

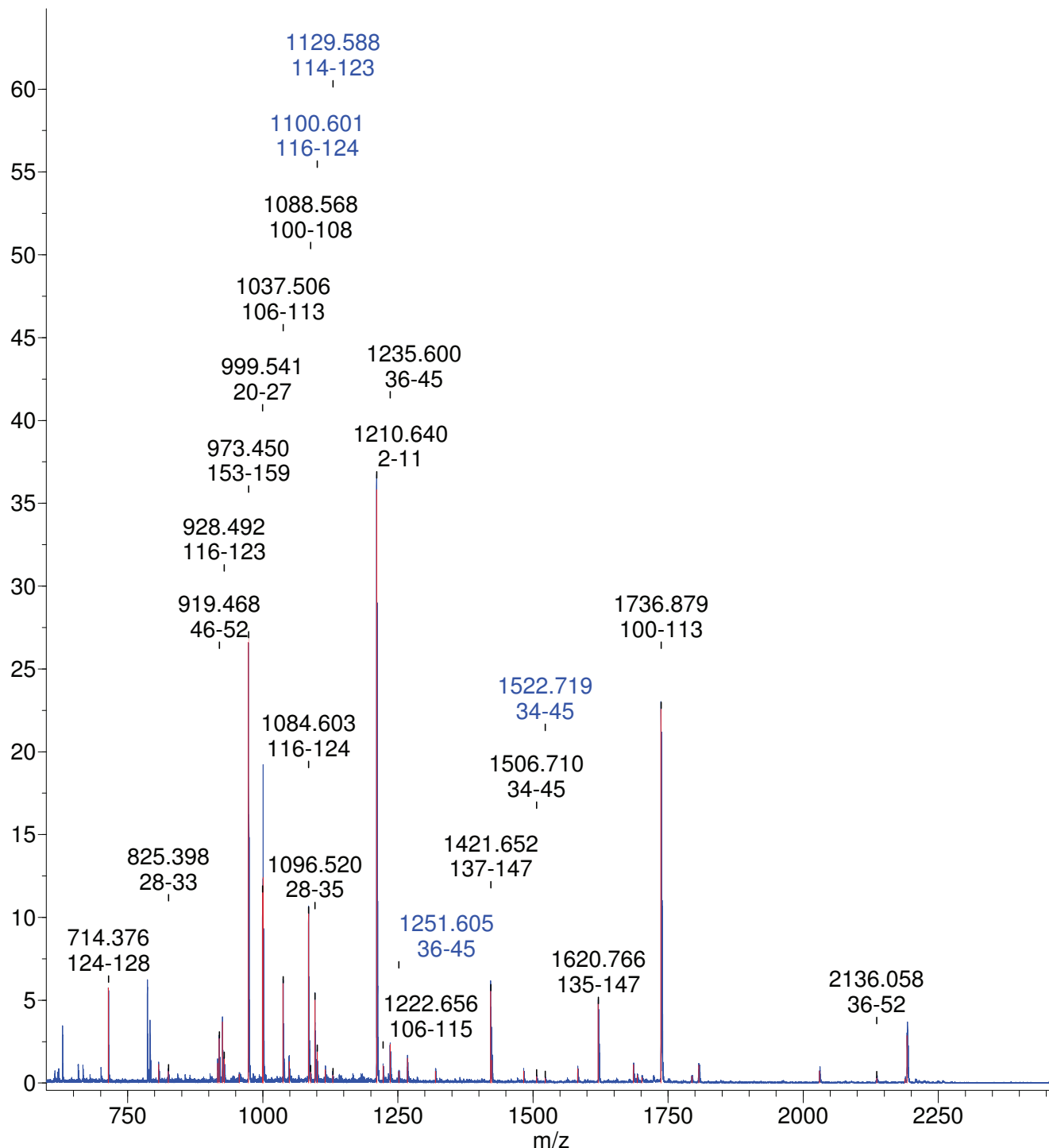
## Spectrum Analysis Report

Date: 01/16/2008 Time: 15:05

FileName: \\Flex-pc\Ashish\16-01-08\beta-sbt\0\_A8\cali\1SRef\data\1\1r

Sequence Name: Chain A, Human Interferon-Beta Crystal Structure  
Formula:  
Parentmass: 1000.000  
Mass Error: 998.992  
MH+ (mono): 1.008  
MH+ (avg): 1.008  
Threshold (a.i.): 0.000  
Tolerance (Da): 1.000  
Number of Peaks: 43  
Above Threshold: 43  
Assigned Peaks: 0  
Not assigned Peaks: 43

[Abs. Int. \* 1000]



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### Sequence data:

Chain A, Human Interferon-Beta Crystal Structure

Intensity Coverage: 81.2 % (139447 cnts) Sequence Coverage MS55.4%  
Sequence Coverage MS0.0% pI (isoelectric point): 9.6

10	20	30	40	50	60	70	80
MSYNLLGFLQ	RSSNFQCQKL	LWQLNGRLEY	CLKDRMNFDI	PEEIKQLQQF	QKEDAALTIY	EMLQNI FAIF	RQDSSSTGWNE
90	100	110	120	130	140	150	160
ETIVENLLAN	VYHQINHLKT	VLEEKLEKED	FTRGKLMSSL	HLKRYYGRIL	HYLKAKEYSH	CAWTIVRVEI	LRNFYFINRL
170	TGYLRLN						

### Display Parameter:

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### Peaklist:

Peak	Mass	Intensity	Peak	Mass	Intensity
1	714.376	5447.000	2	807.394	1073.583
3	825.398	663.657	4	916.510	1133.172
5	919.468	2549.031	6	925.404	3504.931
7	928.492	1389.643	8	956.512	496.874
9	973.450	25461.686	10	999.541	10896.483
11	1000.541	11767.331	12	1037.506	5710.604
13	1048.867	1224.548	14	1084.603	9695.067
15	1088.568	630.618	16	1096.520	4756.274
17	1100.601	1787.048	18	1115.619	766.068
19	1129.588	444.165	20	1210.640	33965.113
21	1222.656	977.708	22	1235.600	2216.236
23	1251.605	664.967	24	1267.676	1415.972
25	1319.702	678.538	26	1421.652	5256.838
27	1423.681	1306.866	28	1482.766	685.638
29	1506.710	382.404	30	1522.719	290.684
31	1582.763	827.703	32	1620.766	4574.009
33	1685.797	1053.995	34	1692.852	456.899
35	1701.530	319.685	36	1736.879	21407.411
37	1793.907	381.327	38	1806.934	1019.174
39	2030.003	691.983	40	2136.058	280.655
41	2188.101	227.766	42	2192.050	2720.070
43	2996.495	478.741			

### Matched Sequences:

#### Chain A, Human Interferon-Beta Crystal Structure

MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQNI FAIFRQDSSSTGWNE  
TIVENLLANVYHQINHLKTIVLEEKLEKEDFTRGKLMSSLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTG

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YLRN

### Digest Matches

Tolerance = 100.000000 ppm, Trypsin/P

Score = 235.000000, Rank = 1, Database = NCBIInr, Accesskey = gi|3318960

Modifications: \ML C -H+CH2CONH2 Carbamidomethyl (C), \MO M O Oxidation (M),

Mass Mr	Dev.	Range	P	Sequence
* 713.369	0.008	124 - 128	1	RYYGR
* 824.390	-0.020	28 - 33	0	LEYCLK
* 918.461	-0.032	46 - 52	0	QLQQFQK
* 927.484	-0.037	116 - 123	0	LMSSLHLK
* 972.443	-0.039	153 - 159	0	NFYFINR
* 998.534	-0.033	20 - 27	0	LLWQLNGR
* 1036.498	-0.021	106 - 113	1	LEKEDFTR
* 1083.596	-0.026	116 - 124	1	LMSSLHLKR
* 1087.561	-0.052	100 - 108	1	TVLEEKLEK
* 1095.512	-0.026	28 - 35	1	LEYCLKDR
* 1099.593	-0.024	116 - 124	1	LMSSLHLKR 117: Oxidation (M)
* 1128.581	-0.052	114 - 123	1	GKLMSSLHLK 117: Oxidation (M)
* 1209.632	-0.018	2 - 11	0	SYNLLGFLQR
* 1221.649	0.014	106 - 115	2	LEKEDFTRGK
* 1234.592	0.002	36 - 45	0	MNFDIPEEIK
* 1250.598	0.013	36 - 45	0	MNFDIPEEIK 36: Oxidation (M)
* 1420.645	-0.011	137 - 147	0	EYSHCAWTIVR
* 1505.703	-0.015	34 - 45	1	DRMNFDIPEEIK
* 1521.711	-0.002	34 - 45	1	DRMNFDIPEEIK 36: Oxidation (M)
* 1619.759	-0.029	135 - 147	1	AKEYSHCAWTIVR
* 1735.871	-0.028	100 - 113	2	TVLEEKLEKEDFTR
* 2135.051	-0.021	36 - 52	1	MNFDIPEEIKQLQQFQK