Supplementary Material for

Quod erat demonstrandum? No restriction endonuclease fold in MIF

Lakshminarayan M. Iyer and L. Aravind

lakshmin@mail.nih.gov / aravind@mail.nih.gov

National Center for Biotechnology Information,

National Library of Medicine,

National Institutes of Health,

Bethesda, MD 20894

Hit list of Dali Search using MIF (PDB:1gd0) as query.

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# Query: mol1A
# No:  Chain   Z    rmsd lali nres  %id PDB  Description
   1:  1gd0-A 24.7  0.0  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
   2:  1gcz-A 23.9  0.1  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
   3:  3l5v-C 23.9  0.1  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
   4:  3l5r-C 23.9  0.1  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
   5:  3l5p-C 23.8  0.1  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
   6:  1gcz-C 23.8  0.2  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
   7:  3l5t-C 23.8  0.1  117   117  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
   8:  3l5s-C 23.8  0.1  117   117  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
   9:  1gd0-C 23.8  0.2  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  10:  3l5r-B 23.7  0.2  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  11:  3jsg-A 23.7  0.2  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  13:  3l5s-B 23.6  0.2  117   117  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  14:  3l5v-A 23.6  0.2  117   117  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  15:  3jsf-C 23.5  0.2  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  16:  3l5p-B 23.5  0.2  117   117  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  18:  3hof-A 23.4  0.3  118   118  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  20:  3jsf-B 23.4  0.2  117   117  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  21:  5eiz-B 23.4  0.2  114   114   99   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  22:  3djh-B 23.4  0.2  114   114  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  45:  3l5v-B 23.3  0.2  114   114  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  56:  3l5u-A 23.2  0.3  116   116  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  63:  4wrb-B 23.2  0.2  114   114  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  64:  4tru-B 23.2  0.2  114   114   98   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  65:  3u18-B 23.2  0.2  114   114  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  68:  5bsi-G 23.2  0.2  114   114   99   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  69:  5eiz-A 23.2  0.2  114   114   99   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  70:  5j7p-C 23.2  0.2  114   114  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  72:  3l5s-A 23.2  0.2  114   114  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  74:  5bsi-B 23.2  0.2  114   114   99   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  75:  5bs9-B 23.2  0.2  114   114   99   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  77:  3djh-A 23.2  0.2  114   114  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  78:  3wns-A 23.2  0.2  114   114  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  83:  5bsi-A 23.2  0.2  114   114   99   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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  87:  4oyq-B 23.2  0.2  114   114  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  88:  3l5t-A 23.2  0.2  114   114  100   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
  89:  5eiz-C 23.2  0.2  114   114   99   MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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91:	4k9g-C	23.2	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
92:	3ce4-C	23.2	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
93:	1ljt-B	23.2	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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95:	3l5u-B	23.1	0.3	115	115	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
96:	3ijg-C	23.1	0.2	114	115	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
97:	5bsc-C	23.1	0.2	114	114	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
98:	4p01-C	23.1	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
99:	4trf-C	23.1	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
100:	4p01-B	23.1	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
101:	4etg-A	23.1	0.2	114	114	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
102:	4plu-A	23.1	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
103:	4gru-A	23.1	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
104:	5cg4-C	23.1	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
105:	4p01-A	23.1	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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108:	3smb-A	23.1	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
109:	5j7q-A	23.1	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
110:	4eui-B	23.1	0.2	114	114	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
111:	4gru-C	23.1	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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122:	5bsj-A	23.1	0.3	114	114	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
123:	5b4o-B	23.1	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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138:	5cg4-A	23.0	0.2	114	115	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
139:	3wnr-C	23.0	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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141:	3b9s-B	23.0	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
142:	4oyq-A	23.0	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
143:	4k9g-A	23.0	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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149:	3dji-A	23.0	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
150:	4tru-A	23.0	0.2	113	113	98	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
151:	4xx8-C	23.0	0.2	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
152:	1cgq-B	23.0	0.2	114	115	99	MOLECULE: PROTEIN (MACROPHAGE MIGRATION INHIBITORY FACTOR);
153:	1cgq-A	23.0	0.2	114	115	99	MOLECULE: PROTEIN (MACROPHAGE MIGRATION INHIBITORY FACTOR);
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156:	4eui-C	22.9	0.3	114	114	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
157:	4p0h-B	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
158:	3dji-B	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
159:	5hvt-A	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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163:	4pkz-C	22.9	0.3	114	114	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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165:	1mff-B	22.9	0.2	114	114	89	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
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167:	4grn-C	22.9	0.2	114	116	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
168:	4grr-A	22.9	0.2	114	116	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
169:	4grn-A	22.9	0.2	114	116	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
170:	4grq-B	22.9	0.2	114	116	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
171:	4gru-B	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
172:	4wr8-E	22.9	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
173:	3u18-A	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
174:	2gdg-C	22.9	0.3	114	114	89	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
175:	3dji-C	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
176:	4wr8-A	22.9	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
177:	5hvs-A	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
178:	3dji-F	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
179:	4trf-B	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
180:	2gdg-A	22.9	0.3	114	114	89	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
181:	2ooh-A	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
182:	5b4o-A	22.9	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
183:	1mff-A	22.8	0.3	114	114	89	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
184:	5j7p-B	22.8	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;

185:	4osf-C	22.8	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
186:	4osf-B	22.8	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
187:	1mfi-B	22.8	0.3	114	114	89	MOLECULE: PROTEIN (MACROPHAGE MIGRATION INHIBITORY FACTOR);
188:	3b9s-A	22.8	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
189:	4wr8-H	22.8	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
190:	1mfi-C	22.8	0.2	114	114	89	MOLECULE: PROTEIN (MACROPHAGE MIGRATION INHIBITORY FACTOR);
191:	3smc-B	22.8	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
192:	5hvs-C	22.8	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
193:	2gdg-B	22.8	0.3	114	114	89	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
194:	4wr8-J	22.8	0.2	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
195:	4wr8-D	22.8	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
196:	4wr8-G	22.8	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
197:	3smb-B	22.8	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
198:	3dji-E	22.8	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
199:	4xx8-B	22.8	0.2	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
200:	4xx8-A	22.8	0.2	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
201:	5hvv-B	22.8	0.2	113	113	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
202:	5hvv-C	22.8	0.2	113	113	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
203:	4grp-A	22.8	0.2	114	118	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
204:	4grp-C	22.8	0.3	114	117	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
205:	4plu-B	22.8	0.2	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
206:	4z1t-B	22.8	0.3	113	113	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
207:	5hvv-A	22.8	0.2	113	113	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
208:	4grp-B	22.7	0.2	114	117	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
209:	4gro-H	22.7	0.2	114	117	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
210:	4gro-G	22.7	0.2	114	117	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
211:	4gro-F	22.7	0.3	114	117	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
212:	4grr-C	22.7	0.3	114	116	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
213:	4wr8-O	22.7	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
214:	4wr8-L	22.7	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
215:	4pkk-C	22.7	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
216:	3wnt-A	22.7	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
217:	4wr8-C	22.7	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
218:	4z1u-C	22.7	0.2	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
219:	4wr8-I	22.7	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
220:	4pkk-A	22.7	0.3	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
221:	4z1u-D	22.7	0.2	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
222:	4z1u-A	22.7	0.2	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
223:	4grq-A	22.7	0.3	114	116	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
224:	4grn-B	22.7	0.3	114	116	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
225:	1gif-C	22.7	0.3	114	115	100	MOLECULE: GLYCOSYLATION-INHIBITING FACTOR;
226:	1gif-A	22.7	0.3	114	115	100	MOLECULE: GLYCOSYLATION-INHIBITING FACTOR;
227:	3wnt-B	22.7	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
228:	4f2k-C	22.7	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
229:	4z1u-F	22.7	0.2	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
230:	1mff-C	22.6	0.3	114	114	89	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
231:	4pkz-A	22.6	0.3	112	112	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
232:	4gro-E	22.6	0.3	114	117	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
233:	4osf-A	22.6	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
234:	4pkk-B	22.6	0.4	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
235:	4gro-A	22.6	0.3	114	117	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
236:	4gro-C	22.6	0.3	114	117	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
237:	4gro-B	22.6	0.3	114	117	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
238:	4gro-D	22.6	0.3	114	117	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
239:	1gif-B	22.6	0.3	114	115	100	MOLECULE: GLYCOSYLATION-INHIBITING FACTOR;
240:	4f2k-B	22.6	0.4	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
241:	4f2k-A	22.6	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
242:	4wr8-R	22.6	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
243:	4z1u-E	22.6	0.2	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
244:	4z1u-B	22.6	0.3	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
245:	3dji-D	22.5	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
246:	4pkz-B	22.5	0.3	113	113	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
247:	4wr8-F	22.5	0.3	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
248:	3wnt-C	22.5	0.4	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
249:	1mfi-A	22.4	0.4	114	114	89	MOLECULE: PROTEIN (MACROPHAGE MIGRATION INHIBITORY FACTOR);
250:	4z15-C	22.4	0.3	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
251:	4z15-B	22.4	0.3	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
252:	4z15-A	22.4	0.3	113	113	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
253:	1mif-C	22.4	0.3	114	114	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
254:	1mif-B	22.4	0.4	114	114	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
255:	1mif-A	22.3	0.4	114	114	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
256:	1uiz-C	22.0	0.4	114	115	68	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
257:	1uiz-D	22.0	0.4	114	115	68	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
258:	1uiz-A	21.9	0.4	114	115	68	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
259:	1uiz-B	21.9	0.4	114	115	68	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
260:	3b9s-C	21.8	0.7	114	114	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
261:	1hfo-A	20.5	0.7	113	113	41	MOLECULE: MIGRATION INHIBITORY FACTOR;
262:	2os5-C	20.3	1.6	118	118	32	MOLECULE: ACEMIF;
263:	3rf5-C	20.3	1.0	116	116	33	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
264:	3rf4-C	20.3	0.8	115	116	33	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
265:	3rf4-B	20.3	0.8	115	116	33	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
266:	3rf5-B	20.3	0.8	115	116	33	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
267:	1hfo-C	20.3	0.7	113	113	41	MOLECULE: MIGRATION INHIBITORY FACTOR;
268:	1hfo-D	20.3	0.7	113	113	41	MOLECULE: MIGRATION INHIBITORY FACTOR;
269:	1hfo-E	20.3	0.7	113	113	41	MOLECULE: MIGRATION INHIBITORY FACTOR;
270:	3rf4-A	20.2	1.0	116	116	33	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
271:	3rf5-A	20.2	1.0	116	116	33	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
272:	1hfo-F	20.2	0.7	113	113	41	MOLECULE: MIGRATION INHIBITORY FACTOR;
273:	2os5-A	20.1	1.0	116	118	33	MOLECULE: ACEMIF;
274:	2os5-B	20.1	1.7	118	118	32	MOLECULE: ACEMIF;
275:	2os5-D	20.1	1.7	118	118	32	MOLECULE: ACEMIF;
276:	1fim-A	20.0	1.2	103	103	87	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
277:	2xcz-A	19.7	1.2	114	114	34	MOLECULE: POSSIBLE ATLS1-LIKE LIGHT-INDUCIBLE PROTEIN;
278:	1hfo-B	19.0	1.0	110	113	41	MOLECULE: MIGRATION INHIBITORY FACTOR;
279:	4gum-C	19.0	1.2	108	112	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;

280:	3kan-C	18.8	1.3	116	117	32	MOLECULE: D-DOPACHROME TAUTOMERASE;
281:	4gum-H	18.8	0.9	99	101	100	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
282:	4q3f-A	18.7	1.3	116	117	32	MOLECULE: D-DOPACHROME DECARBOXYLASE;
283:	4q3f-C	18.7	1.3	116	117	32	MOLECULE: D-DOPACHROME DECARBOXYLASE;
284:	3kan-A	18.7	1.3	116	117	32	MOLECULE: D-DOPACHROME TAUTOMERASE;
285:	1dpt-A	18.6	1.4	116	117	32	MOLECULE: D-DOPACHROME TAUTOMERASE;
286:	3kan-B	18.6	1.2	115	117	32	MOLECULE: D-DOPACHROME TAUTOMERASE;
287:	4q3f-B	18.6	1.4	116	117	32	MOLECULE: D-DOPACHROME DECARBOXYLASE;
288:	1dpt-C	18.6	1.3	116	117	32	MOLECULE: D-DOPACHROME TAUTOMERASE;
289:	1dpt-B	18.6	1.4	116	117	32	MOLECULE: D-DOPACHROME TAUTOMERASE;
290:	4gum-I	18.6	1.4	110	112	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
291:	4gum-F	18.6	1.3	107	108	93	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
292:	3ker-A	18.5	1.4	116	117	28	MOLECULE: D-DOPACHROME DECARBOXYLASE;
293:	3ker-B	18.5	1.4	116	117	28	MOLECULE: D-DOPACHROME DECARBOXYLASE;
294:	3ker-C	18.5	1.4	116	117	28	MOLECULE: D-DOPACHROME DECARBOXYLASE;
295:	3ker-D	18.5	1.4	116	117	28	MOLECULE: D-DOPACHROME DECARBOXYLASE;
296:	4gum-E	18.2	1.5	107	111	93	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
297:	4gum-D	18.2	1.7	107	110	99	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
298:	3gac-A	18.0	1.4	113	115	30	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE
299:	3gac-C	17.9	1.5	115	117	31	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE
300:	3gad-F	17.9	1.5	115	117	31	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
301:	3gad-C	17.9	1.4	115	117	31	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
302:	3gac-F	17.9	1.4	114	116	31	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE
303:	3gad-D	17.9	1.4	113	115	30	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
304:	3gac-D	17.9	1.4	113	115	30	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE
305:	3gac-E	17.8	1.4	113	115	30	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE
306:	3gad-A	17.8	1.5	113	115	30	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
307:	4gum-B	17.8	1.4	109	114	97	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
308:	4gum-A	17.8	1.4	109	114	97	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
309:	3gad-E	17.7	1.5	114	117	31	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
310:	3gac-B	17.7	1.4	114	116	31	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE
311:	4dh4-A	17.6	1.4	112	114	28	MOLECULE: MIF;
312:	3gad-B	17.5	1.4	113	115	30	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
313:	4gum-G	16.3	1.6	106	110	96	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
314:	1vw5-j	15.8	1.8	111	114	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
315:	1vw6-B	15.8	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
316:	1vw6-x	15.8	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
317:	1vw6-X	15.8	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
318:	1vw5-b	15.8	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
319:	1vw5-p	15.8	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
320:	1vw5-P	15.8	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
321:	1vw5-V	15.8	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
322:	1vw6-b	15.7	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
323:	1vw6-f	15.7	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
324:	1vw6-3	15.7	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
325:	1vw5-h	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
326:	1vw5-F	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
327:	1vw5-L	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
328:	1vw5-R	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
329:	1vw5-D	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
330:	1vw5-r	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
331:	1vw5-B	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
332:	1vw6-z	15.7	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
333:	1vw6-1	15.7	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
334:	1vw6-N	15.7	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
335:	1vw6-R	15.7	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
336:	1vw6-H	15.7	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
337:	1vw5-N	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
338:	1vw5-T	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
339:	1vw6-L	15.7	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
340:	1vw6-F	15.7	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
341:	1vw5-v	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
342:	1vw5-l	15.7	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
343:	3b64-A	15.7	1.8	110	112	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE
344:	1vw5-Z	15.6	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
345:	1vw6-9	15.6	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
346:	1vw6-V	15.6	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
347:	1vw6-5	15.6	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
348:	1vw5-d	15.6	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
349:	1vw5-H	15.6	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
350:	1vw5-X	15.6	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
351:	1vw6-J	15.6	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
352:	1vw6-d	15.6	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
353:	3fwu-A	15.6	1.8	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE
354:	2wkf-A	15.6	1.7	99	101	28	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
355:	1vw5-t	15.5	1.8	110	113	19	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
356:	1vw6-7	15.5	1.9	110	113	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
357:	3t5s-A	15.3	1.3	93	97	35	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
358:	1vw6-Z	15.3	1.8	109	113	20	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
359:	1vw6-h	15.3	1.8	109	113	20	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
360:	1vw6-P	15.3	1.8	109	113	20	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
361:	1vw5-f	15.3	1.8	109	113	20	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
362:	1vw6-T	15.2	1.8	109	113	20	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
363:	1vw5-J	15.2	1.8	109	113	20	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
364:	1vw5-n	15.2	1.8	109	113	20	MOLECULE: INTEGRON GENE CASSETTE PROTEIN;
365:	1vw6-D	15.2	1.8	109	113	20	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
366:	3fwt-A	14.6	1.9	110	116	19	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE
367:	2wkb-B	14.0	2.3	107	111	29	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
368:	2wkb-D	13.9	2.3	105	111	29	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
369:	2wkb-E	13.8	2.3	109	116	29	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
370:	2wkb-C	13.7	2.3	109	115	29	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
371:	2wkb-F	13.7	2.2	109	115	28	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
372:	2wkf-B	13.5	2.4	99	103	26	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
373:	4p7s-B	13.5	1.8	96	99	25	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
374:	4p7m-A	13.4	4.2	102	104	26	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE

375:	4p7m-B	13.4	1.8	96	99	25	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
376:	4p7s-A	13.4	4.2	102	104	25	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
377:	2wkb-A	13.0	2.3	100	106	28	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR;
378:	4p7s-C	12.6	2.0	88	92	24	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
379:	3n4h-A	12.2	2.5	111	118	10	MOLECULE: PUTATIVE TAUTOMERASE;
380:	3n4d-A	12.0	2.4	112	145	10	MOLECULE: PUTATIVE TAUTOMERASE;
381:	4p7m-C	11.9	2.1	89	93	28	MOLECULE: MACROPHAGE MIGRATION INHIBITORY FACTOR-LIKE PROTE
382:	3n4g-B	11.8	2.4	113	143	11	MOLECULE: PUTATIVE TAUTOMERASE;
383:	2flt-A	11.7	2.6	111	117	9	MOLECULE: CIS-3-CHLOROACRYLIC ACID DEHALOGENASE;
384:	1mww-B	11.6	2.5	113	118	14	MOLECULE: HYPOTHETICAL PROTEIN HI1388.1;
385:	3mf8-A	11.6	2.6	111	117	9	MOLECULE: CIS-3-CHLOROACRYLIC ACID DEHALOGENASE;
386:	1mww-A	11.5	2.5	112	120	14	MOLECULE: HYPOTHETICAL PROTEIN HI1388.1;
387:	1mww-C	11.5	2.5	113	120	14	MOLECULE: HYPOTHETICAL PROTEIN HI1388.1;
388:	3n4d-D	11.4	2.4	112	145	10	MOLECULE: PUTATIVE TAUTOMERASE;
389:	3mjz-G	11.3	2.9	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
390:	4lho-C	11.3	2.9	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
391:	4lhp-B	11.3	3.0	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
392:	4lhp-F	11.3	2.9	114	130	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
393:	3mjz-F	11.3	2.9	114	130	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
394:	3mlc-D	11.3	2.8	114	129	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
395:	3mlc-C	11.3	3.0	115	129	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
396:	3n4d-B	11.3	2.4	113	145	10	MOLECULE: PUTATIVE TAUTOMERASE;
397:	3n4g-C	11.3	2.3	112	143	12	MOLECULE: PUTATIVE TAUTOMERASE;
398:	4lhp-G	11.3	2.9	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
399:	3n4d-C	11.2	2.3	112	146	10	MOLECULE: PUTATIVE TAUTOMERASE;
400:	3mjz-J	11.2	2.9	114	131	8	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
401:	3mjz-C	11.2	2.9	114	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
402:	4lhp-L	11.2	3.0	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
403:	4lho-E	11.2	2.9	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
404:	4lho-B	11.2	3.0	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
405:	4lhp-D	11.2	2.9	114	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
406:	3mjz-I	11.2	3.0	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
407:	4lhp-E	11.2	2.9	114	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
408:	4lhp-H	11.2	2.8	114	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
409:	4lhp-I	11.2	3.0	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
410:	4lho-A	11.2	3.0	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
411:	4lhp-K	11.2	2.9	115	130	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
412:	3mlc-B	11.2	2.9	115	129	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
413:	3mjz-K	11.2	2.9	115	130	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
414:	3n4g-A	11.2	2.4	113	146	11	MOLECULE: PUTATIVE TAUTOMERASE;
415:	3mjz-E	11.2	3.0	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
416:	4lho-D	11.2	2.9	114	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
417:	4lhp-C	11.2	2.9	114	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
418:	4lhp-J	11.2	3.0	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
419:	3mjz-H	11.2	2.7	114	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
420:	2aal-F	11.2	2.8	112	129	21	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
421:	3mjz-B	11.2	2.9	114	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
422:	3mjz-L	11.2	2.9	114	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
423:	2aal-E	11.2	2.8	112	129	21	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
424:	3mlc-E	11.2	2.9	115	129	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
425:	2aal-A	11.2	2.8	112	129	21	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
426:	2aal-D	11.2	2.9	112	129	21	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
427:	2aal-C	11.2	2.9	112	129	21	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
428:	3mjz-A	11.1	3.0	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
429:	3mjz-D	11.1	2.9	114	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
430:	4lhp-A	11.1	2.9	115	131	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
431:	2aag-A	11.1	2.9	112	129	21	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
432:	2aag-F	11.1	3.0	113	129	20	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
433:	3mlc-A	11.1	3.0	115	129	9	MOLECULE: FG41 MALONATE SEMIALDEHYDE DECARBOXYLASE;
434:	2aag-E	11.1	3.0	113	129	20	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
435:	2aal-B	11.1	2.9	112	130	21	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
436:	2aag-B	11.1	3.0	113	130	20	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
437:	2aag-D	11.1	3.0	113	129	20	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
438:	2aag-C	11.1	3.0	113	129	20	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
439:	3n4d-G	10.9	2.5	112	145	10	MOLECULE: PUTATIVE TAUTOMERASE;
440:	3n4d-F	10.9	2.5	113	145	10	MOLECULE: PUTATIVE TAUTOMERASE;
441:	3n4d-H	10.9	2.5	113	140	10	MOLECULE: PUTATIVE TAUTOMERASE;
442:	2aaj-A	10.9	3.0	113	129	19	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
443:	2aaj-B	10.9	3.0	113	129	19	MOLECULE: MALONATE SEMIALDEHYDE DECARBOXYLASE;
444:	2flz-B	10.8	2.6	113	145	9	MOLECULE: CIS-3-CHLOROACRYLIC ACID DEHALOGENASE;
445:	3n4d-I	10.7	2.5	113	145	10	MOLECULE: PUTATIVE TAUTOMERASE;
446:	3mf7-A	10.7	2.7	112	118	8	MOLECULE: CIS-3-CHLOROACRYLIC ACID DEHALOGENASE;
447:	2flz-A	10.6	2.6	113	147	11	MOLECULE: CIS-3-CHLOROACRYLIC ACID DEHALOGENASE;
448:	3n4d-E	10.6	2.6	114	145	10	MOLECULE: PUTATIVE TAUTOMERASE;
449:	2flz-C	10.4	2.7	114	145	9	MOLECULE: CIS-3-CHLOROACRYLIC ACID DEHALOGENASE;
450:	4nwp-H	10.2	2.8	102	117	15	MOLECULE: PUTATIVE UNCHARACTERIZED PROTEIN;
451:	4nwp-E	10.1	2.7	101	118	15	MOLECULE: PUTATIVE UNCHARACTERIZED PROTEIN;
452:	4nwp-G	10.1	2.7	101	118	15	MOLECULE: PUTATIVE UNCHARACTERIZED PROTEIN;
453:	1u9d-B	10.0	2.6	104	122	7	MOLECULE: HYPOTHETICAL PROTEIN VC0714;
454:	1u9d-A	10.0	2.6	104	122	7	MOLECULE: HYPOTHETICAL PROTEIN VC0714;
455:	4nwp-F	10.0	2.7	101	118	15	MOLECULE: PUTATIVE UNCHARACTERIZED PROTEIN;
456:	4nwq-B	9.9	2.8	102	121	15	MOLECULE: PUTATIVE UNCHARACTERIZED PROTEIN PH0671;
457:	3e6q-B	9.8	2.7	101	126	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
458:	3e6q-I	9.8	2.6	100	126	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
459:	3e6q-E	9.7	2.7	101	127	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
460:	3e6q-K	9.7	2.7	101	127	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
461:	3e6q-G	9.7	2.6	102	126	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
462:	3e6q-L	9.7	2.5	101	127	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
463:	3e6q-J	9.7	2.5	101	127	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
464:	3e6q-F	9.7	2.7	100	128	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
465:	3e6q-A	9.7	2.5	102	126	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
466:	3e6q-C	9.7	2.7	103	126	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
467:	3e6q-H	9.7	2.6	102	126	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER
468:	1otg-A	9.5	2.8	104	125	13	MOLECULE: 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMERASE;
469:	3e6q-D	9.5	2.7	103	128	14	MOLECULE: PUTATIVE 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMER

470:	1otg-B	9.5	2.9	104	125	13	MOLECULE: 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMERASE;
471:	1otg-C	9.4	2.9	104	125	13	MOLECULE: 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMERASE;
472:	4jcu-B	9.2	2.8	101	130	10	MOLECULE: 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMERASE;
473:	4jcu-C	9.0	2.8	101	134	10	MOLECULE: 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMERASE;
474:	4jcu-A	9.0	2.9	101	134	10	MOLECULE: 5-CARBOXYMETHYL-2-HYDROXYMUCONATE ISOMERASE;
475:	4u5p-C	8.9	2.7	108	141	12	MOLECULE: RHCC;
476:	4u5r-A	8.8	3.3	112	151	12	MOLECULE: RHCC;
477:	4u5p-A	8.8	2.8	108	140	12	MOLECULE: RHCC;
478:	4u5r-C	8.7	3.2	112	151	12	MOLECULE: RHCC;
479:	4u5r-B	8.7	3.2	112	152	12	MOLECULE: RHCC;
480:	4u5p-B	8.5	2.8	108	141	12	MOLECULE: RHCC;
481:	3c6v-A	8.5	3.0	107	143	12	MOLECULE: PROBABLE TAUTOMERASE/DEHALOGENASE AU4130;
482:	3c6v-C	8.5	3.0	107	143	12	MOLECULE: PROBABLE TAUTOMERASE/DEHALOGENASE AU4130;
483:	4jj9-C	8.0	3.0	103	145	11	MOLECULE: 5-CARBOXYMETHYL-2-HYDROXYMUCONATE DELTA-ISOMERASE
484:	3c6v-B	7.9	2.6	93	147	16	MOLECULE: PROBABLE TAUTOMERASE/DEHALOGENASE AU4130;
485:	4jj9-B	7.8	3.0	104	151	11	MOLECULE: 5-CARBOXYMETHYL-2-HYDROXYMUCONATE DELTA-ISOMERASE
486:	4jj9-A	7.6	3.1	103	152	11	MOLECULE: 5-CARBOXYMETHYL-2-HYDROXYMUCONATE DELTA-ISOMERASE
487:	2x4k-A	5.9	1.5	62	62	5	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
488:	3m21-B	5.6	2.4	62	66	10	MOLECULE: PROBABLE TAUTOMERASE HP_0924;
489:	1ghh-A	5.6	3.0	70	81	16	MOLECULE: DNA-DAMAGE-INDUCIBLE PROTEIN I;
490:	3abf-A	5.6	2.0	63	64	11	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
491:	2orm-D	5.5	2.9	62	67	8	MOLECULE: PROBABLE TAUTOMERASE HP0924;
492:	3m21-F	5.5	3.1	62	67	8	MOLECULE: PROBABLE TAUTOMERASE HP_0924;
493:	3m21-D	5.5	2.6	62	66	10	MOLECULE: PROBABLE TAUTOMERASE HP_0924;
494:	3m21-A	5.5	1.3	59	65	8	MOLECULE: PROBABLE TAUTOMERASE HP_0924;
495:	3m21-E	5.5	1.2	59	65	8	MOLECULE: PROBABLE TAUTOMERASE HP_0924;
496:	2orm-F	5.5	2.1	61	64	8	MOLECULE: PROBABLE TAUTOMERASE HP0924;
497:	3m21-C	5.5	1.2	59	63	8	MOLECULE: PROBABLE TAUTOMERASE HP_0924;
498:	4fdx-B	5.4	2.6	62	64	15	MOLECULE: 4-OXALOCROTONASE TAUTOMERASE ISOZYME;
499:	3ry0-A	5.4	2.8	62	65	10	MOLECULE: PUTATIVE TAUTOMERASE;
500:	3ry0-B	5.4	2.5	62	63	10	MOLECULE: PUTATIVE TAUTOMERASE;
501:	2x4k-B	5.4	1.6	60	62	5	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
502:	2orm-A	5.4	2.6	62	67	8	MOLECULE: PROBABLE TAUTOMERASE HP0924;
503:	2orm-E	5.4	1.2	59	66	8	MOLECULE: PROBABLE TAUTOMERASE HP0924;
504:	3abf-B	5.4	2.6	63	63	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
505:	3abf-D	5.4	1.7	60	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
506:	2opa-B	5.4	1.9	61	61	8	MOLECULE: PROBABLE TAUTOMERASE YWHB;
507:	2op8-B	5.4	1.9	61	61	8	MOLECULE: PROBABLE TAUTOMERASE YWHB;
508:	2opa-A	5.4	2.0	61	61	8	MOLECULE: PROBABLE TAUTOMERASE YWHB;
509:	3ej7-I	5.4	1.9	58	59	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
510:	3ej7-C	5.4	1.9	58	59	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
511:	3abf-E	5.4	2.0	61	61	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
512:	4fdx-A	5.4	1.5	59	61	15	MOLECULE: 4-OXALOCROTONASE TAUTOMERASE ISOZYME;
513:	2op8-A	5.3	2.0	61	61	8	MOLECULE: PROBABLE TAUTOMERASE YWHB;
514:	1s0y-C	5.3	1.9	58	60	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
515:	2orm-C	5.3	1.3	59	64	8	MOLECULE: PROBABLE TAUTOMERASE HP0924;
516:	3abf-F	5.3	2.8	63	63	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
517:	3abf-C	5.3	1.9	60	63	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
518:	3m20-A	5.3	1.5	59	59	17	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE, PUTATIVE;
519:	3m20-C	5.3	1.3	58	58	17	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE, PUTATIVE;
520:	3ej7-E	5.3	1.9	58	58	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
521:	3mb2-C	5.2	2.2	62	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
522:	1s0y-K	5.2	1.9	58	61	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
523:	1s0y-I	5.2	1.8	58	62	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
524:	1s0y-E	5.2	1.9	58	61	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
525:	4x1c-D	5.2	1.6	59	59	10	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
526:	4x1c-E	5.2	1.6	59	59	10	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
527:	4x1c-A	5.2	1.5	58	58	10	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
528:	2orm-B	5.2	1.3	59	65	8	MOLECULE: PROBABLE TAUTOMERASE HP0924;
529:	3m20-B	5.2	1.3	58	58	17	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE, PUTATIVE;
530:	3ej3-K	5.2	2.0	58	62	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
531:	3ej3-E	5.2	2.0	58	62	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
532:	3ej3-G	5.2	2.0	58	62	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
533:	3ej3-A	5.2	2.0	58	62	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
534:	4faz-A	5.1	1.6	59	62	14	MOLECULE: 4-OXALOCROTONATE ISOMERASE PROTEIN;
535:	4x1c-F	5.1	1.5	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
536:	3ej9-C	5.1	1.9	58	63	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
537:	3mb2-K	5.1	2.2	62	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
538:	4faz-B	5.1	1.6	59	62	14	MOLECULE: 4-OXALOCROTONATE ISOMERASE PROTEIN;
539:	1s0y-A	5.1	1.9	58	62	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
540:	4x1c-H	5.1	1.6	59	62	10	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
541:	3mb2-A	5.1	1.9	61	61	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
542:	4x1c-G	5.1	1.6	59	61	10	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
543:	3mb2-E	5.1	1.9	61	61	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
544:	3mb2-G	5.1	1.9	61	61	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
545:	3ej7-K	5.1	1.9	58	59	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
546:	4x1c-C	5.1	1.7	58	58	10	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
547:	3ej3-I	5.1	2.0	58	64	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
548:	3ej9-A	5.1	1.9	58	62	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
549:	3ej3-L	5.1	2.3	59	60	10	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
550:	4ota-E	5.1	1.7	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
551:	4ota-J	5.1	2.0	60	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
552:	4ota-A	5.1	2.0	60	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
553:	4ota-K	5.1	1.7	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
554:	4ota-D	5.1	1.7	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
555:	4ota-L	5.1	1.7	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
556:	4ota-G	5.1	2.0	60	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
557:	4ota-I	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
558:	4ota-F	5.1	1.7	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
559:	4ota-H	5.1	1.7	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
560:	4ota-N	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
561:	3mb2-I	5.1	1.8	60	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
562:	4ota-C	5.1	1.7	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
563:	4ota-O	5.1	1.7	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
564:	1bjp-D	5.1	1.7	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;

565:	4otb-D	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
566:	4ota-B	5.1	1.7	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
567:	4otb-H	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
568:	4otb-I	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
569:	4otb-G	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
570:	1otf-D	5.1	1.7	59	59	15	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
571:	3ej3-J	5.1	1.9	58	58	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
572:	4otb-C	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
573:	4otb-E	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
574:	4otb-J	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
575:	4otb-B	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
576:	1otf-B	5.1	1.6	59	59	15	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
577:	4otb-K	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
578:	4otb-F	5.1	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
579:	1otf-E	5.1	1.7	59	59	15	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
580:	1bjp-A	5.0	1.7	59	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
581:	1otf-A	5.0	1.7	59	59	15	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
582:	3ej9-E	5.0	1.9	58	64	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
583:	1s0y-G	5.0	1.9	58	62	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
584:	5clo-L	5.0	1.7	59	59	8	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
585:	4x1c-N	5.0	1.7	58	58	10	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
586:	4x19-E	5.0	1.5	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
587:	4x19-P	5.0	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
588:	4x1c-J	5.0	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
589:	4x19-F	5.0	1.5	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
590:	3ej3-C	5.0	2.0	58	64	12	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
591:	3ej9-B	5.0	2.2	59	59	10	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
592:	4x1c-O	5.0	1.6	58	58	10	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
593:	4x19-V	5.0	1.7	58	58	10	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
594:	4x19-c	5.0	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
595:	4x19-Y	5.0	1.5	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
596:	4x19-X	5.0	1.5	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
597:	4x19-A	5.0	1.5	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
598:	4x19-T	5.0	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
599:	4x1c-B	5.0	1.5	56	56	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
600:	1bjp-B	5.0	1.7	59	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
601:	4ota-M	5.0	1.6	59	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
602:	4ota-P	5.0	1.7	59	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
603:	1bjp-E	5.0	1.7	59	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
604:	4ota-Q	5.0	1.7	59	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
605:	4faz-C	5.0	1.7	59	62	14	MOLECULE: 4-OXALOCROTONATE ISOMERASE PROTEIN;
606:	4otc-G	5.0	1.8	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
607:	4otc-E	5.0	1.8	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
608:	4otc-F	5.0	1.8	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
609:	4otb-A	5.0	1.7	59	59	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
610:	4otc-I	5.0	1.8	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
611:	1otf-C	5.0	1.7	59	59	15	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
612:	4otc-D	5.0	1.8	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
613:	4otc-H	5.0	1.8	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
614:	4otc-B	5.0	1.8	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
615:	4otc-C	5.0	1.8	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
616:	4otc-A	5.0	1.8	59	60	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
617:	3ej7-F	5.0	2.0	59	59	10	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
618:	4ota-R	5.0	1.6	58	58	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
619:	1bjp-C	5.0	1.6	58	58	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
620:	4otb-L	5.0	1.6	58	58	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
621:	3ej3-F	5.0	1.8	57	58	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
622:	3ej3-D	5.0	1.8	57	57	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
623:	4bsz-A	5.0	5.5	83	187	11	MOLECULE: ANKYRIN REPEAT-CONTAINING PROTEIN YAR1;
624:	4x19-M	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
625:	4x19-b	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
626:	5clo-E	4.9	1.6	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
627:	5clo-J	4.9	1.8	58	58	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
628:	4x1c-I	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
629:	5cln-K	4.9	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
630:	4x19-L	4.9	1.7	59	62	10	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
631:	4x19-R	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
632:	4x19-C	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
633:	5clo-B	4.9	1.6	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
634:	4x19-N	4.9	1.5	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
635:	5clo-O	4.9	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
636:	4x19-Z	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
637:	4x1c-L	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
638:	4x1c-K	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
639:	5cln-A	4.9	1.6	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
640:	4x19-D	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
641:	5clo-D	4.9	1.6	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
642:	4x19-d	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
643:	4x19-G	4.9	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
644:	3ej3-H	4.9	1.9	59	59	8	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
645:	1otf-F	4.9	1.7	59	59	15	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
646:	3ej9-F	4.9	2.0	58	58	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
647:	3ej7-L	4.9	1.9	58	58	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
648:	3ej7-G	4.9	2.0	56	56	13	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
649:	1s0y-H	4.9	1.9	56	56	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
650:	1s0y-B	4.9	1.9	55	55	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
651:	5clo-F	4.8	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
652:	4x19-Q	4.8	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
653:	4x19-O	4.8	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
654:	4x19-W	4.8	1.7	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
655:	4x19-I	4.8	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
656:	5clo-Q	4.8	1.6	56	56	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
657:	4x19-U	4.8	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
658:	4x1c-M	4.8	1.7	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
659:	5clo-A	4.8	1.6	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;

660:	5clo-M	4.8	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
661:	4x19-K	4.8	1.6	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
662:	5cln-D	4.8	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
663:	5clo-K	4.8	1.6	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
664:	4x19-H	4.8	1.7	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
665:	5clo-P	4.8	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
666:	5clo-R	4.8	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
667:	5clo-N	4.8	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
668:	5clo-I	4.8	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
669:	4x19-a	4.8	1.5	56	56	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
670:	4x19-J	4.8	1.7	57	57	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
671:	5clo-H	4.8	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
672:	5cln-H	4.8	1.8	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
673:	4x19-B	4.8	1.6	56	56	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
674:	3ej9-D	4.8	2.1	58	58	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
675:	3ej7-B	4.8	1.9	57	57	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
676:	3ej7-D	4.8	1.9	57	57	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
677:	1s0y-J	4.8	2.0	55	55	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
678:	3ej7-A	4.8	1.9	53	53	13	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
679:	2fm7-E	4.8	1.8	59	61	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
680:	5cln-F	4.7	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
681:	5cln-G	4.7	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
682:	4x19-S	4.7	1.6	56	56	11	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
683:	5clo-C	4.7	1.6	54	54	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
684:	3ej3-B	4.7	2.7	59	61	8	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
685:	5clo-G	4.7	1.6	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
686:	5cln-L	4.7	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
687:	5cln-J	4.7	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
688:	5cln-I	4.7	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
689:	2fm7-C	4.7	1.8	59	61	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
690:	3mb2-B	4.7	1.9	56	59	5	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
691:	1s0y-F	4.7	1.8	56	57	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
692:	1s0y-D	4.7	2.0	56	56	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
693:	3ej7-J	4.7	1.9	56	56	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
694:	1s0y-L	4.7	1.9	55	55	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID DEHAL
695:	3ej7-H	4.7	1.6	54	54	9	MOLECULE: ALPHA-SUBUNIT OF TRANS-3-CHLOROACRYLIC ACID
696:	2fm7-A	4.7	1.8	59	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
697:	2fm7-B	4.7	1.8	59	62	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
698:	2fm7-F	4.7	1.8	59	61	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
699:	2fm7-D	4.7	1.8	59	61	10	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE;
700:	3mb2-H	4.7	1.5	55	58	5	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
701:	4uku-E	4.7	4.6	81	223	12	MOLECULE: SACCHAROMYCES CEREVISIAE CHROMOSOME XII COSMID 96
702:	4ulj-E	4.7	4.6	82	223	12	MOLECULE: SACCHAROMYCES CEREVISIAE CHROMOSOME XII COSMID 96
703:	4ujz-E	4.7	4.6	82	223	12	MOLECULE: 18S RRNA;
704:	4uk6-h	4.7	4.7	81	223	11	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
705:	4ulm-h	4.7	4.6	81	223	11	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
706:	4ukz-E	4.7	4.6	80	223	10	MOLECULE: SACCHAROMYCES CEREVISIAE CHROMOSOME XII COSMID 96
707:	5cln-B	4.6	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
708:	5cln-E	4.6	1.7	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
709:	5cln-C	4.6	1.8	57	57	9	MOLECULE: 2-HYDROXYMUCONATE TAUTOMERASE;
710:	3byr-A	4.6	3.2	70	88	7	MOLECULE: CZRB PROTEIN;
711:	3mb2-J	4.6	2.1	56	59	5	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
712:	3mb2-D	4.6	1.5	54	58	6	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
713:	4ule-E	4.6	4.6	80	223	11	MOLECULE: SACCHAROMYCES CEREVISIAE CHROMOSOME XII COSMID 96
714:	4byl-D	4.6	4.6	81	223	10	MOLECULE: 40S RIBOSOMAL PROTEIN S27-A;
715:	4byt-D	4.6	4.7	82	223	11	MOLECULE: 40S RIBOSOMAL PROTEIN S27-A;
716:	4ukp-E	4.6	4.6	82	223	13	MOLECULE: SACCHAROMYCES CEREVISIAE CHROMOSOME XII COSMID 96
717:	4ujf-E	4.6	4.6	83	223	12	MOLECULE: SACCHAROMYCES CEREVISIAE CHROMOSOME XII COSMID 96
718:	4ulg-h	4.6	4.6	81	223	11	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
719:	4ul9-E	4.6	4.6	81	223	10	MOLECULE: TPA_INF: SACCHAROMYCES CEREVISIAE S288C CHROMOSOM
720:	4ujr-h	4.6	4.6	82	223	12	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
721:	4ulp-E	4.6	5.2	86	223	10	MOLECULE: SACCHAROMYCES CEREVISIAE CHROMOSOME XII COSMID 96
722:	4ukm-h	4.6	4.6	82	223	12	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
723:	4uju-E	4.6	5.2	86	223	10	MOLECULE: SACCHAROMYCES CEREVISIAE CHROMOSOME XII COSMID 96
724:	3hbb-D	4.6	5.3	59	507	14	MOLECULE: DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE;
725:	4uer-C	4.5	4.6	81	223	10	MOLECULE: ES28;
726:	4ukf-E	4.5	4.5	80	223	13	MOLECULE: SACCHAROMYCES CEREVISIAE CHROMOSOME XII COSMID 96
727:	4ul6-h	4.5	4.6	82	223	12	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
728:	4ulb-h	4.5	4.6	82	223	12	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
729:	4ukh-h	4.5	4.6	82	223	11	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
730:	4ujm-h	4.5	4.6	81	223	12	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
731:	4uk4-E	4.5	5.2	85	223	11	MOLECULE: 18S RRNA;
732:	3u5g-D	4.5	4.6	81	223	11	MOLECULE: 40S RIBOSOMAL PROTEIN S0-A;
733:	4ukb-h	4.5	5.2	86	223	10	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
734:	3u5c-D	4.5	5.2	86	223	10	MOLECULE: 40S RIBOSOMAL PROTEIN S0-A;
735:	1wh9-A	4.4	4.8	78	92	13	MOLECULE: 40S RIBOSOMAL PROTEIN S3;
736:	3byp-B	4.4	3.1	67	82	7	MOLECULE: CZRB PROTEIN;
737:	3mb2-F	4.4	1.7	51	54	6	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
738:	3mb2-L	4.4	1.7	51	54	6	MOLECULE: 4-OXALOCROTONATE TAUTOMERASE FAMILY ENZYME - ALPH
739:	3j81-D	4.4	4.8	84	223	10	MOLECULE: 18S RRNA;
740:	4ujw-h	4.4	4.6	82	223	9	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
741:	3j80-D	4.4	4.6	81	223	11	MOLECULE: 18S RRNA;
742:	3clb-C	4.4	5.3	59	510	14	MOLECULE: DHFR-TS;
743:	3hbb-C	4.4	5.3	59	510	14	MOLECULE: DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE;
744:	3kjs-C	4.4	5.3	59	507	14	MOLECULE: DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE;
745:	3byp-A	4.3	3.0	65	82	8	MOLECULE: CZRB PROTEIN;
746:	1vwv-E	4.3	5.2	88	223	9	MOLECULE: 18S RIBOSOMAL RNA;
747:	4ujh-h	4.3	4.2	76	223	12	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
748:	5a2q-D	4.3	3.0	75	225	13	MOLECULE: 18S RRNA;
749:	4pug-B	4.2	3.4	73	84	10	MOLECULE: BOLA LIKE PROTEIN;
750:	1ylq-A	4.2	3.7	66	92	6	MOLECULE: PUTATIVE NUCLEOTIDYLTRANSFERASE, HYPOTHETICAL PRO
751:	2h2q-A	4.2	2.9	55	514	13	MOLECULE: BIFUNCTIONAL DIHYDROFOLATE REDUCTASE-THYMIDYLATE
752:	4ul1-h	4.2	4.6	81	223	11	MOLECULE: 60S RIBOSOMAL PROTEIN L15-A;
753:	3o2z-C	4.2	4.4	81	189	11	MOLECULE: 18S RIBOSOMAL RNA;
754:	3o30-C	4.2	4.1	81	189	11	MOLECULE: 18S RIBOSOMAL RNA;

755:	3j3a-D	4.2	5.1	86	227	10	MOLECULE: ELONGATION FACTOR 2;
756:	2dhm-A	4.1	4.8	87	107	7	MOLECULE: PROTEIN BOLA;
757:	1qax-A	4.1	4.5	89	425	7	MOLECULE: PROTEIN (3-HYDROXY-3-METHYLGLUTARYL-COENZYME A
758:	4kzy-D	4.1	5.2	86	227	9	MOLECULE: 40S RIBOSOMAL PROTEIN SA;
759:	1vx5-D	4.1	4.5	80	227	13	MOLECULE: 18S RIBOSOMAL RNA;
760:	4bpn-C	4.1	3.8	81	228	12	MOLECULE: TRANSLATION INITIATION FACTOR EIF-1A FAMILY PROTE
761:	4bpo-C	4.1	3.8	81	228	12	MOLECULE: TRANSLATION INITIATION FACTOR EIF-1A FAMILY PROTE
762:	4bpp-C	4.1	3.8	81	228	12	MOLECULE: TRANSLATION INITIATION FACTOR EIF-1A FAMILY PROTE
763:	5k0y-g	4.1	4.4	77	227	13	MOLECULE: RNA (75-MER);
764:	4w28-D	4.0	4.5	80	227	14	MOLECULE: 18S RIBOSOMAL RNA;
765:	5flx-D	4.0	3.6	81	220	11	MOLECULE: 18S RRNA;
766:	2gy9-C	4.0	4.3	80	206	14	MOLECULE: 16S RIBOSOMAL RNA;
767:	1vxz-D	4.0	4.7	81	223	12	MOLECULE: 40S RIBOSOMAL PROTEIN S0;
768:	3zey-X	4.0	3.4	81	205	12	MOLECULE: 40S RIBOSOMAL PROTEIN S4, PUTATIVE;
769:	3j38-D	4.0	5.2	86	227	9	MOLECULE: ELONGATION FACTOR 2;
770:	2xzm-C	4.0	4.9	84	229	11	MOLECULE: RIBOSOMAL PROTEIN S28E CONTAINING PROTEIN;
771:	3hbb-B	4.0	5.5	59	505	14	MOLECULE: DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE;
772:	3kjs-D	4.0	5.3	59	504	14	MOLECULE: DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE;
773:	4pui-B	3.9	3.6	72	86	11	MOLECULE: SUFE-LIKE PROTEIN, CHLOROPLASTIC;
774:	3ofx-C	3.9	4.2	79	206	13	MOLECULE: 16S RRNA;
775:	3oaq-C	3.9	4.2	79	206	13	MOLECULE: 16S RRNA;
776:	2gyb-C	3.9	4.6	82	206	16	MOLECULE: 16S RIBOSOMAL RNA;
777:	3i1s-C	3.9	4.2	78	206	13	MOLECULE: 30S RIBOSOMAL PROTEIN S2;
778:	4uq4-D	3.9	4.0	80	212	11	MOLECULE: 18S RRNA;
779:	4uq5-D	3.9	4.0	80	212	11	MOLECULE: 18S RRNA;
780:	4cxc-D	3.9	4.0	80	212	11	MOLECULE: 18S RRNA;
781:	4qjt-c	3.9	4.3	80	206	10	MOLECULE: E-SITE TRNA;
782:	3k2h-B	3.9	5.4	59	503	15	MOLECULE: DIHYDROFOLATE REDUCTASE/THYMIDYLATE SYNTHASE;
783:	3clb-A	3.9	5.4	58	510	14	MOLECULE: DHFR-TS;
784:	4pug-A	3.8	3.4	72	94	10	MOLECULE: BOLA LIKE PROTEIN;
785:	4pui-A	3.8	3.3	69	85	13	MOLECULE: SUFE-LIKE PROTEIN, CHLOROPLASTIC;
786:	3j6d-m	3.8	3.5	73	148	19	MOLECULE: PROTEIN PRGH;
787:	3r8n-C	3.8	4.1	79	206	13	MOLECULE: 16S RRNA;
788:	3i1m-C	3.8	4.3	78	206	13	MOLECULE: 30S RIBOSOMAL PROTEIN S2;
789:	3ofa-C	3.8	4.3	78	206	13	MOLECULE: 16S RRNA;
790:	3uoq-C	3.8	4.3	79	206	13	MOLECULE: 16S RRNA;
791:	3ora-C	3.8	4.2	78	206	13	MOLECULE: 16S RRNA;
792:	3ofp-C	3.8	4.3	77	206	12	MOLECULE: 16S RRNA;
793:	3i21-C	3.8	4.2	77	206	13	MOLECULE: 30S RIBOSOMAL PROTEIN S2;
794:	3oar-C	3.8	4.0	81	206	11	MOLECULE: 16S RRNA;
795:	1vw9-E	3.8	4.7	81	223	11	MOLECULE: 18S RIBOSOMAL RNA;
796:	4d61-D	3.8	4.0	80	212	11	MOLECULE: 18S RRNA;
797:	4gd1-C	3.8	4.2	78	206	13	MOLECULE: 16S RRNA;
798:	4w2a-C	3.8	4.2	80	205	10	MOLECULE: 16S RIBOSOMAL RNA;
799:	4w2c-C	3.8	4.1	79	205	11	MOLECULE: 16S RIBOSOMAL RNA;
800:	4nvy-C	3.8	4.2	79	206	10	MOLECULE: 16S RIBOSOMAL RNA;
801:	3clb-B	3.8	5.4	59	508	14	MOLECULE: DHFR-TS;
802:	1gyx-A	3.7	1.8	54	76	7	MOLECULE: HYPOTHETICAL PROTEIN YDCE;
803:	1gyy-A	3.7	1.8	54	76	7	MOLECULE: HYPOTHETICAL PROTEIN YDCE;
804:	1hnx-C	3.7	4.2	82	206	10	MOLECULE: 16S RIBOSOMAL RNA;
805:	3j18-C	3.7	4.2	78	206	13	MOLECULE: 16S RIBOSOMAL RNA;
806:	3sfs-C	3.7	4.3	79	206	14	MOLECULE: 16S RRNA;
807:	4gd2-C	3.7	5.0	81	206	11	MOLECULE: 16S RRNA;
808:	3i1z-C	3.7	4.9	80	206	13	MOLECULE: 30S RIBOSOMAL PROTEIN S2;
809:	3ofo-C	3.7	4.9	83	206	12	MOLECULE: 16S RRNA;
810:	3jyv-C	3.7	5.0	82	188	11	MOLECULE: 18S RRNA;
811:	3j20-C	3.7	4.0	79	186	9	MOLECULE: 16S RRNA;
812:	1gyj-A	3.6	2.1	54	76	6	MOLECULE: HYPOTHETICAL PROTEIN YDCE;
813:	2qbd-C	3.6	3.9	79	206	14	MOLECULE: 16S RRNA;
814:	4gas-C	3.6	4.5	78	206	12	MOLECULE: 16S RIBOSOMAL RNA;
815:	4kbt-C	3.6	3.4	78	207	10	MOLECULE: 30S RIBOSOMAL PROTEIN S2;
816:	2aw7-C	3.5	4.9	82	206	12	MOLECULE: 16S RIBOSOMAL RNA;
817:	1v9j-A	3.5	4.5	82	113	11	MOLECULE: BOLA-LIKE PROTEIN RIKEN CDNA 1110025L05;
818:	1vla-A	3.5	3.3	75	144	5	MOLECULE: HYDROPEROXIDE RESISTANCE PROTEIN OSMC;
819:	3ux3-A	3.5	4.1	71	130	8	MOLECULE: MIP18 FAMILY PROTEIN FAM96A;
820:	3h90-B	3.5	3.1	67	283	7	MOLECULE: FERROUS-IRON EFFLUX PUMP FIEF;
821:	3h90-D	3.5	3.1	67	283	7	MOLECULE: FERROUS-IRON EFFLUX PUMP FIEF;
822:	1gyj-B	3.5	1.8	54	76	7	MOLECULE: HYPOTHETICAL PROTEIN YDCE;
823:	3aqo-D	3.5	3.0	69	221	9	MOLECULE: PROBABLE SECDF PROTEIN-EXPORT MEMBRANE PROTEIN;
824:	2qbj-C	3.5	4.9	81	206	11	MOLECULE: 16S RRNA;
825:	2qbh-C	3.5	4.9	80	206	11	MOLECULE: 16S RRNA;
826:	2z4k-C	3.5	4.3	77	206	12	MOLECULE: 16S RRNA;
827:	2z4m-C	3.5	4.3	77	206	12	MOLECULE: 16S RRNA;
828:	3j0x-F	3.5	3.8	73	232	11	MOLECULE: 16S RIBOSOMAL RNA;
829:	3izb-B	3.5	4.9	79	204	10	MOLECULE: 40S RIBOSOMAL PROTEIN RACK1 (RACK1);
830:	2oip-C	3.5	2.7	56	514	16	MOLECULE: CHAIN A, CRYSTAL STRUCTURE OF DHFR;
831:	2ivy-A	3.4	2.8	63	88	8	MOLECULE: HYPOTHETICAL PROTEIN SSO1404;
832:	3h90-A	3.4	3.1	67	283	7	MOLECULE: FERROUS-IRON EFFLUX PUMP FIEF;
833:	3h90-C	3.4	3.1	67	283	7	MOLECULE: FERROUS-IRON EFFLUX PUMP FIEF;
834:	4gaq-C	3.4	3.9	83	206	11	MOLECULE: 16S RIBOSOMAL RNA;
835:	2qoy-C	3.4	4.9	82	206	12	MOLECULE: 16S RRNA;
836:	2qp0-C	3.4	4.0	81	206	12	MOLECULE: 16S RRNA;
837:	4adv-C	3.4	4.3	78	206	13	MOLECULE: 16S RIBOSOMAL RNA;
838:	4a2i-C	3.4	5.2	83	206	13	MOLECULE: 16S RIBOSOMAL RNA;
839:	2i2p-C	3.4	4.9	81	206	11	MOLECULE: 16S RIBOSOMAL RNA;
840:	3df1-C	3.4	5.0	80	206	11	MOLECULE: 16S RIBOSOMAL RNA;
841:	3aqo-C	3.3	2.8	64	222	8	MOLECULE: PROBABLE SECDF PROTEIN-EXPORT MEMBRANE PROTEIN;
842:	3j1x-I	3.3	3.4	77	191	9	MOLECULE: PROTEIN PRGH;
843:	3o2e-A	3.3	3.6	70	86	6	MOLECULE: BOLA-LIKE PROTEIN;
844:	3aqo-B	3.3	3.0	68	220	10	MOLECULE: PROBABLE SECDF PROTEIN-EXPORT MEMBRANE PROTEIN;
845:	3j1z-P	3.3	3.4	74	296	3	MOLECULE: CATION EFFLUX FAMILY PROTEIN;
846:	2qou-C	3.3	5.0	83	206	11	MOLECULE: 16S RRNA;
847:	3fih-C	3.3	4.0	79	206	14	MOLECULE: 30S RIBOSOMAL PROTEIN S10;
848:	3hj3-D	3.3	5.4	60	506	18	MOLECULE: CHAIN A, CRYSTAL STRUCTURE OF DHFR;
849:	1ega-A	3.2	3.8	78	292	9	MOLECULE: PROTEIN (GTP-BINDING PROTEIN ERA);

850:	2xzn-C	3.2	3.5	79	229	10	MOLECULE: RIBOSOMAL PROTEIN S28E CONTAINING PROTEIN;
851:	3j13-E	3.2	5.4	78	232	14	MOLECULE: 16S RIBOSOMAL RNA;
852:	2pn2-A	3.1	3.3	75	137	4	MOLECULE: UNCHARACTERIZED PROTEIN;
853:	4puh-A	3.1	3.9	66	81	9	MOLECULE: AT5G09830;
854:	4puh-B	3.1	3.9	66	81	9	MOLECULE: AT5G09830;
855:	2mma-B	3.1	3.8	66	80	9	MOLECULE: MONOTHIOL GLUTAREDOXIN-S14, CHLOROPLASTIC;
856:	3e1c-O	3.1	4.6	75	206	12	MOLECULE: A/T, P AND E-SITE TRNAS;
857:	3j10-F	3.1	5.5	81	232	12	MOLECULE: 16S RIBOSOMAL RNA;
858:	3nrr-B	3.1	5.4	59	503	15	MOLECULE: DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE;
859:	2ykr-C	3.0	3.6	74	206	11	MOLECULE: 16S RRNA;
860:	3e1a-O	3.0	4.6	76	206	12	MOLECULE: A/T, P AND E-SITE TRNAS;
861:	3j0z-F	3.0	4.5	78	232	14	MOLECULE: 16S RIBOSOMAL RNA;
862:	1lql-A	2.9	3.6	73	141	4	MOLECULE: OSMOTICAL INDUCIBLE PROTEIN C LIKE FAMILY;
863:	5j7r-B	2.9	3.6	70	149	7	MOLECULE: PUTATIVE LIPOPROTEIN;
864:	2mm9-A	2.9	4.3	67	93	7	MOLECULE: BOLA2;
865:	4kzz-D	2.9	4.3	81	227	12	MOLECULE: 40S RIBOSOMAL PROTEIN SA;
866:	3j0u-F	2.9	4.6	77	232	14	MOLECULE: 16S RIBOSOMAL RNA;
867:	1kkg-A	2.8	3.6	73	108	14	MOLECULE: RIBOSOME-BINDING FACTOR A;
868:	5lci-A	2.8	4.2	69	88	10	MOLECULE: BOLA-LIKE PROTEIN 1;
869:	1th5-A	2.8	2.8	59	74	5	MOLECULE: NIFU1;
870:	3j60-D	2.8	6.0	75	208	13	MOLECULE: 40S RIBOSOMAL PROTEIN S24E;
871:	2wwl-C	2.8	4.4	79	206	11	MOLECULE: 16S RIBOSOMAL RNA;
872:	1ml8-A	2.7	3.4	75	131	8	MOLECULE: HYPOTHETICAL PROTEIN (CRP REGION);
873:	3w64-D	2.7	3.3	64	82	3	MOLECULE: MAGNETOSOME PROTEIN MAMM;
874:	3w64-A	2.7	3.5	63	81	5	MOLECULE: MAGNETOSOME PROTEIN MAMM;
875:	4alz-A	2.7	4.1	66	194	9	MOLECULE: YOP PROTEINS TRANSLOCATION PROTEIN D;
876:	3w5y-B	2.6	3.3	62	80	3	MOLECULE: MAGNETOSOME PROTEIN MAMM;
877:	3w65-A	2.6	3.5	62	83	3	MOLECULE: MAGNETOSOME PROTEIN MAMM;
878:	3w5x-A	2.6	3.1	63	80	5	MOLECULE: MAGNETOSOME PROTEIN MAMM;
879:	3w62-A	2.6	3.1	62	79	2	MOLECULE: MAGNETOSOME PROTEIN MAMM;
880:	3izw-G	2.6	4.3	76	232	9	MOLECULE: 16S RIBOSOMAL RNA;
881:	2kdn-A	2.5	4.0	70	108	7	MOLECULE: PUTATIVE UNCHARACTERIZED PROTEIN PFE0790C;
882:	1vmb-A	2.5	4.0	80	107	5	MOLECULE: 30S RIBOSOMAL PROTEIN S6;
883:	1n2f-A	2.5	3.8	74	142	9	MOLECULE: ORGANIC HYDROPEROXIDE RESISTANCE PROTEIN;
884:	3tr3-B	2.5	3.7	67	81	4	MOLECULE: BOLA;
885:	3w61-A	2.5	3.4	63	80	2	MOLECULE: MAGNETOSOME PROTEIN MAMM;
886:	2dyj-B	2.5	3.8	68	90	12	MOLECULE: RIBOSOME-BINDING FACTOR A;
887:	3w63-A	2.5	3.1	62	79	3	MOLECULE: MAGNETOSOME PROTEIN MAMM;
888:	3w64-B	2.5	3.6	63	81	3	MOLECULE: MAGNETOSOME PROTEIN MAMM;
889:	4kzx-D	2.5	4.5	81	227	11	MOLECULE: 40S RIBOSOMAL PROTEIN SA;
890:	3j0v-F	2.5	3.6	78	232	15	MOLECULE: 16S RIBOSOMAL RNA;
891:	4rho-B	2.4	3.1	71	257	4	MOLECULE: UNCHARACTERIZED PROTEIN;
892:	3ouy-A	2.4	7.0	73	441	10	MOLECULE: CCA-ADDING ENZYME;
893:	3w64-C	2.4	3.4	59	78	5	MOLECULE: MAGNETOSOME PROTEIN MAMM;
894:	4nw0-C	2.4	4.3	80	206	10	MOLECULE: 16S RIBOSOMAL RNA;
895:	3iz6-B	2.4	3.2	68	208	10	MOLECULE: 40S RIBOSOMAL PROTEIN RACK1 (RACK1);
896:	1zg9-A	2.3	3.5	66	305	8	MOLECULE: PROCARBOXYPEPTIDASE B;
897:	3e8o-B	2.3	3.7	68	101	12	MOLECULE: UNCHARACTERIZED PROTEIN WITH ERREDOXIN-LIKE FOLD;
898:	2qfi-B	2.3	3.3	67	286	9	MOLECULE: FERROUS-IRON EFFLUX PUMP FIEF;
899:	3h3w-E	2.3	4.0	67	326	9	MOLECULE: BASEPLATE STRUCTURAL PROTEIN GP6;
900:	3tr3-A	2.3	4.0	66	78	5	MOLECULE: BOLA;
901:	3h3w-G	2.3	4.0	67	326	9	MOLECULE: BASEPLATE STRUCTURAL PROTEIN GP6;
902:	3h3w-I	2.3	4.0	66	326	9	MOLECULE: BASEPLATE STRUCTURAL PROTEIN GP6;
903:	3w5y-A	2.3	3.4	60	80	3	MOLECULE: MAGNETOSOME PROTEIN MAMM;
904:	4ujp-E	2.3	4.5	68	223	9	MOLECULE: 18S RRNA;
905:	3h3w-F	2.3	6.2	70	324	6	MOLECULE: BASEPLATE STRUCTURAL PROTEIN GP6;
906:	3h3w-D	2.3	4.1	64	324	6	MOLECULE: BASEPLATE STRUCTURAL PROTEIN GP6;
907:	1sej-E	2.3	2.8	56	519	16	MOLECULE: BIFUNCTIONAL DIHYDROFOLATE REDUCTASE-THYMIDYLATE
908:	1sej-C	2.3	1.9	54	519	15	MOLECULE: BIFUNCTIONAL DIHYDROFOLATE REDUCTASE-THYMIDYLATE
909:	1sej-D	2.3	2.8	56	519	16	MOLECULE: BIFUNCTIONAL DIHYDROFOLATE REDUCTASE-THYMIDYLATE
910:	2xr1-B	2.2	3.3	57	611	16	MOLECULE: CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 1
911:	2zze-A	2.2	3.9	64	744	5	MOLECULE: ALANYL-TRNA SYNTHETASE;
912:	2ec2-E	2.2	3.6	73	129	4	MOLECULE: 136AA LONG HYPOTHETICAL TRANSPOSASE;
913:	2lpi-A	2.2	3.9	84	137	5	MOLECULE: MAJOR AMPULLATE SPIDROIN 1;
914:	3h2t-A	2.2	4.7	71	326	6	MOLECULE: BASEPLATE STRUCTURAL PROTEIN GP6;
915:	2qfi-A	2.2	3.3	68	286	9	MOLECULE: FERROUS-IRON EFFLUX PUMP FIEF;
916:	3h3w-A	2.2	4.0	66	326	9	MOLECULE: BASEPLATE STRUCTURAL PROTEIN GP6;
917:	3j7a-D	2.2	6.6	52	157	21	MOLECULE: 18S RIBOSOMAL RNA;
918:	3h3w-C	2.1	4.0	66	326	6	MOLECULE: BASEPLATE STRUCTURAL PROTEIN GP6;
919:	3hb8-A	2.1	5.5	59	281	14	MOLECULE: THYMIDYLATE SYNTHASE;
920:	3h9k-D	2.1	5.4	59	280	14	MOLECULE: THYMIDYLATE SYNTHASE;
921:	3ejl-A	2.1	5.4	59	283	14	MOLECULE: THYMIDYLATE SYNTHASE;
922:	3hj3-C	2.1	2.7	56	512	16	MOLECULE: CHAIN A, CRYSTAL STRUCTURE OF DHFR;
923:	3j1z-Q	2.0	4.8	66	296	2	MOLECULE: CATION EFFLUX FAMILY PROTEIN;
924:	3ihh-B	2.0	2.1	53	287	11	MOLECULE: THYMIDYLATE SYNTHASE;
925:	3ihh-E	2.0	1.9	53	287	11	MOLECULE: THYMIDYLATE SYNTHASE;
926:	3ejl-C	2.0	5.5	59	283	14	MOLECULE: THYMIDYLATE SYNTHASE;