40 (8)	11 (6)	betaA1c-crystallin [Danio rerio]
5	gi 72011255	600	100 (34)	11 (8)	betaA2-2-crystallin [Danio rerio]
6	gi 110626137	261	57 (17)	9 (7)	beta-crystallin A4 [Danio rerio]
7	gi 198282145	392	125 (27)	14 (8)	beta-crystallin B2 [Danio rerio]
8	gi 347543831	350	93 (25)	14 (10)	beta-crystallin B3 [Danio rerio]
9	gi 16751457	392	84 (34)	14 (10)	crystallin B1 protein [Danio rerio]
10	gi 50540408	92	13 (4)	4 (2)	crystallin, alpha B, b [Danio rerio]
11	gi 50539880	194	104 (22)	8 (5)	crystallin, beta A1a [Danio rerio]
12	gi 50540238	95	27 (6)	5 (5)	crystallin, beta A1b [Danio rerio]
13	gi 50344752	422	71 (29)	11 (9)	crystallin, beta A2a [Danio rerio]
14	gi 154426250	107	63 (11)	12 (5)	crystallin, beta B1, like 2 [Danio rerio]
15	gi 56090499	1245	161 (62)	13 (10)	crystallin, gamma M1 [Danio rerio]
16	gi 66392178	53	45 (5)	8 (2)	crystallin, gamma M2a [Danio rerio]
17	gi 56090503	427	90 (25)	8 (5)	crystallin, gamma M2c [Danio rerio]
18	gi 158534013	52	13 (3)	4 (2)	crystallin, gamma M2f [Danio rerio]
19	gi 56090493	693	170 (57)	11 (6)	crystallin, gamma M3 [Danio rerio]
20	gi 56090491	119	51 (10)	7 (5)	crystallin, gamma M4 [Danio rerio]
21	gi 55742553	130	24 (10)	4 (3)	crystallin, gamma M5 [Danio rerio]
22	gi 66472840	153	40 (13)	7 (5)	crystallin, gamma M6 [Danio rerio]
23	gi 169158622	145	37 (12)	7 (5)	crystallin, gamma M6 [Danio rerio]

24	gi 66472834	289	74 (21)	13 (8)	crystallin, gamma M7 [Danio rerio]
25	gi 61651684	173	39 (12)	7 (5)	crystallin, gamma MX [Danio rerio]
26	gi 61651710	333	104 (26)	11 (7)	crystallin, gamma S1 [Danio rerio]
27	gi 61651706	60	20 (6)	5 (2)	crystallin, gamma S4 [Danio rerio]
28	gi 66773094	85	13 (7)	4 (4)	gamma-crystallin D [Danio rerio]
29	gi 56090497	187	38 (12)	10 (5)	gamma-crystallin N-A [Danio rerio]
30	gi 51010939	77	19 (6)	6 (3)	gamma-crystallin N-B [Danio rerio]
31	gi 80751129	18	10 (1)	5 (1)	60S ribosomal protein L40 [Danio rerio]
32	gi 27762270	29	6 (3)	5 (3)	annexin 5 [Danio rerio]
33	gi 197247193	299	53 (18)	6 (5)	Crygs3 protein [Danio rerio]
34	gi 52219194	90	18 (8)	7 (5)	fatty acid binding protein 11a [Danio rerio]
35	gi 9800189	25	15 (2)	9 (2)	gelsolin [Danio rerio]
36	gi 51010943	57	28 (4)	7 (4)	grifin [Danio rerio]
37	gi 342187202	49	3 (1)	2 (1)	high mobility group nucleosome-binding domain-containing protein 3 isoform 1 [Danio rerio]
38	gi 115496922	1139	155 (60)	13 (10)	hypothetical protein LOC767711 [Danio rerio]
39	gi 116267939	49	14 (4)	5 (3)	hypothetical protein LOC768128 [Danio rerio]
40	gi 165972443	49	16 (3)	6 (3)	hypothetical protein LOC796074 [Danio rerio]
41	gi 160333607	36	18 (3)	7 (3)	hypothetical protein LOC796228 [Danio rerio]
42	gi 63100935	113	36 (10)	8 (6)	LOC553473 protein [Danio rerio]
43	gi 55962804	61	59 (7)	9 (4)	novel protein similar to vertebrate crystallin gamma S (CRYGS) [Danio rerio]
44	gi 41152400	43	18 (2)	2 (1)	peptidylprolyl isomerase A, like [Danio rerio]
45	gi 41388972	14	1 (1)	1 (1)	Pgk1 protein [Danio rerio]
46	gi 56693334	24	5 (1)	3 (1)	phakinin [Danio rerio]
47	gi 326672749	26	3 (1)	3 (1)	PREDICTED: filensin-like [Danio rerio]
48	gi 292615694	17	3 (1)	1 (1)	PREDICTED: hypothetical protein LOC100320788 [Danio rerio]
49	gi 125842397	38	1 (1)	1 (1)	PREDICTED: metastasis-associated protein MTA1-like [Danio rerio]

50	gi 292620311	16	3 (1)	1 (1)	PREDICTED: potassium voltage-gated channel subfamily H member 5-like [Danio rerio]
51	gi 113255	59	10 (4)	6 (2)	RecName: Full=Actin, clone 403; Flags: Precursor
52	gi 47085671	54	2 (2)	1 (1)	S100 calcium binding protein A10b [Danio rerio]
53	gi 50540374	42	19 (3)	9 (3)	serpin peptidase inhibitor, clade B (ovalbumin), member 1 [Danio rerio]
54	gi 148596963	32	4 (1)	4 (1)	spectrin alpha chain, brain [Danio rerio]
55	gi 18859549	37	12 (2)	7 (2)	vimentin [Danio rerio]

Table S4-II. Results obtained from shotgun proteomic analyses on rice eel

Identified Protein No.	Accession No.	Score	Matches	Sequences	Description
1	gi 110626137	74	20 (4)	4 (2)	beta-crystallin A4 [Danio rerio]
2	gi 16751457	66	25 (8)	6 (4)	crystallin B1 protein [Danio rerio]
3	gi 50540238	23	4 (1)	1 (1)	crystallin, beta A1b [Danio rerio]
4	gi 50344752	40	29 (4)	3 (2)	crystallin, beta A2a [Danio rerio]
5	gi 169159105	22	4 (1)	1 (1)	crystallin, beta B2 [Danio rerio]
6	gi 56090503	24	18 (2)	2 (1)	crystallin, gamma M2c [Danio rerio]
7	gi 35902900	120	15 (4)	7 (2)	fructose-bisphosphate aldolase C-B [Danio rerio]
8	gi 181330284	40	5 (2)	1 (1)	gamma-crystallin A [Danio rerio]
9	gi 59933282	42	17 (5)	2 (2)	gamma-crystallin B [Danio rerio]
10	gi 41056025	17	3 (1)	1 (1)	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1, like 4 [Danio rerio]
11	gi 113681112	60	12 (4)	6 (3)	heat shock protein 90-alpha 2 [Danio rerio]
12	gi 4504301	25	6 (2)	3 (2)	histone H4 [Homo sapiens]
13	gi 41152128	54	3 (2)	2 (1)	hypothetical protein LOC393746 [Danio rerio]
14	gi 71152817	52	2 (2)	1 (1)	lengsin [Danio rerio]
15	gi 18858959	37	2 (1)	1 (1)	L-lactate dehydrogenase A chain [Danio rerio]
16	gi 63100935	284	52 (16)	7 (4)	LOC553473 protein [Danio rerio]
17	gi 41055570	28	7 (1)	2 (1)	parvalbumin isoform 1b [Danio rerio]
18	gi 50539996	19	4 (1)	3 (1)	peroxiredoxin-2 [Danio rerio]
19	gi 45501385	21	2 (1)	2 (1)	Pkm2a protein [Danio rerio]
20	gi 125825824	40	11 (3)	2 (1)	PREDICTED: gamma-crystallin M2 [Danio rerio]
21	gi 113255	132	32 (10)	13 (8)	RecName: Full=Actin, clone 403; Flags: Precursor
22	gi 50540374	47	4 (1)	1 (1)	serpin peptidase inhibitor, clade B (ovalbumin), member 1 [Danio rerio]
23	gi 148596963	189	46 (10)	31 (8)	spectrin alpha chain, brain [Danio rerio]

24	gi153791743	47	8 (3)	5 (2)	spectrin beta chain, brain 1 [Danio rerio]
25	gi110005909	18	17 (1)	14 (1)	titin a [Danio rerio]

Table S4-III. Results obtained from shotgun proteomic analyses on catfish

Identified Protein No.	Accession No.	Score	Matches	Sequences	Description
1	gi 110626137	40	7 (1)	2 (1)	beta-crystallin A4 [Danio rerio]
2	gi 16751457	47	12 (3)	4 (2)	crystallin B1 protein [Danio rerio]
3	gi 50539880	44	12 (1)	1 (1)	crystallin, beta A1a [Danio rerio]
4	gi 169159105	34	3 (1)	1 (1)	crystallin, beta B2 [Danio rerio]
5	gi 55742553	38	3 (2)	1 (1)	crystallin, gamma M5 [Danio rerio]
6	gi 52219194	29	3 (2)	1 (1)	fatty acid binding protein 11a [Danio rerio]
7	gi 59933282	20	4 (1)	2 (1)	gamma-crystallin B [Danio rerio]
8	gi 29335504	38	3 (1)	2 (1)	keratin 18 [Danio rerio]
9	gi 50540008	48	1 (1)	1 (1)	L-lactate dehydrogenase B-B chain [Danio rerio]
10	gi 63100935	35	19 (3)	5 (1)	LOC553473 protein [Danio rerio]
11	gi 326671791	26	12 (1)	1 (1)	PREDICTED: protein kinase C-binding protein 1 [Danio rerio]

Table S5. Protein identification in rice eel and catfish based on sequence databases of zebrafish

I. beta A2a crystallin

rice eel	protein identification name: crystallin, beta A2a [Danio rerio]
	Accession No.: gi 50344752
	sequences: 23810
	amino acid No.: 197aa
	Score: 103
	Theoretical Mr/PI: 23810/6.44
	Protein sequence coverage: 6%
	Matched peptides shown in bold red.
	 1 MNQREQMEQQ CQWR ITVWEE ENFQGK RCEF RLECPNILDR DFQKIRSIKV 51 DNGPWVGYEY PEYQGQQFIL EKGDYPCYQA WSGNSSYRTE HMLSFRPIKC 101 ANHSDSKITM YECEDMMGRK FEMCDDYPSL MAMGWCSKEV PSIKVNSGAW 151 VGYQFPGYRG YQYIFERDRR QGEYRKYYEF GTQAHSNQIQ SMRRIQH Unformatted sequence string: 197 residues (for pasting into other applications).

II. **gamma M3 crystallin**

rice eel protein identification name: **crystallin, gamma M3 [Danio rerio]**

Accession No.: **gi|56090493**

sequences: **20961**

amino acid No.: 174aa

Score: **44**

Theoretical Mr/PI: 20961/ 8.02

Protein sequence coverage: 9%

Matched peptides shown in bold red.

1 MGK**IIFYEDR** NFQGRSYECS TDCADMSTYL SRCNSCRVES GCFVVYDRPN
51 FMGNQFFMRR GEYADYMRMG MSDGIRSCRVPQYRGPYRM
RIYERDNFGG
101 QMYELTDDCD SFMDRYRISD CQSCHVMDGH WLMYEQPHYR
GR**MIYFRPGE**
151 YRSFRDMGYS NVRFSSVRRI VDLC

Unformatted sequence string: 174 residues (for pasting into other applications)

III. **alpha-crystallin A chain**

catfish	protein identification name: alpha-crystallin A chain [Danio rerio]
---------	--

Accession No.: **gi|23308655**

sequences: **19702**

amino acid No.: **173aa**

Score: **59**

Theoretical Mr/PI: 19702/ 5.84

Protein sequence coverage: 5%

Matched peptides shown in bold red.

1 MDIAIQHPWF RRTLGYPTL FDQFFGEGLF DYDLFPFTTS TVSPYYRHSL
51 FRNILDSSNS GVSEVRSDRE KFTVYLDVKH FSPDELSVKV TDDYVEIQGK
101 HGER**QDDHGY IS**REFHRRYR LPSNVDQSAI TCTLSADGLL TLCGPKTSGI
151 DAGRGDRTIP VTREDKSNSG SSS

Unformatted sequence string: 173 residues (for pasting into other applications).

IV. **beta B1 crystallin**

catfish	protein identification name: crystallin, beta B1 [Danio rerio]
---------	---

Accession No.: **gi|154426250**

sequences: **25941**

amino acid No.: **221aa**

Score: **248**

Theoretical Mr/PI: 25941/ 6.53

Protein sequence coverage: 18%

Matched peptides shown in bold red.

1 MSTGGEKSKP ASQPDGKAAQ TQKKTEMGMG NYK**MYVFDQE NFQGR**MIEIS

51 NECMNVCEMG MDRVRLRVE CGPWVGWEQM NFCGEMYILE

KGEYPRWDCW

101 SNCHRNDYLL SFRPIRMDPE KHKICLYEVG DFKGRKMEII DDDVPSMYTF

151 GFTDR**VGSIM VSCGTWVG**YQ **YPGYR**GSQYL LEKGDYR**HFN**

EYGARHPQFQ

201 SVRRIRDMQW HPDGCYTMAT K

Unformatted sequence string: 221 residues (for pasting into other applications).
