

Operator: manfred  
Date/time: 2017-09-09/11:40:36am  
Title/Comment:

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**Reference series:** gly1

**hdx\_kin-File:** c:\massmap\web\_site\reports\hdx\hdx\_kin version\_sept\_17\gly1.hdx\_kin

**Experiment series:** degly1

**hdx\_kin-File:** c:\massmap\web\_site\reports\hdx\hdx\_kin version\_sept\_17\degly1.hdx\_kin

**lis-File:** C:\massmap\web\_site\reports\hdx\lis\_etc\MAB\_Demo.lis

Total number lis-entries: 239  
Number entries molecule HC: 143  
Number entries molecule LC: 96

**Standards:** C:\massmap\vertrieb\web\_site\reports\hdx\standards\series1\_1101\_t2.mmp  
C:\massmap\vertrieb\web\_site\reports\hdx\standards\series1\_1201\_t2.mmp  
C:\massmap\vertrieb\web\_site\reports\hdx\standards\series1\_1301\_t2.mmp

**Data sets of reference series:**

Exchange Time	Path
0.0 min	C:\massmap\web_site\reports\hdx\gly_1\series2_1101_t2.mmp
0.5 min	C:\massmap\web_site\reports\hdx\gly_1\series2_1201_t2.mmp
1.0 min	C:\massmap\web_site\reports\hdx\gly_1\series2_1301_t2.mmp
10.0 min	C:\massmap\web_site\reports\hdx\gly_1\series2_1401_t2.mmp
60.0 min	C:\massmap\web_site\reports\hdx\gly_1\series2_1501_t2.mmp
240.0 min	C:\massmap\web_site\reports\hdx\gly_1\series2_1601_t2.mmp

**Data sets of experiment series:**

Exchange Time	Path
0.0 min	C:\massmap\web_site\reports\hdx\degly_1\series2_1801_t2.mmp
0.5 min	C:\massmap\web_site\reports\hdx\degly_1\series2_1901_t2.mmp
1.0 min	C:\massmap\web_site\reports\hdx\degly_1\series2_2001_t2.mmp
10.0 min	C:\massmap\web_site\reports\hdx\degly_1\series2_2101_t2.mmp
60.0 min	C:\massmap\web_site\reports\hdx\degly_1\series2_2201_t2.mmp
240.0 min	C:\massmap\web_site\reports\hdx\degly_1\series2_2301_t2.mmp

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Printout of HDX plots restricted to peptides with significant differences or problems

No printout of DU overview plot(s)

Printout of kinetics difference plot(s) for all peptides with sufficient HDX data

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Molecule HC: Peptides with sufficient kinetics data, part 1

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC001-017	1	0.0 min	7.058	7.050	0.00	0.00	0.00	0.00
		0.5 min	7.043	7.038	37.01	35.51	5.55	5.33
		1.0 min	7.042	7.047	39.13	38.36	5.87	5.75
		10.0 min	7.038	7.034	<b>45.72</b>	45.54	<b>6.86</b>	6.83
		60.0 min	7.028	7.043	47.96	48.13	7.19	7.22
		240.0 min	7.029	7.041	47.93	48.16	7.19	7.22
		Score1:	0.61	DU sum difference:-0.34 u				
Score2:	0.77							
HC001-018	1	0.0 min	8.996	8.986	0.00	0.00	0.00	0.00
		0.5 min	8.988	8.989	30.84	28.29	4.94	4.53
		1.0 min	8.989	8.991	32.11	32.11	5.14	5.14
		10.0 min	8.985	8.981	38.13	39.13	6.10	6.26
		60.0 min	8.973	8.988	43.34	43.34	6.94	6.94
		240.0 min	8.972	8.986	43.34	44.75	6.94	7.16
		Score1:	0.04	DU sum difference:-0.02 u				
Score2:	<b>1.20</b>							
HC001-020	1	0.0 min	9.604	9.581	0.00	0.00	0.00	0.00
		0.5 min	9.592	9.576	28.39	25.48	5.11	4.59
		1.0 min	9.593	9.595	29.69	28.88	5.34	5.20
		10.0 min	9.591	9.579	33.15	34.21	5.97	6.16
		60.0 min	9.572	9.591	37.27	38.14	6.71	6.86
		240.0 min	9.568	9.596	38.17	39.87	6.87	7.18
		Score1:	0.03	DU sum difference:-0.02 u				
Score2:	<b>1.77</b>							
HC001-022	1	0.0 min	9.422	9.415	0.00	0.00	0.00	0.00
		0.5 min	9.426	9.431	<b>28.57</b>	26.07	<b>5.71</b>	5.21
		1.0 min	9.436	9.443	30.93	29.66	6.19	5.93
		10.0 min	9.432	9.426	37.04	38.13	7.41	7.63
		60.0 min	9.427	9.439	42.55	43.66	8.51	8.73
		240.0 min	9.415	9.442	44.22	45.77	8.84	9.15
		Score1:	0.81	DU sum difference: 0.60 u				
Score2:	<b>1.46</b>							
HC001-023	1	0.0 min	9.374	9.366	0.00	0.00	0.00	0.00
		0.5 min	9.377	9.371	29.19	26.99	6.13	5.67
		1.0 min	9.380	9.381	31.48	<b>30.47</b>	6.61	<b>6.40</b>
		10.0 min	9.376	9.369	36.72	37.65	7.71	7.91
		60.0 min	9.362	9.390	41.97	42.58	8.81	8.94
		240.0 min	9.373	9.379	42.94	45.15	9.02	9.48
		Score1:	0.50	DU sum difference: 0.39 u				
Score2:	<b>1.68p</b>							
HC002-044	1	0.0 min	9.804	9.772	0.00	0.00	0.00	0.00
		0.5 min	9.801	9.779	22.57	21.70	9.03	8.68
		1.0 min	9.794	9.783	23.42	22.90	9.37	9.16
		10.0 min	9.793	9.774	27.09	26.24	10.84	10.50
		60.0 min	9.778	9.793	28.69	28.99	11.47	11.60
		240.0 min	9.761	9.791	28.78	29.50	11.51	11.80
		Score1:	0.36	DU sum difference:-0.48 u				
Score2:	0.79							
HC012-043	1	0.0 min	12.929	12.894	0.00	0.00	0.00	0.00
		0.5 min	12.921	12.904	6.63	6.42	1.92	1.86
		1.0 min	12.944	12.940	7.22	7.10	2.10	2.06
		10.0 min	12.919	12.902	8.15	8.61	2.36	2.50
		60.0 min	12.915	12.931	11.52	11.45	3.34	3.32
		240.0 min	12.909	12.910	14.95	15.42	4.34	4.47
		Score1:	0.15	DU sum difference: 0.15 u				
Score2:	0.32							

Molecule HC: Peptides with sufficient kinetics data, part 2

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC019-037	1	0.0 min	7.989	7.965	0.00	0.00	0.00	0.00
		0.5 min	7.987	7.973	0.00	0.00	0.00	0.00
		1.0 min	7.988	7.990	0.00	0.00	0.00	0.00
		10.0 min	7.967	7.976	0.00	0.06	0.00	0.01
		60.0 min	7.967	7.990	0.60	0.71	0.11	0.13
		240.0 min	7.959	7.989	2.59	2.28	0.47	0.41
Score1:	0.04	DU sum difference:-0.03 u						
Score2:	0.11							
HC024-032	1	0.0 min	12.452	12.452	0.00	0.00	0.00	0.00
		0.5 min	12.452	12.453	34.30	32.45	2.74	2.60
		1.0 min	12.456	12.458	35.54	34.97	2.84	2.80
		10.0 min	12.455	12.442	<b>34.33</b>	<b>35.40</b>	<b>2.75</b>	<b>2.83</b>
		60.0 min	12.445	12.459	37.61	39.00	3.01	3.12
		240.0 min	12.448	12.460	39.61	41.78	3.17	3.34
Score1:	0.37	DU sum difference: 0.11 u						
Score2:	<b>1.70p</b>							
HC026-057	1	0.0 min	12.786	12.771	0.38	0.00	0.11	0.00
		0.5 min	12.781	12.781	5.11	4.99	1.53	1.50
		1.0 min	12.781	12.786	5.76	5.56	1.73	1.67
		10.0 min	12.771	12.769	6.75	7.06	2.03	2.12
		60.0 min	12.767	12.783	10.64	10.79	3.19	3.24
		240.0 min	12.759	12.783	14.25	14.85	4.27	4.45
Score1:	0.11	DU sum difference: 0.11 u						
Score2:	0.42							
HC027-031	1	0.0 min	10.195	10.180	0.40	0.00	0.02	0.00
		0.5 min	10.164	10.171	41.54	33.31	1.66	1.33
		1.0 min	10.178	10.161	<b>44.55</b>	<b>37.32</b>	<b>1.78</b>	<b>1.49</b>
		10.0 min	10.169	10.152	40.94	40.94	1.64	1.64
		60.0 min	10.166	10.164	42.94	42.34	1.72	1.69
		240.0 min	10.181	10.164	42.34	42.34	1.69	1.69
Score1:	<b>3.00</b>	DU sum difference:-0.44 u						
Score2:	2.68							
HC027-032	1	0.0 min	12.120	12.120	0.00	0.00	0.00	0.00
		0.5 min	12.105	12.120	21.07	18.66	1.05	0.93
		1.0 min	12.117	12.121	22.48	21.67	1.12	1.08
		10.0 min	12.117	12.106	<b>21.45</b>	<b>22.88</b>	<b>1.07</b>	<b>1.14</b>
		60.0 min	12.109	12.118	27.12	27.89	1.36	1.39
		240.0 min	12.109	12.120	30.70	32.43	1.54	1.62
Score1:	0.23	DU sum difference:-0.04 u						
Score2:	<b>1.66</b>							
HC035-047	1	0.0 min	9.678	9.646	0.40	0.03	0.04	0.00
		0.5 min	9.669	9.655	5.92	5.19	0.65	0.57
		1.0 min	9.669	9.669	6.12	5.95	0.67	0.66
		10.0 min	9.655	9.656	9.53	10.37	1.05	1.14
		60.0 min	9.648	9.669	18.23	18.57	2.01	2.04
		240.0 min	9.640	9.670	22.72	24.04	2.50	2.64
Score1:	0.37	DU sum difference: 0.14 u						
Score2:	0.91							
HC035-050	1	0.0 min	8.990	8.966	0.00	0.00	0.00	0.00
		0.5 min	8.979	8.976	6.02	5.57	0.84	0.78
		1.0 min	8.979	8.982	6.32	6.20	0.89	0.87
		10.0 min	8.974	8.969	9.77	10.03	1.37	1.40
		60.0 min	8.969	8.983	16.74	17.04	2.34	2.39
		240.0 min	8.963	8.984	20.94	21.67	2.93	3.03
Score1:	0.21	DU sum difference: 0.10 u						
Score2:	0.45							

Molecule HC: Peptides with sufficient kinetics data, part 3

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC036-047	1	0.0 min	8.845	8.822	0.09	0.09	0.01	0.01
		0.5 min	8.833	8.821	6.97	6.53	0.70	0.65
		1.0 min	8.835	8.822	7.34	7.05	0.73	0.70
		10.0 min	8.814	8.822	11.90	12.32	1.19	1.23
		60.0 min	8.817	8.833	21.72	22.31	2.17	2.23
		240.0 min	8.805	8.832	<b>27.18</b>	28.05	<b>2.72</b>	2.81
		Score1: Score2:	0.09 0.50	DU sum difference: 0.04 u				
HC036-049	1	0.0 min	9.246	9.233	0.00	0.00	0.00	0.00
		0.5 min	9.243	9.230	6.37	5.23	0.76	0.63
		1.0 min	9.244	9.238	6.62	6.32	0.79	0.76
		10.0 min	9.229	9.231	10.38	10.47	1.25	1.26
		60.0 min	9.219	9.244	18.42	18.52	2.21	2.22
		240.0 min	9.214	9.247	22.68	23.88	2.72	2.87
		Score1: Score2:	0.01 0.68	DU sum difference: -0.01 u				
HC037-050	1	0.0 min	7.939	7.916	0.00	0.00	0.00	0.00
		0.5 min	7.933	7.913	8.25	7.98	0.99	0.96
		1.0 min	7.931	7.936	8.61	8.61	1.03	1.03
		10.0 min	7.913	7.918	13.65	13.81	1.64	1.66
		60.0 min	7.912	7.927	22.65	22.66	2.72	2.72
		240.0 min	7.902	7.924	<b>27.56</b>	28.29	<b>3.31</b>	3.40
		Score1: Score2:	0.03 0.13	DU sum difference: -0.01 u				
HC051-068	1	0.0 min	9.709	9.706	0.00	0.00	0.00	0.00
		0.5 min	9.699	9.707	19.79	<b>18.78</b>	3.17	<b>3.00</b>
		1.0 min	9.700	9.703	<b>19.17</b>	19.17	<b>3.07</b>	3.07
		10.0 min	9.702	9.695	29.44	30.30	4.71	4.85
		60.0 min	9.692	9.699	37.53	37.53	6.00	6.00
		240.0 min	9.680	9.707	38.67	40.54	6.19	6.49
		Score1: Score2:	0.99 0.99	DU sum difference: 0.65 u				
HC051-079	1	0.0 min	9.270	9.266	0.20	0.20	0.05	0.05
		0.5 min	9.276	9.263	13.95	12.74	3.77	3.44
		1.0 min	9.272	9.269	15.70	15.09	4.24	4.07
		10.0 min	9.254	9.253	22.47	22.87	6.07	6.17
		60.0 min	9.239	9.251	30.70	31.10	8.29	8.40
		240.0 min	9.238	9.253	32.91	34.28	8.89	9.25
		Score1: Score2:	0.10 0.96	DU sum difference: 0.10 u				
HC057-068	1	0.0 min	9.025	9.008	0.00	0.00	0.00	0.00
		0.5 min	9.031	9.021	<b>9.97</b>	8.84	<b>1.00</b>	0.88
		1.0 min	9.031	9.023	11.84	<b>11.39</b>	1.18	<b>1.14</b>
		10.0 min	9.015	9.013	25.32	25.89	2.53	2.59
		60.0 min	9.005	9.021	37.44	38.04	3.74	3.80
		240.0 min	9.002	9.019	39.86	40.94	3.99	4.09
		Score1: Score2:	0.81 0.81	DU sum difference: 0.34 u				
HC057-079	1	0.0 min	8.725	8.724	0.00	0.00	0.00	0.00
		0.5 min	8.728	8.723	11.16	9.69	2.34	2.03
		1.0 min	8.723	8.729	<b>12.78</b>	12.65	<b>2.68</b>	2.66
		10.0 min	8.721	8.713	20.28	20.81	4.26	4.37
		60.0 min	8.717	8.728	30.31	30.90	6.36	6.49
		240.0 min	8.711	8.728	33.28	34.89	6.99	7.33
		Score1: Score2:	0.41 <b>1.05p</b>	DU sum difference: 0.32 u				

Molecule HC: Peptides with sufficient kinetics data, part 4

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC058-079	1	0.0 min	8.234	8.206	0.00	0.00	0.00	0.00
		0.5 min	8.234	8.216	12.22	11.09	2.44	2.22
		1.0 min	8.223	8.227	13.94	13.76	2.79	2.75
		10.0 min	8.208	8.215	<b>21.94</b>	22.48	<b>4.39</b>	4.50
		60.0 min	8.197	8.210	32.23	32.83	6.45	6.57
		240.0 min	8.191	8.216	35.37	37.12	7.07	7.42
		Score1: 0.34	DU sum difference: 0.25 u					
Score2: <b>1.02p</b>								
HC065-101	1	0.0 min	13.413	13.412	0.20	0.00	0.07	0.00
		0.5 min	13.413	13.412	4.98	4.47	1.79	1.61
		1.0 min	13.397	13.435	5.11	5.08	1.84	1.83
		10.0 min	13.398	13.414	6.00	6.33	2.16	2.28
		60.0 min	13.381	13.418	8.79	8.73	3.16	3.14
		240.0 min	13.389	13.417	11.65	12.35	4.19	4.44
		Score1: 0.07	DU sum difference: 0.08 u					
Score2: 0.44								
HC069-079	1	0.0 min	4.824	4.822	0.00	0.00	0.00	0.00
		0.5 min	4.812	4.803	27.49	26.70	2.75	2.67
		1.0 min	4.811	4.808	30.52	29.90	3.05	2.99
		10.0 min	4.803	4.792	34.51	34.71	3.45	3.47
		60.0 min	4.795	4.809	42.56	42.35	4.26	4.23
		240.0 min	4.790	4.801	45.95	45.94	4.59	4.59
		Score1: 0.42	DU sum difference: -0.14 u					
Score2: 0.44								
HC069-080	1	0.0 min	6.160	6.165	0.00	0.00	0.00	0.00
		0.5 min	6.161	6.146	23.48	21.87	2.58	2.41
		1.0 min	6.160	6.154	25.69	24.68	2.83	2.72
		10.0 min	6.154	6.145	28.90	27.89	3.18	3.07
		60.0 min	6.144	6.155	35.72	34.92	3.93	3.84
		240.0 min	6.148	6.153	39.53	37.32	4.35	4.11
		Score1: <b>1.96</b>	DU sum difference: -0.73 u					
Score2: 1.60								
HC070-078	1	0.0 min	4.824	4.812	0.00	0.00	0.00	0.00
		0.5 min	4.804	4.798	29.90	28.29	2.39	2.26
		1.0 min	4.800	4.804	31.59	32.86	2.53	2.63
		10.0 min	4.791	4.789	39.33	37.53	3.15	3.00
		60.0 min	4.791	4.804	45.45	45.95	3.64	3.68
		240.0 min	4.786	4.795	<b>48.16</b>	49.37	<b>3.85</b>	3.95
		Score1: 0.53	DU sum difference: -0.16 u					
Score2: <b>1.50</b>								
HC080-083	1	0.0 min	9.808	9.808	0.00	0.00	0.00	0.00
		0.5 min	9.808	9.808	0.40	0.60	0.01	0.02
		1.0 min	9.808	9.808	1.00	1.00	0.03	0.03
		10.0 min	9.811	9.802	1.20	0.60	0.04	0.02
		60.0 min	9.808	9.808	2.21	1.00	0.07	0.03
		240.0 min	9.808	9.813	4.41	4.21	0.13	0.13
		Score1: 0.53	DU sum difference: -0.05 u					
Score2: 0.53								
HC084-093	1	0.0 min	5.957	5.944	0.00	0.00	0.00	0.00
		0.5 min	5.953	5.943	13.66	13.43	1.23	1.21
		1.0 min	5.952	5.954	13.85	13.45	1.25	1.21
		10.0 min	5.950	5.940	13.84	14.06	1.25	1.27
		60.0 min	5.942	5.952	15.31	15.44	1.38	1.39
		240.0 min	5.939	5.945	18.25	18.64	1.64	1.68
		Score1: 0.03	DU sum difference: 0.01 u					
Score2: 0.33								

Molecule HC: Peptides with sufficient kinetics data, part 5

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC087-093	1	0.0 min	4.255	4.250	0.00	0.00	0.00	0.00
		0.5 min	4.248	4.248	8.36	8.15	0.50	0.49
		1.0 min	4.250	4.248	8.25	8.28	0.50	0.50
		10.0 min	4.262	4.245	8.18	8.29	0.49	0.50
		60.0 min	4.247	4.251	8.36	8.54	0.50	0.51
		240.0 min	4.243	4.248	8.88	9.12	0.53	0.55
		Score1: Score2:	0.10 0.19	DU sum difference: 0.02 u				
HC089-127	1	0.0 min	7.544	7.534	0.00	0.00	0.00	0.00
		0.5 min	7.540	7.521	6.41	6.01	2.44	2.28
		1.0 min	7.534	7.536	7.82	7.30	2.97	2.77
		10.0 min	7.529	7.531	10.10	9.57	3.84	3.63
		60.0 min	7.536	7.532	11.82	11.70	4.49	4.45
		240.0 min	7.529	7.528	13.76	13.75	5.23	5.23
		Score1: Score2:	0.47 0.38	DU sum difference:-0.60 u				
HC094-109	1	0.0 min	7.857	7.841	0.00	0.00	0.00	0.00
		0.5 min	7.854	7.848	33.42	31.91	5.01	4.79
		1.0 min	7.853	7.855	34.58	34.43	5.19	5.16
		10.0 min	7.843	7.843	35.35	36.11	5.30	5.42
		60.0 min	7.839	7.856	36.22	36.22	5.43	5.43
		240.0 min	7.835	7.856	36.52	37.49	5.48	5.62
		Score1: Score2:	0.02 0.82	DU sum difference: 0.01 u				
HC094-110	1	0.0 min	8.913	8.885	0.00	0.00	0.00	0.00
		0.5 min	8.908	8.887	35.87	33.24	5.74	5.32
		1.0 min	8.912	8.902	36.98	36.02	5.92	5.76
		10.0 min	8.890	8.887	38.27	39.43	6.12	6.31
		60.0 min	8.894	8.894	41.21	41.80	6.59	6.69
		240.0 min	8.897	8.898	42.24	41.78	6.76	6.69
		Score1: Score2:	0.68 <b>1.40</b>	DU sum difference:-0.37 u				
HC094-137	1	0.0 min	9.707	9.684	0.00	0.00	0.00	0.00
		0.5 min	9.680	9.690	21.81	19.48	8.51	7.60
		1.0 min	9.686	9.684	23.75	22.78	9.26	8.88
		10.0 min	9.685	9.683	26.44	26.38	10.31	10.29
		60.0 min	9.678	9.685	28.44	28.92	11.09	11.28
		240.0 min	9.671	9.692	28.45	28.91	11.10	11.27
		Score1: Score2:	0.72 <b>1.04</b>	DU sum difference:-0.95 u				
HC095-112	1	0.0 min	8.686	8.674	0.00	0.00	0.00	0.00
		0.5 min	8.680	8.671	30.22	28.23	5.14	4.80
		1.0 min	8.680	8.679	31.51	31.45	5.36	5.35
		10.0 min	8.677	8.669	34.38	34.33	5.85	5.84
		60.0 min	8.672	8.676	36.89	37.20	6.27	6.32
		240.0 min	8.673	8.676	36.64	38.30	6.23	6.51
		Score1: Score2:	0.04 0.98	DU sum difference:-0.02 u				
HC105-143	1	0.0 min	13.165	13.145	0.20	0.13	0.07	0.04
		0.5 min	13.159	13.154	5.65	5.57	1.92	1.90
		1.0 min	13.165	13.172	6.10	6.08	2.07	2.07
		10.0 min	13.144	13.156	7.17	7.23	2.44	2.46
		60.0 min	13.142	13.168	9.89	9.90	3.36	3.36
		240.0 min	13.138	13.160	12.75	12.81	4.34	4.35
		Score1: Score2:	0.01 0.07	DU sum difference:-0.01 u				

Molecule HC: Peptides with sufficient kinetics data, part 6

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC111-120	1	0.0 min	10.269	10.262	0.00	0.00	0.00	0.00
		0.5 min	10.257	10.273	20.74	<b>18.44</b>	1.87	<b>1.66</b>
		1.0 min	10.254	10.258	<b>22.20</b>	21.39	<b>2.00</b>	1.93
		10.0 min	10.275	10.241	28.11	28.90	2.53	2.60
		60.0 min	10.247	10.253	36.32	37.12	3.27	3.34
		240.0 min	10.250	10.256	39.71	40.19	3.57	3.62
		Score1:	0.75	DU sum difference: 0.28 u				
Score2:	0.75							
HC111-139	1	0.0 min	11.324	11.324	0.00	0.00	0.00	0.00
		0.5 min	11.322	11.324	15.84	14.54	3.80	3.49
		1.0 min	11.321	11.320	18.26	17.64	4.38	4.23
		10.0 min	11.322	11.310	22.63	22.71	5.43	5.45
		60.0 min	11.307	11.320	29.68	28.94	7.12	6.95
		240.0 min	11.306	11.321	32.94	34.33	7.91	8.24
		Score1:	0.35	DU sum difference: -0.29 u				
Score2:	<b>1.00</b>							
HC111-145	1	0.0 min	11.441	11.438	<b>0.80</b>	0.78	<b>0.24</b>	0.24
		0.5 min	11.437	11.440	19.60	18.15	5.88	5.45
		1.0 min	11.437	11.426	21.45	21.05	6.44	6.32
		10.0 min	11.438	11.426	24.28	25.25	7.28	7.57
		60.0 min	11.422	11.436	31.50	29.74	9.45	8.92
		240.0 min	11.416	11.436	32.92	33.59	9.88	10.08
		Score1:	0.64	DU sum difference: -0.71 u				
Score2:	<b>1.27p</b>							
HC112-120	1	0.0 min	9.765	9.759	0.25	0.00	0.02	0.00
		0.5 min	9.763	9.759	23.48	22.88	1.88	1.83
		1.0 min	9.761	9.756	25.44	24.87	2.04	1.99
		10.0 min	9.769	9.746	28.90	29.78	2.31	2.38
		60.0 min	9.760	9.762	35.36	36.28	2.83	2.90
		240.0 min	9.756	9.764	38.74	40.80	3.10	3.26
		Score1:	0.72	DU sum difference: 0.19 u				
Score2:	<b>1.27</b>							
HC112-139	1	0.0 min	11.032	11.056	0.00	0.00	0.00	0.00
		0.5 min	11.045	11.043	17.01	15.83	3.91	3.64
		1.0 min	11.041	11.040	19.02	18.05	4.37	4.15
		10.0 min	11.043	11.036	21.91	22.68	5.04	5.22
		60.0 min	11.029	11.043	27.26	27.49	6.27	6.32
		240.0 min	11.028	11.043	30.35	32.29	6.98	7.43
		Score1:	0.24	DU sum difference: 0.18 u				
Score2:	<b>1.23</b>							
HC112-145	1	0.0 min	11.152	11.186	<b>1.00</b>	<b>1.20</b>	<b>0.29</b>	<b>0.35</b>
		0.5 min	11.148	11.158	20.67	20.45	6.00	5.93
		1.0 min	11.142	11.159	22.41	22.62	6.50	6.56
		10.0 min	11.153	11.150	25.06	25.06	7.27	7.27
		60.0 min	11.146	11.146	28.56	29.19	8.28	8.46
		240.0 min	11.146	11.140	32.85	32.85	9.53	9.53
		Score1:	0.20	DU sum difference: 0.21 u				
Score2:	0.31							
HC113-120	1	0.0 min	7.617	7.623	0.00	0.00	0.00	0.00
		0.5 min	7.606	7.601	20.05	19.48	1.40	1.36
		1.0 min	7.607	7.606	20.44	<b>20.00</b>	1.43	<b>1.40</b>
		10.0 min	7.601	7.594	24.04	25.17	1.68	1.76
		60.0 min	7.594	7.607	33.01	32.71	2.31	2.29
		240.0 min	7.594	7.601	38.53	38.93	2.70	2.73
		Score1:	0.21	DU sum difference: 0.06 u				
Score2:	0.70							

Molecule HC: Peptides with sufficient kinetics data, part 7

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC113-139	1	0.0 min	10.222	10.226	0.00	0.00	0.00	0.00
		0.5 min	10.218	10.220	16.05	14.45	3.53	3.18
		1.0 min	10.221	10.218	17.26	<b>16.25</b>	3.80	<b>3.58</b>
		10.0 min	10.210	10.207	20.07	21.67	4.41	4.77
		60.0 min	10.218	10.224	25.93	25.65	5.71	5.64
		240.0 min	10.209	10.218	31.91	32.11	7.02	7.06
		Score1: 0.03	DU sum difference: -0.02 u					
Score2: <b>1.07</b>								
HC115-140	1	0.0 min	10.582	10.569	0.00	0.00	0.00	0.00
		0.5 min	10.592	10.575	22.28	20.26	4.68	4.25
		1.0 min	10.578	10.597	23.85	23.00	5.01	4.83
		10.0 min	10.589	10.590	28.27	29.30	5.94	6.15
		60.0 min	10.579	10.600	32.91	33.72	6.91	7.08
		240.0 min	10.580	10.604	<b>34.87</b>	35.94	<b>7.32</b>	7.55
		Score1: 0.34	DU sum difference: -0.26 u					
Score2: <b>1.37</b>								
HC118-156	1	0.0 min	10.805	10.794	0.00	0.16	0.00	0.05
		0.5 min	10.814	10.802	4.49	4.54	1.53	1.54
		1.0 min	10.815	10.819	4.93	5.33	1.68	1.81
		10.0 min	10.817	10.810	7.55	7.39	2.57	2.51
		60.0 min	10.800	10.819	10.68	11.50	3.63	3.91
		240.0 min	10.794	10.815	15.03	15.46	5.11	5.26
		Score1: 0.50	DU sum difference: 0.58 u					
Score2: 0.49								
HC119-139	1	0.0 min	9.110	9.090	0.00	0.00	0.00	0.00
		0.5 min	9.092	9.095	17.13	15.93	2.74	2.55
		1.0 min	9.093	9.100	19.39	18.94	3.10	3.03
		10.0 min	9.091	9.086	22.86	23.80	3.66	3.81
		60.0 min	9.078	9.097	26.69	26.96	4.27	4.31
		240.0 min	9.076	9.091	29.79	30.80	4.77	4.93
		Score1: 0.17	DU sum difference: 0.09 u					
Score2: 0.94								
HC119-142	1	0.0 min	8.807	8.797	0.00	0.00	0.00	0.00
		0.5 min	8.810	8.804	25.54	24.47	4.85	4.65
		1.0 min	8.800	8.814	28.66	26.62	5.44	5.06
		10.0 min	8.806	8.804	29.39	29.20	5.58	5.55
		60.0 min	8.793	8.807	31.30	32.31	5.95	6.14
		240.0 min	8.793	8.806	38.10	38.10	7.24	7.24
		Score1: 0.68	DU sum difference: -0.44 u					
Score2: <b>1.04</b>								
HC119-145	1	0.0 min	9.545	9.539	0.80	0.60	0.18	0.13
		0.5 min	9.533	9.536	25.08	25.28	5.52	5.56
		1.0 min	9.536	9.541	29.10	27.09	6.40	5.96
		10.0 min	9.536	9.528	31.71	<b>31.71</b>	6.98	<b>6.98</b>
		60.0 min	9.525	9.537	<b>32.71</b>	33.51	<b>7.20</b>	7.37
		240.0 min	9.522	9.538	36.21	36.21	7.97	7.97
		Score1: 0.73	DU sum difference: -0.66 u					
Score2: 0.87								
HC121-139	1	0.0 min	8.878	8.869	0.00	0.00	0.00	0.00
		0.5 min	8.876	8.878	19.55	17.90	2.74	2.51
		1.0 min	8.880	8.883	21.91	20.91	3.07	2.93
		10.0 min	8.877	8.875	24.73	25.54	3.46	3.58
		60.0 min	8.868	8.881	26.52	27.16	3.71	3.80
		240.0 min	8.866	8.881	<b>29.10</b>	<b>29.90</b>	<b>4.07</b>	<b>4.19</b>
		Score1: 0.39	DU sum difference: -0.20 u					
Score2: <b>1.19p</b>								



Molecule HC: Peptides with sufficient kinetics data, part 8

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC121-142	1	0.0 min	8.578	8.561	0.00	0.00	0.00	0.00
		0.5 min	8.567	8.562	28.60	26.74	4.86	4.55
		1.0 min	8.563	8.567	30.90	29.56	5.25	5.03
		10.0 min	8.561	8.559	32.71	33.01	5.56	5.61
		60.0 min	8.553	8.570	34.20	34.29	5.81	5.83
		240.0 min	8.549	8.558	35.37	36.84	6.01	6.26
		Score1:	0.39	DU sum difference: -0.23 u				
Score2:	<b>1.23</b>							
HC121-145	1	0.0 min	9.380	9.384	<b>2.01</b>	<b>1.86</b>	<b>0.40</b>	<b>0.37</b>
		0.5 min	9.370	9.370	28.09	28.09	5.62	5.62
		1.0 min	9.373	9.372	30.72	31.30	6.14	6.26
		10.0 min	9.374	9.373	33.91	33.91	6.78	6.78
		60.0 min	9.368	9.378	34.11	35.12	6.82	7.02
		240.0 min	9.366	9.381	35.66	36.72	7.13	7.34
		Score1:	0.86	DU sum difference: 0.64 u				
Score2:	0.77							
HC132-184	1	0.0 min	11.609	11.626	0.00	0.00	0.00	0.00
		0.5 min	11.610	11.612	3.52	3.61	1.65	1.70
		1.0 min	11.619	11.602	4.58	4.80	2.15	2.25
		10.0 min	11.598	11.610	6.42	8.43	3.02	3.96
		60.0 min	11.590	11.603	9.43	11.64	4.43	5.47
		240.0 min	11.597	11.599	15.25	15.25	7.17	7.17
		Score1:	<b>1.34</b>	DU sum difference: 2.13 u				
Score2:	1.09							
HC138-177	1	0.0 min	11.229	11.212	0.40	0.20	0.14	0.07
		0.5 min	11.230	11.218	4.41	4.41	1.59	1.59
		1.0 min	11.233	11.231	4.62	5.02	1.66	1.81
		10.0 min	11.218	11.216	6.62	7.83	2.38	2.82
		60.0 min	11.209	11.217	10.23	11.64	3.68	4.19
		240.0 min	11.201	11.224	14.05	15.25	5.06	5.49
		Score1:	<b>1.19</b>	DU sum difference: 1.44 u				
Score2:	1.07							
HC146-151	1	0.0 min	11.832	11.832	0.00	0.00	0.00	0.00
		0.5 min	11.829	11.832	0.00	0.00	0.00	0.00
		1.0 min	11.832	11.833	1.00	1.00	0.05	0.05
		10.0 min	11.832	11.813	1.00	1.00	0.05	0.05
		60.0 min	11.818	11.843	0.60	1.00	0.03	0.05
		240.0 min	11.825	11.839	<b>0.40</b>	0.60	<b>0.02</b>	0.03
		Score1:	0.13	DU sum difference: 0.02 u				
Score2:	0.12							
HC146-161	1	0.0 min	13.370	13.361	0.00	0.00	0.00	0.00
		0.5 min	13.366	13.361	0.75	0.72	0.10	0.09
		1.0 min	13.368	13.390	1.51	1.17	0.20	0.15
		10.0 min	13.363	13.363	2.77	3.12	0.36	0.41
		60.0 min	13.358	13.375	5.79	6.59	0.75	0.86
		240.0 min	13.349	13.372	6.72	6.88	0.87	0.89
		Score1:	0.27	DU sum difference: 0.12 u				
Score2:	0.40							
HC151-161	1	0.0 min	9.995	9.993	0.00	0.00	0.00	0.00
		0.5 min	10.001	10.004	3.09	3.04	0.25	0.24
		1.0 min	10.004	9.994	3.50	3.61	0.28	0.29
		10.0 min	9.997	9.994	10.88	10.91	0.87	0.87
		60.0 min	9.989	10.003	23.28	23.28	1.86	1.86
		240.0 min	9.981	10.001	25.09	25.49	2.01	2.04
		Score1:	0.15	DU sum difference: 0.04 u				
Score2:	0.14							

Molecule HC: Peptides with sufficient kinetics data, part 9

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC152-161	1	0.0 min	9.388	9.381	0.01	0.00	0.00	0.00
		0.5 min	9.390	9.386	2.22	2.23	0.16	0.16
		1.0 min	9.385	9.389	3.02	3.04	0.21	0.21
		10.0 min	9.383	9.379	11.83	11.85	0.83	0.83
		60.0 min	9.372	9.385	24.88	24.90	1.74	1.74
		240.0 min	9.372	9.388	26.93	29.39	1.89	2.06
		Score1:	0.75	DU sum difference: 0.18 u				
Score2:	0.62							
HC152-164	1	0.0 min	13.017	13.003	0.00	0.00	0.00	0.00
		0.5 min	13.019	13.007	10.03	<b>9.43</b>	1.00	<b>0.94</b>
		1.0 min	13.028	13.022	11.92	11.72	1.19	1.17
		10.0 min	13.003	13.007	<b>21.07</b>	21.73	<b>2.11</b>	2.17
		60.0 min	13.005	13.017	28.90	28.70	2.89	2.87
		240.0 min	12.993	13.019	29.50	30.30	2.95	3.03
		Score1:	0.15	DU sum difference: 0.06 u				
Score2:	0.44							
HC160-195	1	0.0 min	12.442	12.424	0.57	0.32	0.19	0.10
		0.5 min	12.441	12.424	5.58	4.98	1.84	1.64
		1.0 min	12.440	12.442	6.18	5.90	2.04	1.95
		10.0 min	12.422	12.429	6.98	7.41	2.30	2.44
		60.0 min	12.414	12.437	10.28	10.33	3.39	3.41
		240.0 min	12.401	12.436	13.44	14.32	4.44	4.73
		Score1:	0.07	DU sum difference: 0.07 u				
Score2:	0.60							
HC161-183	1	0.0 min	14.792	14.791	0.02	0.19	0.00	0.04
		0.5 min	14.789	14.786	<b>9.31</b>	7.07	<b>1.96</b>	1.48
		1.0 min	14.789	14.806	7.49	7.56	1.57	1.59
		10.0 min	14.787	14.786	8.12	8.43	1.70	1.77
		60.0 min	14.779	14.793	10.83	10.91	2.27	2.29
		240.0 min	14.777	14.791	14.48	14.09	3.04	2.96
		Score1:	0.08	DU sum difference: 0.06 u				
Score2:	0.30							
HC162-169	1	0.0 min	10.815	10.822	0.00	0.00	0.00	0.00
		0.5 min	10.813	10.814	24.94	22.18	1.75	1.55
		1.0 min	10.817	10.815	30.39	30.11	2.13	2.11
		10.0 min	10.815	10.804	38.19	40.00	2.67	2.80
		60.0 min	10.802	10.810	42.77	43.02	2.99	3.01
		240.0 min	10.803	10.814	43.87	45.88	3.07	3.21
		Score1:	0.31	DU sum difference: 0.07 u				
Score2:	<b>1.73</b>							
HC162-180	1	0.0 min	12.889	12.893	0.00	0.00	0.00	0.00
		0.5 min	12.891	12.890	15.37	13.58	2.61	2.31
		1.0 min	12.887	12.898	18.66	17.66	3.17	3.00
		10.0 min	12.887	12.881	21.27	22.88	3.62	3.89
		60.0 min	12.877	12.892	23.48	23.77	3.99	4.04
		240.0 min	12.869	12.890	24.05	25.63	4.09	4.36
		Score1:	0.20	DU sum difference: 0.12 u				
Score2:	<b>1.52</b>							
HC163-180	1	0.0 min	12.683	12.678	0.46	0.56	0.07	0.09
		0.5 min	12.681	12.675	16.52	12.57	2.64	2.01
		1.0 min	12.671	12.679	18.73	17.47	3.00	2.79
		10.0 min	12.665	12.671	19.79	21.07	3.17	3.37
		60.0 min	12.663	12.682	21.67	21.60	3.47	3.46
		240.0 min	12.660	12.679	21.33	23.06	3.41	3.69
		Score1:	0.64	DU sum difference: -0.35 u				
Score2:	<b>2.03</b>							

Molecule HC: Peptides with sufficient kinetics data, part 10

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC164-180	1	0.0 min	12.566	12.551	0.20	0.00	0.03	0.00
		0.5 min	12.562	12.555	18.04	15.57	2.71	2.34
		1.0 min	12.559	12.570	20.34	20.59	3.05	3.09
		10.0 min	12.551	12.550	21.98	23.36	3.30	3.50
		60.0 min	12.546	12.560	23.49	23.85	3.52	3.58
		240.0 min	12.541	12.558	22.77	26.80	3.42	4.02
		Score1:	0.99	DU sum difference: 0.50 u				
Score2:	<b>2.10</b>							
HC165-180	1	0.0 min	11.493	11.488	0.00	0.00	0.00	0.00
		0.5 min	11.483	11.479	15.91	12.19	2.23	1.71
		1.0 min	11.483	11.491	18.83	17.41	2.64	2.44
		10.0 min	11.484	11.485	19.48	20.97	2.73	2.94
		60.0 min	11.481	11.488	20.59	21.69	2.88	3.04
		240.0 min	11.482	11.491	20.93	22.74	2.93	3.18
		Score1:	0.22	DU sum difference: -0.10 u				
Score2:	<b>2.31</b>							
HC170-180	1	0.0 min	10.830	10.827	0.01	0.05	0.00	0.00
		0.5 min	10.834	10.833	12.73	11.50	1.15	1.03
		1.0 min	10.835	10.837	16.53	15.73	1.49	1.42
		10.0 min	10.829	10.832	20.30	21.31	1.83	1.92
		60.0 min	10.827	10.838	21.19	21.90	1.91	1.97
		240.0 min	10.817	10.844	22.84	23.44	2.06	2.11
		Score1:	0.09	DU sum difference: 0.03 u				
Score2:	<b>1.06</b>							
HC170-180	2	0.0 min	11.189	11.170	0.01	0.01	0.00	0.00
		0.5 min	11.184	11.178	12.64	11.45	1.14	1.03
		1.0 min	11.194	11.186	16.10	15.66	1.45	1.41
		10.0 min	11.173	11.182	21.47	22.68	1.93	2.04
		60.0 min	11.182	11.187	23.48	22.90	2.11	2.06
		240.0 min	11.168	11.200	23.67	24.88	2.13	2.24
		Score1:	0.06	DU sum difference: 0.02 u				
Score2:	<b>1.12</b>							
HC175-182	1	0.0 min	11.861	11.899	0.00	0.00	0.00	0.00
		0.5 min	11.863	11.882	5.49	5.23	0.33	0.31
		1.0 min	11.880	11.873	7.69	6.67	0.46	0.40
		10.0 min	11.888	11.871	18.01	18.79	1.08	1.13
		60.0 min	11.870	11.878	20.94	21.62	1.26	1.30
		240.0 min	11.870	11.877	<b>19.32</b>	<b>20.76</b>	<b>1.16</b>	<b>1.25</b>
		Score1:	0.06	DU sum difference: 0.01 u				
Score2:	0.80							
HC185-190	1	0.0 min	6.578	6.572	0.00	0.00	0.00	0.00
		0.5 min	6.569	6.572	3.41	3.61	0.17	0.18
		1.0 min	6.575	6.578	3.41	3.44	0.17	0.17
		10.0 min	6.578	6.561	3.21	3.61	0.16	0.18
		60.0 min	6.561	6.575	3.61	3.41	0.18	0.17
		240.0 min	6.564	6.575	3.81	4.01	0.19	0.20
		Score1:	0.19	DU sum difference: 0.03 u				
Score2:	0.25							
HC185-201	1	0.0 min	11.603	11.612	0.00	0.00	0.00	0.00
		0.5 min	11.607	11.613	7.58	6.23	1.06	0.87
		1.0 min	11.602	11.594	8.19	8.70	1.15	1.22
		10.0 min	11.595	11.586	10.48	10.81	1.47	1.51
		60.0 min	11.600	11.592	14.24	14.43	1.99	2.02
		240.0 min	11.610	11.610	16.86	21.38	2.36	2.99
		Score1:	<b>1.25</b>	DU sum difference: 0.59 u				
Score2:	1.67							

Molecule HC: Peptides with sufficient kinetics data, part 11

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC185-202	1	0.0 min	11.436	11.473	0.65	0.04	0.10	0.01
		0.5 min	11.458	11.473	7.46	6.44	1.12	0.97
		1.0 min	11.444	11.458	<b>6.04</b>	8.65	<b>0.91</b>	1.30
		10.0 min	11.491	11.455	10.23	12.94	1.53	1.94
		60.0 min	11.461	11.460	12.99	13.22	1.95	1.98
		240.0 min	11.488	11.464	15.95	16.91	2.39	2.54
	Score1:	0.74	DU sum difference: 0.41 u					
	Score2:	<b>1.61</b>						
HC191-201	1	0.0 min	9.921	9.947	0.00	0.80	0.00	0.06
		0.5 min	9.939	9.952	21.53	18.70	1.72	1.50
		1.0 min	9.940	9.943	24.97	23.58	2.00	1.89
		10.0 min	9.956	9.932	30.52	31.76	2.44	2.54
		60.0 min	9.933	9.941	36.71	37.36	2.94	2.99
		240.0 min	9.935	9.944	37.84	39.53	3.03	3.16
	Score1:	0.05	DU sum difference: 0.01 u					
	Score2:	<b>2.08</b>						
HC191-202	1	0.0 min	9.821	9.823	0.60	0.80	0.05	0.07
		0.5 min	9.815	9.823	18.45	18.86	1.66	1.70
		1.0 min	9.815	9.817	24.74	23.88	2.23	2.15
		10.0 min	9.826	9.810	31.42	31.91	2.83	2.87
		60.0 min	9.814	9.825	35.69	36.79	3.21	3.31
		240.0 min	9.809	9.820	38.41	39.33	3.46	3.54
	Score1:	0.67	DU sum difference: 0.20 u					
	Score2:	0.96						
HC210-239	1	0.0 min	12.395	12.394	0.00	0.00	0.00	0.00
		0.5 min	12.385	12.386	30.59	27.74	7.65	6.93
		1.0 min	12.385	12.388	32.71	31.51	8.18	7.88
		10.0 min	12.385	12.382	<b>36.45</b>	38.33	<b>9.11</b>	9.58
		60.0 min	12.380	12.388	40.85	42.73	10.21	10.68
		240.0 min	12.373	12.380	43.05	<b>45.32</b>	10.76	<b>11.33</b>
	Score1:	0.79	DU sum difference: -0.82 u					
	Score2:	<b>2.15</b>						
HC212-229	1	0.0 min	9.128	9.114	0.00	0.00	0.00	0.00
		0.5 min	9.128	9.117	4.82	4.49	0.72	0.67
		1.0 min	9.134	9.134	4.88	4.69	0.73	0.70
		10.0 min	9.120	9.135	7.78	8.77	1.17	1.31
		60.0 min	9.118	9.140	13.85	14.96	2.08	2.24
		240.0 min	9.117	9.135	18.33	18.66	2.75	2.80
	Score1:	0.56	DU sum difference: 0.29 u					
	Score2:	0.71						
HC214-225	1	0.0 min	9.813	9.808	0.00	0.00	0.00	0.00
		0.5 min	9.814	9.809	5.22	4.64	0.52	0.46
		1.0 min	9.812	9.818	7.49	7.42	0.75	0.74
		10.0 min	9.809	9.806	14.65	17.39	1.46	1.74
		60.0 min	9.799	9.814	22.78	23.25	2.28	2.33
		240.0 min	9.794	9.817	24.31	32.31	2.43	3.23
	Score1:	<b>3.13</b>	DU sum difference: 1.06 u					
	Score2:	2.87						
HC219-253	1	0.0 min	10.718	10.702	0.00	0.00	0.00	0.00
		0.5 min	10.716	10.709	3.91	4.01	1.10	1.12
		1.0 min	10.715	10.714	4.47	5.00	1.25	1.40
		10.0 min	10.714	10.712	7.10	7.67	1.99	2.15
		60.0 min	10.701	10.724	10.92	12.00	3.06	3.36
		240.0 min	10.697	10.723	16.10	16.88	4.51	4.73
	Score1:	0.91	DU sum difference: 0.86 u					
	Score2:	0.74						

Molecule HC: Peptides with sufficient kinetics data, part 12

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC240-251	1	0.0 min	10.988	10.965	0.35	0.14	0.03	0.01
		0.5 min	10.986	10.985	7.16	7.92	0.57	0.63
		1.0 min	10.980	10.980	10.40	<b>9.89</b>	0.83	<b>0.79</b>
		10.0 min	10.979	10.967	18.64	20.74	1.49	1.66
		60.0 min	10.964	10.985	22.23	26.77	1.78	2.14
		240.0 min	10.959	10.982	27.33	37.91	2.19	3.03
		Score1:	<b>5.11p</b>	<b>DU sum difference: 1.38 u</b>				
Score2:	4.52p							
HC240-252	1	0.0 min	10.386	10.360	0.08	0.00	0.01	0.00
		0.5 min	10.379	10.371	6.47	5.88	0.58	0.53
		1.0 min	10.377	10.377	9.45	9.18	0.85	0.83
		10.0 min	10.365	10.370	16.73	19.78	1.51	1.78
		60.0 min	10.366	10.375	21.77	28.84	1.96	2.60
		240.0 min	10.352	10.376	29.30	41.38	2.64	3.72
		Score1:	<b>6.30</b>	<b>DU sum difference: 1.91 u</b>				
Score2:	5.60							
HC241-251	1	0.0 min	10.415	10.409	0.00	0.00	0.00	0.00
		0.5 min	10.417	10.405	6.82	6.22	0.48	0.44
		1.0 min	10.416	10.415	11.04	10.23	0.77	0.72
		10.0 min	10.406	10.404	19.67	21.87	1.38	1.53
		60.0 min	10.400	10.418	22.88	27.77	1.60	1.94
		240.0 min	10.390	10.419	25.49	35.92	1.78	2.51
		Score1:	<b>4.78</b>	<b>DU sum difference: 1.13 u</b>				
Score2:	4.58							
HC241-252	1	0.0 min	9.813	9.808	0.00	0.00	0.00	0.00
		0.5 min	9.815	9.809	6.42	5.82	0.51	0.47
		1.0 min	9.812	9.818	9.83	9.25	0.79	0.74
		10.0 min	9.809	9.806	18.26	21.23	1.46	1.70
		60.0 min	9.799	9.814	23.97	28.77	1.92	2.30
		240.0 min	9.794	9.816	28.95	40.31	2.32	3.22
		Score1:	<b>5.32</b>	<b>DU sum difference: 1.44 u</b>				
Score2:	4.91							
HC242-252	1	0.0 min	7.828	7.814	0.00	0.00	0.00	0.00
		0.5 min	7.816	7.804	8.83	8.03	0.62	0.56
		1.0 min	7.819	7.817	12.84	12.04	0.90	0.84
		10.0 min	7.802	7.802	23.28	25.69	1.63	1.80
		60.0 min	7.789	7.809	28.50	36.12	1.99	2.53
		240.0 min	7.781	7.802	37.53	50.37	2.63	3.53
		Score1:	<b>6.30</b>	<b>DU sum difference: 1.49 u</b>				
Score2:	5.92							
HC243-251	1	0.0 min	10.413	10.402	0.00	0.00	0.00	0.00
		0.5 min	10.409	10.406	9.22	8.23	0.46	0.41
		1.0 min	10.414	10.414	13.82	12.84	0.69	0.64
		10.0 min	10.411	10.405	24.48	27.69	1.22	1.38
		60.0 min	10.402	10.414	28.70	34.31	1.43	1.72
		240.0 min	10.391	10.416	31.51	44.75	1.58	2.24
		Score1:	<b>5.96</b>	<b>DU sum difference: 1.01 u</b>				
Score2:	5.81							
HC243-252	1	0.0 min	9.815	9.804	0.00	0.00	0.00	0.00
		0.5 min	9.819	9.808	8.03	7.07	0.48	0.42
		1.0 min	9.811	9.822	12.04	11.44	0.72	0.69
		10.0 min	9.811	9.808	22.27	25.28	1.34	1.52
		60.0 min	9.801	9.816	27.49	35.12	1.65	2.11
		240.0 min	9.792	9.816	35.32	47.94	2.12	2.88
		Score1:	<b>6.43</b>	<b>DU sum difference: 1.30 u</b>				
Score2:	6.00							

Molecule HC: Peptides with sufficient kinetics data, part 13

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC252-261	1	0.0 min	8.813	8.794	0.00	0.39	0.00	0.03
		0.5 min	8.804	8.802	19.06	19.67	1.53	1.57
		1.0 min	8.806	8.805	19.87	20.66	1.59	1.65
		10.0 min	8.793	8.794	23.88	26.29	1.91	2.10
		60.0 min	8.786	8.804	32.91	34.31	2.63	2.75
		240.0 min	8.782	8.809	37.52	38.53	3.00	3.08
		Score1:	<b>1.96</b>	<b>DU sum difference: 0.53 u</b>				
Score2:	1.60							
HC253-261	1	0.0 min	8.420	8.406	0.00	0.00	0.00	0.00
		0.5 min	8.422	8.415	7.06	7.83	0.49	0.55
		1.0 min	8.425	8.425	<b>7.62</b>	<b>8.44</b>	<b>0.53</b>	<b>0.59</b>
		10.0 min	8.413	8.409	16.66	18.68	1.17	1.31
		60.0 min	8.407	8.422	26.08	28.29	1.83	1.98
		240.0 min	8.407	8.423	31.31	33.51	2.19	2.35
		Score1:	<b>2.34</b>	<b>DU sum difference: 0.61 u</b>				
Score2:	1.95p							
HC263-274	1	0.0 min	7.302	7.278	0.00	0.00	0.00	0.00
		0.5 min	7.292	7.281	<b>18.46</b>	18.26	<b>1.85</b>	1.83
		1.0 min	7.285	7.292	22.68	22.68	2.27	2.27
		10.0 min	7.281	7.274	32.11	<b>34.72</b>	3.21	<b>3.47</b>
		60.0 min	7.270	7.281	38.13	38.13	3.81	3.81
		240.0 min	7.268	7.281	40.74	40.74	4.07	4.07
		Score1:	0.00	<b>DU sum difference: 0.00 u</b>				
Score2:	0.00							
HC263-275	1	0.0 min	10.560	10.553	0.40	0.20	0.04	0.02
		0.5 min	10.557	10.560	18.72	16.94	2.06	1.86
		1.0 min	10.560	10.558	20.55	20.55	2.26	2.26
		10.0 min	10.560	10.549	<b>29.46</b>	32.77	<b>3.24</b>	3.60
		60.0 min	10.547	10.560	32.50	35.12	3.58	3.86
		240.0 min	10.545	10.562	39.33	<b>39.33</b>	4.33	<b>4.33</b>
		Score1:	0.23	<b>DU sum difference: 0.10 u</b>				
Score2:	<b>1.67</b>							
HC266-274	1	0.0 min	4.687	4.675	0.00	0.00	0.00	0.00
		0.5 min	4.686	4.677	22.72	20.68	1.59	1.45
		1.0 min	4.685	4.682	26.68	24.73	1.87	1.73
		10.0 min	4.684	4.669	<b>33.75</b>	<b>33.31</b>	<b>2.36</b>	<b>2.33</b>
		60.0 min	4.671	4.681	34.11	34.20	2.39	2.39
		240.0 min	4.668	4.676	36.74	36.65	2.57	2.57
		Score1:	<b>1.29</b>	<b>DU sum difference: -0.34 u</b>				
Score2:	1.11p							
HC266-275	1	0.0 min	9.286	9.260	0.01	0.00	0.00	0.00
		0.5 min	9.281	9.267	<b>17.65</b>	14.29	<b>1.41</b>	1.14
		1.0 min	9.281	9.281	22.27	20.08	1.78	1.61
		10.0 min	9.267	9.266	30.50	29.74	2.44	2.38
		60.0 min	9.258	9.283	31.68	32.09	2.53	2.57
		240.0 min	9.254	9.279	33.24	34.28	2.66	2.74
		Score1:	0.49	<b>DU sum difference: -0.15 u</b>				
Score2:	<b>1.28</b>							
HC272-294	1	0.0 min	11.509	11.481	0.40	0.60	0.08	0.13
		0.5 min	11.495	11.497	11.81	10.65	2.48	2.24
		1.0 min	11.501	11.493	11.08	11.67	2.33	2.45
		10.0 min	11.497	11.496	10.95	11.58	2.30	2.43
		60.0 min	11.488	11.510	13.57	13.37	2.85	2.81
		240.0 min	11.476	11.496	17.66	18.67	3.71	3.92
		Score1:	0.32	<b>DU sum difference: 0.22 u</b>				
Score2:	0.91							

Molecule HC: Peptides with sufficient kinetics data, part 14

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC278-281	1	0.0 min	5.706	5.716	0.00	0.00	0.00	0.00
		0.5 min	5.706	5.706	6.22	6.38	0.19	0.19
		1.0 min	5.707	5.707	6.82	7.37	0.20	0.22
		10.0 min	5.721	5.696	12.84	12.64	0.39	0.38
		60.0 min	5.707	5.713	19.67	19.87	0.59	0.60
		240.0 min	5.707	5.707	20.67	20.47	0.62	0.61
		Score1:	0.15	DU sum difference: 0.02 u				
Score2:	0.32							
HC280-292	1	0.0 min	9.332	9.311	0.71	0.33	0.08	0.04
		0.5 min	9.303	9.314	<b>9.53</b>	8.86	<b>1.05</b>	0.97
		1.0 min	9.316	9.302	11.80	<b>10.53</b>	1.30	<b>1.16</b>
		10.0 min	9.295	9.291	23.88	23.01	2.63	2.53
		60.0 min	9.285	9.299	33.28	34.91	3.66	3.84
		240.0 min	9.277	9.303	36.76	37.76	4.04	4.15
		Score1:	0.50	DU sum difference: 0.23 u				
Score2:	<b>1.41p</b>							
HC291-315	1	0.0 min	11.414	11.381	0.00	0.20	0.00	0.04
		0.5 min	11.432	11.410	5.89	4.94	1.30	1.09
		1.0 min	11.428	11.422	7.05	7.02	1.55	1.55
		10.0 min	11.425	11.438	10.64	10.69	2.34	2.35
		60.0 min	11.428	11.411	14.65	15.05	3.22	3.31
		240.0 min	11.423	11.426	16.17	16.74	3.56	3.68
		Score1:	0.07	DU sum difference: 0.06 u				
Score2:	0.53							
HC297-350	1	0.0 min	10.049	10.023	0.10	0.08	0.05	0.04
		0.5 min	10.055	10.034	5.16	5.28	2.48	2.53
		1.0 min	10.049	10.046	5.93	6.25	2.85	3.00
		10.0 min	10.034	10.051	8.53	9.12	4.09	4.38
		60.0 min	10.026	10.048	11.19	11.78	5.37	5.65
		240.0 min	10.020	10.059	13.94	15.27	6.69	7.33
		Score1:	0.87	DU sum difference: 1.41 u				
Score2:	0.72							
HC301-306	1	0.0 min	6.288	6.297	0.00	0.00	0.00	0.00
		0.5 min	6.291	6.295	1.44	2.14	0.07	0.11
		1.0 min	6.291	6.283	1.62	2.41	0.08	0.12
		10.0 min	6.274	6.283	3.07	3.79	0.15	0.19
		60.0 min	6.279	6.282	9.42	9.23	0.47	0.46
		240.0 min	6.262	6.282	20.90	19.71	1.05	0.99
		Score1:	0.24	DU sum difference: 0.04 u				
Score2:	0.86							
HC301-318	1	0.0 min	11.121	11.092	0.00	0.00	0.00	0.00
		0.5 min	11.130	11.101	1.92	1.81	0.31	0.29
		1.0 min	11.118	11.119	1.92	2.34	0.31	0.37
		10.0 min	11.108	11.119	4.04	4.38	0.65	0.70
		60.0 min	11.101	11.126	8.62	8.74	1.38	1.40
		240.0 min	11.092	11.125	13.04	14.42	2.09	2.31
		Score1:	0.63	DU sum difference: 0.34 u				
Score2:	0.57							
HC307-333	1	0.0 min	11.167	11.146	0.00	0.00	0.00	0.00
		0.5 min	11.166	11.162	4.54	4.64	1.04	1.07
		1.0 min	11.170	11.172	5.28	5.71	1.22	1.31
		10.0 min	11.173	11.174	8.70	9.32	2.00	2.14
		60.0 min	11.159	11.173	12.42	14.03	2.86	3.23
		240.0 min	11.150	11.160	16.07	19.03	3.70	4.38
		Score1:	<b>1.70</b>	DU sum difference: <b>1.32 u</b>				
Score2:	1.38							

Molecule HC: Peptides with sufficient kinetics data, part 15

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC308-340	1	0.0 min	10.978	10.958	0.19	0.11	0.06	0.03
		0.5 min	10.959	10.952	3.08	2.90	0.93	0.87
		1.0 min	10.955	10.963	3.54	3.44	1.06	1.03
		10.0 min	10.948	10.968	5.43	5.58	1.63	1.67
		60.0 min	10.971	10.969	9.47	10.86	2.84	3.26
		240.0 min	10.961	10.989	13.94	15.10	4.18	4.53
		Score1: Score2:	0.69 0.74	DU sum difference: 0.70 u				
HC318-359	1	0.0 min	8.728	8.716	0.11	0.07	0.04	0.02
		0.5 min	8.730	8.712	8.25	7.85	2.81	2.67
		1.0 min	8.728	8.733	<b>9.25</b>	9.64	<b>3.14</b>	3.28
		10.0 min	8.714	8.719	13.39	14.11	4.55	4.80
		60.0 min	8.706	8.725	16.37	17.11	5.56	5.82
		240.0 min	8.697	8.718	18.61	20.15	6.33	6.85
		Score1: Score2:	0.83 0.99	DU sum difference: 1.04 u				
HC319-333	1	0.0 min	9.379	9.372	0.00	0.00	0.00	0.00
		0.5 min	9.379	9.378	7.45	8.33	0.89	1.00
		1.0 min	9.383	9.385	10.29	<b>10.29</b>	1.23	<b>1.23</b>
		10.0 min	9.378	9.377	16.86	18.66	2.02	2.24
		60.0 min	9.372	9.390	22.13	23.68	2.66	2.84
		240.0 min	9.370	9.393	29.30	29.30	3.52	3.52
		Score1: Score2:	<b>1.25p</b> 1.02p	DU sum difference: 0.51 u				
HC326-348	1	0.0 min	7.475	7.451	0.01	0.00	0.00	0.00
		0.5 min	7.463	7.447	<b>16.25</b>	15.83	<b>2.93</b>	2.85
		1.0 min	7.464	7.470	18.86	<b>18.88</b>	3.40	<b>3.40</b>
		10.0 min	7.435	7.438	26.08	26.49	4.69	4.77
		60.0 min	7.427	7.446	28.88	29.15	5.20	5.25
		240.0 min	7.418	7.439	31.93	33.11	5.75	5.96
		Score1: Score2:	0.67 0.67	DU sum difference: 0.50 u				
HC334-348	1	0.0 min	3.580	3.587	0.00	0.00	0.00	0.00
		0.5 min	3.579	3.588	22.42	21.67	2.69	2.60
		1.0 min	3.580	3.587	24.88	24.23	2.99	2.91
		10.0 min	3.587	3.574	28.09	28.04	3.37	3.36
		60.0 min	3.574	3.587	28.44	28.24	3.41	3.39
		240.0 min	3.577	3.582	29.44	29.24	3.53	3.51
		Score1: Score2:	0.55 0.45	DU sum difference:-0.22 u				
HC334-361	1	0.0 min	5.389	5.375	0.00	0.00	0.00	0.00
		0.5 min	5.380	5.368	27.97	27.22	6.15	5.99
		1.0 min	5.382	5.379	30.60	29.52	6.73	6.50
		10.0 min	5.373	5.370	32.46	32.05	7.14	7.05
		60.0 min	5.367	5.384	32.60	32.52	7.17	7.15
		240.0 min	5.357	5.377	32.66	32.77	7.18	7.21
		Score1: Score2:	0.65 0.59	DU sum difference:-0.48 u				
HC334-365	1	0.0 min	6.768	6.751	0.00	0.00	0.00	0.00
		0.5 min	6.751	6.737	22.55	21.47	5.86	5.58
		1.0 min	6.756	6.758	24.79	24.24	6.45	6.30
		10.0 min	6.739	6.746	26.54	27.12	6.90	7.05
		60.0 min	6.732	6.758	27.07	27.25	7.04	7.08
		240.0 min	6.731	6.755	28.55	28.74	7.42	7.47
		Score1: Score2:	0.20 0.63	DU sum difference:-0.18 u				



Molecule HC: Peptides with sufficient kinetics data, part 16

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC334-368	1	0.0 min	7.742	7.723	0.00	0.00	0.00	0.00
		0.5 min	7.730	7.716	17.21	<b>19.59</b>	4.99	<b>5.68</b>
		1.0 min	7.727	7.737	19.24	19.09	5.58	5.54
		10.0 min	7.713	7.717	<b>23.48</b>	23.22	<b>6.81</b>	6.73
		60.0 min	7.709	7.735	25.60	25.35	7.42	7.35
		240.0 min	7.706	7.726	28.85	28.57	8.37	8.29
		Score1:	0.25	DU sum difference:-0.30 u				
Score2:	0.25							
HC336-348	1	0.0 min	3.696	3.703	0.00	0.00	0.00	0.00
		0.5 min	3.693	3.695	26.48	25.94	2.65	2.59
		1.0 min	3.696	3.697	30.08	29.01	3.01	2.90
		10.0 min	3.704	3.688	32.43	32.29	3.24	3.23
		60.0 min	3.696	3.701	33.67	33.62	3.37	3.36
		240.0 min	3.696	3.692	35.44	33.06	3.54	3.31
		Score1:	<b>1.24</b>	DU sum difference:-0.42 u				
Score2:	1.01							
HC342-366	1	0.0 min	10.631	10.613	<b>0.91</b>	0.11	<b>0.17</b>	0.02
		0.5 min	10.629	10.618	7.70	7.70	1.46	1.46
		1.0 min	10.628	10.619	9.19	9.86	1.75	1.87
		10.0 min	10.631	10.628	13.01	14.93	2.47	2.84
		60.0 min	10.629	10.688	20.40	21.31	3.88	4.05
		240.0 min	10.625	10.613	25.62	27.54	4.87	5.23
		Score1:	<b>1.37p</b>	DU sum difference: 0.88 u				
Score2:	1.50p							
HC345-374	1	0.0 min	12.929	12.907	0.00	0.00	0.00	0.00
		0.5 min	12.932	12.906	10.49	9.51	2.52	2.28
		1.0 min	12.931	12.938	12.94	12.83	3.10	3.08
		10.0 min	12.902	12.921	<b>17.64</b>	17.08	<b>4.23</b>	4.10
		60.0 min	12.897	12.932	19.82	19.39	4.76	4.65
		240.0 min	12.887	12.921	22.99	22.24	5.52	5.34
		Score1:	0.74	DU sum difference:-0.66 u				
Score2:	0.66							
HC347-370	1	0.0 min	10.474	10.463	0.00	0.00	0.00	0.00
		0.5 min	10.471	10.459	5.65	5.67	1.13	1.13
		1.0 min	10.440	10.423	6.21	6.64	1.24	1.33
		10.0 min	10.454	10.442	9.37	11.84	1.87	2.37
		60.0 min	10.443	10.459	15.28	16.86	3.06	3.37
		240.0 min	10.436	10.417	20.58	20.48	4.12	4.10
		Score1:	<b>1.30</b>	DU sum difference: 0.88 u				
Score2:	1.11							
HC349-365	1	0.0 min	8.012	8.003	0.00	0.00	0.00	0.00
		0.5 min	8.002	7.997	30.86	28.28	4.01	3.68
		1.0 min	8.001	8.004	32.35	31.38	4.20	4.08
		10.0 min	7.996	7.999	31.29	31.87	4.07	4.14
		60.0 min	7.988	8.004	32.07	32.64	4.17	4.24
		240.0 min	7.982	7.999	34.31	35.34	4.46	4.59
		Score1:	0.41	DU sum difference:-0.18 u				
Score2:	<b>1.39</b>							
HC357-385	1	0.0 min	7.175	7.149	0.00	0.00	0.00	0.00
		0.5 min	7.167	7.150	2.14	2.21	0.58	0.60
		1.0 min	7.166	7.167	2.37	2.19	0.64	0.59
		10.0 min	7.151	7.155	2.59	2.63	0.70	0.71
		60.0 min	7.146	7.165	3.67	3.49	0.99	0.94
		240.0 min	7.144	7.165	4.85	4.79	1.31	1.29
		Score1:	0.09	DU sum difference:-0.09 u				
Score2:	0.13							

Molecule HC: Peptides with sufficient kinetics data, part 17

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC364-393	1	0.0 min	6.353	6.333	0.00	0.00	0.00	0.00
		0.5 min	6.356	6.340	5.62	5.26	1.52	1.42
		1.0 min	6.353	6.358	6.82	6.48	1.84	1.75
		10.0 min	6.345	6.347	9.23	9.43	2.49	2.55
		60.0 min	6.337	6.354	11.55	11.61	3.12	3.13
		240.0 min	6.332	6.350	14.05	14.05	3.79	3.79
		Score1: 0.13	DU sum difference: -0.12 u					
Score2: 0.23								
HC367-390	1	0.0 min	8.258	8.249	0.20	0.11	0.04	0.02
		0.5 min	8.256	8.247	24.04	22.07	5.05	4.64
		1.0 min	8.259	8.255	25.36	24.96	5.33	5.24
		10.0 min	8.246	8.247	28.51	29.68	5.99	6.23
		60.0 min	8.243	8.254	30.45	31.37	6.39	6.59
		240.0 min	8.236	8.257	31.03	32.83	6.52	6.89
		Score1: 0.43	DU sum difference: 0.30 u					
Score2: 1.54								
HC368-387	1	0.0 min	8.312	8.295	0.00	0.00	0.00	0.00
		0.5 min	8.309	8.293	2.91	2.30	0.49	0.39
		1.0 min	8.310	8.309	3.67	3.53	0.62	0.60
		10.0 min	8.293	8.299	4.72	5.24	0.80	0.89
		60.0 min	8.288	8.306	5.97	6.18	1.02	1.05
		240.0 min	8.279	8.305	8.09	8.61	1.38	1.46
		Score1: 0.15	DU sum difference: 0.08 u					
Score2: 0.48								
HC369-372	1	0.0 min	9.057	9.053	0.00	0.00	0.00	0.00
		0.5 min	9.057	9.052	2.81	2.41	0.08	0.07
		1.0 min	9.055	9.055	2.81	2.81	0.08	0.08
		10.0 min	9.057	9.048	3.41	3.61	0.10	0.11
		60.0 min	9.050	9.055	6.02	5.62	0.18	0.17
		240.0 min	9.046	9.055	10.03	9.63	0.30	0.29
		Score1: 0.30	DU sum difference: -0.03 u					
Score2: 0.34								
HC369-380	1	0.0 min	13.996	13.995	0.00	0.00	0.00	0.00
		0.5 min	13.991	13.989	6.41	5.15	0.64	0.51
		1.0 min	13.995	13.992	8.58	7.61	0.86	0.76
		10.0 min	13.990	13.984	11.19	11.58	1.12	1.16
		60.0 min	13.984	13.997	13.62	12.82	1.36	1.28
		240.0 min	13.985	13.990	16.81	16.44	1.68	1.64
		Score1: 0.89	DU sum difference: -0.30 u					
Score2: 0.92								
HC372-397	1	0.0 min	12.785	12.772	0.20	0.30	0.04	0.07
		0.5 min	12.788	12.784	6.42	6.21	1.41	1.37
		1.0 min	12.784	12.791	6.43	6.40	1.41	1.41
		10.0 min	12.780	12.771	6.81	7.40	1.50	1.63
		60.0 min	12.780	12.799	9.74	9.53	2.14	2.10
		240.0 min	12.781	12.797	13.23	13.77	2.91	3.03
		Score1: 0.23	DU sum difference: 0.17 u					
Score2: 0.41								
HC373-376	1	0.0 min	6.353	6.353	0.00	0.00	0.00	0.00
		0.5 min	6.353	6.353	16.18	13.63	0.32	0.27
		1.0 min	6.353	6.353	<b>21.67</b>	<b>18.86</b>	<b>0.43</b>	<b>0.38</b>
		10.0 min	6.353	6.339	38.13	37.53	0.76	0.75
		60.0 min	6.348	6.353	40.94	41.54	0.82	0.83
		240.0 min	6.353	6.353	46.76	45.95	0.94	0.92
		Score1: 1.09	DU sum difference: -0.08 u					
Score2: 1.32								

Molecule HC: Peptides with sufficient kinetics data, part 18

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC377-390	1	0.0 min	12.318	12.365	0.00	0.00	0.00	0.00
		0.5 min	12.313	12.386	19.67	19.67	2.36	2.36
		1.0 min	12.317	12.334	26.69	24.08	3.20	2.89
		10.0 min	12.373	12.309	31.71	<b>33.11</b>	3.80	<b>3.97</b>
		60.0 min	12.346	12.317	33.31	33.91	4.00	4.07
		240.0 min	12.386	12.313	35.12	35.12	4.21	4.21
		Score1: 0.65	DU sum difference:-0.29 u					
Score2: 0.93								
HC381-390	1	0.0 min	10.616	10.601	0.07	0.00	0.01	0.00
		0.5 min	10.611	10.617	36.57	33.34	2.93	2.67
		1.0 min	10.611	10.612	39.82	38.11	3.19	3.05
		10.0 min	10.619	10.593	46.57	47.12	3.73	3.77
		60.0 min	10.608	10.613	49.34	50.45	3.95	4.04
		240.0 min	10.606	10.624	48.84	50.83	3.91	4.07
		Score1: 0.40	DU sum difference:-0.11 u					
Score2: 2.10								
HC381-398	1	0.0 min	11.474	11.463	0.23	0.13	0.03	0.02
		0.5 min	11.472	11.469	19.84	18.33	2.98	2.75
		1.0 min	11.473	11.470	24.56	<b>21.91</b>	3.68	<b>3.29</b>
		10.0 min	11.459	11.462	<b>33.76</b>	34.15	<b>5.06</b>	5.12
		60.0 min	11.454	11.468	38.11	37.58	5.72	5.64
		240.0 min	11.448	11.473	38.62	41.40	5.79	6.21
		Score1: 0.24	DU sum difference: 0.15 u					
Score2: 1.78								
HC390-398	1	0.0 min	7.290	7.269	0.00	0.00	0.00	0.00
		0.5 min	7.283	7.278	8.03	7.02	0.56	0.49
		1.0 min	7.289	7.281	<b>10.43</b>	10.43	<b>0.73</b>	0.73
		10.0 min	7.269	7.271	25.89	24.08	1.81	1.69
		60.0 min	7.264	7.276	31.71	31.71	2.22	2.22
		240.0 min	7.264	7.278	39.93	39.33	2.80	2.75
		Score1: 1.01p	DU sum difference:-0.24 u					
Score2: 0.99								
HC391-398	1	0.0 min	7.036	7.028	0.00	0.00	0.00	0.00
		0.5 min	7.042	7.027	7.81	6.06	0.47	0.36
		1.0 min	7.044	7.037	12.18	9.81	0.73	0.59
		10.0 min	7.028	7.029	26.69	25.08	1.60	1.51
		60.0 min	7.029	7.033	33.97	33.47	2.04	2.01
		240.0 min	7.020	7.034	37.22	37.45	2.23	2.25
		Score1: 1.78	DU sum difference:-0.36 u					
Score2: 1.56								
HC391-404	1	0.0 min	8.554	8.541	0.22	0.04	0.03	0.00
		0.5 min	8.537	8.514	13.12	10.89	1.57	1.31
		1.0 min	8.534	8.527	<b>14.90</b>	<b>13.60</b>	<b>1.79</b>	<b>1.63</b>
		10.0 min	8.520	8.507	20.37	21.84	2.44	2.62
		60.0 min	8.526	8.532	26.34	26.08	3.16	3.13
		240.0 min	8.524	8.529	29.02	30.10	3.48	3.61
		Score1: 0.04	DU sum difference:-0.02 u					
Score2: 1.52								
HC399-404	1	0.0 min	5.253	5.269	0.00	0.00	0.00	0.00
		0.5 min	5.256	5.267	15.25	14.65	0.76	0.73
		1.0 min	5.256	5.264	17.06	16.86	0.85	0.84
		10.0 min	5.262	5.242	19.67	19.26	0.98	0.96
		60.0 min	5.251	5.267	24.28	23.68	1.21	1.18
		240.0 min	5.251	5.264	29.10	28.09	1.45	1.40
		Score1: 0.83	DU sum difference:-0.14 u					
Score2: 0.68								

Molecule HC: Peptides with sufficient kinetics data, part 19

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC405-410	1	0.0 min	9.178	9.165	0.00	0.00	0.00	0.00
		0.5 min	9.173	9.176	1.58	1.48	0.08	0.07
		1.0 min	9.176	9.178	1.44	1.59	0.07	0.08
		10.0 min	9.177	9.165	1.47	1.60	0.07	0.08
		60.0 min	9.165	9.180	1.40	1.57	0.07	0.08
		240.0 min	9.161	9.180	2.02	1.94	0.10	0.10
		Score1: Score2:	0.08 0.15	DU sum difference: 0.01 u				
HC407-418	1	0.0 min	9.025	9.015	0.00	0.04	0.00	0.00
		0.5 min	9.031	9.022	<b>9.38</b>	<b>8.43</b>	<b>1.03</b>	<b>0.93</b>
		1.0 min	9.029	9.023	11.04	10.48	1.21	1.15
		10.0 min	9.015	9.013	23.88	23.88	2.63	2.63
		60.0 min	9.005	9.021	33.75	33.51	3.71	3.69
		240.0 min	9.003	9.019	36.68	37.53	4.04	4.13
		Score1: Score2:	0.03 0.49	DU sum difference: 0.01 u				
HC411-417	1	0.0 min	6.891	6.863	0.00	0.00	0.00	0.00
		0.5 min	6.881	6.863	32.33	31.33	1.94	1.88
		1.0 min	6.879	6.875	<b>36.30</b>	35.38	<b>2.18</b>	2.12
		10.0 min	6.866	6.864	39.32	39.35	2.36	2.36
		60.0 min	6.864	6.873	41.33	41.12	2.48	2.47
		240.0 min	6.863	6.869	45.18	45.35	2.71	2.72
		Score1: Score2:	0.32 0.41	DU sum difference:-0.07 u				
HC411-422	1	0.0 min	6.352	6.338	0.00	0.00	0.00	0.00
		0.5 min	6.347	6.336	37.55	36.32	4.13	3.99
		1.0 min	6.345	6.342	40.33	39.34	4.44	4.33
		10.0 min	6.341	6.333	42.14	40.68	4.64	4.47
		60.0 min	6.333	6.344	44.61	44.58	4.91	4.90
		240.0 min	6.329	6.341	49.71	49.94	5.47	5.49
		Score1: Score2:	<b>1.03</b> 0.96	DU sum difference:-0.38 u				
HC411-447	1	0.0 min	8.626	8.586	0.09	0.00	0.03	0.00
		0.5 min	8.603	8.577	9.44	8.61	3.30	3.01
		1.0 min	8.597	8.595	10.35	11.14	3.62	3.90
		10.0 min	8.572	8.586	11.29	11.65	3.95	4.08
		60.0 min	8.580	8.585	13.85	14.10	4.85	4.93
		240.0 min	8.577	8.591	16.86	17.14	5.90	6.00
		Score1: Score2:	0.22 0.63	DU sum difference: 0.26 u				
HC426-446	1	0.0 min	4.260	4.249	0.00	0.00	0.00	0.00
		0.5 min	4.251	4.248	6.29	6.47	1.19	1.23
		1.0 min	4.251	4.249	6.64	6.40	1.26	1.22
		10.0 min	4.264	4.240	8.17	7.83	1.55	1.49
		60.0 min	4.240	4.251	9.66	9.86	1.84	1.87
		240.0 min	4.237	4.249	12.22	11.88	2.32	2.26
		Score1: Score2:	0.16 0.32	DU sum difference:-0.10 u				
HC429-446	1	0.0 min	3.538	3.544	0.00	0.00	0.00	0.00
		0.5 min	3.535	3.545	8.63	8.49	1.38	1.36
		1.0 min	3.537	3.540	8.92	8.83	1.43	1.41
		10.0 min	3.544	3.533	10.03	9.78	1.61	1.56
		60.0 min	3.534	3.540	12.40	11.90	1.98	1.90
		240.0 min	3.535	3.539	14.79	14.45	2.37	2.31
		Score1: Score2:	0.40 0.32	DU sum difference:-0.21 u				

Molecule HC: Peptides/Ranges with insufficient kinetics data, part 1

Ref: reference series, Exp: experiment series

**Bold typing: problematic DU values**

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
HC016-027	1	0.0 min	9.237	9.242	<b>0.00</b>	0.39	<b>0.00</b>	0.04
		0.5 min	9.197	9.211	<b>14.97</b>	13.24	<b>1.65</b>	1.46
		1.0 min	9.217	9.195	<b>15.75</b>	14.43	<b>1.73</b>	1.59
		10.0 min	9.198	9.191	<b>15.05</b>	15.85	<b>1.66</b>	1.74
		60.0 min	9.188	9.200	<b>13.36</b>	17.06	<b>1.47</b>	1.88
		240.0 min	9.187	9.197	<b>14.32</b>	16.66	<b>1.57</b>	1.83
HC162-180	2	0.0 min	13.051	13.131	<b>0.00</b>	0.00	<b>0.00</b>	0.00
		0.5 min	n.d.	13.129	n.d.	13.09	n.d.	2.23
		1.0 min	n.d.	13.144	n.d.	17.75	n.d.	3.02
		10.0 min	13.124	13.130	<b>21.54</b>	22.96	<b>3.66</b>	3.90
		60.0 min	13.125	13.142	<b>23.19</b>	24.00	<b>3.94</b>	4.08
		240.0 min	13.117	13.134	<b>23.80</b>	25.84	<b>4.05</b>	4.39
HC185-189	1	0.0 min	6.826	6.824	<b>0.00</b>	0.00	<b>0.00</b>	0.00
		0.5 min	6.820	6.829	<b>3.81</b>	4.01	<b>0.15</b>	0.16
		1.0 min	6.820	6.821	<b>3.95</b>	4.19	<b>0.16</b>	0.17
		10.0 min	6.826	6.809	<b>4.16</b>	4.21	<b>0.17</b>	0.17
		60.0 min	6.821	6.827	<b>3.61</b>	4.01	<b>0.14</b>	0.16
		240.0 min	6.818	6.832	<b>3.41</b>	4.62	<b>0.14</b>	0.18
HC334-358	1	0.0 min	6.144	6.119	<b>4.95</b>	<b>4.83</b>	<b>0.94</b>	<b>0.92</b>
		0.5 min	6.132	6.111	<b>25.46</b>	<b>22.50</b>	<b>4.84</b>	<b>4.27</b>
		1.0 min	6.134	6.128	<b>24.81</b>	<b>26.12</b>	<b>4.71</b>	<b>4.96</b>
		10.0 min	6.119	6.120	<b>27.67</b>	<b>29.65</b>	<b>5.26</b>	<b>5.63</b>
		60.0 min	6.117	6.128	<b>26.48</b>	<b>26.86</b>	<b>5.03</b>	<b>5.10</b>
		240.0 min	6.109	6.129	<b>29.49</b>	<b>26.61</b>	<b>5.60</b>	<b>5.06</b>
HC377-380	1	0.0 min	5.858	5.858	n.d.	n.d.	n.d.	n.d.
		0.5 min	5.855	5.857	n.d.	n.d.	n.d.	n.d.
		1.0 min	5.855	5.858	n.d.	n.d.	n.d.	n.d.
		10.0 min	5.858	5.846	n.d.	n.d.	n.d.	n.d.
		60.0 min	5.852	5.857	n.d.	n.d.	n.d.	n.d.
		240.0 min	5.855	5.855	n.d.	n.d.	n.d.	n.d.
HC379-390	1	0.0 min	11.318	11.319	<b>0.88</b>	0.80	<b>0.09</b>	0.08
		0.5 min	11.318	11.323	<b>31.94</b>	26.69	<b>3.19</b>	2.67
		1.0 min	11.320	11.318	<b>30.68</b>	29.56	<b>3.07</b>	2.96
		10.0 min	11.325	11.307	<b>40.16</b>	<b>42.88</b>	<b>4.02</b>	<b>4.29</b>
		60.0 min	11.312	11.320	<b>41.22</b>	39.50	<b>4.12</b>	3.95
		240.0 min	11.310	11.321	<b>42.06</b>	44.27	<b>4.21</b>	4.43
HC395-426	1	0.0 min	11.121	11.099	<b>0.91</b>	0.87	<b>0.27</b>	0.26
		0.5 min	11.115	11.105	<b>18.55</b>	15.86	<b>5.57</b>	4.76
		1.0 min	11.118	11.117	<b>17.29</b>	17.44	<b>5.19</b>	5.23
		10.0 min	11.100	11.098	<b>19.85</b>	19.31	<b>5.95</b>	5.79
		60.0 min	11.098	11.125	<b>19.73</b>	22.58	<b>5.92</b>	6.78
		240.0 min	11.081	11.128	<b>20.84</b>	22.40	<b>6.25</b>	6.72
HC411-446	1	0.0 min	9.168	9.138	<b>0.04</b>	<b>0.00</b>	<b>0.01</b>	<b>0.00</b>
		0.5 min	9.158	9.152	n.d.	n.d.	n.d.	n.d.
		1.0 min	9.114	9.144	n.d.	n.d.	n.d.	n.d.
		10.0 min	9.134	9.145	n.d.	n.d.	n.d.	n.d.
		60.0 min	9.088	9.142	n.d.	n.d.	n.d.	n.d.
		240.0 min	9.111	9.153	n.d.	n.d.	n.d.	n.d.

# Comparison Report HDX, Exchange Data - Tabular Overview

(Experiment series: deglyl, reference series: glyl)

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## Molecule HC: Peptides lacking equivalent range, part 1

Peptide	Peptide	Peptide
HC279-300_p1444.53	HC282-306_p1216.42	HC293-312_p1095.4

Molecule HC: no peptides lacking HDX data in experiment series available

Molecule HC: no peptides lacking HDX data in reference series available

## Molecule HC: Peptides lacking HDX data in both series, part 1

Peptide	Peptide	Peptide
HC133-159		

Molecule LC: Peptides with sufficient kinetics data, part 1

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC001-004	1	0.0 min	10.719	10.733	0.00	0.00	0.00	0.00
		0.5 min	10.719	10.735	23.28	22.07	0.70	0.66
		1.0 min	10.721	10.725	<b>34.31</b>	33.11	<b>1.03</b>	0.99
		10.0 min	10.736	10.718	54.38	54.78	1.63	1.64
		60.0 min	10.724	10.727	54.78	54.98	1.64	1.65
		240.0 min	10.724	10.733	54.18	54.98	1.63	1.65
		Score1:	0.07	DU sum difference: 0.01 u				
Score2:	0.76							
LC001-042	1	0.0 min	11.570	11.555	0.38	0.20	0.15	0.08
		0.5 min	11.581	11.569	4.34	4.62	1.69	1.80
		1.0 min	11.570	11.581	4.94	5.32	1.92	2.08
		10.0 min	11.562	11.577	7.15	8.40	2.79	3.28
		60.0 min	11.557	11.582	11.31	12.61	4.41	4.92
		240.0 min	11.549	11.575	15.37	16.71	5.99	6.52
		Score1:	<b>1.30</b>	DU sum difference: 1.71 u				
Score2:	1.15							
	2	0.0 min	11.705	11.696	0.66	0.63	0.26	0.25
		0.5 min	11.712	11.699	4.49	4.66	1.75	1.82
		1.0 min	11.704	11.713	4.94	5.36	1.93	2.09
		10.0 min	11.704	11.698	7.09	7.78	2.77	3.03
		60.0 min	11.692	11.711	11.03	12.33	4.30	4.81
		240.0 min	11.682	11.702	15.81	17.05	6.17	6.65
		Score1:	<b>1.12</b>	DU sum difference: 1.47 u				
Score2:	0.93							
LC003-018	1	0.0 min	11.493	11.489	0.00	0.20	0.00	0.03
		0.5 min	11.483	11.480	16.86	13.85	2.19	1.80
		1.0 min	11.484	11.489	18.66	18.66	2.43	2.43
		10.0 min	11.486	11.483	<b>23.08</b>	<b>23.08</b>	<b>3.00</b>	3.00
		60.0 min	11.481	11.487	22.27	23.28	2.90	3.03
		240.0 min	11.480	11.491	24.08	24.08	3.13	3.13
		Score1:	0.59	DU sum difference: -0.28 u				
Score2:	<b>1.02p</b>							
LC004-021	1	0.0 min	9.966	9.956	0.40	0.82	0.06	0.12
		0.5 min	9.973	9.965	18.66	15.85	2.80	2.38
		1.0 min	9.969	9.975	18.86	18.06	2.83	2.71
		10.0 min	9.968	9.964	20.87	21.67	3.13	3.25
		60.0 min	9.961	9.981	25.69	25.69	3.85	3.85
		240.0 min	9.957	9.980	26.89	27.89	4.03	4.18
		Score1:	0.41	DU sum difference: -0.21 u				
Score2:	<b>1.41</b>							
LC005-011	1	0.0 min	7.056	7.056	0.00	0.00	0.00	0.00
		0.5 min	7.056	7.056	39.33	39.72	1.97	1.99
		1.0 min	7.056	7.059	42.74	43.55	2.14	2.18
		10.0 min	7.060	7.048	43.95	43.14	2.20	2.16
		60.0 min	7.054	7.060	45.95	45.93	2.30	2.30
		240.0 min	7.050	7.058	50.01	50.26	2.50	2.51
		Score1:	0.18	DU sum difference: 0.03 u				
Score2:	0.55							
LC005-018	1	0.0 min	7.868	7.868	0.00	0.00	0.00	0.00
		0.5 min	7.854	7.864	27.09	25.89	2.98	2.85
		1.0 min	7.861	7.871	27.89	28.09	3.07	3.09
		10.0 min	7.871	7.848	28.90	30.10	3.18	3.31
		60.0 min	7.850	7.862	34.47	35.55	3.79	3.91
		240.0 min	7.854	7.865	40.33	40.74	4.44	4.48
		Score1:	0.50	DU sum difference: 0.18 u				
Score2:	0.99							

Molecule LC: Peptides with sufficient kinetics data, part 2

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC005-039	1	0.0 min	6.755	6.743	0.14	0.18	0.05	0.06
		0.5 min	6.757	6.741	6.14	5.54	1.97	1.77
		1.0 min	6.757	6.758	7.58	7.25	2.43	2.32
		10.0 min	6.745	6.744	10.14	10.29	3.24	3.29
		60.0 min	6.740	6.753	12.64	12.47	4.04	3.99
		240.0 min	6.731	6.751	14.84	15.19	4.75	4.86
		Score1: 0.16	DU sum difference: -0.18 u					
Score2: 0.39								
LC10-043	1	0.0 min	6.951	6.923	0.06	0.18	0.02	0.06
		0.5 min	6.947	6.926	3.58	3.66	1.15	1.17
		1.0 min	6.947	6.947	3.98	3.93	1.27	1.26
		10.0 min	6.932	6.938	4.27	4.18	1.37	1.34
		60.0 min	6.927	6.950	5.48	5.41	1.75	1.73
		240.0 min	6.921	6.945	7.28	7.16	2.33	2.29
		Score1: 0.04	DU sum difference: -0.04 u					
Score2: 0.13								
LC012-018	1	0.0 min	4.097	4.097	0.00	0.00	0.00	0.00
		0.5 min	4.097	4.097	12.44	12.64	0.62	0.63
		1.0 min	4.094	4.094	15.65	15.65	0.78	0.78
		10.0 min	4.100	4.083	21.27	21.27	1.06	1.06
		60.0 min	4.083	4.097	33.31	32.91	1.67	1.65
		240.0 min	4.083	4.088	42.94	42.34	2.15	2.12
		Score1: 0.24	DU sum difference: -0.04 u					
Score2: 0.29								
LC012-020	1	0.0 min	5.253	5.257	0.00	0.00	0.00	0.00
		0.5 min	5.251	5.253	18.22	17.82	1.28	1.25
		1.0 min	5.251	5.253	20.05	19.82	1.40	1.39
		10.0 min	5.256	5.243	24.09	23.71	1.69	1.66
		60.0 min	5.248	5.255	32.52	32.13	2.28	2.25
		240.0 min	5.242	5.250	39.11	39.69	2.74	2.78
		Score1: 0.24	DU sum difference: -0.06 u					
Score2: 0.48								
LC019-023	1	0.0 min	7.882	7.879	0.00	0.00	0.00	0.00
		0.5 min	7.882	7.882	4.41	4.41	0.18	0.18
		1.0 min	7.879	7.879	4.41	4.62	0.18	0.18
		10.0 min	7.886	7.871	6.62	6.42	0.26	0.26
		60.0 min	7.875	7.882	15.64	16.05	0.63	0.64
		240.0 min	7.885	7.874	21.07	21.27	0.84	0.85
		Score1: 0.18	DU sum difference: 0.02 u					
Score2: 0.24								
LC019-046	1	0.0 min	11.621	11.605	0.00	0.40	0.00	0.10
		0.5 min	11.585	11.587	6.62	6.22	1.72	1.62
		1.0 min	11.581	11.612	7.63	7.42	1.98	1.93
		10.0 min	11.589	11.586	10.23	11.44	2.66	2.97
		60.0 min	11.563	11.586	14.65	15.05	3.81	3.91
		240.0 min	11.556	11.581	16.25	16.86	4.23	4.38
		Score1: 0.59	DU sum difference: 0.52 u					
Score2: 0.78								
LC021-032	1	0.0 min	7.535	7.523	0.00	0.00	0.00	0.00
		0.5 min	7.504	7.492	17.74	<b>18.46</b>	1.95	<b>2.03</b>
		1.0 min	7.505	7.506	<b>22.07</b>	19.66	<b>2.43</b>	2.16
		10.0 min	7.487	7.486	28.29	27.49	3.11	3.02
		60.0 min	7.481	7.497	35.32	34.92	3.88	3.84
		240.0 min	7.471	7.482	40.33	41.14	4.44	4.53
		Score1: 0.15	DU sum difference: -0.07 u					
Score2: 0.73								



Molecule LC: Peptides with sufficient kinetics data, part 3

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC022-035	1	0.0 min	9.974	9.965	0.00	0.00	0.00	0.00
		0.5 min	9.970	9.957	15.71	13.65	2.04	1.77
		1.0 min	9.975	9.965	17.66	16.66	2.30	2.17
		10.0 min	9.963	9.975	<b>22.27</b>	22.41	<b>2.90</b>	2.91
		60.0 min	9.960	9.970	27.09	26.96	3.52	3.51
		240.0 min	9.950	9.974	31.46	32.11	4.09	4.17
		Score1:	0.83	DU sum difference:-0.40 u				
Score2:	0.96p							
LC022-046	1	0.0 min	8.822	8.801	0.00	0.00	0.00	0.00
		0.5 min	8.816	8.801	10.20	9.41	2.35	2.16
		1.0 min	8.812	8.811	11.79	11.46	2.71	2.64
		10.0 min	8.794	8.795	15.51	15.85	3.57	3.65
		60.0 min	8.788	8.803	19.35	19.57	4.45	4.50
		240.0 min	8.779	8.799	20.71	21.33	4.76	4.91
		Score1:	0.02	DU sum difference: 0.02 u				
Score2:	0.56							
LC024-033	1	0.0 min	6.863	6.839	0.00	0.00	0.00	0.00
		0.5 min	6.849	6.834	<b>20.17</b>	<b>18.86</b>	<b>1.82</b>	<b>1.70</b>
		1.0 min	6.863	6.847	21.79	22.07	1.96	1.99
		10.0 min	6.853	6.842	30.50	28.70	2.75	2.58
		60.0 min	6.832	6.851	36.72	36.72	3.31	3.31
		240.0 min	6.828	6.842	42.14	42.14	3.79	3.79
		Score1:	0.49	DU sum difference:-0.16 u				
Score2:	0.61							
LC024-035	1	0.0 min	9.650	9.628	0.09	0.38	0.01	0.04
		0.5 min	9.650	9.632	10.98	9.75	1.21	1.07
		1.0 min	9.643	9.643	14.26	14.07	1.57	1.55
		10.0 min	9.630	9.630	19.38	19.75	2.13	2.17
		60.0 min	9.624	9.641	23.01	23.81	2.53	2.62
		240.0 min	9.614	9.641	26.05	27.66	2.87	3.04
		Score1:	0.48	DU sum difference: 0.18 u				
Score2:	<b>1.08</b>							
LC024-046	1	0.0 min	8.256	8.239	0.00	0.00	0.00	0.00
		0.5 min	8.249	8.237	7.79	7.00	1.64	1.47
		1.0 min	8.250	8.248	9.03	8.83	1.90	1.85
		10.0 min	8.236	8.236	11.88	12.44	2.49	2.61
		60.0 min	8.229	8.244	14.85	15.25	3.12	3.20
		240.0 min	8.220	8.244	15.45	16.25	3.24	3.41
		Score1:	0.23	DU sum difference: 0.16 u				
Score2:	0.67							
LC027-084	1	0.0 min	8.995	8.975	0.57	0.49	0.32	0.27
		0.5 min	8.985	8.975	9.75	9.57	5.36	5.26
		1.0 min	8.982	8.979	10.31	10.26	5.67	5.64
		10.0 min	8.972	8.974	11.12	11.24	6.11	6.18
		60.0 min	8.972	8.976	12.40	12.83	6.82	7.06
		240.0 min	8.956	8.977	14.43	14.49	7.94	7.97
		Score1:	0.09	DU sum difference: 0.16 u				
Score2:	0.23							
LC028-047	1	0.0 min	9.476	9.467	0.70	0.70	0.13	0.13
		0.5 min	9.466	9.469	23.61	21.36	4.25	3.85
		1.0 min	9.472	9.476	25.16	24.69	4.53	4.44
		10.0 min	9.461	9.458	34.42	<b>33.41</b>	6.20	<b>6.01</b>
		60.0 min	9.442	9.458	42.66	40.82	7.68	7.35
		240.0 min	9.438	9.462	43.34	46.33	7.80	8.34
		Score1:	0.51	DU sum difference:-0.34 u				
Score2:	<b>2.07p</b>							

Molecule LC: Peptides with sufficient kinetics data, part 4

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC028-084	1	0.0 min	9.199	9.180	0.43	0.42	0.23	0.22
		0.5 min	9.184	9.169	9.51	9.12	5.13	4.93
		1.0 min	9.182	9.182	9.95	9.79	5.37	5.29
		10.0 min	9.172	9.171	10.54	10.79	5.69	5.82
		60.0 min	9.164	9.180	12.37	12.29	6.68	6.64
		240.0 min	9.152	9.179	14.20	14.50	7.67	7.83
		Score1:	0.03	DU sum difference:-0.05 u				
Score2:	0.29							
LC030-046	1	0.0 min	8.239	8.233	0.00	0.00	0.00	0.00
		0.5 min	8.236	8.225	7.63	7.22	1.14	1.08
		1.0 min	8.241	8.237	8.56	8.43	1.28	1.26
		10.0 min	8.238	8.226	11.84	12.44	1.78	1.87
		60.0 min	8.221	8.242	15.25	16.05	2.29	2.41
		240.0 min	8.221	8.241	15.85	15.27	2.38	2.29
		Score1:	0.08	DU sum difference: 0.04 u				
Score2:	0.61							
LC033-046	1	0.0 min	7.441	7.419	0.00	0.00	0.00	0.00
		0.5 min	7.441	7.419	3.97	3.50	0.48	0.42
		1.0 min	7.440	7.438	4.74	4.66	0.57	0.56
		10.0 min	7.419	7.429	8.07	8.21	0.97	0.98
		60.0 min	7.415	7.443	9.51	9.37	1.14	1.12
		240.0 min	7.413	7.440	9.54	10.38	1.14	1.25
		Score1:	0.09	DU sum difference: 0.04 u				
Score2:	0.41							
LC034-046	1	0.0 min	6.222	6.202	0.00	0.00	0.00	0.00
		0.5 min	6.215	6.198	5.56	4.94	0.61	0.54
		1.0 min	6.211	6.215	6.95	6.23	0.76	0.69
		10.0 min	6.201	6.203	10.86	10.36	1.19	1.14
		60.0 min	6.200	6.214	12.61	12.86	1.39	1.41
		240.0 min	6.198	6.215	12.16	12.72	1.34	1.40
		Score1:	0.30	DU sum difference:-0.11 u				
Score2:	0.64							
LC036-046	1	0.0 min	4.522	4.508	0.00	0.00	0.00	0.00
		0.5 min	4.522	4.508	<b>9.83</b>	9.14	<b>0.88</b>	0.82
		1.0 min	4.522	4.522	11.58	11.24	1.04	1.01
		10.0 min	4.522	4.508	16.66	16.46	1.50	1.48
		60.0 min	4.516	4.522	18.86	19.06	1.70	1.72
		240.0 min	4.505	4.522	19.47	19.06	1.75	1.72
		Score1:	0.24	DU sum difference:-0.08 u				
Score2:	0.33							
LC041-078	1	0.0 min	15.652	15.659	0.16	0.20	0.06	0.07
		0.5 min	15.660	15.657	0.35	0.40	0.12	0.14
		1.0 min	15.660	15.675	0.40	0.56	0.14	0.20
		10.0 min	15.656	15.660	0.53	0.20	0.19	0.07
		60.0 min	15.646	15.669	0.20	0.40	0.07	0.14
		240.0 min	15.646	15.660	0.54	0.58	0.19	0.20
		Score1:	0.04	DU sum difference: 0.05 u				
Score2:	0.20							
LC047-053	1	0.0 min	5.612	5.612	0.00	0.00	0.00	0.00
		0.5 min	5.612	5.612	5.23	5.31	0.31	0.32
		1.0 min	5.614	5.612	6.42	6.49	0.39	0.39
		10.0 min	5.610	5.602	<b>23.10</b>	22.95	<b>1.39</b>	1.38
		60.0 min	5.598	5.613	48.16	48.10	2.89	2.89
		240.0 min	5.594	5.607	54.73	<b>54.77</b>	3.28	<b>3.29</b>
		Score1:	0.03	DU sum difference: 0.01 u				
Score2:	0.07							

Molecule LC: Peptides with sufficient kinetics data, part 5

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC047-062	1	0.0 min	10.325	10.301	0.54	0.60	0.08	0.08
		0.5 min	10.300	10.293	21.79	<b>20.39</b>	3.05	<b>2.85</b>
		1.0 min	10.297	10.301	23.48	23.08	3.29	3.23
		10.0 min	10.284	10.283	<b>31.71</b>	32.64	<b>4.44</b>	4.57
		60.0 min	10.273	10.289	42.72	43.89	5.98	6.14
		240.0 min	10.262	10.287	45.47	47.12	6.37	6.60
		Score1:	0.90	DU sum difference: 0.52 u				
Score2:	<b>1.19</b>							
LC047-071	1	0.0 min	10.700	10.688	0.00	0.00	0.00	0.00
		0.5 min	10.695	10.686	15.51	13.87	3.57	3.19
		1.0 min	10.695	10.693	16.76	16.00	3.86	3.68
		10.0 min	10.684	10.685	21.32	21.79	4.90	5.01
		60.0 min	10.675	10.689	26.56	27.70	6.11	6.37
		240.0 min	10.669	10.691	28.09	30.17	6.46	6.94
		Score1:	0.38	DU sum difference: 0.30 u				
Score2:	<b>1.48</b>							
LC054-062	1	0.0 min	9.881	9.867	0.00	0.00	0.00	0.00
		0.5 min	9.872	9.864	<b>30.10</b>	27.49	<b>2.11</b>	1.92
		1.0 min	9.876	9.874	30.70	<b>29.70</b>	2.15	<b>2.08</b>
		10.0 min	9.864	9.862	36.60	36.92	2.56	2.58
		60.0 min	9.853	9.869	42.94	43.34	3.01	3.03
		240.0 min	9.852	9.872	46.96	48.36	3.29	3.39
		Score1:	0.77	DU sum difference: 0.22 u				
Score2:	0.77							
LC054-070	1	0.0 min	8.598	8.588	0.00	0.00	0.00	0.00
		0.5 min	8.591	8.592	26.55	23.84	3.98	3.58
		1.0 min	8.588	8.593	28.12	<b>27.47</b>	4.22	<b>4.12</b>
		10.0 min	8.589	8.584	32.21	33.77	4.83	5.07
		60.0 min	8.577	8.589	36.08	37.42	5.41	5.61
		240.0 min	8.576	8.587	37.62	39.71	5.64	5.96
		Score1:	0.74	DU sum difference: 0.41 u				
Score2:	<b>2.02p</b>							
LC054-071	1	0.0 min	10.534	10.521	<b>0.95</b>	0.57	<b>0.15</b>	0.09
		0.5 min	10.535	10.528	14.45	13.44	2.31	2.15
		1.0 min	10.531	10.532	17.46	16.40	2.79	2.62
		10.0 min	10.524	10.523	19.03	20.59	3.04	3.29
		60.0 min	10.515	10.540	21.92	23.36	3.51	3.74
		240.0 min	10.512	10.534	22.66	25.52	3.63	4.08
		Score1:	<b>1.01p</b>	DU sum difference: 0.55 u				
Score2:	2.01p							
LC054-095	1	0.0 min	8.936	8.915	0.05	0.08	0.02	0.03
		0.5 min	8.925	8.913	22.61	20.87	8.82	8.14
		1.0 min	8.923	8.921	23.88	22.78	9.31	8.89
		10.0 min	8.920	8.909	26.60	27.98	10.37	10.91
		60.0 min	8.907	8.918	29.51	30.04	11.51	11.72
		240.0 min	8.902	8.909	29.60	31.21	11.54	12.17
		Score1:	0.22	DU sum difference: 0.28 u				
Score2:	<b>1.55</b>							
LC055-070	1	0.0 min	8.291	8.281	0.04	0.04	0.01	0.01
		0.5 min	8.263	8.258	26.26	<b>23.77</b>	3.68	<b>3.33</b>
		1.0 min	8.264	8.271	28.22	27.89	3.95	3.91
		10.0 min	8.280	8.246	<b>33.39</b>	34.38	<b>4.67</b>	4.81
		60.0 min	8.243	8.258	37.43	38.58	5.24	5.40
		240.0 min	8.282	8.257	39.13	40.88	5.48	5.72
		Score1:	0.94	DU sum difference: 0.54 u				
Score2:	<b>1.17</b>							

Molecule LC: Peptides with sufficient kinetics data, part 6

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC055-085	1	0.0 min	12.573	12.563	0.17	0.44	0.05	0.13
		0.5 min	12.575	12.562	6.81	6.79	1.97	1.97
		1.0 min	12.572	12.580	7.50	7.27	2.18	2.11
		10.0 min	12.564	12.568	8.02	8.71	2.33	2.53
		60.0 min	12.550	12.576	10.56	10.73	3.06	3.11
		240.0 min	12.545	12.566	14.04	14.54	4.07	4.22
		Score1:	0.42	DU sum difference: 0.41 u				
Score2:	0.46							
LC059-100	1	0.0 min	9.938	9.921	0.65	0.88	0.25	0.34
		0.5 min	9.928	9.920	19.33	17.31	7.54	6.75
		1.0 min	9.932	9.933	20.55	19.95	8.01	7.78
		10.0 min	9.926	9.918	23.17	23.69	9.03	9.24
		60.0 min	9.915	9.932	25.04	26.99	9.76	10.52
		240.0 min	9.909	9.936	25.06	26.93	9.77	10.50
		Score1:	0.58	DU sum difference: 0.76 u				
Score2:	<b>1.74</b>							
LC071-077	1	0.0 min	10.798	10.807	0.00	0.00	0.00	0.00
		0.5 min	10.787	10.812	<b>6.46</b>	<b>6.75</b>	<b>0.39</b>	<b>0.40</b>
		1.0 min	10.785	10.788	8.35	8.03	0.50	0.48
		10.0 min	10.811	10.787	23.68	23.48	1.42	1.41
		60.0 min	10.803	10.806	26.09	27.09	1.57	1.63
		240.0 min	10.812	10.797	27.09	26.89	1.63	1.61
		Score1:	0.09	DU sum difference: 0.02 u				
Score2:	0.50							
LC071-079	1	0.0 min	11.866	11.879	0.00	0.00	0.00	0.00
		0.5 min	11.864	11.879	5.30	5.31	0.42	0.43
		1.0 min	11.865	11.869	6.69	6.81	0.54	0.54
		10.0 min	11.877	11.855	<b>16.96</b>	17.32	<b>1.36</b>	1.39
		60.0 min	11.861	11.866	19.27	19.39	1.54	1.55
		240.0 min	11.864	11.867	19.07	19.57	1.53	1.57
		Score1:	0.25	DU sum difference: 0.07 u				
Score2:	0.22							
LC072-079	1	0.0 min	9.207	9.211	0.04	0.00	0.00	0.00
		0.5 min	9.206	9.214	4.91	<b>6.29</b>	0.34	<b>0.44</b>
		1.0 min	9.202	9.209	6.81	5.86	0.48	0.41
		10.0 min	9.205	9.197	<b>17.06</b>	16.98	<b>1.19</b>	1.19
		60.0 min	9.198	9.219	18.88	18.71	1.32	1.31
		240.0 min	9.197	9.200	19.84	19.10	1.39	1.34
		Score1:	0.69	DU sum difference: -0.20 u				
Score2:	0.69							
LC074-079	1	0.0 min	5.584	5.593	0.00	0.00	0.00	0.00
		0.5 min	5.584	5.588	<b>6.02</b>	6.22	<b>0.30</b>	0.31
		1.0 min	5.587	5.584	8.02	<b>8.15</b>	0.40	<b>0.41</b>
		10.0 min	5.591	5.577	24.08	24.48	1.20	1.22
		60.0 min	5.581	5.586	27.69	27.49	1.38	1.37
		240.0 min	5.578	5.584	27.49	27.69	1.37	1.38
		Score1:	0.15	DU sum difference: 0.03 u				
Score2:	0.29							
LC078-085	1	0.0 min	10.900	10.900	0.00	0.00	0.00	0.00
		0.5 min	10.898	10.910	18.78	16.86	1.31	1.18
		1.0 min	10.902	10.900	20.84	19.34	1.46	1.35
		10.0 min	10.912	10.895	22.49	23.90	1.57	1.67
		60.0 min	10.898	10.906	26.32	27.52	1.84	1.93
		240.0 min	10.898	10.912	30.23	30.86	2.12	2.16
		Score1:	0.06	DU sum difference: -0.01 u				
Score2:	<b>1.61</b>							

Molecule LC: Peptides with sufficient kinetics data, part 7

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC080-086	1	0.0 min	11.385	11.379	0.00	0.00	0.00	0.00
		0.5 min	11.384	11.391	6.50	5.78	0.39	0.35
		1.0 min	11.385	11.382	8.88	7.84	0.53	0.47
		10.0 min	11.393	11.377	11.14	11.66	0.67	0.70
		60.0 min	11.379	11.393	13.53	14.90	0.81	0.89
		240.0 min	11.379	11.390	19.89	20.12	1.19	1.21
		Score1:	0.11	DU sum difference: 0.02 u				
Score2:	0.94							
LC086-101	1	0.0 min	14.519	14.532	0.00	0.20	0.00	0.03
		0.5 min	14.515	14.536	9.98	<b>9.58</b>	1.40	<b>1.34</b>
		1.0 min	14.541	14.557	9.84	8.26	1.38	1.16
		10.0 min	14.535	14.514	11.84	11.90	1.66	1.67
		60.0 min	14.539	14.525	15.45	13.72	2.16	1.92
		240.0 min	14.545	14.531	17.86	18.26	2.50	2.56
		Score1:	0.86	DU sum difference:-0.45 u				
Score2:	<b>1.06p</b>							
LC086-104	1	0.0 min	14.014	14.008	0.00	0.06	0.00	0.01
		0.5 min	14.013	14.008	8.03	6.62	1.36	1.13
		1.0 min	14.014	14.027	8.03	8.03	1.36	1.36
		10.0 min	14.008	14.009	8.63	8.43	1.47	1.43
		60.0 min	13.999	14.020	12.04	12.17	2.05	2.07
		240.0 min	13.992	14.010	16.82	15.51	2.86	2.64
		Score1:	0.81	DU sum difference:-0.47 u				
Score2:	0.75							
LC086-106	1	0.0 min	14.792	14.791	0.00	0.00	0.00	0.00
		0.5 min	14.789	14.785	<b>9.52</b>	7.27	<b>1.81</b>	1.38
		1.0 min	14.788	14.807	7.61	7.80	1.45	1.48
		10.0 min	14.788	14.787	8.36	8.62	1.59	1.64
		60.0 min	14.779	14.793	11.42	11.46	2.17	2.18
		240.0 min	14.777	14.789	15.36	14.96	2.92	2.84
		Score1:	0.03	DU sum difference: 0.02 u				
Score2:	0.26							
LC087-101	1	0.0 min	13.823	13.834	0.00	0.89	0.00	0.12
		0.5 min	13.833	13.845	10.89	9.77	1.42	1.27
		1.0 min	13.841	13.845	11.12	9.57	1.45	1.24
		10.0 min	13.843	13.826	11.73	11.09	1.53	1.44
		60.0 min	13.837	13.834	15.62	15.98	2.03	2.08
		240.0 min	13.841	13.834	20.27	20.47	2.63	2.66
		Score1:	0.55	DU sum difference:-0.24 u				
Score2:	<b>1.15</b>							
LC087-104	1	0.0 min	13.322	13.315	0.11	0.20	0.02	0.03
		0.5 min	13.316	13.309	7.22	6.58	1.16	1.05
		1.0 min	13.317	13.327	<b>6.17</b>	8.15	<b>0.99</b>	1.30
		10.0 min	13.307	13.308	9.01	<b>6.58</b>	1.44	<b>1.05</b>
		60.0 min	13.303	13.322	12.41	14.13	1.99	2.26
		240.0 min	13.295	13.304	17.54	18.23	2.81	2.92
		Score1:	0.67	DU sum difference: 0.45 u				
Score2:	<b>1.14</b>							
LC087-106	1	0.0 min	14.335	14.329	0.00	0.00	0.00	0.00
		0.5 min	14.334	14.325	8.48	8.21	1.53	1.48
		1.0 min	14.335	14.352	8.87	8.63	1.60	1.55
		10.0 min	14.332	14.325	9.03	9.63	1.63	1.73
		60.0 min	14.323	14.340	12.63	12.78	2.27	2.30
		240.0 min	14.321	14.335	17.22	17.69	3.10	3.19
		Score1:	0.21	DU sum difference: 0.13 u				
Score2:	0.42							

Molecule LC: Peptides with sufficient kinetics data, part 8

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC098-106	1	0.0 min	10.461	10.440	0.00	0.00	0.00	0.00
		0.5 min	10.461	10.451	5.47	4.42	0.44	0.35
		1.0 min	10.461	10.461	6.16	5.59	0.49	0.45
		10.0 min	10.452	10.440	5.68	7.78	0.45	0.62
		60.0 min	10.435	10.454	7.89	9.41	0.63	0.75
		240.0 min	10.496	10.457	11.30	12.24	0.90	0.98
Score1:	0.87	DU sum difference: 0.24 u						
Score2:	<b>1.50</b>							
LC102-106	1	0.0 min	8.553	8.526	0.00	0.00	0.00	0.00
		0.5 min	8.543	8.531	2.25	2.41	0.09	0.10
		1.0 min	8.541	8.543	2.26	2.74	0.09	0.11
		10.0 min	8.540	8.529	2.78	3.13	0.11	0.13
		60.0 min	8.529	8.546	4.27	4.95	0.17	0.20
		240.0 min	8.530	8.546	6.01	5.89	0.24	0.24
Score1:	0.46	DU sum difference: 0.06 u						
Score2:	0.44							
LC104-124	1	0.0 min	11.562	11.543	0.00	0.19	0.00	0.03
		0.5 min	11.561	11.554	17.66	16.26	3.00	2.76
		1.0 min	11.561	11.563	19.26	18.40	3.27	3.13
		10.0 min	11.547	11.554	24.48	<b>25.08</b>	4.16	<b>4.26</b>
		60.0 min	11.552	11.564	29.10	29.30	4.95	4.98
		240.0 min	11.547	11.562	30.30	32.11	5.15	5.46
Score1:	0.02	DU sum difference: -0.01 u						
Score2:	<b>1.23p</b>							
LC105-123	1	0.0 min	9.840	9.832	0.00	0.00	0.00	0.00
		0.5 min	9.847	9.836	20.30	20.24	3.04	3.04
		1.0 min	9.849	9.849	21.20	21.05	3.18	3.16
		10.0 min	9.849	9.839	22.69	22.97	3.40	3.44
		60.0 min	9.830	9.849	26.29	26.89	3.94	4.03
		240.0 min	9.828	9.843	27.18	28.94	4.08	4.34
Score1:	0.72	DU sum difference: 0.37 u						
Score2:	0.69							
LC105-124	1	0.0 min	9.681	9.664	0.00	0.00	0.00	0.00
		0.5 min	9.671	9.669	19.49	17.63	3.12	2.82
		1.0 min	9.670	9.672	20.30	19.77	3.25	3.16
		10.0 min	9.666	9.667	23.15	24.11	3.70	3.86
		60.0 min	9.658	9.672	27.25	28.06	4.36	4.49
		240.0 min	9.656	9.672	28.75	29.90	4.60	4.78
Score1:	0.16	DU sum difference: 0.08 u						
Score2:	<b>1.29</b>							
LC105-125	1	0.0 min	11.117	11.108	0.00	0.00	0.00	0.00
		0.5 min	11.116	11.114	17.63	16.25	3.00	2.76
		1.0 min	11.116	11.122	18.84	18.23	3.20	3.10
		10.0 min	11.118	11.119	23.85	24.64	4.06	4.19
		60.0 min	11.102	11.120	28.09	28.67	4.78	4.87
		240.0 min	11.099	11.123	29.27	30.53	4.98	5.19
Score1:	0.19	DU sum difference: 0.11 u						
Score2:	<b>1.11</b>							
LC105-131	1	0.0 min	10.295	10.302	0.00	0.00	0.00	0.00
		0.5 min	10.291	10.290	22.48	20.79	5.17	4.78
		1.0 min	10.298	10.296	23.88	23.26	5.49	5.35
		10.0 min	10.292	10.282	27.48	28.50	6.32	6.55
		60.0 min	10.280	10.297	31.88	32.69	7.33	7.52
		240.0 min	10.271	10.295	33.51	35.23	7.71	8.10
Score1:	0.37	DU sum difference: 0.29 u						
Score2:	<b>1.42</b>							

Molecule LC: Peptides with sufficient kinetics data, part 9

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC105-131	2	0.0 min	10.715	10.735	0.00	0.00	0.00	0.00
		0.5 min	10.707	10.712	24.15	22.31	5.55	5.13
		1.0 min	10.713	10.705	25.42	23.95	5.85	5.51
		10.0 min	10.714	10.709	29.33	29.87	6.75	6.87
		60.0 min	10.692	10.711	34.65	34.82	7.97	8.01
		240.0 min	10.714	10.706	35.31	36.58	8.12	8.41
Score1:	0.39	DU sum difference:-0.30 u						
Score2:	<b>1.28</b>							
LC105-132	1	0.0 min	10.849	10.841	0.00	0.00	0.00	0.00
		0.5 min	10.833	10.828	22.27	18.26	5.35	4.38
		1.0 min	10.815	10.831	23.42	22.07	5.62	5.30
		10.0 min	10.827	10.804	26.49	26.49	6.36	6.36
		60.0 min	10.830	10.832	30.30	31.55	7.27	7.57
		240.0 min	10.802	10.820	32.51	34.11	7.80	8.19
Score1:	0.74	DU sum difference:-0.60 u						
Score2:	<b>1.99</b>							
LC107-122	1	0.0 min	9.392	9.384	0.00	0.09	0.00	0.01
		0.5 min	9.397	9.392	25.49	21.27	3.06	2.55
		1.0 min	9.400	9.398	24.68	27.29	2.96	3.27
		10.0 min	9.389	9.387	26.49	<b>27.69</b>	3.18	<b>3.32</b>
		60.0 min	9.382	9.399	30.50	34.31	3.66	4.12
		240.0 min	9.378	9.404	33.71	34.52	4.05	4.14
Score1:	<b>1.01</b>	DU sum difference: 0.45 u						
Score2:	3.08p							
LC107-123	1	0.0 min	9.556	9.541	0.00	0.00	0.00	0.00
		0.5 min	9.550	9.544	21.47	20.19	2.79	2.62
		1.0 min	9.551	9.554	22.62	21.58	2.94	2.81
		10.0 min	9.546	9.542	24.18	25.10	3.14	3.26
		60.0 min	9.535	9.553	28.15	28.09	3.66	3.65
		240.0 min	9.532	9.554	29.23	30.63	3.80	3.98
Score1:	0.02	DU sum difference:-0.01 u						
Score2:	<b>1.14</b>							
LC107-124	1	0.0 min	9.355	9.342	0.00	0.00	0.00	0.00
		0.5 min	9.355	9.355	20.29	18.89	2.84	2.65
		1.0 min	9.355	9.357	22.00	20.90	3.08	2.93
		10.0 min	9.350	9.346	25.08	25.89	3.51	3.62
		60.0 min	9.342	9.358	29.58	30.02	4.14	4.20
		240.0 min	9.341	9.358	31.02	32.28	4.34	4.52
Score1:	0.00	DU sum difference: 0.00 u						
Score2:	<b>1.21</b>							
LC107-125	1	0.0 min	10.886	10.881	0.00	0.00	0.00	0.00
		0.5 min	10.883	10.879	18.62	17.02	2.79	2.55
		1.0 min	10.887	10.888	20.16	19.26	3.02	2.89
		10.0 min	10.883	10.878	26.25	27.13	3.94	4.07
		60.0 min	10.880	10.889	31.27	32.00	4.69	4.80
		240.0 min	10.867	10.890	32.11	33.76	4.82	5.06
Score1:	0.22	DU sum difference: 0.11 u						
Score2:	<b>1.39</b>							
LC107-131	1	0.0 min	10.062	10.057	0.00	0.00	0.00	0.00
		0.5 min	10.070	10.066	23.53	21.51	4.94	4.52
		1.0 min	10.071	10.069	25.08	24.27	5.27	5.10
		10.0 min	10.061	10.065	29.39	30.15	6.17	6.33
		60.0 min	10.056	10.068	34.02	35.01	7.14	7.35
		240.0 min	10.055	10.075	35.59	37.21	7.47	7.81
Score1:	0.16	DU sum difference: 0.11 u						
Score2:	<b>1.50</b>							

Molecule LC: Peptides with sufficient kinetics data, part 10

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC107-131	2	0.0 min	10.582	10.569	0.00	0.00	0.00	0.00
		0.5 min	10.586	10.580	22.31	20.20	4.69	4.24
		1.0 min	10.580	10.597	23.85	22.90	5.01	4.81
		10.0 min	10.589	10.589	28.35	29.31	5.95	6.16
		60.0 min	10.578	10.598	33.08	33.92	6.95	7.12
		240.0 min	10.581	10.606	<b>34.87</b>	36.14	<b>7.32</b>	7.59
		Score1: 0.41	DU sum difference: -0.32 u					
Score2: <b>1.41</b>								
LC110-120	1	0.0 min	10.836	10.831	0.03	0.09	0.00	0.01
		0.5 min	10.840	10.838	16.22	14.54	1.14	1.02
		1.0 min	10.841	10.840	21.28	20.24	1.49	1.42
		10.0 min	10.837	10.839	25.77	27.02	1.80	1.89
		60.0 min	10.830	10.845	26.99	27.58	1.89	1.93
		240.0 min	10.826	10.848	28.94	30.10	2.03	2.11
		Score1: 0.10	DU sum difference: 0.02 u					
Score2: <b>1.40</b>								
	2	0.0 min	11.189	11.172	0.03	0.05	0.00	0.00
		0.5 min	11.184	11.178	16.05	14.67	1.12	1.03
		1.0 min	11.194	11.186	21.48	20.07	1.50	1.41
		10.0 min	11.178	11.186	26.89	27.69	1.88	1.94
		60.0 min	11.178	11.192	27.11	28.69	1.90	2.01
		240.0 min	11.168	11.199	30.29	31.10	2.12	2.18
		Score1: 0.13	DU sum difference: 0.03 u					
Score2: <b>1.46</b>								
LC111-153	1	0.0 min	11.571	11.550	0.20	0.18	0.08	0.07
		0.5 min	11.584	11.564	4.59	4.51	1.75	1.72
		1.0 min	11.577	11.579	4.95	4.78	1.88	1.82
		10.0 min	11.565	11.576	7.34	8.12	2.79	3.09
		60.0 min	11.556	11.583	11.99	11.91	4.56	4.52
		240.0 min	11.549	11.569	15.75	17.44	5.99	6.63
		Score1: 0.63	DU sum difference: 0.81 u					
Score2: 0.68								
	2	0.0 min	11.708	11.696	0.30	0.08	0.11	0.03
		0.5 min	11.709	11.699	4.46	4.47	1.69	1.70
		1.0 min	11.704	11.713	4.81	5.22	1.83	1.98
		10.0 min	11.705	11.700	7.14	7.68	2.71	2.92
		60.0 min	11.692	11.712	11.04	12.39	4.19	4.71
		240.0 min	11.681	11.701	16.02	17.20	6.09	6.54
		Score1: 0.97	DU sum difference: 1.25 u					
Score2: 0.90								
LC124-131	1	0.0 min	4.140	4.139	0.00	0.00	0.00	0.00
		0.5 min	4.128	4.130	37.73	36.92	2.64	2.58
		1.0 min	4.125	4.128	39.53	39.42	2.77	2.76
		10.0 min	4.140	4.121	42.54	42.06	2.98	2.94
		60.0 min	4.123	4.127	47.76	47.36	3.34	3.32
		240.0 min	4.121	4.125	51.57	51.37	3.61	3.60
		Score1: 0.59	DU sum difference: -0.14 u					
Score2: 0.48								
LC132-145	1	0.0 min	13.786	13.781	0.00	0.00	0.00	0.00
		0.5 min	13.786	13.780	<b>9.03</b>	8.38	<b>1.08</b>	1.01
		1.0 min	13.791	13.802	10.34	9.95	1.24	1.19
		10.0 min	13.785	13.783	15.51	15.77	1.86	1.89
		60.0 min	13.776	13.793	18.14	18.70	2.18	2.24
		240.0 min	13.770	13.788	18.67	19.74	2.24	2.37
		Score1: 0.48	DU sum difference: 0.21 u					
Score2: 0.66								



Molecule LC: Peptides with sufficient kinetics data, part 11

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC136-143	1	0.0 min	7.903	7.894	0.00	0.00	0.00	0.00
		0.5 min	7.905	7.898	16.05	15.45	0.96	0.93
		1.0 min	7.906	7.905	<b>15.85</b>	<b>15.45</b>	<b>0.95</b>	<b>0.93</b>
		10.0 min	7.901	7.898	23.08	23.08	1.38	1.38
		60.0 min	7.892	7.906	23.68	23.68	1.42	1.42
		240.0 min	7.890	7.904	23.88	23.88	1.43	1.43
		Score1:	0.20	DU sum difference:-0.04 u				
Score2:	0.17							
LC136-146	1	0.0 min	10.532	10.512	0.60	0.00	0.05	0.00
		0.5 min	10.523	10.522	20.06	19.26	1.81	1.73
		1.0 min	10.524	10.524	22.87	22.07	2.06	1.99
		10.0 min	10.522	10.511	<b>31.30</b>	<b>22.04</b>	<b>2.82</b>	<b>2.88</b>
		60.0 min	10.510	10.523	34.11	34.72	3.07	3.12
		240.0 min	10.506	10.524	33.90	<b>35.32</b>	3.05	<b>3.18</b>
		Score1:	0.58	DU sum difference:-0.22 u				
Score2:	<b>1.01</b>							
LC136-154	1	0.0 min	10.557	10.539	0.00	0.00	0.00	0.00
		0.5 min	10.555	10.547	15.25	14.33	2.59	2.44
		1.0 min	10.554	10.553	16.46	16.25	2.80	2.76
		10.0 min	10.550	10.543	<b>21.84</b>	<b>22.07</b>	<b>3.71</b>	<b>3.75</b>
		60.0 min	10.537	10.551	25.34	25.68	4.31	4.37
		240.0 min	10.538	10.556	27.88	28.90	4.74	4.91
		Score1:	0.07	DU sum difference: 0.05 u				
Score2:	0.72							
LC137-161	1	0.0 min	10.747	10.735	0.18	0.00	0.04	0.00
		0.5 min	10.758	10.735	14.00	<b>13.11</b>	3.22	<b>3.02</b>
		1.0 min	10.750	10.750	<b>15.99</b>	15.37	<b>3.68</b>	3.54
		10.0 min	10.737	10.731	20.47	21.53	4.71	4.95
		60.0 min	10.735	10.748	23.88	24.23	5.49	5.57
		240.0 min	10.727	10.760	27.70	28.88	6.37	6.64
		Score1:	0.88	DU sum difference: 0.84 u				
Score2:	<b>1.01</b>							
LC140-161	1	0.0 min	10.662	10.656	0.00	0.00	0.00	0.00
		0.5 min	10.662	10.661	24.68	<b>23.02</b>	4.94	<b>4.60</b>
		1.0 min	10.670	10.668	26.09	25.70	5.22	5.14
		10.0 min	10.661	10.656	<b>30.90</b>	31.51	<b>6.18</b>	6.30
		60.0 min	10.667	10.678	34.92	36.93	6.98	7.39
		240.0 min	10.658	10.682	38.53	39.43	7.71	7.89
		Score1:	0.91	DU sum difference: 0.76 u				
Score2:	<b>1.20</b>							
LC146-160	1	0.0 min	8.632	8.595	0.00	0.00	0.00	0.00
		0.5 min	8.624	8.613	16.83	15.88	2.36	2.22
		1.0 min	8.621	8.622	<b>18.62</b>	17.90	<b>2.61</b>	2.51
		10.0 min	8.605	8.602	22.65	<b>22.78</b>	3.17	<b>3.19</b>
		60.0 min	8.595	8.620	26.29	26.91	3.68	3.77
		240.0 min	8.604	8.631	30.34	31.08	4.25	4.35
		Score1:	0.15	DU sum difference: 0.08 u				
Score2:	0.84							
LC147-160	1	0.0 min	8.183	8.164	0.03	0.00	0.00	0.00
		0.5 min	8.185	8.170	<b>17.07</b>	16.18	<b>2.22</b>	2.10
		1.0 min	8.186	8.186	18.99	18.22	2.47	2.37
		10.0 min	8.171	8.173	23.15	<b>23.33</b>	3.01	<b>3.03</b>
		60.0 min	8.173	8.182	26.05	26.31	3.39	3.42
		240.0 min	8.157	8.184	28.09	28.93	3.65	3.76
		Score1:	0.11	DU sum difference: 0.06 u				
Score2:	0.69							

Molecule LC: Peptides with sufficient kinetics data, part 12

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC152-162	1	0.0 min	11.927	11.927	0.20	0.09	0.02	0.01
		0.5 min	11.927	11.937	1.18	1.25	0.12	0.13
		1.0 min	11.927	11.927	1.47	1.54	0.15	0.15
		10.0 min	11.934	11.927	0.97	1.62	0.10	0.16
		60.0 min	11.921	11.929	1.81	1.58	0.18	0.16
		240.0 min	11.921	11.934	1.40	<b>1.25</b>	0.14	<b>0.12</b>
Score1:	0.15	DU sum difference: 0.06 u						
Score2:	0.33							
LC155-160	1	0.0 min	5.900	5.900	0.00	0.00	0.00	0.00
		0.5 min	5.900	5.900	25.08	23.88	1.25	1.19
		1.0 min	5.900	5.900	<b>29.10</b>	27.89	<b>1.45</b>	1.39
		10.0 min	5.900	5.891	34.31	<b>34.11</b>	1.72	<b>1.71</b>
		60.0 min	5.900	5.903	35.12	35.52	1.76	1.78
		240.0 min	5.886	5.902	37.73	37.93	1.89	1.90
Score1:	0.22	DU sum difference: -0.05 u						
Score2:	0.66							
LC161-172	1	0.0 min	6.274	6.259	0.00	0.00	0.00	0.00
		0.5 min	6.261	6.250	23.25	22.69	2.56	2.50
		1.0 min	6.260	6.258	<b>24.91</b>	24.32	<b>2.74</b>	2.68
		10.0 min	6.259	6.246	30.86	30.50	3.39	3.36
		60.0 min	6.247	6.256	37.93	38.13	4.17	4.19
		240.0 min	6.246	6.250	41.12	41.94	4.52	4.61
Score1:	0.03	DU sum difference: 0.01 u						
Score2:	0.56							
LC161-175	1	0.0 min	9.357	9.324	0.01	0.00	0.00	0.00
		0.5 min	9.338	9.336	12.05	10.84	1.69	1.52
		1.0 min	9.340	9.332	12.88	11.81	1.80	1.65
		10.0 min	9.339	9.327	14.55	15.29	2.04	2.14
		60.0 min	9.330	9.334	18.91	19.96	2.65	2.79
		240.0 min	9.324	9.337	20.40	22.41	2.86	3.14
Score1:	0.45	DU sum difference: 0.21 u						
Score2:	<b>1.48</b>							
LC161-178	1	0.0 min	8.607	8.605	0.00	0.00	0.00	0.00
		0.5 min	8.602	8.604	10.23	10.23	1.74	1.74
		1.0 min	8.603	8.605	12.44	11.84	2.12	2.01
		10.0 min	8.607	8.597	14.65	14.65	2.49	2.49
		60.0 min	8.597	8.599	17.26	18.26	2.93	3.10
		240.0 min	8.599	8.606	20.27	20.27	3.45	3.45
Score1:	0.12	DU sum difference: 0.07 u						
Score2:	0.39							
LC161-179	1	0.0 min	10.570	10.558	0.00	0.00	0.00	0.00
		0.5 min	10.566	10.561	7.69	6.42	1.38	1.16
		1.0 min	10.568	10.566	8.09	7.93	1.46	1.43
		10.0 min	10.565	10.557	8.37	9.64	1.51	1.74
		60.0 min	10.554	10.567	11.47	12.60	2.06	2.27
		240.0 min	10.549	10.570	12.94	14.49	2.33	2.61
Score1:	0.75	DU sum difference: 0.46 u						
Score2:	<b>1.30</b>							
LC164-189	1	0.0 min	12.729	12.708	0.60	0.20	0.15	0.05
		0.5 min	12.721	12.717	6.19	5.82	1.55	1.45
		1.0 min	12.725	12.750	6.02	6.42	1.51	1.61
		10.0 min	12.717	12.729	6.62	6.82	1.66	1.71
		60.0 min	12.715	12.753	9.24	9.21	2.31	2.30
		240.0 min	12.702	12.739	12.64	13.24	3.16	3.31
Score1:	0.12	DU sum difference: 0.10 u						
Score2:	0.48							

Molecule LC: Peptides with sufficient kinetics data, part 13

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC173-179	1	0.0 min	9.794	9.794	0.00	0.00	0.00	0.00
		0.5 min	9.794	9.802	1.61	1.61	0.10	0.10
		1.0 min	9.795	9.794	2.21	1.81	0.13	0.11
		10.0 min	9.801	9.790	1.61	2.01	0.10	0.12
		60.0 min	9.794	9.801	1.81	2.01	0.11	0.12
		240.0 min	9.790	9.801	2.21	2.61	0.13	0.16
		Score1: 0.18	DU sum difference: 0.04 u					
Score2: 0.34								
LC173-199	1	0.0 min	12.573	12.563	0.00	0.24	0.00	0.06
		0.5 min	12.572	12.562	7.34	7.30	1.91	1.90
		1.0 min	12.572	12.580	8.07	7.87	2.10	2.05
		10.0 min	12.564	12.566	8.69	9.40	2.26	2.44
		60.0 min	12.555	12.576	12.70	12.33	3.30	3.21
		240.0 min	12.548	12.567	15.43	16.05	4.01	4.17
		Score1: 0.28	DU sum difference: 0.25 u					
Score2: 0.52								
LC174-199	1	0.0 min	12.384	12.362	0.06	0.00	0.01	0.00
		0.5 min	12.382	12.360	8.83	7.76	2.21	1.94
		1.0 min	12.383	12.390	9.28	8.83	2.32	2.21
		10.0 min	12.368	12.372	10.50	10.69	2.62	2.67
		60.0 min	12.360	12.380	13.59	13.90	3.40	3.47
		240.0 min	12.356	12.380	17.46	18.46	4.36	4.62
		Score1: 0.02	DU sum difference: -0.02 u					
Score2: 0.75								
LC179-195	1	0.0 min	7.222	7.207	0.00	0.00	0.00	0.00
		0.5 min	7.221	7.208	5.94	5.45	0.95	0.87
		1.0 min	7.221	7.222	7.41	7.31	1.19	1.17
		10.0 min	7.216	7.214	9.61	9.83	1.54	1.57
		60.0 min	7.207	7.221	11.74	12.18	1.88	1.95
		240.0 min	7.206	7.221	15.56	15.63	2.49	2.50
		Score1: 0.04	DU sum difference: 0.02 u					
Score2: 0.32								
LC179-206	1	0.0 min	11.018	11.021	0.00	0.00	0.00	0.00
		0.5 min	11.009	11.016	20.64	18.86	5.37	4.90
		1.0 min	11.016	11.017	22.27	<b>21.28</b>	5.79	<b>5.53</b>
		10.0 min	11.019	11.004	25.08	26.89	6.52	6.99
		60.0 min	11.005	11.015	31.91	31.91	8.30	8.30
		240.0 min	11.003	11.018	35.52	35.72	9.23	9.29
		Score1: 0.08	DU sum difference: 0.07 u					
Score2: <b>1.10</b>								
LC180-195	1	0.0 min	6.085	6.067	0.00	0.00	0.00	0.00
		0.5 min	6.077	6.059	6.10	5.85	0.92	0.88
		1.0 min	6.073	6.071	7.94	7.61	1.19	1.14
		10.0 min	6.065	6.059	10.12	10.48	1.52	1.57
		60.0 min	6.057	6.070	12.08	12.04	1.81	1.81
		240.0 min	6.052	6.063	15.16	15.54	2.27	2.33
		Score1: 0.03	DU sum difference: 0.02 u					
Score2: 0.33								
LC180-214	1	0.0 min	6.962	6.947	0.00	0.00	0.00	0.00
		0.5 min	6.950	6.937	10.41	9.95	3.44	3.28
		1.0 min	6.943	6.948	12.58	12.24	4.15	4.04
		10.0 min	6.926	6.931	15.67	15.72	5.17	5.19
		60.0 min	6.918	6.934	18.80	18.94	6.20	6.25
		240.0 min	6.915	6.927	21.82	22.31	7.20	7.36
		Score1: 0.04	DU sum difference: -0.05 u					
Score2: 0.36								

**Molecule LC: Peptides with sufficient kinetics data, part 14**

Ref: reference series, Exp: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sums)**

Score1/Score2: DU sum / behavior curve; significance limit both scores: 1; added 'p': plus probl. DU values

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC182-195	1	0.0 min	5.206	5.197	0.00	0.00	0.00	0.00
		0.5 min	5.211	5.197	2.63	2.50	0.34	0.32
		1.0 min	5.210	5.198	2.50	2.77	0.33	0.36
		10.0 min	5.197	5.197	2.84	3.09	0.37	0.40
		60.0 min	5.197	5.208	4.53	4.28	0.59	0.56
		240.0 min	5.183	5.195	7.89	7.81	1.03	1.02
	Score1:	0.01	DU sum difference: 0.01 u					
	Score2:	0.24						
=====								
LC196-214	1	0.0 min	6.165	6.142	0.00	0.00	0.00	0.00
		0.5 min	6.158	6.132	<b>17.64</b>	16.30	<b>3.00</b>	2.77
		1.0 min	6.155	6.154	20.47	<b>19.32</b>	3.48	<b>3.28</b>
		10.0 min	6.129	6.134	24.87	24.67	4.23	4.19
		60.0 min	6.120	6.143	28.11	27.90	4.78	4.74
		240.0 min	6.112	6.138	31.12	31.12	5.29	5.29
	Score1:	0.15	DU sum difference:-0.11 u					
	Score2:	0.15						
=====								

**Molecule LC: Peptides/Ranges with insufficient kinetics data, part 1**

Ref: reference series, Exp: experiment series

**Bold typing: problematic DU values**

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC027-042	1	0.0 min	6.401	6.381	<b>1.00</b>	0.48	<b>0.15</b>	0.07
		0.5 min	6.394	6.380	<b>19.87</b>	18.82	<b>2.98</b>	2.82
		1.0 min	6.393	6.393	<b>21.56</b>	21.17	<b>3.23</b>	3.18
		10.0 min	6.385	6.384	<b>26.70</b>	<b>26.90</b>	<b>4.01</b>	<b>4.04</b>
		60.0 min	6.377	6.393	<b>28.86</b>	28.56	<b>4.33</b>	4.28
		240.0 min	6.376	6.388	<b>30.90</b>	32.07	<b>4.64</b>	4.81
=====								
LC029-046	1	0.0 min	8.007	7.977	<b>8.43</b>	<b>8.55</b>	<b>1.35</b>	<b>1.37</b>
		0.5 min	8.006	7.985	13.04	<b>13.65</b>	2.09	<b>2.18</b>
		1.0 min	8.005	7.999	14.33	<b>16.05</b>	2.29	<b>2.57</b>
		10.0 min	7.995	7.987	14.55	<b>13.04</b>	2.33	<b>2.09</b>
		60.0 min	7.990	8.004	13.56	<b>13.79</b>	2.17	<b>2.21</b>
		240.0 min	7.984	7.999	13.56	<b>15.50</b>	2.17	<b>2.48</b>
=====								
LC051-070	1	0.0 min	8.747	8.745	<b>1.45</b>	0.72	<b>0.26</b>	0.13
		0.5 min	8.728	8.736	<b>20.37</b>	22.98	<b>3.67</b>	4.14
		1.0 min	8.726	8.750	<b>23.93</b>	26.85	<b>4.31</b>	4.83
		10.0 min	8.730	8.733	<b>27.50</b>	33.78	<b>4.95</b>	6.08
		60.0 min	8.721	8.734	<b>39.13</b>	40.85	<b>7.04</b>	7.35
		240.0 min	8.729	8.737	<b>31.46</b>	44.43	<b>5.66</b>	8.00
=====								
LC051-093	1	0.0 min	9.463	9.440	0.00	n.d.	0.00	n.d.
		0.5 min	9.453	9.440	11.59	n.d.	4.75	n.d.
		1.0 min	9.455	9.433	12.04	n.d.	4.94	n.d.
		10.0 min	9.435	9.435	13.00	n.d.	5.33	n.d.
		60.0 min	9.440	9.475	15.85	n.d.	6.50	n.d.
		240.0 min	9.427	9.436	19.29	n.d.	7.91	n.d.
=====								
LC071-076	1	0.0 min	11.140	11.171	<b>1.00</b>	1.00	<b>0.05</b>	0.05
		0.5 min	11.122	11.140	<b>6.52</b>	6.81	<b>0.33</b>	0.34
		1.0 min	11.118	11.126	<b>8.23</b>	8.23	<b>0.41</b>	0.41
		10.0 min	11.129	11.104	<b>17.86</b>	18.46	<b>0.89</b>	0.92
		60.0 min	11.121	11.132	<b>19.67</b>	20.27	<b>0.98</b>	1.01
		240.0 min	11.119	11.129	<b>19.67</b>	<b>19.67</b>	<b>0.98</b>	<b>0.98</b>
=====								

Molecule LC: Peptides/Ranges with insufficient kinetics data, part 2

Ref: reference series, Exp: experiment series

**Bold typing: problematic DU values**

Peptide	Range	Exchange Time	Retention Times (min)		Exchange Rates (%)		DU Values (u)	
			Ref	Exp	Ref	Exp	Ref	Exp
LC136-145	2	0.0 min	8.957	8.940	n.d.	<b>0.00</b>	n.d.	<b>0.00</b>
		0.5 min	8.957	8.955	n.d.	<b>12.24</b>	n.d.	<b>0.98</b>
		1.0 min	n.d.	8.958	n.d.	n.d.	n.d.	n.d.
		10.0 min	8.949	8.938	<b>26.29</b>	<b>26.09</b>	<b>2.10</b>	<b>2.09</b>
		60.0 min	8.934	8.955	<b>29.30</b>	n.d.	<b>2.34</b>	n.d.
		240.0 min	8.932	8.943	<b>29.30</b>	n.d.	<b>2.34</b>	n.d.
=====								
LC140-160	1	0.0 min	9.341	9.333	<b>10.84</b>	<b>16.66</b>	<b>2.06</b>	<b>3.16</b>
		0.5 min	9.347	9.344	<b>47.96</b>	<b>45.15</b>	<b>9.11</b>	<b>8.58</b>
		1.0 min	9.343	9.353	<b>49.65</b>	<b>47.96</b>	<b>9.43</b>	<b>9.11</b>
		10.0 min	9.338	9.341	<b>44.71</b>	<b>52.98</b>	<b>8.50</b>	<b>10.07</b>
		60.0 min	9.329	9.343	<b>46.49</b>	<b>52.98</b>	<b>8.83</b>	<b>10.07</b>
		240.0 min	9.329	9.346	<b>49.45</b>	<b>48.64</b>	<b>9.39</b>	<b>9.24</b>
=====								
LC173-178	1	0.0 min	6.339	6.325	n.d.	n.d.	n.d.	n.d.
		0.5 min	6.339	6.328	n.d.	n.d.	n.d.	n.d.
		1.0 min	6.339	6.332	n.d.	n.d.	n.d.	n.d.
		10.0 min	6.333	6.325	n.d.	n.d.	n.d.	n.d.
		60.0 min	6.325	6.330	n.d.	n.d.	n.d.	n.d.
		240.0 min	6.325	6.333	n.d.	n.d.	n.d.	n.d.

Molecule LC: no peptides lacking equivalent range available

Molecule LC: no peptides lacking HDX data in experiment series available

Molecule LC: no peptides lacking HDX data in reference series available

Molecule LC: no peptides lacking HDX data in both series available

Molecule: **HC**  
 Peptide: **HC001-018**  
 Exchangeable protons: 16  
 Index lis-file: 89  
 Sequence: EVQGVESGGGLVKPGGSL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

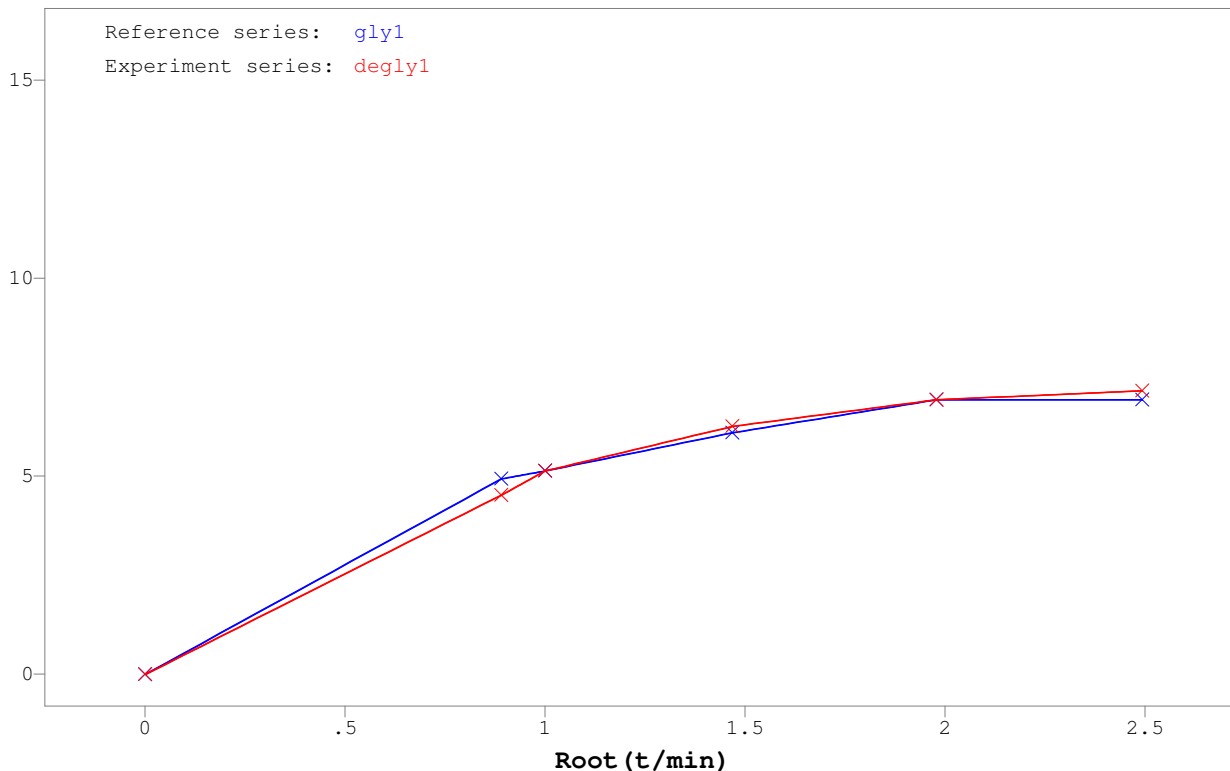
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.996	8.986	0.00	0.00	0.00	0.00
0.5	8.988	8.989	30.84	28.29	4.94	4.53
1.0	8.989	8.991	32.11	32.11	5.14	5.14
10.0	8.985	8.981	38.13	39.13	6.10	6.26
60.0	8.973	8.988	43.34	43.34	6.94	6.94
240.0	8.972	8.986	43.34	44.75	6.94	7.16

Score1 (DU sum): 0.04  
 Score2 (DU Profile): **1.20**  
 DU sum difference (u): -0.02

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC001-020**  
 Exchangeable protons: 18  
 Index lis-file: 90  
 Sequence: EVQGVESGGGLVKPGGSLKL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

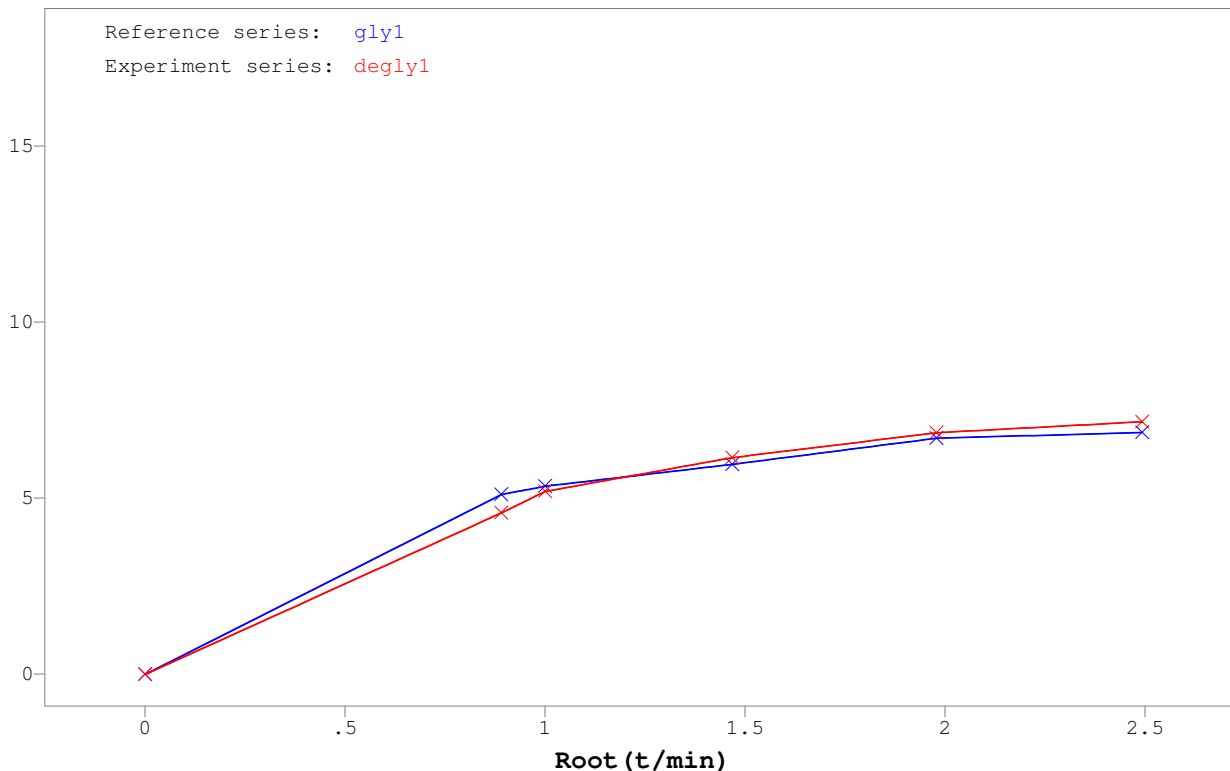
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.604	9.581	0.00	0.00	0.00	0.00
0.5	9.592	9.576	28.39	25.48	5.11	4.59
1.0	9.593	9.595	29.69	28.88	5.34	5.20
10.0	9.591	9.579	33.15	34.21	5.97	6.16
60.0	9.572	9.591	37.27	38.14	6.71	6.86
240.0	9.568	9.596	38.17	39.87	6.87	7.18

Score1 (DU sum): 0.03  
 Score2 (DU Profile): **1.77**  
 DU sum difference (u): -0.02

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC001-022**  
 Exchangeable protons: 20  
 Index lis-file: 205  
 Sequence: EVQGVESGGGLVKPGGSLKLSK  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

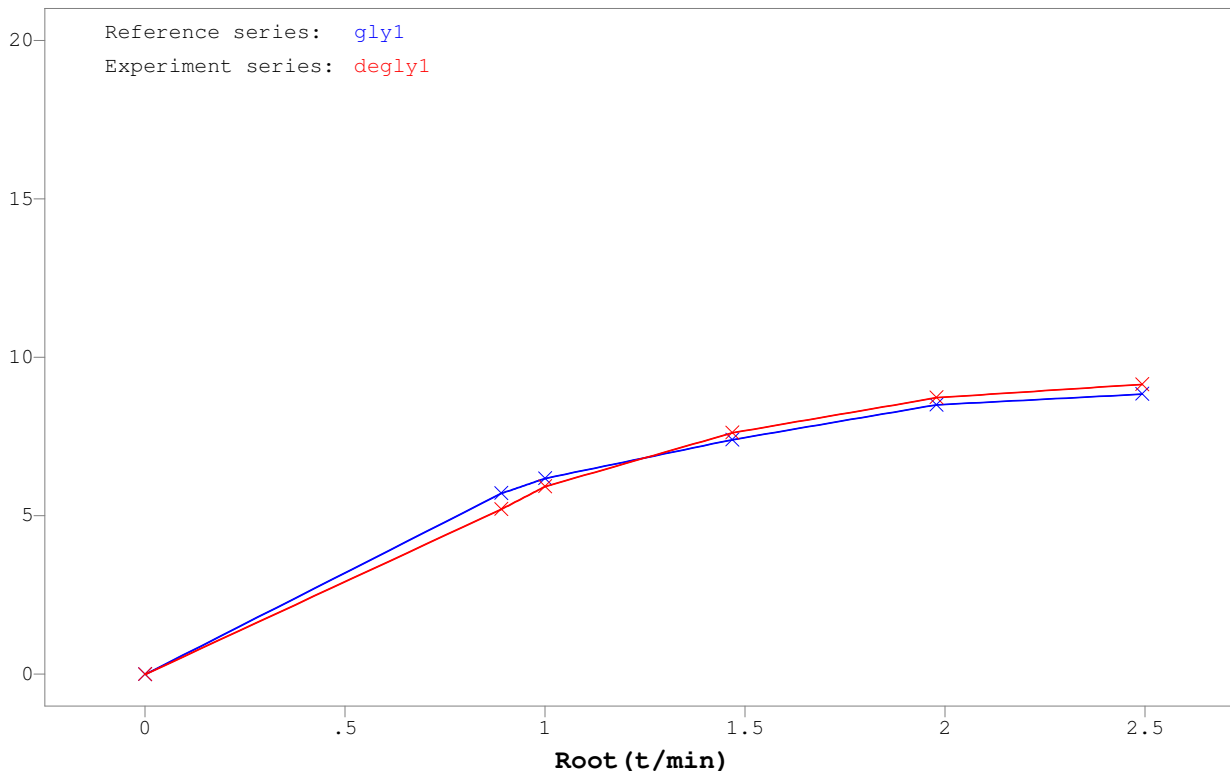
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.422	9.415	0.00	0.00	0.00	0.00
0.5	9.426	9.431	<b>28.57</b>	26.07	<b>5.71</b>	5.21
1.0	9.436	9.443	30.93	29.66	6.19	5.93
10.0	9.432	9.426	37.04	38.13	7.41	7.63
60.0	9.427	9.439	42.55	43.66	8.51	8.73
240.0	9.415	9.442	44.22	45.77	8.84	9.15

Score1 (DU sum): 0.81  
 Score2 (DU Profile): **1.46**  
 DU sum difference (u): 0.60

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **HC**  
 Peptide: **HC001-023**  
 Exchangeable protons: 21  
 Index lis-file: 91  
 Sequence: EVQGVESGGGLVKPGGSLKLSKA  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

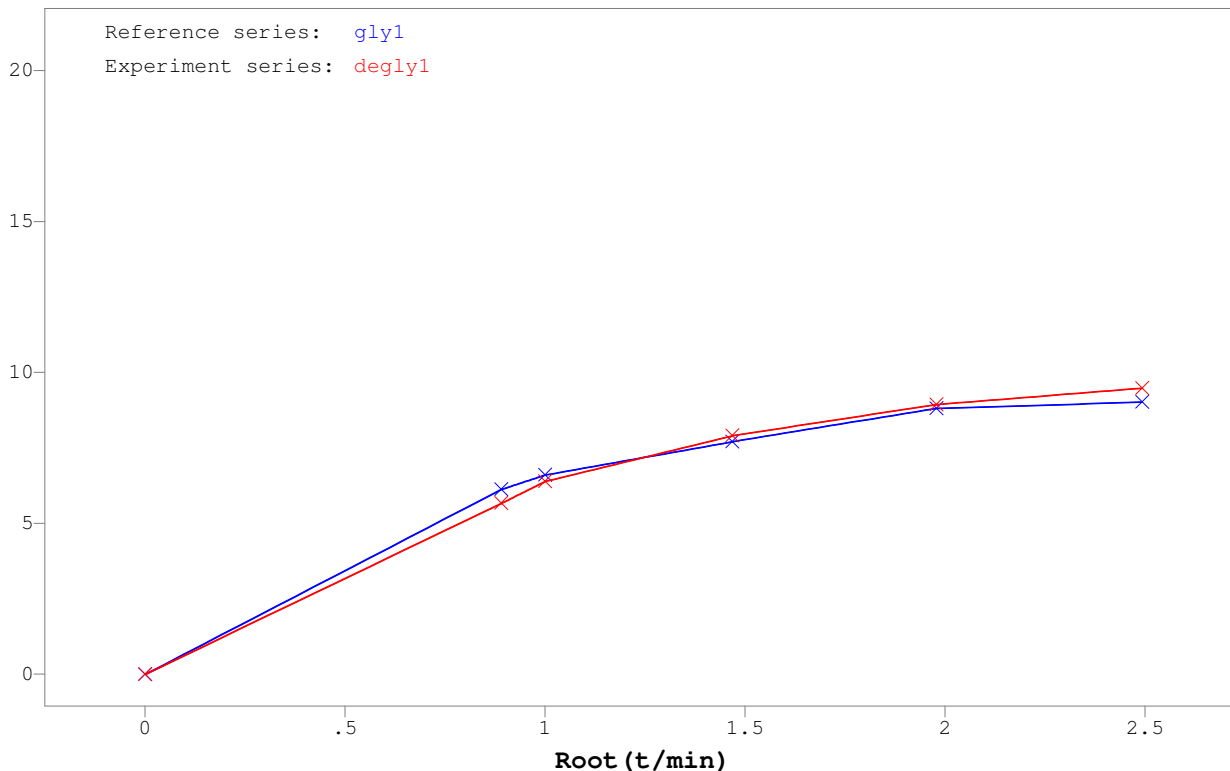
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.374	9.366	0.00	0.00	0.00	0.00
0.5	9.377	9.371	29.19	26.99	6.13	5.67
1.0	9.380	9.381	31.48	<b>30.47</b>	6.61	<b>6.40</b>
10.0	9.376	9.369	36.72	37.65	7.71	7.91
60.0	9.362	9.390	41.97	42.58	8.81	8.94
240.0	9.373	9.379	42.94	45.15	9.02	9.48

Score1 (DU sum): 0.50  
 Score2 (DU Profile): **1.68p**  
 DU sum difference (u): 0.39

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC024-032**  
 Exchangeable protons: 8  
 Index lis-file: 95  
 Sequence: ASGFTFSDY  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

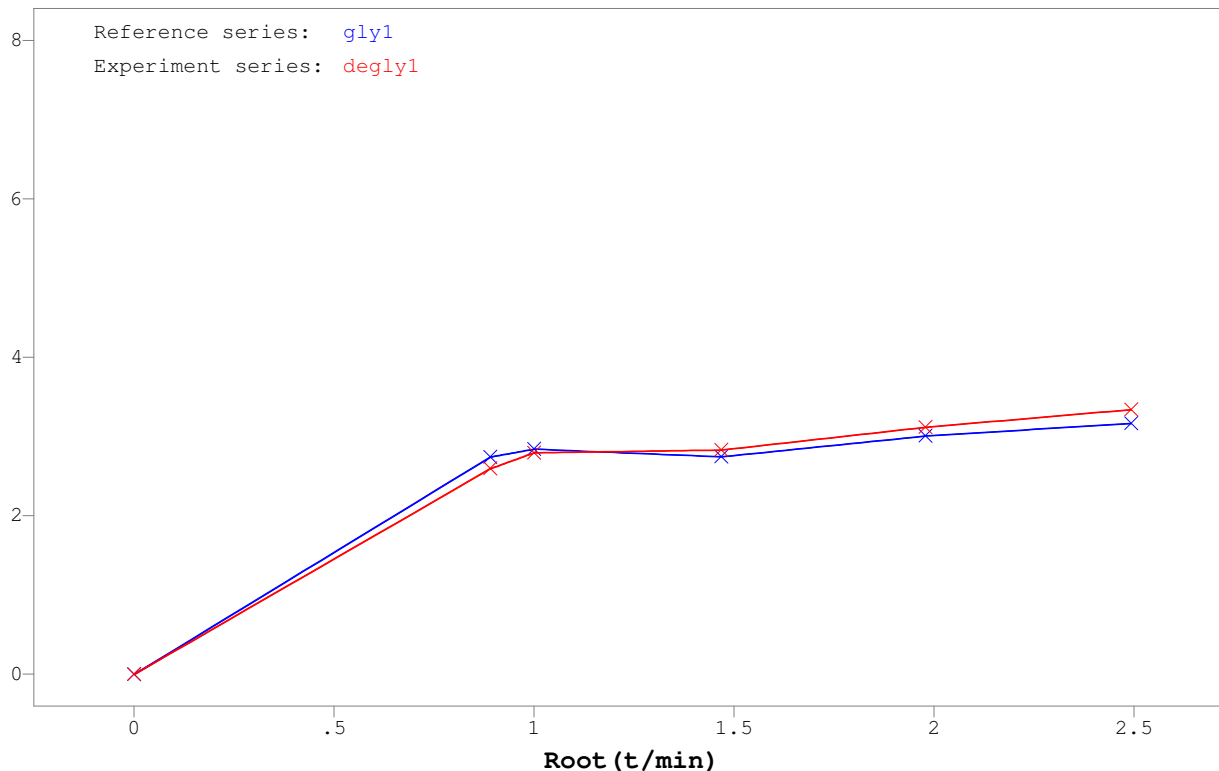
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	12.452	12.452	0.00	0.00	0.00	0.00
0.5	12.452	12.453	34.30	32.45	2.74	2.60
1.0	12.456	12.458	35.54	34.97	2.84	2.80
10.0	12.455	12.442	<b>34.33</b>	35.40	<b>2.75</b>	2.83
60.0	12.445	12.459	37.61	39.00	3.01	3.12
240.0	12.448	12.460	39.61	41.78	3.17	3.34

Score1 (DU sum): 0.37  
 Score2 (DU Profile): **1.70p**  
 DU sum difference (u): 0.11

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC027-031**  
 Exchangeable protons: 4  
 Index lis-file: 96  
 Sequence: FTFS  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

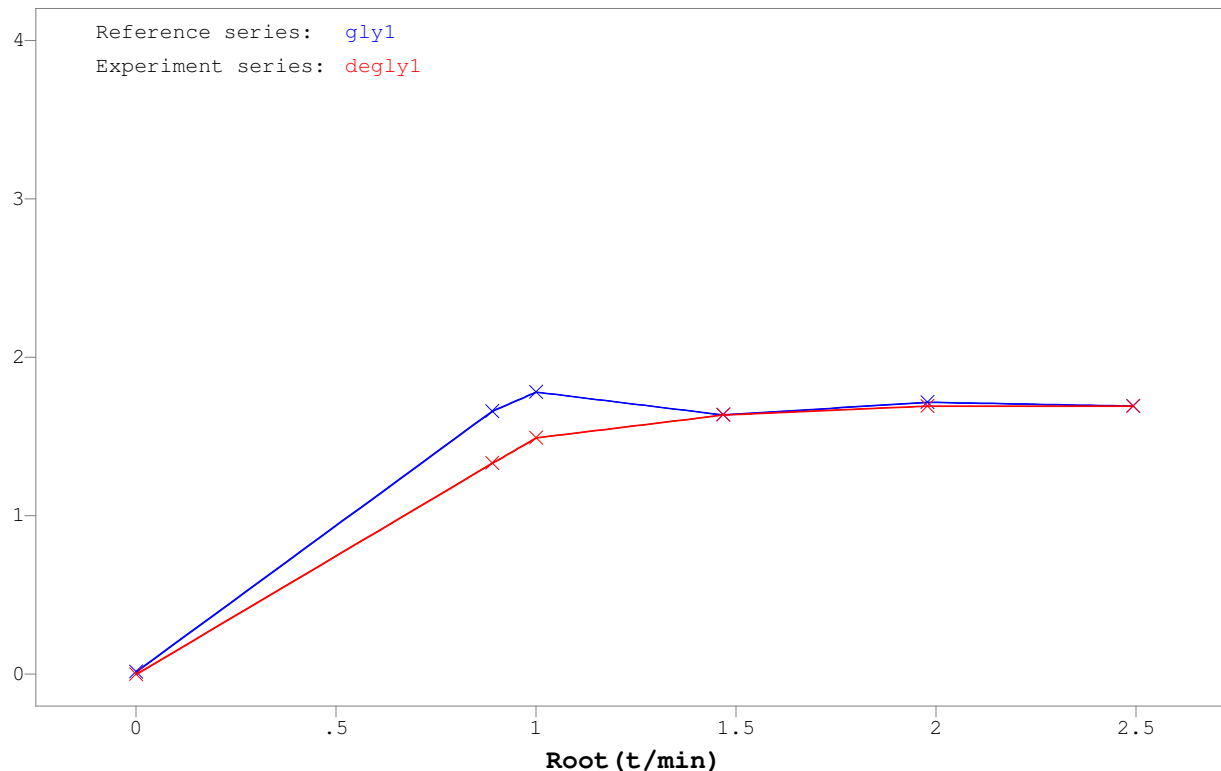
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.195	10.180	0.40	0.00	0.02	0.00
0.5	10.164	10.171	41.54	33.31	1.66	1.33
1.0	10.178	10.161	<b>44.55</b>	37.32	<b>1.78</b>	1.49
10.0	10.169	10.152	40.94	40.94	1.64	1.64
60.0	10.166	10.164	42.94	42.34	1.72	1.69
240.0	10.181	10.164	42.34	42.34	1.69	1.69

Score1 (DU sum): **3.00**  
 Score2 (DU Profile): 2.68  
**DU sum difference (u): -0.44**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC027-032**  
 Exchangeable protons: 5  
 Index lis-file: 97  
 Sequence: FTFS DY  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

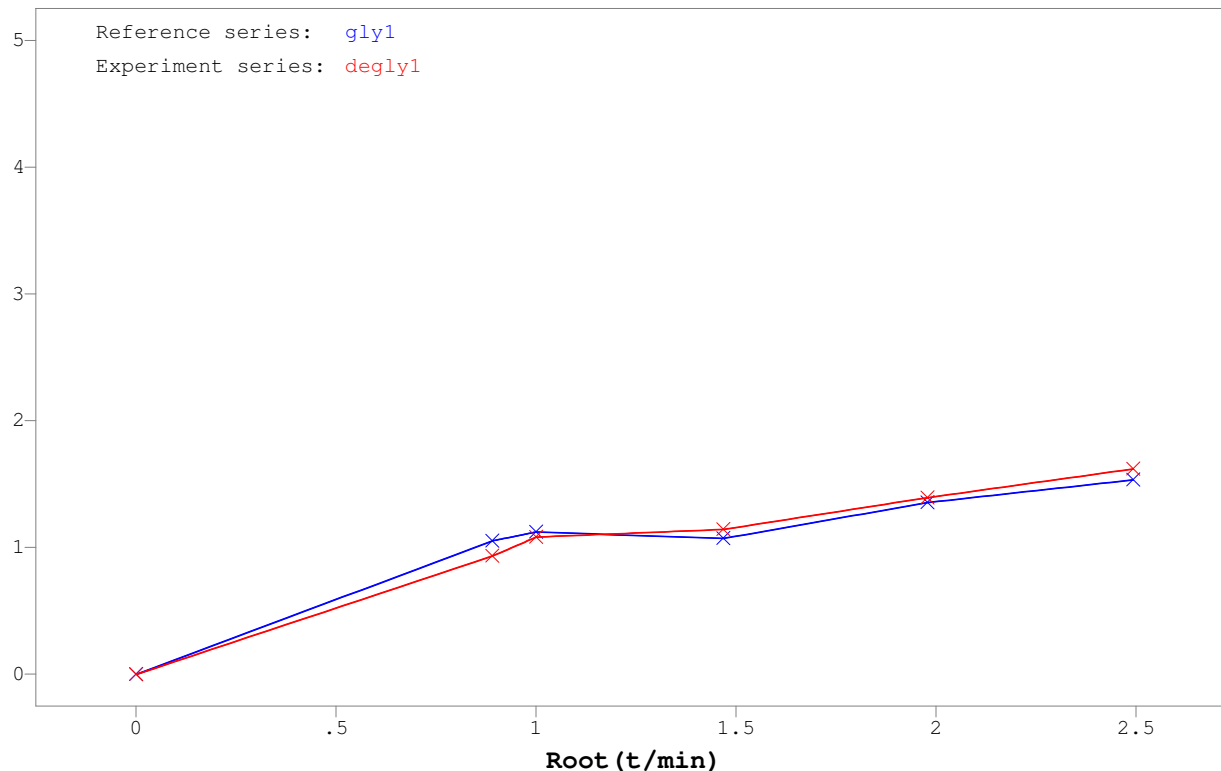
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	12.120	12.120	0.00	0.00	0.00	0.00
0.5	12.105	12.120	21.07	18.66	1.05	0.93
1.0	12.117	12.121	22.48	21.67	1.12	1.08
10.0	12.117	12.106	<b>21.45</b>	22.88	<b>1.07</b>	1.14
60.0	12.109	12.118	27.12	27.89	1.36	1.39
240.0	12.109	12.120	30.70	32.43	1.54	1.62

Score1 (DU sum): 0.23  
 Score2 (DU Profile): **1.66**  
 DU sum difference (u): -0.04

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC057-079**  
 Exchangeable protons: 21  
 Index lis-file: 105  
 Sequence: YTYYPDSVKGRFTISRDNKNNL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

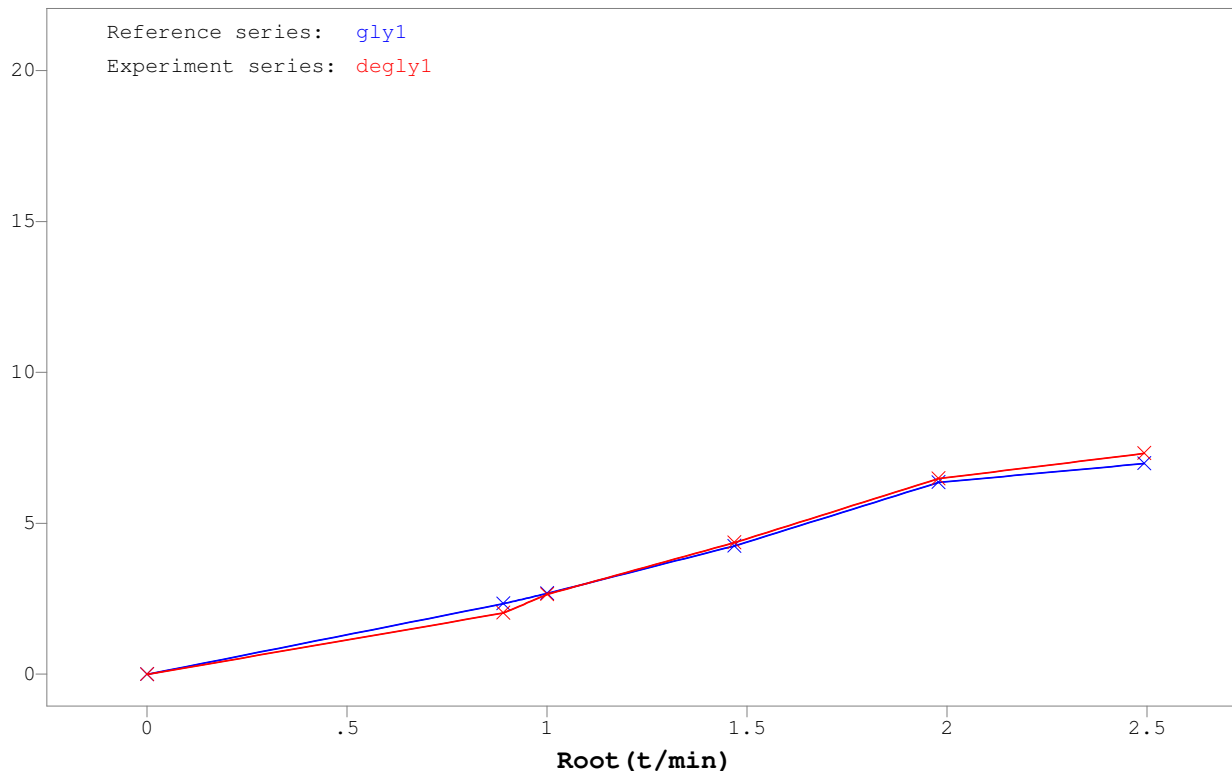
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.725	8.724	0.00	0.00	0.00	0.00
0.5	8.728	8.723	11.16	9.69	2.34	2.03
1.0	8.723	8.729	<b>12.78</b>	12.65	<b>2.68</b>	2.66
10.0	8.721	8.713	20.28	20.81	4.26	4.37
60.0	8.717	8.728	30.31	30.90	6.36	6.49
240.0	8.711	8.728	33.28	34.89	6.99	7.33

Score1 (DU sum): 0.41  
 Score2 (DU Profile): **1.05p**  
 DU sum difference (u): 0.32

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC058-079**  
 Exchangeable protons: 20  
 Index lis-file: 209  
 Sequence: TYPDSVKGRFTISRDNKNNL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

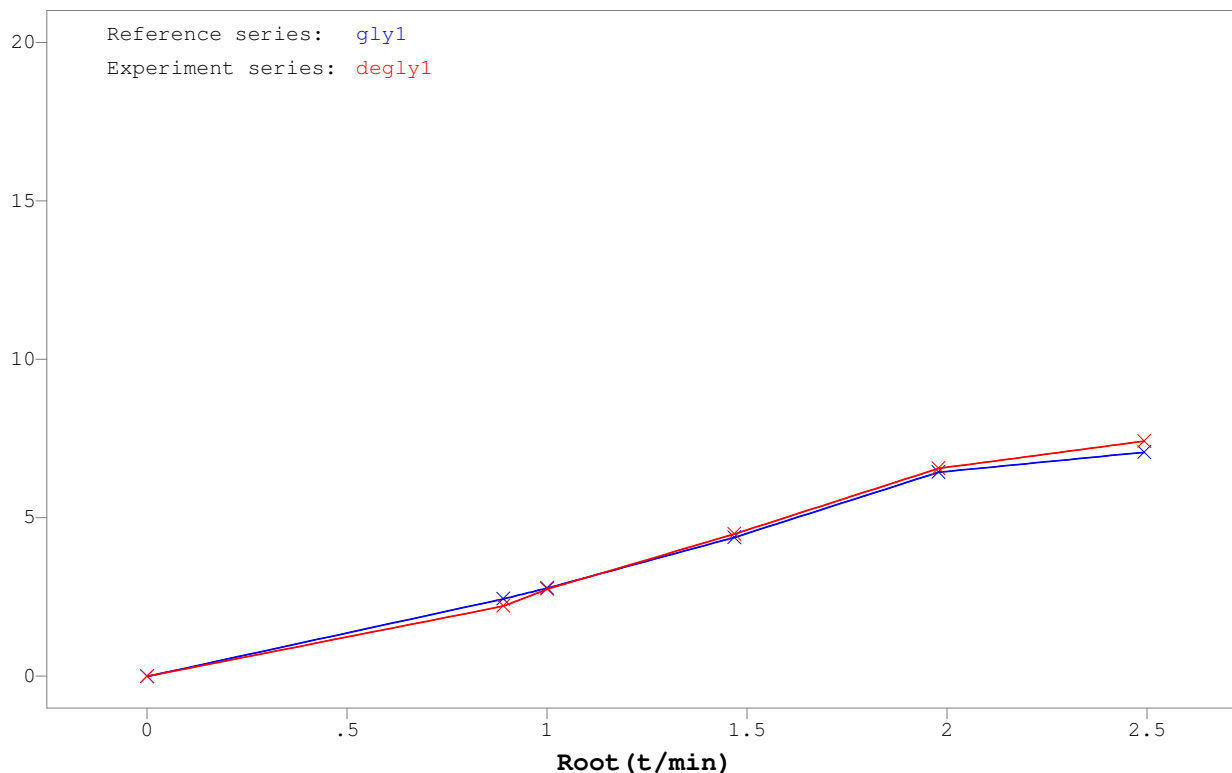
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.234	8.206	0.00	0.00	0.00	0.00
0.5	8.234	8.216	12.22	11.09	2.44	2.22
1.0	8.223	8.227	13.94	13.76	2.79	2.75
10.0	8.208	8.215	<b>21.94</b>	22.48	<b>4.39</b>	4.50
60.0	8.197	8.210	32.23	32.83	6.45	6.57
240.0	8.191	8.216	35.37	37.12	7.07	7.42

Score1 (DU sum): 0.34  
 Score2 (DU Profile): **1.02p**  
 DU sum difference (u): 0.25

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC069-080**  
 Exchangeable protons: 11  
 Index lis-file: 108  
 Sequence: TISRDNAKNNLY  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

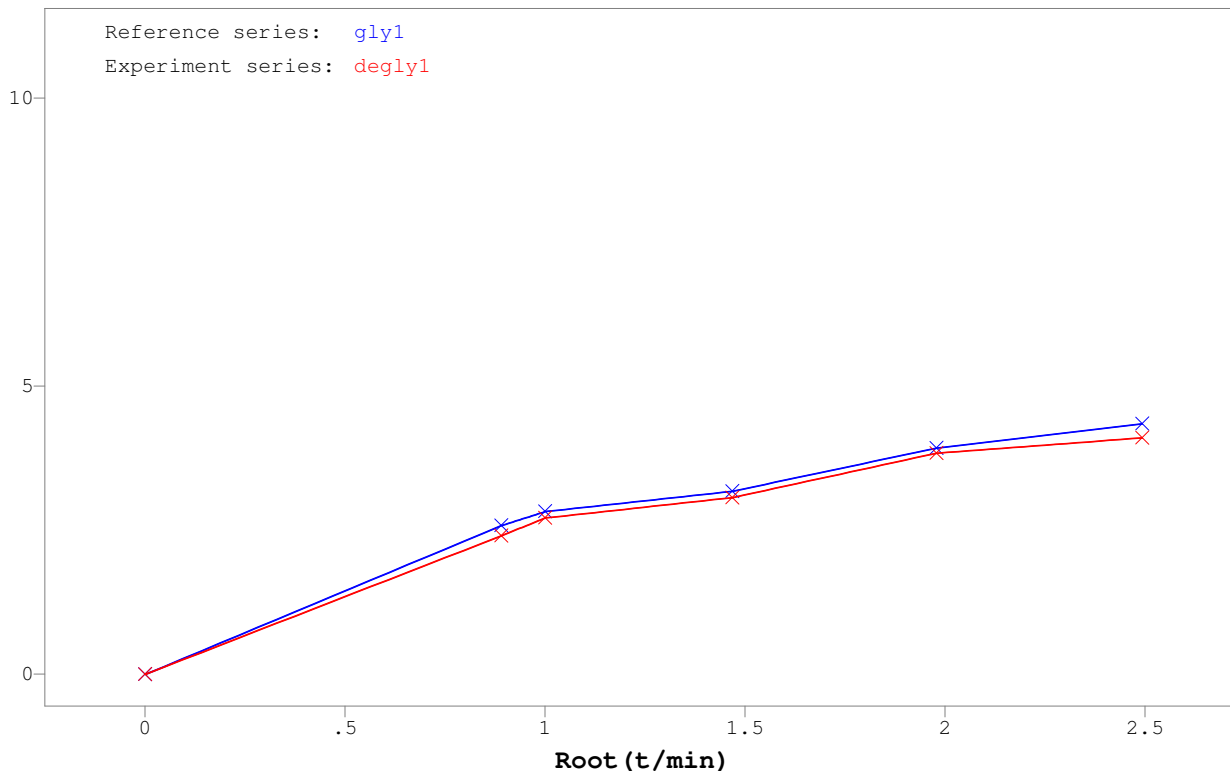
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.160	6.165	0.00	0.00	0.00	0.00
0.5	6.161	6.146	23.48	21.87	2.58	2.41
1.0	6.160	6.154	25.69	24.68	2.83	2.72
10.0	6.154	6.145	28.90	27.89	3.18	3.07
60.0	6.144	6.155	35.72	34.92	3.93	3.84
240.0	6.148	6.153	39.53	37.32	4.35	4.11

Score1 (DU sum): **1.96**  
 Score2 (DU Profile): 1.60  
**DU sum difference (u): -0.73**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC070-078**  
 Exchangeable protons: 8  
 Index lis-file: 109  
 Sequence: ISRDNAKNN  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

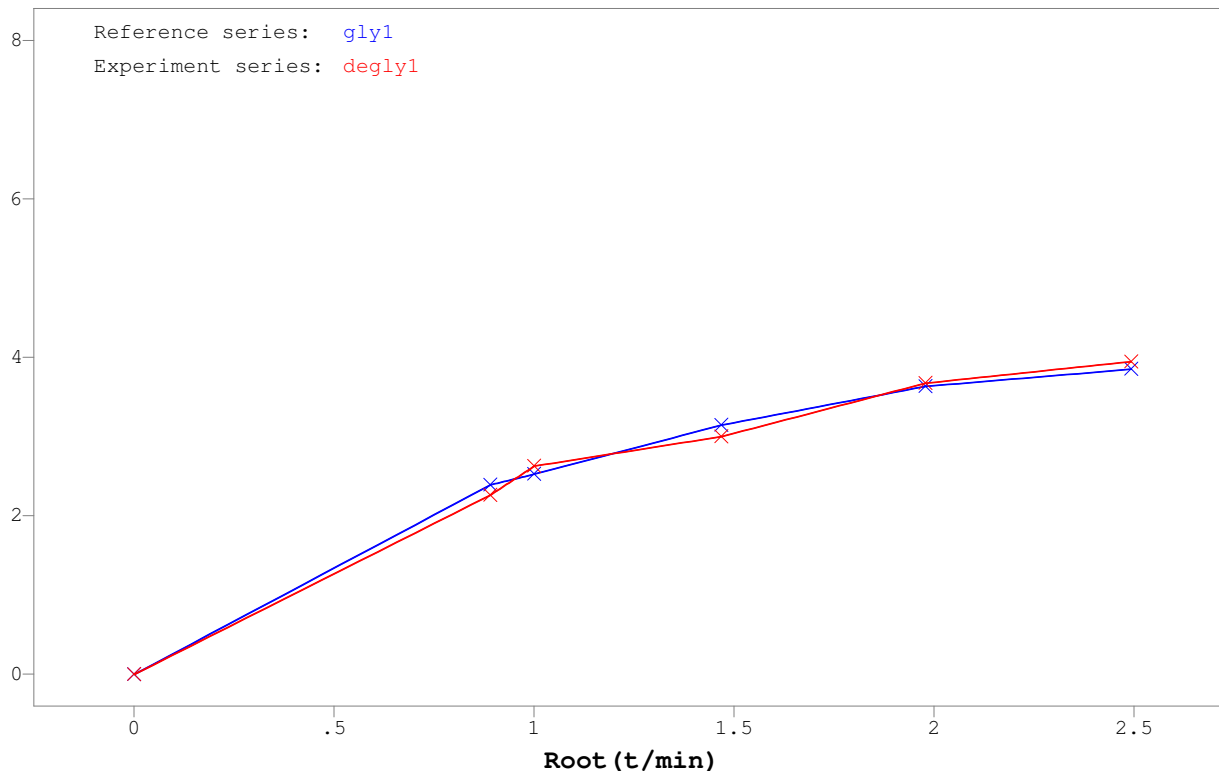
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	4.824	4.812	0.00	0.00	0.00	0.00
0.5	4.804	4.798	29.90	28.29	2.39	2.26
1.0	4.800	4.804	31.59	32.86	2.53	2.63
10.0	4.791	4.789	39.33	37.53	3.15	3.00
60.0	4.791	4.804	45.45	45.95	3.64	3.68
240.0	4.786	4.795	<b>48.16</b>	49.37	<b>3.85</b>	3.95

Score1 (DU sum): 0.53  
 Score2 (DU Profile): **1.50**  
 DU sum difference (u): -0.16

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **HC**  
 Peptide: **HC094-110**  
 Exchangeable protons: 16  
 Index lis-file: 115  
 Sequence: YYCARDKAYYGNYGDAM  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

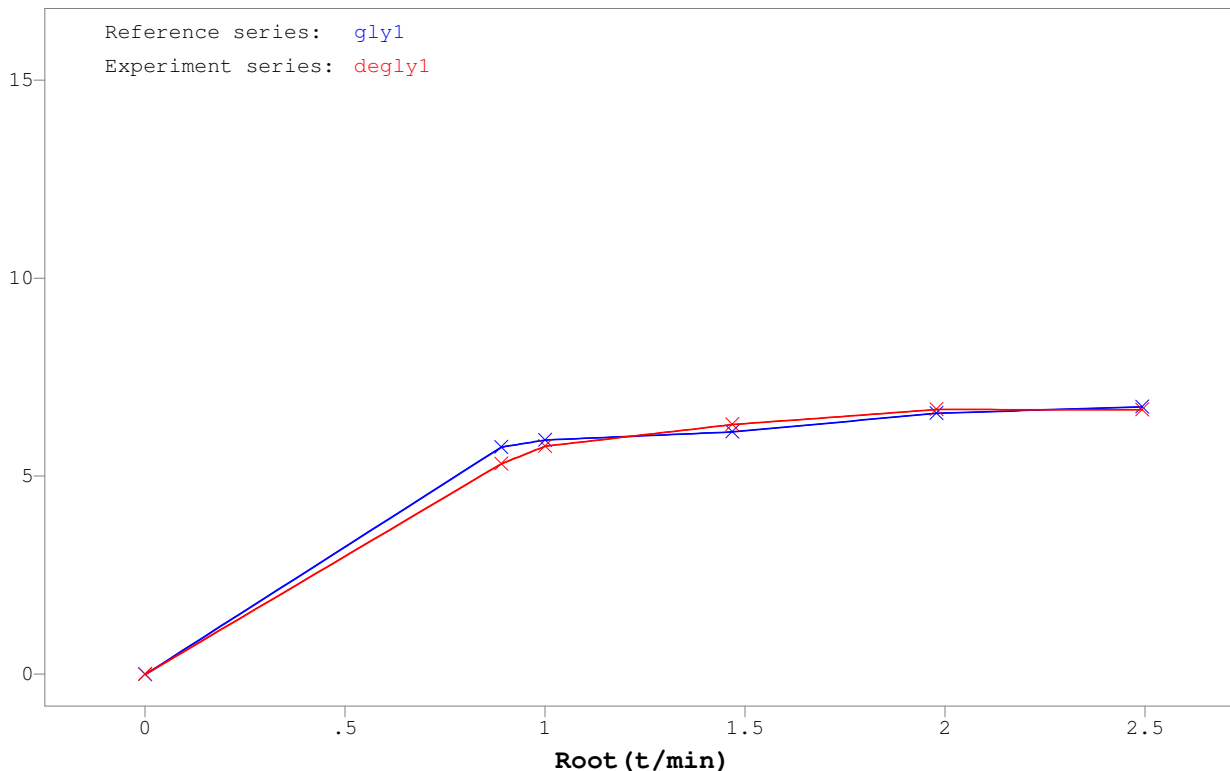
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.913	8.885	0.00	0.00	0.00	0.00
0.5	8.908	8.887	35.87	33.24	5.74	5.32
1.0	8.912	8.902	36.98	36.02	5.92	5.76
10.0	8.890	8.887	38.27	39.43	6.12	6.31
60.0	8.894	8.894	41.21	41.80	6.59	6.69
240.0	8.897	8.898	42.24	41.78	6.76	6.69

Score1 (DU sum): 0.68  
 Score2 (DU Profile): **1.40**  
 DU sum difference (u): -0.37

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC094-137**  
 Exchangeable protons: 39  
 Index lis-file: 116  
 Sequence: YYCARDKAYYGNYGDAMDYWGQTSVTVSSAKTTPPSVYPLAPG  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

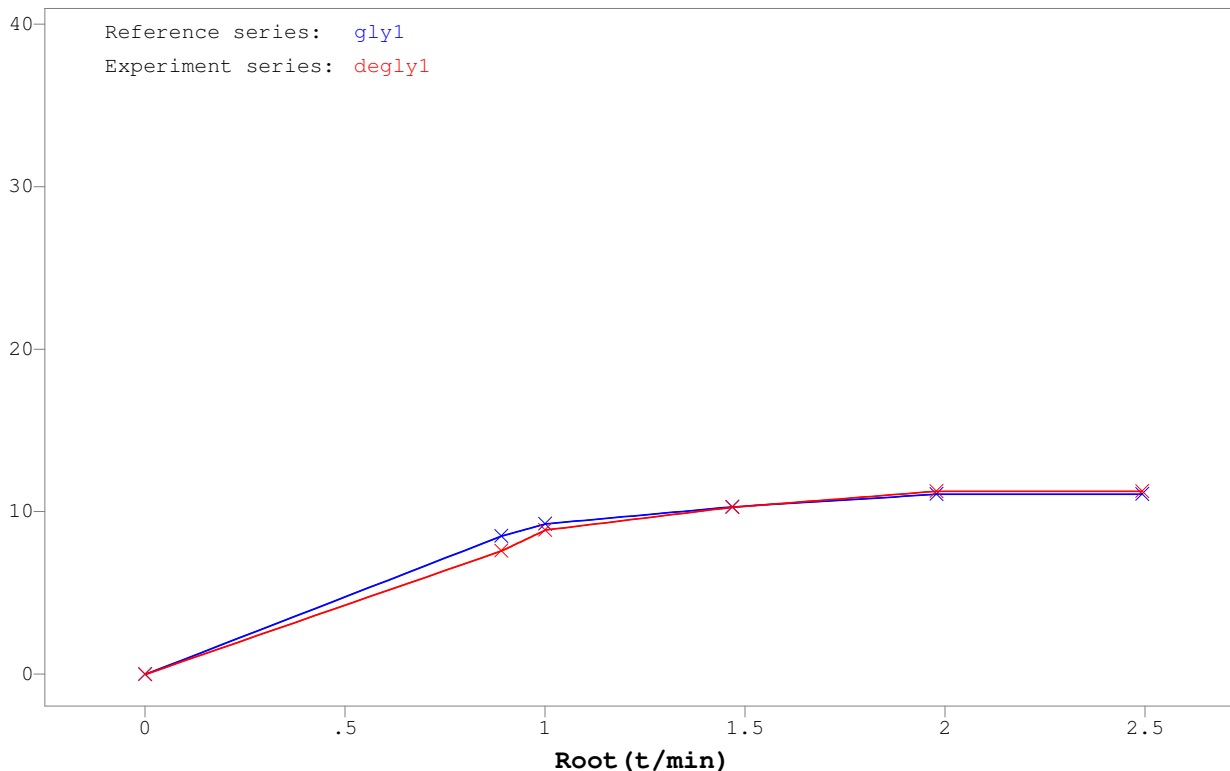
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.707	9.684	0.00	0.00	0.00	0.00
0.5	9.680	9.690	21.81	19.48	8.51	7.60
1.0	9.686	9.684	23.75	22.78	9.26	8.88
10.0	9.685	9.683	26.44	26.38	10.31	10.29
60.0	9.678	9.685	28.44	28.92	11.09	11.28
240.0	9.671	9.692	28.45	28.91	11.10	11.27

Score1 (DU sum): 0.72  
 Score2 (DU Profile): **1.04**  
 DU sum difference (u): -0.95

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC111-139**  
 Exchangeable protons: 24  
 Index lis-file: 211  
 Sequence: DYWGQGTSTVTSSAKITPPSVYPLAPGSA  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

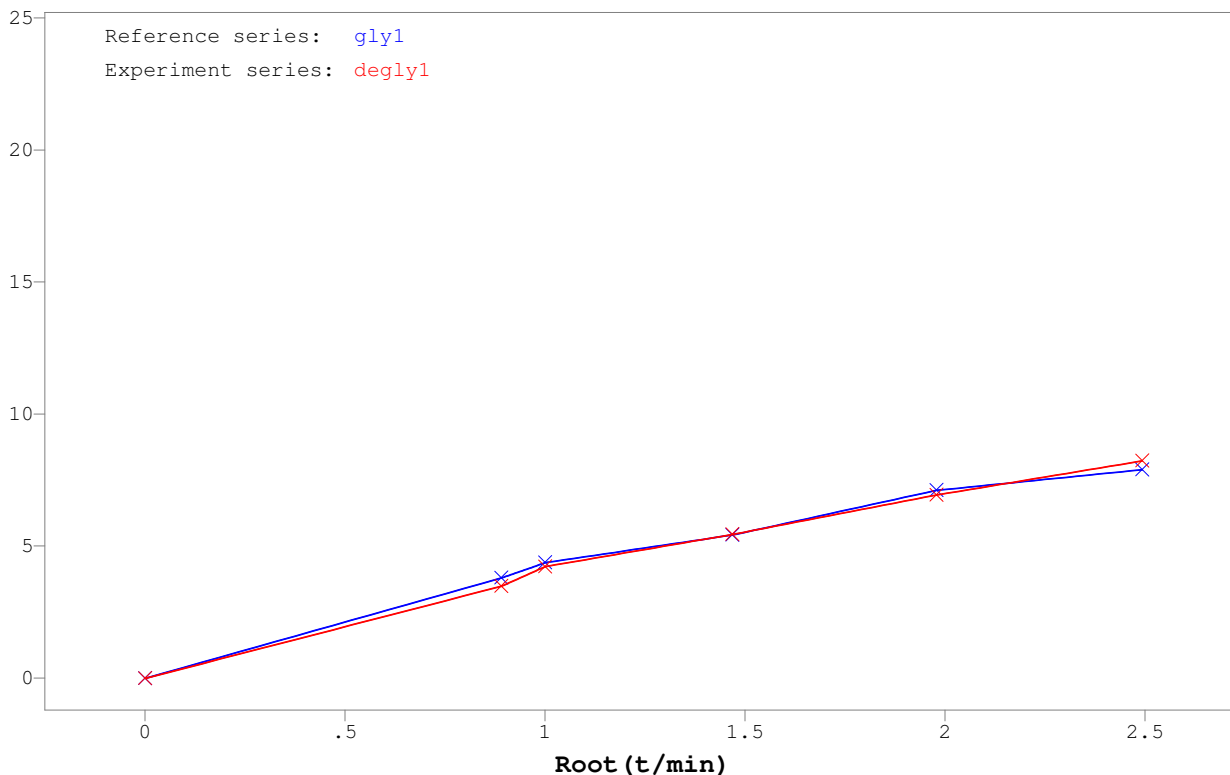
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.324	11.324	0.00	0.00	0.00	0.00
0.5	11.322	11.324	15.84	14.54	3.80	3.49
1.0	11.321	11.320	18.26	17.64	4.38	4.23
10.0	11.322	11.310	22.63	22.71	5.43	5.45
60.0	11.307	11.320	29.68	28.94	7.12	6.95
240.0	11.306	11.321	32.94	34.33	7.91	8.24

Score1 (DU sum): 0.35  
 Score2 (DU Profile): **1.00**  
 DU sum difference (u): -0.29

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC111-145**  
 Exchangeable protons: 30  
 Index lis-file: 119  
 Sequence: DYWGQGTSVTVSSAKITPPSVYPLAPGSAAQTNSM  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

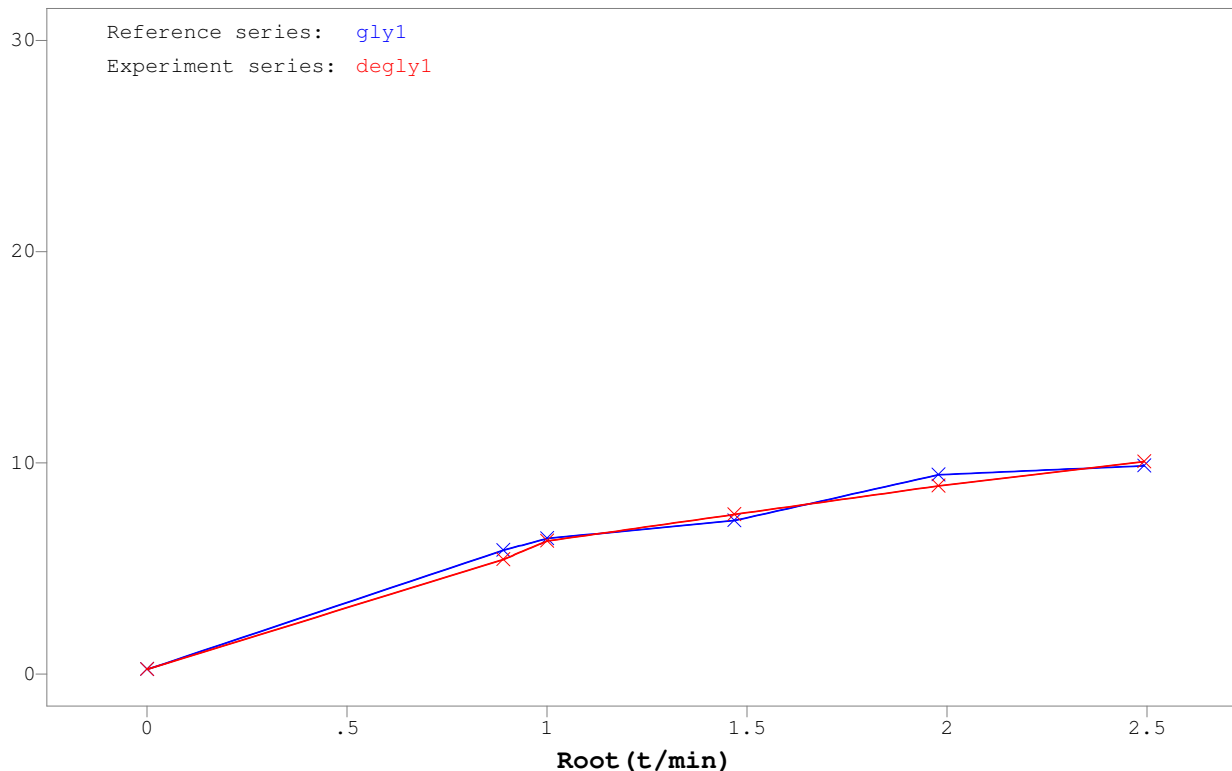
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.441	11.438	<b>0.80</b>	0.78	<b>0.24</b>	0.24
0.5	11.437	11.440	19.60	18.15	5.88	5.45
1.0	11.437	11.426	21.45	21.05	6.44	6.32
10.0	11.438	11.426	24.28	25.25	7.28	7.57
60.0	11.422	11.436	31.50	29.74	9.45	8.92
240.0	11.416	11.436	32.92	33.59	9.88	10.08

Score1 (DU sum): 0.64  
 Score2 (DU Profile): **1.27p**  
 DU sum difference (u): -0.71

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC112-120**  
 Exchangeable protons: 8  
 Index lis-file: 120  
 Sequence: YWGQTSVT  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

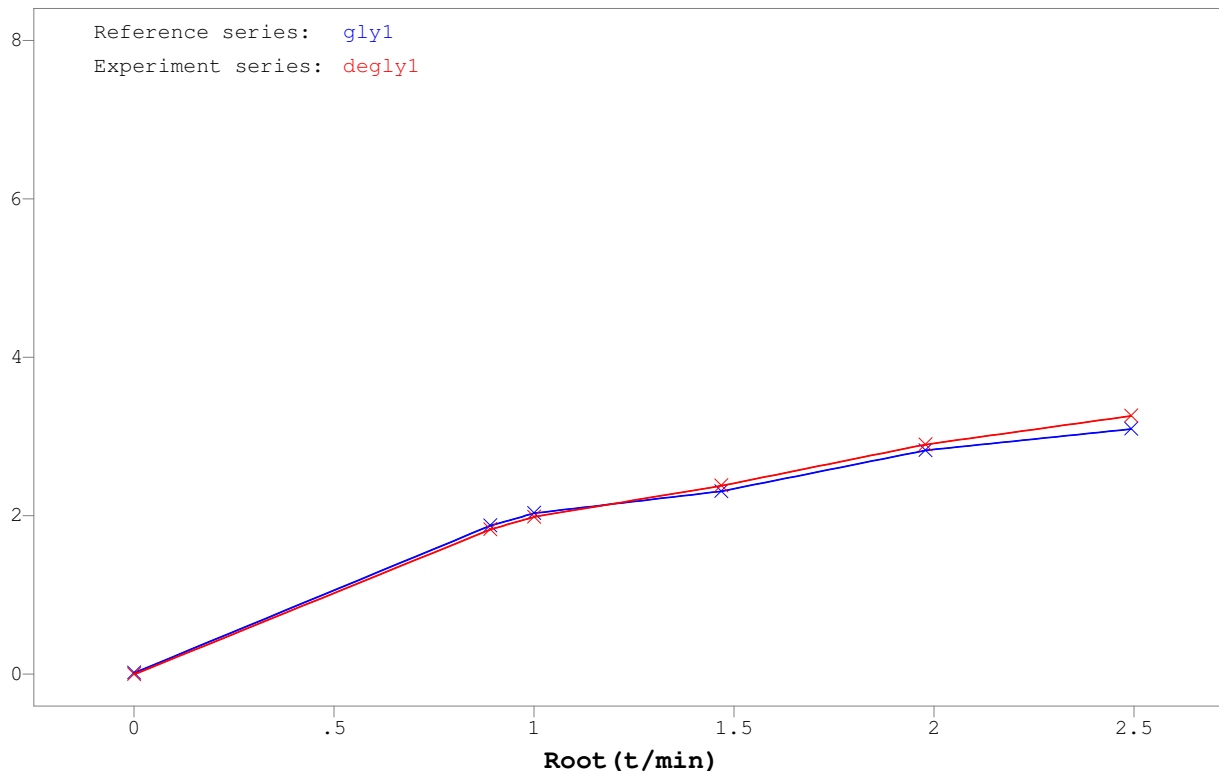
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.765	9.759	0.25	0.00	0.02	0.00
0.5	9.763	9.759	23.48	22.88	1.88	1.83
1.0	9.761	9.756	25.44	24.87	2.04	1.99
10.0	9.769	9.746	28.90	29.78	2.31	2.38
60.0	9.760	9.762	35.36	36.28	2.83	2.90
240.0	9.756	9.764	38.74	40.80	3.10	3.26

Score1 (DU sum): 0.72  
 Score2 (DU Profile): **1.27**  
 DU sum difference (u): 0.19

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC112-139**  
 Exchangeable protons: 23  
 Index lis-file: 121  
 Sequence: YWGQGSVTVSSAKTTPPSVYPLAPGSA  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

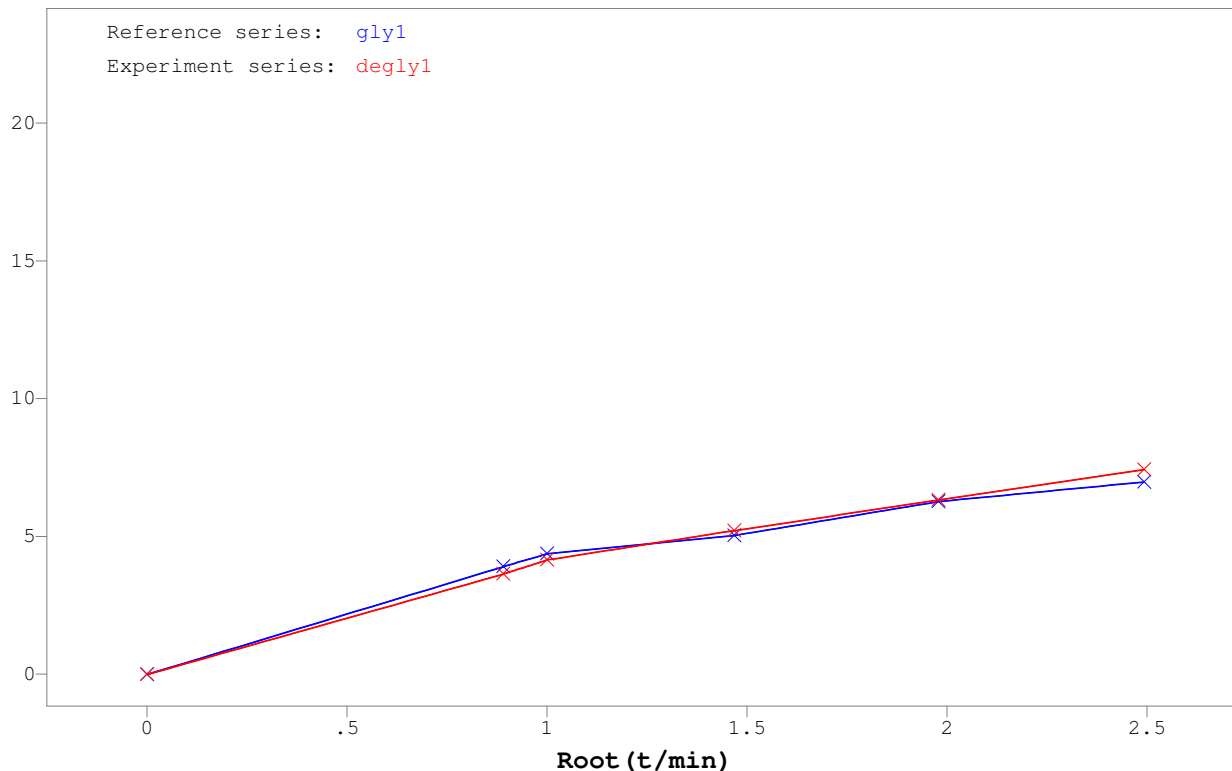
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.032	11.056	0.00	0.00	0.00	0.00
0.5	11.045	11.043	17.01	15.83	3.91	3.64
1.0	11.041	11.040	19.02	18.05	4.37	4.15
10.0	11.043	11.036	21.91	22.68	5.04	5.22
60.0	11.029	11.043	27.26	27.49	6.27	6.32
240.0	11.028	11.043	30.35	32.29	6.98	7.43

Score1 (DU sum): 0.24  
 Score2 (DU Profile): **1.23**  
 DU sum difference (u): 0.18

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC113-139**  
 Exchangeable protons: 22  
 Index lis-file: 124  
 Sequence: WGQGTSVTVSSAKTTPPSVYPLAPGSA  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

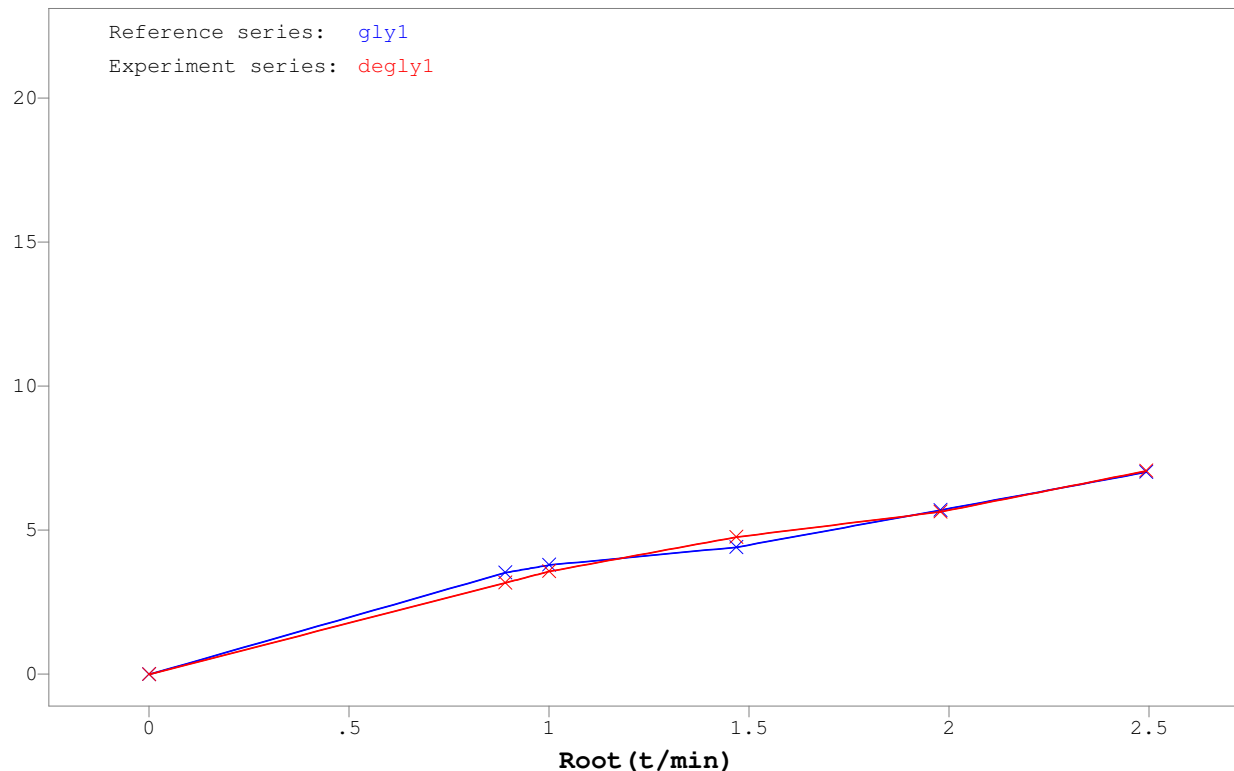
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.222	10.226	0.00	0.00	0.00	0.00
0.5	10.218	10.220	16.05	14.45	3.53	3.18
1.0	10.221	10.218	17.26	<b>16.25</b>	3.80	<b>3.58</b>
10.0	10.210	10.207	20.07	21.67	4.41	4.77
60.0	10.218	10.224	25.93	25.65	5.71	5.64
240.0	10.209	10.218	31.91	32.11	7.02	7.06

Score1 (DU sum): 0.03  
 Score2 (DU Profile): **1.07**  
 DU sum difference (u): -0.02

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC115-140**  
 Exchangeable protons: 21  
 Index lis-file: 212  
 Sequence: QGTSVTVSSAKITPPSVYPLAPGSAA  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

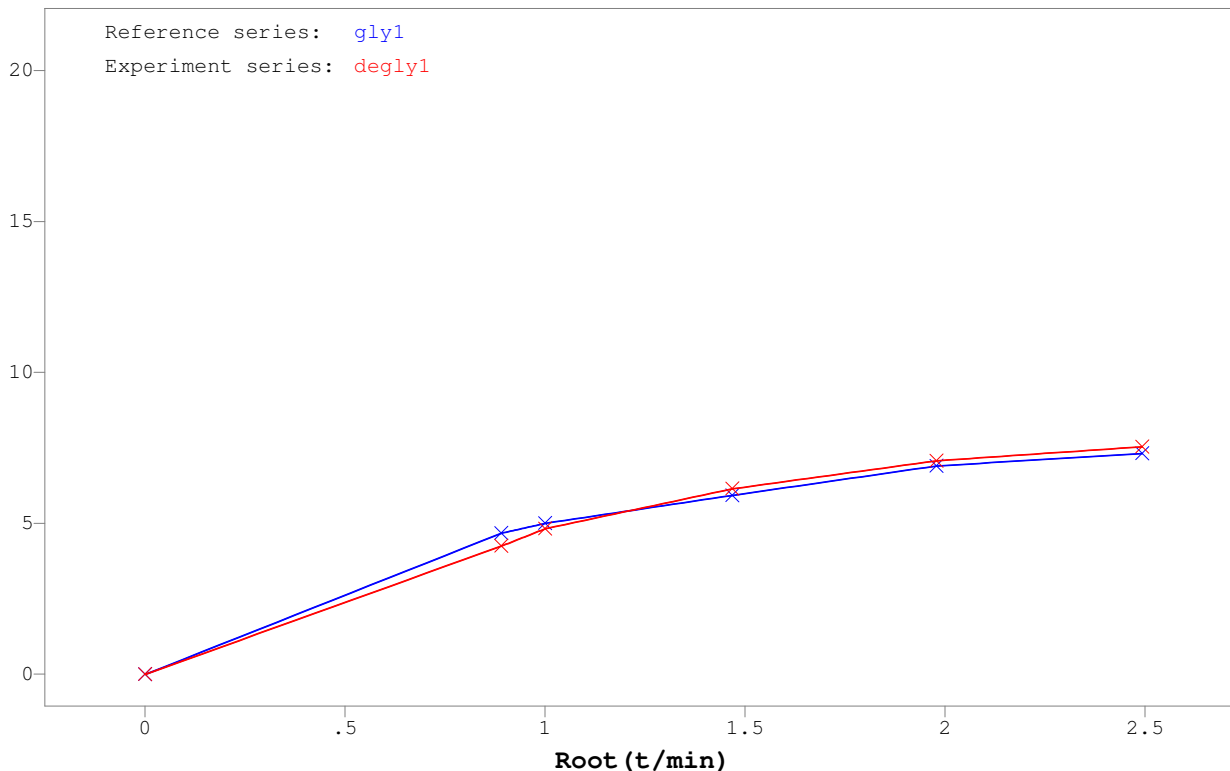
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.582	10.569	0.00	0.00	0.00	0.00
0.5	10.592	10.575	22.28	20.26	4.68	4.25
1.0	10.578	10.597	23.85	23.00	5.01	4.83
10.0	10.589	10.590	28.27	29.30	5.94	6.15
60.0	10.579	10.600	32.91	33.72	6.91	7.08
240.0	10.580	10.604	<b>34.87</b>	35.94	<b>7.32</b>	7.55

Score1 (DU sum): 0.34  
 Score2 (DU Profile): **1.37**  
 DU sum difference (u): -0.26

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **HC**  
 Peptide: **HC119-142**  
 Exchangeable protons: 19  
 Index lis-file: 127  
 Sequence: VTVSSAKTTPPSVYPLAPGSAAQT  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

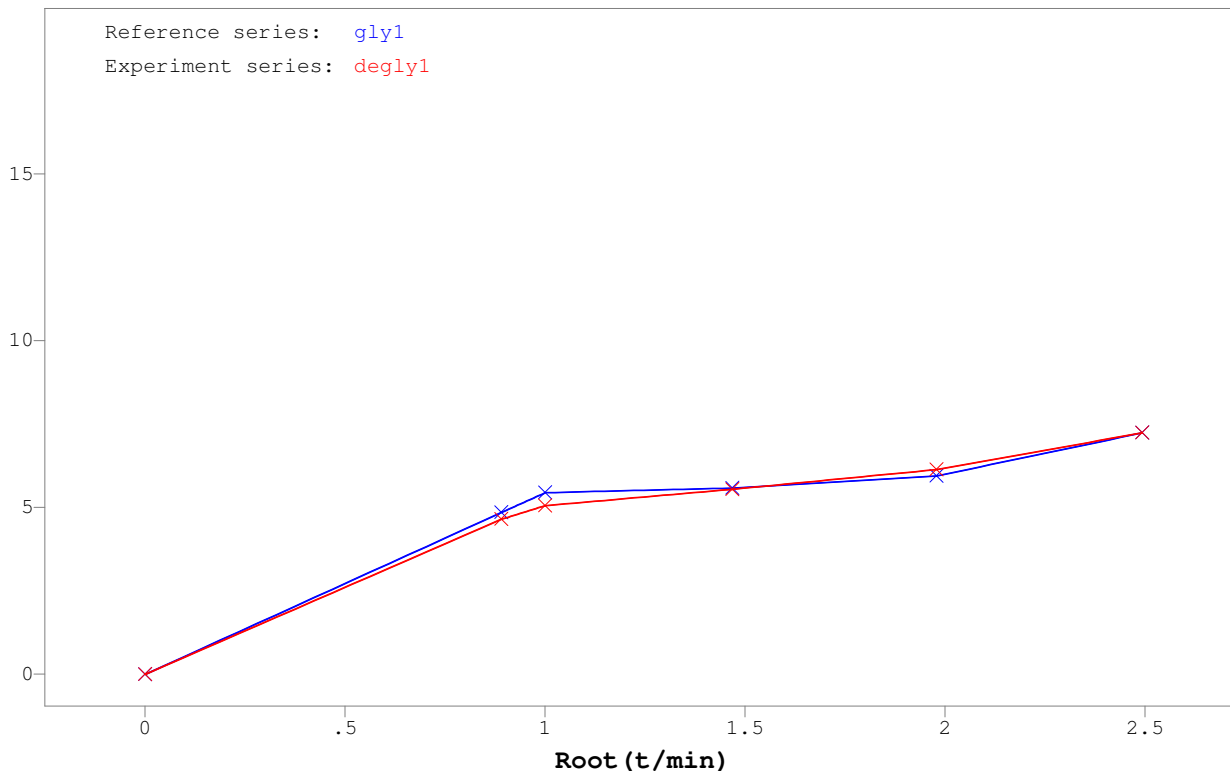
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.807	8.797	0.00	0.00	0.00	0.00
0.5	8.810	8.804	25.54	24.47	4.85	4.65
1.0	8.800	8.814	28.66	26.62	5.44	5.06
10.0	8.806	8.804	29.39	29.20	5.58	5.55
60.0	8.793	8.807	31.30	32.31	5.95	6.14
240.0	8.793	8.806	38.10	38.10	7.24	7.24

Score1 (DU sum): 0.68  
 Score2 (DU Profile): **1.04**  
 DU sum difference (u): -0.44

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC121-139**  
 Exchangeable protons: 14  
 Index lis-file: 129  
 Sequence: VSSAKTTPPSVYPLAPGSA  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

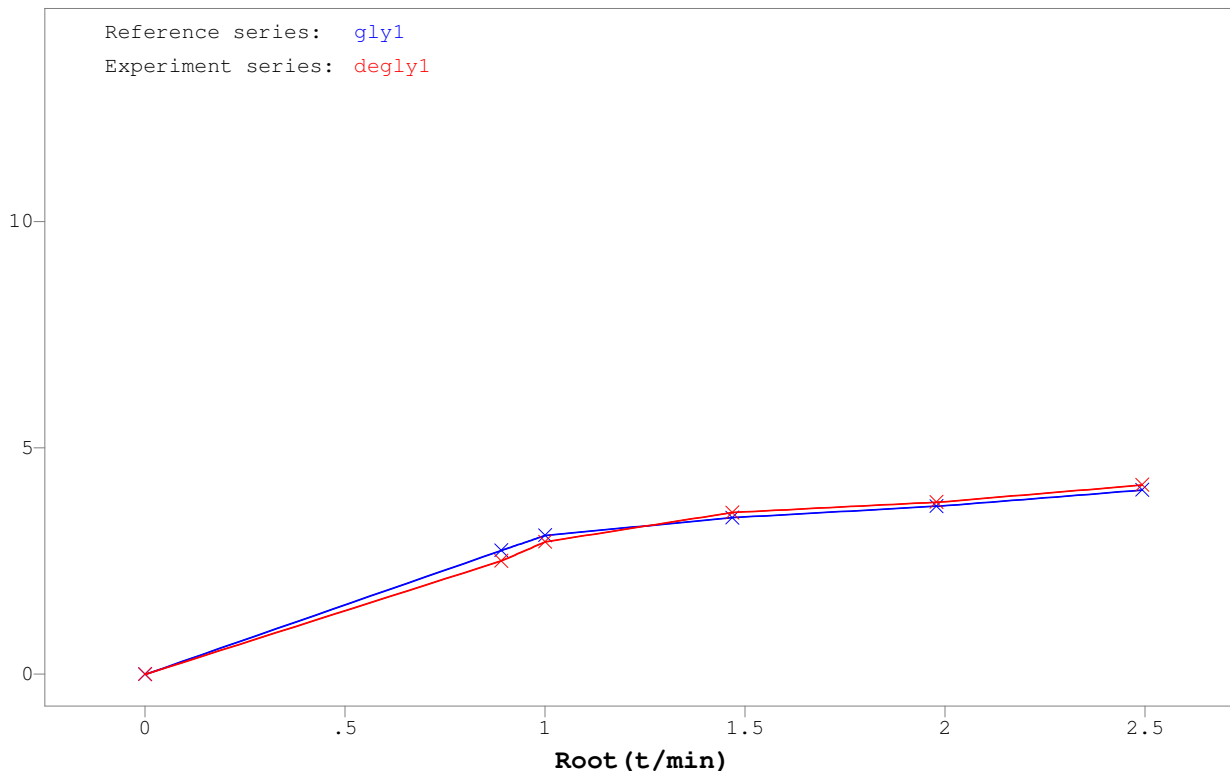
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.878	8.869	0.00	0.00	0.00	0.00
0.5	8.876	8.878	19.55	17.90	2.74	2.51
1.0	8.880	8.883	21.91	20.91	3.07	2.93
10.0	8.877	8.875	24.73	25.54	3.46	3.58
60.0	8.868	8.881	26.52	27.16	3.71	3.80
240.0	8.866	8.881	<b>29.10</b>	<b>29.90</b>	<b>4.07</b>	<b>4.19</b>

Score1 (DU sum): 0.39  
 Score2 (DU Profile): **1.19p**  
 DU sum difference (u): -0.20

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC121-142**  
 Exchangeable protons: 17  
 Index lis-file: 130  
 Sequence: VSSAKTTPPSVYPLAPGSAAQT  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

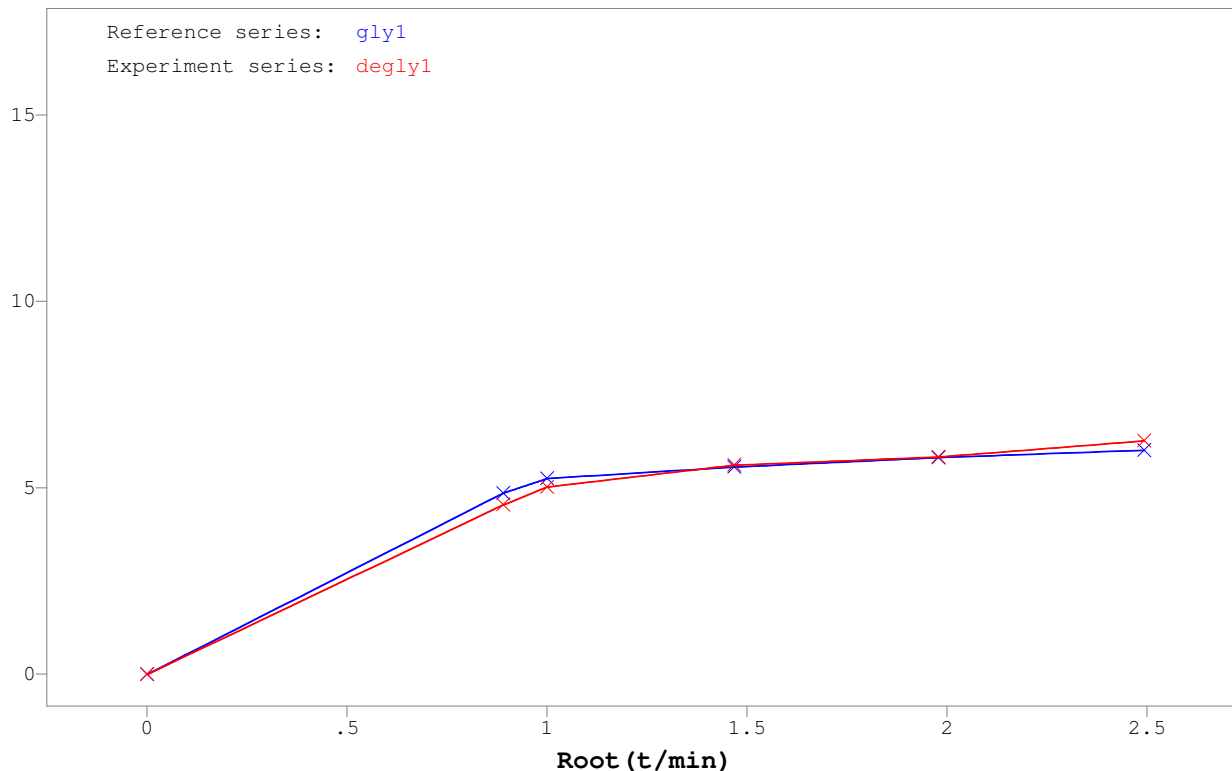
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.578	8.561	0.00	0.00	0.00	0.00
0.5	8.567	8.562	28.60	26.74	4.86	4.55
1.0	8.563	8.567	30.90	29.56	5.25	5.03
10.0	8.561	8.559	32.71	33.01	5.56	5.61
60.0	8.553	8.570	34.20	34.29	5.81	5.83
240.0	8.549	8.558	35.37	36.84	6.01	6.26

Score1 (DU sum): 0.39  
 Score2 (DU Profile): **1.23**  
 DU sum difference (u): -0.23

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC132-184**  
 Exchangeable protons: 47  
 Index lis-file: 213  
 Sequence: YPLAPGSAAQTNSMVLGCLVKGYFPEPVITVWNSGSLSSGVHTFFPAVLQSDL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

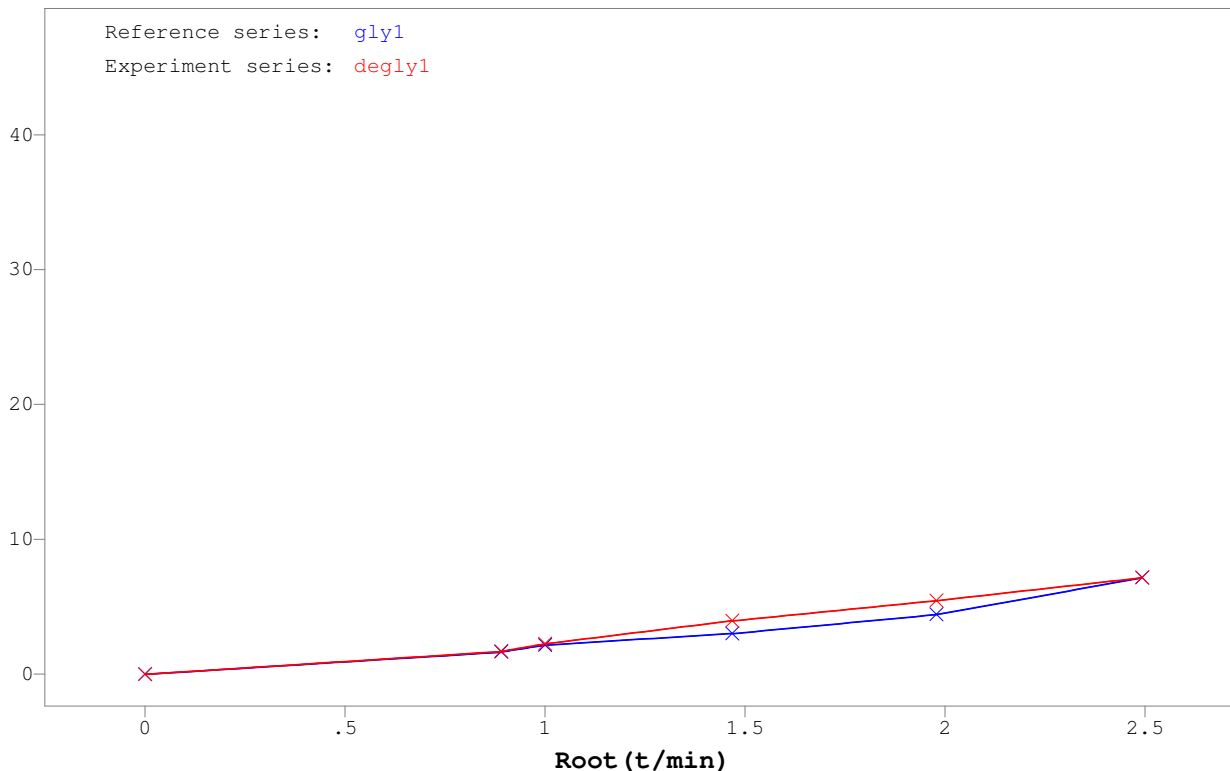
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.609	11.626	0.00	0.00	0.00	0.00
0.5	11.610	11.612	3.52	3.61	1.65	1.70
1.0	11.619	11.602	4.58	4.80	2.15	2.25
10.0	11.598	11.610	6.42	8.43	3.02	3.96
60.0	11.590	11.603	9.43	11.64	4.43	5.47
240.0	11.597	11.599	15.25	15.25	7.17	7.17

Score1 (DU sum): **1.34**  
 Score2 (DU Profile): 1.09  
**DU sum difference (u): 2.13**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC138-177**  
 Exchangeable protons: 36  
 Index lis-file: 133  
 Sequence: SAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFP  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

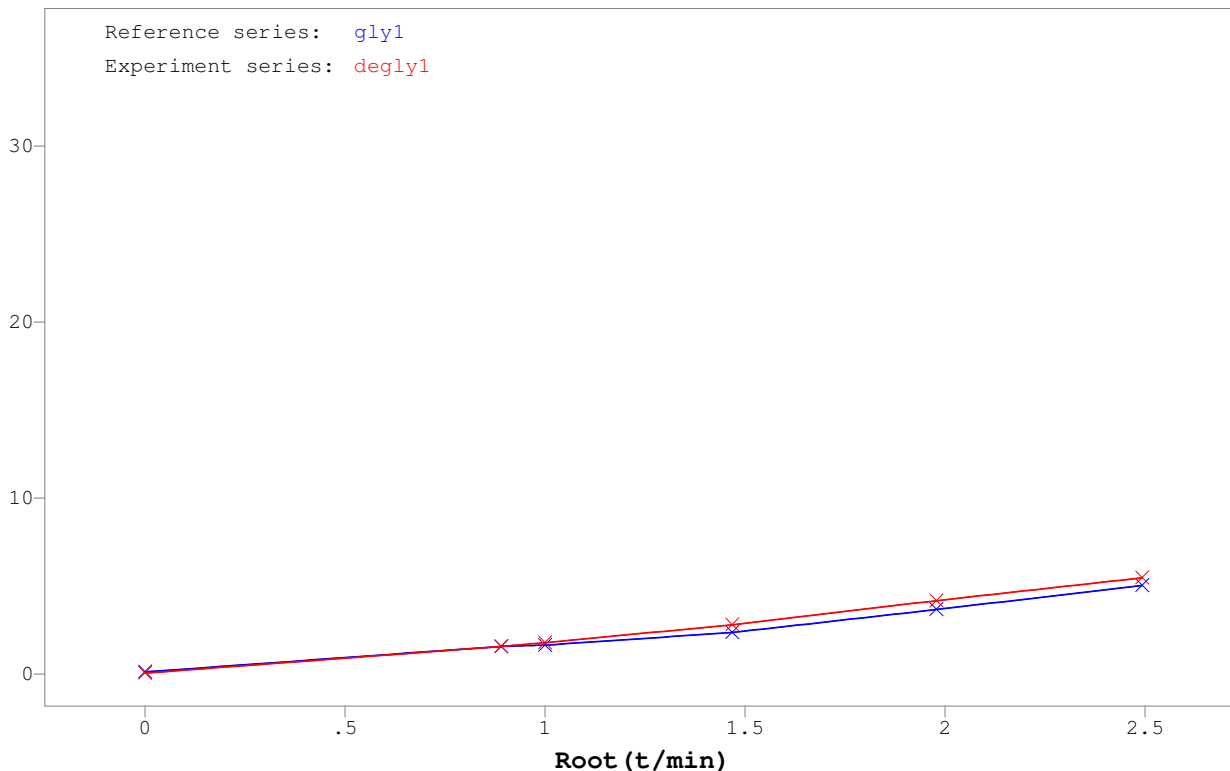
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.229	11.212	0.40	0.20	0.14	0.07
0.5	11.230	11.218	4.41	4.41	1.59	1.59
1.0	11.233	11.231	4.62	5.02	1.66	1.81
10.0	11.218	11.216	6.62	7.83	2.38	2.82
60.0	11.209	11.217	10.23	11.64	3.68	4.19
240.0	11.201	11.224	14.05	15.25	5.06	5.49

Score1 (DU sum): **1.19**  
 Score2 (DU Profile): 1.07  
**DU sum difference (u): 1.44**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC162-169**  
 Exchangeable protons: 7  
 Index lis-file: 217  
 Sequence: VTWNSGSL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

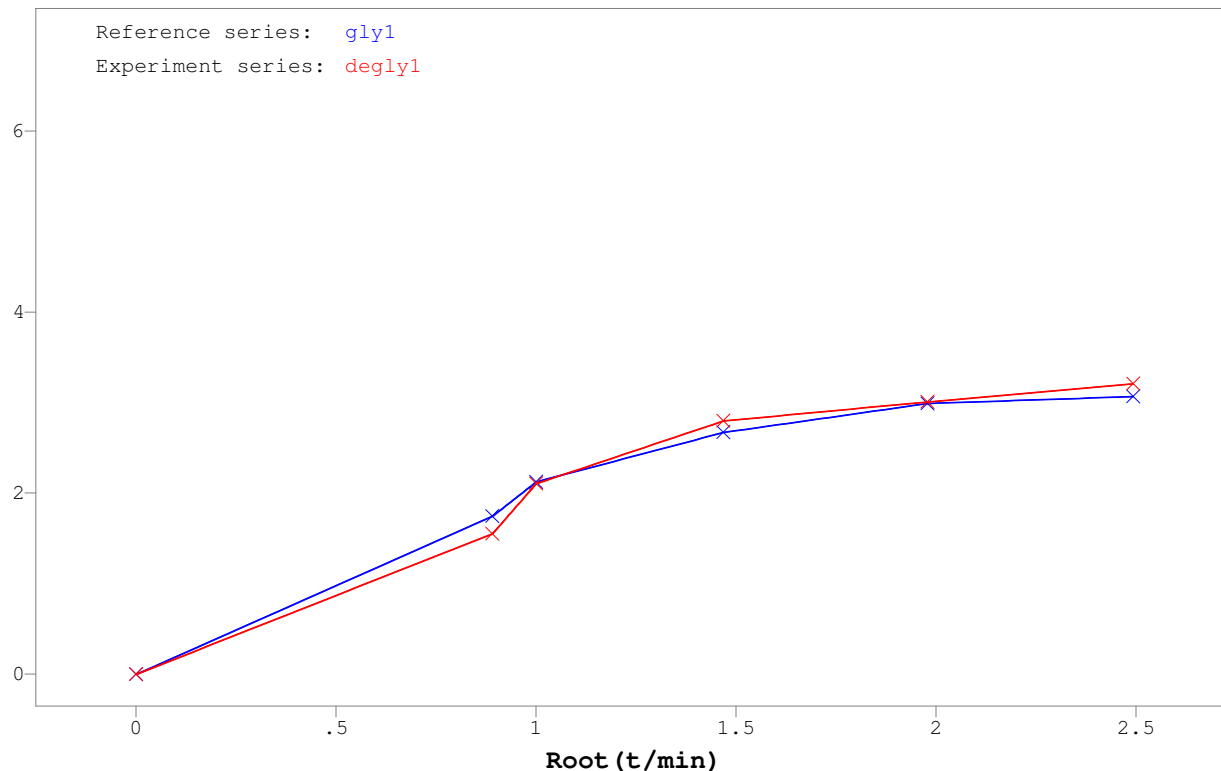
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.815	10.822	0.00	0.00	0.00	0.00
0.5	10.813	10.814	24.94	22.18	1.75	1.55
1.0	10.817	10.815	30.39	30.11	2.13	2.11
10.0	10.815	10.804	38.19	40.00	2.67	2.80
60.0	10.802	10.810	42.77	43.02	2.99	3.01
240.0	10.803	10.814	43.87	45.88	3.07	3.21

Score1 (DU sum): 0.31  
 Score2 (DU Profile): **1.73**  
 DU sum difference (u): 0.07

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC162-180**  
 Exchangeable protons: 17  
 Index lis-file: 138  
 Sequence: VTWNSGSLSSGVHTFFAVL  
 Range: 1 / 3

Reference: reference series, experiment: experiment series

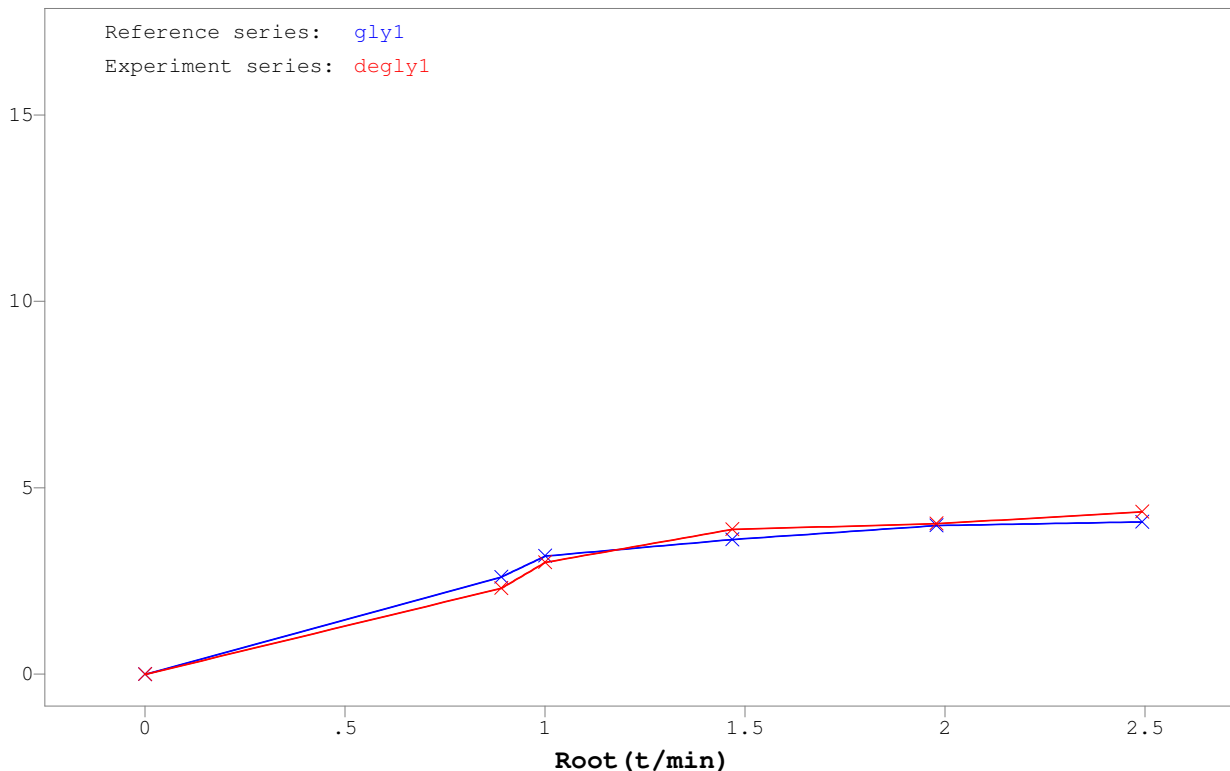
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	12.889	12.893	0.00	0.00	0.00	0.00
0.5	12.891	12.890	15.37	13.58	2.61	2.31
1.0	12.887	12.898	18.66	17.66	3.17	3.00
10.0	12.887	12.881	21.27	22.88	3.62	3.89
60.0	12.877	12.892	23.48	23.77	3.99	4.04
240.0	12.869	12.890	24.05	25.63	4.09	4.36

Score1 (DU sum): 0.20  
 Score2 (DU Profile): **1.52**  
 DU sum difference (u): 0.12

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC163-180**  
 Exchangeable protons: 16  
 Index lis-file: 218  
 Sequence: TWNSGSLSSGVHTFPAVL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

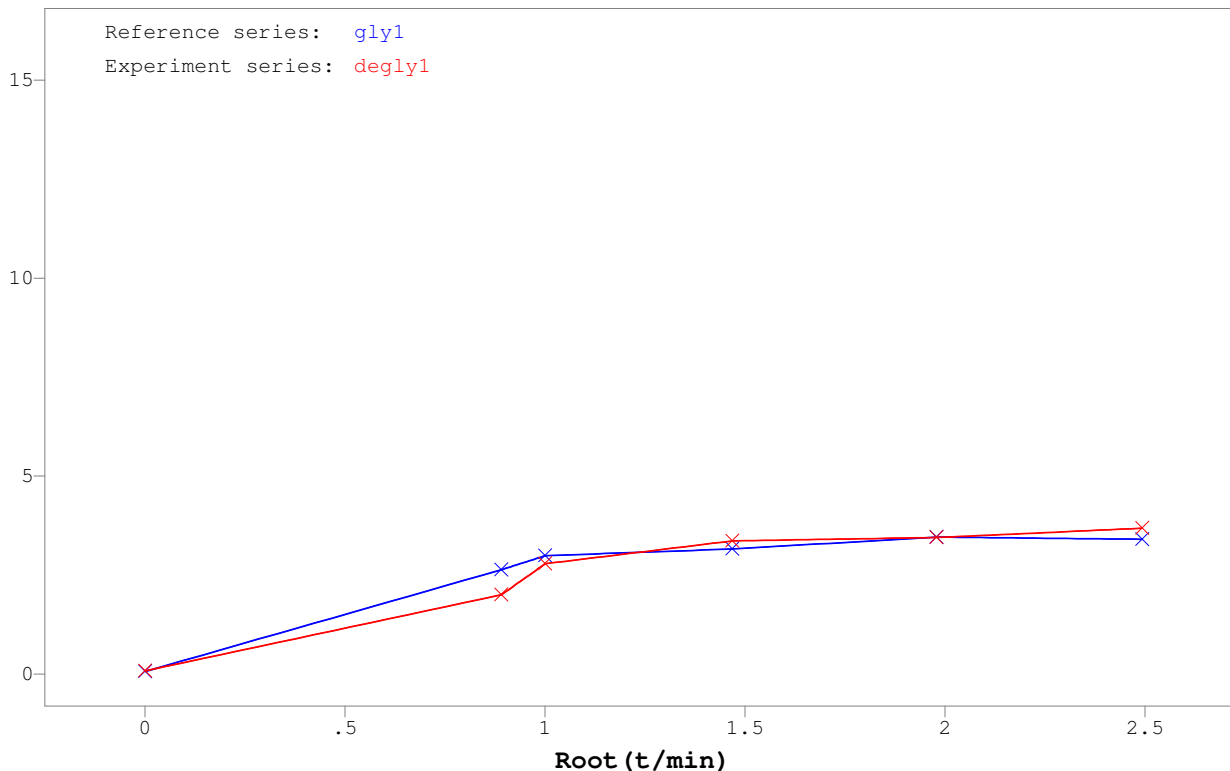
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	12.683	12.678	0.46	0.56	0.07	0.09
0.5	12.681	12.675	16.52	12.57	2.64	2.01
1.0	12.671	12.679	18.73	17.47	3.00	2.79
10.0	12.665	12.671	19.79	21.07	3.17	3.37
60.0	12.663	12.682	21.67	21.60	3.47	3.46
240.0	12.660	12.679	21.33	23.06	3.41	3.69

Score1 (DU sum): 0.64  
 Score2 (DU Profile): **2.03**  
 DU sum difference (u): -0.35

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **HC**  
 Peptide: **HC164-180**  
 Exchangeable protons: 15  
 Index lis-file: 219  
 Sequence: WNSGSLSSGVHTFPAVL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

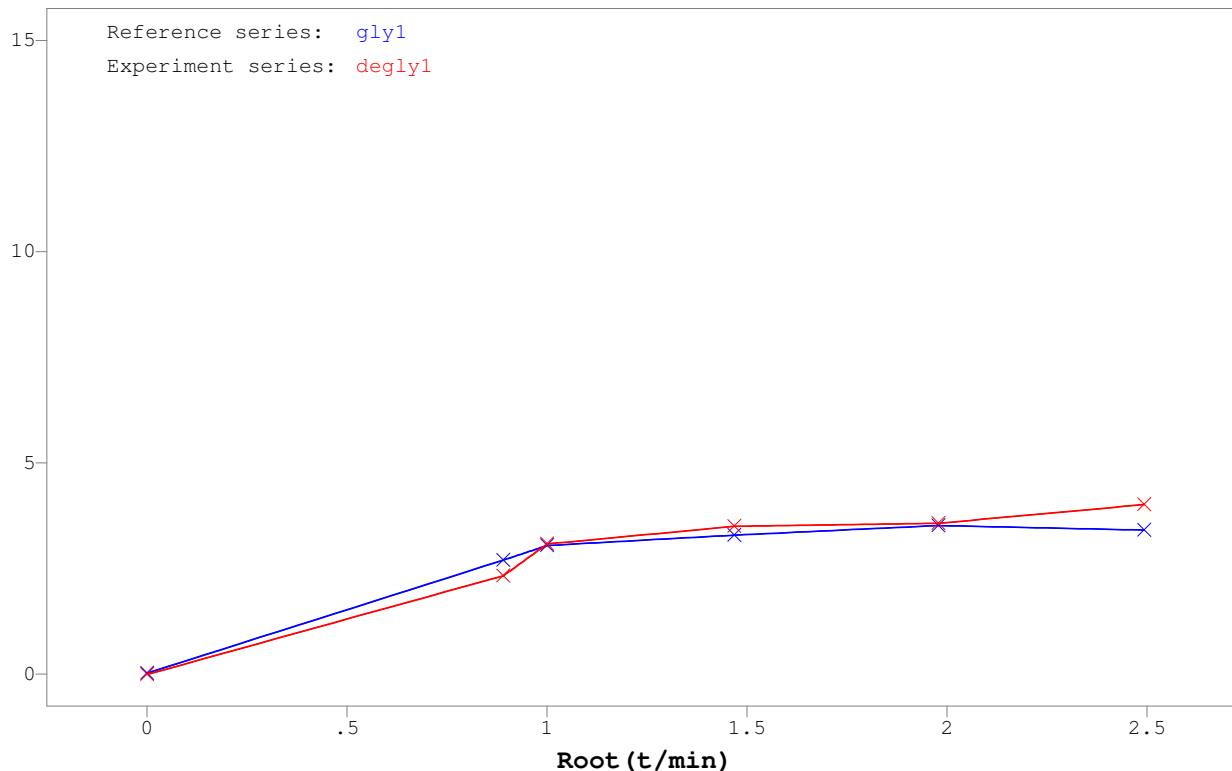
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	12.566	12.551	0.20	0.00	0.03	0.00
0.5	12.562	12.555	18.04	15.57	2.71	2.34
1.0	12.559	12.570	20.34	20.59	3.05	3.09
10.0	12.551	12.550	21.98	23.36	3.30	3.50
60.0	12.546	12.560	23.49	23.85	3.52	3.58
240.0	12.541	12.558	22.77	26.80	3.42	4.02

Score1 (DU sum): 0.99  
 Score2 (DU Profile): **2.10**  
 DU sum difference (u): 0.50

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC165-180**  
 Exchangeable protons: 14  
 Index lis-file: 139  
 Sequence: NSGSLSSGVHTFPAVL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

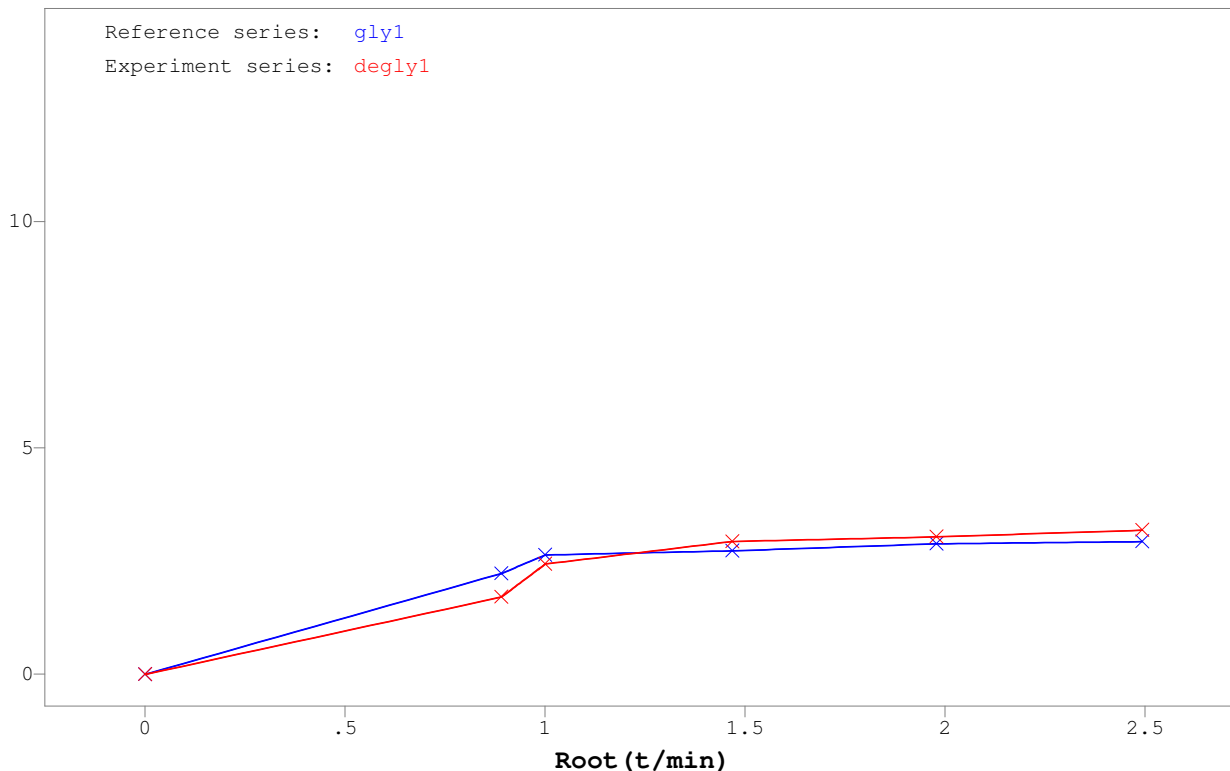
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.493	11.488	0.00	0.00	0.00	0.00
0.5	11.483	11.479	15.91	12.19	2.23	1.71
1.0	11.483	11.491	18.83	17.41	2.64	2.44
10.0	11.484	11.485	19.48	20.97	2.73	2.94
60.0	11.481	11.488	20.59	21.69	2.88	3.04
240.0	11.482	11.491	20.93	22.74	2.93	3.18

Score1 (DU sum): 0.22  
 Score2 (DU Profile): **2.31**  
 DU sum difference (u): -0.10

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC170-180**  
 Exchangeable protons: 9  
 Index lis-file: 140  
 Sequence: SSGVHTFPAVL  
 Range: 1 / 2

Reference: reference series, experiment: experiment series

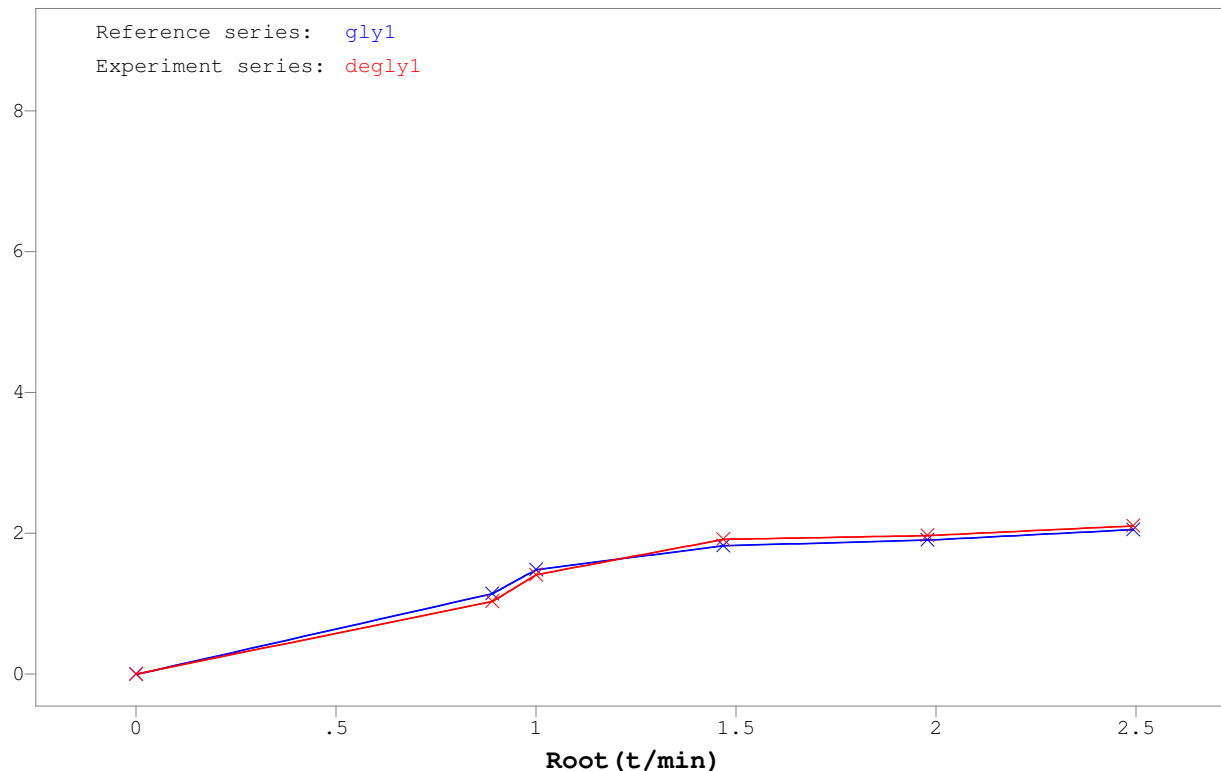
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.830	10.827	0.01	0.05	0.00	0.00
0.5	10.834	10.833	12.73	11.50	1.15	1.03
1.0	10.835	10.837	16.53	15.73	1.49	1.42
10.0	10.829	10.832	20.30	21.31	1.83	1.92
60.0	10.827	10.838	21.19	21.90	1.91	1.97
240.0	10.817	10.844	22.84	23.44	2.06	2.11

Score1 (DU sum): 0.09  
 Score2 (DU Profile): **1.06**  
 DU sum difference (u): 0.03

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC170-180**  
 Exchangeable protons: 9  
 Index lis-file: 140  
 Sequence: SSGVHTFPAVL  
 Range: 2 / 2

Reference: reference series, experiment: experiment series

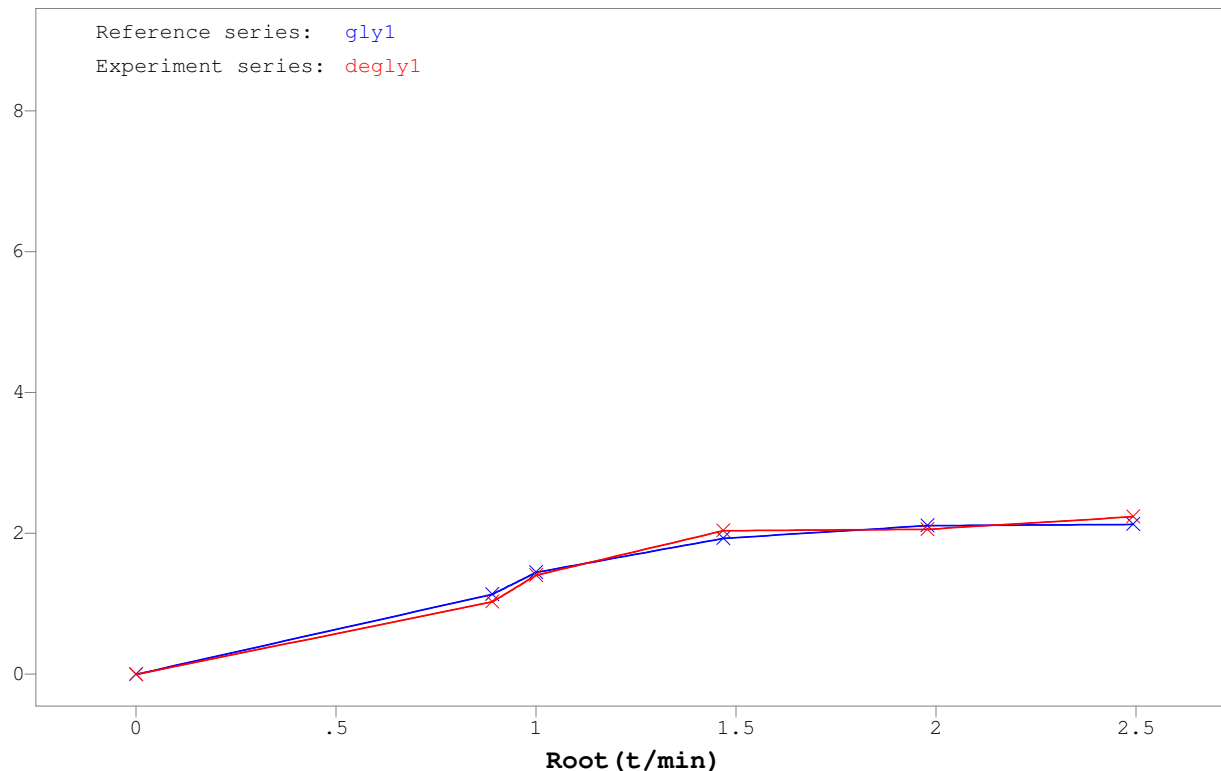
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.189	11.170	0.01	0.01	0.00	0.00
0.5	11.184	11.178	12.64	11.45	1.14	1.03
1.0	11.194	11.186	16.10	15.66	1.45	1.41
10.0	11.173	11.182	21.47	22.68	1.93	2.04
60.0	11.182	11.187	23.48	22.90	2.11	2.06
240.0	11.168	11.200	23.67	24.88	2.13	2.24

Score1 (DU sum): 0.06  
 Score2 (DU Profile): **1.12**  
 DU sum difference (u): 0.02

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC185-201**  
 Exchangeable protons: 14  
 Index lis-file: 143  
 Sequence: YTLSSSVTVPSSTWPSE  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

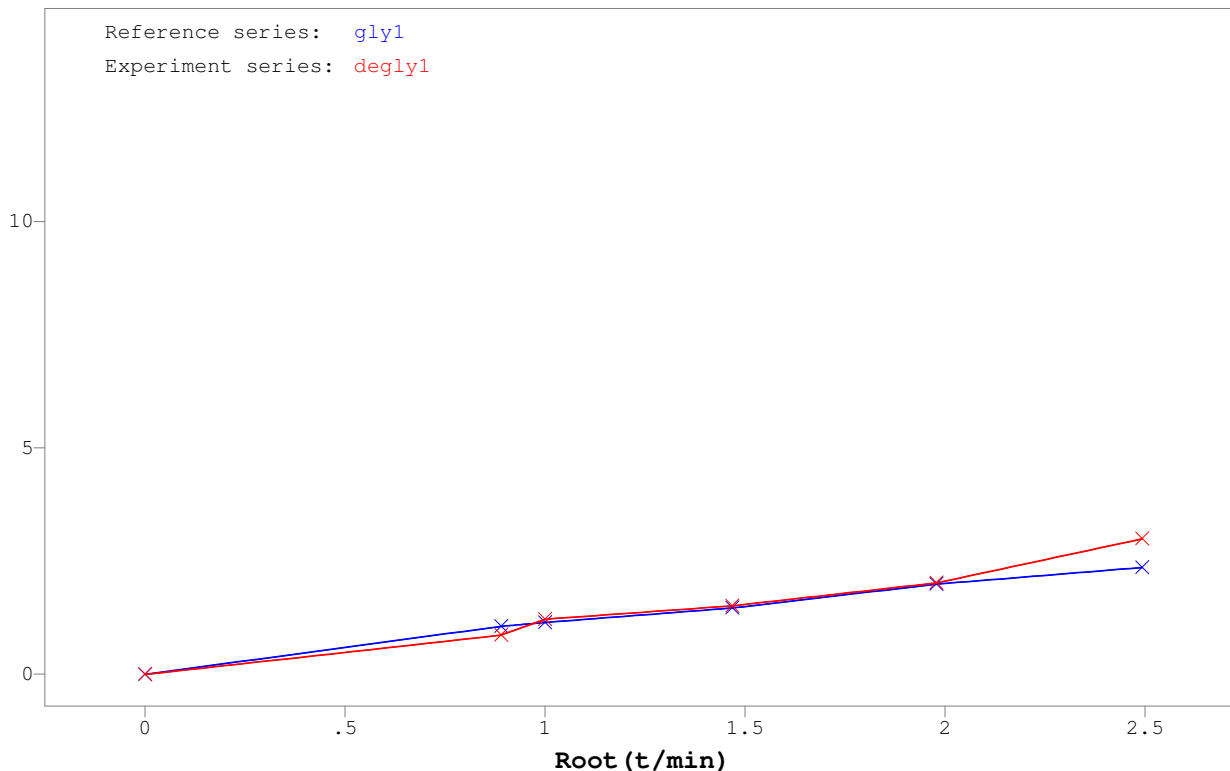
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.603	11.612	0.00	0.00	0.00	0.00
0.5	11.607	11.613	7.58	6.23	1.06	0.87
1.0	11.602	11.594	8.19	8.70	1.15	1.22
10.0	11.595	11.586	10.48	10.81	1.47	1.51
60.0	11.600	11.592	14.24	14.43	1.99	2.02
240.0	11.610	11.610	16.86	21.38	2.36	2.99

Score1 (DU sum): **1.25**  
 Score2 (DU Profile): 1.67  
**DU sum difference (u): 0.59**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC185-202**  
 Exchangeable protons: 15  
 Index lis-file: 144  
 Sequence: YTLSSSVTVPSSTWPSET  
 Range: 1 / 2

Reference: reference series, experiment: experiment series

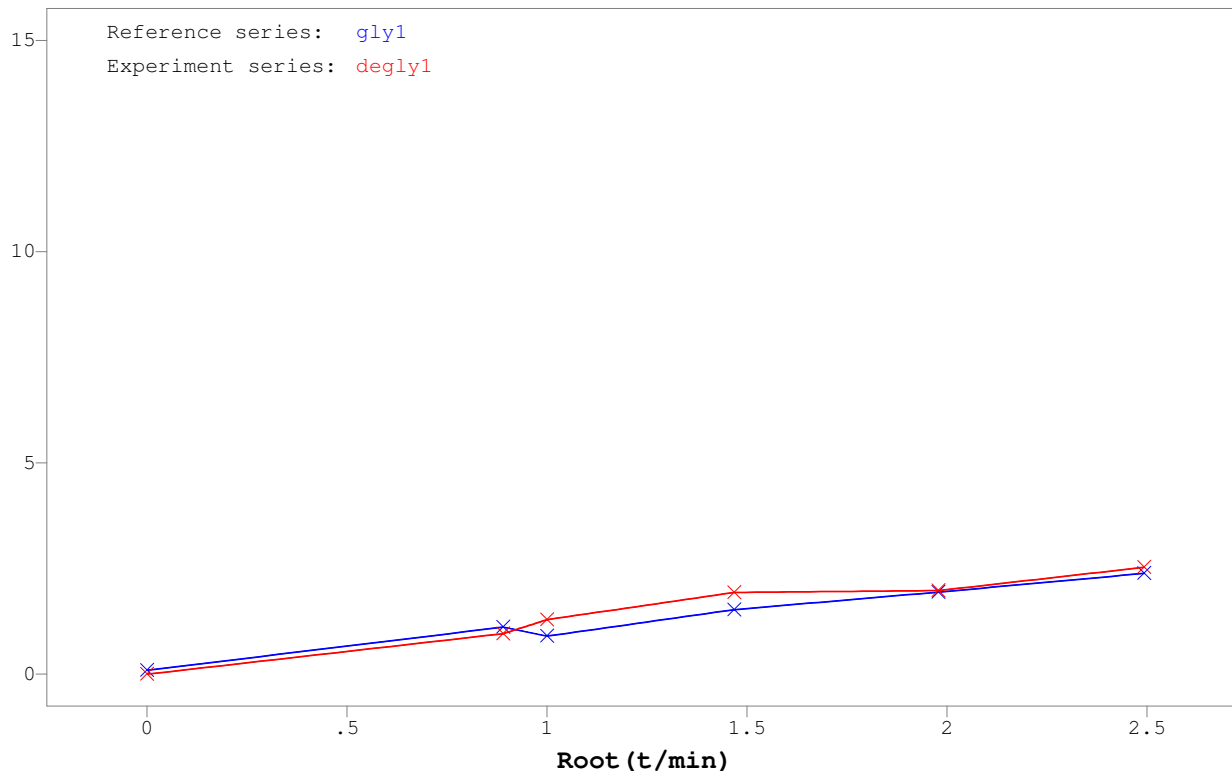
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.436	11.473	0.65	0.04	0.10	0.01
0.5	11.458	11.473	7.46	6.44	1.12	0.97
1.0	11.444	11.458	<b>6.04</b>	8.65	<b>0.91</b>	1.30
10.0	11.491	11.455	10.23	12.94	1.53	1.94
60.0	11.461	11.460	12.99	13.22	1.95	1.98
240.0	11.488	11.464	15.95	16.91	2.39	2.54

Score1 (DU sum): 0.74  
 Score2 (DU Profile): **1.61**  
 DU sum difference (u): 0.41

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC191-201**  
 Exchangeable protons: 8  
 Index lis-file: 145  
 Sequence: VIVPSSTWPSE  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

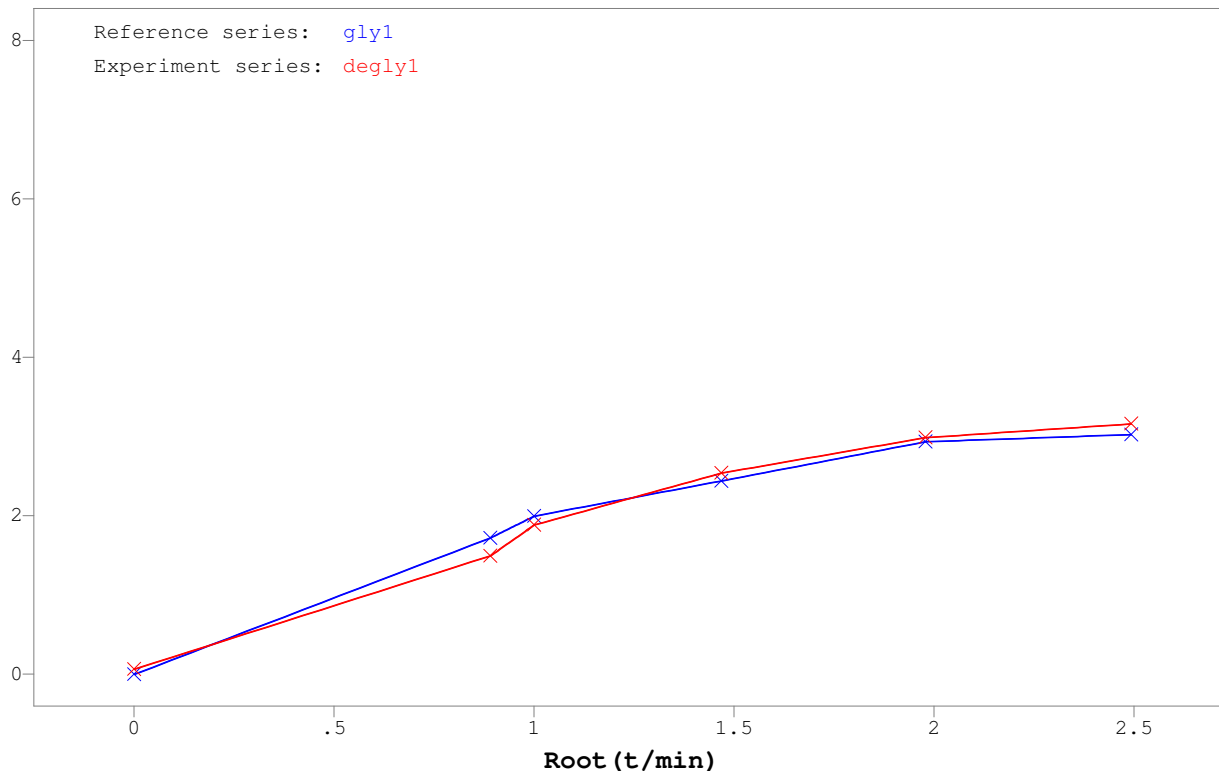
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.921	9.947	0.00	0.80	0.00	0.06
0.5	9.939	9.952	21.53	18.70	1.72	1.50
1.0	9.940	9.943	24.97	23.58	2.00	1.89
10.0	9.956	9.932	30.52	31.76	2.44	2.54
60.0	9.933	9.941	36.71	37.36	2.94	2.99
240.0	9.935	9.944	37.84	39.53	3.03	3.16

Score1 (DU sum): 0.05  
 Score2 (DU Profile): **2.08**  
 DU sum difference (u): 0.01

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC210-239**  
 Exchangeable protons: 25  
 Index lis-file: 221  
 Sequence: PASSTKVDDKKIVPRDCGCKPCICTVPEVSS  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

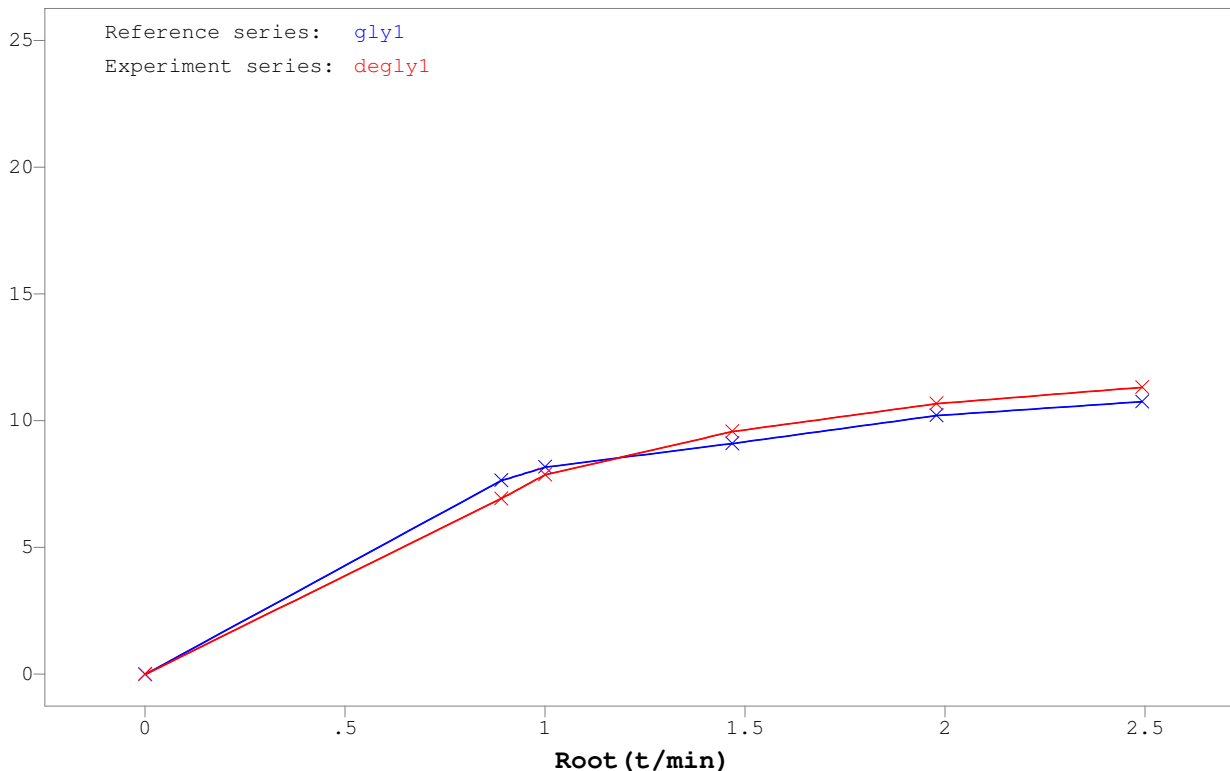
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	12.395	12.394	0.00	0.00	0.00	0.00
0.5	12.385	12.386	30.59	27.74	7.65	6.93
1.0	12.385	12.388	32.71	31.51	8.18	7.88
10.0	12.385	12.382	<b>36.45</b>	38.33	<b>9.11</b>	9.58
60.0	12.380	12.388	40.85	42.73	10.21	10.68
240.0	12.373	12.380	43.05	<b>45.32</b>	10.76	<b>11.33</b>

Score1 (DU sum): 0.79  
 Score2 (DU Profile): **2.15**  
 DU sum difference (u): -0.82

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **HC**  
 Peptide: **HC214-225**  
 Exchangeable protons: 10  
 Index lis-file: 147  
 Sequence: TKVDKKIVPRDC  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

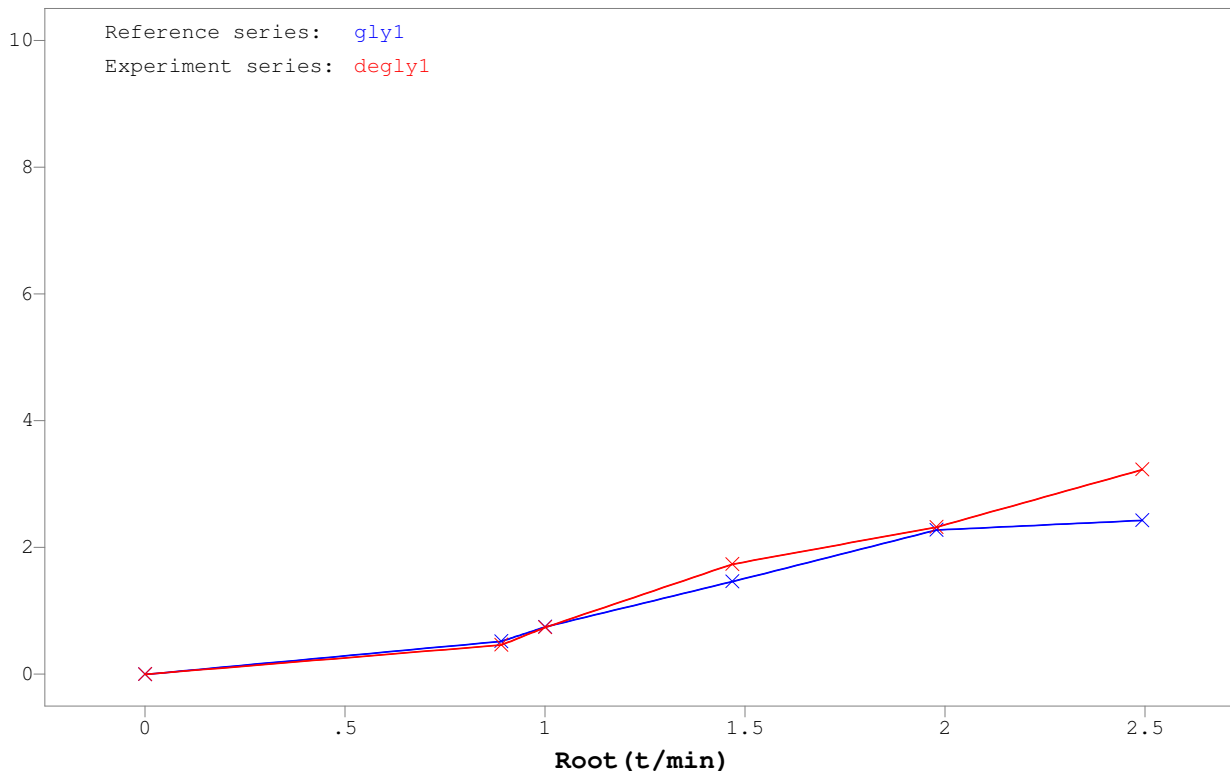
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.813	9.808	0.00	0.00	0.00	0.00
0.5	9.814	9.809	5.22	4.64	0.52	0.46
1.0	9.812	9.818	7.49	7.42	0.75	0.74
10.0	9.809	9.806	14.65	17.39	1.46	1.74
60.0	9.799	9.814	22.78	23.25	2.28	2.33
240.0	9.794	9.817	24.31	32.31	2.43	3.23

Score1 (DU sum): **3.13**  
 Score2 (DU Profile): 2.87  
**DU sum difference (u): 1.06**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC240-251**  
 Exchangeable protons: 8  
 Index lis-file: 149  
 Sequence: VFIFPPKPKDVL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

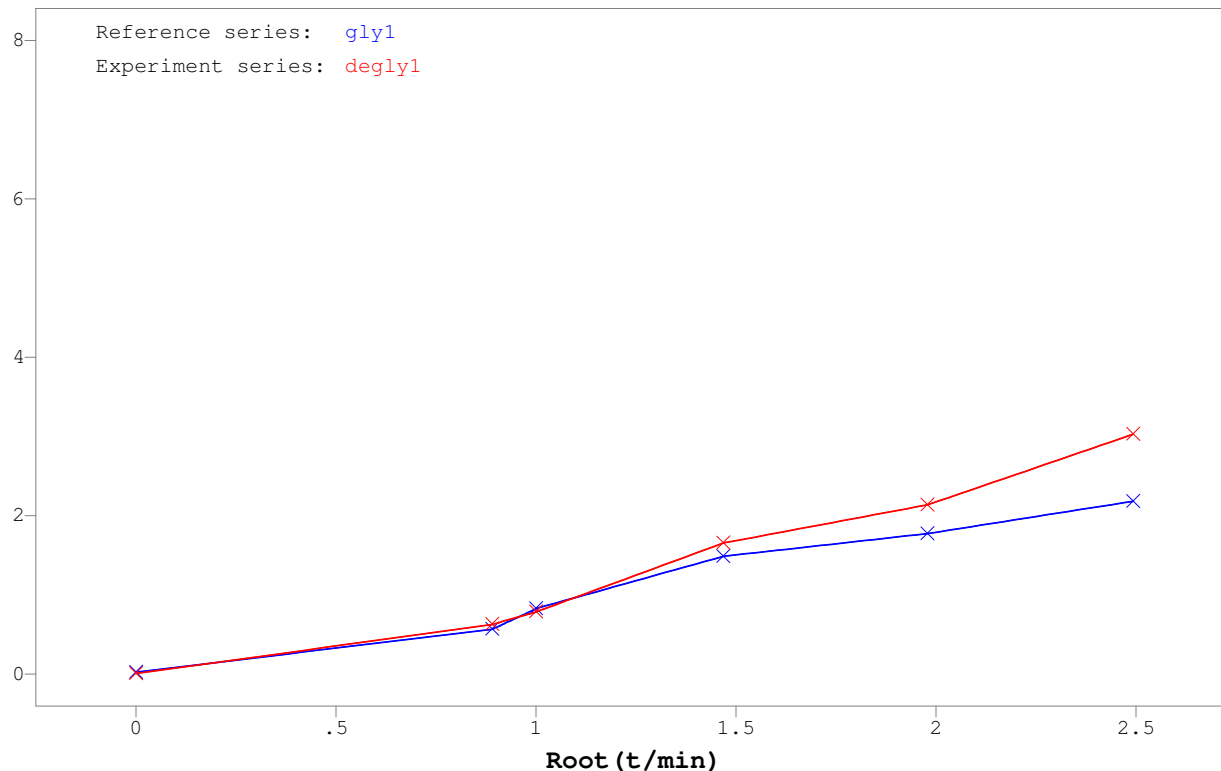
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.988	10.965	0.35	0.14	0.03	0.01
0.5	10.986	10.985	7.16	7.92	0.57	0.63
1.0	10.980	10.980	10.40	<b>9.89</b>	0.83	<b>0.79</b>
10.0	10.979	10.967	18.64	20.74	1.49	1.66
60.0	10.964	10.985	22.23	26.77	1.78	2.14
240.0	10.959	10.982	27.33	37.91	2.19	3.03

Score1 (DU sum): **5.11p**  
 Score2 (DU Profile): 4.52p  
**DU sum difference (u): 1.38**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC240-252**  
 Exchangeable protons: 9  
 Index lis-file: 223  
 Sequence: VFIFPPKPKDVLV  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

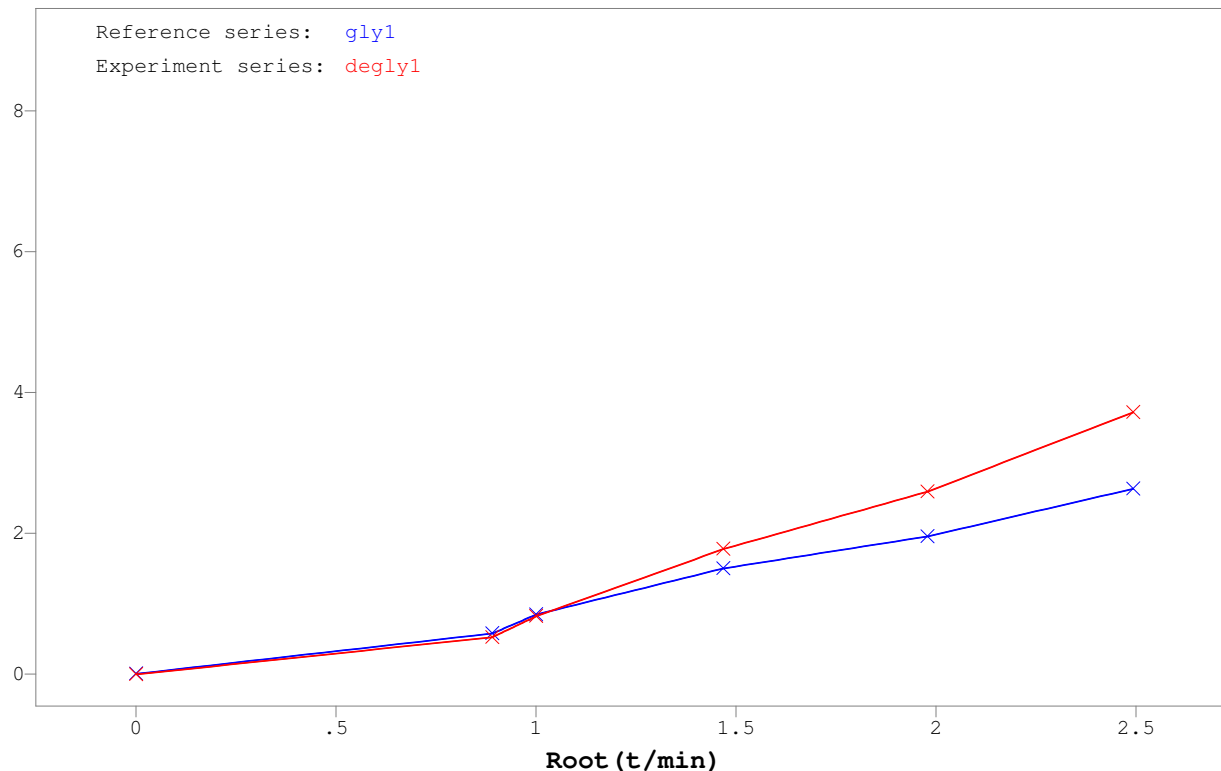
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.386	10.360	0.08	0.00	0.01	0.00
0.5	10.379	10.371	6.47	5.88	0.58	0.53
1.0	10.377	10.377	9.45	9.18	0.85	0.83
10.0	10.365	10.370	16.73	19.78	1.51	1.78
60.0	10.366	10.375	21.77	28.84	1.96	2.60
240.0	10.352	10.376	29.30	41.38	2.64	3.72

Score1 (DU sum): **6.30**  
 Score2 (DU Profile): 5.60  
**DU sum difference (u): 1.91**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC241-251**  
 Exchangeable protons: 7  
 Index lis-file: 150  
 Sequence: FIFPPKPKDVL  
 Range: 1 / 2

Reference: reference series, experiment: experiment series

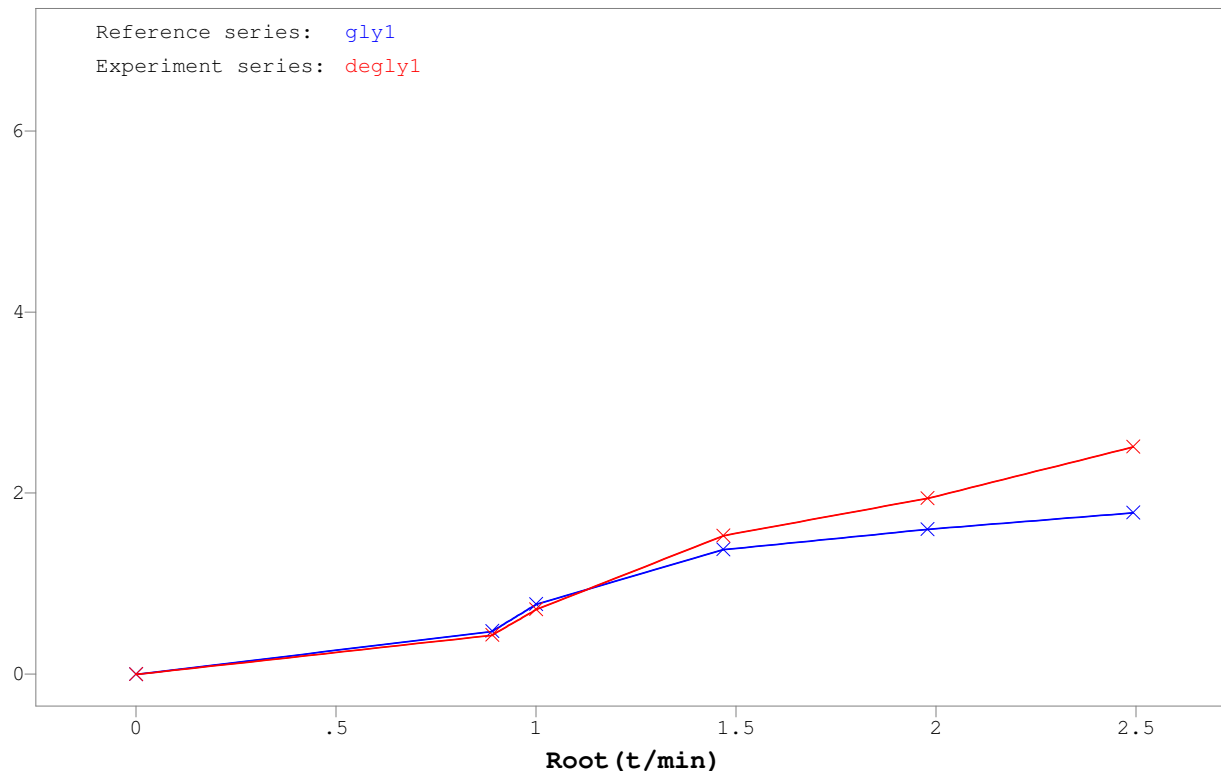
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.415	10.409	0.00	0.00	0.00	0.00
0.5	10.417	10.405	6.82	6.22	0.48	0.44
1.0	10.416	10.415	11.04	10.23	0.77	0.72
10.0	10.406	10.404	19.67	21.87	1.38	1.53
60.0	10.400	10.418	22.88	27.77	1.60	1.94
240.0	10.390	10.419	25.49	35.92	1.78	2.51

Score1 (DU sum): **4.78**  
 Score2 (DU Profile): 4.58  
**DU sum difference (u): 1.13**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC241-252**  
 Exchangeable protons: 8  
 Index lis-file: 224  
 Sequence: FIFPPKPKDVLT  
 Range: 1 / 2

Reference: reference series, experiment: experiment series

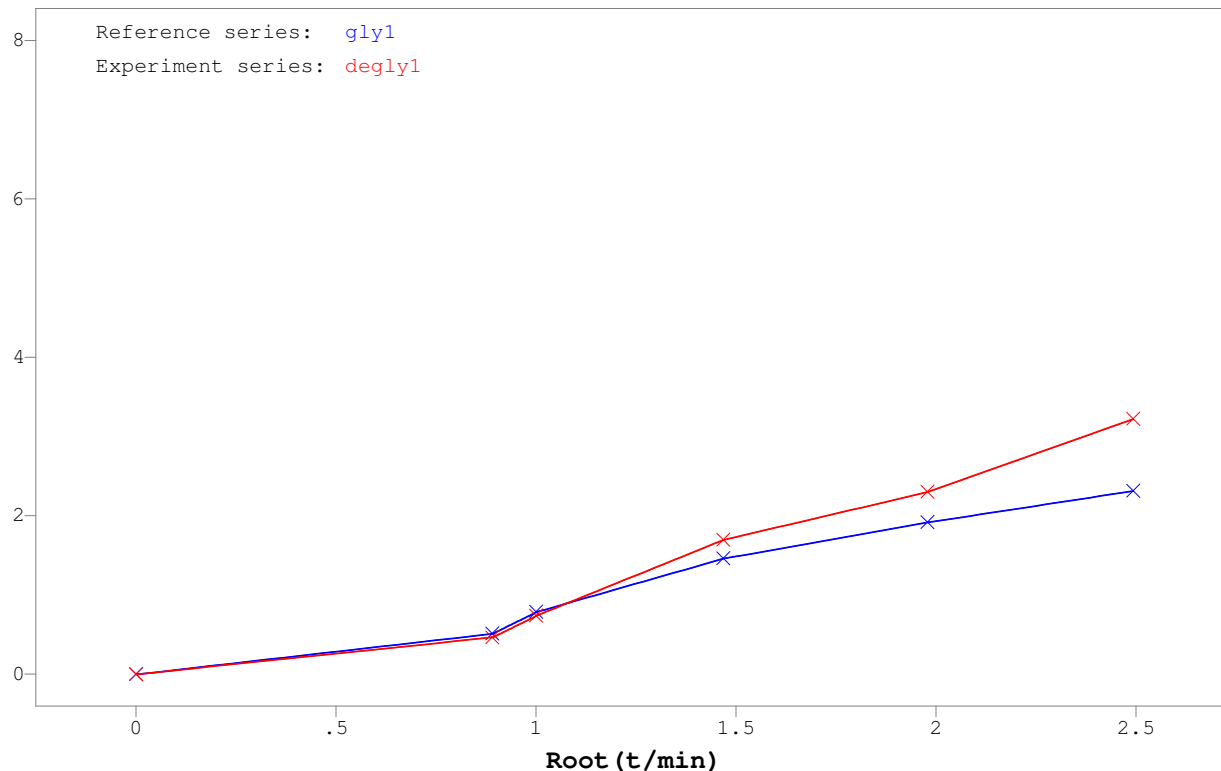
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.813	9.808	0.00	0.00	0.00	0.00
0.5	9.815	9.809	6.42	5.82	0.51	0.47
1.0	9.812	9.818	9.83	9.25	0.79	0.74
10.0	9.809	9.806	18.26	21.23	1.46	1.70
60.0	9.799	9.814	23.97	28.77	1.92	2.30
240.0	9.794	9.816	28.95	40.31	2.32	3.22

Score1 (DU sum): **5.32**  
 Score2 (DU Profile): 4.91  
**DU sum difference (u): 1.44**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC242-252**  
 Exchangeable protons: 7  
 Index lis-file: 151  
 Sequence: IFPPKPKDVLV  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

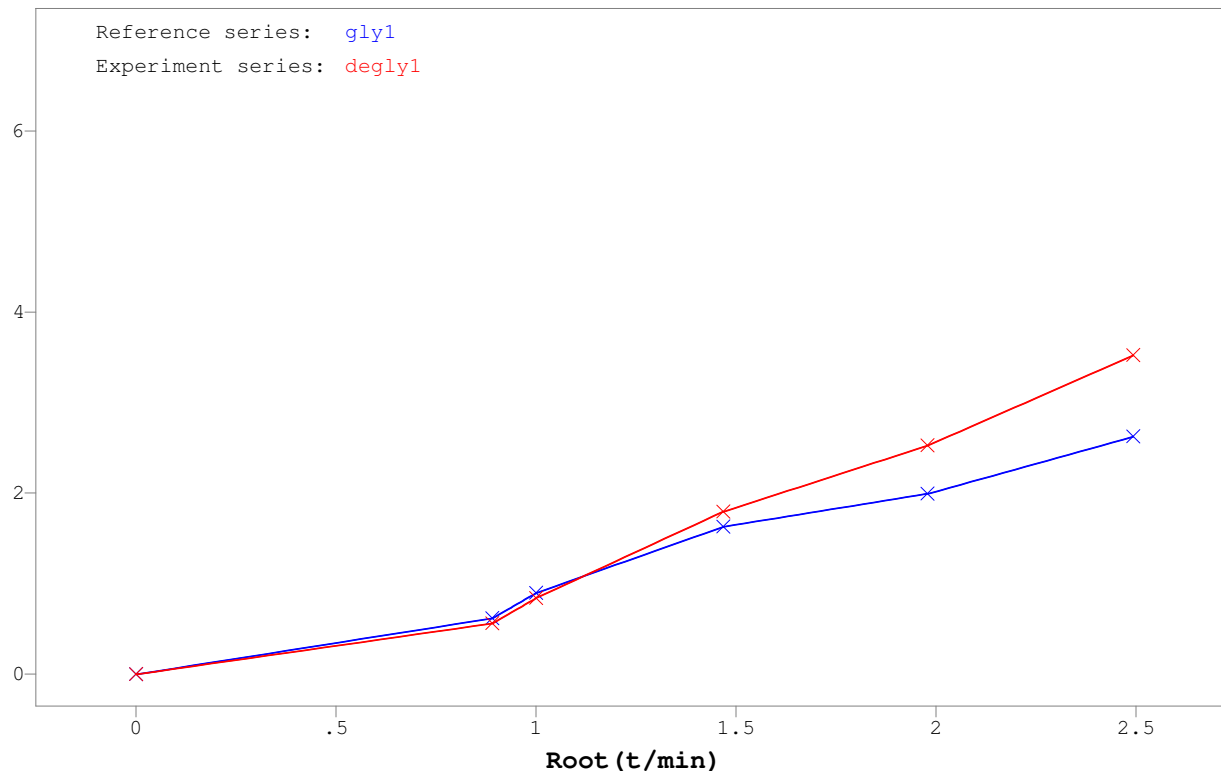
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.828	7.814	0.00	0.00	0.00	0.00
0.5	7.816	7.804	8.83	8.03	0.62	0.56
1.0	7.819	7.817	12.84	12.04	0.90	0.84
10.0	7.802	7.802	23.28	25.69	1.63	1.80
60.0	7.789	7.809	28.50	36.12	1.99	2.53
240.0	7.781	7.802	37.53	50.37	2.63	3.53

Score1 (DU sum): **6.30**  
 Score2 (DU Profile): 5.92  
**DU sum difference (u): 1.49**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC243-251**  
 Exchangeable protons: 5  
 Index lis-file: 225  
 Sequence: FPPKPKDVL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

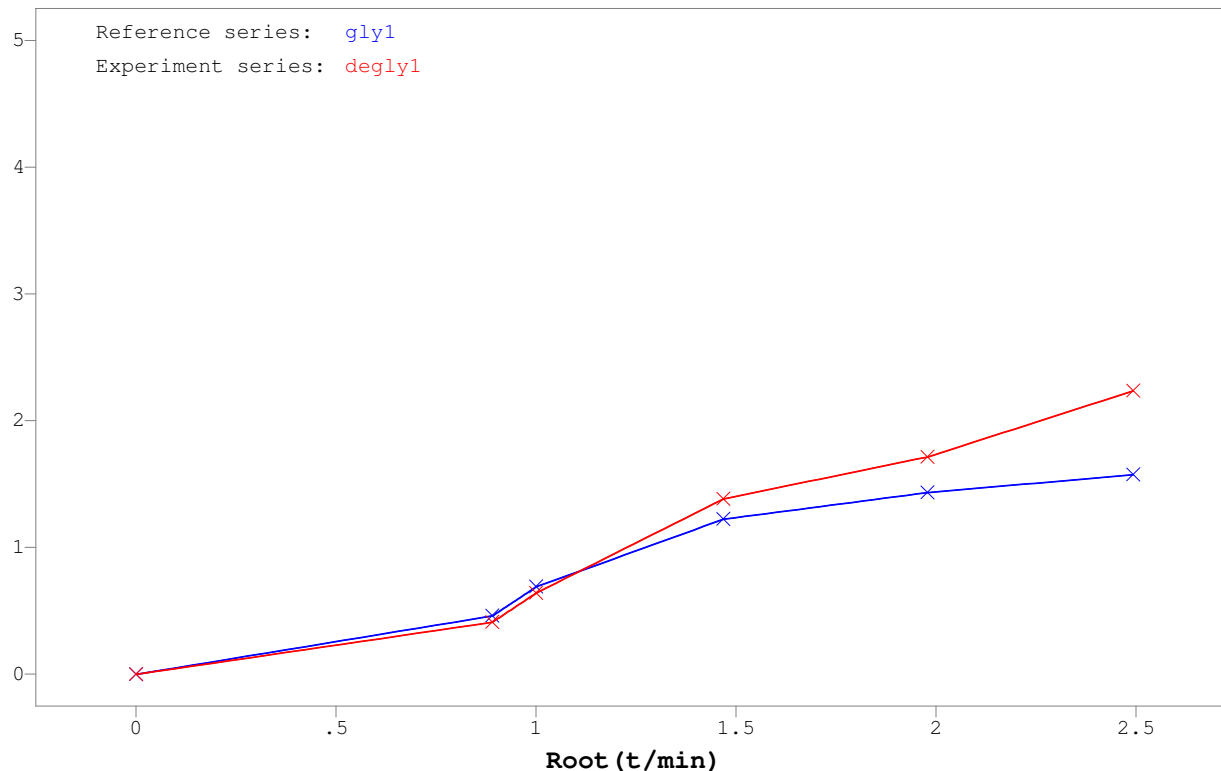
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.413	10.402	0.00	0.00	0.00	0.00
0.5	10.409	10.406	9.22	8.23	0.46	0.41
1.0	10.414	10.414	13.82	12.84	0.69	0.64
10.0	10.411	10.405	24.48	27.69	1.22	1.38
60.0	10.402	10.414	28.70	34.31	1.43	1.72
240.0	10.391	10.416	31.51	44.75	1.58	2.24

Score1 (DU sum): **5.96**  
 Score2 (DU Profile): 5.81  
**DU sum difference (u): 1.01**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC243-252**  
 Exchangeable protons: 6  
 Index lis-file: 152  
 Sequence: FPPKPKDVLV  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

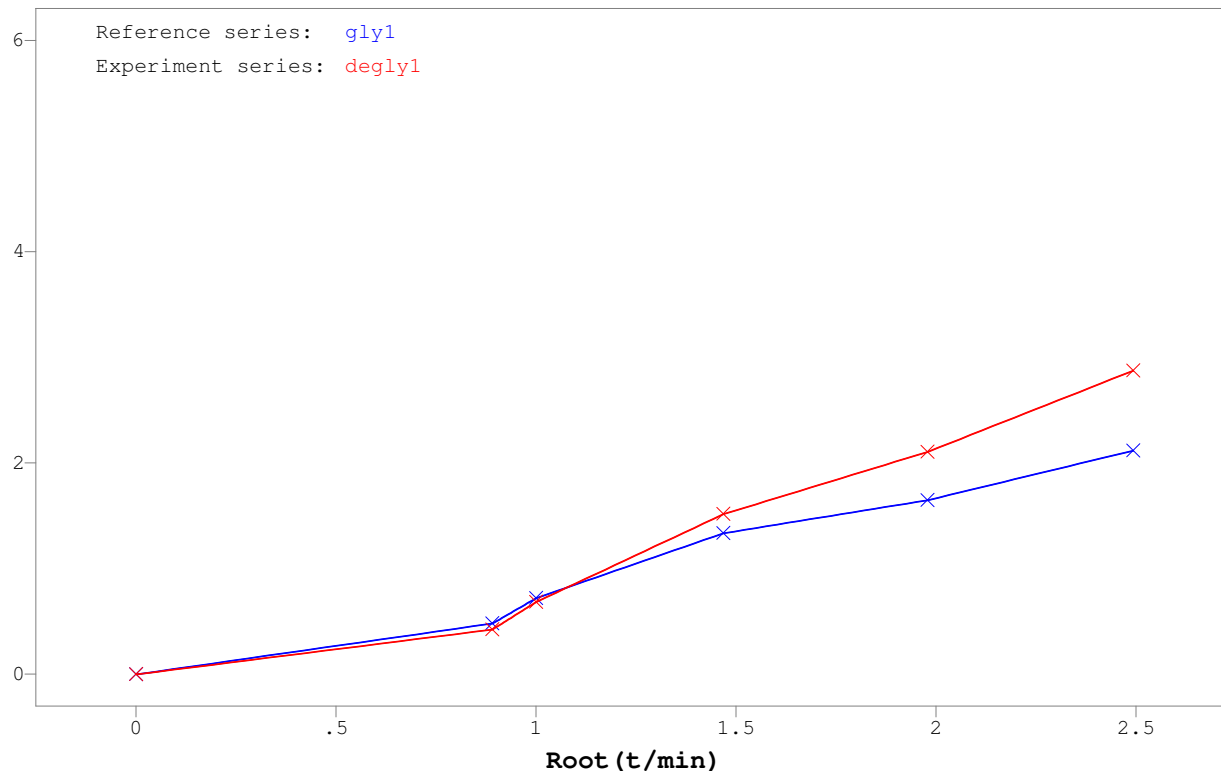
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.815	9.804	0.00	0.00	0.00	0.00
0.5	9.819	9.808	8.03	7.07	0.48	0.42
1.0	9.811	9.822	12.04	11.44	0.72	0.69
10.0	9.811	9.808	22.27	25.28	1.34	1.52
60.0	9.801	9.816	27.49	35.12	1.65	2.11
240.0	9.792	9.816	35.32	47.94	2.12	2.88

Score1 (DU sum): **6.43**  
 Score2 (DU Profile): 6.00  
**DU sum difference (u): 1.30**

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **HC**  
 Peptide: **HC252-261**  
 Exchangeable protons: 8  
 Index lis-file: 153  
 Sequence: TITLTPKVTC  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

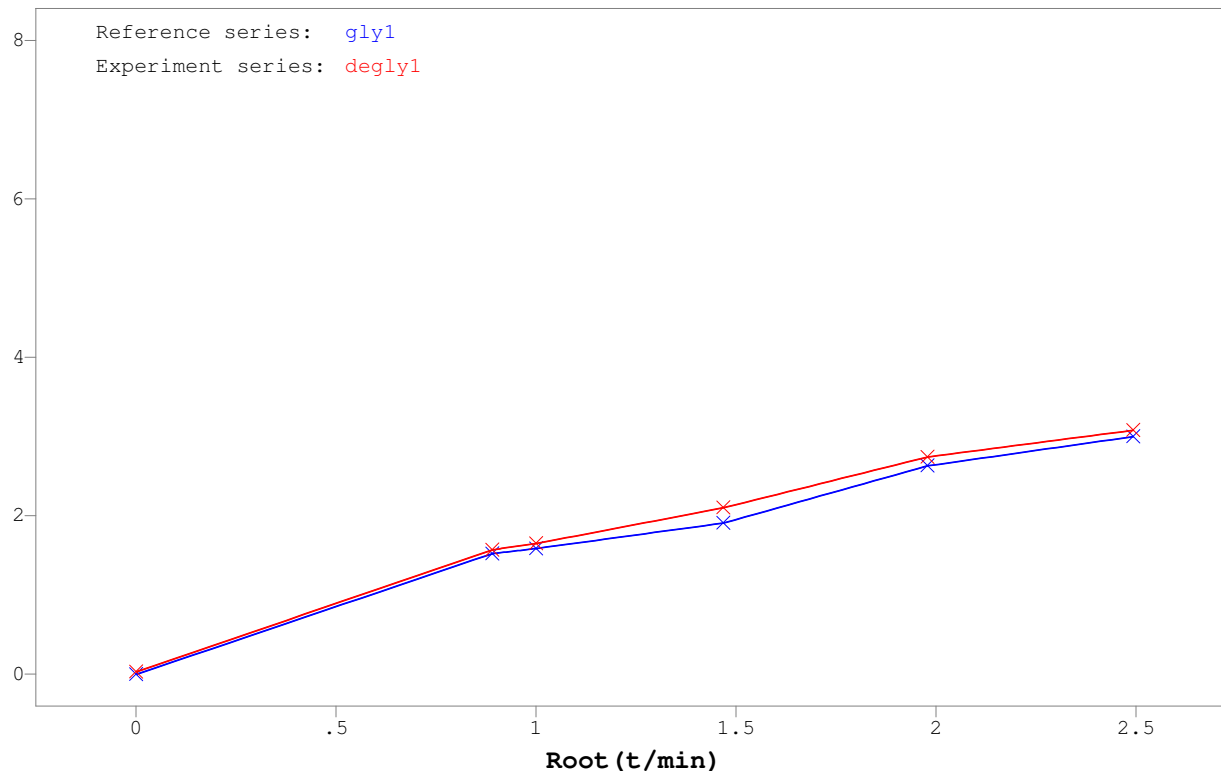
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.813	8.794	0.00	0.39	0.00	0.03
0.5	8.804	8.802	19.06	19.67	1.53	1.57
1.0	8.806	8.805	19.87	20.66	1.59	1.65
10.0	8.793	8.794	23.88	26.29	1.91	2.10
60.0	8.786	8.804	32.91	34.31	2.63	2.75
240.0	8.782	8.809	37.52	38.53	3.00	3.08

Score1 (DU sum): **1.96**  
 Score2 (DU Profile): 1.60  
**DU sum difference (u): 0.53**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC253-261**  
 Exchangeable protons: 7  
 Index lis-file: 154  
 Sequence: ITLTPKVTC  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

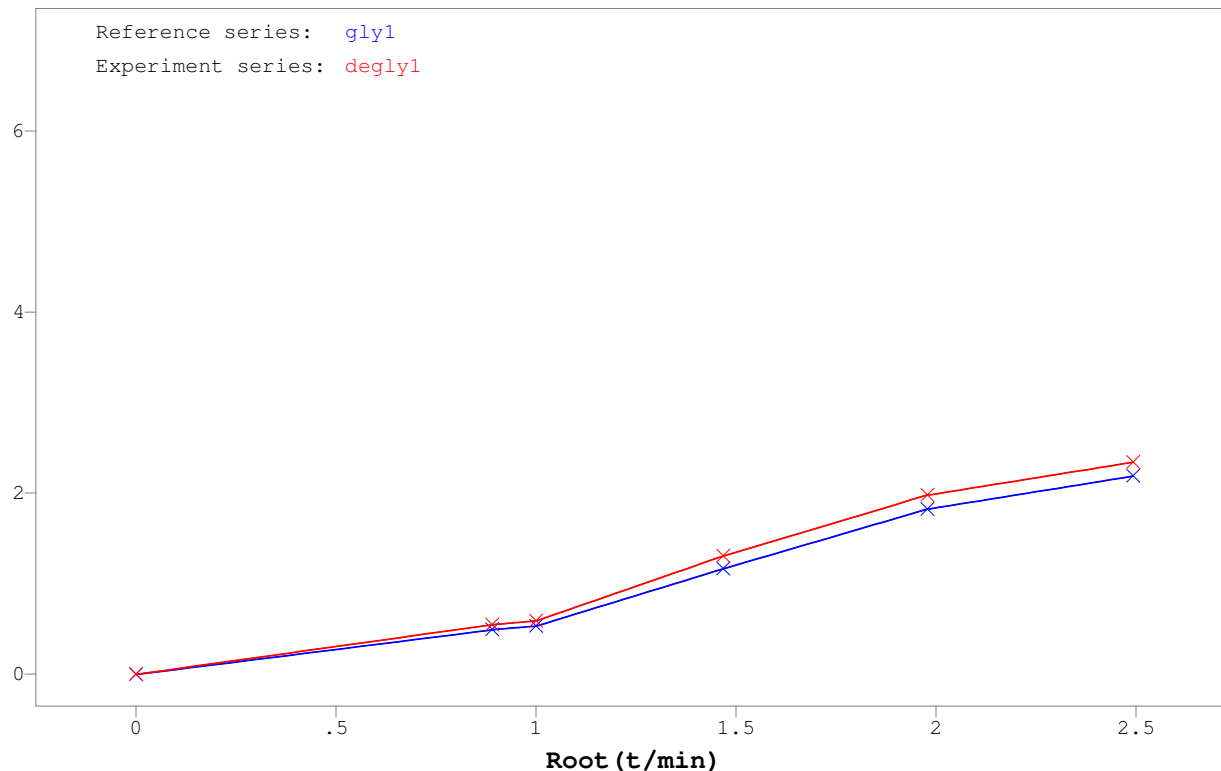
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.420	8.406	0.00	0.00	0.00	0.00
0.5	8.422	8.415	7.06	7.83	0.49	0.55
1.0	8.425	8.425	<b>7.62</b>	<b>8.44</b>	<b>0.53</b>	<b>0.59</b>
10.0	8.413	8.409	16.66	18.68	1.17	1.31
60.0	8.407	8.422	26.08	28.29	1.83	1.98
240.0	8.407	8.423	31.31	33.51	2.19	2.35

Score1 (DU sum): **2.34**  
 Score2 (DU Profile): 1.95p  
**DU sum difference (u): 0.61**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC263-275**  
 Exchangeable protons: 11  
 Index lis-file: 156  
 Sequence: VVDISKDDPEVQF  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

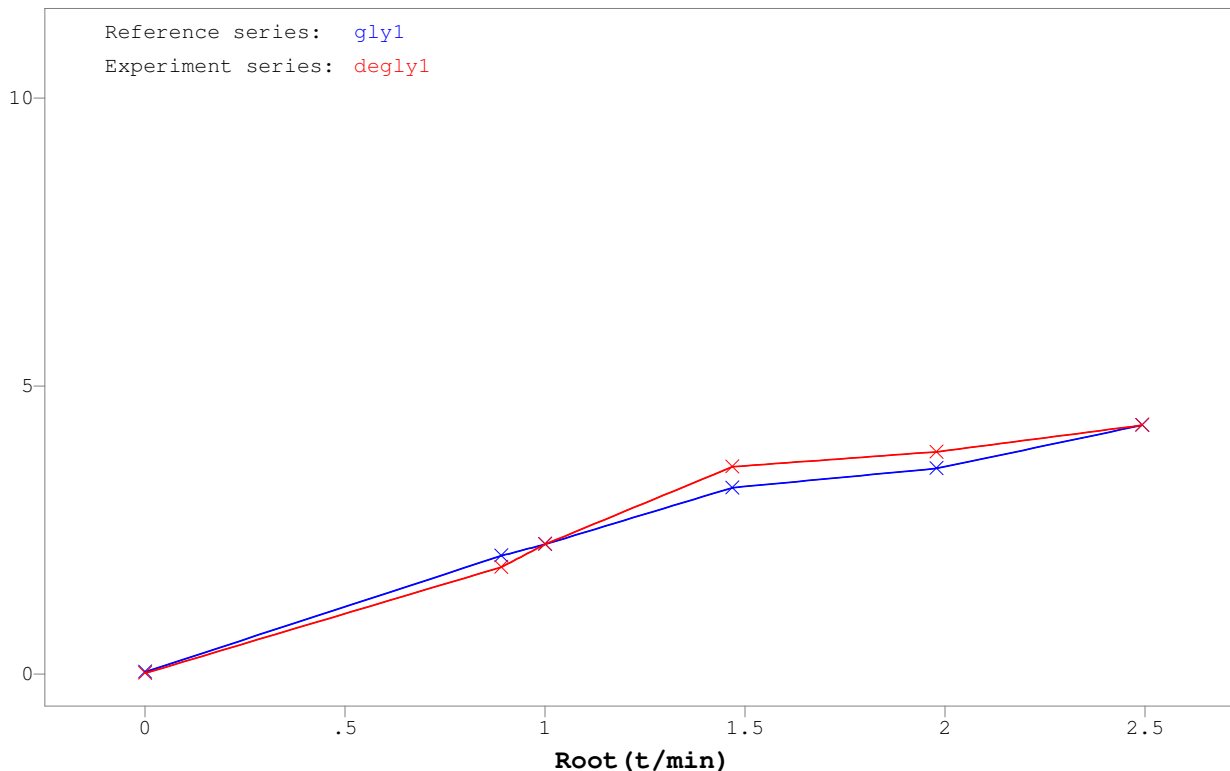
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.560	10.553	0.40	0.20	0.04	0.02
0.5	10.557	10.560	18.72	16.94	2.06	1.86
1.0	10.560	10.558	20.55	20.55	2.26	2.26
10.0	10.560	10.549	<b>29.46</b>	32.77	<b>3.24</b>	3.60
60.0	10.547	10.560	32.50	35.12	3.58	3.86
240.0	10.545	10.562	39.33	<b>39.33</b>	4.33	<b>4.33</b>

Score1 (DU sum): 0.23  
 Score2 (DU Profile): **1.67**  
 DU sum difference (u): 0.10

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC266-274**  
 Exchangeable protons: 7  
 Index lis-file: 157  
 Sequence: ISKDDPEVQ  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

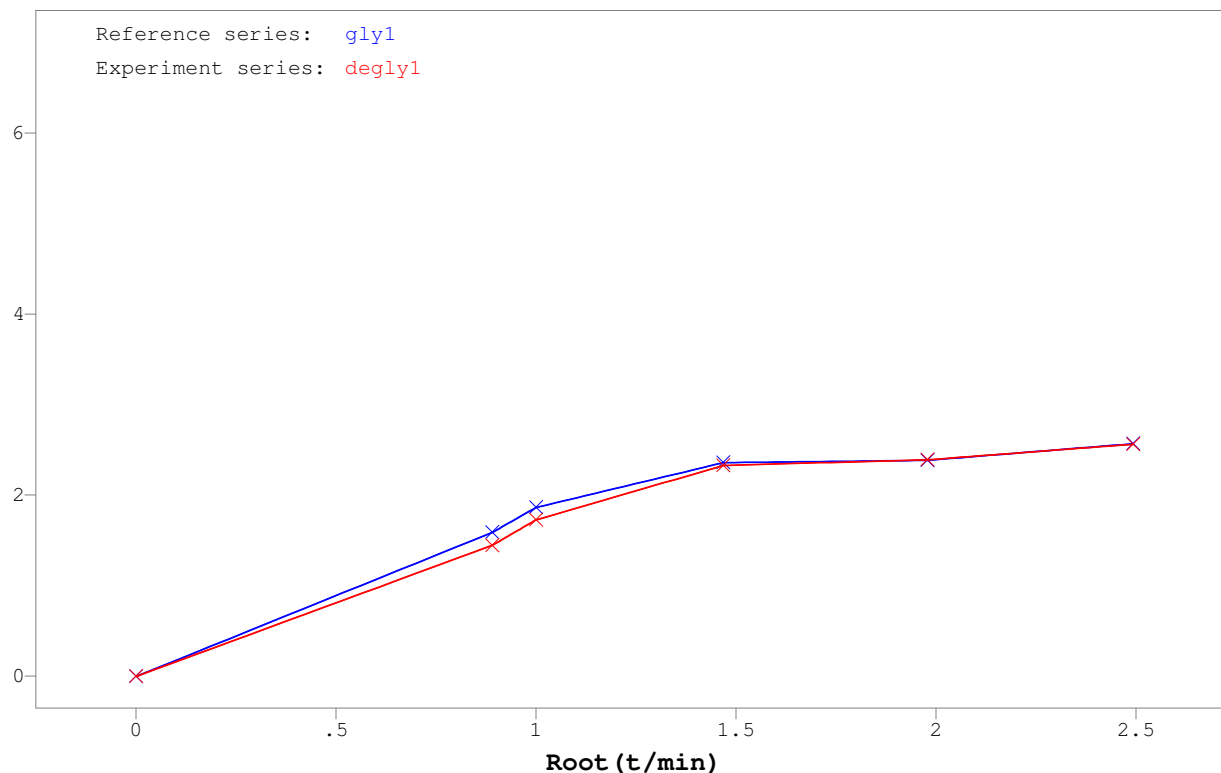
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	4.687	4.675	0.00	0.00	0.00	0.00
0.5	4.686	4.677	22.72	20.68	1.59	1.45
1.0	4.685	4.682	26.68	24.73	1.87	1.73
10.0	4.684	4.669	<b>33.75</b>	<b>33.31</b>	<b>2.36</b>	<b>2.33</b>
60.0	4.671	4.681	34.11	34.20	2.39	2.39
240.0	4.668	4.676	36.74	36.65	2.57	2.57

Score1 (DU sum): **1.29**  
 Score2 (DU Profile): 1.11p  
**DU sum difference (u): -0.34**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC266-275**  
 Exchangeable protons: 8  
 Index lis-file: 158  
 Sequence: ISKDDPEVQF  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

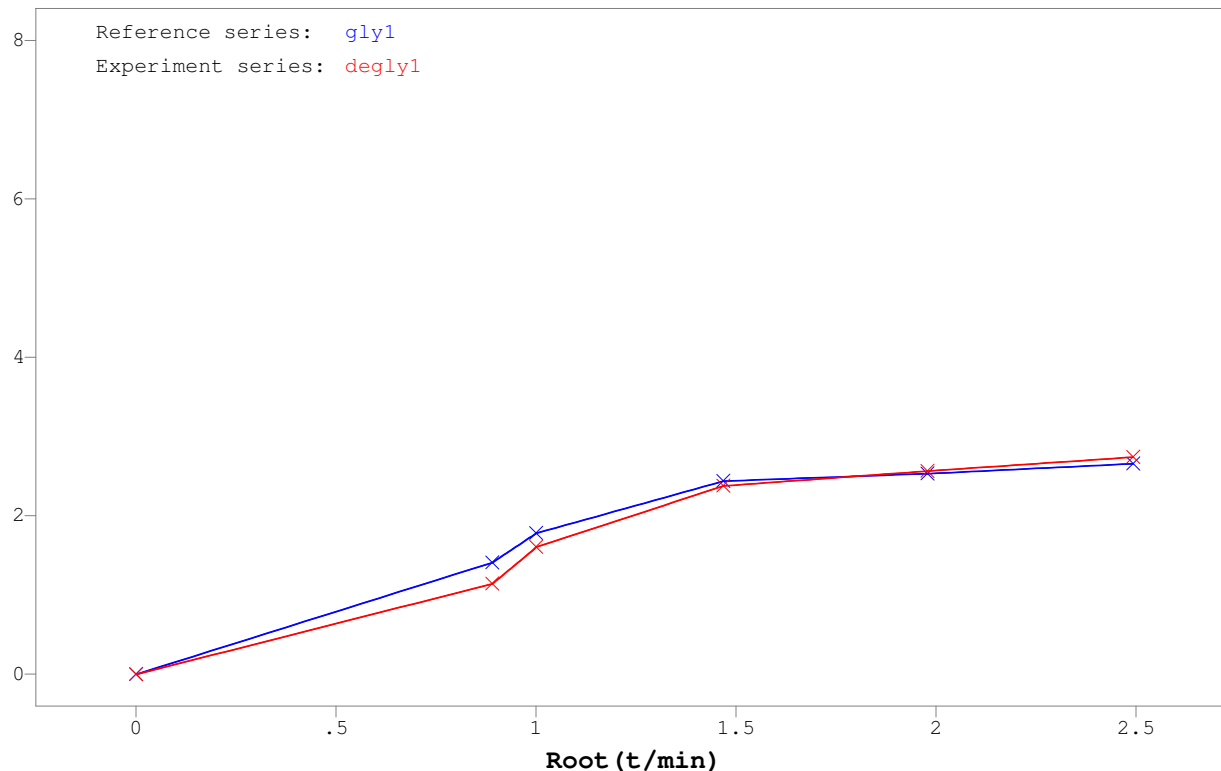
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.286	9.260	0.01	0.00	0.00	0.00
0.5	9.281	9.267	<b>17.65</b>	14.29	<b>1.41</b>	1.14
1.0	9.281	9.281	22.27	20.08	1.78	1.61
10.0	9.267	9.266	30.50	29.74	2.44	2.38
60.0	9.258	9.283	31.68	32.09	2.53	2.57
240.0	9.254	9.279	33.24	34.28	2.66	2.74

Score1 (DU sum): 0.49  
 Score2 (DU Profile): **1.28**  
 DU sum difference (u): -0.15

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC280-292**  
 Exchangeable protons: 11  
 Index lis-file: 227  
 Sequence: DDVEVHTAQTQPR  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

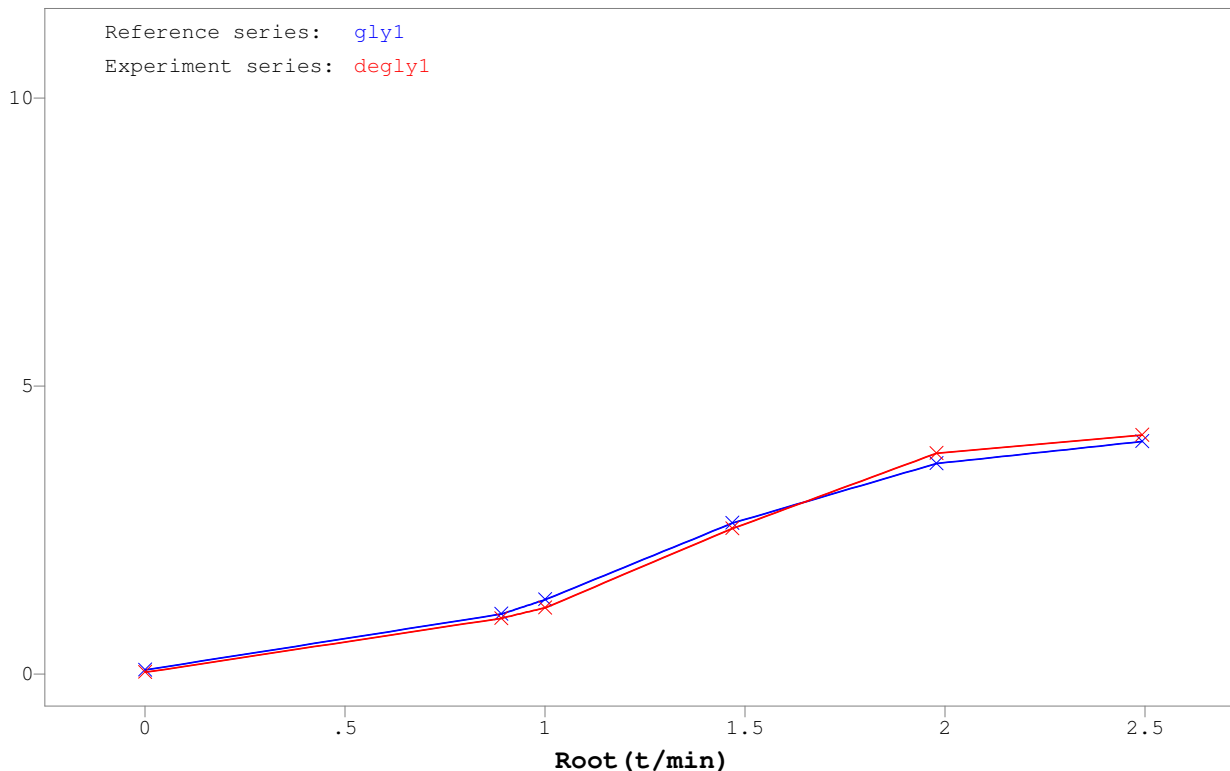
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.332	9.311	0.71	0.33	0.08	0.04
0.5	9.303	9.314	<b>9.53</b>	8.86	<b>1.05</b>	0.97
1.0	9.316	9.302	11.80	<b>10.53</b>	1.30	<b>1.16</b>
10.0	9.295	9.291	23.88	23.01	2.63	2.53
60.0	9.285	9.299	33.28	34.91	3.66	3.84
240.0	9.277	9.303	36.76	37.76	4.04	4.15

Score1 (DU sum): 0.50  
 Score2 (DU Profile): **1.41p**  
 DU sum difference (u): 0.23

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC307-333**  
 Exchangeable protons: 23  
 Index lis-file: 232  
 Sequence: PIMHQDWLNGKEFKCRVNSAAFPAPIE  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

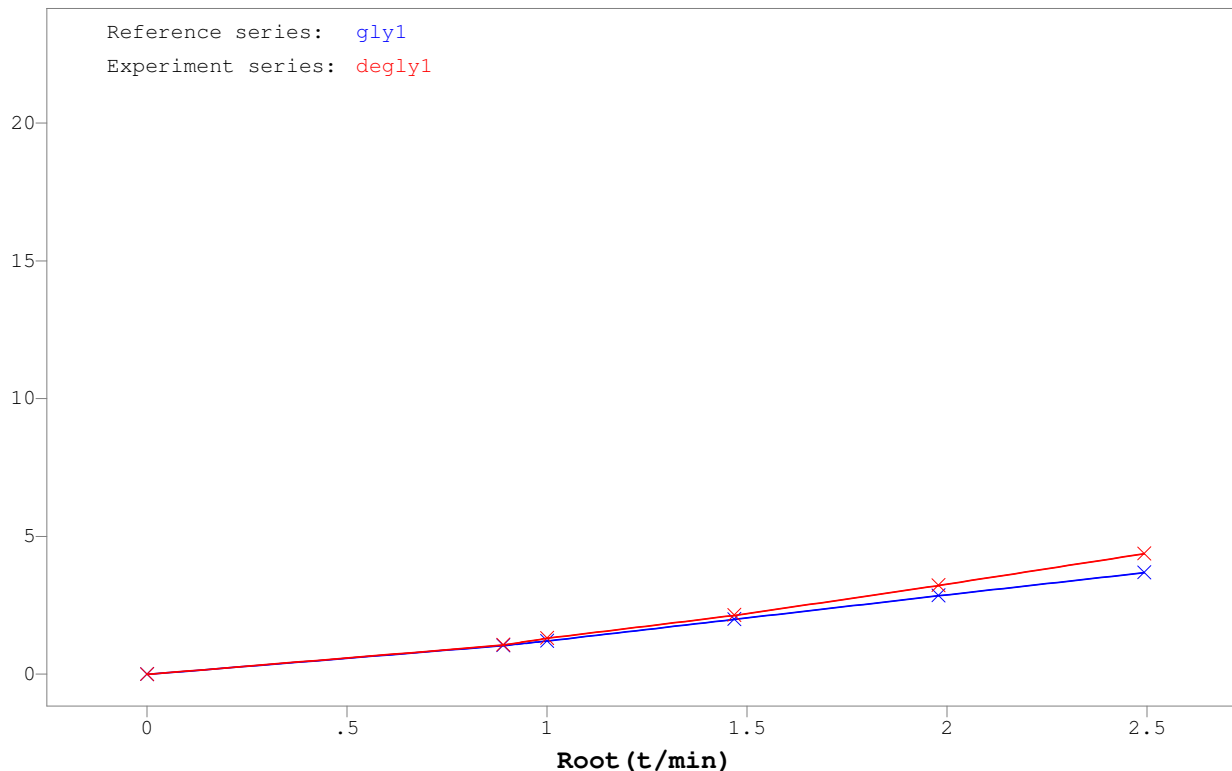
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.167	11.146	0.00	0.00	0.00	0.00
0.5	11.166	11.162	4.54	4.64	1.04	1.07
1.0	11.170	11.172	5.28	5.71	1.22	1.31
10.0	11.173	11.174	8.70	9.32	2.00	2.14
60.0	11.159	11.173	12.42	14.03	2.86	3.23
240.0	11.150	11.160	16.07	19.03	3.70	4.38

Score1 (DU sum): **1.70**  
 Score2 (DU Profile): 1.38  
**DU sum difference (u): 1.32**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC319-333**  
 Exchangeable protons: 12  
 Index lis-file: 164  
 Sequence: FKCRVNSAAFPAPIE  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

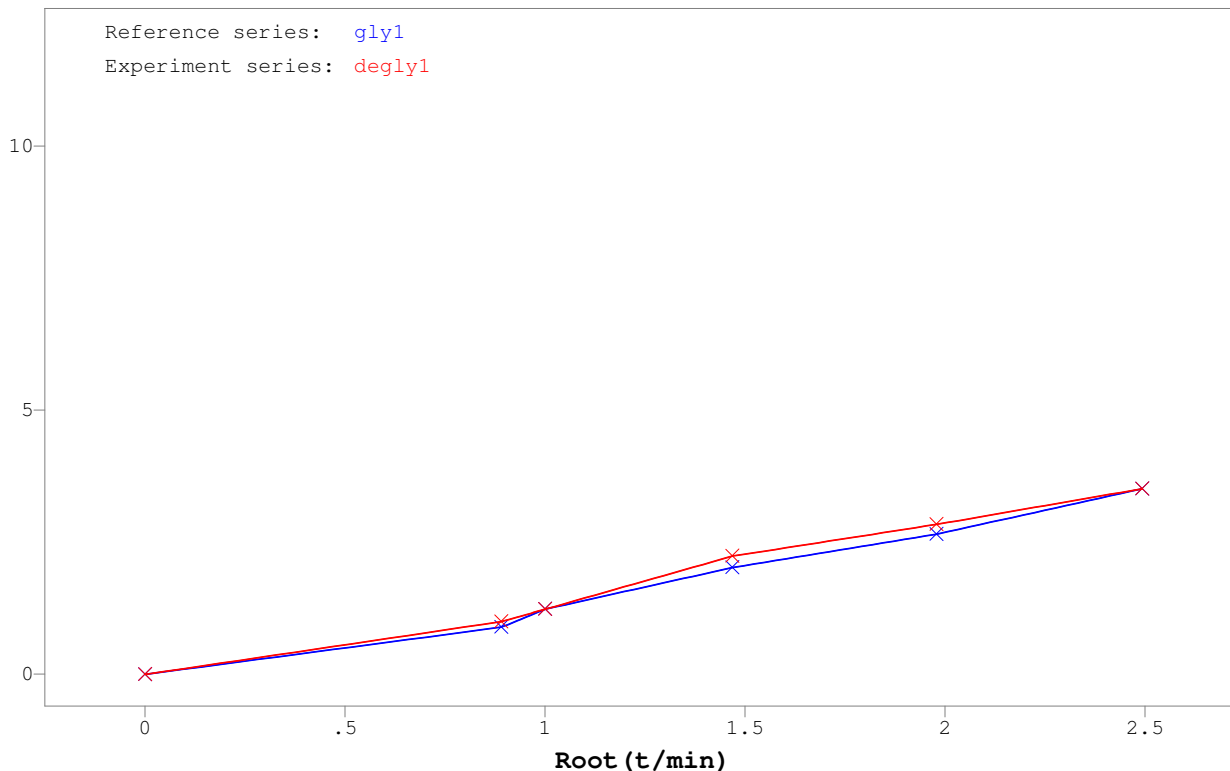
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.379	9.372	0.00	0.00	0.00	0.00
0.5	9.379	9.378	7.45	8.33	0.89	1.00
1.0	9.383	9.385	10.29	<b>10.29</b>	1.23	<b>1.23</b>
10.0	9.378	9.377	16.86	18.66	2.02	2.24
60.0	9.372	9.390	22.13	23.68	2.66	2.84
240.0	9.370	9.393	29.30	29.30	3.52	3.52

Score1 (DU sum): **1.25p**  
 Score2 (DU Profile): 1.02p  
**DU sum difference (u): 0.51**

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **HC**  
 Peptide: **HC336-348**  
 Exchangeable protons: 10  
 Index lis-file: 171  
 Sequence: ISKTKGRPKAPQV  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

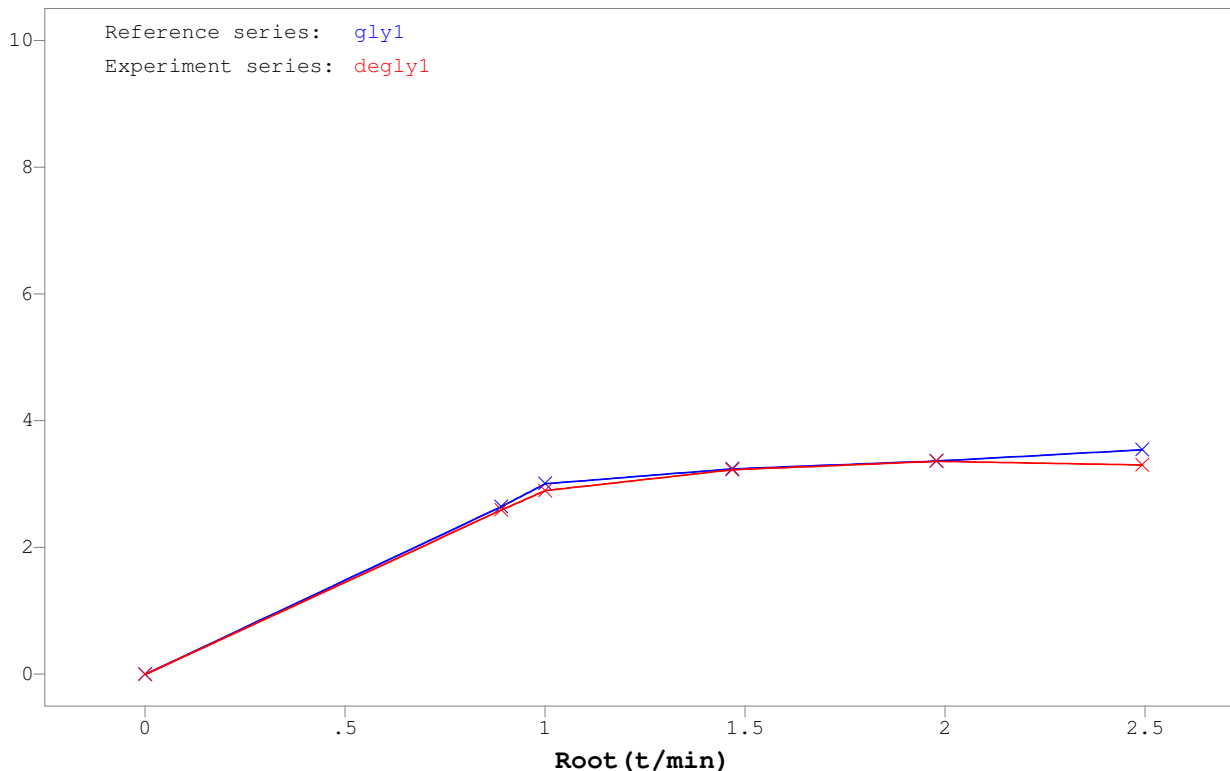
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	3.696	3.703	0.00	0.00	0.00	0.00
0.5	3.693	3.695	26.48	25.94	2.65	2.59
1.0	3.696	3.697	30.08	29.01	3.01	2.90
10.0	3.704	3.688	32.43	32.29	3.24	3.23
60.0	3.696	3.701	33.67	33.62	3.37	3.36
240.0	3.696	3.692	35.44	33.06	3.54	3.31

Score1 (DU sum): **1.24**  
 Score2 (DU Profile): 1.01  
**DU sum difference (u): -0.42**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC342-366**  
 Exchangeable protons: 19  
 Index lis-file: 234  
 Sequence: RPKAPQVYTIPPPKEQMAKDKVSLT  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

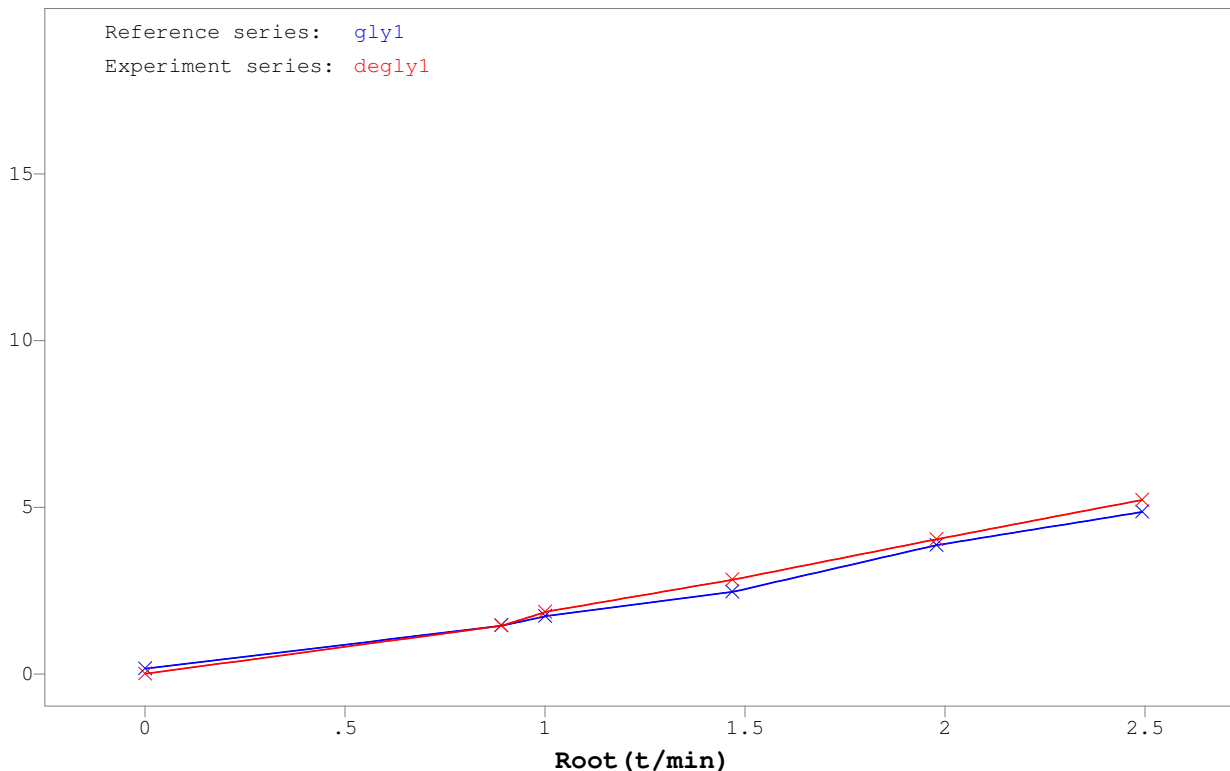
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.631	10.613	<b>0.91</b>	0.11	<b>0.17</b>	0.02
0.5	10.629	10.618	7.70	7.70	1.46	1.46
1.0	10.628	10.619	9.19	9.86	1.75	1.87
10.0	10.631	10.628	13.01	14.93	2.47	2.84
60.0	10.629	10.688	20.40	21.31	3.88	4.05
240.0	10.625	10.613	25.62	27.54	4.87	5.23

Score1 (DU sum): **1.37p**  
 Score2 (DU Profile): 1.50p  
**DU sum difference (u): 0.88**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC347-370**  
 Exchangeable protons: 20  
 Index lis-file: 173  
 Sequence: QVYTIPPPKEQMAKDKVSLTCMIT  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

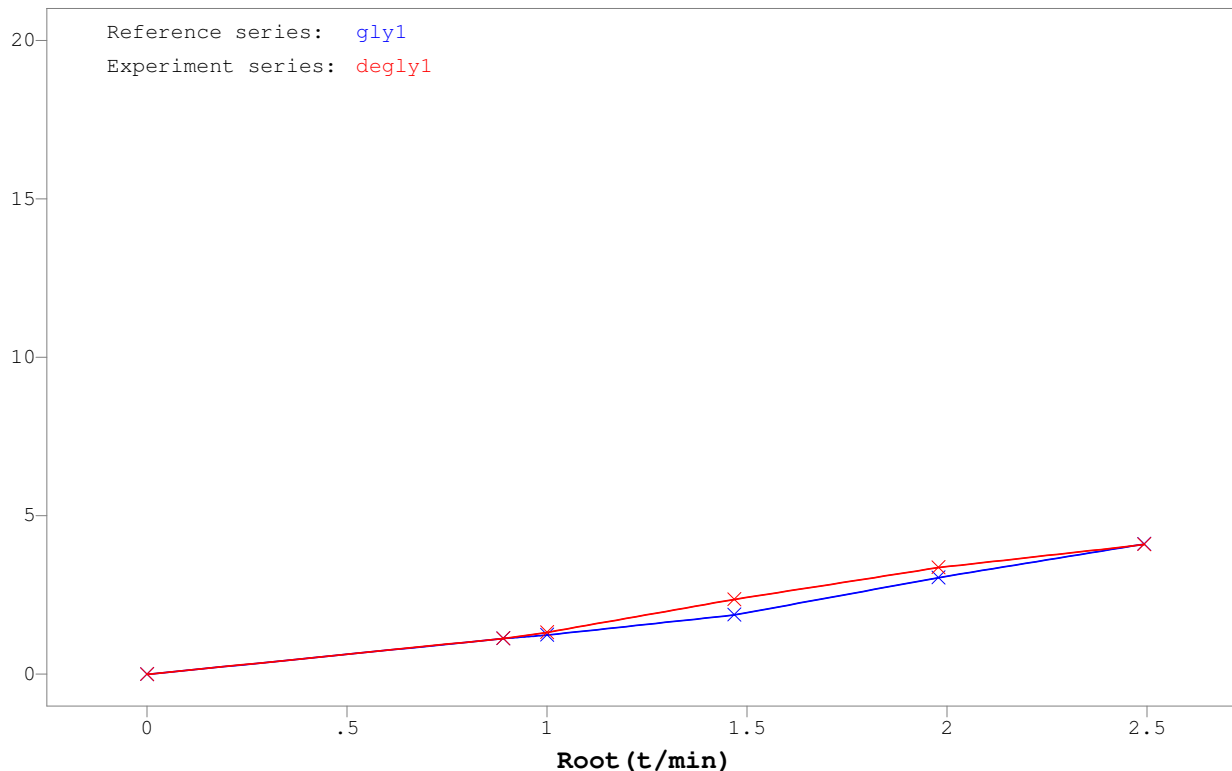
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.474	10.463	0.00	0.00	0.00	0.00
0.5	10.471	10.459	5.65	5.67	1.13	1.13
1.0	10.440	10.423	6.21	6.64	1.24	1.33
10.0	10.454	10.442	9.37	11.84	1.87	2.37
60.0	10.443	10.459	15.28	16.86	3.06	3.37
240.0	10.436	10.417	20.58	20.48	4.12	4.10

Score1 (DU sum): **1.30**  
 Score2 (DU Profile): 1.11  
**DU sum difference (u): 0.88**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC349-365**  
 Exchangeable protons: 13  
 Index lis-file: 174  
 Sequence: YTIPPPKEQMAKDKVSL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

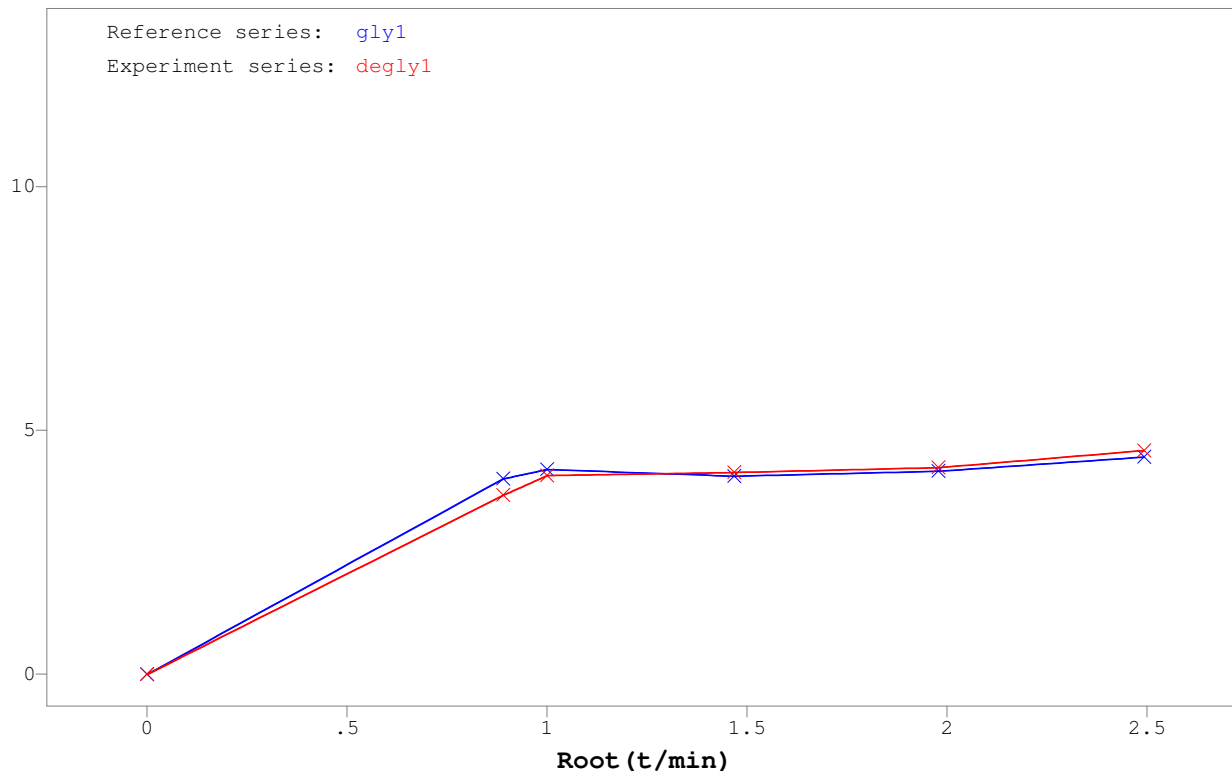
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.012	8.003	0.00	0.00	0.00	0.00
0.5	8.002	7.997	30.86	28.28	4.01	3.68
1.0	8.001	8.004	32.35	31.38	4.20	4.08
10.0	7.996	7.999	31.29	31.87	4.07	4.14
60.0	7.988	8.004	32.07	32.64	4.17	4.24
240.0	7.982	7.999	34.31	35.34	4.46	4.59

Score1 (DU sum): 0.41  
 Score2 (DU Profile): **1.39**  
 DU sum difference (u): -0.18

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC367-390**  
 Exchangeable protons: 21  
 Index lis-file: 177  
 Sequence: CMITDFFPEDITVEWQWNGQPAEN  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

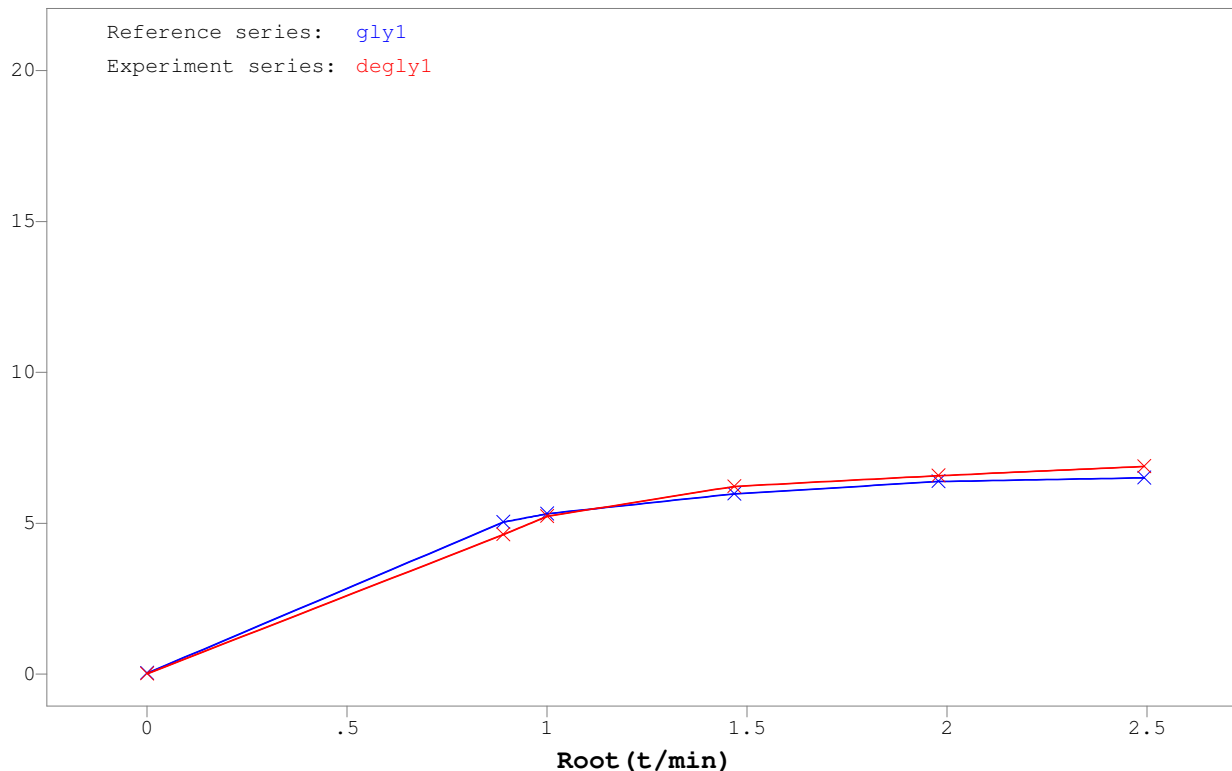
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.258	8.249	0.20	0.11	0.04	0.02
0.5	8.256	8.247	24.04	22.07	5.05	4.64
1.0	8.259	8.255	25.36	24.96	5.33	5.24
10.0	8.246	8.247	28.51	29.68	5.99	6.23
60.0	8.243	8.254	30.45	31.37	6.39	6.59
240.0	8.236	8.257	31.03	32.83	6.52	6.89

Score1 (DU sum): 0.43  
 Score2 (DU Profile): **1.54**  
 DU sum difference (u): 0.30

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC373-376**  
 Exchangeable protons: 2  
 Index lis-file: 181  
 Sequence: FPED  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

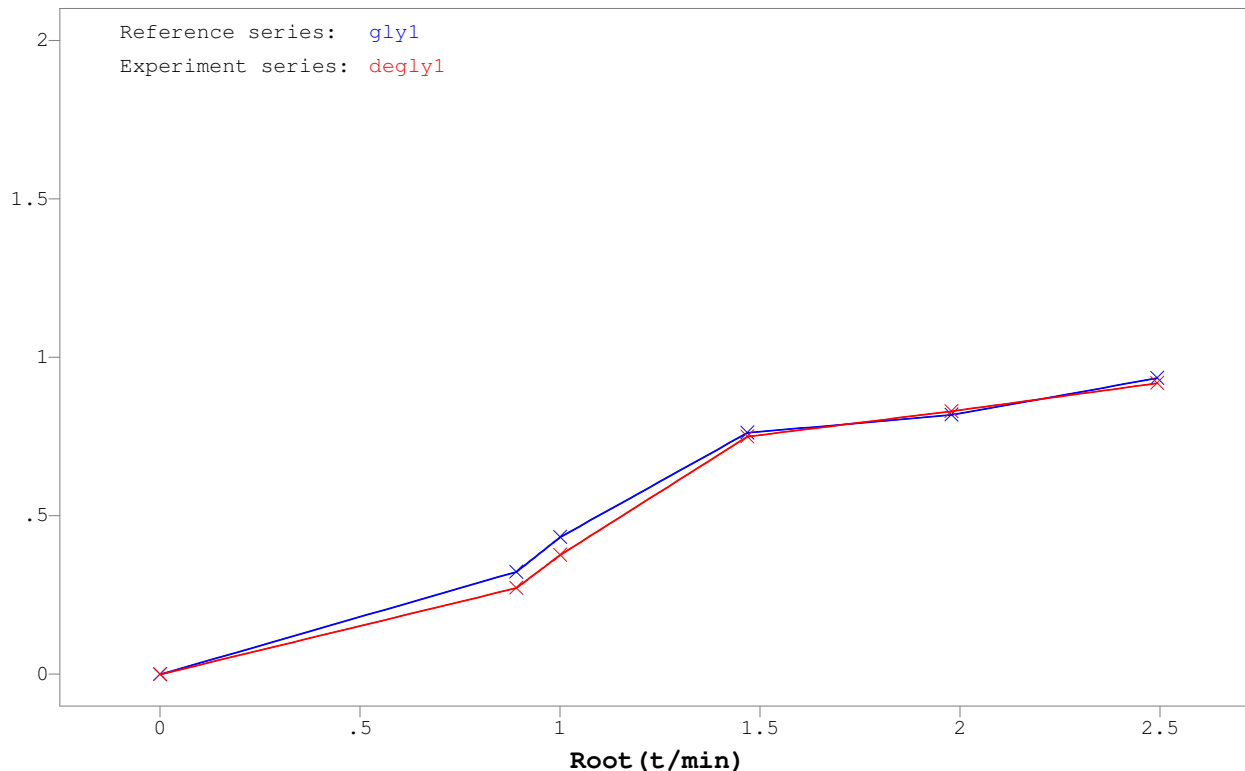
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.353	6.353	0.00	0.00	0.00	0.00
0.5	6.353	6.353	16.18	13.63	0.32	0.27
1.0	6.353	6.353	<b>21.67</b>	<b>18.86</b>	<b>0.43</b>	<b>0.38</b>
10.0	6.353	6.339	38.13	37.53	0.76	0.75
60.0	6.348	6.353	40.94	41.54	0.82	0.83
240.0	6.353	6.353	46.76	45.95	0.94	0.92

Score1 (DU sum): **1.09**  
 Score2 (DU Profile): 1.32  
**DU sum difference (u): -0.08**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC381-390**  
 Exchangeable protons: 8  
 Index lis-file: 183  
 Sequence: WQWNGQPAEN  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

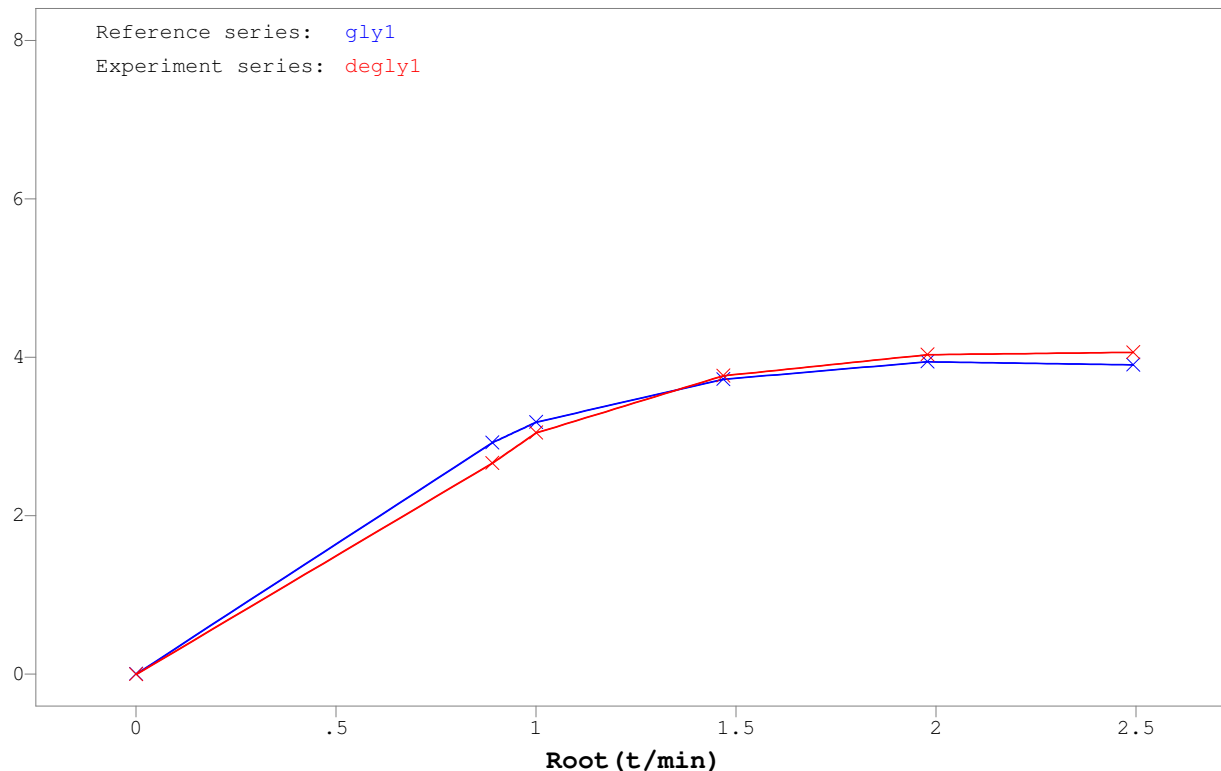
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.616	10.601	0.07	0.00	0.01	0.00
0.5	10.611	10.617	36.57	33.34	2.93	2.67
1.0	10.611	10.612	39.82	38.11	3.19	3.05
10.0	10.619	10.593	46.57	47.12	3.73	3.77
60.0	10.608	10.613	49.34	50.45	3.95	4.04
240.0	10.606	10.624	48.84	50.83	3.91	4.07

Score1 (DU sum): 0.40  
 Score2 (DU Profile): **2.10**  
 DU sum difference (u): -0.11

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC381-398**  
 Exchangeable protons: 15  
 Index lis-file: 184  
 Sequence: WQWNGQPAENYKNTQPIM  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

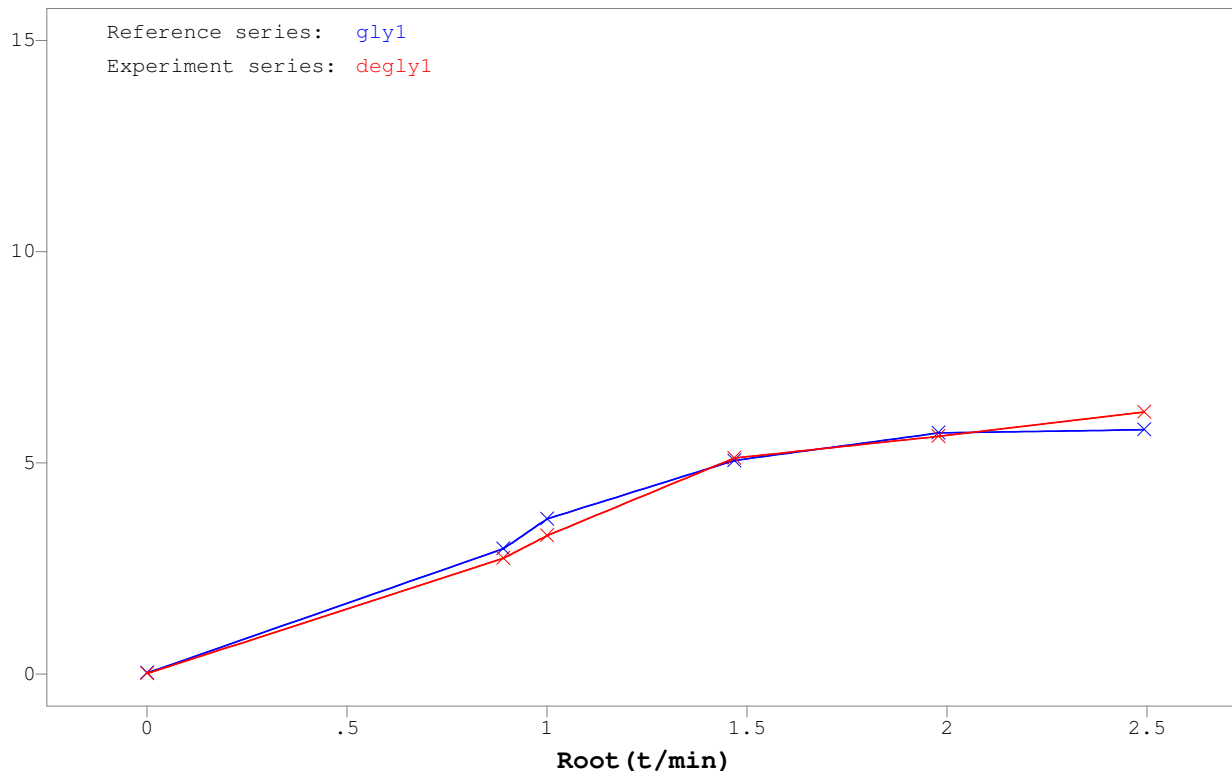
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.474	11.463	0.23	0.13	0.03	0.02
0.5	11.472	11.469	19.84	18.33	2.98	2.75
1.0	11.473	11.470	24.56	<b>21.91</b>	3.68	<b>3.29</b>
10.0	11.459	11.462	<b>33.76</b>	34.15	<b>5.06</b>	5.12
60.0	11.454	11.468	38.11	37.58	5.72	5.64
240.0	11.448	11.473	38.62	41.40	5.79	6.21

Score1 (DU sum): 0.24  
 Score2 (DU Profile): **1.78**  
 DU sum difference (u): 0.15

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **HC**  
 Peptide: **HC390-398**  
 Exchangeable protons: 7  
 Index lis-file: 185  
 Sequence: NYKNTQPIM  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

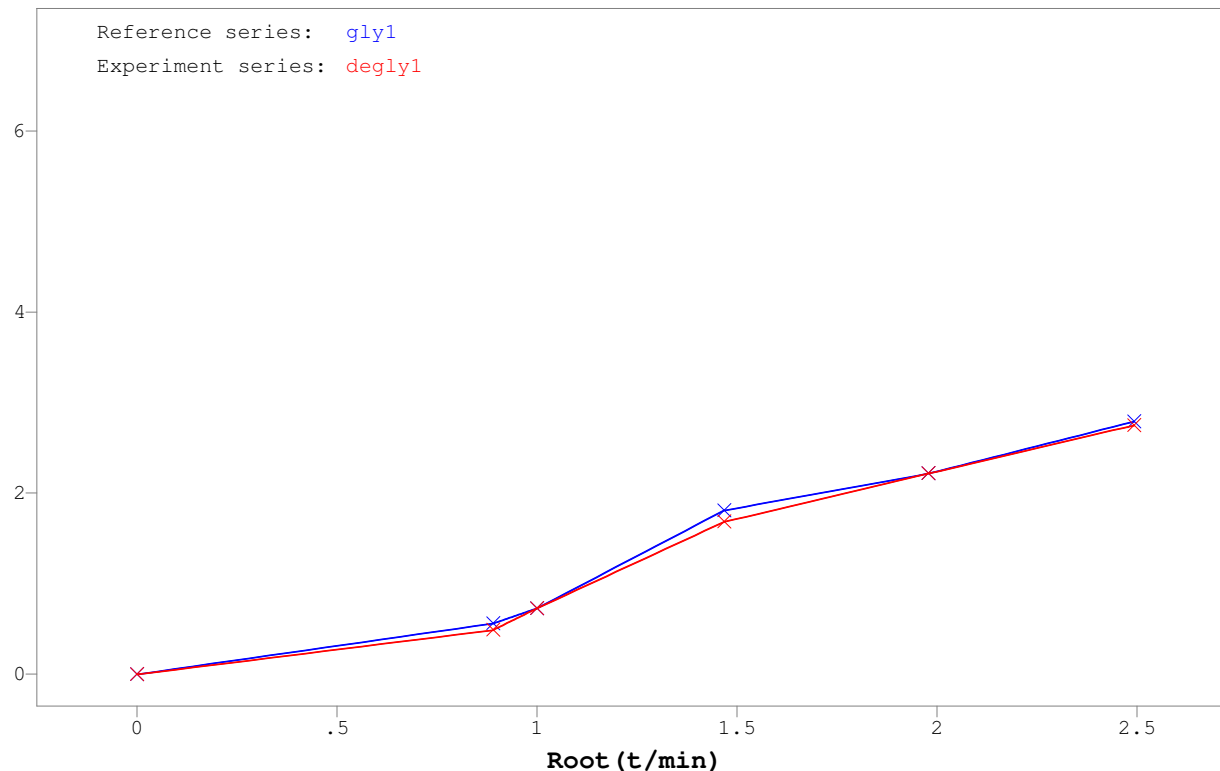
Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.290	7.269	0.00	0.00	0.00	0.00
0.5	7.283	7.278	8.03	7.02	0.56	0.49
1.0	7.289	7.281	<b>10.43</b>	10.43	<b>0.73</b>	0.73
10.0	7.269	7.271	25.89	24.08	1.81	1.69
60.0	7.264	7.276	31.71	31.71	2.22	2.22
240.0	7.264	7.278	39.93	39.33	2.80	2.75

Score1 (DU sum): **1.01p**

Score2 (DU Profile): 0.99

DU sum difference (u): **-0.24**

### DU Value



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC391-398**  
 Exchangeable protons: 6  
 Index lis-file: 238  
 Sequence: YKNTQPIM  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

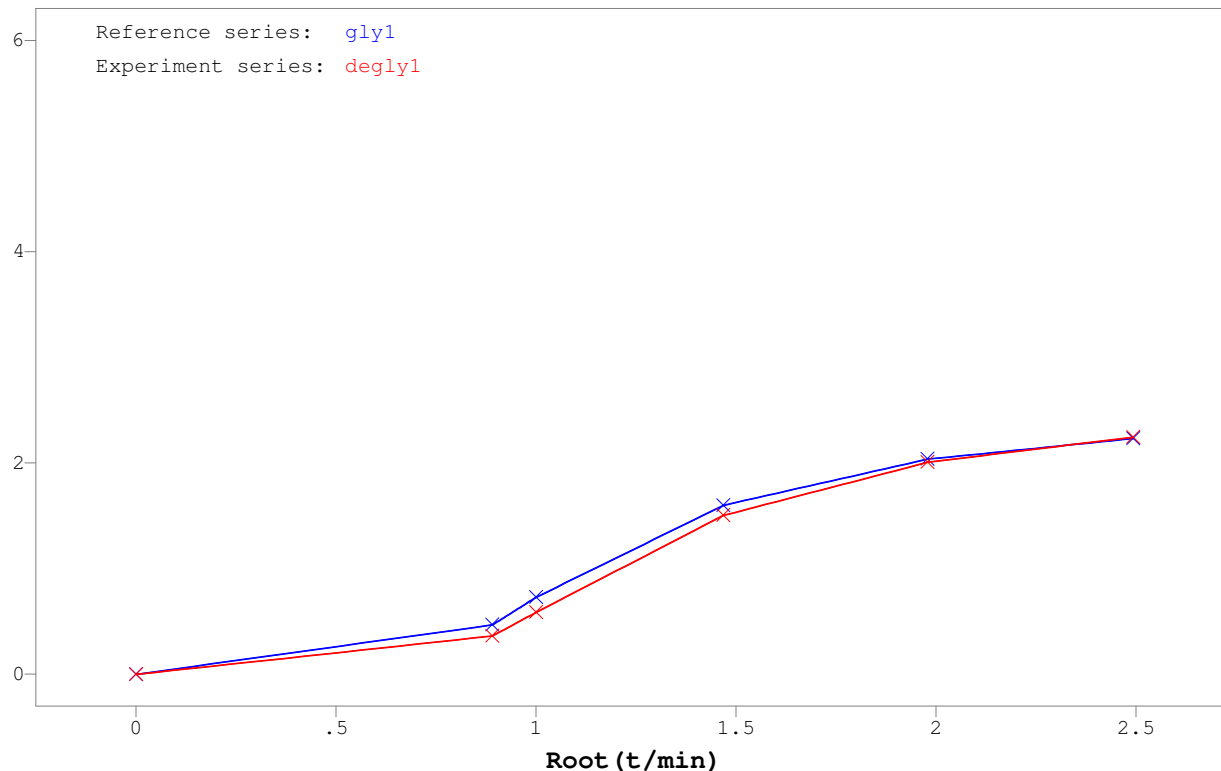
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	7.036	7.028	0.00	0.00	0.00	0.00
0.5	7.042	7.027	7.81	6.06	0.47	0.36
1.0	7.044	7.037	12.18	9.81	0.73	0.59
10.0	7.028	7.029	26.69	25.08	1.60	1.51
60.0	7.029	7.033	33.97	33.47	2.04	2.01
240.0	7.020	7.034	37.22	37.45	2.23	2.25

Score1 (DU sum): **1.78**  
 Score2 (DU Profile): 1.56  
**DU sum difference (u): -0.36**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC391-404**  
 Exchangeable protons: 12  
 Index lis-file: 186  
 Sequence: YKNTQPIMDTDGSY  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

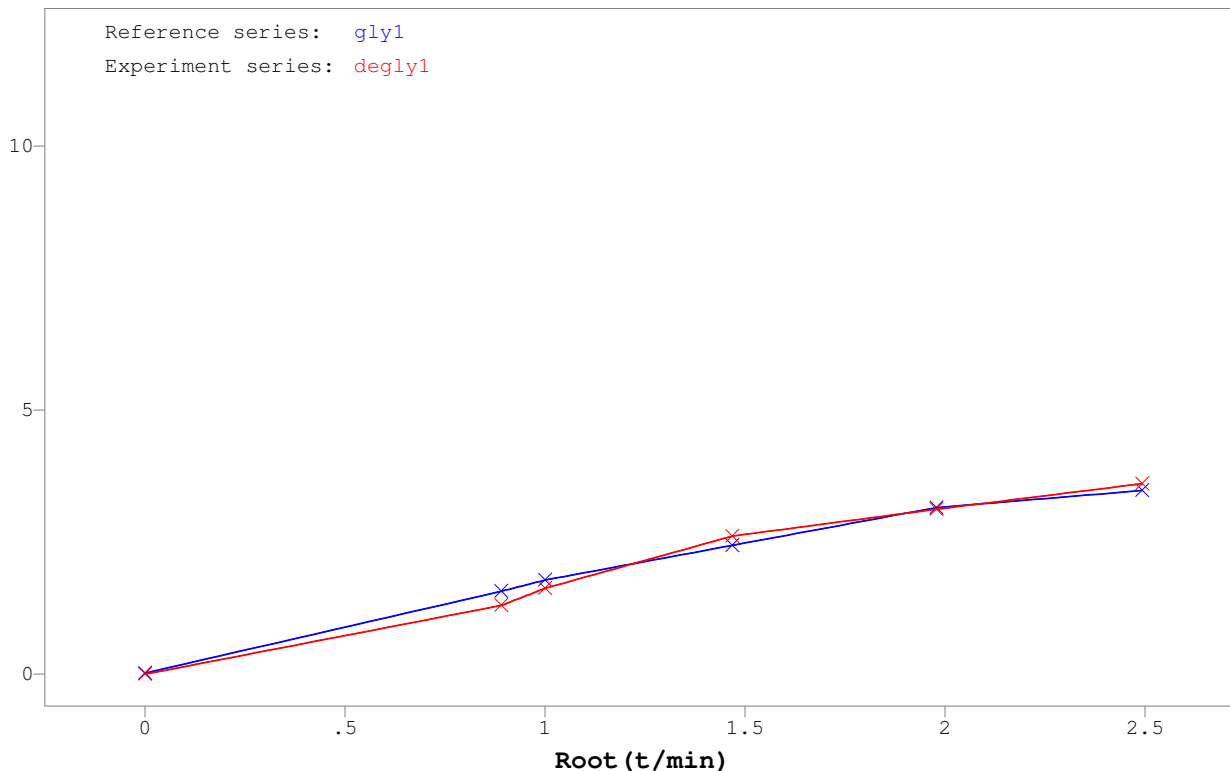
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.554	8.541	0.22	0.04	0.03	0.00
0.5	8.537	8.514	13.12	10.89	1.57	1.31
1.0	8.534	8.527	<b>14.90</b>	<b>13.60</b>	<b>1.79</b>	<b>1.63</b>
10.0	8.520	8.507	20.37	21.84	2.44	2.62
60.0	8.526	8.532	26.34	26.08	3.16	3.13
240.0	8.524	8.529	29.02	30.10	3.48	3.61

Score1 (DU sum): 0.04  
 Score2 (DU Profile): **1.52**  
 DU sum difference (u): -0.02

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **HC**  
 Peptide: **HC411-422**  
 Exchangeable protons: 11  
 Index lis-file: 192  
 Sequence: NVQKSNWEAGNT  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

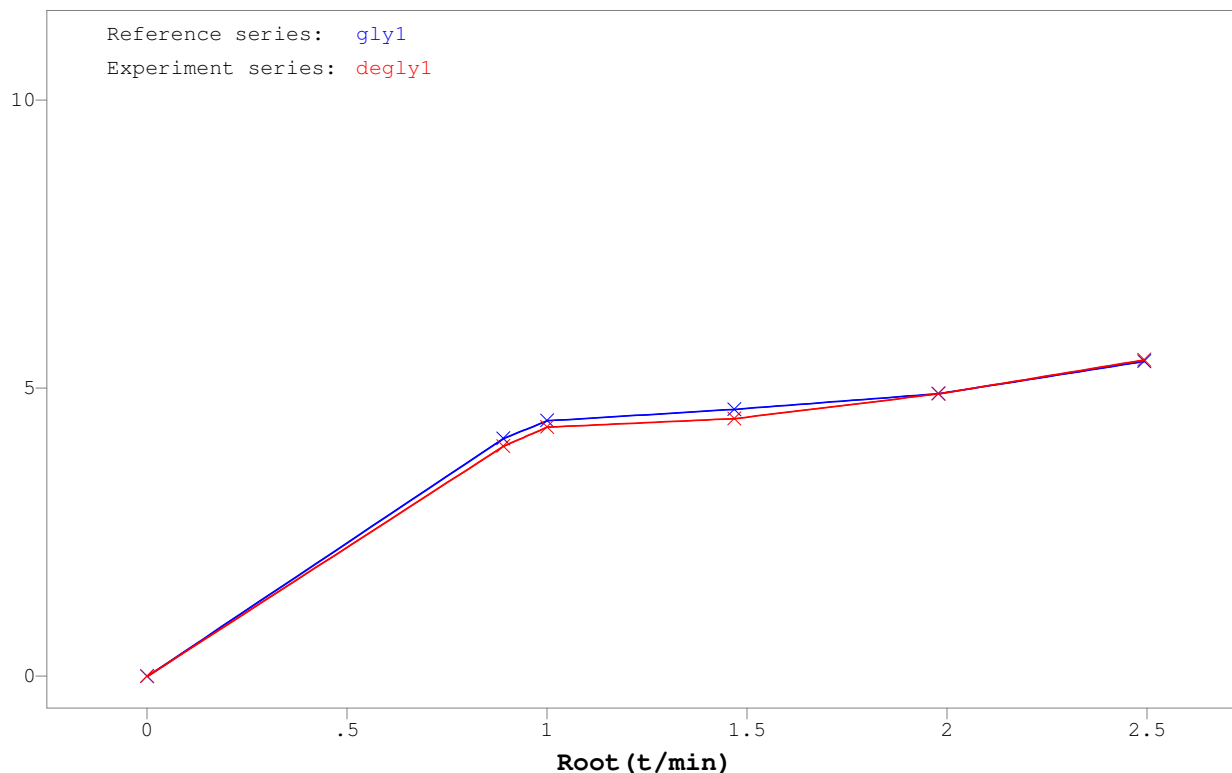
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.352	6.338	0.00	0.00	0.00	0.00
0.5	6.347	6.336	37.55	36.32	4.13	3.99
1.0	6.345	6.342	40.33	39.34	4.44	4.33
10.0	6.341	6.333	42.14	40.68	4.64	4.47
60.0	6.333	6.344	44.61	44.58	4.91	4.90
240.0	6.329	6.341	49.71	49.94	5.47	5.49

Score1 (DU sum): **1.03**  
 Score2 (DU Profile): 0.96  
**DU sum difference (u): -0.38**

**DU Value**



Root(t/min): 6th roots of exchange times

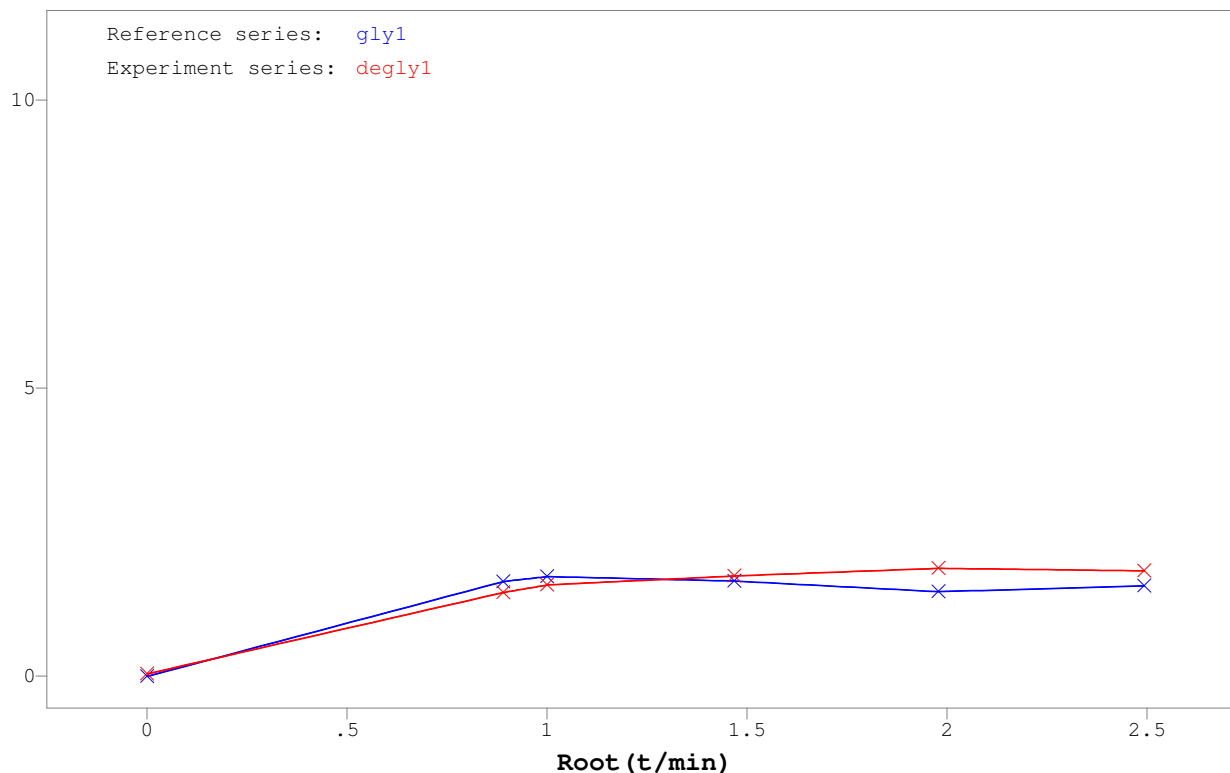
Molecule: **HC**  
 Peptide: **HC016-027**  
 Exchangeable protons: 11  
 Index lis-file: 93  
 Sequence: GSLKLSCAASGF  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.237	9.242	<b>0.00</b>	0.39	<b>0.00</b>	0.04
0.5	9.197	9.211	<b>14.97</b>	13.24	<b>1.65</b>	1.46
1.0	9.217	9.195	<b>15.75</b>	14.43	<b>1.73</b>	1.59
10.0	9.198	9.191	<b>15.05</b>	15.85	<b>1.66</b>	1.74
60.0	9.188	9.200	<b>13.36</b>	17.06	<b>1.47</b>	1.88
240.0	9.187	9.197	<b>14.32</b>	16.66	<b>1.57</b>	1.83

**DU Value**



Root(t/min): 6th roots of exchange times

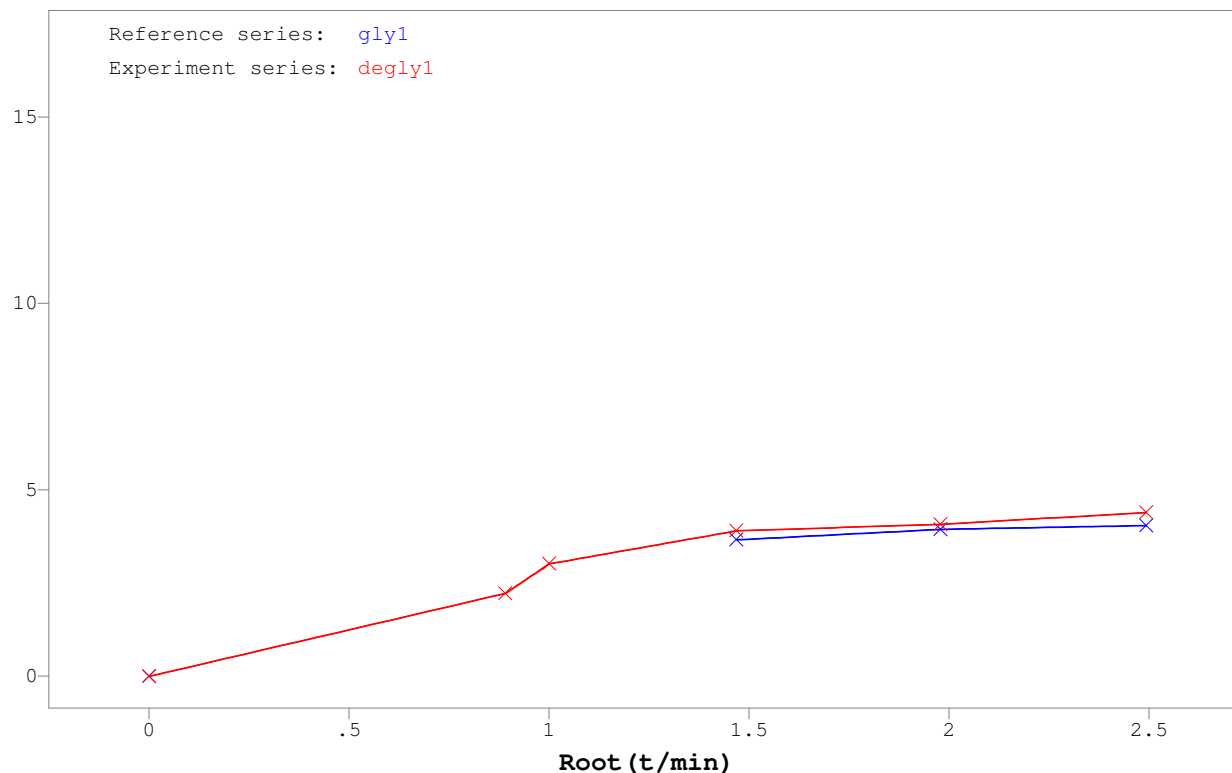
Molecule: **HC**  
 Peptide: **HC162-180**  
 Exchangeable protons: 17  
 Index lis-file: 138  
 Sequence: VTWNSGSLSSGVHTFPAVL  
 Range: 2 / 3

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	13.051	13.131	<b>0.00</b>	0.00	<b>0.00</b>	0.00
0.5	n.d.	13.129	n.d.	13.09	n.d.	2.23
1.0	n.d.	13.144	n.d.	17.75	n.d.	3.02
10.0	13.124	13.130	<b>21.54</b>	22.96	<b>3.66</b>	3.90
60.0	13.125	13.142	<b>23.19</b>	24.00	<b>3.94</b>	4.08
240.0	13.117	13.134	<b>23.80</b>	25.84	<b>4.05</b>	4.39

**DU Value**



Root(t/min): 6th roots of exchange times

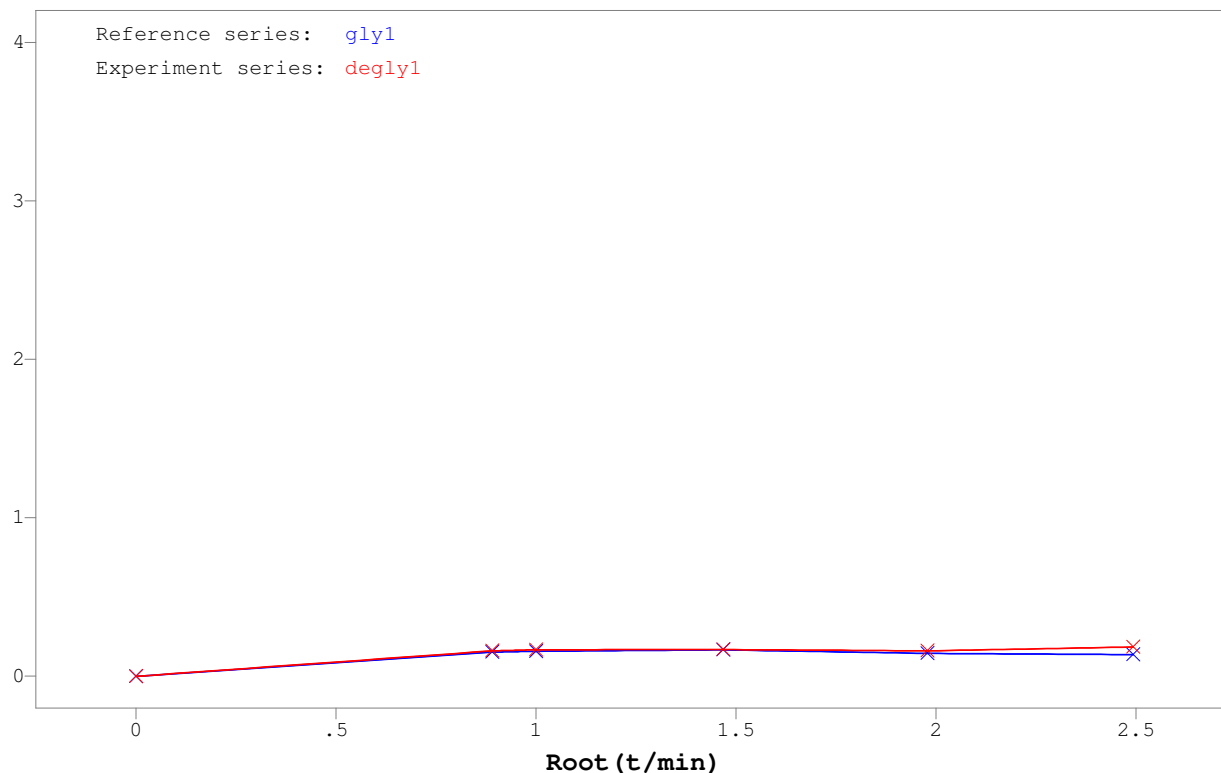
Molecule: **HC**  
 Peptide: **HC185-189**  
 Exchangeable protons: 4  
 Index lis-file: 141  
 Sequence: YTLSS  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.826	6.824	<b>0.00</b>	0.00	<b>0.00</b>	0.00
0.5	6.820	6.829	<b>3.81</b>	4.01	<b>0.15</b>	0.16
1.0	6.820	6.821	<b>3.95</b>	4.19	<b>0.16</b>	0.17
10.0	6.826	6.809	<b>4.16</b>	4.21	<b>0.17</b>	0.17
60.0	6.821	6.827	<b>3.61</b>	4.01	<b>0.14</b>	0.16
240.0	6.818	6.832	<b>3.41</b>	4.62	<b>0.14</b>	0.18

**DU Value**



Root(t/min): 6th roots of exchange times

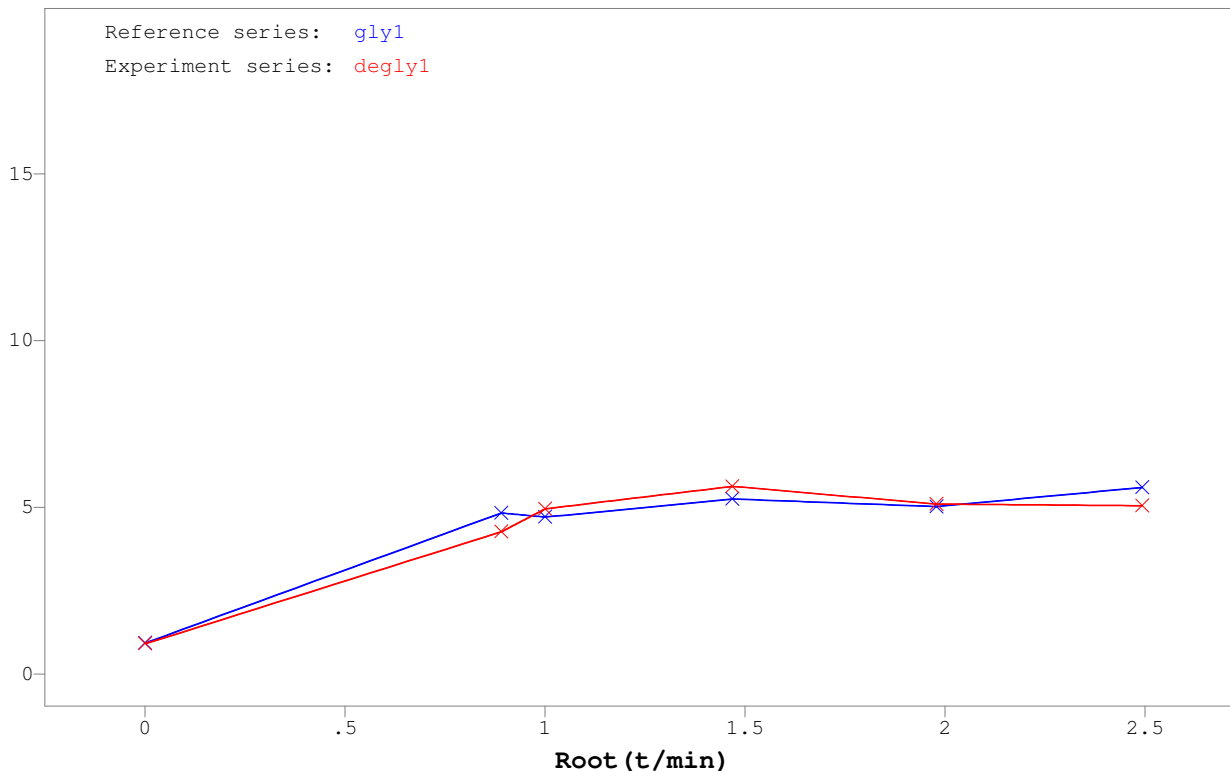
Molecule: **HC**  
 Peptide: **HC334-358**  
 Exchangeable protons: 19  
 Index lis-file: 167  
 Sequence: KTISKTKGRPKAPQVYTIPPPKEQM  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.144	6.119	<b>4.95</b>	<b>4.83</b>	<b>0.94</b>	<b>0.92</b>
0.5	6.132	6.111	<b>25.46</b>	<b>22.50</b>	<b>4.84</b>	<b>4.27</b>
1.0	6.134	6.128	<b>24.81</b>	<b>26.12</b>	<b>4.71</b>	<b>4.96</b>
10.0	6.119	6.120	<b>27.67</b>	<b>29.65</b>	<b>5.26</b>	<b>5.63</b>
60.0	6.117	6.128	<b>26.48</b>	<b>26.86</b>	<b>5.03</b>	<b>5.10</b>
240.0	6.109	6.129	<b>29.49</b>	<b>26.61</b>	<b>5.60</b>	<b>5.06</b>

**DU Value**



Root(t/min): 6th roots of exchange times



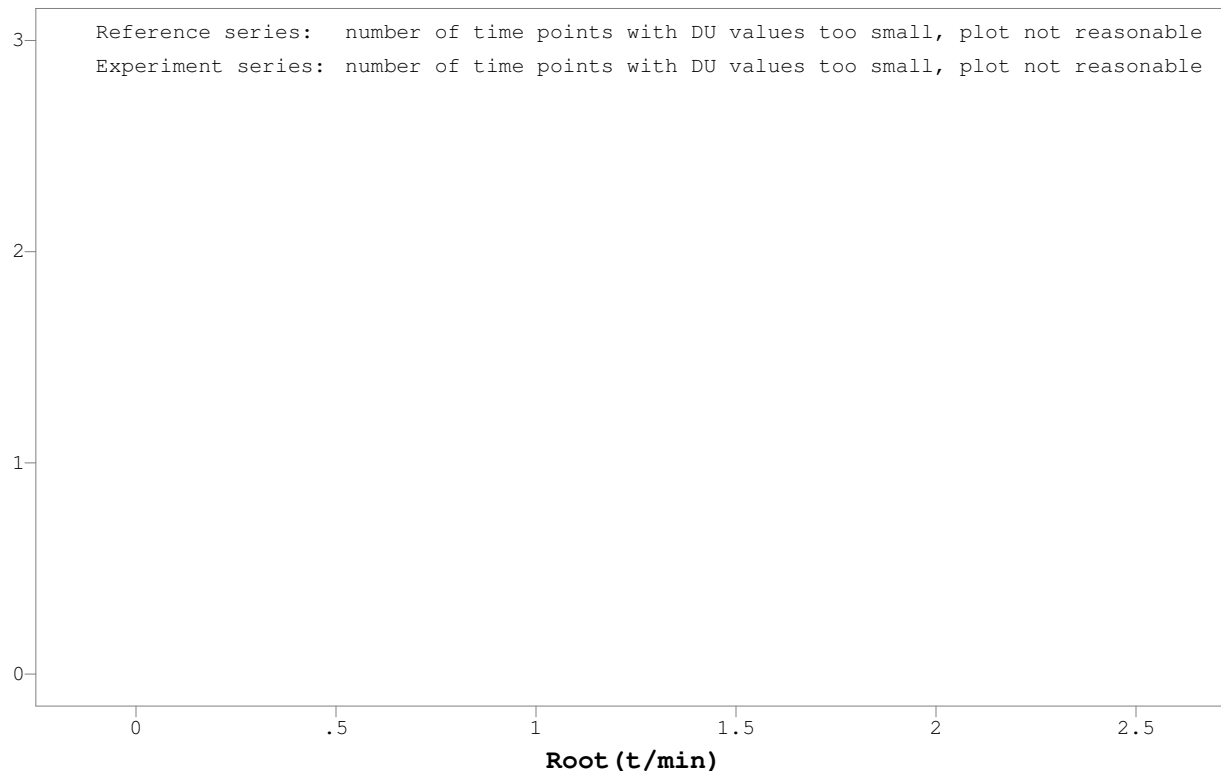
Molecule: **HC**  
 Peptide: **HC377-380**  
 Exchangeable protons: 3  
 Index lis-file: 182  
 Sequence: ITVE  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	5.858	5.858	n.d.	n.d.	n.d.	n.d.
0.5	5.855	5.857	n.d.	n.d.	n.d.	n.d.
1.0	5.855	5.858	n.d.	n.d.	n.d.	n.d.
10.0	5.858	5.846	n.d.	n.d.	n.d.	n.d.
60.0	5.852	5.857	n.d.	n.d.	n.d.	n.d.
240.0	5.855	5.855	n.d.	n.d.	n.d.	n.d.

**DU Value**



Root(t/min): 6th roots of exchange times

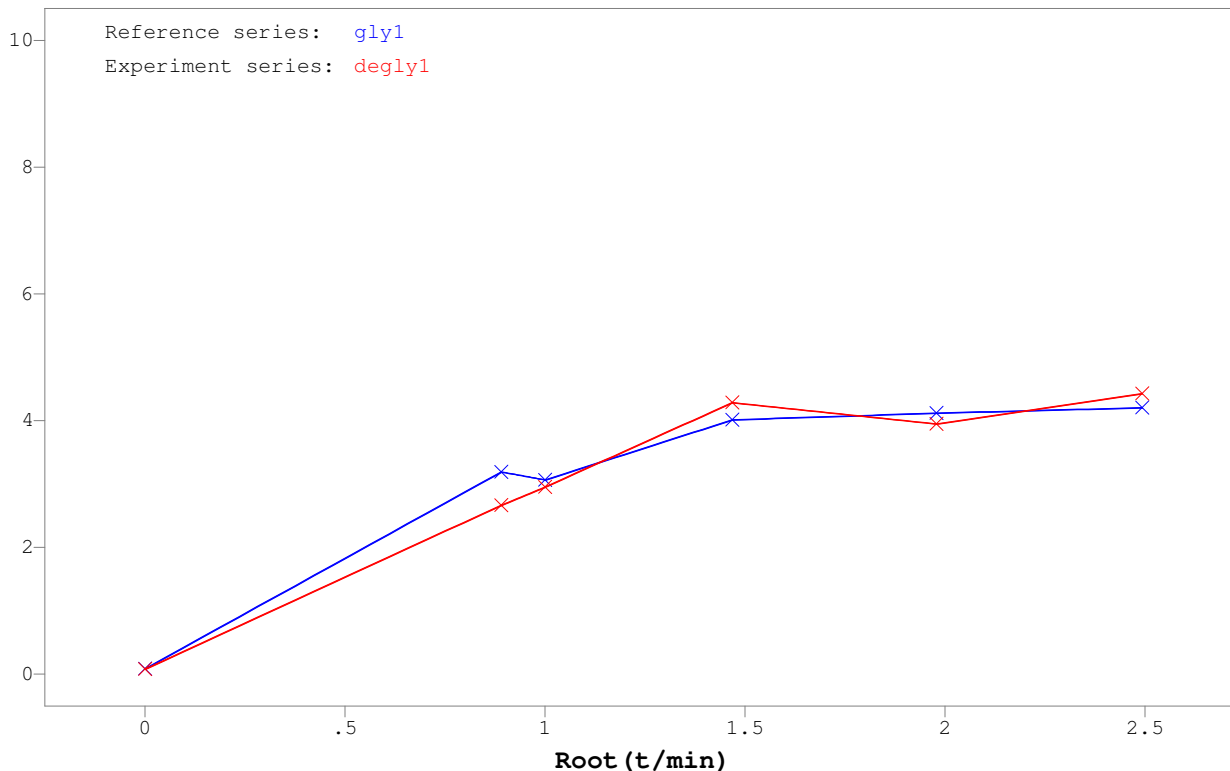
Molecule: **HC**  
 Peptide: **HC379-390**  
 Exchangeable protons: 10  
 Index lis-file: 237  
 Sequence: VEWQWNGQPAEN  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.318	11.319	<b>0.88</b>	0.80	<b>0.09</b>	0.08
0.5	11.318	11.323	<b>31.94</b>	26.69	<b>3.19</b>	2.67
1.0	11.320	11.318	<b>30.68</b>	29.56	<b>3.07</b>	2.96
10.0	11.325	11.307	<b>40.16</b>	<b>42.88</b>	<b>4.02</b>	<b>4.29</b>
60.0	11.312	11.320	<b>41.22</b>	39.50	<b>4.12</b>	3.95
240.0	11.310	11.321	<b>42.06</b>	44.27	<b>4.21</b>	4.43

**DU Value**



Root(t/min): 6th roots of exchange times

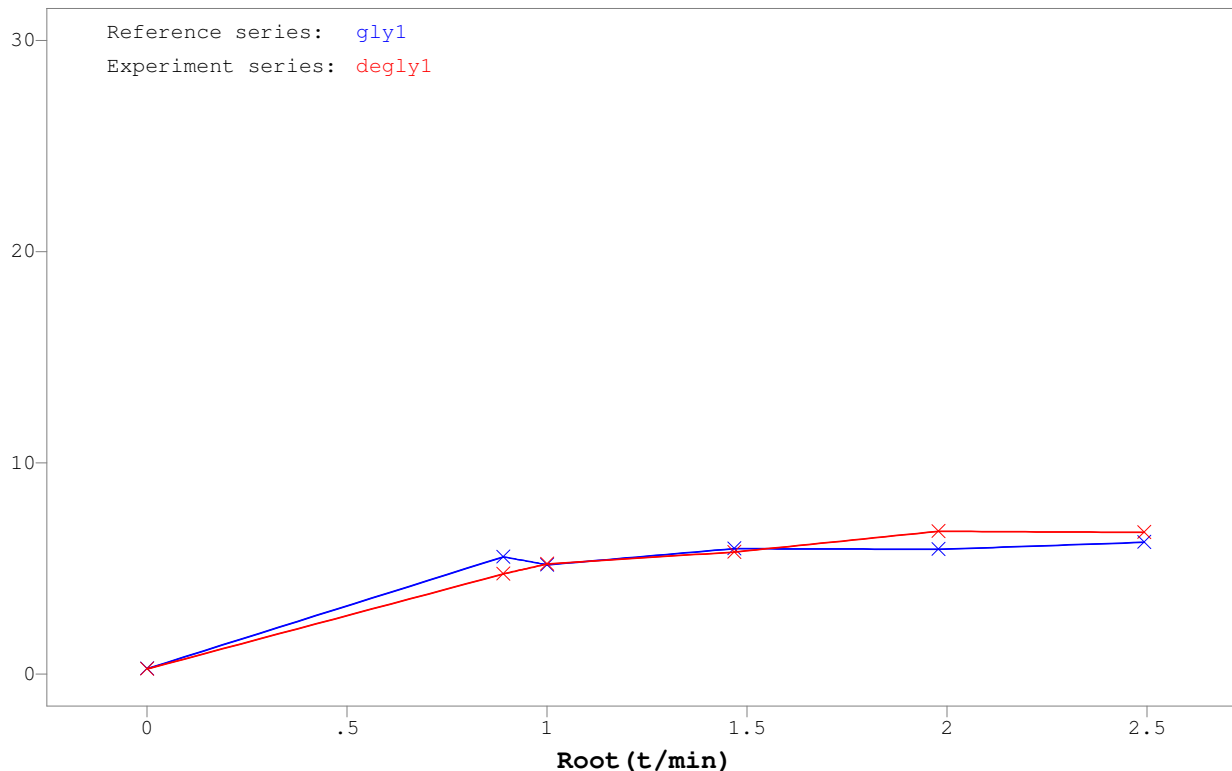
Molecule: **HC**  
 Peptide: **HC395-426**  
 Exchangeable protons: 30  
 Index lis-file: 187  
 Sequence: QPIMDTDGSYFVYSKLVQKSNWEAGNTFTCS  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.121	11.099	<b>0.91</b>	0.87	<b>0.27</b>	0.26
0.5	11.115	11.105	<b>18.55</b>	15.86	<b>5.57</b>	4.76
1.0	11.118	11.117	<b>17.29</b>	17.44	<b>5.19</b>	5.23
10.0	11.100	11.098	<b>19.85</b>	19.31	<b>5.95</b>	5.79
60.0	11.098	11.125	<b>19.73</b>	22.58	<b>5.92</b>	6.78
240.0	11.081	11.128	<b>20.84</b>	22.40	<b>6.25</b>	6.72

**DU Value**



Root(t/min): 6th roots of exchange times

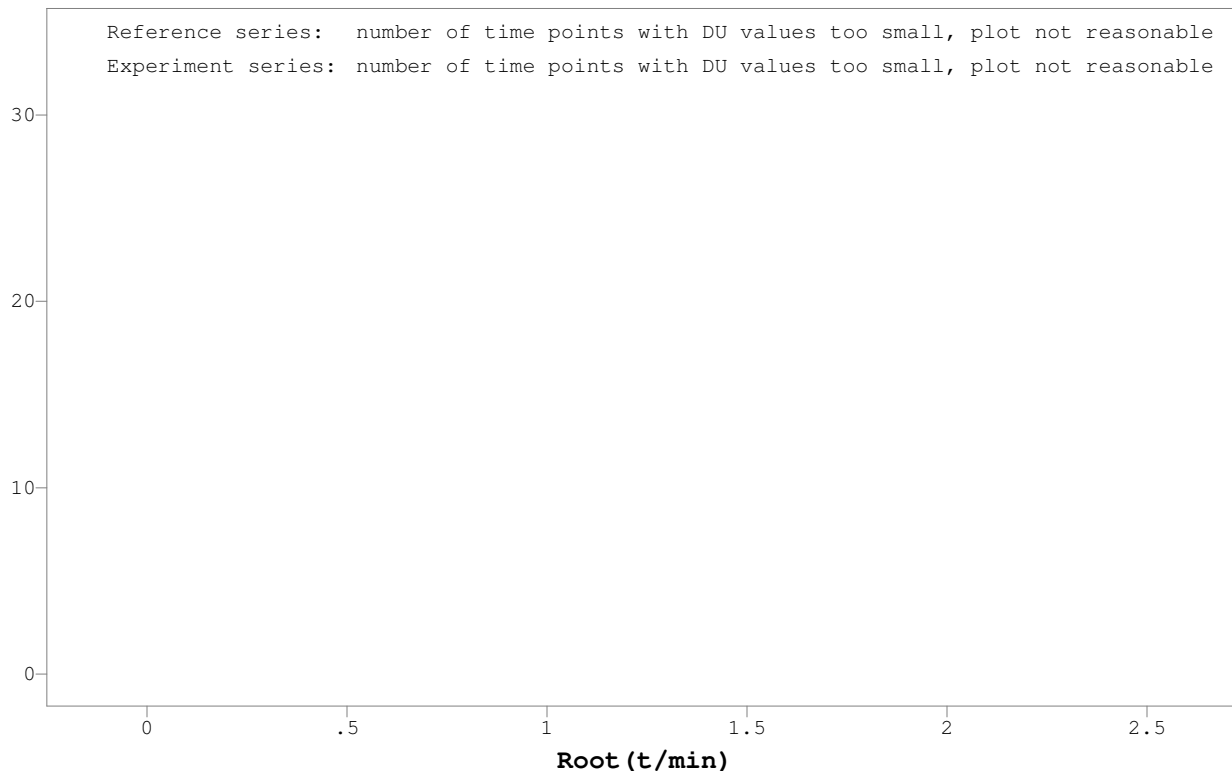
Molecule: **HC**  
 Peptide: **HC411-446**  
 Exchangeable protons: 34  
 Index lis-file: 193  
 Sequence: NVQKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPG  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.168	9.138	<b>0.04</b>	<b>0.00</b>	<b>0.01</b>	<b>0.00</b>
0.5	9.158	9.152	n.d.	n.d.	n.d.	n.d.
1.0	9.114	9.144	n.d.	n.d.	n.d.	n.d.
10.0	9.134	9.145	n.d.	n.d.	n.d.	n.d.
60.0	9.088	9.142	n.d.	n.d.	n.d.	n.d.
240.0	9.111	9.153	n.d.	n.d.	n.d.	n.d.

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC001-042**  
 Exchangeable protons: 39  
 Index lis-file: 1  
 Sequence: DIVLTQSPATLSVTPGDSVLSLSCRASQSIISNNLHWYQQKSHE  
 Range: 1 / 2

Reference: reference series, experiment: experiment series

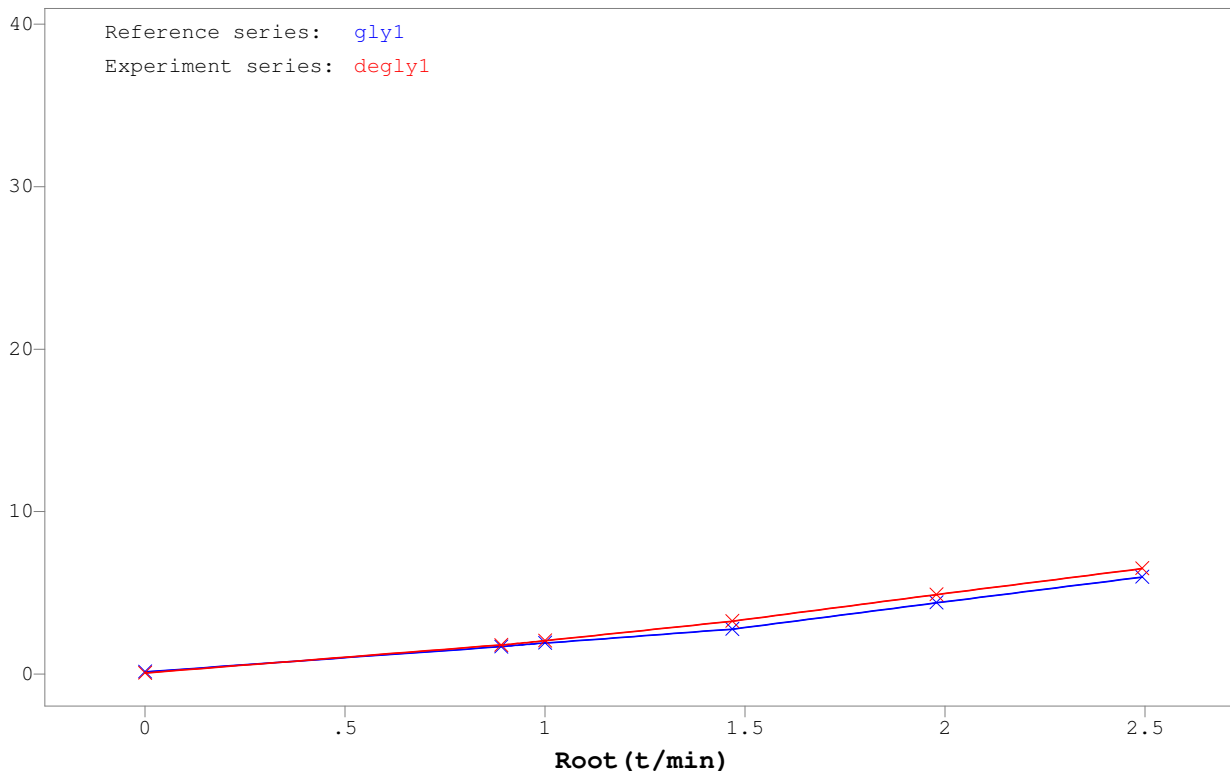
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.570	11.555	0.38	0.20	0.15	0.08
0.5	11.581	11.569	4.34	4.62	1.69	1.80
1.0	11.570	11.581	4.94	5.32	1.92	2.08
10.0	11.562	11.577	7.15	8.40	2.79	3.28
60.0	11.557	11.582	11.31	12.61	4.41	4.92
240.0	11.549	11.575	15.37	16.71	5.99	6.52

Score1 (DU sum): **1.30**  
 Score2 (DU Profile): 1.15  
**DU sum difference (u): 1.71**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC001-042**  
 Exchangeable protons: 39  
 Index lis-file: 1  
 Sequence: DIVLTQSPATLSVTPGDSVLSLSCRASQSIISNNLHWYQKSHE  
 Range: 2 / 2

Reference: reference series, experiment: experiment series

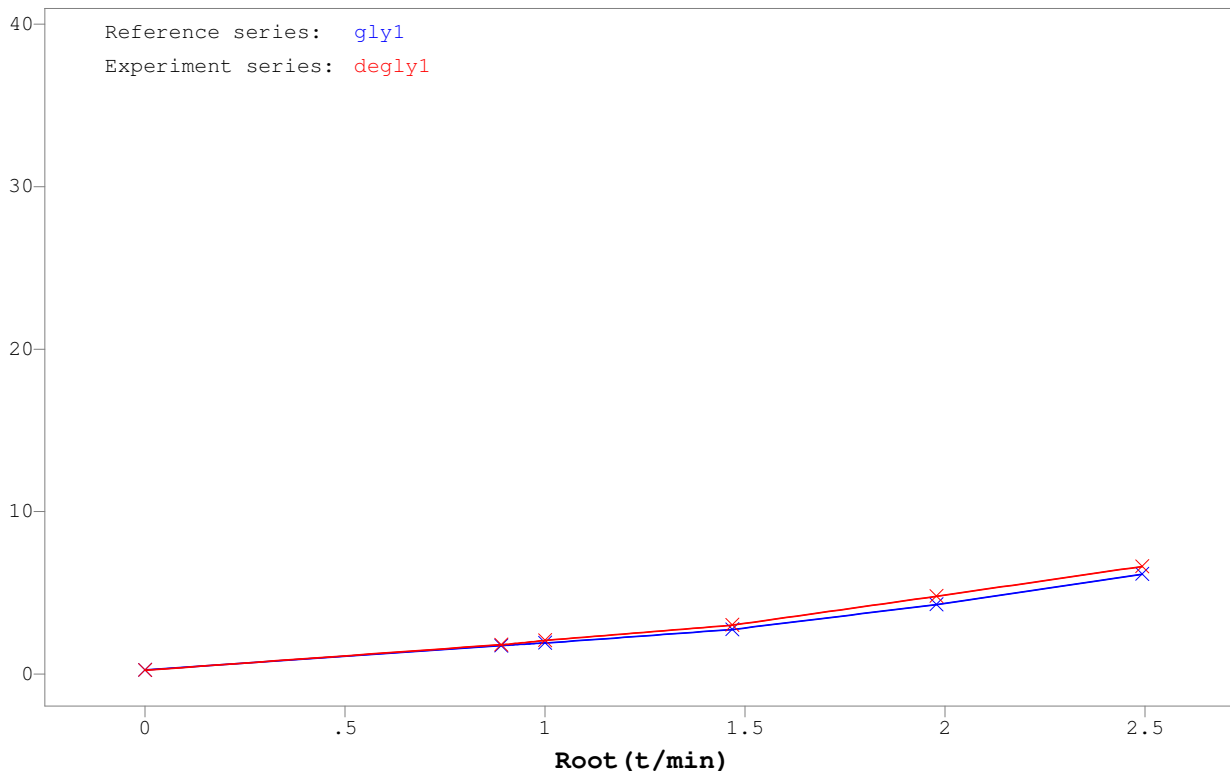
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.705	11.696	0.66	0.63	0.26	0.25
0.5	11.712	11.699	4.49	4.66	1.75	1.82
1.0	11.704	11.713	4.94	5.36	1.93	2.09
10.0	11.704	11.698	7.09	7.78	2.77	3.03
60.0	11.692	11.711	11.03	12.33	4.30	4.81
240.0	11.682	11.702	15.81	17.05	6.17	6.65

Score1 (DU sum): **1.12**  
 Score2 (DU Profile): 0.93  
**DU sum difference (u): 1.47**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC003-018**  
 Exchangeable protons: 13  
 Index lis-file: 197  
 Sequence: VLTQSPATLSVTPGDS  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

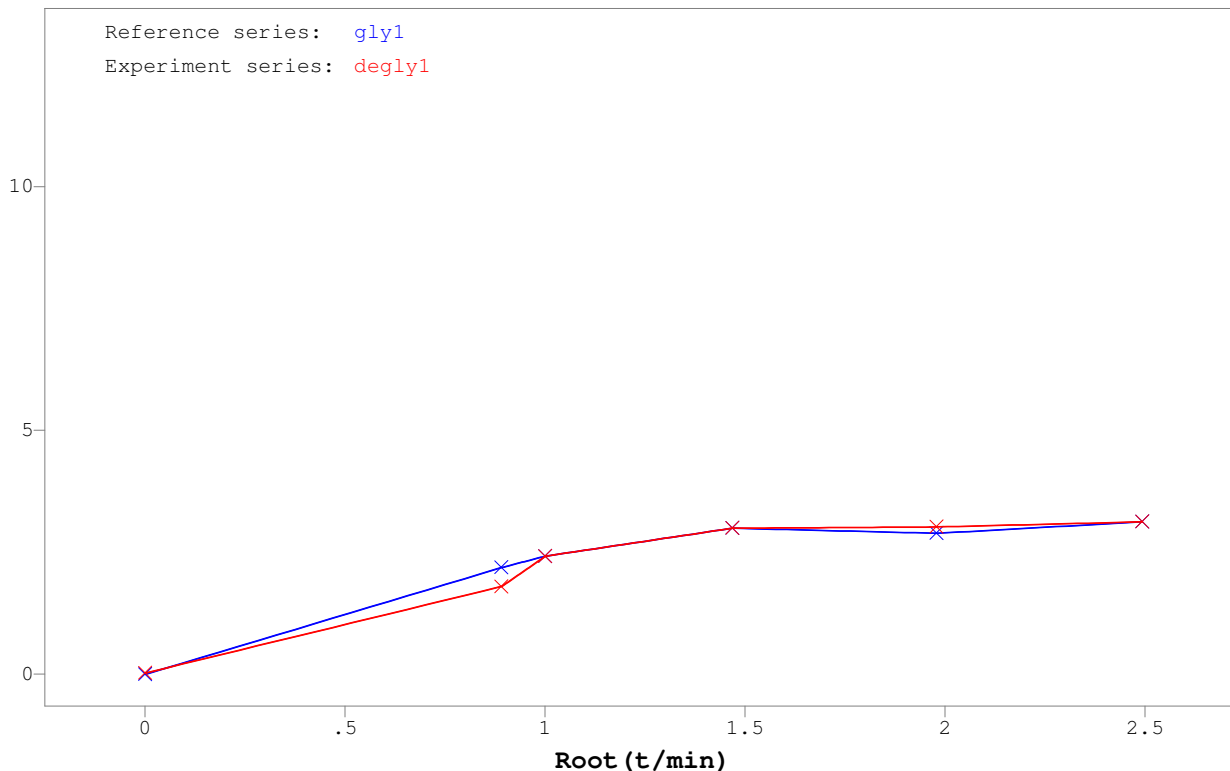
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.493	11.489	0.00	0.20	0.00	0.03
0.5	11.483	11.480	16.86	13.85	2.19	1.80
1.0	11.484	11.489	18.66	18.66	2.43	2.43
10.0	11.486	11.483	<b>23.08</b>	23.08	<b>3.00</b>	3.00
60.0	11.481	11.487	22.27	23.28	2.90	3.03
240.0	11.480	11.491	24.08	24.08	3.13	3.13

Score1 (DU sum): 0.59  
 Score2 (DU Profile): **1.02p**  
 DU sum difference (u): -0.28

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC004-021**  
 Exchangeable protons: 15  
 Index lis-file: 2  
 Sequence: LTQSPATLSVTPGDSVSL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

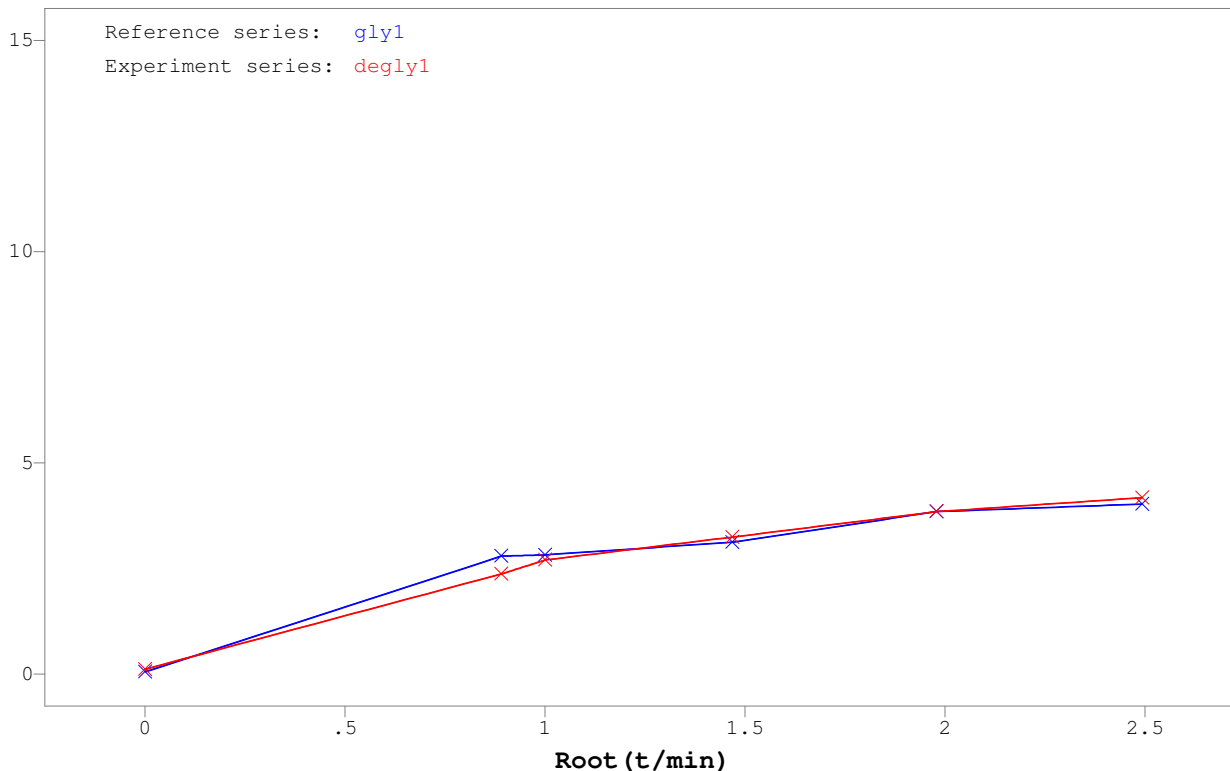
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.966	9.956	0.40	0.82	0.06	0.12
0.5	9.973	9.965	18.66	15.85	2.80	2.38
1.0	9.969	9.975	18.86	18.06	2.83	2.71
10.0	9.968	9.964	20.87	21.67	3.13	3.25
60.0	9.961	9.981	25.69	25.69	3.85	3.85
240.0	9.957	9.980	26.89	27.89	4.03	4.18

Score1 (DU sum): 0.41  
 Score2 (DU Profile): **1.41**  
 DU sum difference (u): -0.21

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **LC**  
 Peptide: **LC024-035**  
 Exchangeable protons: 11  
 Index lis-file: 13  
 Sequence: RASQSISSNNLHW  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

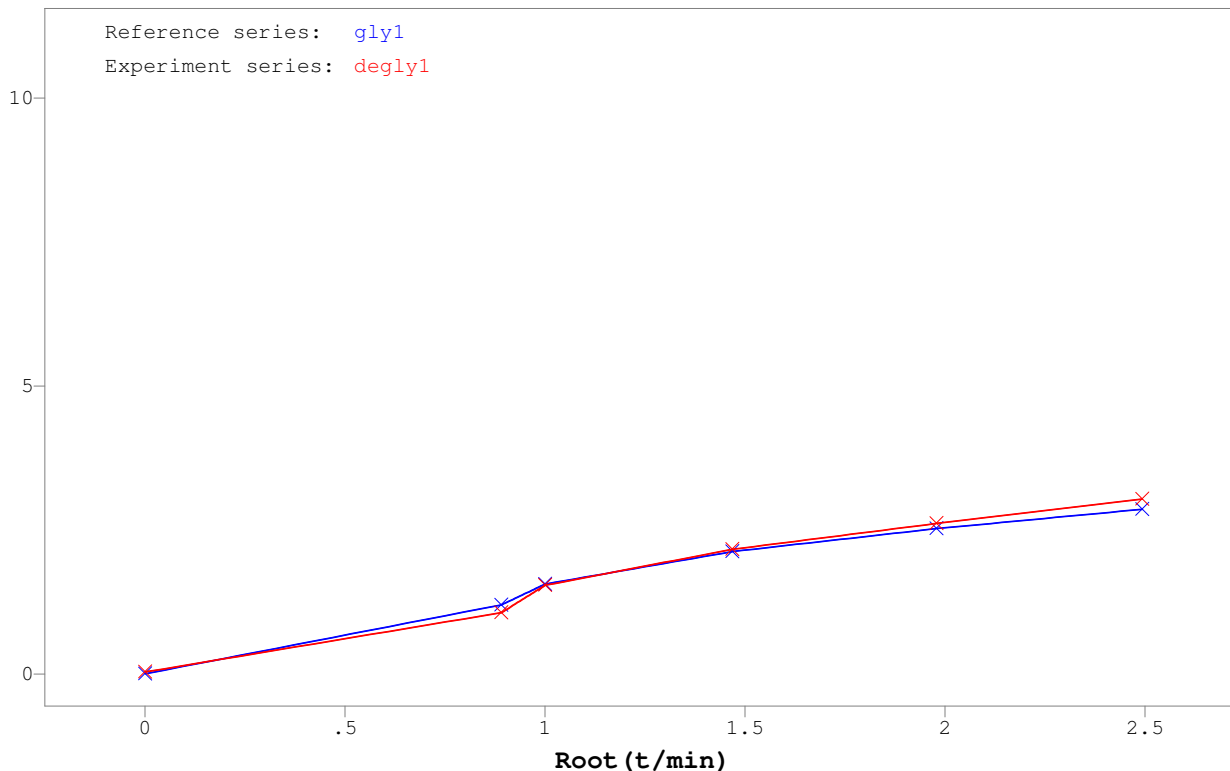
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.650	9.628	0.09	0.38	0.01	0.04
0.5	9.650	9.632	10.98	9.75	1.21	1.07
1.0	9.643	9.643	14.26	14.07	1.57	1.55
10.0	9.630	9.630	19.38	19.75	2.13	2.17
60.0	9.624	9.641	23.01	23.81	2.53	2.62
240.0	9.614	9.641	26.05	27.66	2.87	3.04

Score1 (DU sum): 0.48  
 Score2 (DU Profile): **1.08**  
 DU sum difference (u): 0.18

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC028-047**  
 Exchangeable protons: 18  
 Index lis-file: 17  
 Sequence: SISNNLHWYQQKSHESPRL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

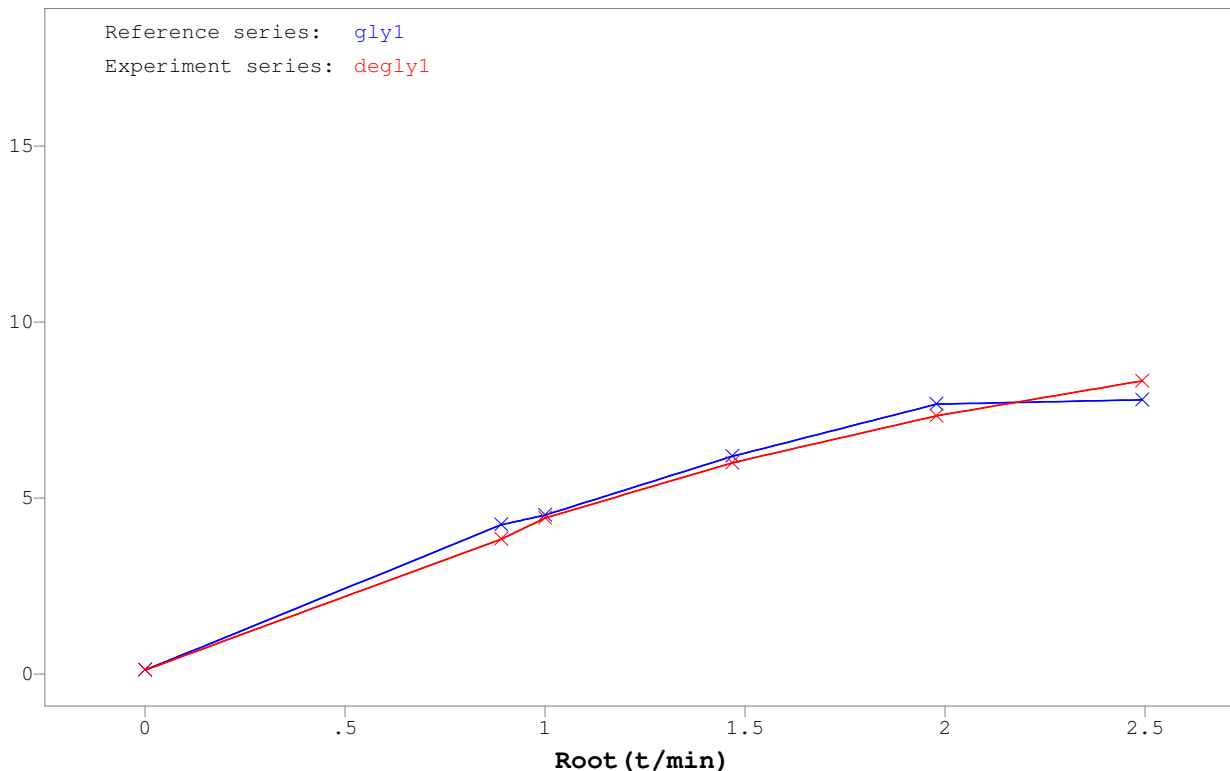
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.476	9.467	0.70	0.70	0.13	0.13
0.5	9.466	9.469	23.61	21.36	4.25	3.85
1.0	9.472	9.476	25.16	24.69	4.53	4.44
10.0	9.461	9.458	34.42	<b>33.41</b>	6.20	<b>6.01</b>
60.0	9.442	9.458	42.66	40.82	7.68	7.35
240.0	9.438	9.462	43.34	46.33	7.80	8.34

Score1 (DU sum): 0.51  
 Score2 (DU Profile): **2.07p**  
 DU sum difference (u): -0.34

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC047-062**  
 Exchangeable protons: 14  
 Index lis-file: 25  
 Sequence: LIKYASQSISGIPSRF  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

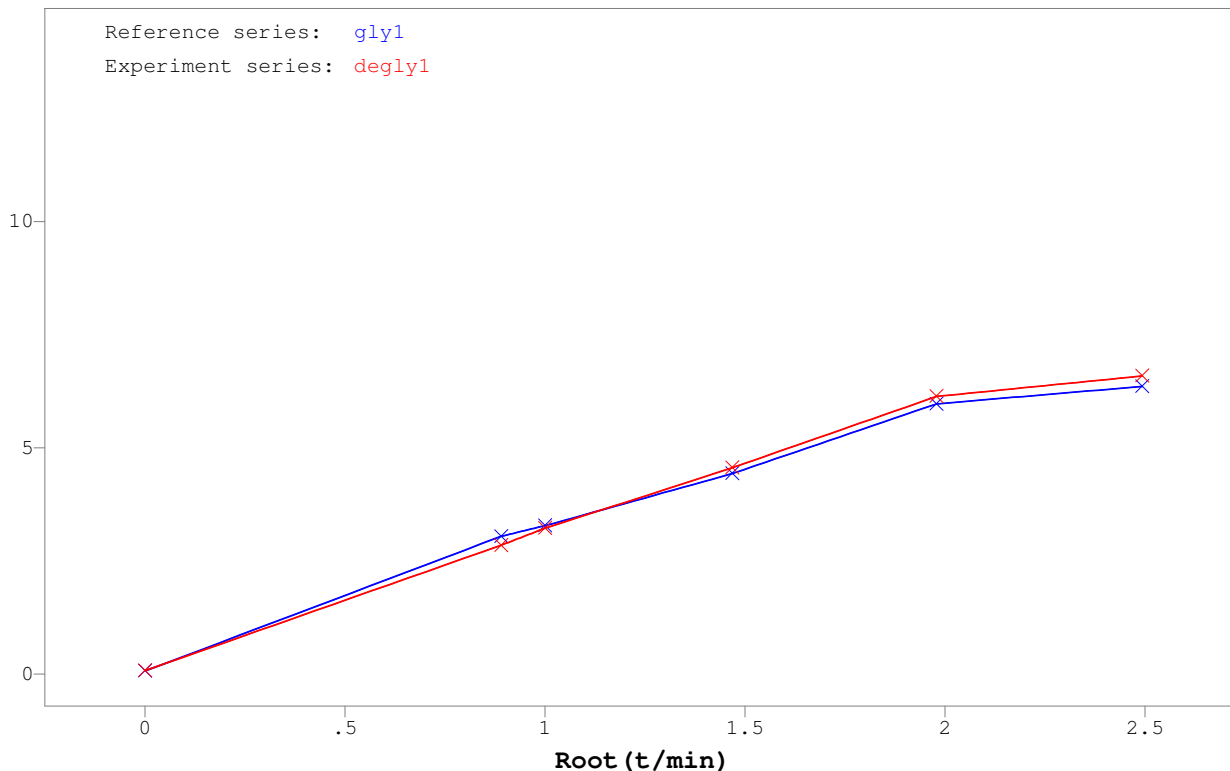
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.325	10.301	0.54	0.60	0.08	0.08
0.5	10.300	10.293	21.79	<b>20.39</b>	3.05	<b>2.85</b>
1.0	10.297	10.301	23.48	23.08	3.29	3.23
10.0	10.284	10.283	<b>31.71</b>	32.64	<b>4.44</b>	4.57
60.0	10.273	10.289	42.72	43.89	5.98	6.14
240.0	10.262	10.287	45.47	47.12	6.37	6.60

Score1 (DU sum): 0.90  
 Score2 (DU Profile): **1.19**  
 DU sum difference (u): 0.52

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC047-071**  
 Exchangeable protons: 23  
 Index lis-file: 26  
 Sequence: LIKYASQSISGIPSRFSGSGSGTDF  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

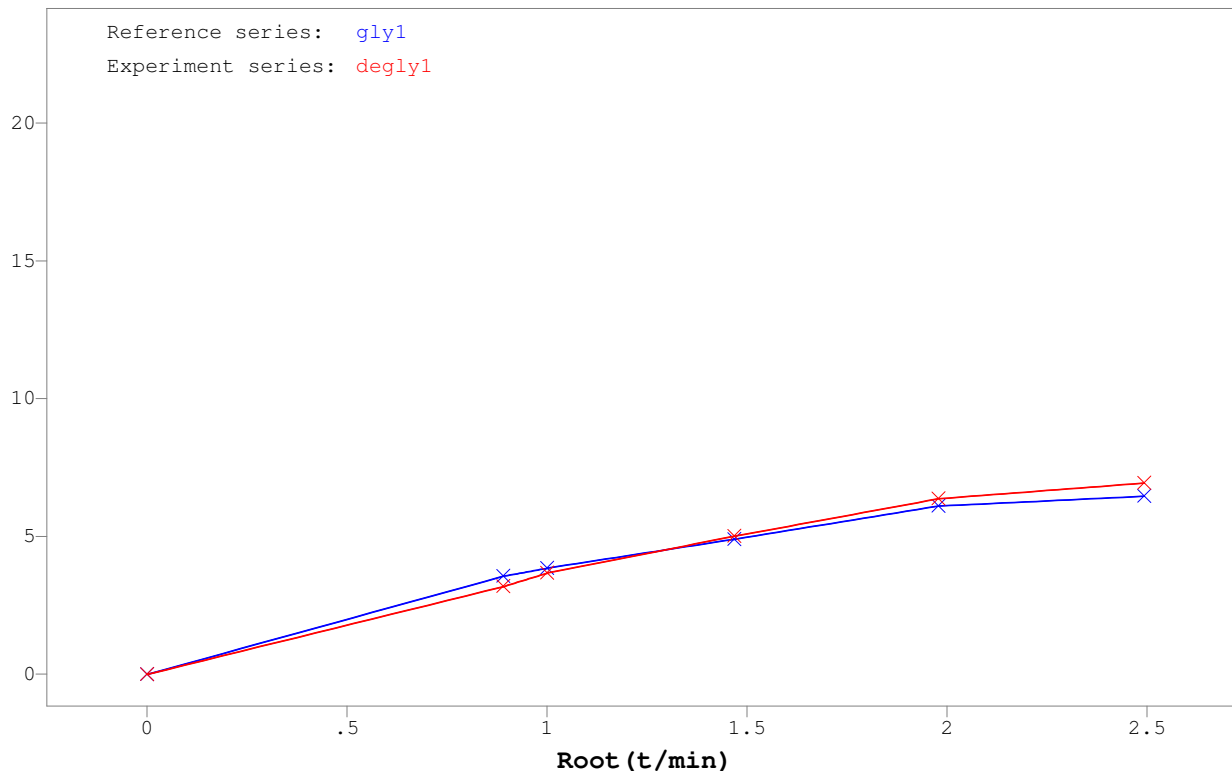
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.700	10.688	0.00	0.00	0.00	0.00
0.5	10.695	10.686	15.51	13.87	3.57	3.19
1.0	10.695	10.693	16.76	16.00	3.86	3.68
10.0	10.684	10.685	21.32	21.79	4.90	5.01
60.0	10.675	10.689	26.56	27.70	6.11	6.37
240.0	10.669	10.691	28.09	30.17	6.46	6.94

Score1 (DU sum): 0.38  
 Score2 (DU Profile): **1.48**  
 DU sum difference (u): 0.30

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC054-070**  
 Exchangeable protons: 15  
 Index lis-file: 30  
 Sequence: SISGIPSRFSGSGSGTD  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

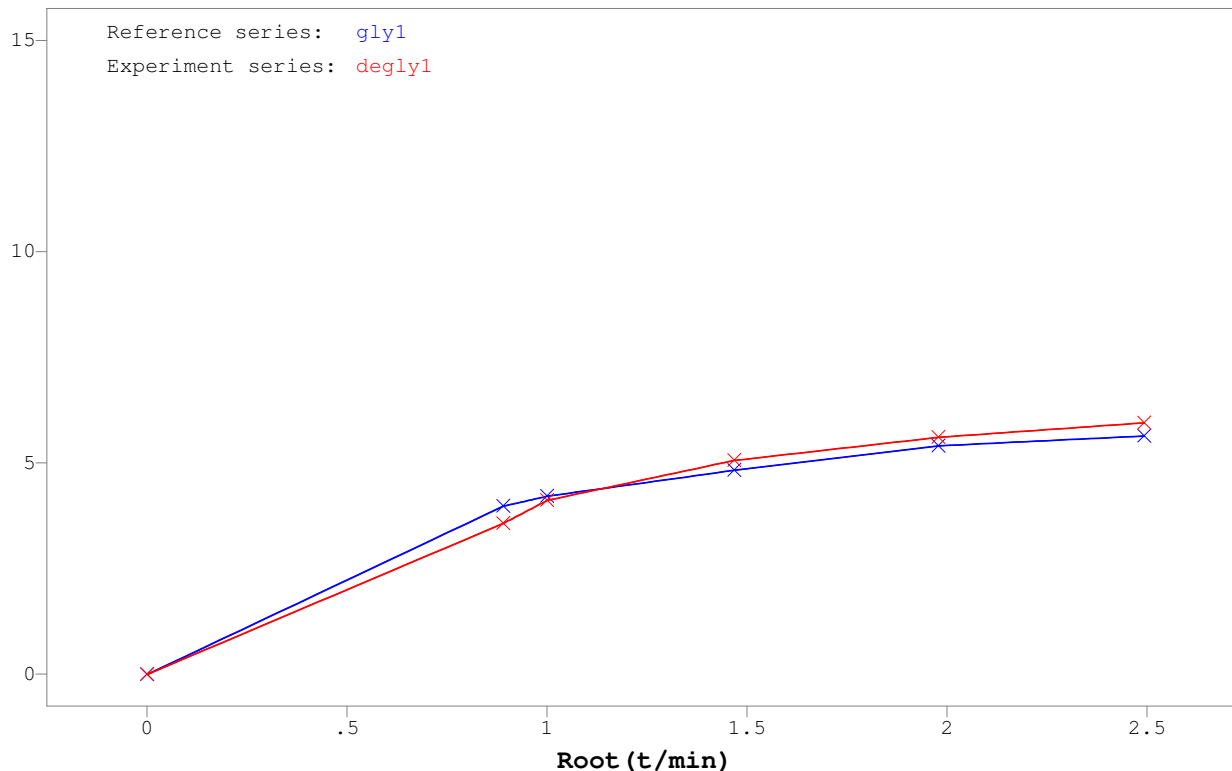
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.598	8.588	0.00	0.00	0.00	0.00
0.5	8.591	8.592	26.55	23.84	3.98	3.58
1.0	8.588	8.593	28.12	<b>27.47</b>	4.22	<b>4.12</b>
10.0	8.589	8.584	32.21	33.77	4.83	5.07
60.0	8.577	8.589	36.08	37.42	5.41	5.61
240.0	8.576	8.587	37.62	39.71	5.64	5.96

Score1 (DU sum): 0.74  
 Score2 (DU Profile): **2.02p**  
 DU sum difference (u): 0.41

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC054-071**  
 Exchangeable protons: 16  
 Index lis-file: 31  
 Sequence: SISGIPSRFSGSGSTDF  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

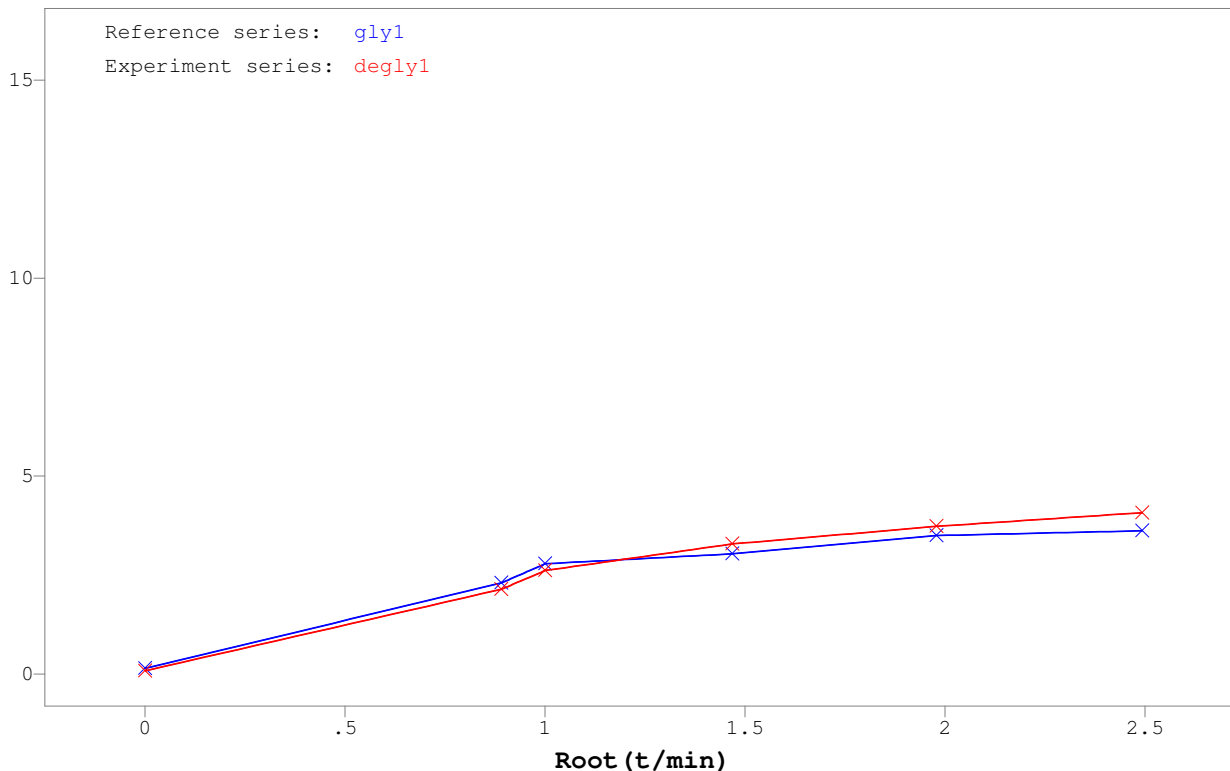
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.534	10.521	<b>0.95</b>	0.57	<b>0.15</b>	0.09
0.5	10.535	10.528	14.45	13.44	2.31	2.15
1.0	10.531	10.532	17.46	16.40	2.79	2.62
10.0	10.524	10.523	19.03	20.59	3.04	3.29
60.0	10.515	10.540	21.92	23.36	3.51	3.74
240.0	10.512	10.534	22.66	25.52	3.63	4.08

Score1 (DU sum): **1.01p**  
 Score2 (DU Profile): 2.01p  
**DU sum difference (u): 0.55**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC054-095**  
 Exchangeable protons: 39  
 Index lis-file: 32  
 Sequence: SISGIPSRFSGSGSGTDFTLINSVETEDFGMYFCQSNNSWP  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

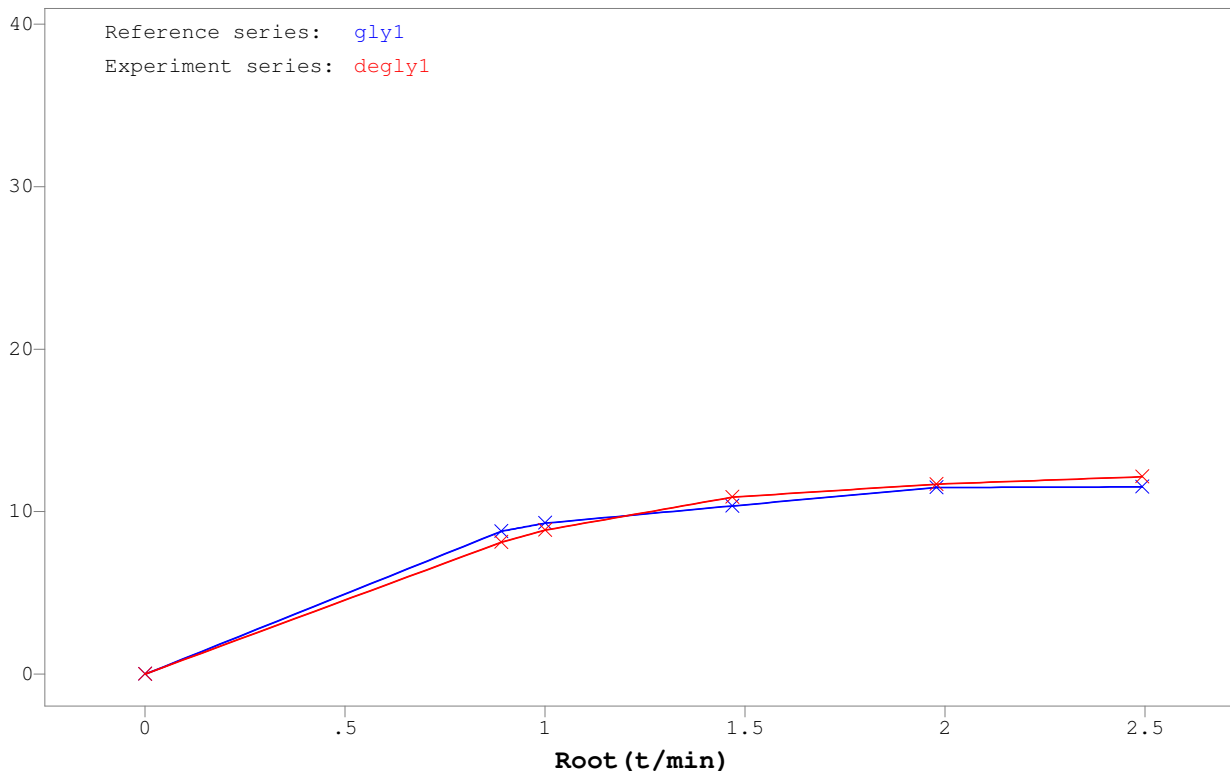
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.936	8.915	0.05	0.08	0.02	0.03
0.5	8.925	8.913	22.61	20.87	8.82	8.14
1.0	8.923	8.921	23.88	22.78	9.31	8.89
10.0	8.920	8.909	26.60	27.98	10.37	10.91
60.0	8.907	8.918	29.51	30.04	11.51	11.72
240.0	8.902	8.909	29.60	31.21	11.54	12.17

Score1 (DU sum): 0.22  
 Score2 (DU Profile): **1.55**  
 DU sum difference (u): 0.28

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC055-070**  
 Exchangeable protons: 14  
 Index lis-file: 33  
 Sequence: ISGIPSRFSGSGSGTD  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

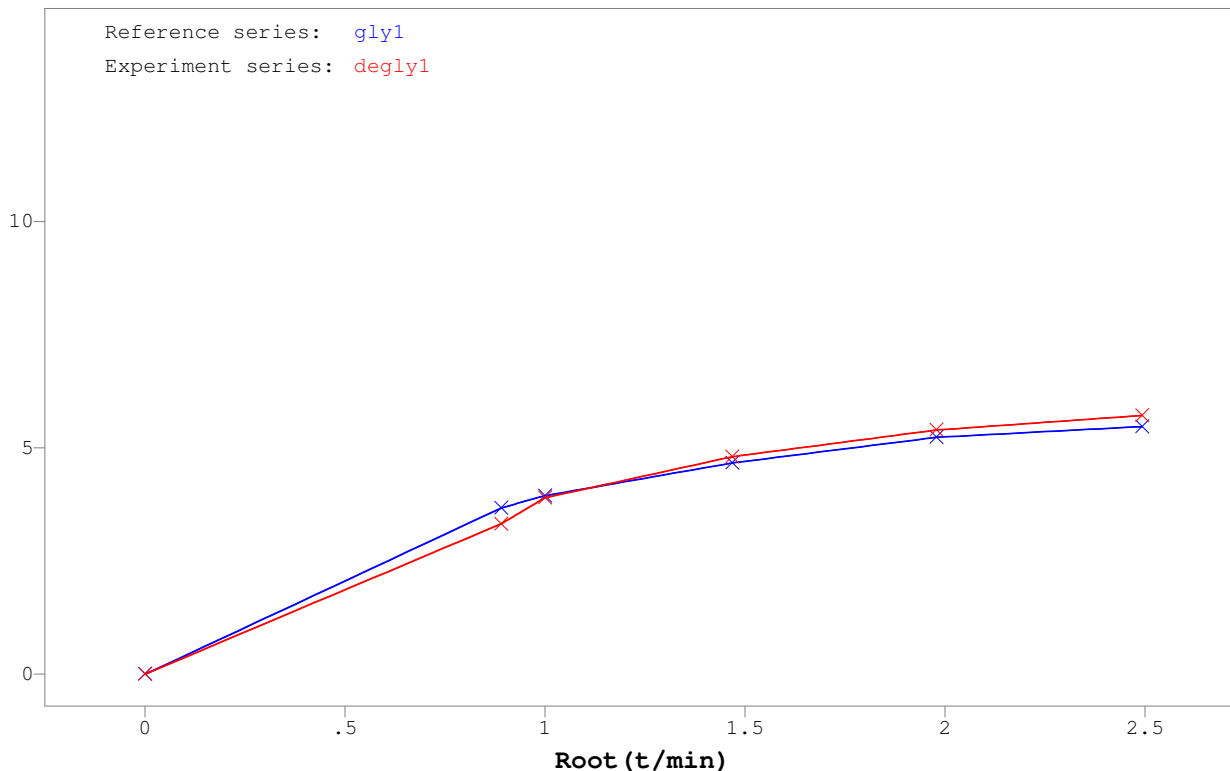
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.291	8.281	0.04	0.04	0.01	0.01
0.5	8.263	8.258	26.26	<b>23.77</b>	3.68	<b>3.33</b>
1.0	8.264	8.271	28.22	27.89	3.95	3.91
10.0	8.280	8.246	<b>33.39</b>	34.38	<b>4.67</b>	4.81
60.0	8.243	8.258	37.43	38.58	5.24	5.40
240.0	8.282	8.257	39.13	40.88	5.48	5.72

Score1 (DU sum): 0.94  
 Score2 (DU Profile): **1.17**  
 DU sum difference (u): 0.54

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **LC**  
 Peptide: **LC059-100**  
 Exchangeable protons: 39  
 Index lis-file: 35  
 Sequence: PSRFSGSGSGTDFTLINSVETEDFGMYFCQQSNSWPLTFGA  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

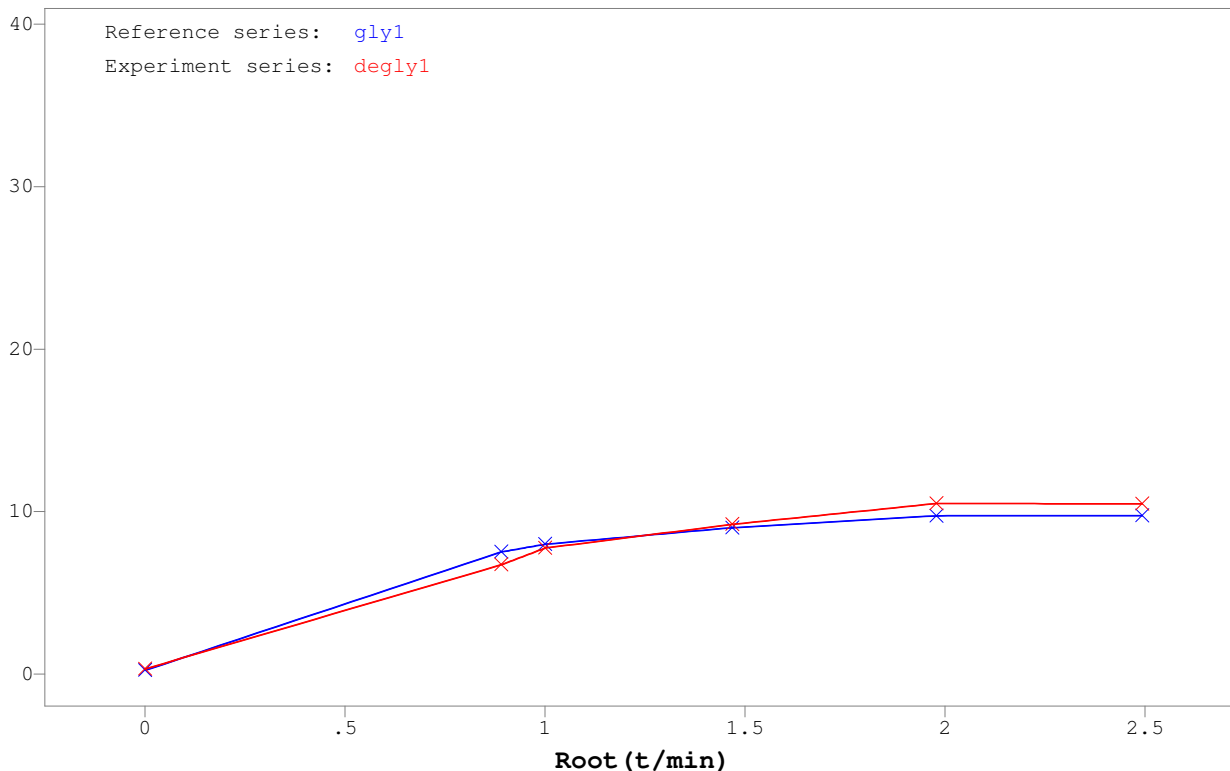
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.938	9.921	0.65	0.88	0.25	0.34
0.5	9.928	9.920	19.33	17.31	7.54	6.75
1.0	9.932	9.933	20.55	19.95	8.01	7.78
10.0	9.926	9.918	23.17	23.69	9.03	9.24
60.0	9.915	9.932	25.04	26.99	9.76	10.52
240.0	9.909	9.936	25.06	26.93	9.77	10.50

Score1 (DU sum): 0.58  
 Score2 (DU Profile): **1.74**  
 DU sum difference (u): 0.76

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC078-085**  
 Exchangeable protons: 7  
 Index lis-file: 41  
 Sequence: VETEDFGM  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

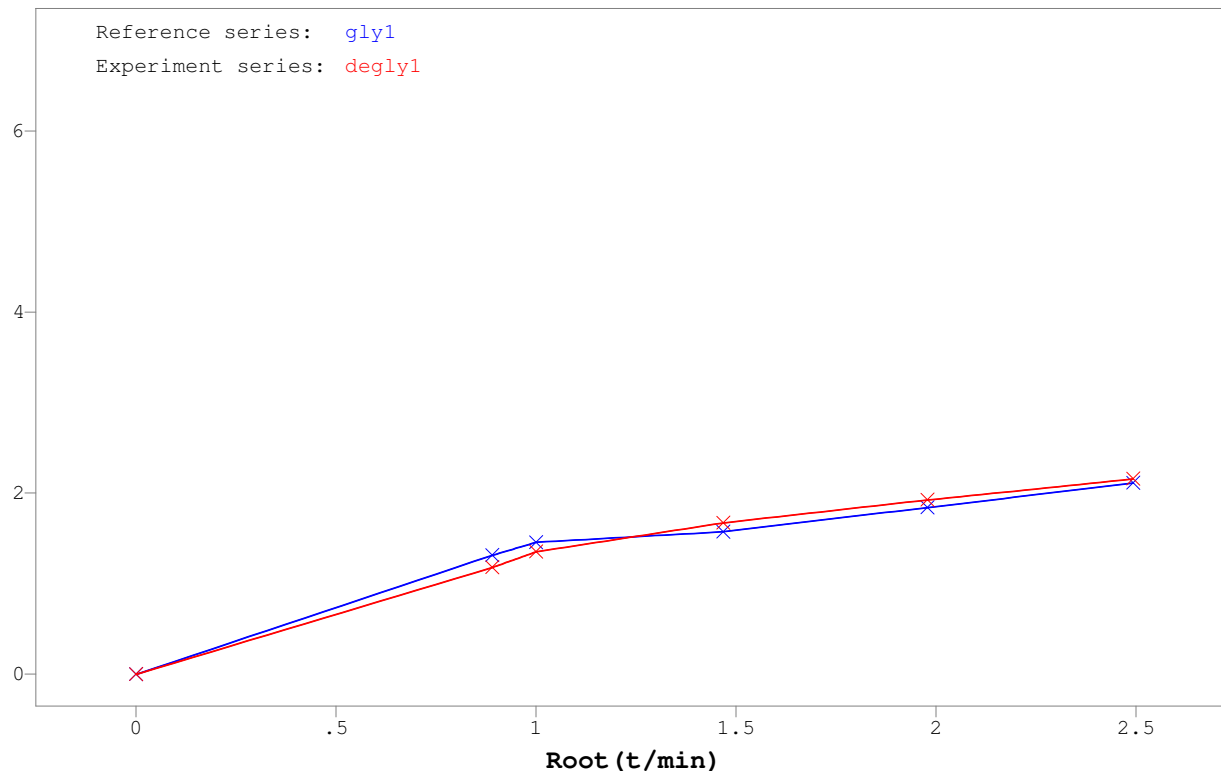
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.900	10.900	0.00	0.00	0.00	0.00
0.5	10.898	10.910	18.78	16.86	1.31	1.18
1.0	10.902	10.900	20.84	19.34	1.46	1.35
10.0	10.912	10.895	22.49	23.90	1.57	1.67
60.0	10.898	10.906	26.32	27.52	1.84	1.93
240.0	10.898	10.912	30.23	30.86	2.12	2.16

Score1 (DU sum): 0.06  
 Score2 (DU Profile): **1.61**  
 DU sum difference (u): -0.01

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC086-101**  
 Exchangeable protons: 14  
 Index lis-file: 43  
 Sequence: YFCQQSNSWPLTFGAG  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

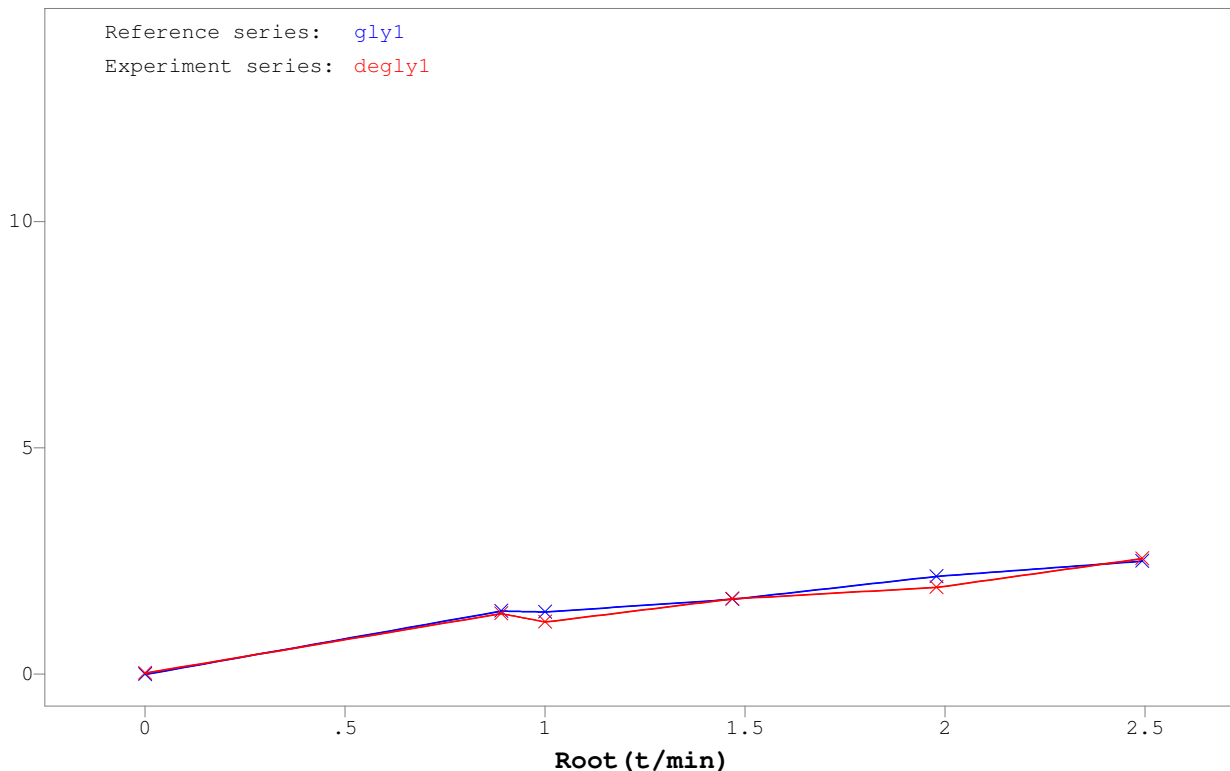
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	14.519	14.532	0.00	0.20	0.00	0.03
0.5	14.515	14.536	9.98	<b>9.58</b>	1.40	<b>1.34</b>
1.0	14.541	14.557	9.84	8.26	1.38	1.16
10.0	14.535	14.514	11.84	11.90	1.66	1.67
60.0	14.539	14.525	15.45	13.72	2.16	1.92
240.0	14.545	14.531	17.86	18.26	2.50	2.56

Score1 (DU sum): 0.86  
 Score2 (DU Profile): **1.06p**  
 DU sum difference (u): -0.45

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC087-101**  
 Exchangeable protons: 13  
 Index lis-file: 45  
 Sequence: FCQQSNSWPLTFGAG  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

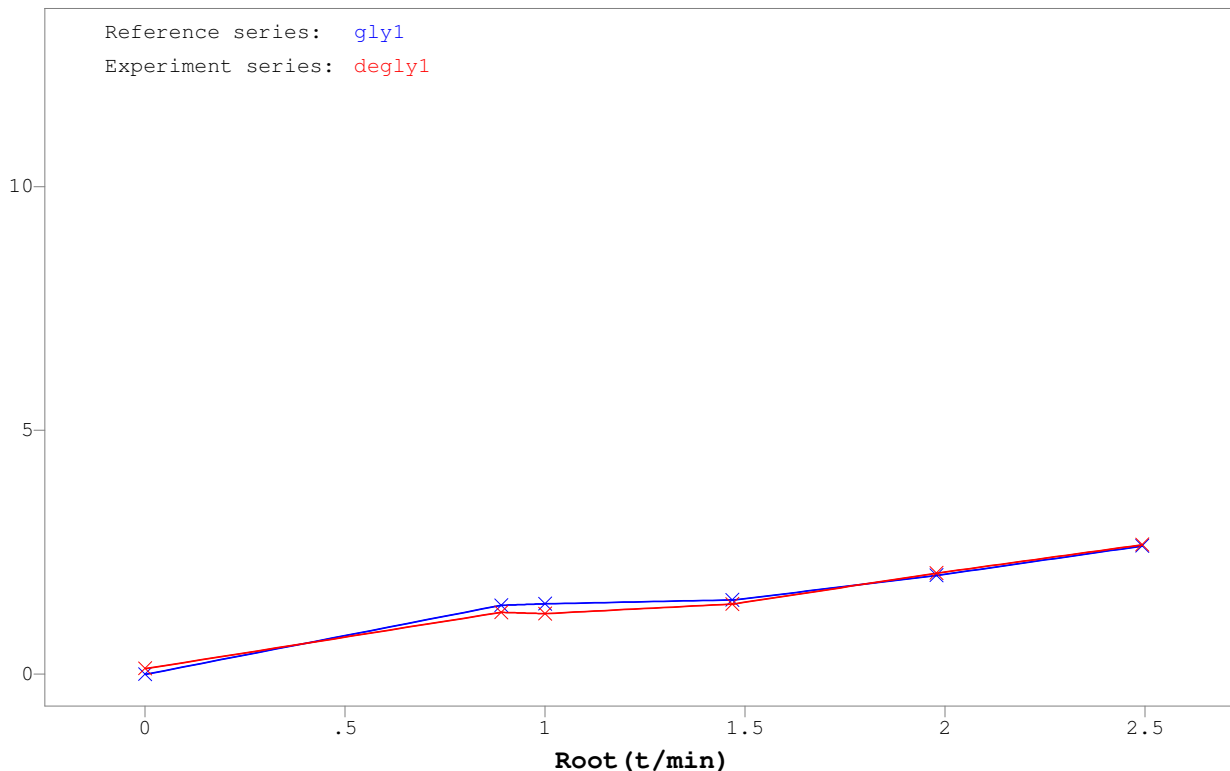
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	13.823	13.834	0.00	0.89	0.00	0.12
0.5	13.833	13.845	10.89	9.77	1.42	1.27
1.0	13.841	13.845	11.12	9.57	1.45	1.24
10.0	13.843	13.826	11.73	11.09	1.53	1.44
60.0	13.837	13.834	15.62	15.98	2.03	2.08
240.0	13.841	13.834	20.27	20.47	2.63	2.66

Score1 (DU sum): 0.55  
 Score2 (DU Profile): **1.15**  
 DU sum difference (u): -0.24

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC087-104**  
 Exchangeable protons: 16  
 Index lis-file: 46  
 Sequence: FCQQSNSWPLTFGAGTKL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

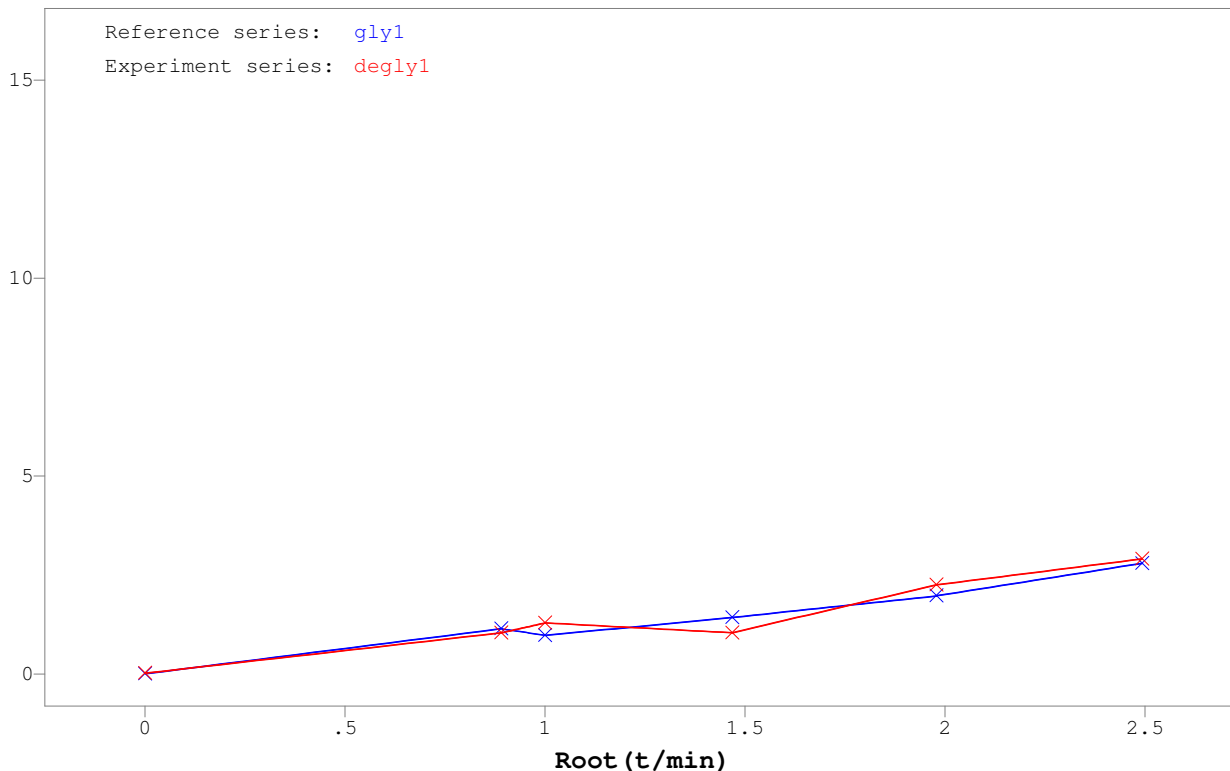
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	13.322	13.315	0.11	0.20	0.02	0.03
0.5	13.316	13.309	7.22	6.58	1.16	1.05
1.0	13.317	13.327	<b>6.17</b>	8.15	<b>0.99</b>	1.30
10.0	13.307	13.308	9.01	<b>6.58</b>	1.44	<b>1.05</b>
60.0	13.303	13.322	12.41	14.13	1.99	2.26
240.0	13.295	13.304	17.54	18.23	2.81	2.92

Score1 (DU sum): 0.67  
 Score2 (DU Profile): **1.14**  
 DU sum difference (u): 0.45

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC098-106**  
 Exchangeable protons: 8  
 Index lis-file: 47  
 Sequence: FGAGTKLEL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

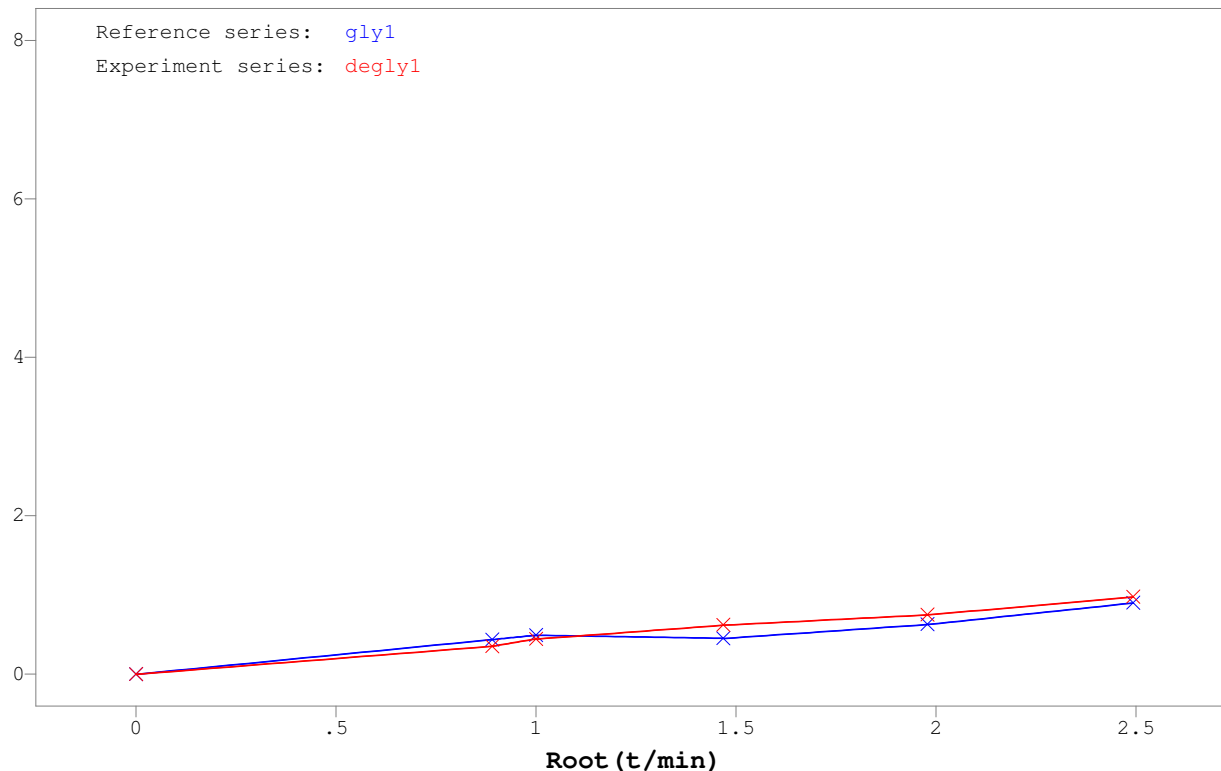
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.461	10.440	0.00	0.00	0.00	0.00
0.5	10.461	10.451	5.47	4.42	0.44	0.35
1.0	10.461	10.461	6.16	5.59	0.49	0.45
10.0	10.452	10.440	5.68	7.78	0.45	0.62
60.0	10.435	10.454	7.89	9.41	0.63	0.75
240.0	10.496	10.457	11.30	12.24	0.90	0.98

Score1 (DU sum): 0.87  
 Score2 (DU Profile): **1.50**  
 DU sum difference (u): 0.24

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: LC  
 Peptide: LC104-124  
 Exchangeable protons: 17  
 Index lis-file: 49  
 Sequence: LELKRADAAPTVSIFPPSSEQ  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

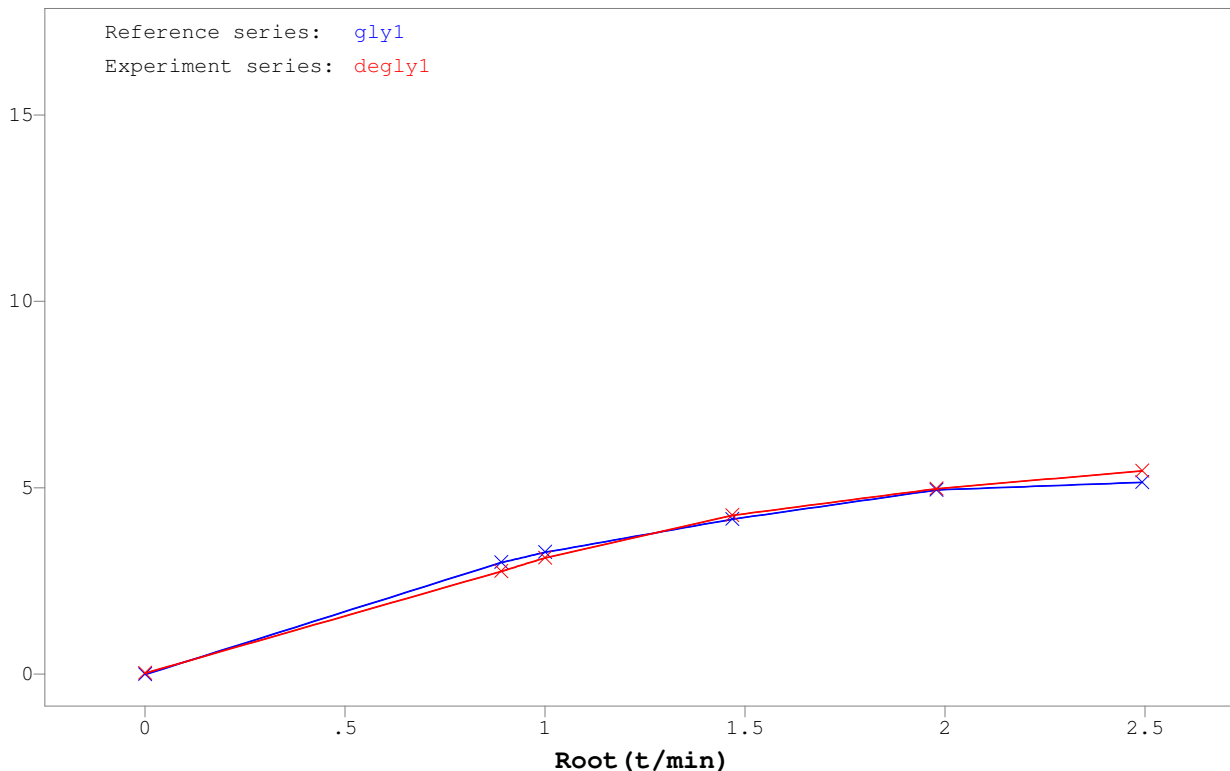
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.562	11.543	0.00	0.19	0.00	0.03
0.5	11.561	11.554	17.66	16.26	3.00	2.76
1.0	11.561	11.563	19.26	18.40	3.27	3.13
10.0	11.547	11.554	24.48	<b>25.08</b>	4.16	<b>4.26</b>
60.0	11.552	11.564	29.10	29.30	4.95	4.98
240.0	11.547	11.562	30.30	32.11	5.15	5.46

Score1 (DU sum): 0.02  
 Score2 (DU Profile): **1.23p**  
 DU sum difference (u): -0.01

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC105-124**  
 Exchangeable protons: 16  
 Index lis-file: 51  
 Sequence: ELKRADAAPTVSIFPPSSEQ  
 Range: 1 / 2

Reference: reference series, experiment: experiment series

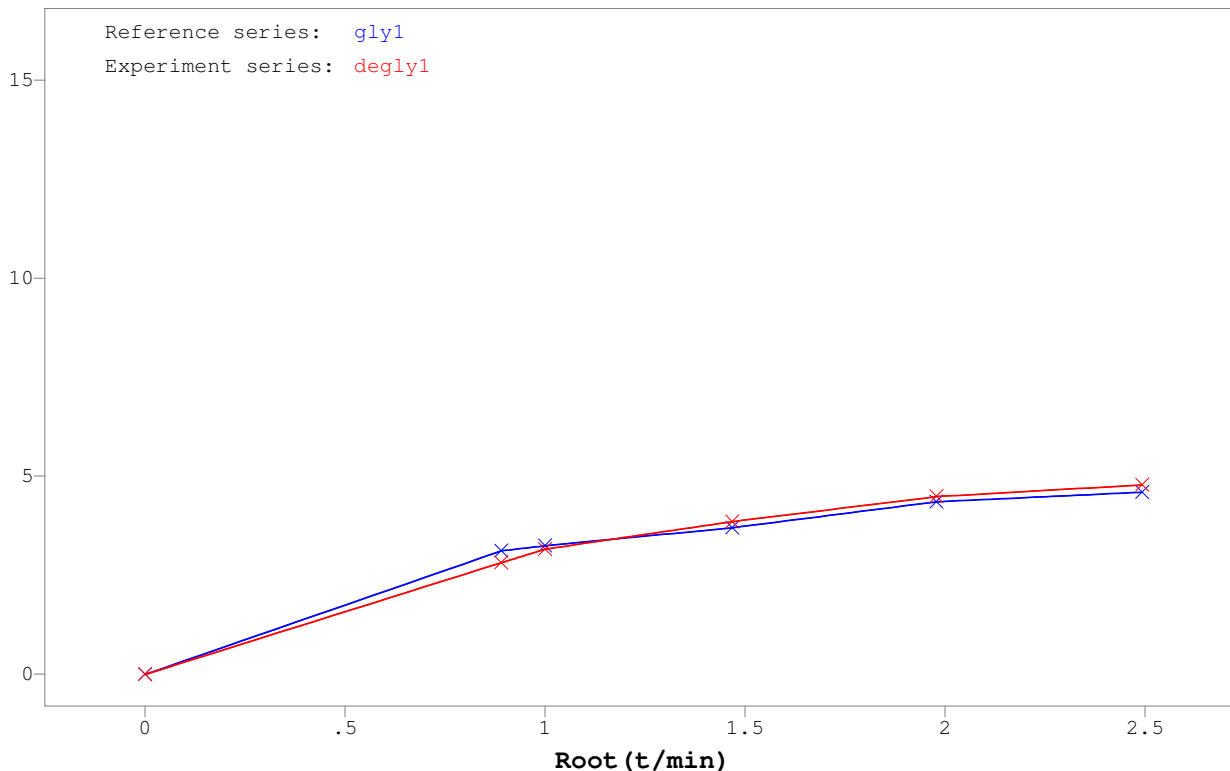
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.681	9.664	0.00	0.00	0.00	0.00
0.5	9.671	9.669	19.49	17.63	3.12	2.82
1.0	9.670	9.672	20.30	19.77	3.25	3.16
10.0	9.666	9.667	23.15	24.11	3.70	3.86
60.0	9.658	9.672	27.25	28.06	4.36	4.49
240.0	9.656	9.672	28.75	29.90	4.60	4.78

Score1 (DU sum): 0.16  
 Score2 (DU Profile): **1.29**  
 DU sum difference (u): 0.08

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **LC**  
 Peptide: **LC105-125**  
 Exchangeable protons: 17  
 Index lis-file: 52  
 Sequence: ELKRADAAPTVSIFPPSSEQL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

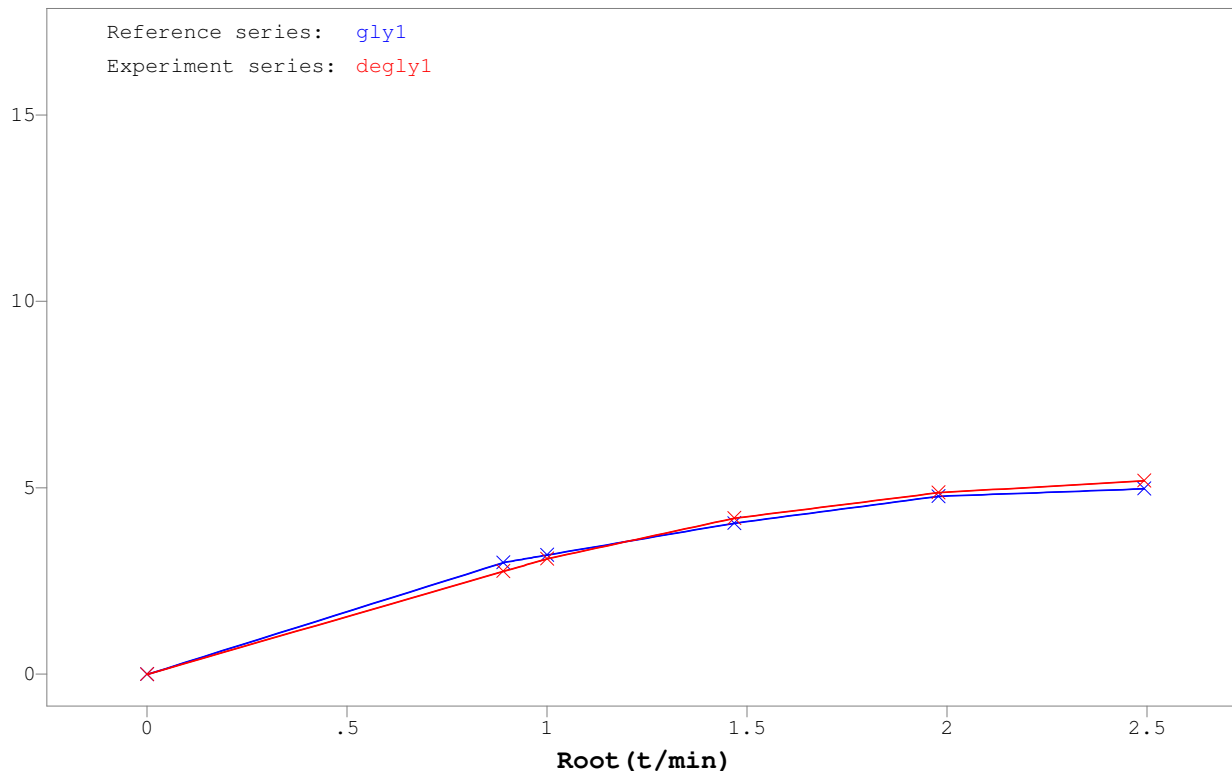
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.117	11.108	0.00	0.00	0.00	0.00
0.5	11.116	11.114	17.63	16.25	3.00	2.76
1.0	11.116	11.122	18.84	18.23	3.20	3.10
10.0	11.118	11.119	23.85	24.64	4.06	4.19
60.0	11.102	11.120	28.09	28.67	4.78	4.87
240.0	11.099	11.123	29.27	30.53	4.98	5.19

Score1 (DU sum): 0.19  
 Score2 (DU Profile): **1.11**  
 DU sum difference (u): 0.11

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC105-131**  
 Exchangeable protons: 23  
 Index lis-file: 53  
 Sequence: ELKRADAAPTVSIFPPSSEQLTSGGAS  
 Range: 1 / 2

Reference: reference series, experiment: experiment series

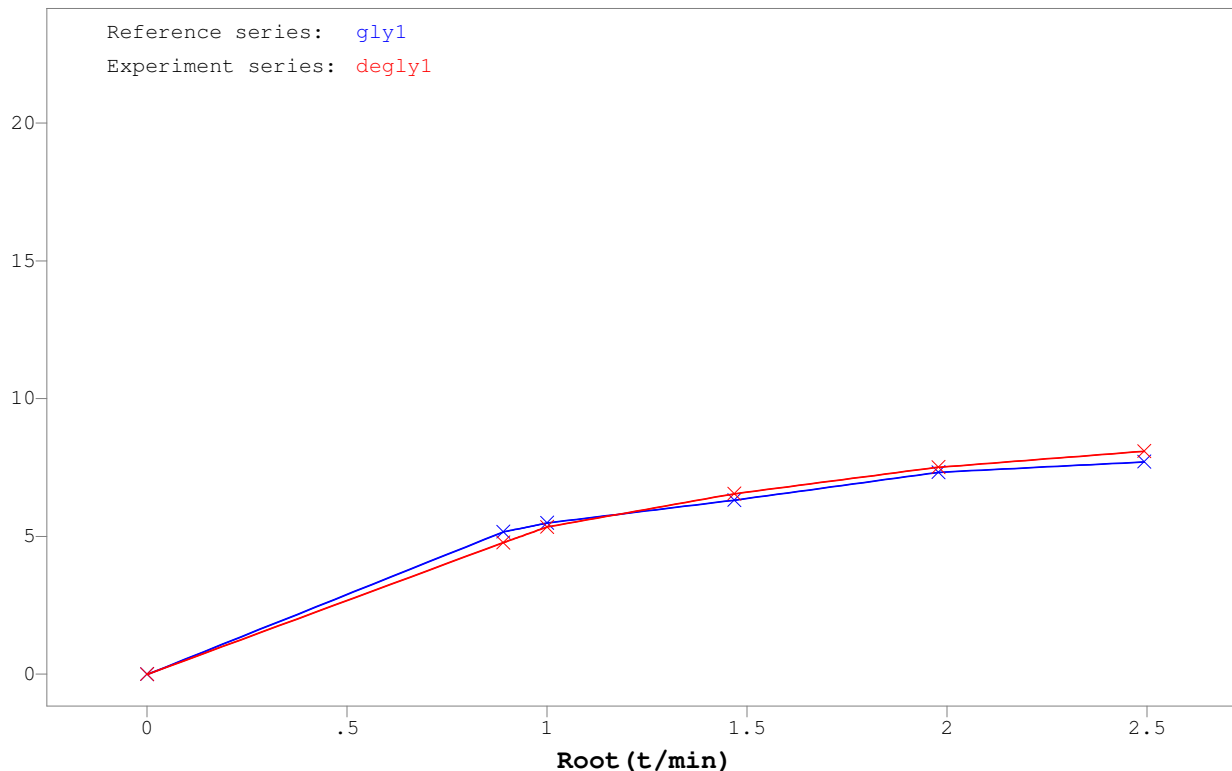
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.295	10.302	0.00	0.00	0.00	0.00
0.5	10.291	10.290	22.48	20.79	5.17	4.78
1.0	10.298	10.296	23.88	23.26	5.49	5.35
10.0	10.292	10.282	27.48	28.50	6.32	6.55
60.0	10.280	10.297	31.88	32.69	7.33	7.52
240.0	10.271	10.295	33.51	35.23	7.71	8.10

Score1 (DU sum): 0.37  
 Score2 (DU Profile): **1.42**  
 DU sum difference (u): 0.29

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC105-131**  
 Exchangeable protons: 23  
 Index lis-file: 53  
 Sequence: ELKRADAAPTVSIFPPSSEQLTSGGAS  
 Range: 2 / 2

Reference: reference series, experiment: experiment series

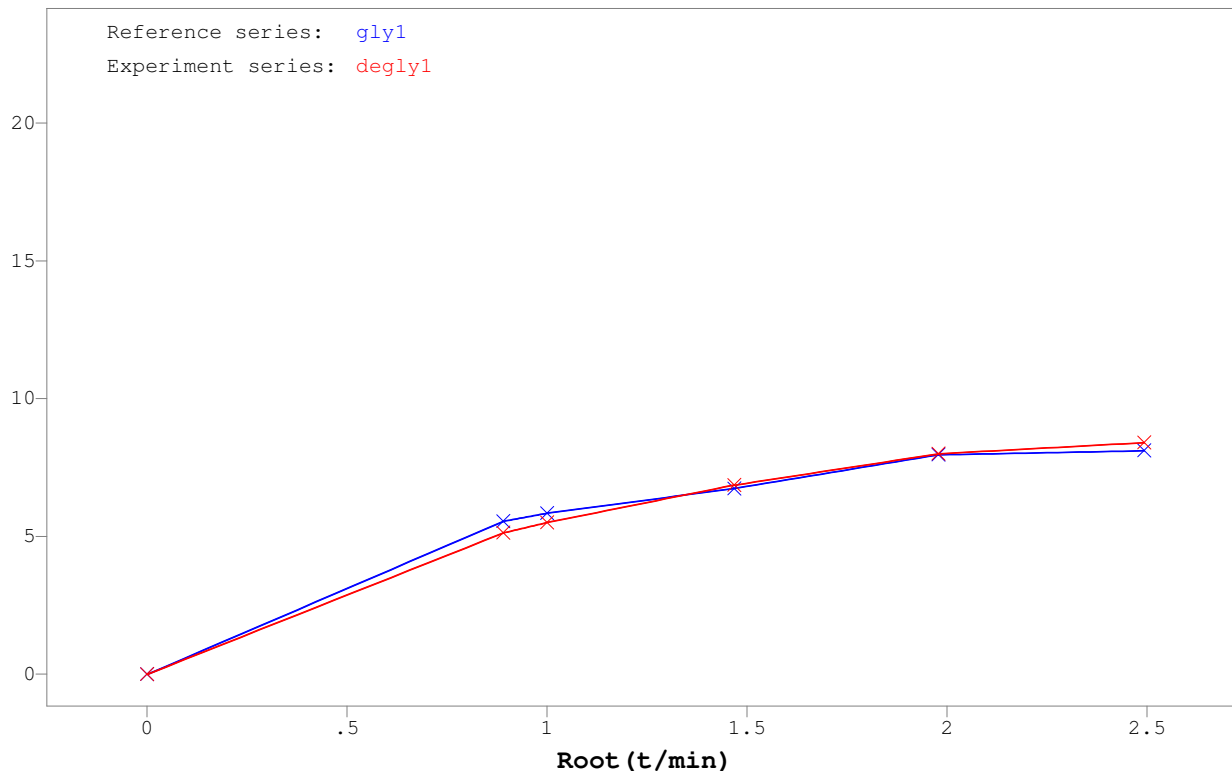
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.715	10.735	0.00	0.00	0.00	0.00
0.5	10.707	10.712	24.15	22.31	5.55	5.13
1.0	10.713	10.705	25.42	23.95	5.85	5.51
10.0	10.714	10.709	29.33	29.87	6.75	6.87
60.0	10.692	10.711	34.65	34.82	7.97	8.01
240.0	10.714	10.706	35.31	36.58	8.12	8.41

Score1 (DU sum): 0.39  
 Score2 (DU Profile): **1.28**  
 DU sum difference (u): -0.30

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC105-132**  
 Exchangeable protons: 24  
 Index lis-file: 54  
 Sequence: ELKRADAAPTVSIFPPSSEQLTSGGASV  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

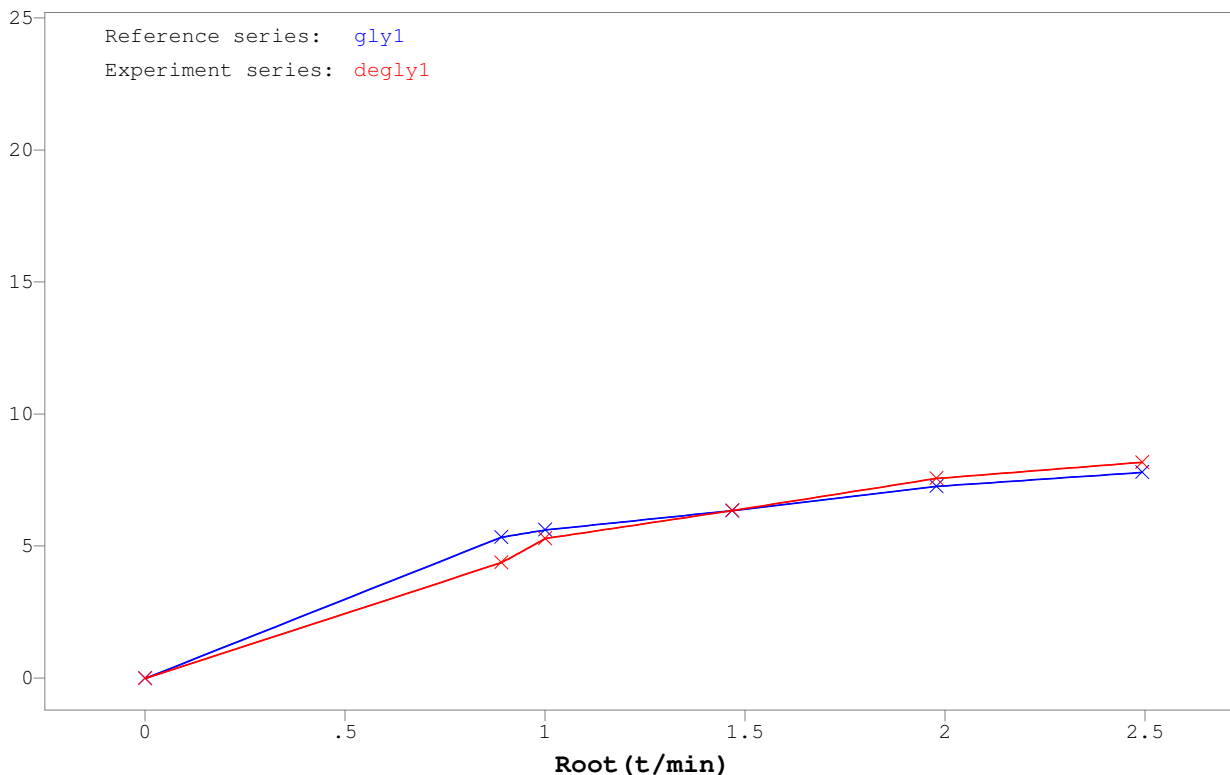
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.849	10.841	0.00	0.00	0.00	0.00
0.5	10.833	10.828	22.27	18.26	5.35	4.38
1.0	10.815	10.831	23.42	22.07	5.62	5.30
10.0	10.827	10.804	26.49	26.49	6.36	6.36
60.0	10.830	10.832	30.30	31.55	7.27	7.57
240.0	10.802	10.820	32.51	34.11	7.80	8.19

Score1 (DU sum): 0.74  
 Score2 (DU Profile): **1.99**  
 DU sum difference (u): -0.60

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC107-122**  
 Exchangeable protons: 12  
 Index lis-file: 203  
 Sequence: KRADAAPTVSIFPPSS  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

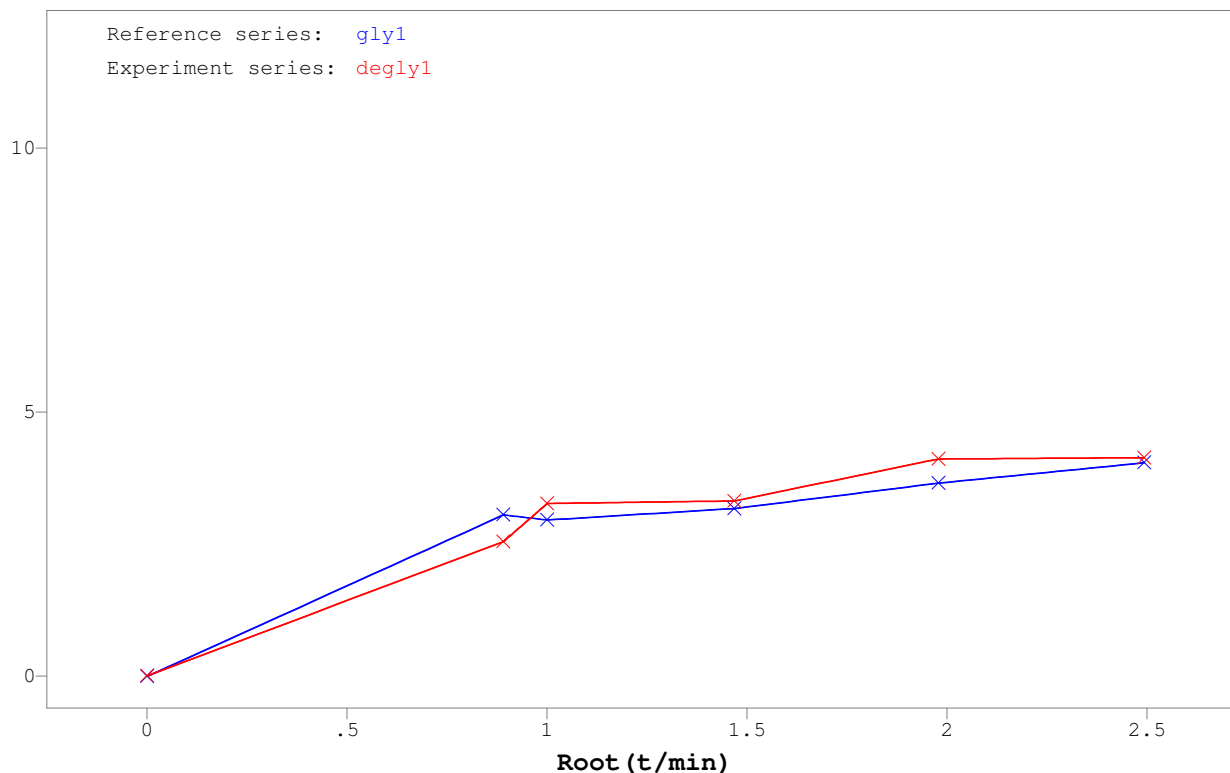
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.392	9.384	0.00	0.09	0.00	0.01
0.5	9.397	9.392	25.49	21.27	3.06	2.55
1.0	9.400	9.398	24.68	27.29	2.96	3.27
10.0	9.389	9.387	26.49	<b>27.69</b>	3.18	<b>3.32</b>
60.0	9.382	9.399	30.50	34.31	3.66	4.12
240.0	9.378	9.404	33.71	34.52	4.05	4.14

Score1 (DU sum): **1.01**  
 Score2 (DU Profile): 3.08p  
**DU sum difference (u): 0.45**

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC107-123**  
 Exchangeable protons: 13  
 Index lis-file: 55  
 Sequence: KRADAAPTVSIFPPSSE  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

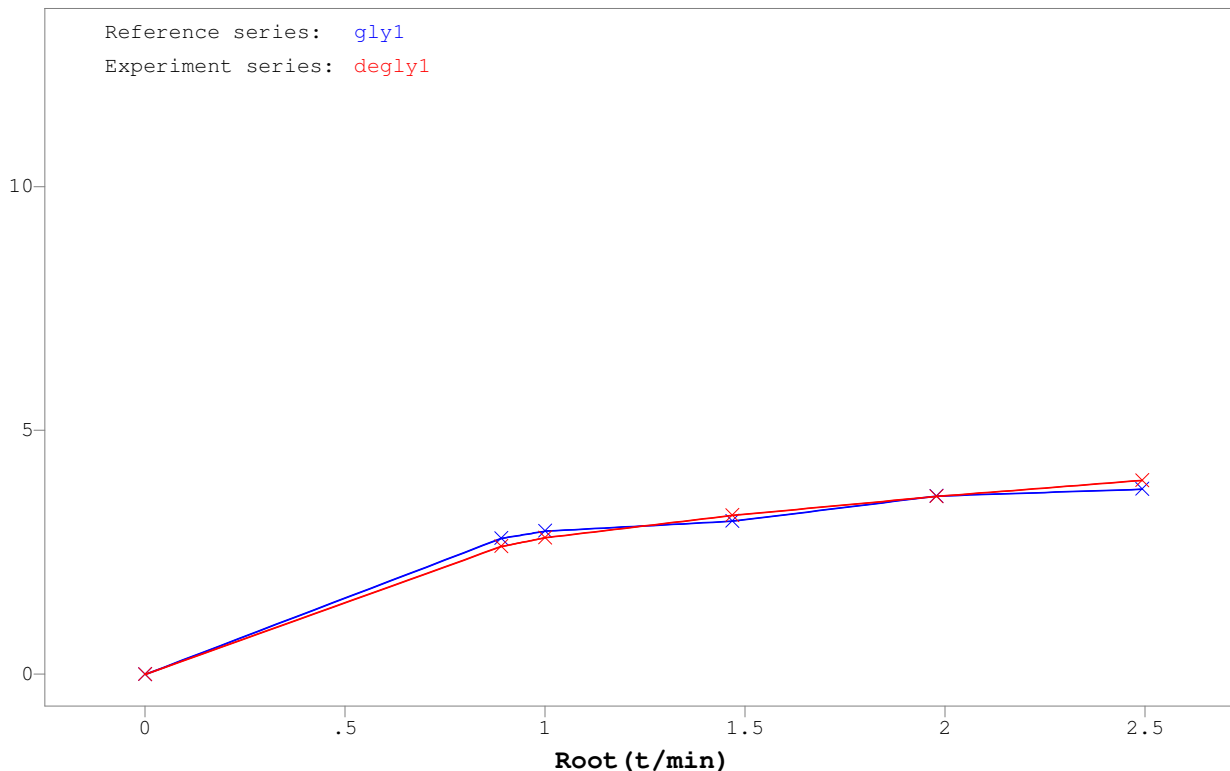
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.556	9.541	0.00	0.00	0.00	0.00
0.5	9.550	9.544	21.47	20.19	2.79	2.62
1.0	9.551	9.554	22.62	21.58	2.94	2.81
10.0	9.546	9.542	24.18	25.10	3.14	3.26
60.0	9.535	9.553	28.15	28.09	3.66	3.65
240.0	9.532	9.554	29.23	30.63	3.80	3.98

Score1 (DU sum): 0.02  
 Score2 (DU Profile): **1.14**  
 DU sum difference (u): -0.01

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC107-124**  
 Exchangeable protons: 14  
 Index lis-file: 56  
 Sequence: KRADAAPTVSIFPPSSEQ  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

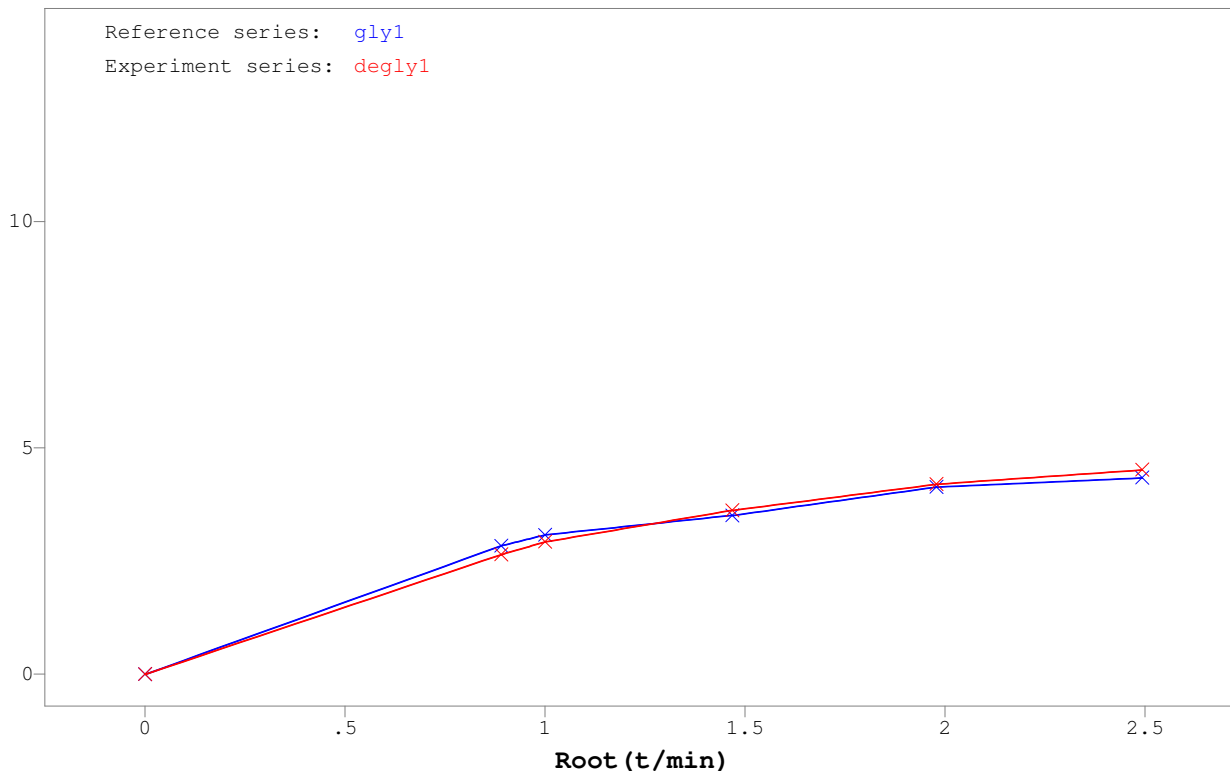
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.355	9.342	0.00	0.00	0.00	0.00
0.5	9.355	9.355	20.29	18.89	2.84	2.65
1.0	9.355	9.357	22.00	20.90	3.08	2.93
10.0	9.350	9.346	25.08	25.89	3.51	3.62
60.0	9.342	9.358	29.58	30.02	4.14	4.20
240.0	9.341	9.358	31.02	32.28	4.34	4.52

Score1 (DU sum): 0.00  
 Score2 (DU Profile): **1.21**  
 DU sum difference (u): 0.00

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC107-125**  
 Exchangeable protons: 15  
 Index lis-file: 204  
 Sequence: KRADAAPTVSIFPPSSEQL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

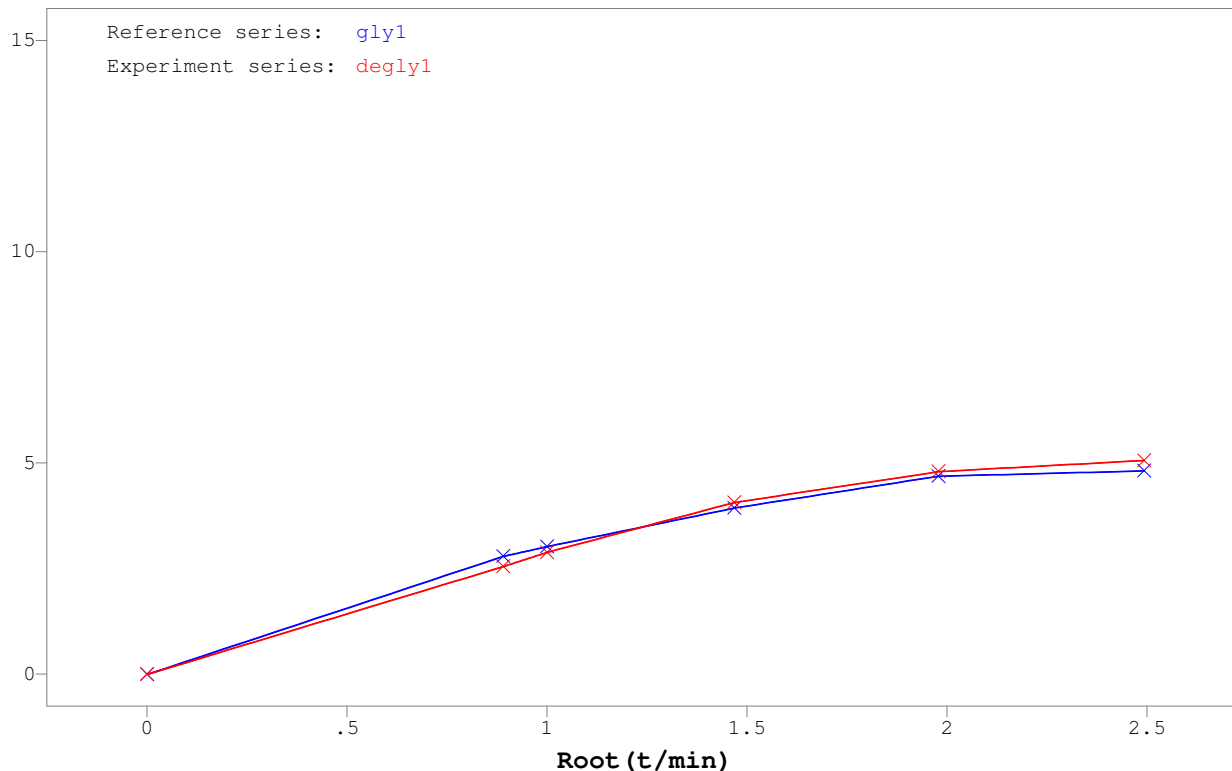
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.886	10.881	0.00	0.00	0.00	0.00
0.5	10.883	10.879	18.62	17.02	2.79	2.55
1.0	10.887	10.888	20.16	19.26	3.02	2.89
10.0	10.883	10.878	26.25	27.13	3.94	4.07
60.0	10.880	10.889	31.27	32.00	4.69	4.80
240.0	10.867	10.890	32.11	33.76	4.82	5.06

Score1 (DU sum): 0.22  
 Score2 (DU Profile): **1.39**  
 DU sum difference (u): 0.11

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **LC**  
 Peptide: **LC107-131**  
 Exchangeable protons: 21  
 Index lis-file: 57  
 Sequence: KRADAAPTVSIFPPSSEQLTSGGAS  
 Range: 1 / 2

Reference: reference series, experiment: experiment series

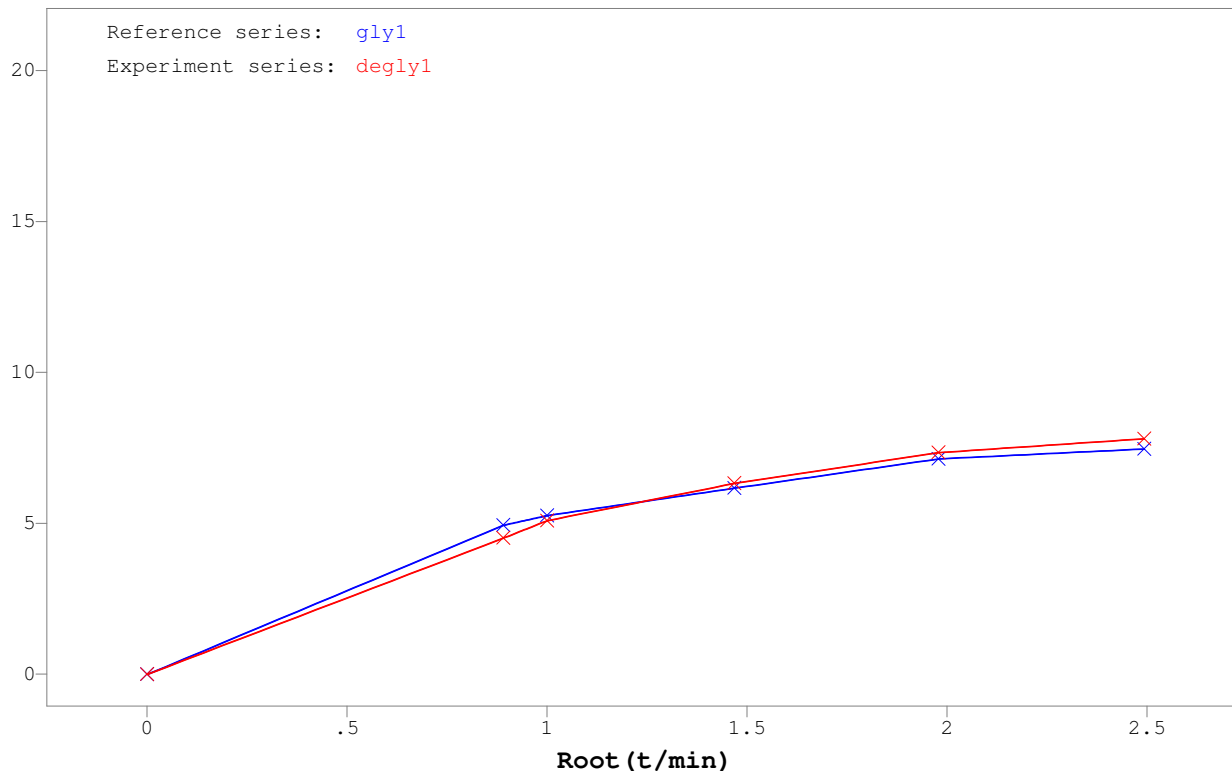
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.062	10.057	0.00	0.00	0.00	0.00
0.5	10.070	10.066	23.53	21.51	4.94	4.52
1.0	10.071	10.069	25.08	24.27	5.27	5.10
10.0	10.061	10.065	29.39	30.15	6.17	6.33
60.0	10.056	10.068	34.02	35.01	7.14	7.35
240.0	10.055	10.075	35.59	37.21	7.47	7.81

Score1 (DU sum): 0.16  
 Score2 (DU Profile): **1.50**  
 DU sum difference (u): 0.11

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC107-131**  
 Exchangeable protons: 21  
 Index lis-file: 57  
 Sequence: KRADAAPTVSIFPPSSEQLTSGGAS  
 Range: 2 / 2

Reference: reference series, experiment: experiment series

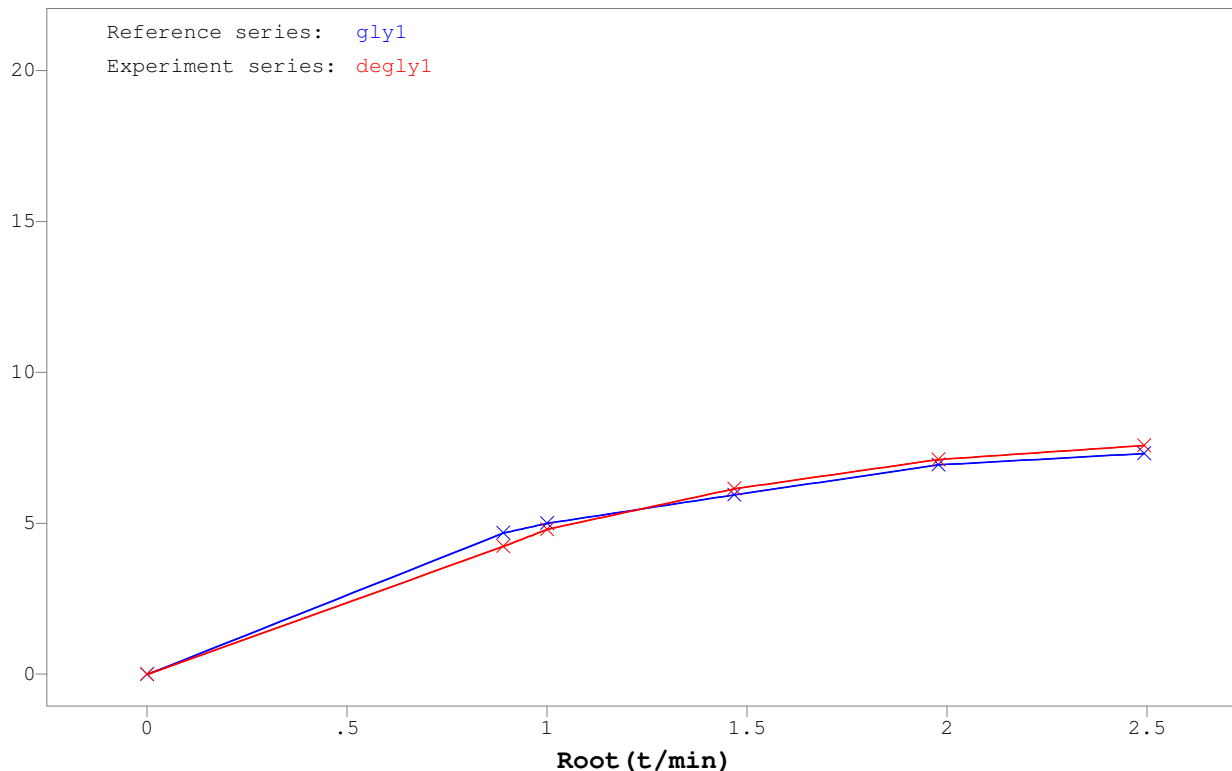
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.582	10.569	0.00	0.00	0.00	0.00
0.5	10.586	10.580	22.31	20.20	4.69	4.24
1.0	10.580	10.597	23.85	22.90	5.01	4.81
10.0	10.589	10.589	28.35	29.31	5.95	6.16
60.0	10.578	10.598	33.08	33.92	6.95	7.12
240.0	10.581	10.606	<b>34.87</b>	36.14	<b>7.32</b>	7.59

Score1 (DU sum): 0.41  
 Score2 (DU Profile): **1.41**  
 DU sum difference (u): -0.32

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC110-120**  
 Exchangeable protons: 7  
 Index lis-file: 58  
 Sequence: DAAPTVSIFPP  
 Range: 1 / 2

Reference: reference series, experiment: experiment series

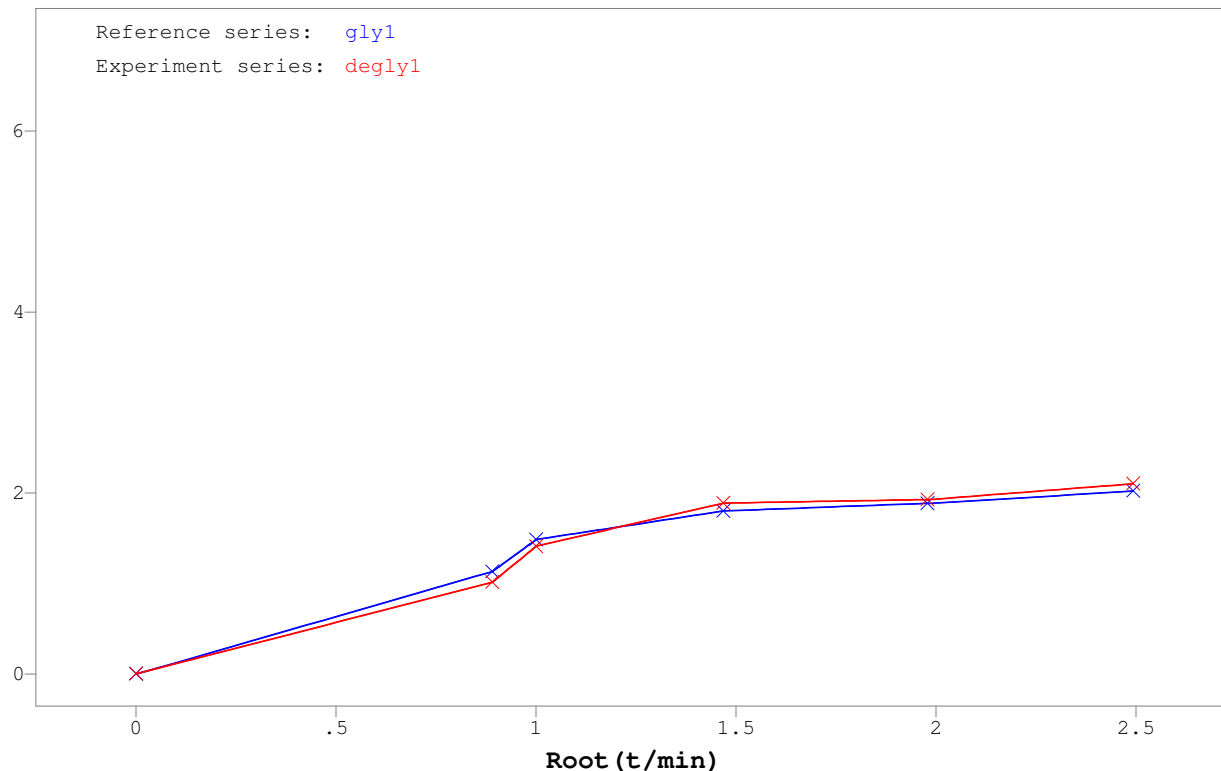
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.836	10.831	0.03	0.09	0.00	0.01
0.5	10.840	10.838	16.22	14.54	1.14	1.02
1.0	10.841	10.840	21.28	20.24	1.49	1.42
10.0	10.837	10.839	25.77	27.02	1.80	1.89
60.0	10.830	10.845	26.99	27.58	1.89	1.93
240.0	10.826	10.848	28.94	30.10	2.03	2.11

Score1 (DU sum): 0.10  
 Score2 (DU Profile): **1.40**  
 DU sum difference (u): 0.02

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC110-120**  
 Exchangeable protons: 7  
 Index lis-file: 58  
 Sequence: DAAPTVSIFPP  
 Range: 2 / 2

Reference: reference series, experiment: experiment series

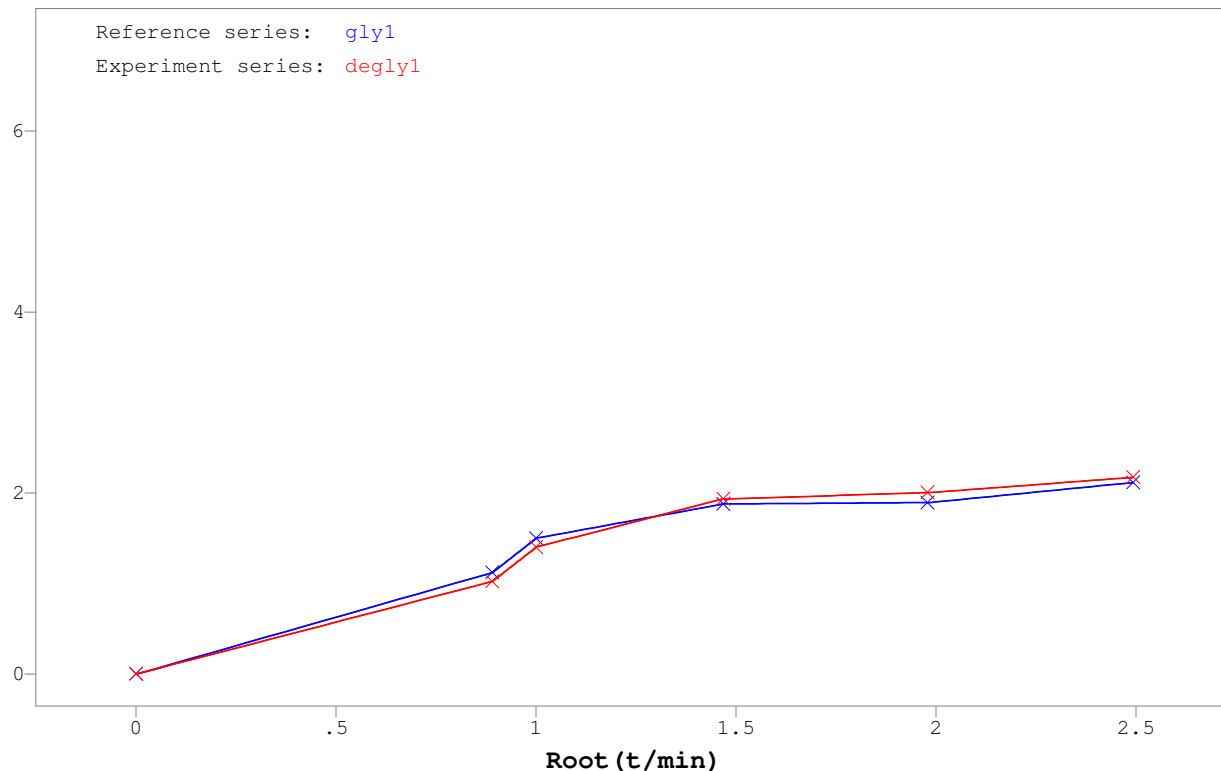
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.189	11.172	0.03	0.05	0.00	0.00
0.5	11.184	11.178	16.05	14.67	1.12	1.03
1.0	11.194	11.186	21.48	20.07	1.50	1.41
10.0	11.178	11.186	26.89	27.69	1.88	1.94
60.0	11.178	11.192	27.11	28.69	1.90	2.01
240.0	11.168	11.199	30.29	31.10	2.12	2.18

Score1 (DU sum): 0.13  
 Score2 (DU Profile): **1.46**  
 DU sum difference (u): 0.03

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC136-146**  
 Exchangeable protons: 9  
 Index lis-file: 64  
 Sequence: LNNFYPKDINV  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

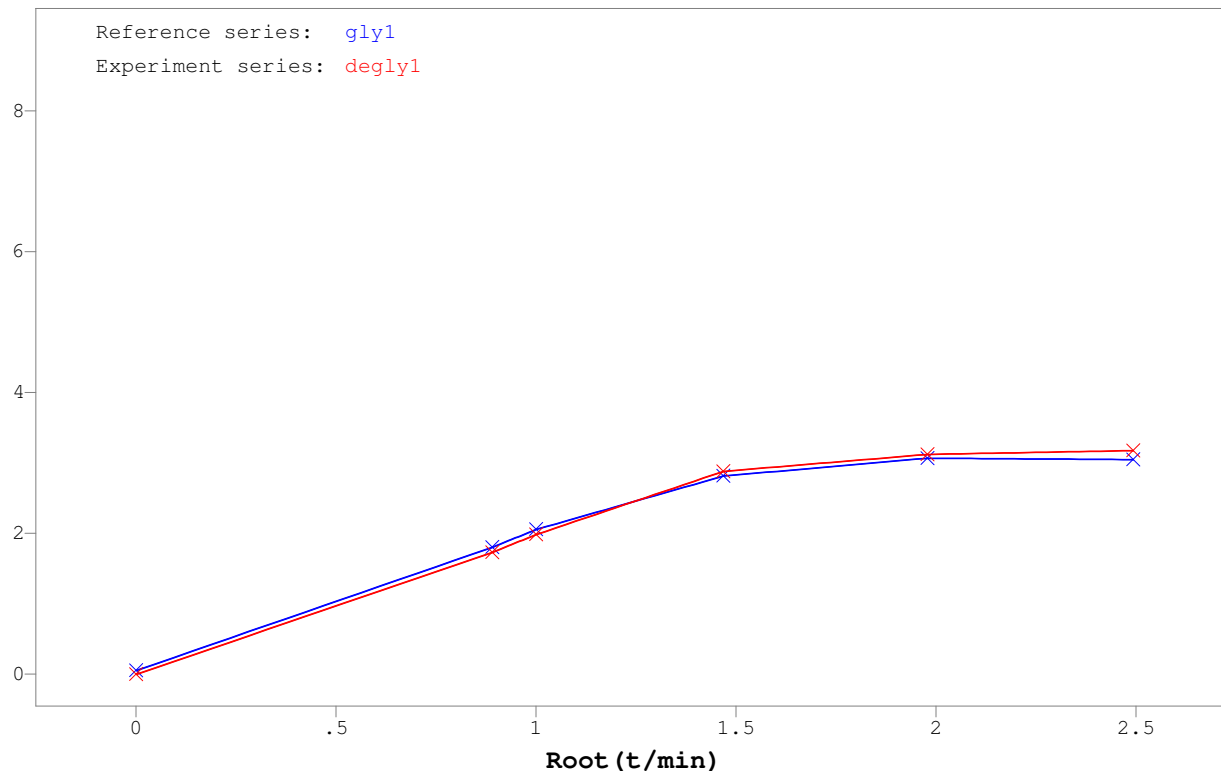
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.532	10.512	0.60	0.00	0.05	0.00
0.5	10.523	10.522	20.06	19.26	1.81	1.73
1.0	10.524	10.524	22.87	22.07	2.06	1.99
10.0	10.522	10.511	<b>31.30</b>	32.04	<b>2.82</b>	2.88
60.0	10.510	10.523	34.11	34.72	3.07	3.12
240.0	10.506	10.524	33.90	<b>35.32</b>	3.05	<b>3.18</b>

Score1 (DU sum): 0.58  
 Score2 (DU Profile): **1.01**  
 DU sum difference (u): -0.22

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC137-161**  
 Exchangeable protons: 23  
 Index lis-file: 66  
 Sequence: NNFYPKDINVKWKIDGSRQNGVLN  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

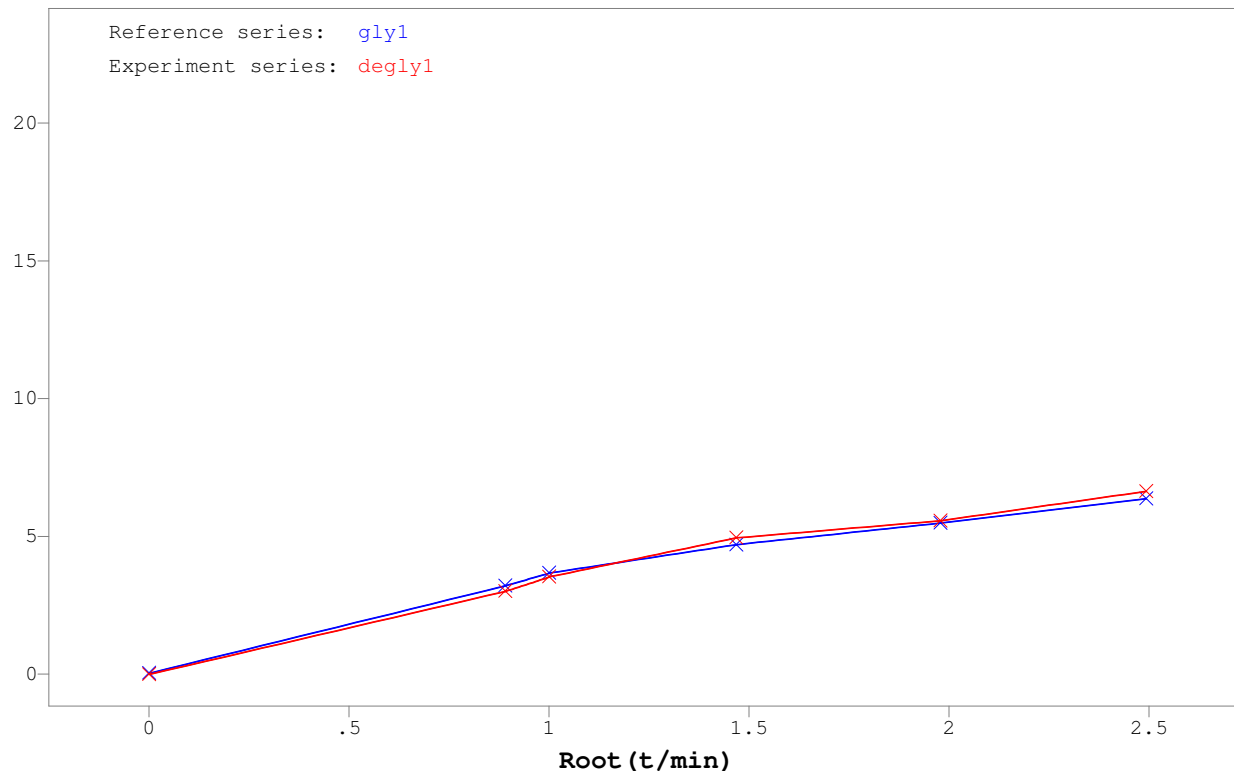
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.747	10.735	0.18	0.00	0.04	0.00
0.5	10.758	10.735	14.00	<b>13.11</b>	3.22	<b>3.02</b>
1.0	10.750	10.750	<b>15.99</b>	15.37	<b>3.68</b>	3.54
10.0	10.737	10.731	20.47	21.53	4.71	4.95
60.0	10.735	10.748	23.88	24.23	5.49	5.57
240.0	10.727	10.760	27.70	28.88	6.37	6.64

Score1 (DU sum): 0.88  
 Score2 (DU Profile): **1.01**  
 DU sum difference (u): 0.84

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC140-161**  
 Exchangeable protons: 20  
 Index lis-file: 68  
 Sequence: YPKDINVKWKIDGSERQNGVLN  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

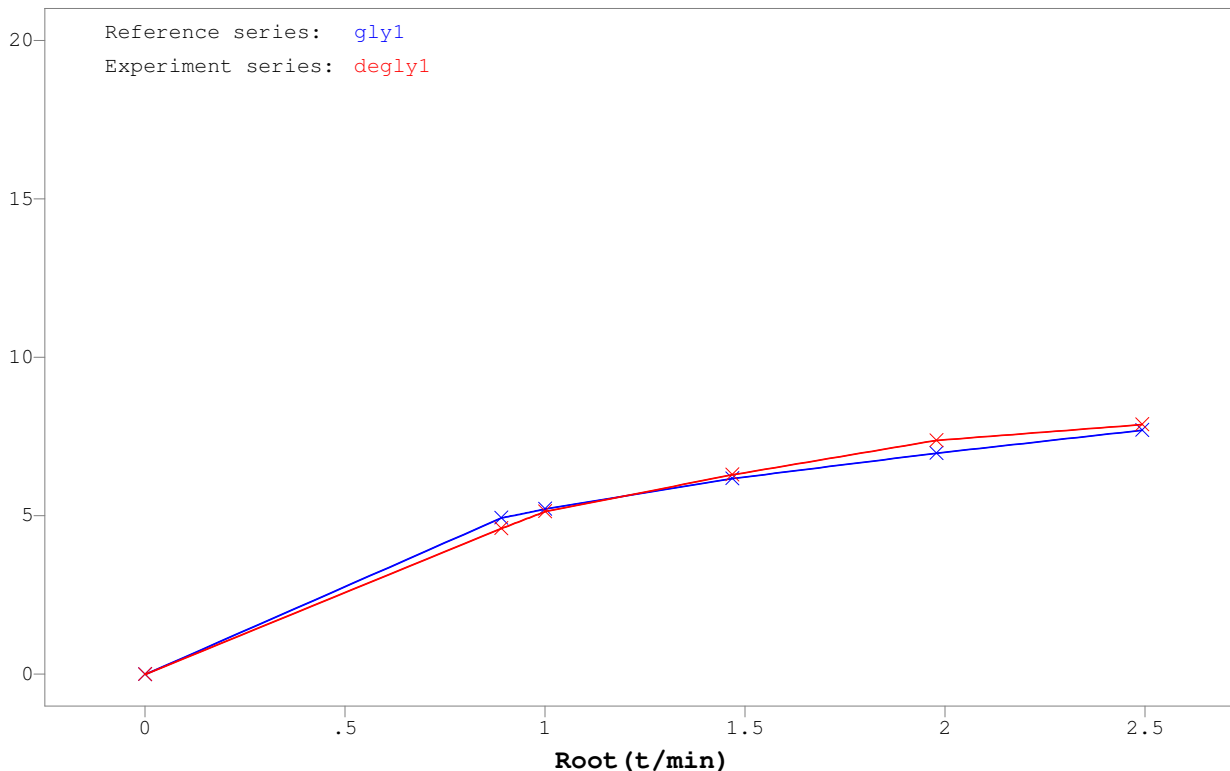
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.662	10.656	0.00	0.00	0.00	0.00
0.5	10.662	10.661	24.68	<b>23.02</b>	4.94	<b>4.60</b>
1.0	10.670	10.668	26.09	25.70	5.22	5.14
10.0	10.661	10.656	<b>30.90</b>	31.51	<b>6.18</b>	6.30
60.0	10.667	10.678	34.92	36.93	6.98	7.39
240.0	10.658	10.682	38.53	39.43	7.71	7.89

Score1 (DU sum): 0.91  
 Score2 (DU Profile): **1.20**  
 DU sum difference (u): 0.76

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC161-175**  
 Exchangeable protons: 14  
 Index lis-file: 74  
 Sequence: NSWTDQDSKDYISM  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

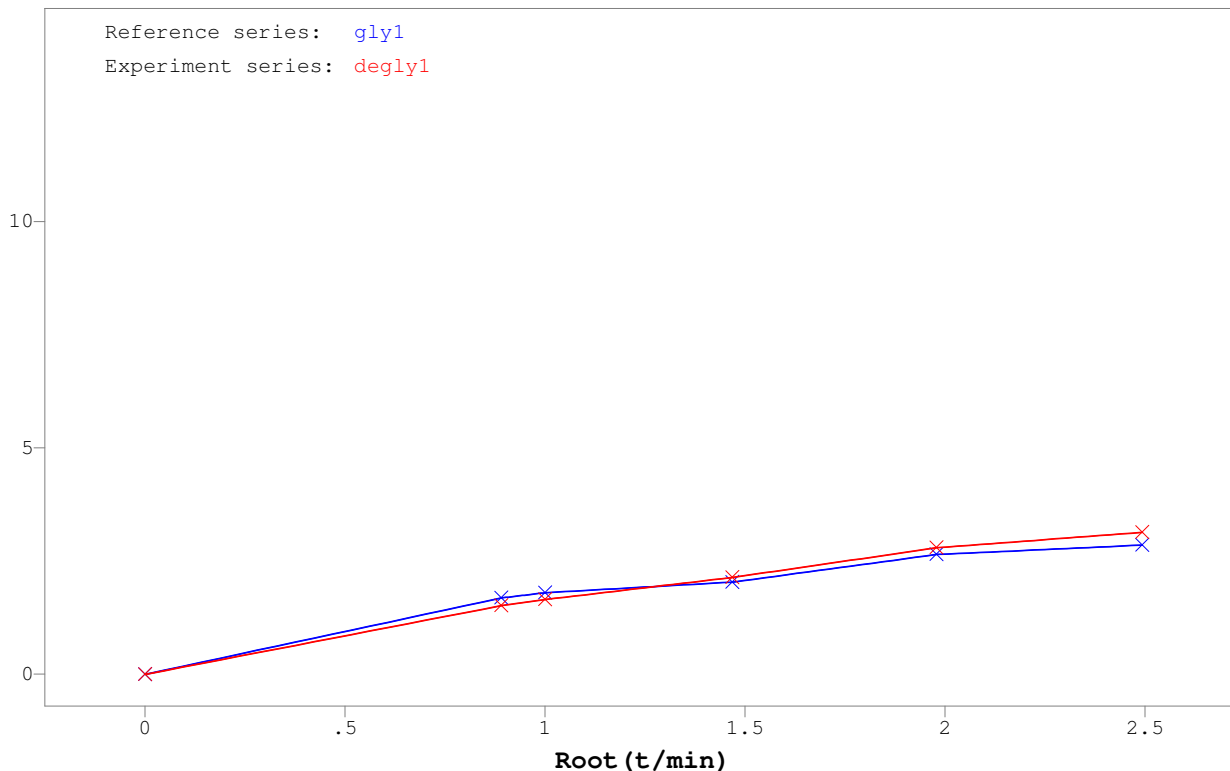
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.357	9.324	0.01	0.00	0.00	0.00
0.5	9.338	9.336	12.05	10.84	1.69	1.52
1.0	9.340	9.332	12.88	11.81	1.80	1.65
10.0	9.339	9.327	14.55	15.29	2.04	2.14
60.0	9.330	9.334	18.91	19.96	2.65	2.79
240.0	9.324	9.337	20.40	22.41	2.86	3.14

Score1 (DU sum): 0.45  
 Score2 (DU Profile): **1.48**  
 DU sum difference (u): 0.21

**DU Value**



Root(t/min): 6th roots of exchange times



Molecule: **LC**  
 Peptide: **LC161-179**  
 Exchangeable protons: 18  
 Index lis-file: 76  
 Sequence: NSWTDQDSKDYMSSTL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

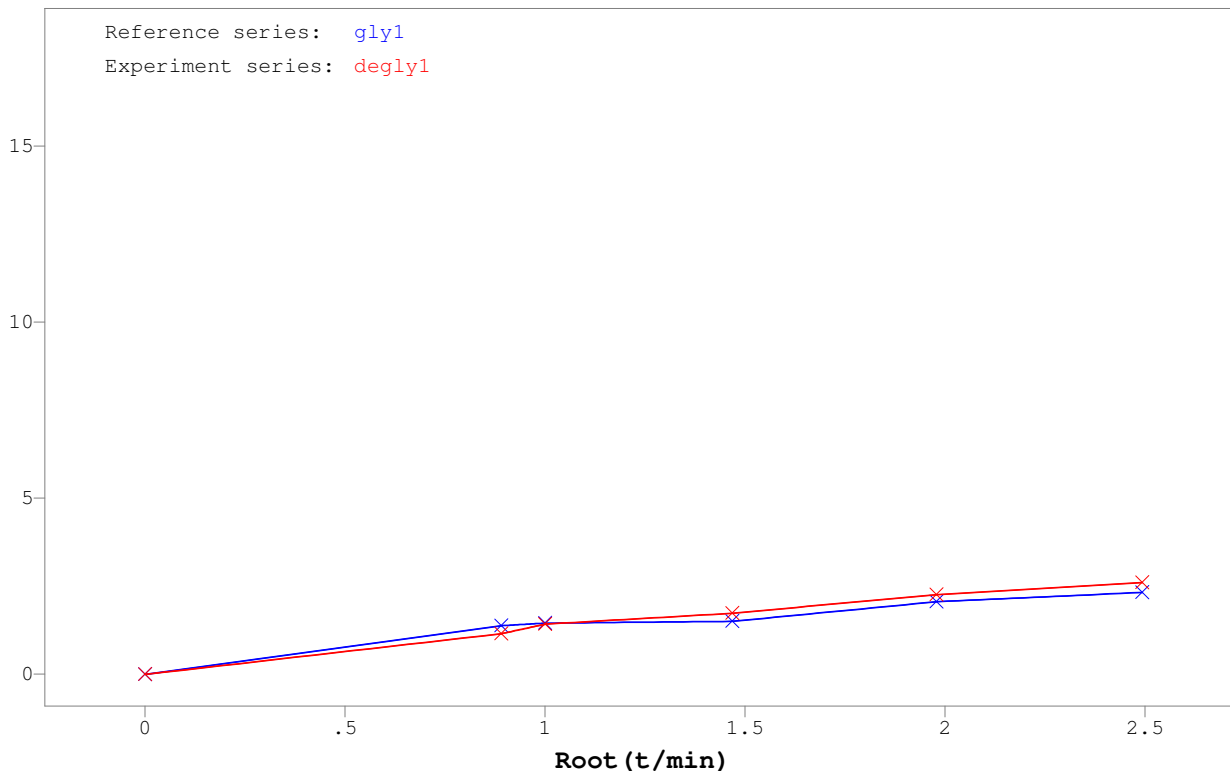
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	10.570	10.558	0.00	0.00	0.00	0.00
0.5	10.566	10.561	7.69	6.42	1.38	1.16
1.0	10.568	10.566	8.09	7.93	1.46	1.43
10.0	10.565	10.557	8.37	9.64	1.51	1.74
60.0	10.554	10.567	11.47	12.60	2.06	2.27
240.0	10.549	10.570	12.94	14.49	2.33	2.61

Score1 (DU sum): 0.75  
 Score2 (DU Profile): **1.30**  
 DU sum difference (u): 0.46

**DU Value**



Root(t/min): 6th roots of exchange times

Molecule: **LC**  
 Peptide: **LC179-206**  
 Exchangeable protons: 26  
 Index lis-file: 83  
 Sequence: LTLTKDEYERHNSYTCEATHKTSTSPIV  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

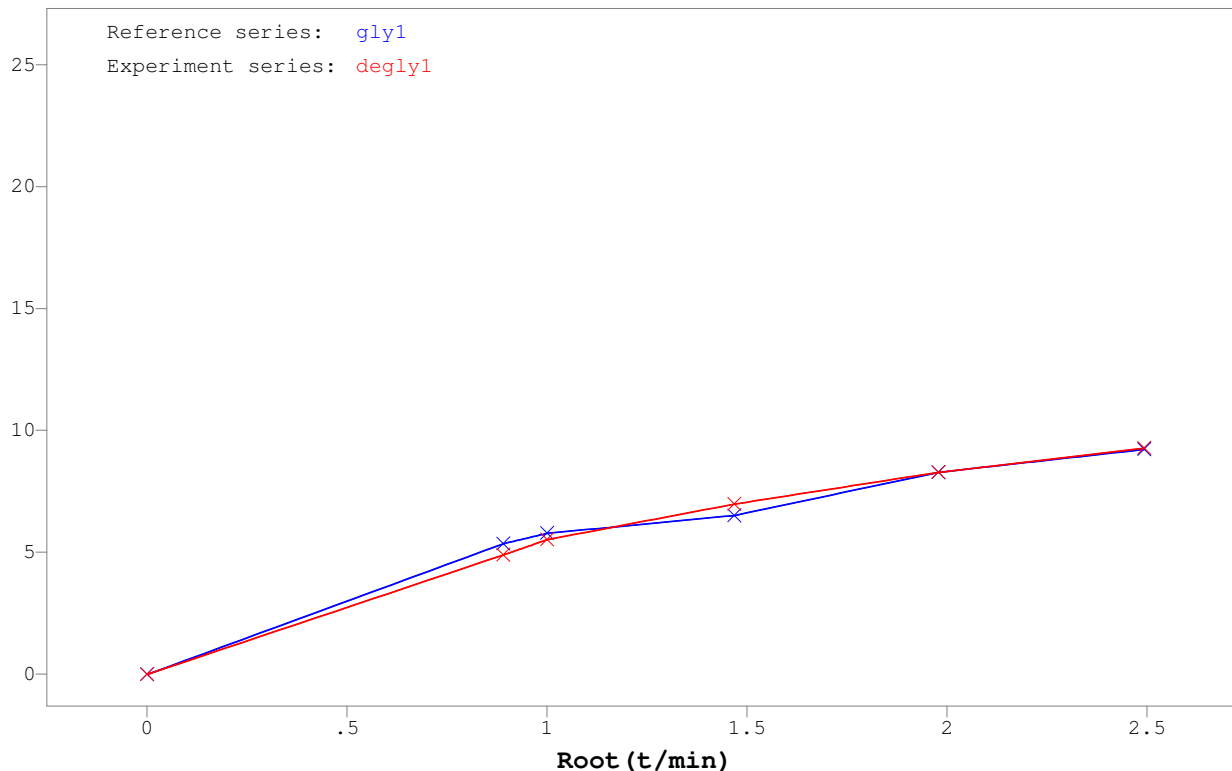
**Bold typing: problematic values (DU values) or significant differences (scores, DU sum difference)**

Significance limit Score1/Score2: 1; added 'p': plus problematic DU values

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.018	11.021	0.00	0.00	0.00	0.00
0.5	11.009	11.016	20.64	18.86	5.37	4.90
1.0	11.016	11.017	22.27	<b>21.28</b>	5.79	<b>5.53</b>
10.0	11.019	11.004	25.08	26.89	6.52	6.99
60.0	11.005	11.015	31.91	31.91	8.30	8.30
240.0	11.003	11.018	35.52	35.72	9.23	9.29

Score1 (DU sum): 0.08  
 Score2 (DU Profile): **1.10**  
 DU sum difference (u): 0.07

**DU Value**



Root(t/min): 6th roots of exchange times

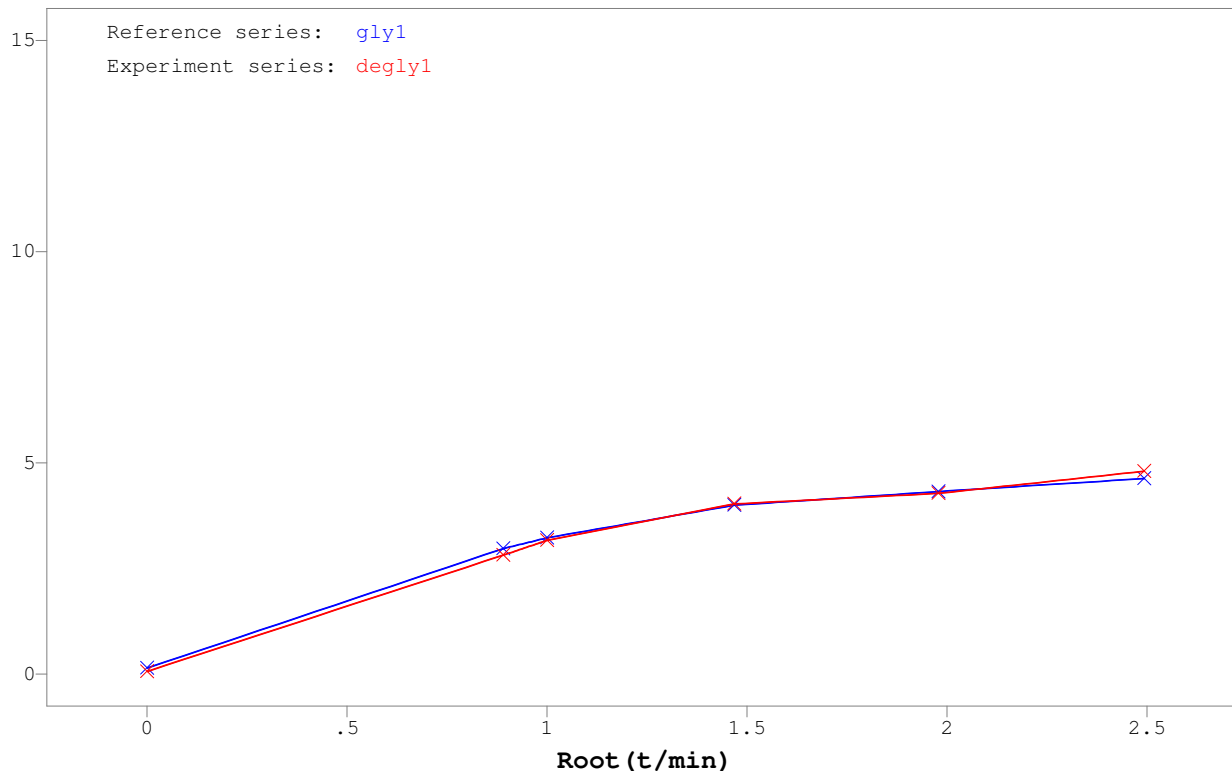
Molecule: **LC**  
 Peptide: **LC027-042**  
 Exchangeable protons: 15  
 Index lis-file: 15  
 Sequence: QSISNNLHWYQQKSHE  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.401	6.381	<b>1.00</b>	0.48	<b>0.15</b>	0.07
0.5	6.394	6.380	<b>19.87</b>	18.82	<b>2.98</b>	2.82
1.0	6.393	6.393	<b>21.56</b>	21.17	<b>3.23</b>	3.18
10.0	6.385	6.384	<b>26.70</b>	<b>26.90</b>	<b>4.01</b>	<b>4.04</b>
60.0	6.377	6.393	<b>28.86</b>	28.56	<b>4.33</b>	4.28
240.0	6.376	6.388	<b>30.90</b>	32.07	<b>4.64</b>	4.81

**DU Value**



Root(t/min): 6th roots of exchange times

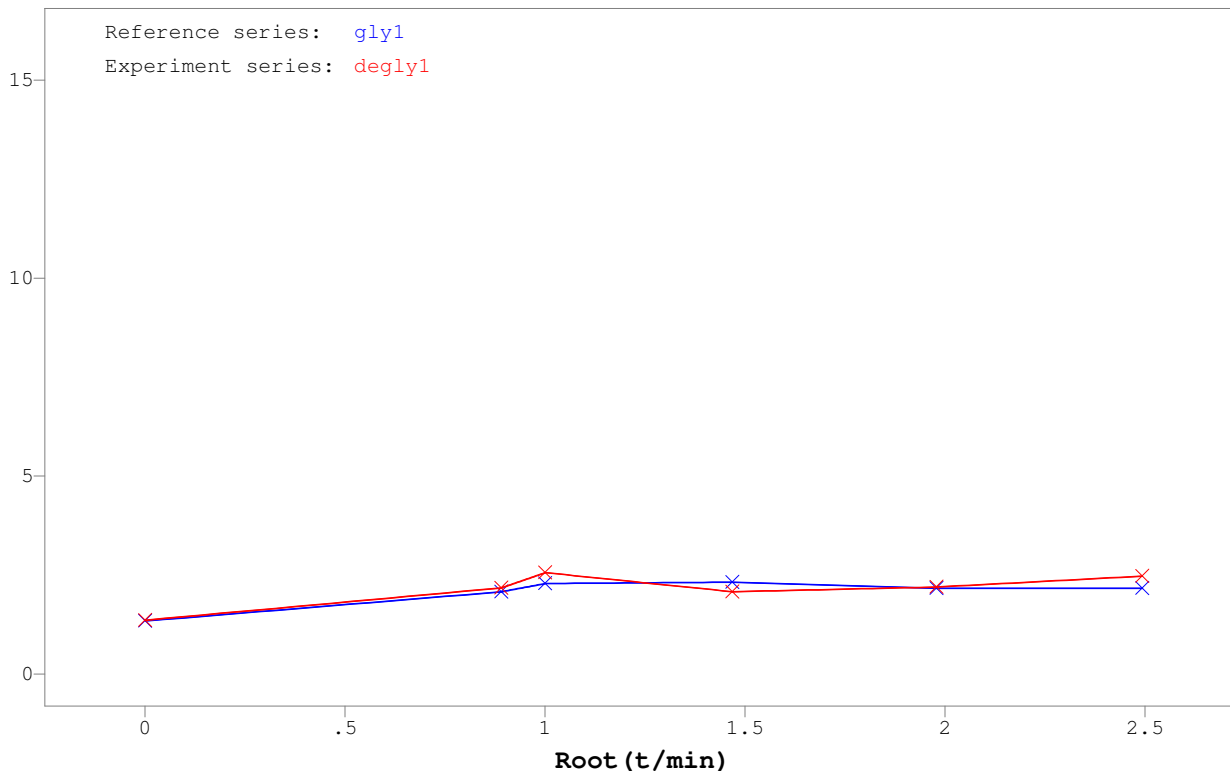
Molecule: **LC**  
 Peptide: **LC029-046**  
 Exchangeable protons: 16  
 Index lis-file: 19  
 Sequence: ISNNLHWYQQKSHESPRL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.007	7.977	<b>8.43</b>	<b>8.55</b>	<b>1.35</b>	<b>1.37</b>
0.5	8.006	7.985	13.04	<b>13.65</b>	2.09	<b>2.18</b>
1.0	8.005	7.999	14.33	<b>16.05</b>	2.29	<b>2.57</b>
10.0	7.995	7.987	14.55	<b>13.04</b>	2.33	<b>2.09</b>
60.0	7.990	8.004	13.56	<b>13.79</b>	2.17	<b>2.21</b>
240.0	7.984	7.999	13.56	<b>15.50</b>	2.17	<b>2.48</b>

**DU Value**



Root(t/min): 6th roots of exchange times

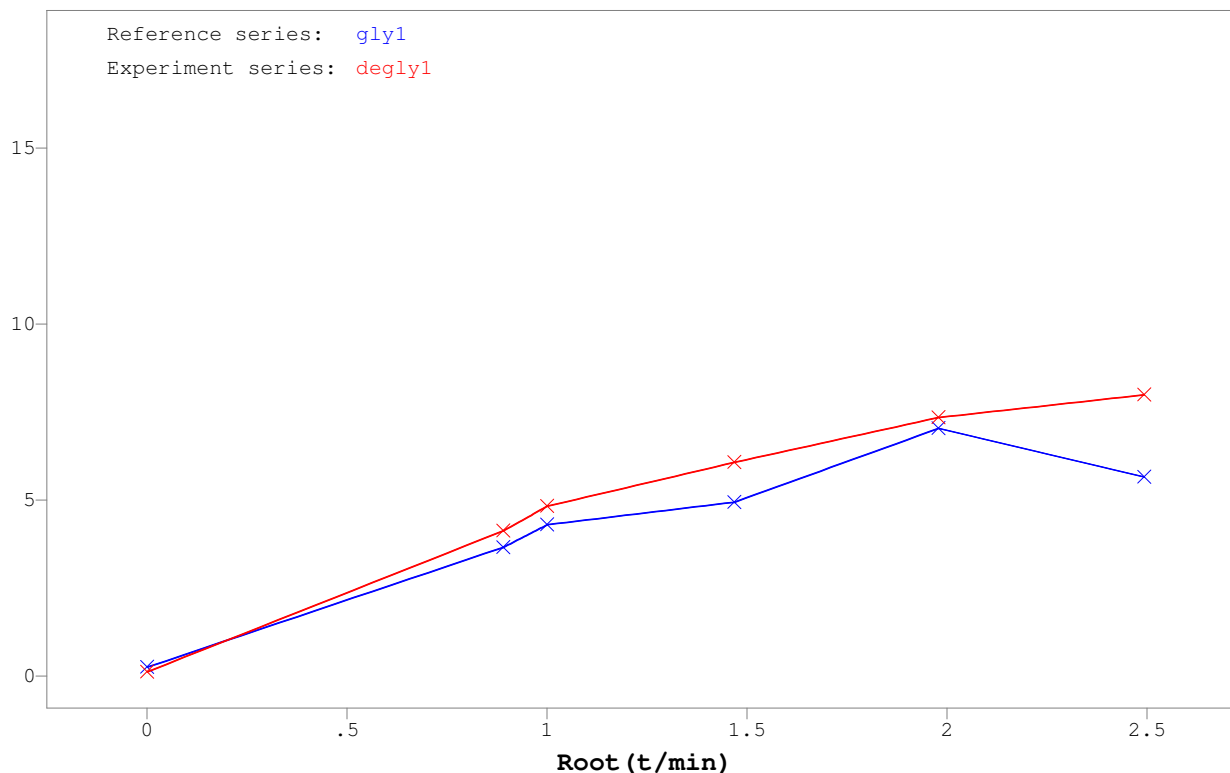
Molecule: **LC**  
 Peptide: **LC051-070**  
 Exchangeable protons: 18  
 Index lis-file: 27  
 Sequence: ASQSISGIPSRFSGSGSGTD  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.747	8.745	<b>1.45</b>	0.72	<b>0.26</b>	0.13
0.5	8.728	8.736	<b>20.37</b>	22.98	<b>3.67</b>	4.14
1.0	8.726	8.750	<b>23.93</b>	26.85	<b>4.31</b>	4.83
10.0	8.730	8.733	<b>27.50</b>	33.78	<b>4.95</b>	6.08
60.0	8.721	8.734	<b>39.13</b>	40.85	<b>7.04</b>	7.35
240.0	8.729	8.737	<b>31.46</b>	44.43	<b>5.66</b>	8.00

**DU Value**



Root(t/min): 6th roots of exchange times

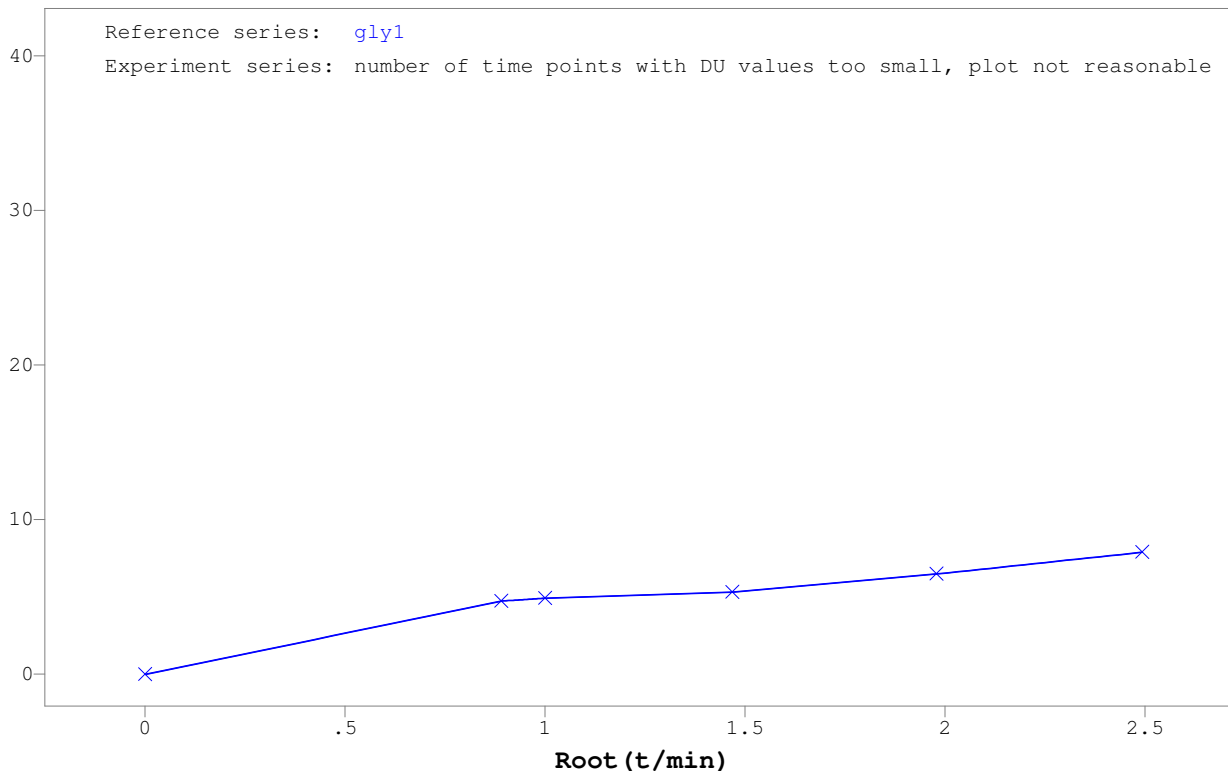
Molecule: **LC**  
 Peptide: **LC051-093**  
 Exchangeable protons: 41  
 Index lis-file: 28  
 Sequence: ASQSISGIPSRFSGSGSGTDFTLINSVETEDFGMYFCQQSNS  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.463	9.440	0.00	n.d.	0.00	n.d.
0.5	9.453	9.440	11.59	n.d.	4.75	n.d.
1.0	9.455	9.433	12.04	n.d.	4.94	n.d.
10.0	9.435	9.435	13.00	n.d.	5.33	n.d.
60.0	9.440	9.475	15.85	n.d.	6.50	n.d.
240.0	9.427	9.436	19.29	n.d.	7.91	n.d.

**DU Value**



Root(t/min): 6th roots of exchange times

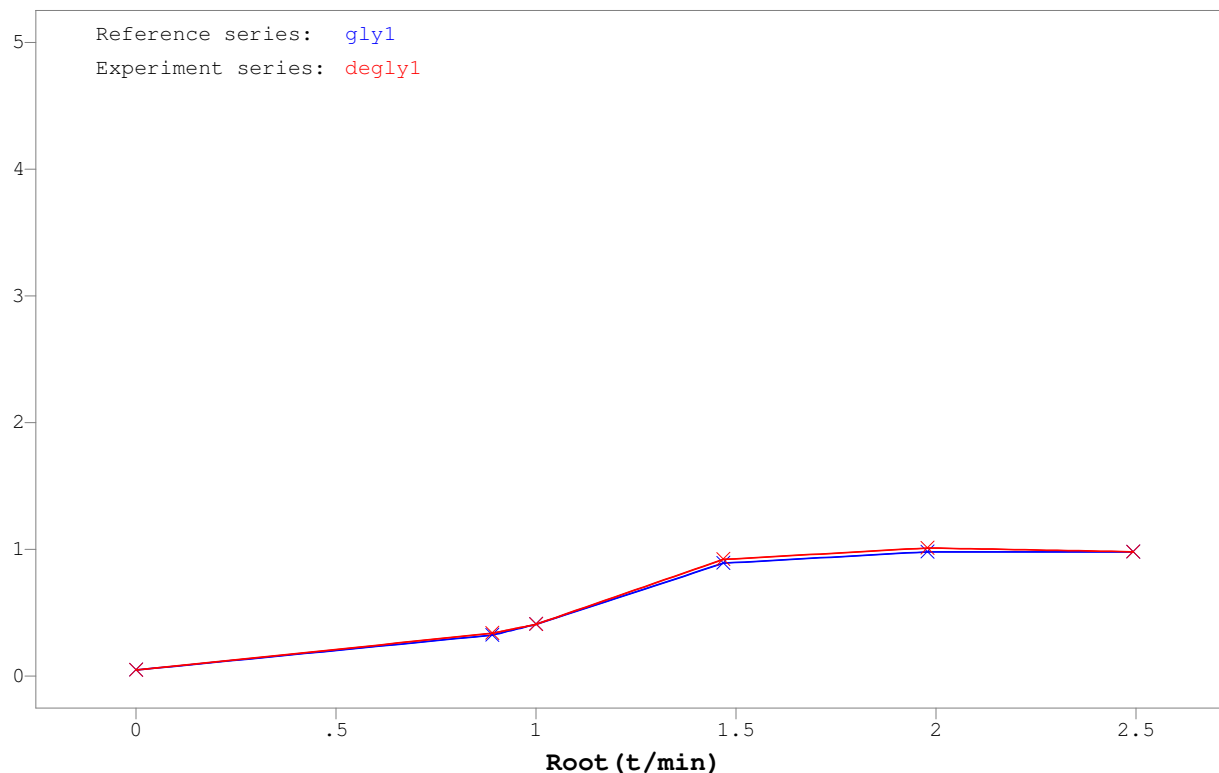
Molecule: **LC**  
 Peptide: **LC071-076**  
 Exchangeable protons: 5  
 Index lis-file: 36  
 Sequence: FTLSIN  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	11.140	11.171	<b>1.00</b>	1.00	<b>0.05</b>	0.05
0.5	11.122	11.140	<b>6.52</b>	6.81	<b>0.33</b>	0.34
1.0	11.118	11.126	<b>8.23</b>	8.23	<b>0.41</b>	0.41
10.0	11.129	11.104	<b>17.86</b>	18.46	<b>0.89</b>	0.92
60.0	11.121	11.132	<b>19.67</b>	20.27	<b>0.98</b>	1.01
240.0	11.119	11.129	<b>19.67</b>	<b>19.67</b>	<b>0.98</b>	<b>0.98</b>

**DU Value**



Root(t/min): 6th roots of exchange times

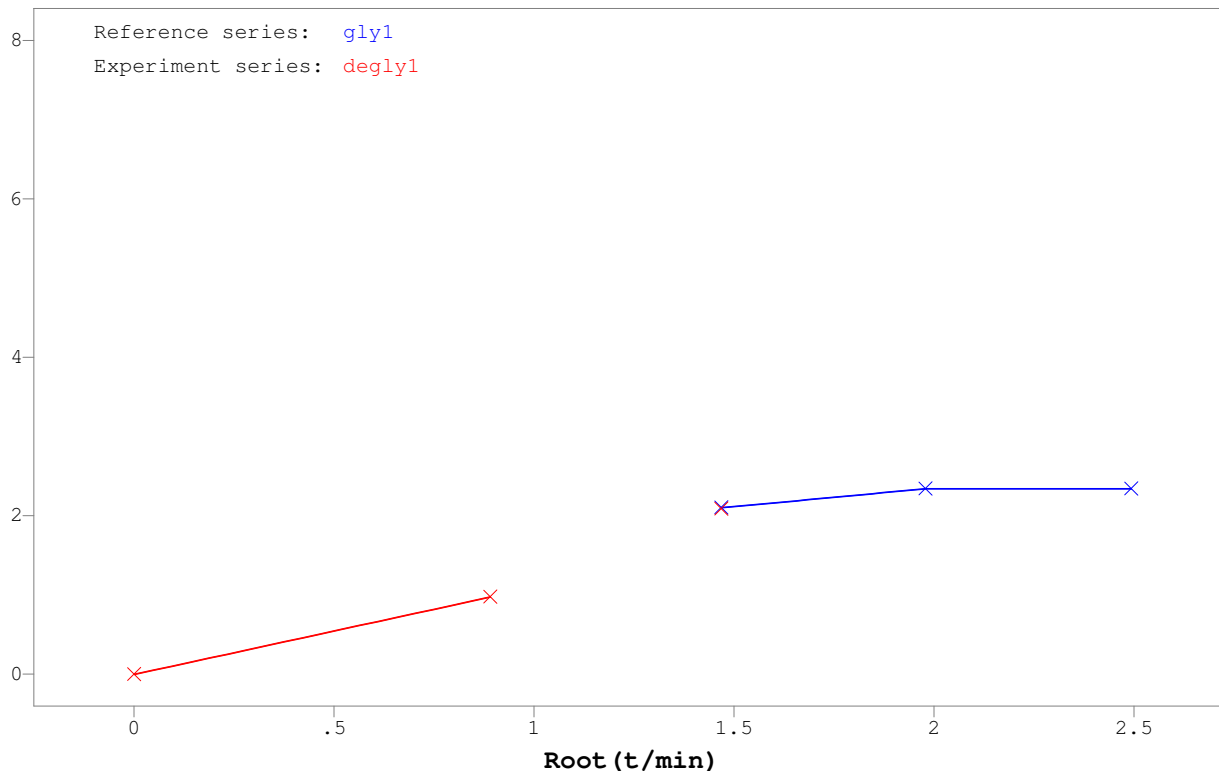
Molecule: **LC**  
 Peptide: **LC136-145**  
 Exchangeable protons: 8  
 Index lis-file: 63  
 Sequence: LNNFYPKDIN  
 Range: 2 / 2

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	8.957	8.940	n.d.	<b>0.00</b>	n.d.	<b>0.00</b>
0.5	8.957	8.955	n.d.	<b>12.24</b>	n.d.	<b>0.98</b>
1.0	n.d.	8.958	n.d.	n.d.	n.d.	n.d.
10.0	8.949	8.938	<b>26.29</b>	<b>26.09</b>	<b>2.10</b>	<b>2.09</b>
60.0	8.934	8.955	<b>29.30</b>	n.d.	<b>2.34</b>	n.d.
240.0	8.932	8.943	<b>29.30</b>	n.d.	<b>2.34</b>	n.d.

**DU Value**



Root(t/min): 6th roots of exchange times



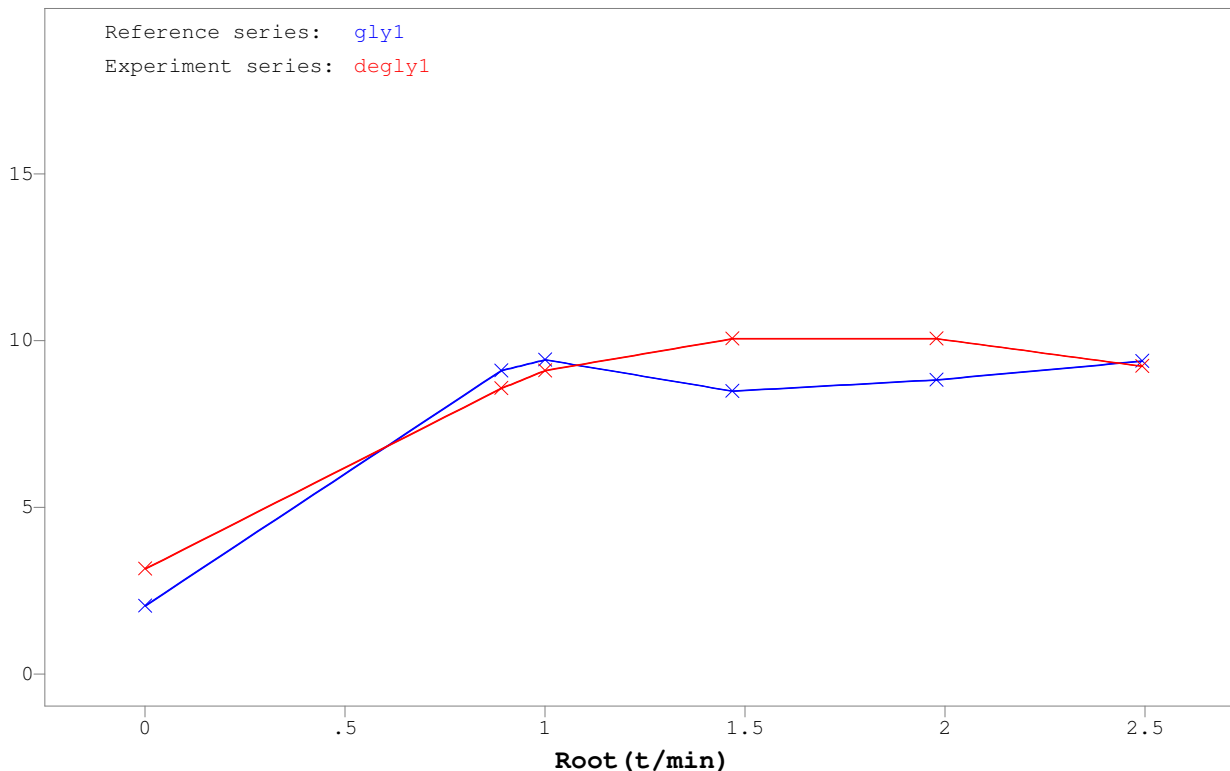
Molecule: **LC**  
 Peptide: **LC140-160**  
 Exchangeable protons: 19  
 Index lis-file: 67  
 Sequence: YPKDINVKWKIDGSERQNGVL  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	9.341	9.333	<b>10.84</b>	<b>16.66</b>	<b>2.06</b>	<b>3.16</b>
0.5	9.347	9.344	<b>47.96</b>	<b>45.15</b>	<b>9.11</b>	<b>8.58</b>
1.0	9.343	9.353	<b>49.65</b>	<b>47.96</b>	<b>9.43</b>	<b>9.11</b>
10.0	9.338	9.341	<b>44.71</b>	<b>52.98</b>	<b>8.50</b>	<b>10.07</b>
60.0	9.329	9.343	<b>46.49</b>	<b>52.98</b>	<b>8.83</b>	<b>10.07</b>
240.0	9.329	9.346	<b>49.45</b>	<b>48.64</b>	<b>9.39</b>	<b>9.24</b>

**DU Value**



Root(t/min): 6th roots of exchange times

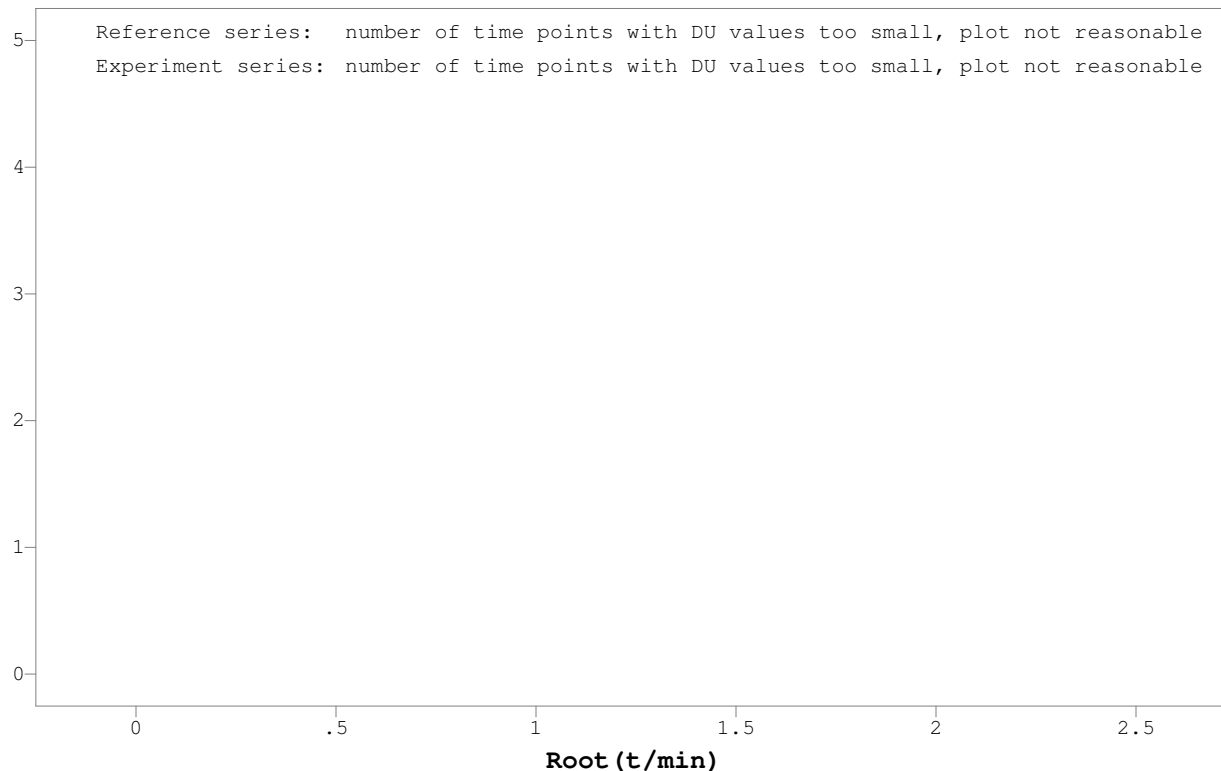
Molecule: **LC**  
 Peptide: **LC173-178**  
 Exchangeable protons: 5  
 Index lis-file: 78  
 Sequence: YSMSST  
 Range: 1 / 1

Reference: reference series, experiment: experiment series

**Bold typing: problematic DU values**

Exchange Time (min)	Retention Time Reference (min)	Retention Time Experiment (min)	Exchange Rate Reference (%)	Exchange Rate Experiment (%)	DU Value (u) Reference	DU Value (u) Experiment
0.0	6.339	6.325	n.d.	n.d.	n.d.	n.d.
0.5	6.339	6.328	n.d.	n.d.	n.d.	n.d.
1.0	6.339	6.332	n.d.	n.d.	n.d.	n.d.
10.0	6.333	6.325	n.d.	n.d.	n.d.	n.d.
60.0	6.325	6.330	n.d.	n.d.	n.d.	n.d.
240.0	6.325	6.333	n.d.	n.d.	n.d.	n.d.

**DU Value**

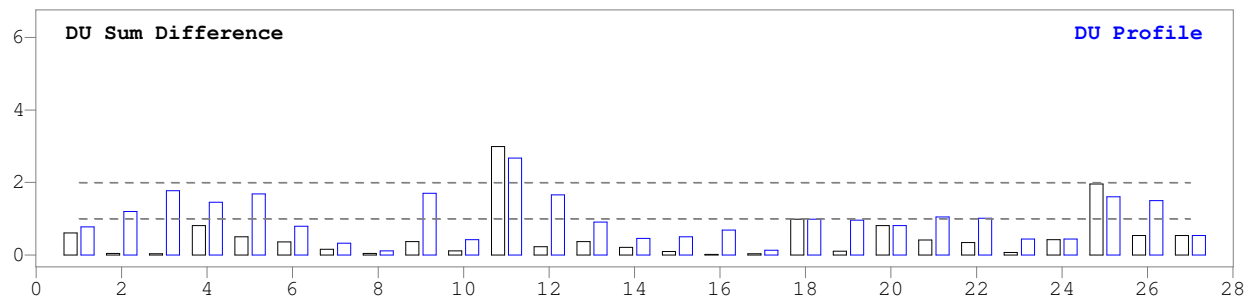


Root(t/min): 6th roots of exchange times

Molecule HC: Peptides with sufficient kinetics data, part 1

No.	Peptide/Range	Sequence
1	HC001-017/1	EVQGVESGGGLVKPGGS
2	HC001-018/1	EVQGVESGGGLVKPGGSL
3	HC001-020/1	EVQGVESGGGLVKPGGSLKL
4	HC001-022/1	EVQGVESGGGLVKPGGSLKLS
5	HC001-023/1	EVQGVESGGGLVKPGGSLKLSA
6	HC002-044/1	VQGVESGGGLVKPGGSLKLSAASGFTFSDYYMYWVRQTPEKR
7	HC012-043/1	VKPGGSLKLSAASGFTFSDYYMYWVRQTPEK
8	HC019-037/1	KLSCAASGFTFSDYYMYW
9	HC024-032/1	ASGFTFSDY
10	HC026-057/1	GFTFSDYYMYWVRQTPEKRLEWVATISDGGSY
11	HC027-031/1	FTFSD
12	HC027-032/1	FTFSDY
13	HC035-047/1	YWVRQTPEKRLEW
14	HC035-050/1	YWVRQTPEKRLEWVAT
15	HC036-047/1	WVRQTPEKRLEW
16	HC036-049/1	WVRQTPEKRLEWVA
17	HC037-050/1	VRQTPEKRLEWVAT
18	HC051-068/1	ISDGGSYTYYPDSVKGRF
19	HC051-079/1	ISDGGSYTYYPDSVKGRFTISRDNKNNL
20	HC057-068/1	YTYYPDSVKGRF
21	HC057-079/1	YTYYPDSVKGRFTISRDNKNNL
22	HC058-079/1	TYYPDSVKGRFTISRDNKNNL
23	HC065-101/1	KGRFTISRDNKNNLYLQMSLKSEDTAMYYCARDKA
24	HC069-079/1	TISRDNKNNL
25	HC069-080/1	TISRDNKNNLY
26	HC070-078/1	ISRDNKNN
27	HC080-083/1	YLQM

Score



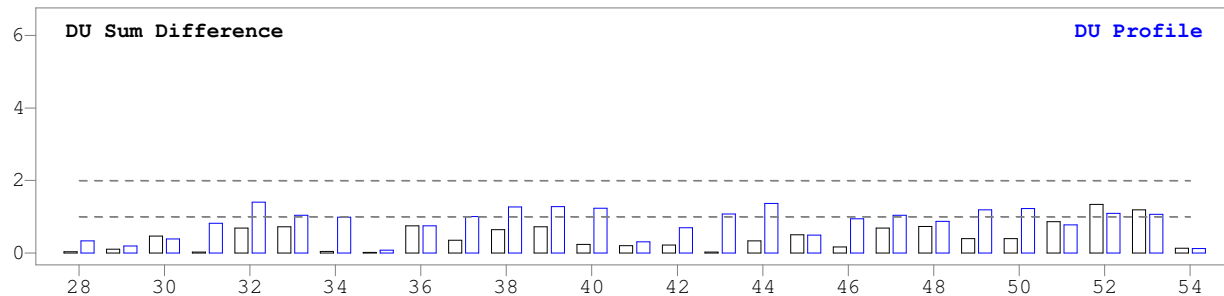
DU Sum Difference (u)



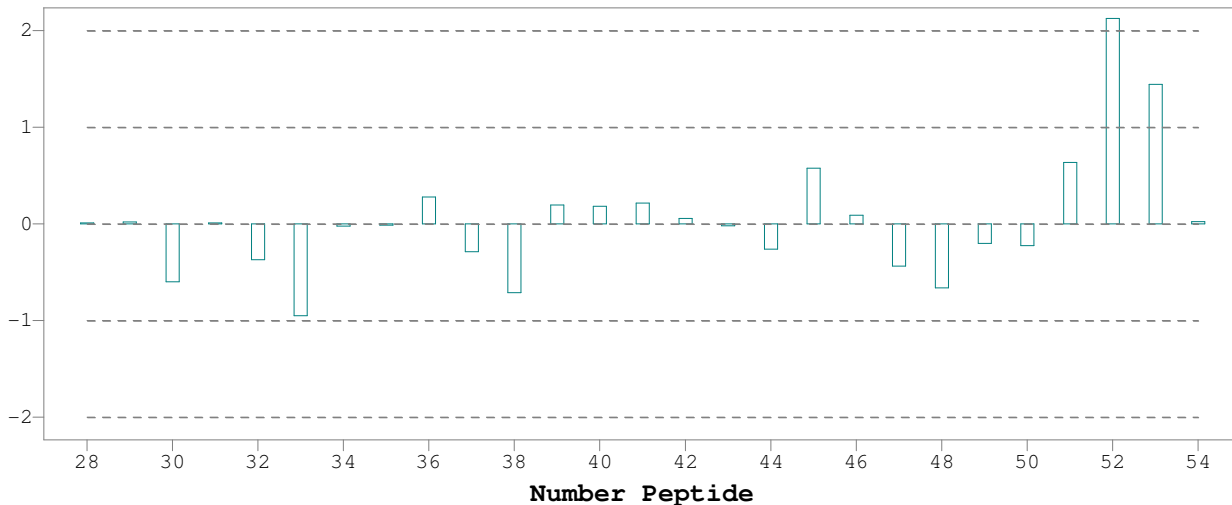
Molecule HC: Peptides with sufficient kinetics data, part 2

No.	Peptide/Range	Sequence
28	HC084-093/1	SSLKSED TAM
29	HC087-093/1	KSED TAM
30	HC089-127/1	EDTAMYICARDKAYYGNYGDMADYWGQGT SVTVSSAKTT
31	HC094-109/1	YYCARDKAYYGNYGDA
32	HC094-110/1	YYCARDKAYYGNYGDM
33	HC094-137/1	YYCARDKAYYGNYGDMADYWGQGT SVTVSSAKTTPPSVYPLAPG
34	HC095-112/1	YCARDKAYYGNYGDMADY
35	HC105-143/1	NYGDAMADYWGQGT SVTVSSAKTTPPSVYPLAPGSAAQTN
36	HC111-120/1	DYWGQGT SVT
37	HC111-139/1	DYWGQGT SVTVSSAKTTPPSVYPLAPGSA
38	HC111-145/1	DYWGQGT SVTVSSAKTTPPSVYPLAPGSAAQTNSM
39	HC112-120/1	YWQGT SVT
40	HC112-139/1	YWQGT SVTVSSAKTTPPSVYPLAPGSA
41	HC112-145/1	YWQGT SVTVSSAKTTPPSVYPLAPGSAAQTNSM
42	HC113-120/1	WGQGT SVT
43	HC113-139/1	WGQGT SVTVSSAKTTPPSVYPLAPGSA
44	HC115-140/1	QGTSVTVSSAKTTPPSVYPLAPGSAA
45	HC118-156/1	SVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYF
46	HC119-139/1	VTVSSAKTTPPSVYPLAPGSA
47	HC119-142/1	VTVSSAKTTPPSVYPLAPGSAAQT
48	HC119-145/1	VTVSSAKTTPPSVYPLAPGSAAQTNSM
49	HC121-139/1	VSSAKTTPPSVYPLAPGSA
50	HC121-142/1	VSSAKTTPPSVYPLAPGSAAQT
51	HC121-145/1	VSSAKTTPPSVYPLAPGSAAQTNSM
52	HC132-184/1	YPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDL
53	HC138-177/1	SAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFP
54	HC146-151/1	VTLGCL

Score



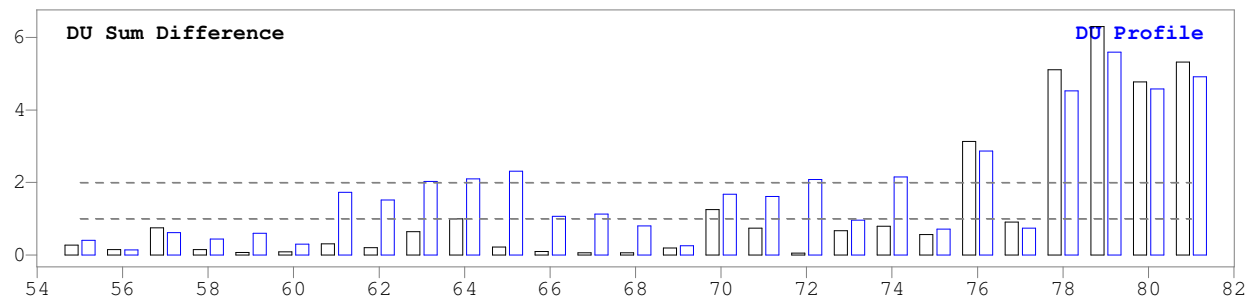
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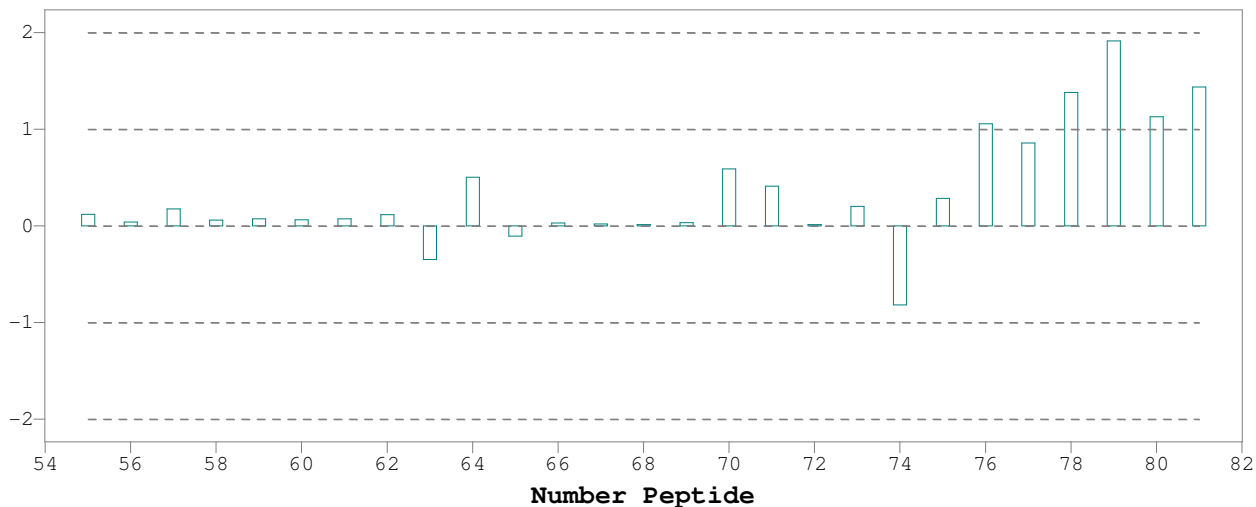
Molecule HC: Peptides with sufficient kinetics data, part 3

No.	Peptide/Range	Sequence
55	HC146-161/1	VTLGCLVKGYFPEPVT
56	HC151-161/1	LVKGYFPEPVT
57	HC152-161/1	VKGYFPEPVT
58	HC152-164/1	VKGYFPEPVTITW
59	HC160-195/1	VTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPS
60	HC161-183/1	TVTWNNSGSLSSGVHTFPAVLQSD
61	HC162-169/1	VTWNSGSL
62	HC162-180/1	VTWNSGSLSSGVHTFPAVL
63	HC163-180/1	TWNSGSLSSGVHTFPAVL
64	HC164-180/1	WNSGSLSSGVHTFPAVL
65	HC165-180/1	NSGSLSSGVHTFPAVL
66	HC170-180/1	SSGVHTFPAVL
67	HC170-180/2	SSGVHTFPAVL
68	HC175-182/1	TFPAVLQS
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69	HC185-190/1	YTLSSS
70	HC185-201/1	YTLSSSVTVPSSTWPSE
71	HC185-202/1	YTLSSSVTVPSSTWPSET
72	HC191-201/1	VTVPSSTWPSE
73	HC191-202/1	VTVPSSTWPSET
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74	HC210-239/1	PASSTKVDKKIVPRDCGCKPCICTVPEVSS
75	HC212-229/1	SSTKVDKKIVPRDCGCKP
76	HC214-225/1	TKVDKKIVPRDC
77	HC219-253/1	KIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTI
78	HC240-251/1	VFIFPPKPKDVL
79	HC240-252/1	VFIFPPKPKDVL
80	HC241-251/1	FIFPPKPKDVL
81	HC241-252/1	FIFPPKPKDVL

Score



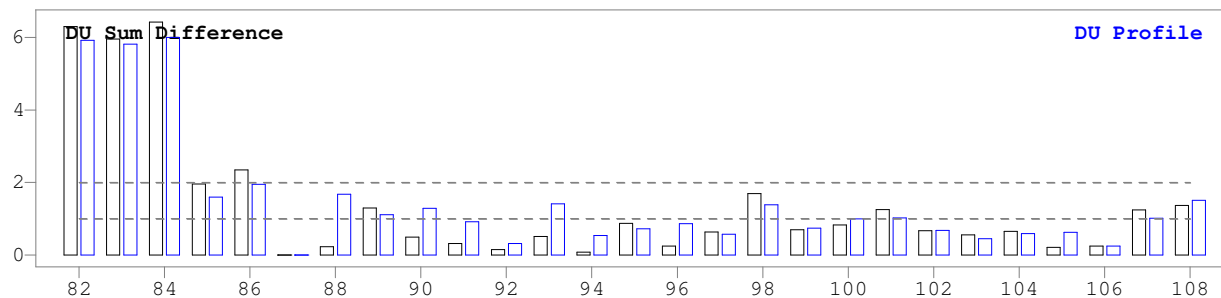
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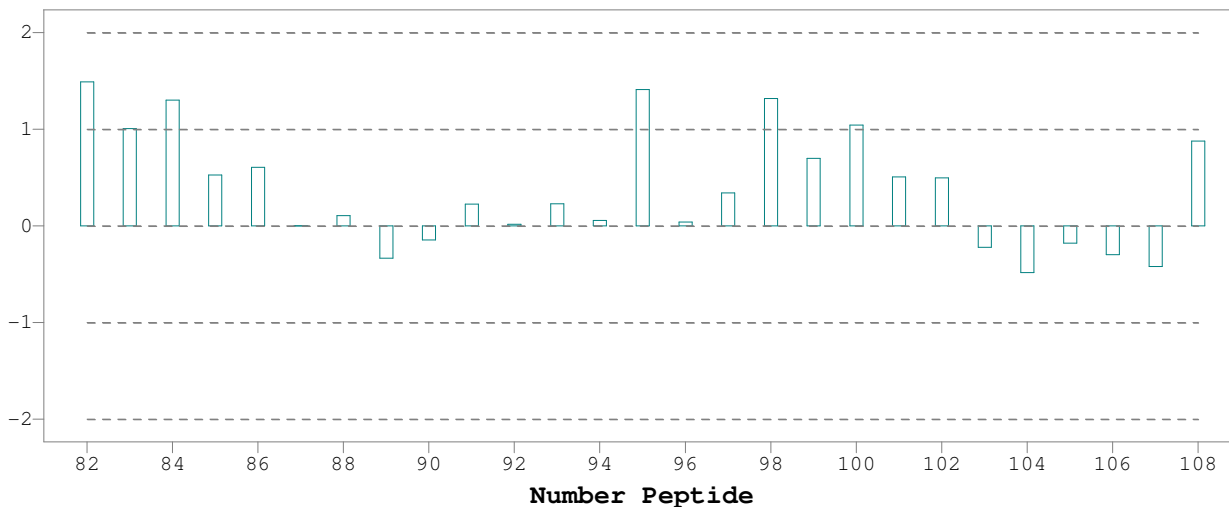
Molecule HC: Peptides with sufficient kinetics data, part 4

No.	Peptide/Range	Sequence
82	HC242-252/1	IFPPKPKDVL
83	HC243-251/1	FPPKPKDVL
84	HC243-252/1	FPPKPKDVL
85	HC252-261/1	TITLTPKVTC
86	HC253-261/1	ITLTPKVTC
87	HC263-274/1	VVDISKDDPEVQ
88	HC263-275/1	VVDISKDDPEVQF
89	HC266-274/1	ISKDDPEVQ
90	HC266-275/1	ISKDDPEVQF
91	HC272-294/1	EVQFSWFVDDDEVHTAQTQPREE
92	HC278-281/1	FVDD
93	HC280-292/1	DDDEVHTAQTQPR
94	HC291-315/1	PREEQFNSTFRSVSELPIMHQDWLN
95	HC297-350/1	NSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAIEKTI SKTKGRPAPQVYT
96	HC301-306/1	RSVSEL
97	HC301-318/1	RSVSELPIMHQDWLNGKE
98	HC307-333/1	PIMHQDWLNGKEFKCRVNSAAFPAIE
99	HC308-340/1	IMHQDWLNGKEFKCRVNSAAFPAIEKTI SKTK
100	HC318-359/1	EFKCRVNSAAFPAIEKTI SKTKGRPAPQVYTI PPPKEQMA
101	HC319-333/1	FKCRVNSAAFPAIE
102	HC326-348/1	AAFPAIEKTI SKTKGRPAPQV
103	HC334-348/1	KTI SKTKGRPAPQV
104	HC334-361/1	KTI SKTKGRPAPQVYTI PPPKEQMAKD
105	HC334-365/1	KTI SKTKGRPAPQVYTI PPPKEQMAKDKVSL
106	HC334-368/1	KTI SKTKGRPAPQVYTI PPPKEQMAKDKVSLTCM
107	HC336-348/1	ISKTGRPAPQV
108	HC342-366/1	RPKAPQVYTI PPPKEQMAKDKVSLT

Score



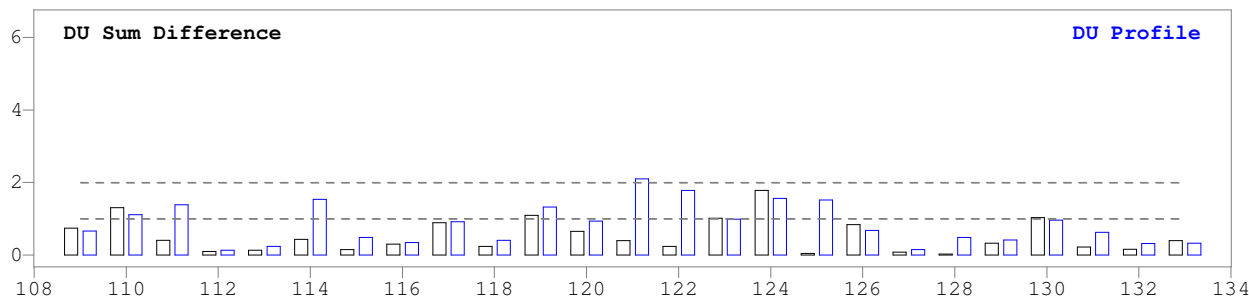
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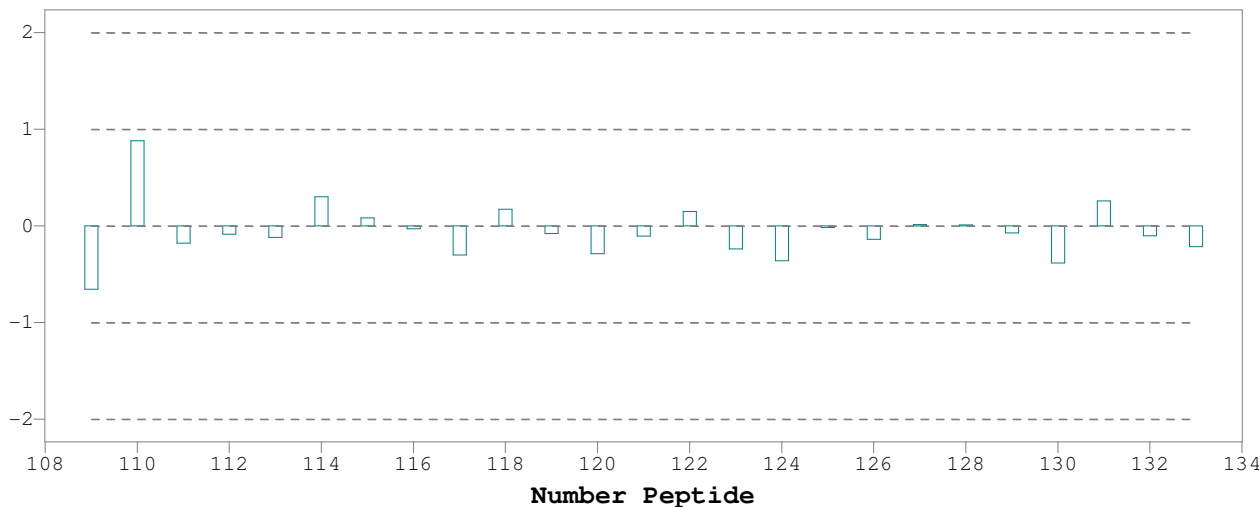
Molecule HC: Peptides with sufficient kinetics data, part 5

No.	Peptide/Range	Sequence
109	HC345-374/1	APQVYTIPPPKEQMAKDKVSLTCMITDFFP
110	HC347-370/1	QVYTIPPPKEQMAKDKVSLTCMIT
111	HC349-365/1	YTIPPPKEQMAKDKVSL
112	HC357-385/1	QMAKDKVSLTCMITDFFPEDITVEWQWNG
113	HC364-393/1	SLTCMITDFFPEDITVEWQWNGQPAENYKN
114	HC367-390/1	CMITDFFPEDITVEWQWNGQPAEN
115	HC368-387/1	MITDFFPEDITVEWQWNGQP
116	HC369-372/1	ITDF
117	HC369-380/1	ITDFFPEDITVE
118	HC372-397/1	FFPEDITVEWQWNGQPAENYKNTQPI
119	HC373-376/1	FPED
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120	HC377-390/1	ITVEWQWNGQPAEN
121	HC381-390/1	WQWNGQPAEN
122	HC381-398/1	WQWNGQPAENYKNTQPI
123	HC390-398/1	NYKNTQPI
124	HC391-398/1	YKNTQPI
125	HC391-404/1	YKNTQPI
126	HC399-404/1	YKNTQPI
127	HC405-410/1	DTDGSY
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127	HC405-410/1	FVYSKL
128	HC407-418/1	YSKLVQKSNWE
129	HC411-417/1	NVQKSNW
130	HC411-422/1	NVQKSNWEAGNT
131	HC411-447/1	NVQKSNWEAGNTFTCSVLHEGLHNNHTEKSLSHSPGK
132	HC426-446/1	SVLHEGLHNNHTEKSLSHSPG
133	HC429-446/1	HEGLHNNHTEKSLSHSPG

Score



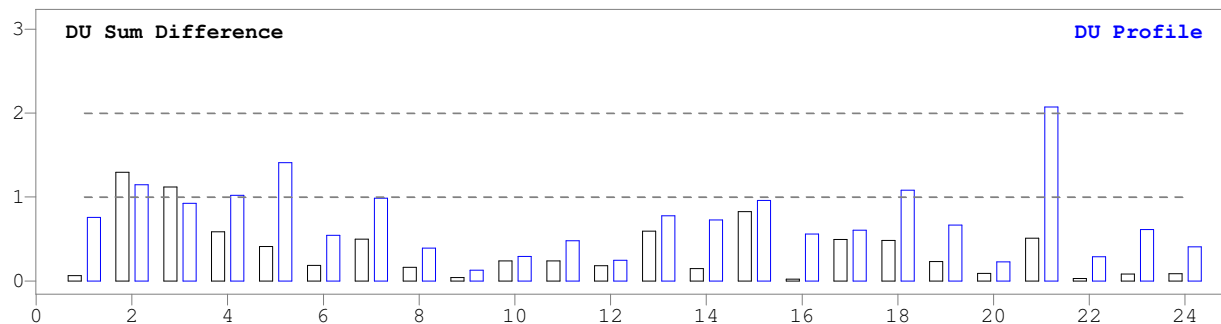
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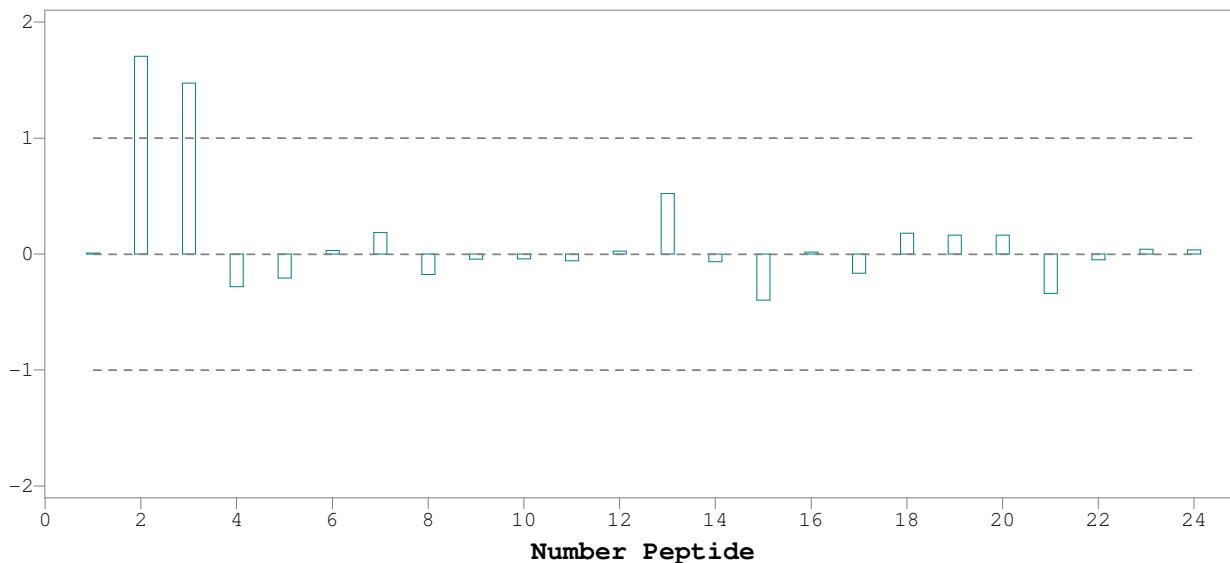
Molecule LC: Peptides with sufficient kinetics data, part 1

No.	Peptide/Range	Sequence
1	LC001-004/1	DIVL
2	LC001-042/1	DIVLTQSPATLSVTPGDSVLSLSCRASQSIENNHLHWYQQKSHE
3	LC001-042/2	DIVLTQSPATLSVTPGDSVLSLSCRASQSIENNHLHWYQQKSHE
4	LC003-018/1	VLTQSPATLSVTPGDS
5	LC004-021/1	LTQSPATLSVTPGDSVSL
6	LC005-011/1	TQSPATL
7	LC005-018/1	TQSPATLSVTPGDS
8	LC005-039/1	TQSPATLSVTPGDSVLSLSCRASQSIENNHLHWYQQK
9	LC10-043/1	TLSVTPGDSVLSLSCRASQSIENNHLHWYQQKSHES
10	LC012-018/1	SVTPGDS
11	LC012-020/1	SVTPGDSVS
12	LC019-023/1	VLSLSC
13	LC019-046/1	VLSLSCRASQSIENNHLHWYQQKSHESPRLL
14	LC021-032/1	LSCRASQSIENN
15	LC022-035/1	SCRASQSIENNLHW
16	LC022-046/1	SCRASQSIENNHLHWYQQKSHESPRLL
17	LC024-033/1	RASQSIENNL
18	LC024-035/1	RASQSIENNLHW
19	LC024-046/1	RASQSIENNHLHWYQQKSHESPRLL
20	LC027-084/1	QSIENNHLHWYQQKSHESPRLLIKYASQSIENSGIPSRFSGSGSGTDFTLINSVETEDFG
21	LC028-047/1	SIENNHLHWYQQKSHESPRLL
22	LC028-084/1	SIENNHLHWYQQKSHESPRLLIKYASQSIENSGIPSRFSGSGSGTDFTLINSVETEDFG
23	LC030-046/1	ENNLHWYQQKSHESPRLL
24	LC033-046/1	LHWYQQKSHESPRLL

Score



DU Sum Difference (u)

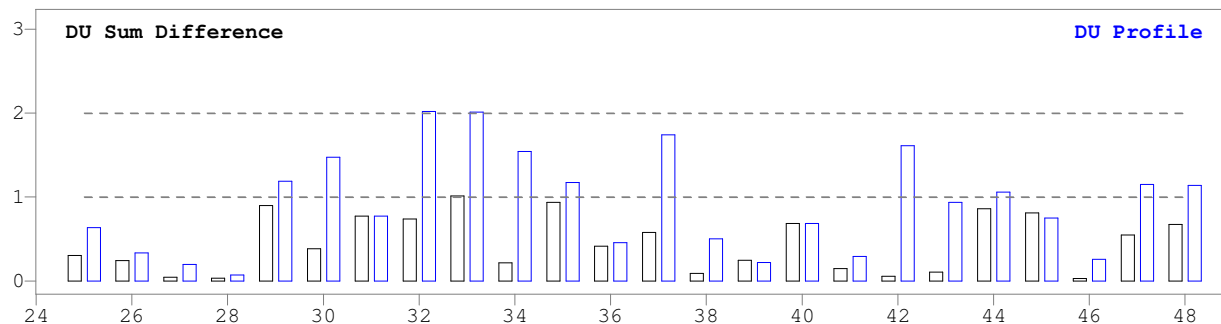




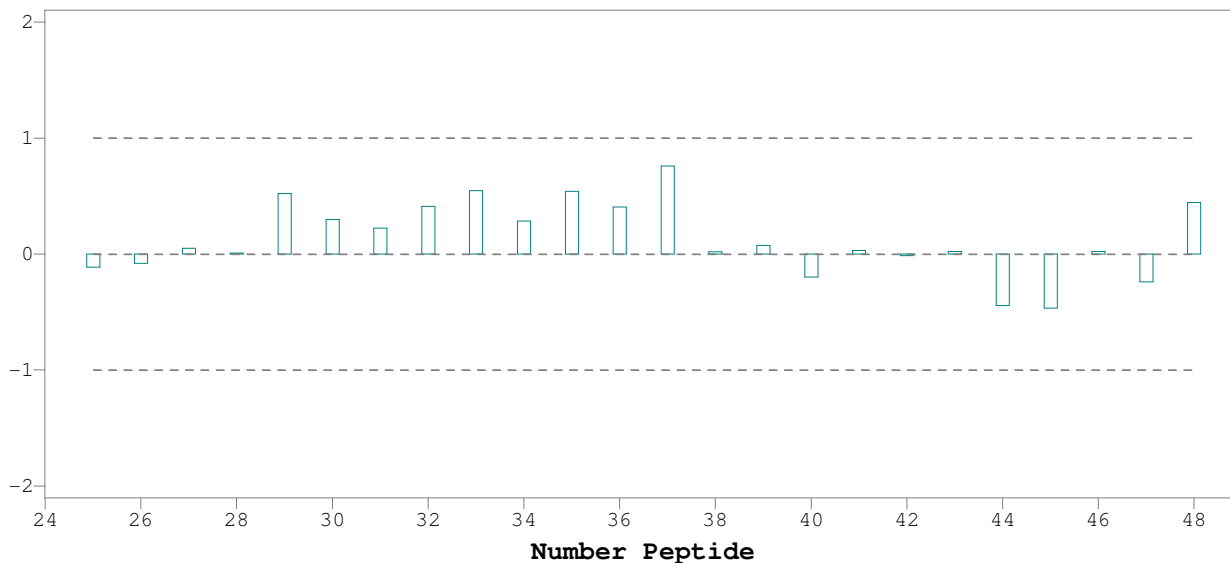
Molecule LC: Peptides with sufficient kinetics data, part 2

No.	Peptide/Range	Sequence
25	LC034-046/1	HWYQQKSHESPRL
26	LC036-046/1	YQQKSHESPRL
27	LC041-078/1	HESPRLLIKYASQSIGIPSRFSGSGSGTDFTLSINSV
28	LC047-053/1	LIKYASQ
29	LC047-062/1	LIKYASQSIGIPSRF
30	LC047-071/1	LIKYASQSIGIPSRFSGSGSGTDF
31	LC054-062/1	SISGIPSRF
32	LC054-070/1	SISGIPSRFSGSGSGTD
33	LC054-071/1	SISGIPSRFSGSGSGTDF
34	LC054-095/1	SISGIPSRFSGSGSGTDFTLSINSVETEDFGMYFCQQNSWP
35	LC055-070/1	ISGIPSRFSGSGSGTD
36	LC055-085/1	ISGIPSRFSGSGSGTDFTLSINSVETEDFGM
37	LC059-100/1	PSRFSGSGSGTDFTLSINSVETEDFGMYFCQQNSWPLTFGA
38	LC071-077/1	FTLSINS
39	LC071-079/1	FTLSINSVE
40	LC072-079/1	TLSINSVE
41	LC074-079/1	SINSVE
42	LC078-085/1	VETEDFGM
43	LC080-086/1	TEDFGMY
44	LC086-101/1	YFCQQNSWPLTFGAG
45	LC086-104/1	YFCQQNSWPLTFGAGTKL
46	LC086-106/1	YFCQQNSWPLTFGAGTKLEL
47	LC087-101/1	FCQQNSWPLTFGAG
48	LC087-104/1	FCQQNSWPLTFGAGTKL

Score



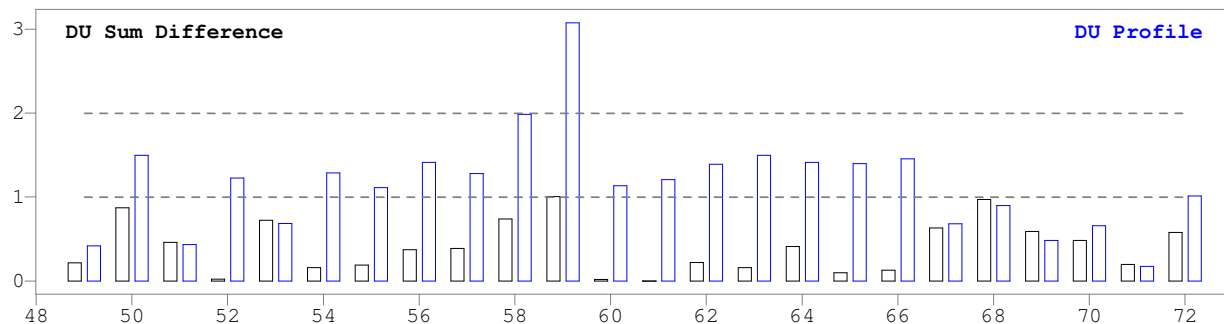
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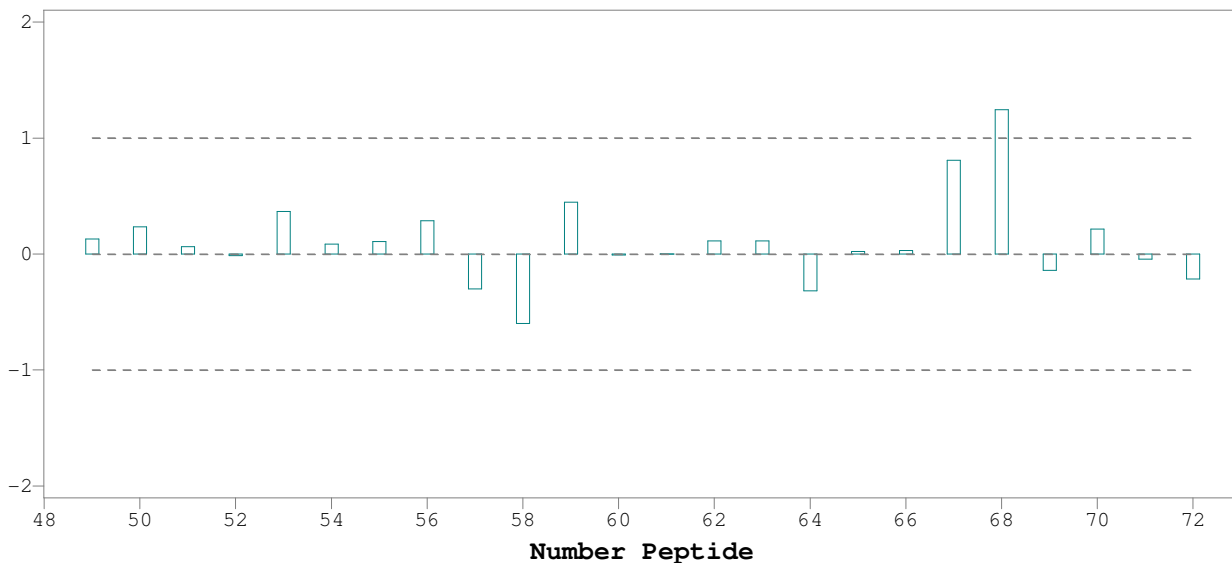
Molecule LC: Peptides with sufficient kinetics data, part 3

No.	Peptide/Range	Sequence
49	LC087-106/1	FCQQSNSWPLTFGAGTKLEL
50	LC098-106/1	FGAGTKLEL
51	LC102-106/1	TKLEL
52	LC104-124/1	LELKRADAAPTVSIFPPSSEQ
53	LC105-123/1	ELKRADAAPTVSIFPPSSE
54	LC105-124/1	ELKRADAAPTVSIFPPSSEQ
55	LC105-125/1	ELKRADAAPTVSIFPPSSEQL
56	LC105-131/1	ELKRADAAPTVSIFPPSSEQLTSGGAS
57	LC105-131/2	ELKRADAAPTVSIFPPSSEQLTSGGAS
58	LC105-132/1	ELKRADAAPTVSIFPPSSEQLTSGGASV
59	LC107-122/1	KRADAAPTVSIFPPSS
60	LC107-123/1	KRADAAPTVSIFPPSSE
61	LC107-124/1	KRADAAPTVSIFPPSSEQ
62	LC107-125/1	KRADAAPTVSIFPPSSEQL
63	LC107-131/1	KRADAAPTVSIFPPSSEQLTSGGAS
64	LC107-131/2	KRADAAPTVSIFPPSSEQLTSGGAS
65	LC110-120/1	DAAPTVSIFPP
66	LC110-120/2	DAAPTVSIFPP
67	LC111-153/1	AAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGS
68	LC111-153/2	AAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGS
69	LC124-131/1	QLTSGGAS
70	LC132-145/1	VVCFLNNFYPKDIN
71	LC136-143/1	LNNFYPKD
72	LC136-146/1	LNNFYPKDINV

Score



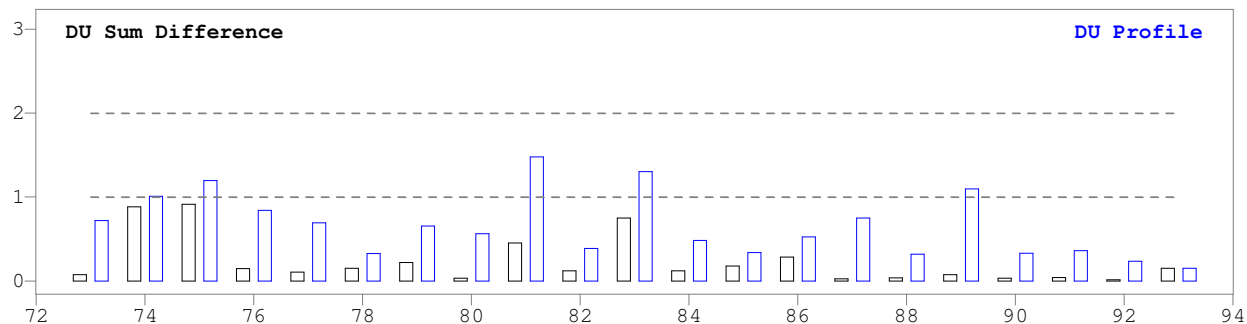
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Molecule LC: Peptides with sufficient kinetics data, part 4

No.	Peptide/Range	Sequence
73	LC136-154/1	LNNFYPKDINVKWKIDGSE
74	LC137-161/1	NNFYPKDINVKWKIDGSERQNGVLN
75	LC140-161/1	YPKDINVKWKIDGSERQNGVLN
76	LC146-160/1	VKWKIDGSERQNGVL
77	LC147-160/1	KWKIDGSERQNGVL
78	LC152-162/1	GSERQNGVLNS
79	LC155-160/1	RQNGVL
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80	LC161-172/1	NSWTDQDSKDST
81	LC161-175/1	NSWTDQDSKDYISM
82	LC161-178/1	NSWTDQDSKDYISMSS
83	LC161-179/1	NSWTDQDSKDYISMSSL
84	LC164-189/1	TDQDSKDYISMSSLTLTKDEYERH
85	LC173-179/1	YSMSSL
86	LC173-199/1	YSMSSLTLTKDEYERHNSYTCEATHK
87	LC174-199/1	SMSSLTLTKDEYERHNSYTCEATHK
88	LC179-195/1	LTLTKDEYERHNSYTCE
89	LC179-206/1	LTLTKDEYERHNSYTCEATHKTSTSPIV
90	LC180-195/1	TLTKDEYERHNSYTCE
91	LC180-214/1	TLTKDEYERHNSYTCEATHKTSTSPIVKSFNREK
92	LC182-195/1	TKDEYERHNSYTCE
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93	LC196-214/1	ATHKTSTSPIVKSFNREK

Score



DU Sum Difference (u)

