wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 07:37 pm GMT

PDB ID	:	5JCS
EMDB ID	:	EMD-3199
Title	:	CRYO-EM STRUCTURE OF THE RIX1-REA1 PRE-60S PARTICLE
Authors	:	Barrio-Garcia, C.; Thoms, M.; Flemming, D.; Kater, L.; Berninghausen, O.; Bassler, J.; Beckmann, R.; Hurt, E.
Deposited on	:	2016-04-15
Resolution	:	9.50 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

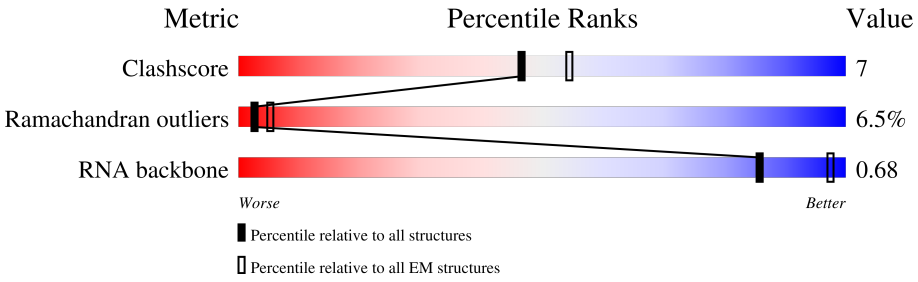
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 9.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	254	39% 85% 13%
2	c	105	12% 91% 8%
3	B	387	18% 92% 7%
4	d	113	15% 93%
5	C	362	25% 90% 9%
6	e	130	22% 96%
7	D	297	13% 95%
8	f	107	15% 92% 6%

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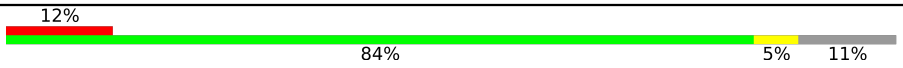
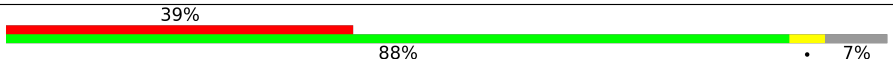
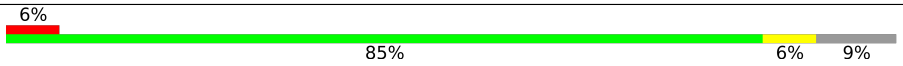
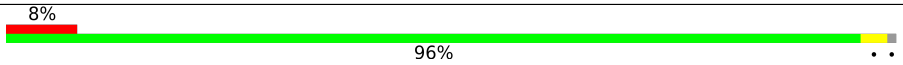
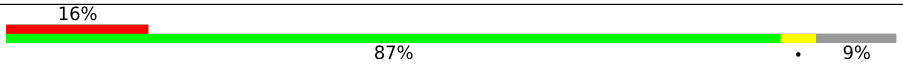
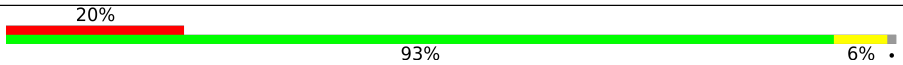
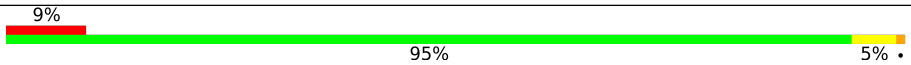
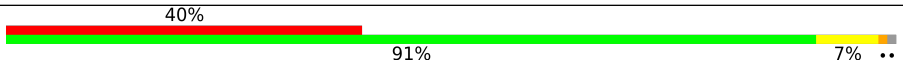
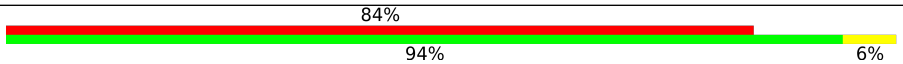
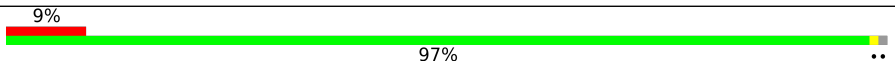
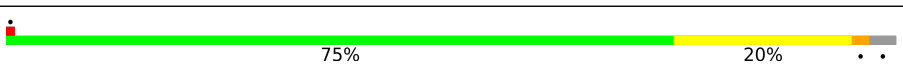
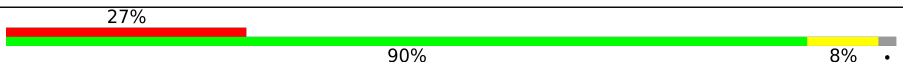
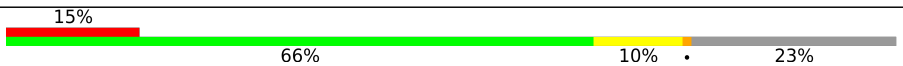
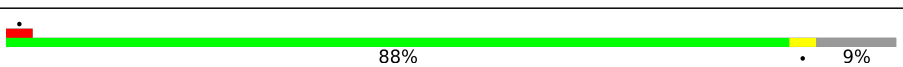
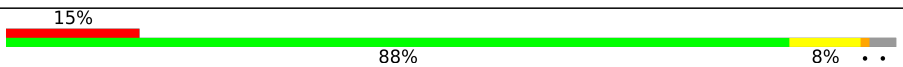
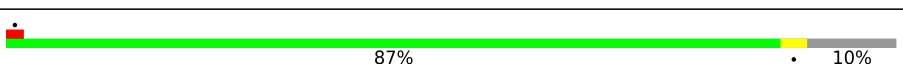
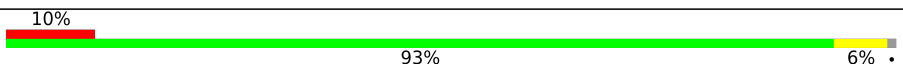
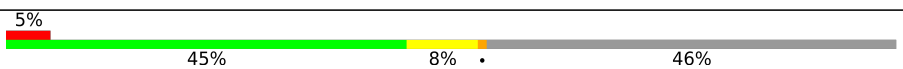
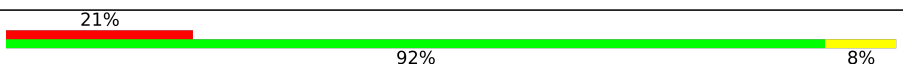
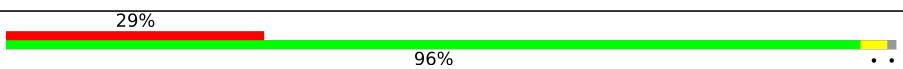
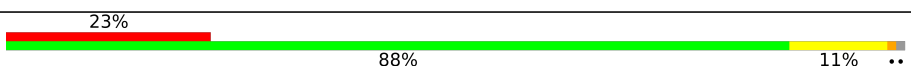
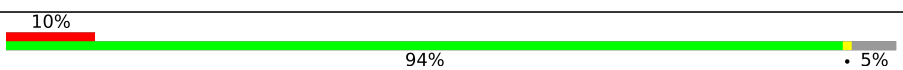
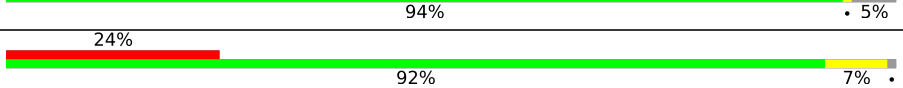
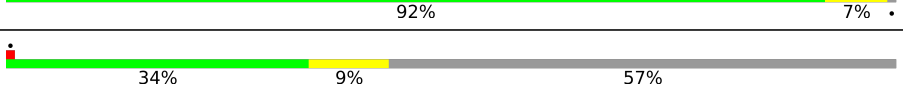
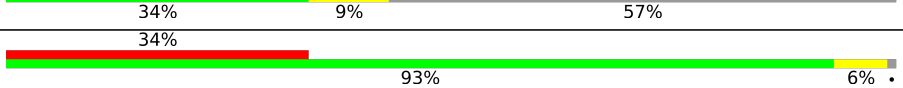
Mol	Chain	Length	Quality of chain
9	E	176	
10	g	121	
11	F	244	
12	h	120	
13	G	256	
14	i	100	
15	H	191	
16	j	88	
17	I	217	
18	k	78	
19	J	174	
20	l	51	
21	K	165	
22	m	245	
23	L	199	
24	n	236	
25	M	138	
26	o	647	
27	N	204	
28	p	92	
29	O	199	
30	q	515	
31	P	184	
32	r	767	
33	Q	186	

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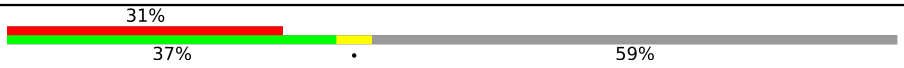
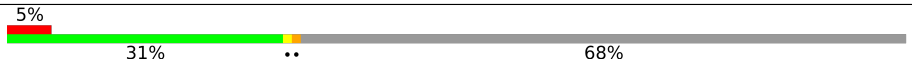
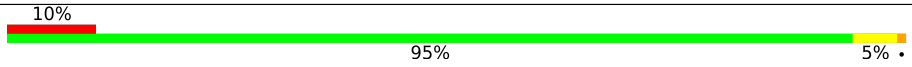
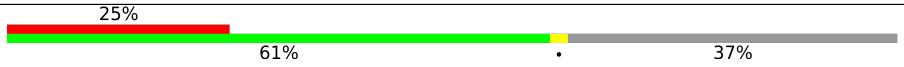
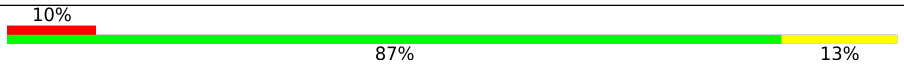
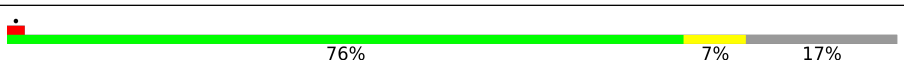
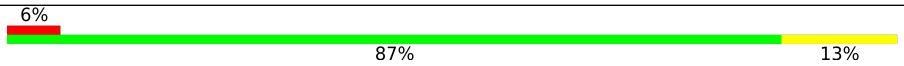
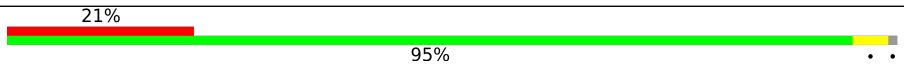
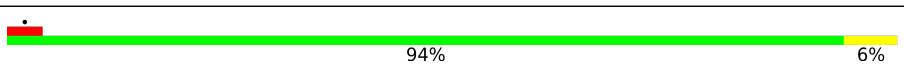
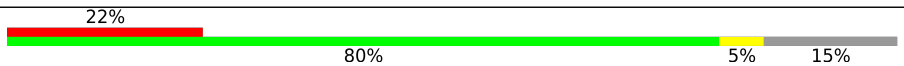
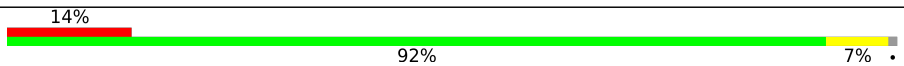
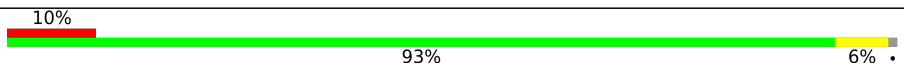
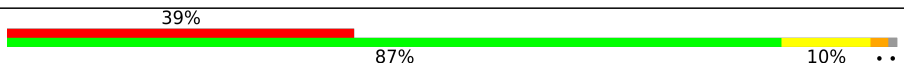
Mol	Chain	Length	Quality of chain
34	s	4910	
35	R	189	
36	t	199	
37	S	172	
38	u	593	
39	T	160	
40	x	3396	
41	U	121	
42	y	158	
43	V	137	
44	z	121	
45	X	142	
46	Y	127	
47	Z	136	
48	a	149	

2 Entry composition (i)

There are 48 unique types of molecules in this entry. The entry contains 118855 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	252	Total 1007	C 504	N 252	O 251	0	0

- Molecule 2 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	c	97	Total 387	C 194	N 97	O 96	0	0

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	B	386	Total 1543	C 772	N 386	O 385	0	0

- Molecule 4 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	d	109	Total 435	C 218	N 109	O 108	0	0

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	C	361	Total 1443	C 722	N 361	O 360	0	0

- Molecule 6 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	e	127	Total 507	C 254	N 127	O 126	0	0

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	D	296	Total 1183	C 592	N 296	O 295	0	0

- Molecule 8 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	f	106	Total 423	C 212	N 106	O 105	0	0

- Molecule 9 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	E	156	Total 622	C 312	N 156	O 154	0	0

- Molecule 10 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	g	112	Total 447	C 224	N 112	O 111	0	0

- Molecule 11 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	F	222	Total 887	C 444	N 222	O 221	0	0

- Molecule 12 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	h	119	Total 475	C 238	N 119	O 118	0	0

- Molecule 13 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	G	233	Total 931	C 466	N 233	O 232	0	0

- Molecule 14 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	i	99	Total 395	C 198	N 99	O 98	0	0

- Molecule 15 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	H	191	Total 763	C 382	N 191	O 190	0	0

- Molecule 16 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	j	87	Total 347	C 174	N 87	O 86	0	0

- Molecule 17 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	I	217	Total 867	C 434	N 217	O 216	0	0

- Molecule 18 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	k	77	Total 307	C 154	N 77	O 76	0	0

- Molecule 19 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	J	169	Total 675	C 338	N 169	O 168	0	0

- Molecule 20 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	l	50	Total 199	C 100	N 50	O 49	0	0

- Molecule 21 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	K	127	Total 507	C 254	N 127	O 126	0	0

- Molecule 22 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	m	224	Total 895	C 448	N 224	O 223	0	0

- Molecule 23 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	L	193	Total 771	C 386	N 193	O 192	0	0

- Molecule 24 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	n	212	Total 847	C 424	N 212	O 211	0	0

- Molecule 25 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	M	136	Total 543	C 272	N 136	O 135	0	0

- Molecule 26 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	o	347	Total 1387	C 694	N 347	O 346	0	0

- Molecule 27 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	N	203	Total 811	C 406	N 203	O 202	0	0

- Molecule 28 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	p	91	Total 363	C 182	N 91	O 90	0	0

- Molecule 29 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	O	197	Total 787	C 394	N 197	O 196	0	0

- Molecule 30 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	q	488	Total 1951	C 976	N 488	O 487	0	0

- Molecule 31 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	P	183	Total 731	C 366	N 183	O 182	0	0

- Molecule 32 is a protein called Protein SDA1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	r	333	Total 1304	C 666	N 333	O 305	0	0

- Molecule 33 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Q	185	Total 739	C 370	N 185	O 184	0	0

- Molecule 34 is a protein called Midasin.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	s	2003	Total 8007	C 4006	N 2003	O 1998	0	0

- Molecule 35 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	R	188	Total 751	C 376	N 188	O 187	0	0

- Molecule 36 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	t	63	Total 251	C 126	N 63	O 62	0	0

- Molecule 37 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	S	172	Total 687	C 344	N 172	O 171	0	0

- Molecule 38 is a protein called Probable metalloprotease ARX1.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	u	373	Total 1491	C 746	N 373	O 372	0	0

- Molecule 39 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	T	159	Total 635	C 318	N 159	O 158	0	0

- Molecule 40 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	x	3394	Total 72570	C 32410	N 13042	O 23725	P 3393	0	0

- Molecule 41 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	U	100	Total 399	C 200	N 100	O 99	0	0

- Molecule 42 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	y	158	Total	C	N	O	P	0	0
			3350	1500	586	1107	157		

- Molecule 43 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	V	136	Total	C	N	O	0	0
			543	272	136	135		

- Molecule 44 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	121	Total	C	N	O	P	0	0
			2576	1152	461	843	120		

- Molecule 45 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	X	121	Total	C	N	O	0	0
			483	242	121	120		

- Molecule 46 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	Y	126	Total	C	N	O	0	0
			503	252	126	125		

- Molecule 47 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	Z	135	Total	C	N	O	0	0
			539	270	135	134		

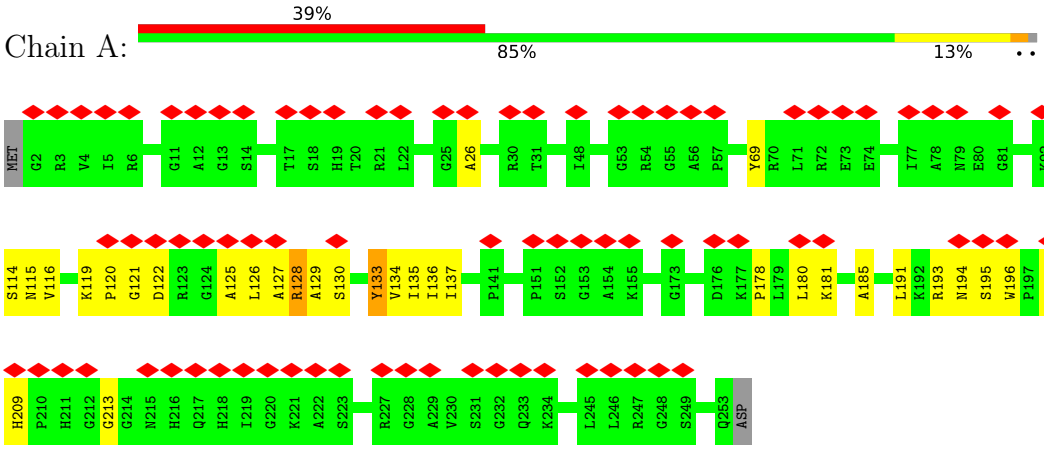
- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	a	148	Total	C	N	O	0	0
			591	296	148	147		

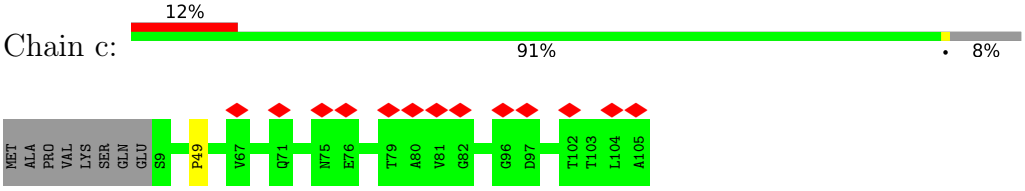
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

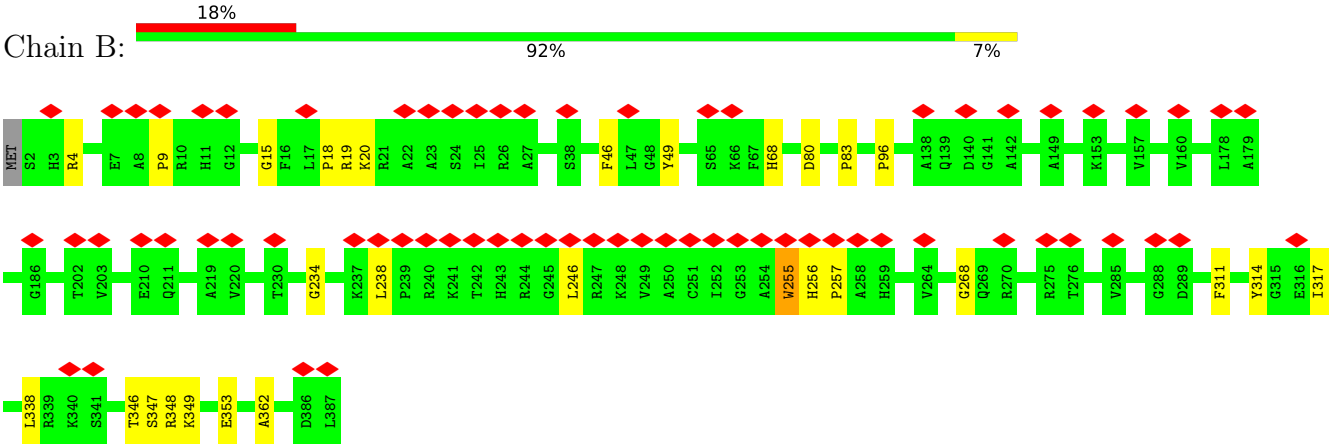
• Molecule 1: 60S ribosomal protein L2-A



• Molecule 2: 60S ribosomal protein L30

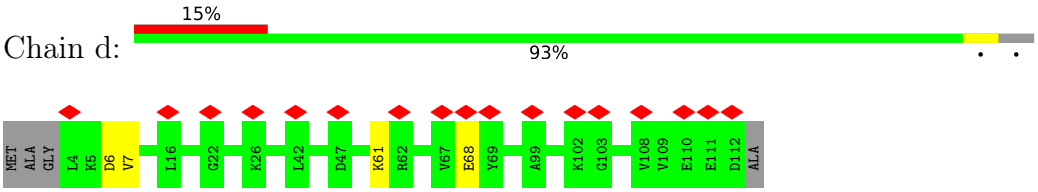


• Molecule 3: 60S ribosomal protein L3



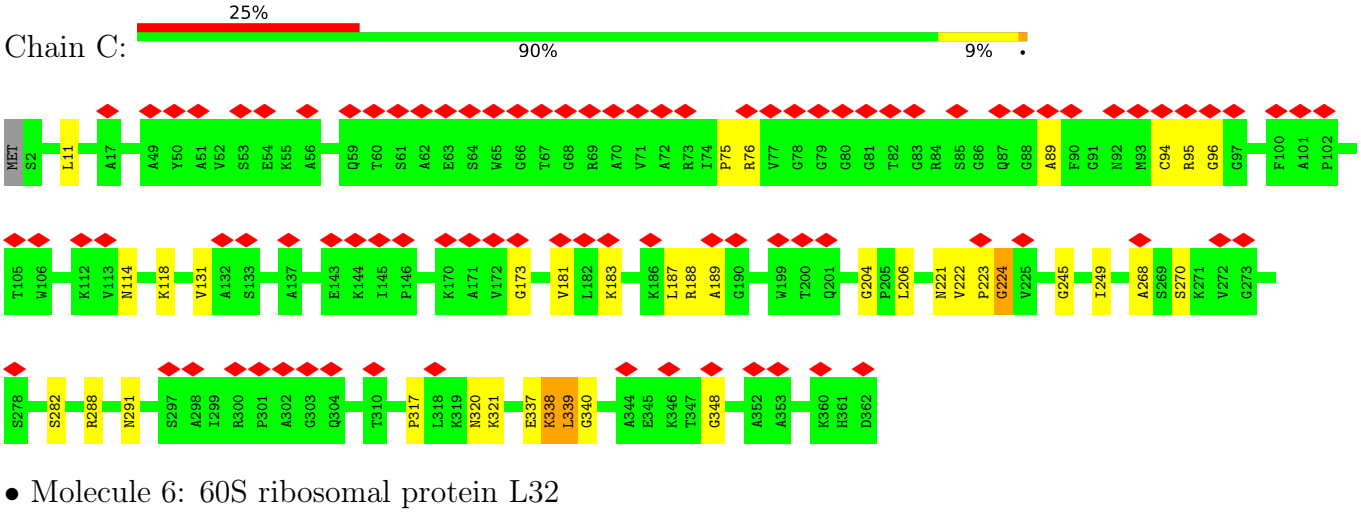
• Molecule 4: 60S ribosomal protein L31-A

Chain d:



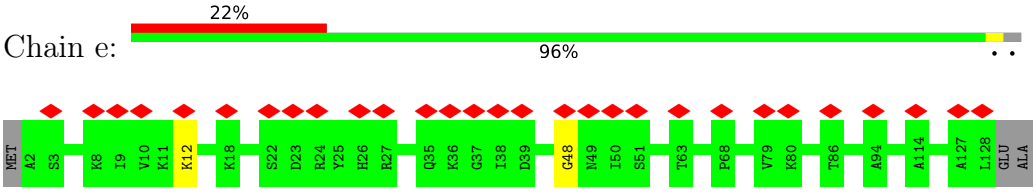
• Molecule 5: 60S ribosomal protein L4-A

Chain C:



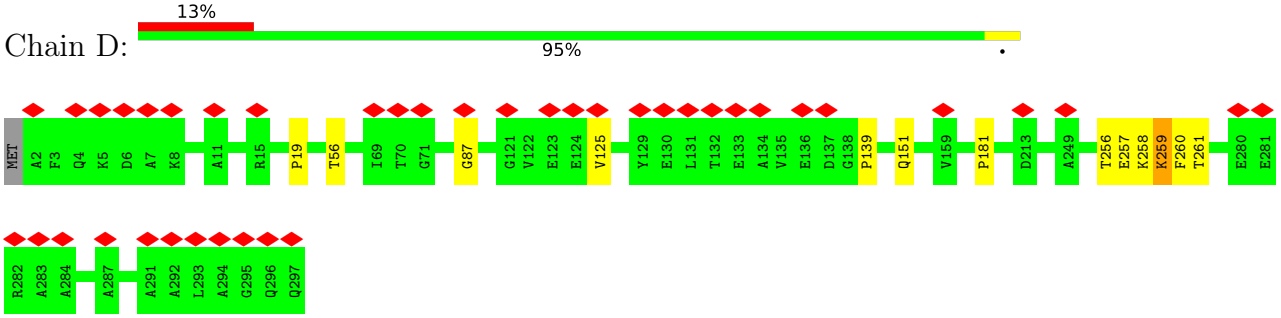
• Molecule 6: 60S ribosomal protein L32

Chain e:



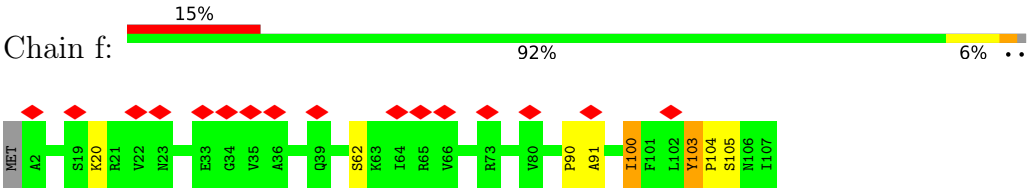
• Molecule 7: 60S ribosomal protein L5

Chain D:



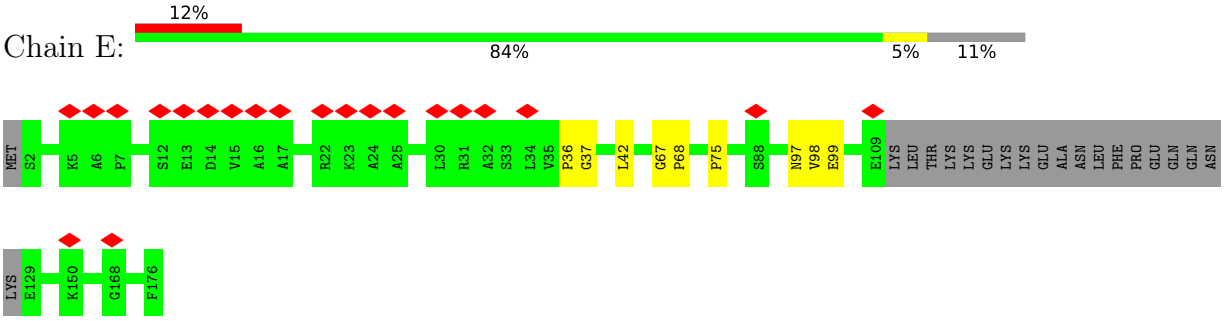
• Molecule 8: 60S ribosomal protein L33-A

Chain f:



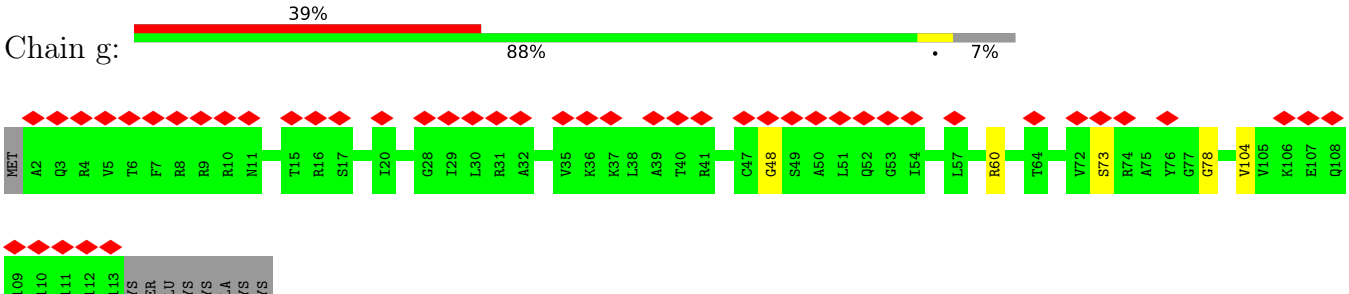
• Molecule 9: 60S ribosomal protein L6-A

Chain E:



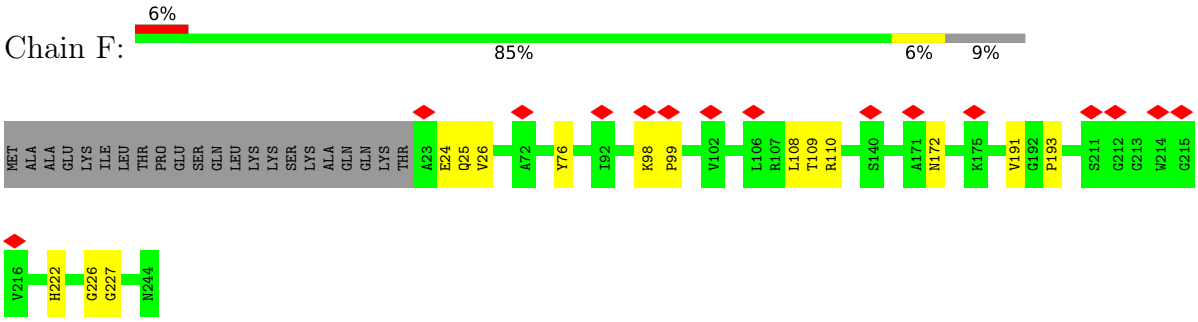
• Molecule 10: 60S ribosomal protein L34-A

Chain g:



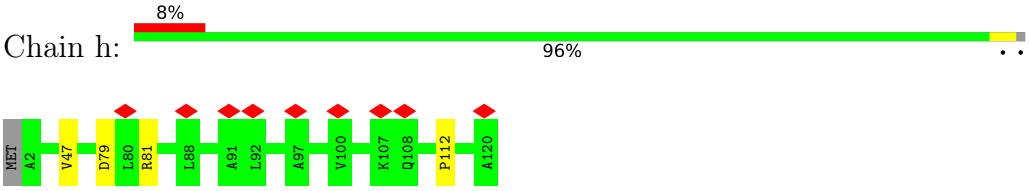
• Molecule 11: 60S ribosomal protein L7-A

Chain F:



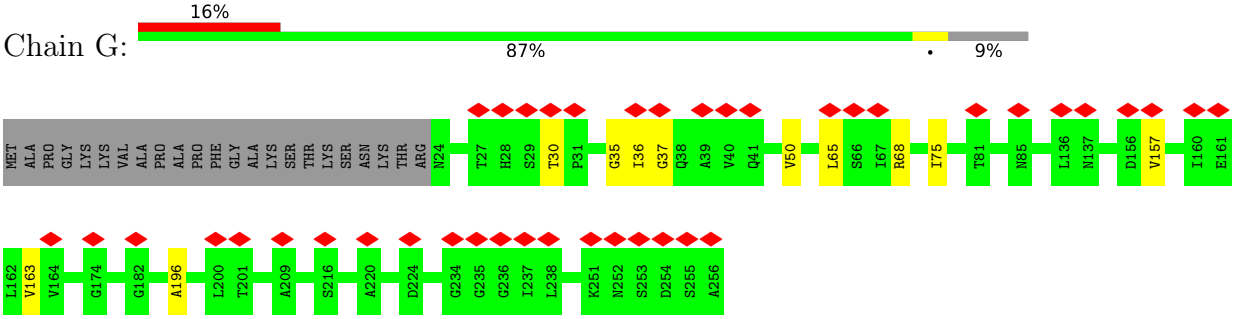
• Molecule 12: 60S ribosomal protein L35-A

Chain h:



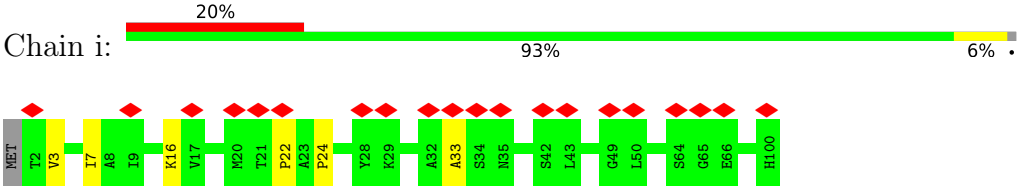
• Molecule 13: 60S ribosomal protein L8-A

Chain G:



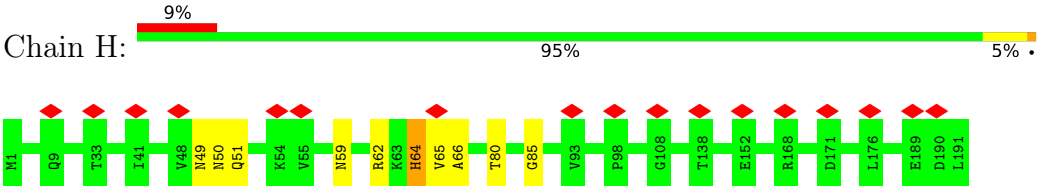
• Molecule 14: 60S ribosomal protein L36-A

Chain i:



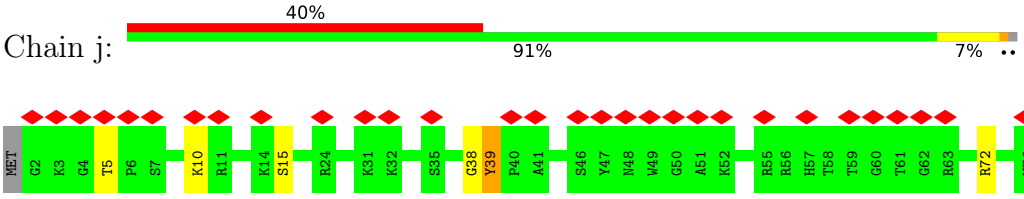
• Molecule 15: 60S ribosomal protein L9-A

Chain H:



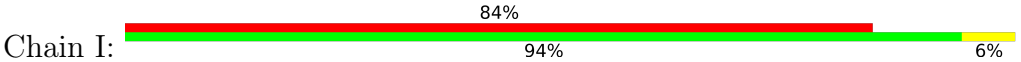
• Molecule 16: 60S ribosomal protein L37-A

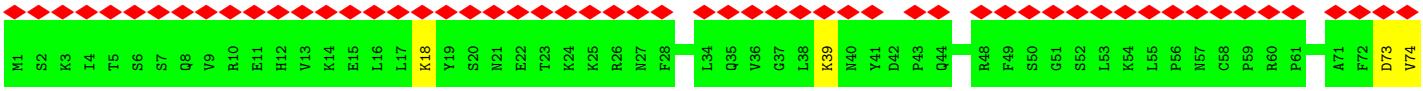
Chain j:

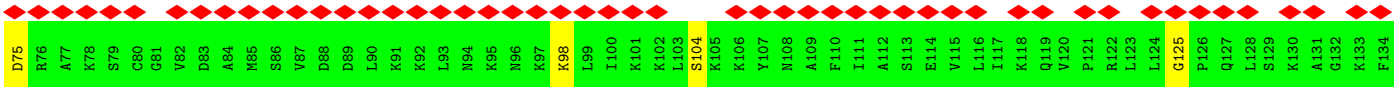


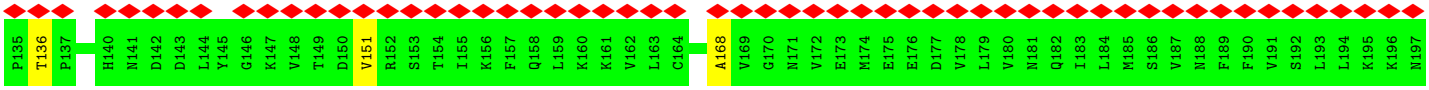
• Molecule 17: 60S ribosomal protein L1-A

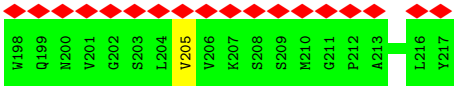
Chain I:





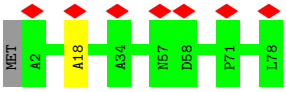






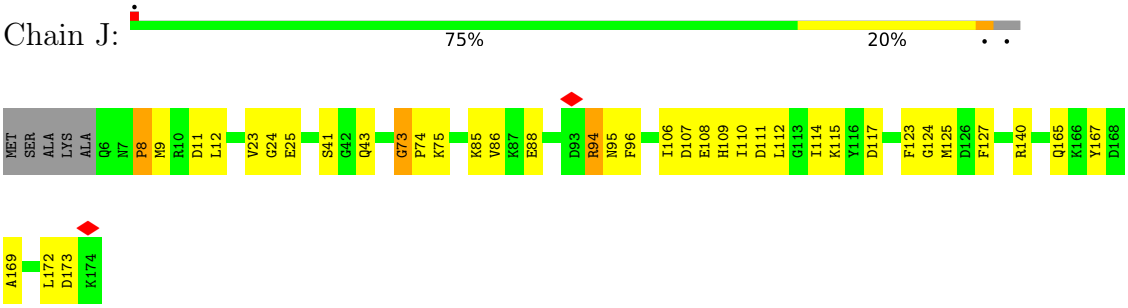
• Molecule 18: 60S ribosomal protein L38

Chain k:



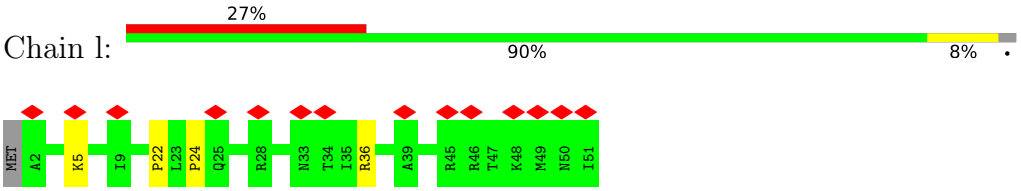
• Molecule 19: 60S ribosomal protein L11-A

Chain J:



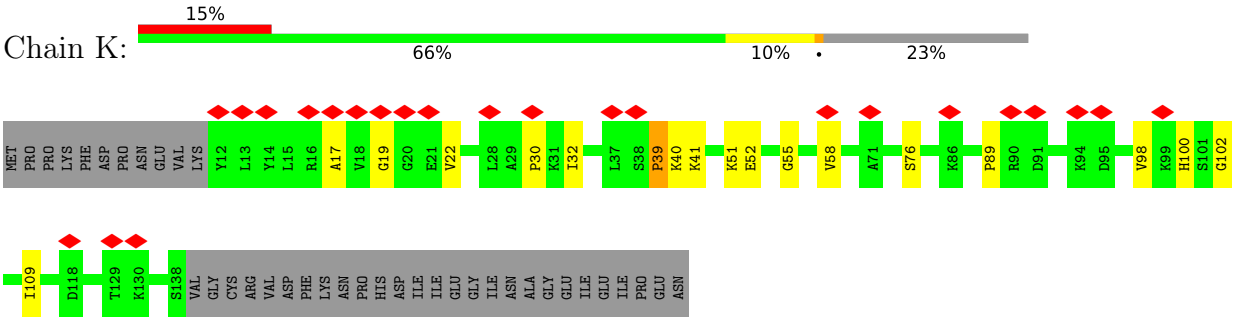
• Molecule 20: 60S ribosomal protein L39

Chain l:



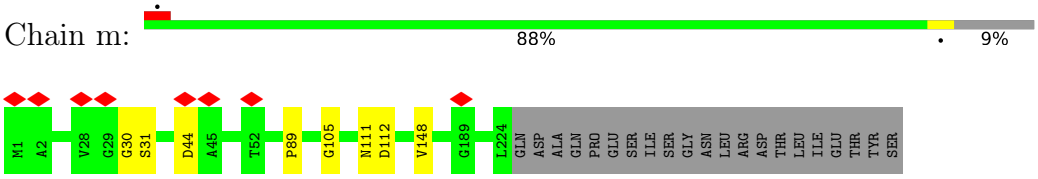
• Molecule 21: 60S ribosomal protein L12-A

Chain K:



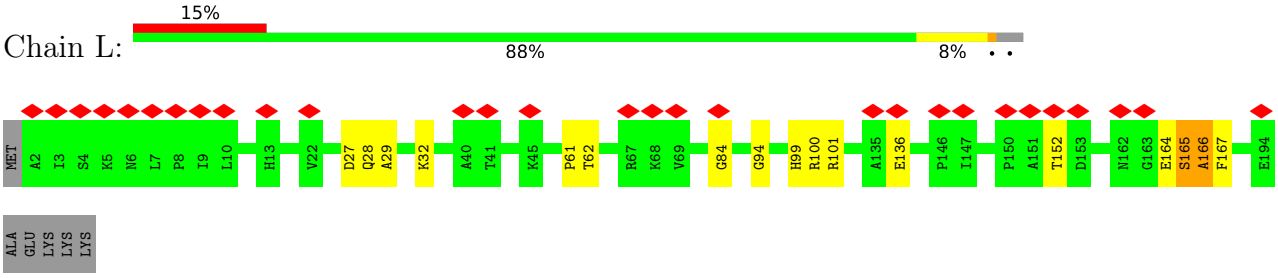
• Molecule 22: Eukaryotic translation initiation factor 6

Chain m:



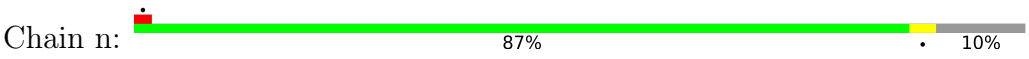
• Molecule 23: 60S ribosomal protein L13-A

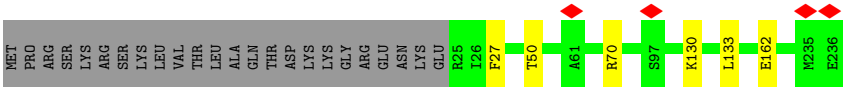
Chain L:



• Molecule 24: Ribosome assembly factor MRT4

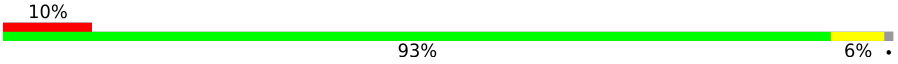
Chain n:

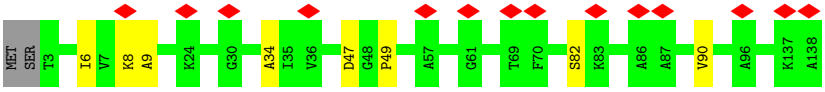




• Molecule 25: 60S ribosomal protein L14-A

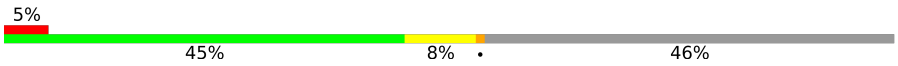
Chain M:

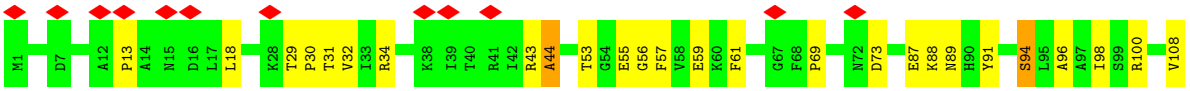


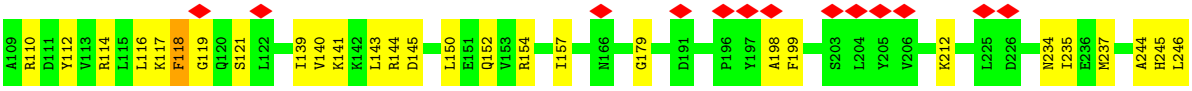


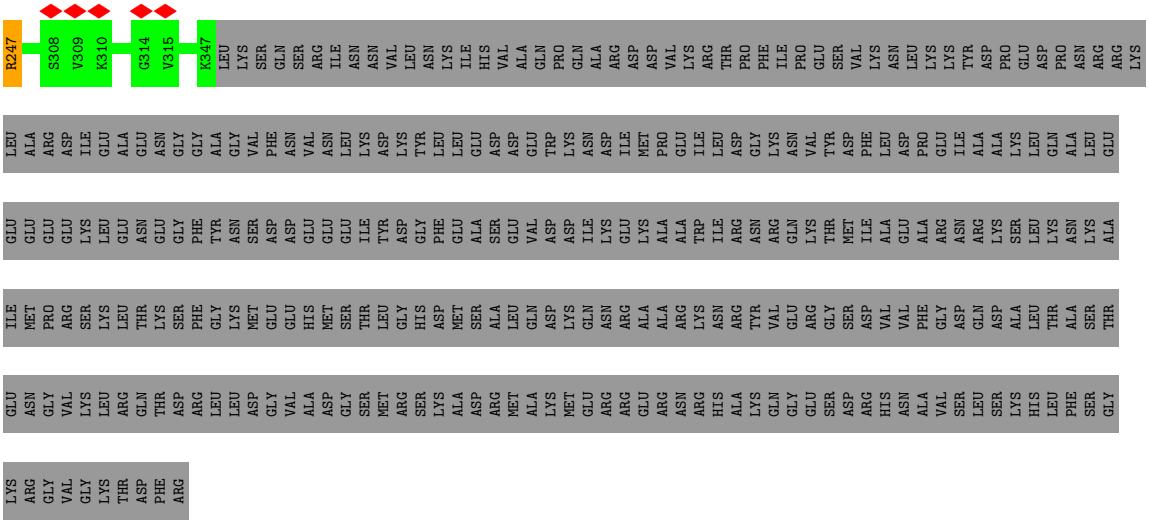
• Molecule 26: Nucleolar GTP-binding protein 1

Chain o:



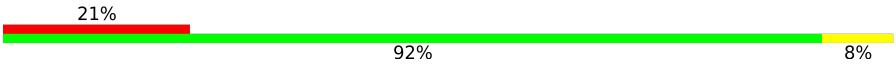


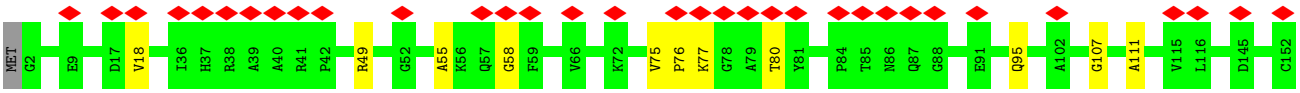


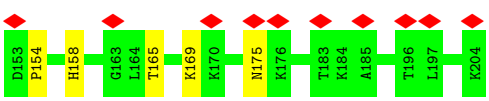


• Molecule 27: 60S ribosomal protein L15-A

Chain N:

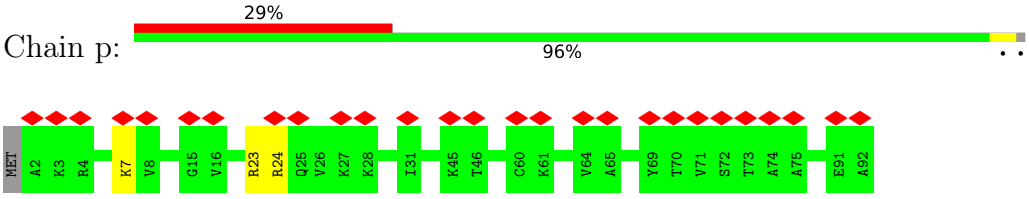






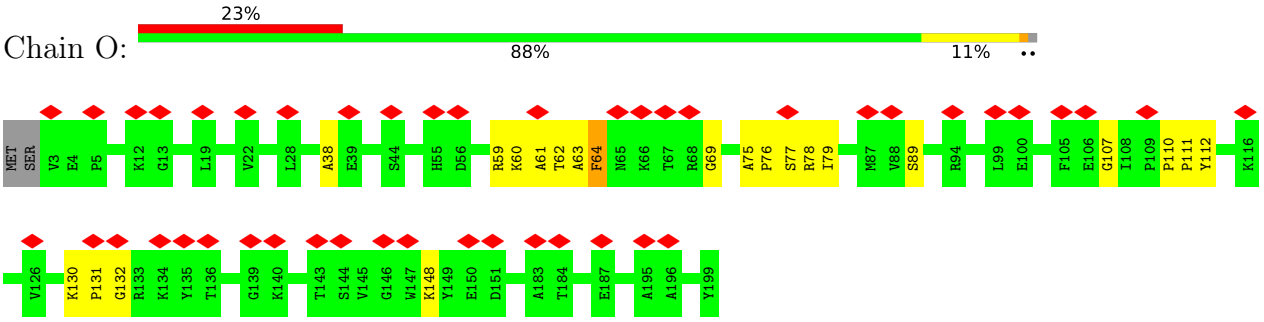
• Molecule 28: 60S ribosomal protein L43-A

Chain p:



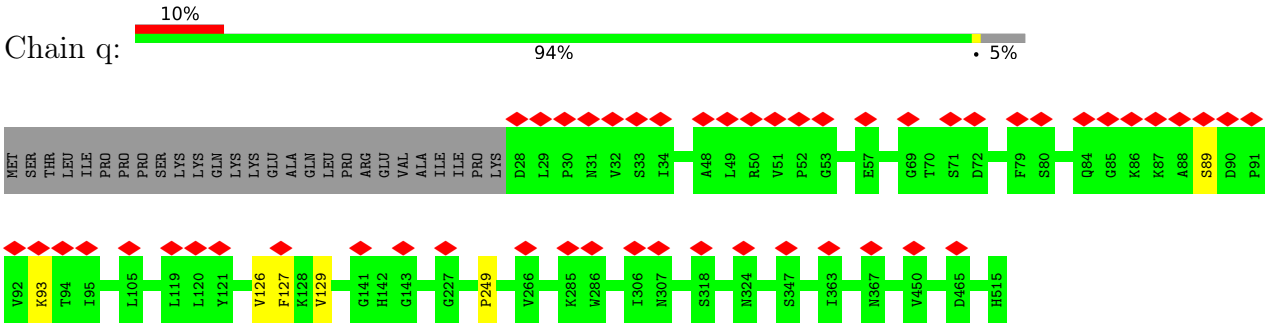
• Molecule 29: 60S ribosomal protein L16-A

Chain O:



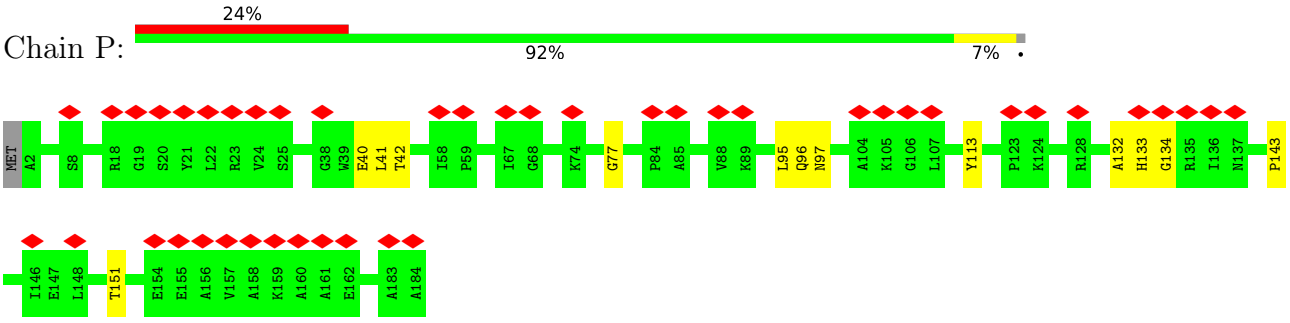
• Molecule 30: Ribosome assembly protein 4

Chain q:



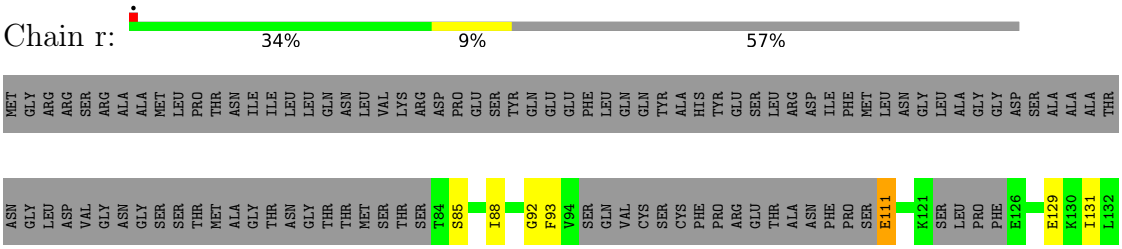
• Molecule 31: 60S ribosomal protein L17-A

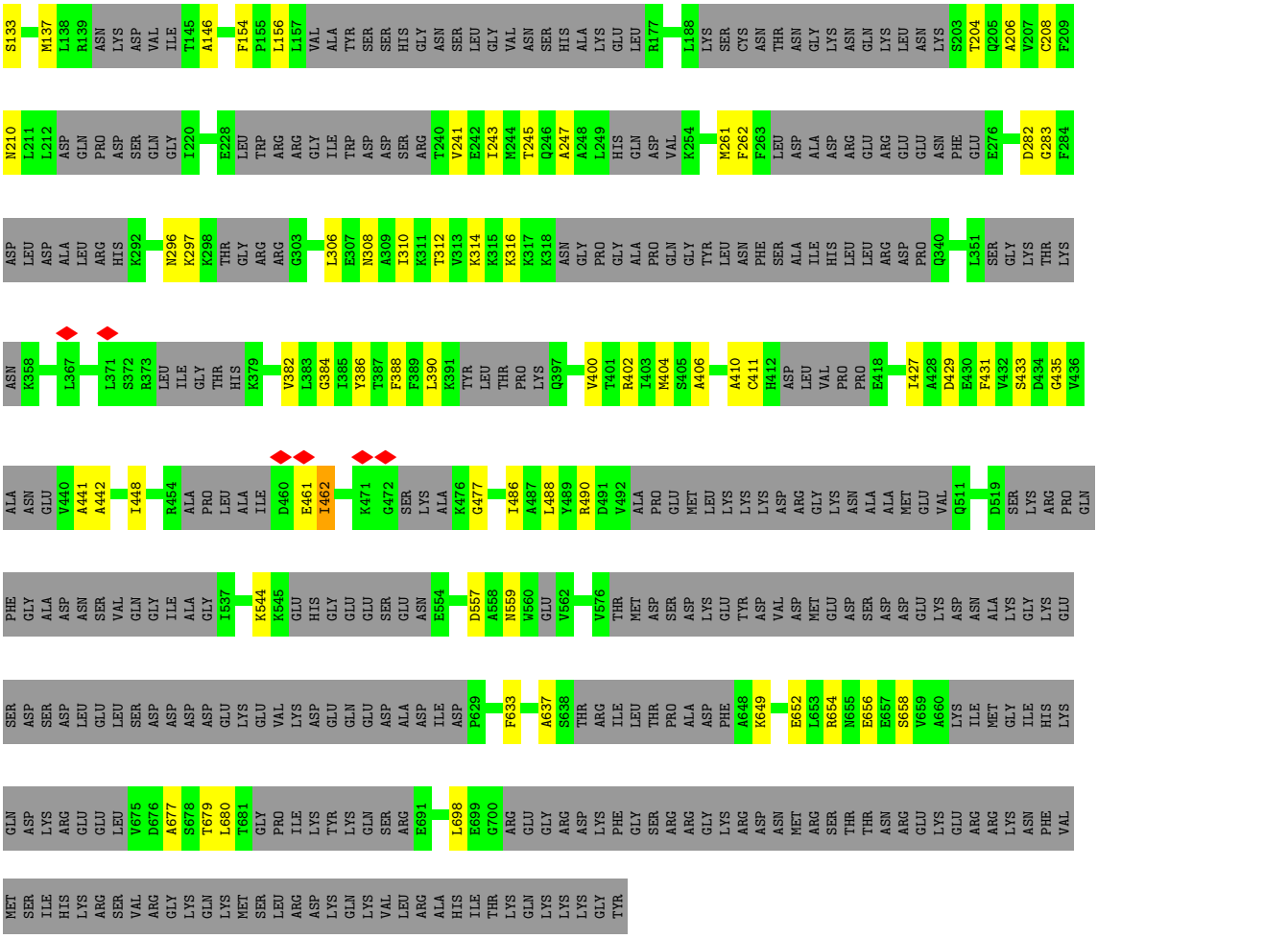
Chain P:



• Molecule 32: Protein SDA1

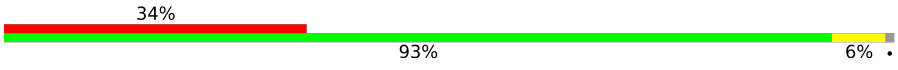
Chain r:

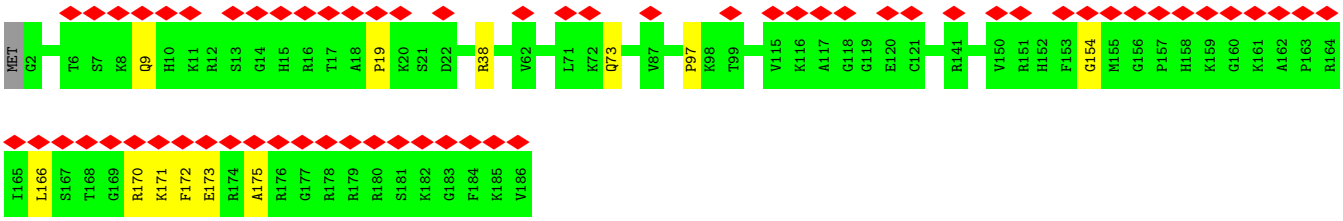




• Molecule 33: 60S ribosomal protein L18-A

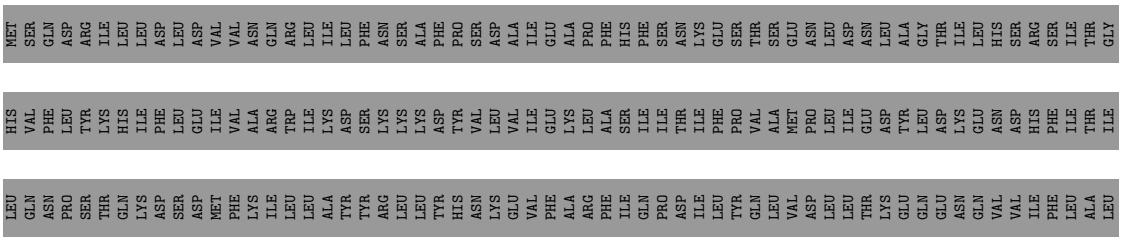
Chain Q:

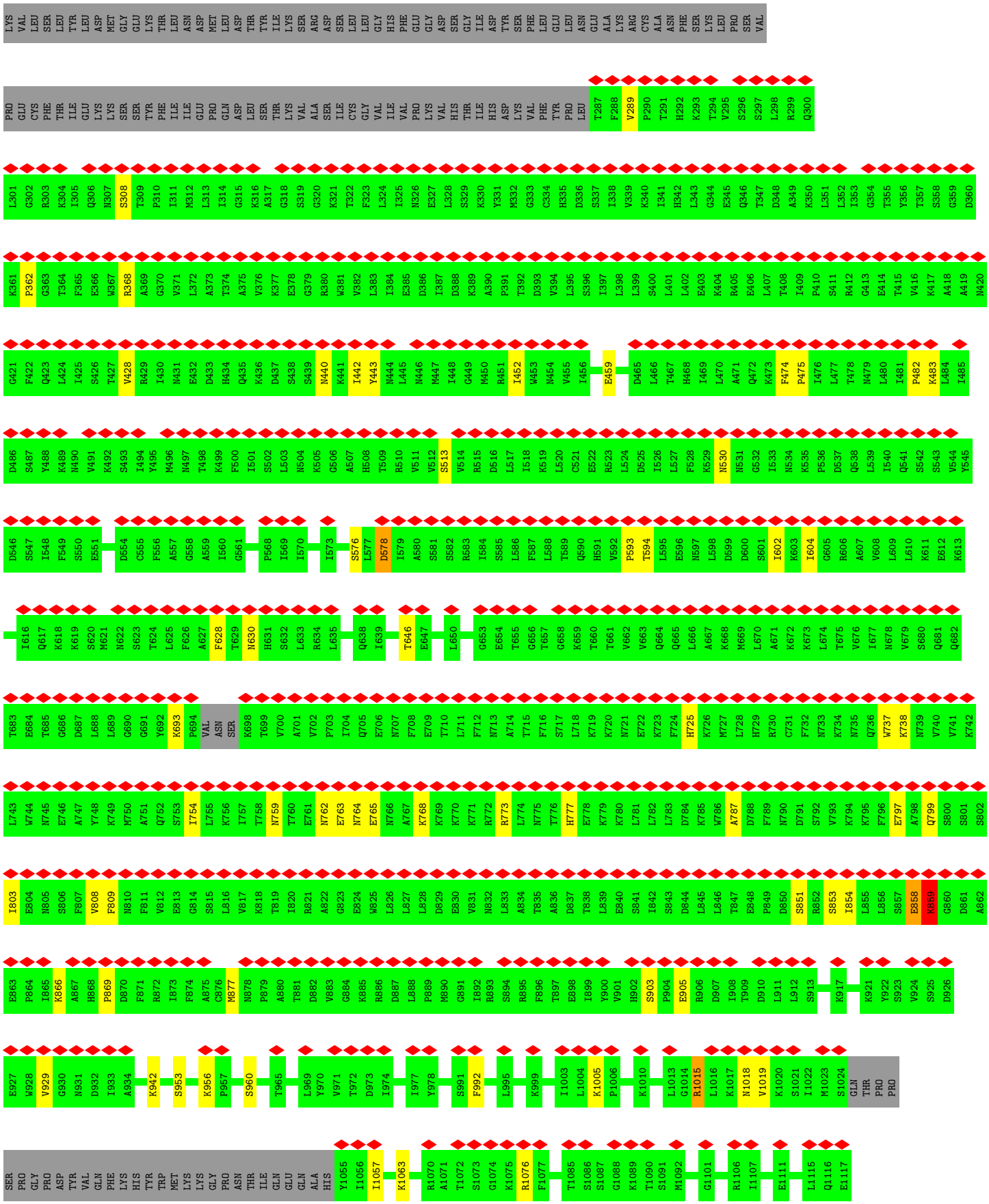




• Molecule 34: Midasin

Chain s:

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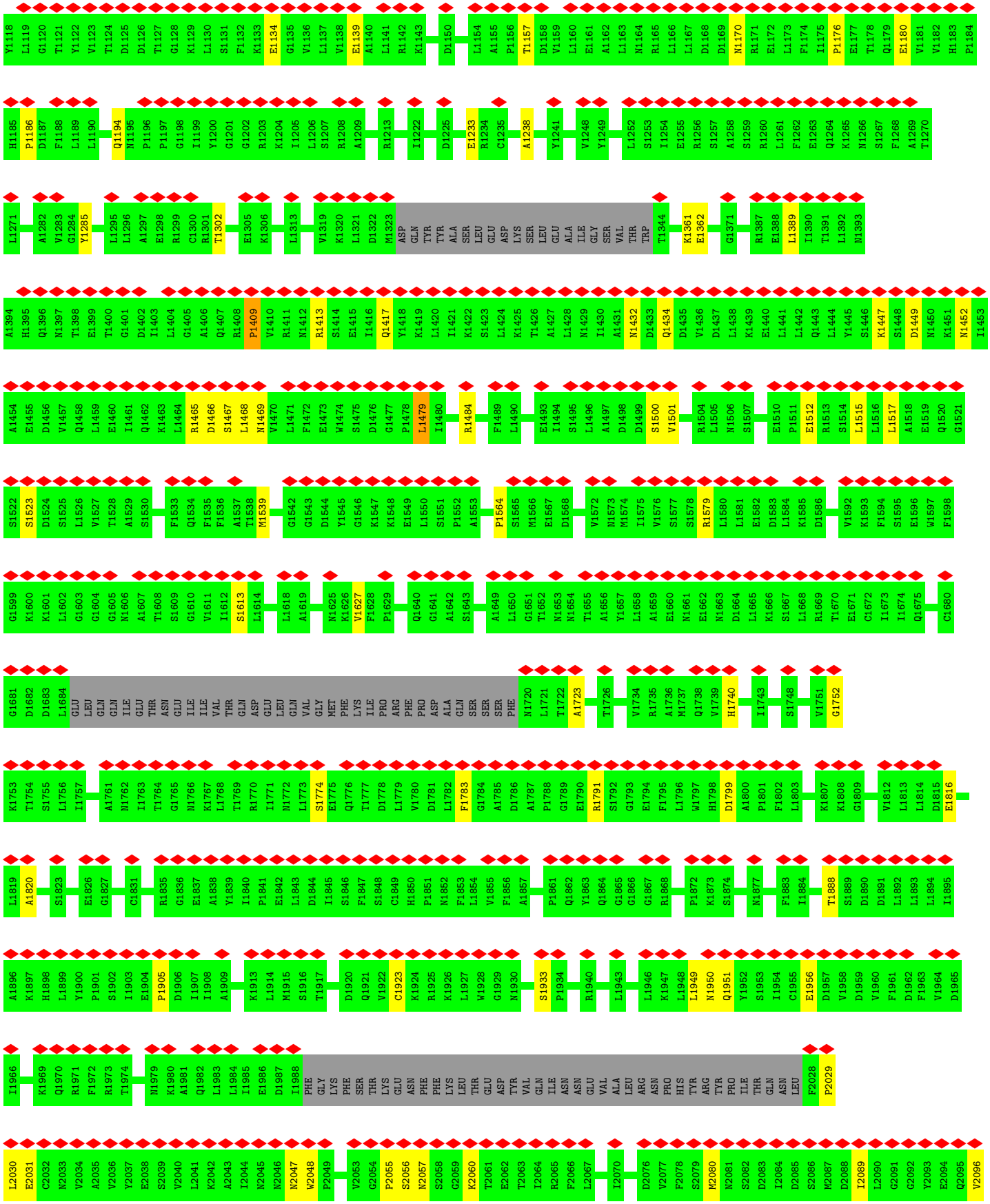
PRO GLU CYS PHE THR ILE GLU LYS LYS SER SER TYR PHE ILE ILE GLU PRO GLN ASP LEU SER THR LYS VAL ALA SER ILE CYS GLY VAL ILE VAL PRO LYS VAL HIS THR ILE HIS ASP LYS VAL PHE TYR PRO LEU T287 F288 V289 P290 T291 H292 K293 T294 V295 S296 S297 L298 R299 Q300
L301 G302 R303 K304 I305 Q306 N307 S308 T309 P310 I311 M312 L313 I314 G315 K316 A317 G318 S319 G320 K321 T322 F323 L324 I325 N326 E327 L328 S329 K330 Y331 M332 G333 C334 H335 D336 S337 I338 V339 K340 I341 H342 L343 G344 E345 Q346 T347 D348 A349 K350 L351 L352 I353 G354 T355 Y356 T357 S358 G359 D360
K361 P362 G363 T364 F365 E366 W367 R368 A369 G370 V371 L372 A373 T374 A375 V376 K377 E378 G379 R380 W381 V382 L383 I384 E385 D386 I387 D388 K389 A390 P391 T392 D393 V394 L395 S396 I397 L398 L399 S400 L401 L402 E403 K404 R405 E406 L407 T408 I409 P410 S411 R412 G413 E414 T415 V416 K417 A418 A419 M420
G421 F422 Q423 L424 I425 S426 T427 V428 R429 I430 N431 E432 D433 H434 Q435 K436 D437 S438 S439 N440 K441 I442 Y443 N444 L445 N446 M447 I448 G449 M450 R451 I452 W453 N454 V455 I456 E459 D465 L466 T467 H468 I469 L470 A471 Q472 K473 F474 P475 I476 L477 T478 N479 L480 I481 P482 K483 L484 I485
D486 S487 Y488 K489 N490 V491 K492 S493 I494 Y495 M496 N497 T498 K499 F500 I501 S502 L503 N504 K505 G506 A507 H508 T509 R510 V511 V512 S513 V514 R515 D516 L517 I518 K519 L520 C521 E522 R523 L524 D525 I526 L527 F528 K529 N530 N531 G532 I533 N534 K535 P536 D537 Q538 L539 I540 Q541 S542 S543 V544 Y545
D546 S547 I548 F549 S550 E551 D554 C555 F556 A557 G558 A559 I560 G561 P568 I569 I570 I573 S576 L577 D578 I579 A580 S581 S582 R583 I584 S585 L586 F587 L588 T589 Q590 H591 V592 P593 T594 L595 E596 N597 L598 D599 D600 S601 I602 K603 I604 G605 R606 A607 V608 L609 L610 K611 E612 K613
I616 Q617 K618 K619 S620 M621 N622 S623 T624 L625 F626 A627 F628 T629 N630 H631 S632 L633 R634 L635 Q638 I639 T646 E647 L650 G653 E654 T655 G656 T657 G658 K659 T660 T661 V662 V663 Q664 Q665 L666 A667 K668 M669 L670 A671 K672 K673 L674 T675 V676 I677 N678 V679 S680 Q681 Q682
T683 E684 T685 G686 D687 L688 L689 G690 G691 Y692 K693 P694 VAL ASN SER K698 T699 V700 A701 V702 P703 I704 Q705 E706 N707 F708 E709 T710 L711 F712 N713 A714 T715 F716 S717 L718 K719 K720 N721 E722 K723 F724 H725 K726 M727 L728 H729 R730 C731 F732 N733 K734 N735 Q736 W737 K738 N739 V740 V741 K742
L743 W744 N745 E746 A747 Y748 K749 M750 A751 Q752 S753 I754 L755 K756 I757 T758 N759 T760 E761 N762 E763 N764 E765 N766 A767 K768 K769 K770 K771 R772 R773 L774 N775 T776 H777 E778 K779 K780 L781 L782 L783 D784 K785 W786 A787 D788 F789 N790 D791 S792 V793 K794 K795 F796 E797 A798 Q799 S800 S801 S802
I803 E804 N805 S806 F807 V808 F809 N810 F811 V812 E813 G814 S815 L816 V817 K818 T819 I820 R821 A822 G823 E824 W825 L826 L827 L828 D829 E830 V831 N832 L833 A834 T835 A836 D837 T838 L839 E840 S841 I842 S843 D844 L845 L846 T847 E848 P849 D850 S851 R852 S853 I854 L855 L856 S857 E858 K859 G860 D861 A862
E863 P864 I865 K866 A867 H868 P869 D870 F871 R872 I873 F874 A875 C876 M877 N878 P879 A880 T881 D882 V883 G884 K885 R886 D887 L888 P889 M890 G891 I892 R893 S894 R895 F896 T897 E898 I899 Y900 Y901 H902 S903 P904 E905 R906 D907 I908 T909 D910 L911 L912 S913 K917 K921 Y922 S923 Y924 S925 D926
E927 W928 V929 G930 N931 D932 I933 A934 K942 S953 K956 P957 S960 T965 L969 Y970 V971 T972 D973 I974 I977 Y978 S991 F992 L995 K999 I1003 L1004 K1005 P1006 K1010 L1013 G1014 R1015 L1016 K1017 N1018 V1019 K1020 S1021 I1022 M1023 S1024 GLN THR PRO PRO
SER PRO GLY PRO ASP TYR VAL GLN PHE LYS HIS TYR TRP MET LYS LYS GLY PRO ASN THR ILE GLN GLU GLN ALA HIS Y1055 I1056 I1057 K1063 R1070 A1071 T1072 S1073 G1074 K1075 R1076 F1077 T1085 S1086 S1087 G1088 K1089 T1090 S1091 M1092 G1101 R1106 I1107 E1111 L1115 Q1116 E1117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H1185 P1186 D1187 F1188 L1189 L1190 Q1194 N1195 P1196 P1197 G1198 I1199 Y1200 G1201 G1202 R1203 K1204 I1205 L1206 S1207 R1208 A1209 R1213 I1222 D1225 E1233 R1234 C1235 A1238 Y1241 V1248 Y1249 L1252 S1253 I1254 E1255 R1256 S1257 A1258 S1259 R1260 L1261 F1262 E1263 Q1264 K1265 N1266 S1267 F1268 A1269 T1270
L1271 A1282 V1283 G1284 Y1285 L1295 L1296 A1297 E1298 R1299 C1300 R1301 T1302 E1305 K1306 L1313 V1319 K1320 L1321 D1322 M1323 ASP GLN TYR TYR ALA SER LEU GLU ASP LYS SER LEU GLU ALA ILE GLY SER VAL THR TRP T1344 K1361 E1362 G1371 R1387 E1388 L1389 I1390 T1391 L1392 N1393
A1394 H1395 Q1396 N1397 T1398 E1399 T1400 G1401 D1402 I1403 L1404 G1405 A1406 Q1407 R1408 P1409 V1410 R1411 N1412 R1413 S1414 E1415 I1416 Q1417 Y1418 K1419 L1420 I1421 K1422 S1423 L1424 K1425 T1426 A1427 L1428 N1429 I1430 A1431 N1432 D1433 Q1434 D1435 V1436 D1437 L1438 K1439 E1440 L1441 L1442 Q1443 L1444 Y1445 S1446 K1447 S1448 D1449 N1450 K1451 N1452 I1453
A1454 E1455 D1456 V1457 Q1458 L1459 E1460 I1461 Q1462 K1463 L1464 R1465 D1466 S1467 L1468 N1469 V1470 L1471 F1472 E1473 W1474 S1475 D1476 G1477 P1478 L1479 I1480 R1484 F1489 L1490 E1493 I1494 S1495 L1496 A1497 D1498 D1499 S1500 V1501 R1504 L1505 N1506 S1507 E1510 P1511 E1512 R1513 S1514 L1515 L1516 L1517 A1518 E1519 Q1520 G1521
S1522 S1523 D1524 S1525 L1526 V1527 T1528 A1529 S1530 F1533 Q1534 F1535 F1536 A1537 T1538 M1539 G1542 G1543 D1544 Y1545 G1546 K1547 K1548 E1549 L1550 S1551 P1552 A1553 P1564 S1565 M1566 E1567 D1568 V1572 N1573 M1574 I1575 V1576 S1577 S1578 R1579 L1580 L1581 E1582 D1583 L1584 K1585 D1586 V1592 K1593 F1594 S1595 E1596 W1597 F1598
G1599 K1600 K1601 L1602 G1603 G1604 G1605 N1606 A1607 T1608 S1609 G1610 V1611 I1612 S1613 L1614 L1618 A1619 N1625 K1626 V1627 F1628 P1629 Q1640 G1641 A1642 S1643 A1649 L1650 G1651 T1652 N1653 N1654 T1655 A1656 Y1657 L1658 A1659 E1660 N1661 E1662 N1663 D1664 L1665 K1666 S1667 L1668 R1669 T1670 E1671 C1672 I1673 I1674 Q1675 C1680
G1681 D1682 D1683 L1684 GLU LEU GLN GLN ILE GLU THR ASN GLU ILE ILE VAL THR GLN ASP GLU LEU GLN VAL GLY MET PHE LYS ILE PRO ARG PHE PRO ASP ALA GLN SER SER SER PHE N1720 L1721 T1722 A1723 T1726 V1734 R1735 A1736 M1737 Q1738 V1739 H1740 I1743 S1748 V1751 G1752
K1753 T1754 S1755 L1756 I1757 A1761 N1762 I1763 T1764 G1765 N1766 K1767 L1768 T1769 R1770 I1771 N1772 L1773 S1774 E1775 Q1776 T1777 D1778 L1779 V1780 D1781 L1782 F1783 G1784 A1785 D1786 A1787 P1788 G1789 E1790 R1791 S1792 G1793 E1794 F1795 L1796 W1797 H1798 D1799 A1800 P1801 F1802 L1803 K1807 K1808 G1809 V1812 L1813 L1814 D1815 E1816
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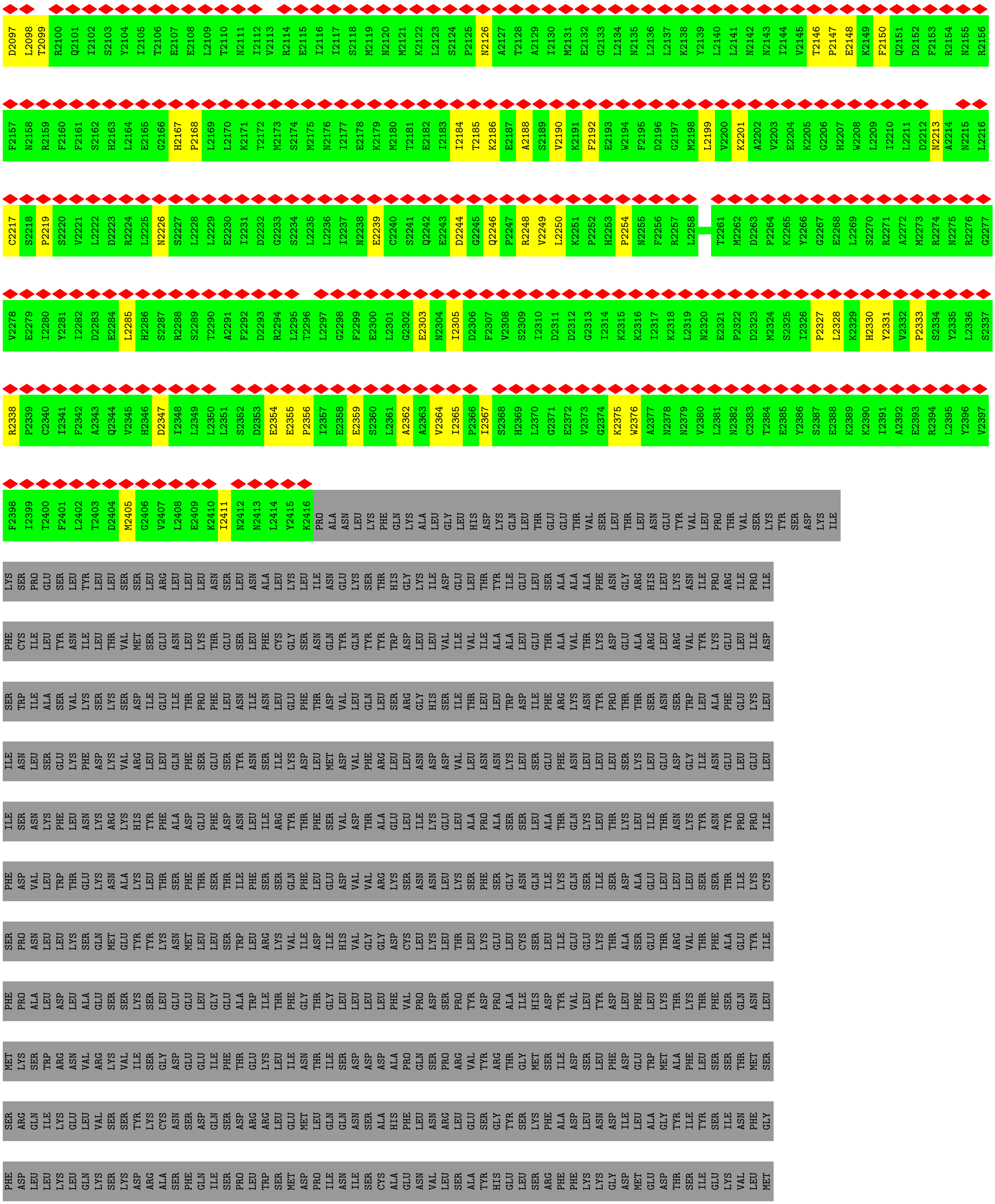
A1896 K1897 H1898 L1899 Y1900 P1901 S1902 I1903 E1904 P1905 D1906 I1907 I1908 A1909 K1913 L1914 M1915 S1916 T1917 D1920 Q1921 V1922 C1923 K1924 R1925 K1926 L1927 W1928 G1929 N1930 S1933 P1934 R1940 L1943 L1946 K1947 L1948 L1949 N1950 Q1951 Y1952 S1953 I1954 C1955 E1956 D1957 V1958 D1959 V1960 F1961 D1962 F1963 V1964 D1965
I1966 K1969 Q1970 R1971 F1972 R1973 T1974 N1979 K1980 A1981 Q1982 L1983 L1984 I1985 E1986 D1987 I1988 PHE GLY LYS PHE SER THR LYS GLU ASN PHE PHE LYS LEU THR GLU ASP TYR VAL GLN ILE ASN ASN GLU VAL ALA LEU ARG ASN PRO HIS TYR ARG TYR PRO ILE THR GLN ASN LEU F2028 P2029
L2030 E2031 C2032 N2033 V2034 A2035 V2036 Y2037 E2038 S2039 V2040 L2041 K2042 A2043 I2044 N2045 N2046 N2047 W2048 P2049 V2053 G2054 P2055 S2056 N2057 S2058 G2059 K2060 T2061 E2062 T2063 I2064 R2065 F2066 L2067 I2070 D2076 V2077 F2078 S2079 M2080 W2081 S2082 D2083 I2084 D2085 S2086 M2087 D2088 I2089 L2090 G2091 C2092 Y2093 E2094 Q2095 V2096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V2278 E2279 I2280 Y2281 I2282 D2283 E2284 L2285 H2286 S2287 R2288 S2289 T2290 A2291 F2292 D2293 R2294 L2295 T2296 L2297 G2298 F2299 E2300 L2301 G2302 E2303 N2304 I2305 D2306 F2307 V2308 S2309 I2310 D2311 D2312 G2313 I2314 K2315 K2316 I2317 K2318 L2319 N2320 E2321 P2322 D2323 M2324 S2325 I2326 P2327 L2328 K2329 H2330 Y2331 V2332 P2333 S2334 Y2335 L2336 S2337
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F2398 I2399 T2400 F2401 L2402 T2403 D2404 M2405 G2406 V2407 L2408 E2409 K2410 I2411 N2412 N2413 L2414 Y2415 K2416 PRO ALA ASN LEU LYS PHE GLN LYS ALA LEU GLY LEU HIS ASP LYS GLN LEU THR GLU GLU THR VAL SER LEU THR LEU ASN GLU TYR VAL LEU PRO THR VAL SER LYS TYR SER ASP LYS ILE
LYS SER PRO GLU SER LEU TYR LEU LEU SER SER LEU ARG LEU LEU LEU ASN SER LEU ASN ALA LEU LYS LEU ILE ASN GLU LYS SER THR HIS GLY LYS ILE ASP GLU LEU THR TYR ILE GLU LEU SER ALA ALA ALA PHE ASN GLY ARG HIS LEU LYS ASN ILE PRO ARG ILE PRO ILE
PHE CYS ILE LEU TYR ASN ILE LEU THR VAL MET SER GLU ASN LEU LYS THR GLU SER LEU PHE CYS GLY SER ASN GLN TYR GLN TYR TRP ASP LEU LEU VAL ILE VAL ILE ALA ALA LEU GLU THR ALA VAL THR LYS ASP GLU ALA ARG LEU ARG VAL TYR LYS GLU LEU ILE ASP
SER TRP ILE ALA SER VAL LYS SER LYS SER ASP ILE GLU ILE THR PRO PHE LEU ASN ILE ASN LEU GLU PHE THR ASP VAL LEU GLN LEU SER ARG GLY HIS SER ILE THR LEU LEU TRP ASP ILE PHE ARG LYS ASN TYR PRO THR THR SER ASN SER TRP LEU ALA PHE GLU LYS LEU
ILE ASN LEU SER GLU LYS PHE ASP LYS VAL ARG LEU LEU GLN PHE SER GLU SER TYR ASN SER ILE LYS ASP LEU MET ASP VAL PHE ARG LEU LEU ASN ASP ASP VAL LEU ASN ASN LYS LEU SER GLU PHE ASN LEU LEU LEU SER LYS LEU GLU ASP GLY ILE ASN GLU LEU GLU LEU
ILE SER ASN LYS PHE LEU ASN LYS ARG LYS HIS TYR PHE ALA ASP GLU PHE ASP ASN LEU ILE ARG TYR THR PHE SER VAL ASP THR ALA GLU LEU ILE LYS GLU LEU ALA PRO ALA SER SER LEU ALA THR GLN LYS LEU THR LYS LEU ILE THR ASN LYS TYR ASN TYR PRO PRO ILE
PHE ASP VAL LEU TRP THR GLU LYS ASN ALA LYS LEU THR SER PHE THR SER THR ILE PHE SER SER GLN PHE LEU GLU ASP VAL VAL ARG LYS SER ASN ASN LEU LYS SER PHE SER GLY ASN GLN ILE LYS GLN SER ILE SER ASP ALA GLU LEU LEU LEU SER SER THR ILE LYS CYS
SER PRO ASN LEU LEU LYS SER GLN MET GLU TYR TYR LYS ASN MET LEU LEU SER TRP LEU ARG LYS VAL ILE ASP ILE HIS VAL GLY GLY ASP CYS LEU LYS LEU THR LEU LYS GLU LEU CYS SER LEU ILE GLU GLU LYS THR ALA SER GLU THR ARG VAL THR PHE ALA GLU TYR ILE
PHE PRO ALA LEU ASP LEU ALA GLU SER SER LYS SER LEU GLU GLU GLU LEU GLY GLU ALA TRP ILE THR PHE GLY THR GLY LEU LEU LEU LEU PHE VAL PRO ASP SER PRO TYR ASP PRO ALA ILE HIS ASP TYR VAL LEU TYR ASP LEU PHE LEU LYS THR LYS THR PHE SER GLN ASN LEU
MET LYS SER TRP ARG ASN VAL ARG LYS VAL ILE SER GLY ASP GLU GLU ILE PHE THR GLU LYS LEU ILE ASN THR ILE SER ASP ASP ALA PRO GLN SER PRO ARG VAL TYR ARG THR GLY MET SER ILE ASP SER LEU PHE ASP GLU TRP MET ALA PHE LEU SER SER THR MET SER
SER ARG GLN ILE LYS GLU LEU VAL SER SER TYR LYS CYS ASN SER ASP GLN SER ASP ARG ARG LEU GLU MET LEU GLN GLN ASN SER ALA HIS PHE LEU ASN ARG LEU GLU SER GLY TYR SER LYS PHE ALA ASP LEU ASN ASP ILE LEU ALA GLY TYR ILE TYR SER ILE ASN PHE GLY
PHE ASP LEU LEU LYS LEU GLN LYS SER LYS ASP ARG ALA SER PHE GLN ILE SER PRO LEU TRP SER MET ASP PRO ILE ASN ILE SER CYS ALA GLU ASN VAL LEU SER ALA TYR HIS GLU LEU SER ARG PHE PHE LYS LYS GLY ASP MET GLU ASP THR SER ILE GLU LYS VAL LEU MET

TYR PHE LEU THR LEU PHE LYS PHE HIS LYS ARG ASP THR ASN LEU LEU GLU ILE PHE GLU ALA ALA LEU TYR THR LEU TYR SER ARG TRP SER VAL ARG ARG PHE ARG GLN GLU GLN GLU ASN GLU LYS SER ASN MET PHE LYS PHE ASN ASP ASN SER ASP ASP TYR GLU ALA ASP

PHE ARG LYS LEU PHE PRO ASP TYR GLU ASP THR ALA LEU VAL THR ASN GLU LYS ASP ILE SER SER PRO GLU ASN LEU ASP ASP ILE TYR PHE LYS LEU ALA ASP THR TYR ILE SER VAL PHE ASP LYS ASP HIS ASP ALA ASN PHE SER SER GLU LEU LYS SER GLY ALA ILE ILE THR

THR ILE LEU SER GLU ASP LEU LYS ASN THR ARG ILE GLU GLU LEU LYS SER GLY SER LEU SER ALA VAL ILE ASN THR LEU ASP ALA GLU THR GLN SER PHE LYS ASN THR GLU VAL PHE GLY ASN ILE ASP PHE TYR HIS ASP PHE SER ILE PRO GLU PHE GLN LYS ALA GLY ASP ILE

ILE GLU THR VAL LEU LYS SER VAL LEU LYS LEU LEU LYS GLN TRP PRO GLU HIS ALA THR LEU LYS GLU LEU TYR ARG VAL SER GLN GLU PHE LEU ASN TYR PRO ILE LYS THR PRO LEU ALA ARG GLN LEU GLN LYS ILE GLU GLN ILE TYR THR TYR LEU ALA GLU TRP GLU LYS TYR

ALA SER SER GLU VAL SER LEU ASN ASN THR VAL LYS LEU ILE THR ASP LEU ILE VAL SER TRP ARG LYS LEU GLU LEU ARG THR TRP LYS GLY LEU PHE ASN SER GLU ASP ALA LYS THR ARG LYS SER ILE GLY LYS TRP TRP PHE TYR LEU TYR GLU SER ILE VAL ILE SER ASN PHE

VAL SER GLU LYS LYS GLU THR ALA PRO ASN ALA THR LEU LEU VAL SER SER LEU ASN LEU PHE PHE SER LYS SER THR LEU GLY GLU PHE ASN ALA ARG LEU ASP LEU VAL LYS ALA PHE TYR LYS HIS ILE GLN LEU ILE GLY LEU ARG SER SER LYS ILE ALA GLY LEU LEU HIS ASN

THR ILE LYS PHE TYR TYR GLN PHE LYS PRO LEU ILE ASP GLU ARG ILE THR ASN GLY LYS LYS SER LEU GLU LYS GLU ILE ASP ASP ILE ILE LEU LEU ALA SER TRP LYS ASP VAL ASN VAL ASP ALA LEU LYS GLN SER SER ARG LYS SER HIS ASN ASN LEU TYR LYS ILE VAL ARG

LYS TYR ARG ASP LEU LEU ASN GLY ASP ALA LYS THR ILE GLU ALA GLY LEU LEU TYR SER ASN GLU ASN LYS LEU LYS LEU PRO THR LEU LYS GLN HIS PHE TYR GLU ASP PRO ASN LEU GLU ALA SER LYS ASN LEU VAL LYS GLU ILE SER THR TRP SER MET ARG ALA ALA PRO

LEU ARG ASN ILE ASP THR VAL ALA SER ASN MET ASP SER TYR LEU GLU LYS ILE SER SER GLN GLU PHE PRO ASN PHE ALA ASP LEU ALA SER ASP PHE TYR ALA GLU ALA GLU ARG LEU ARG LYS GLU THR PRO ASN VAL TYR THR LYS GLU ASN LYS LYS ARG LEU ALA TYR LEU LYS

THR GLN LYS SER LYS LEU LEU GLY ASP ALA LEU LYS GLU LEU ARG ARG ILE GLY LEU LYS VAL ASN PHE ARG GLU ASP ILE GLN LYS VAL GLN SER SER THR THR ILE LEU ALA ASN ILE ALA PRO PHE ASN ASN GLU TYR LEU ASN SER SER ASP ALA PHE PHE PHE LYS ILE LEU

ASP LEU LEU PRO LYS LEU ARG SER ALA ALA SER ASN PRO SER ASP ASP ILE PRO VAL ALA ALA ILE GLU ARG GLY MET ALA LEU ALA GLN SER LEU MET PHE SER LEU ILE THR VAL ARG HIS PRO LEU SER GLU PHE THR ASN ASP TYR CYS LYS ILE ASN GLY MET MET LEU ASP LEU

GLU HIS PHE THR CYS LEU LYS GLY ASP ILE VAL HIS SER SER LEU LYS ALA ASN VAL ASP ASN VAL ARG LEU PHE GLU LYS TRP LEU PRO SER LEU LEU ASP TYR ALA ALA GLN THR LEU SER VAL ILE SER LYS TYR SER ALA THR SER GLU GLN GLN LYS ILE LEU LEU ASP ALA LYS

SER THR LEU SER SER PHE PHE VAL HIS PHE ASN SER SER ARG ILE PHE ASP SER SER PHE ILE GLU SER TYR SER ARG PHE GLU LEU PHE ILE ASN GLU LEU LEU LYS LYS LEU GLU ASN ALA LYS GLU THR GLY ASN ALA PHE VAL PHE ASP ILE ILE ILE GLU TRP ILE LYS ALA ASN

LYS GLY GLY PRO ILE LYS LYS GLU GLN LYS ARG GLY PRO SER VAL GLU ASP VAL GLU GLN ALA PHE ARG ARG THR PHE THR SER ILE ILE LEU SER PHE GLN LYS VAL ILE GLY ASP GLY ILE GLU SER ILE SER GLU THR ASP ASP ASN TRP LEU SER ALA SER PHE LYS LYS VAL MET

VAL ASN VAL LYS LEU LEU ARG SER SER VAL VAL SER LYS ASN ILE GLU THR ALA LEU SER LEU LEU LYS ASP PHE ASP PHE THR THR THR GLU SER ILE TYR VAL LYS SER VAL ILE SER PHE THR LEU PRO VAL ILE THR ARG TYR TYR ASN ALA MET THR THR VAL VAL LEU GLU ARG SER

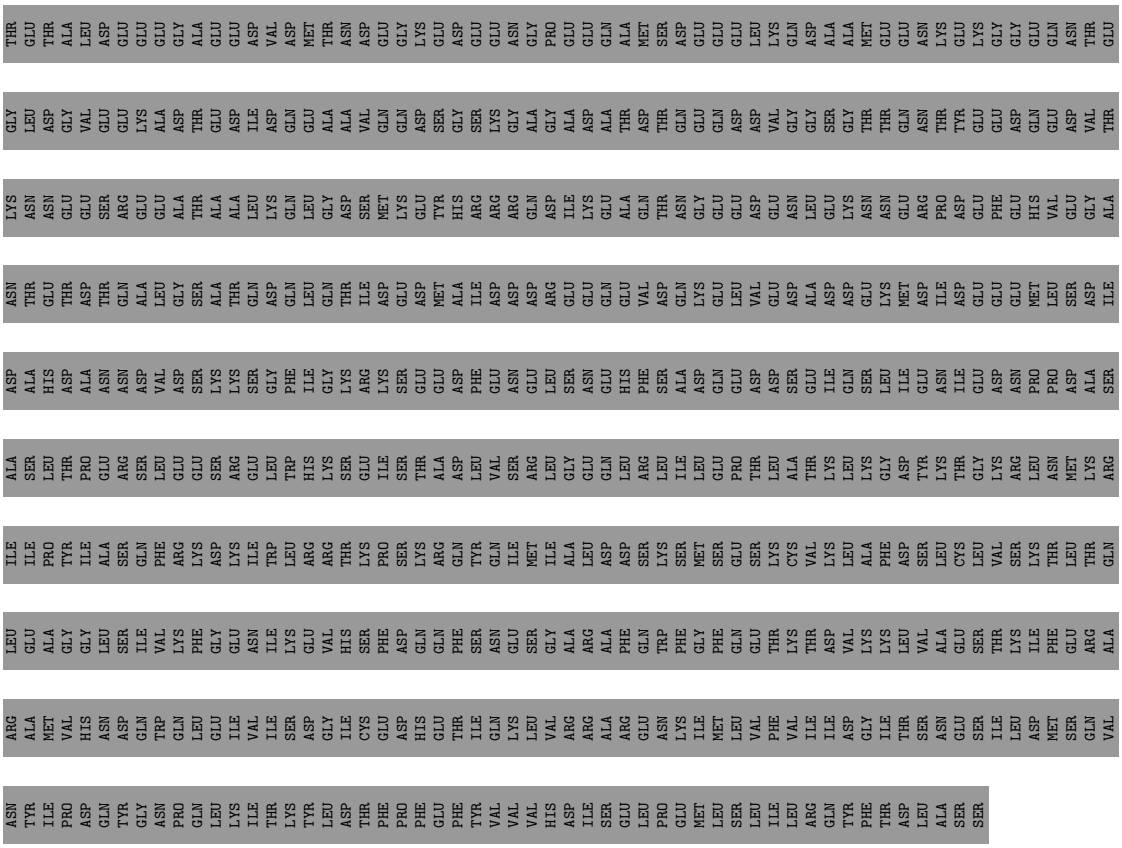
ARG ILE TYR TYR THR ASN THR SER ARG GLY MET TYR ILE LEU SER THR ILE LEU HIS SER LEU ALA LYS ASN GLY PHE CYS SER PRO GLN PRO PRO SER GLU GLU VAL ASP ASP LYS ASN LEU GLN GLU GLY THR GLY LEU GLY ASP GLY GLU GLY ALA GLN ASN ASN ASN LYS ASP VAL

GLU GLN ASP GLU ASP LEU THR GLU ASP ALA GLN ASN GLU ASN LYS GLU GLN GLN ASP LYS ASP GLU ARG ASP ASP GLU ASN GLU ASP ASP ALA VAL GLU MET GLU GLY ASP MET ALA GLY GLU LEU GLU GLU ASP LEU SER ASN GLY GLU GLU ASN ASP ASP GLU ASP THR ASP SER GLU GLU

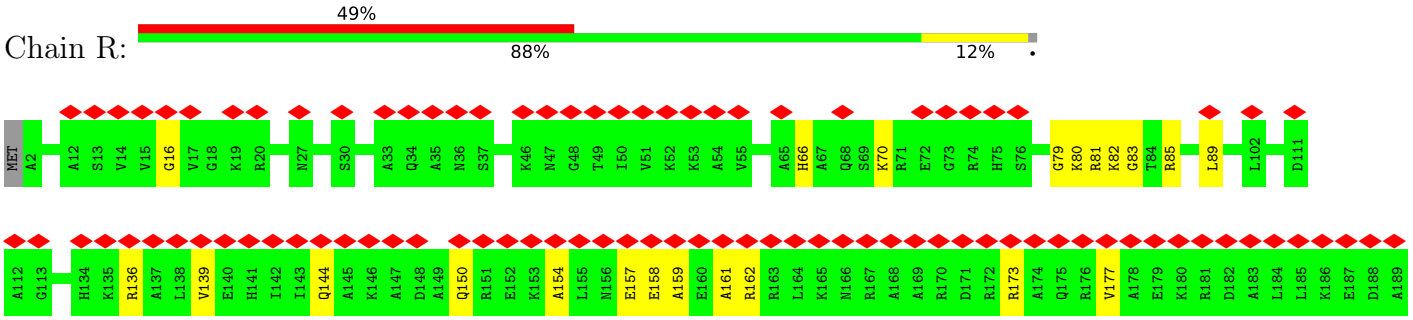
GLU GLU LEU ASP GLU GLU ILE ASP ASP LEU ASN GLU ASP ASP PRO ASN ALA ILE ASP LYS LYS MET TRP ASP ASP LYS ALA SER ASP ASN SER LYS GLU LYS ASP THR ASP GLN ASN LEU ASP GLY LYS ASN GLN GLU ASP VAL GLN ALA ALA GLU ASN ASP GLU GLN GLN ARG ASP

ASN LYS GLU GLY GLY ASP GLU ASP PRO ASN ALA PRO GLU ASP ASP GLY ASP GLU GLU ILE GLU ASN ASP GLU ASN ALA GLU GLU ASN ASP VAL GLY GLU GLN GLU ASP GLU VAL LYS ASP GLU GLU GLY GLU ASP LEU GLU ALA ASN VAL PRO GLU ILE GLU THR LEU ASP LEU PRO GLU

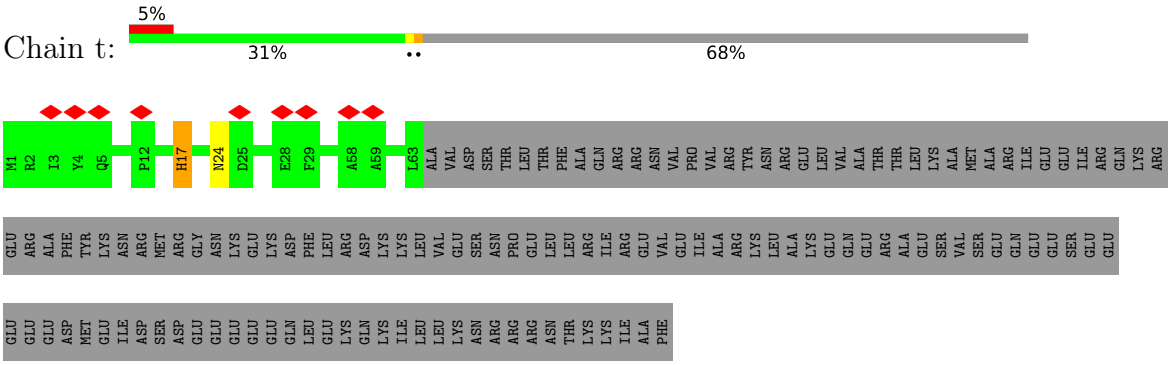
ASP MET ASN LEU ASP SER GLU HIS GLU GLU SER ASP GLU ASP VAL ASP MET SER ASP GLY MET PRO ASP LEU ASN LYS GLU GLU VAL GLY ASN GLU ASP GLU GLU VAL LYS GLN GLU SER GLY ILE GLU SER ASP ASN GLU ASN ASP GLU PRO GLY PRO GLU GLU ASP ALA GLY GLU



• Molecule 35: 60S ribosomal protein L19-A

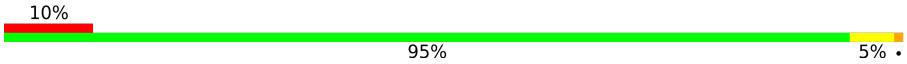


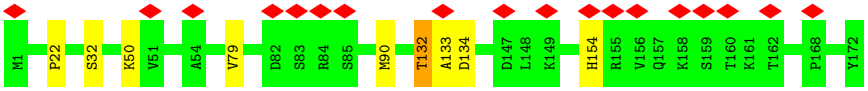
• Molecule 36: Ribosome biogenesis protein RLP24



• Molecule 37: 60S ribosomal protein L20-A

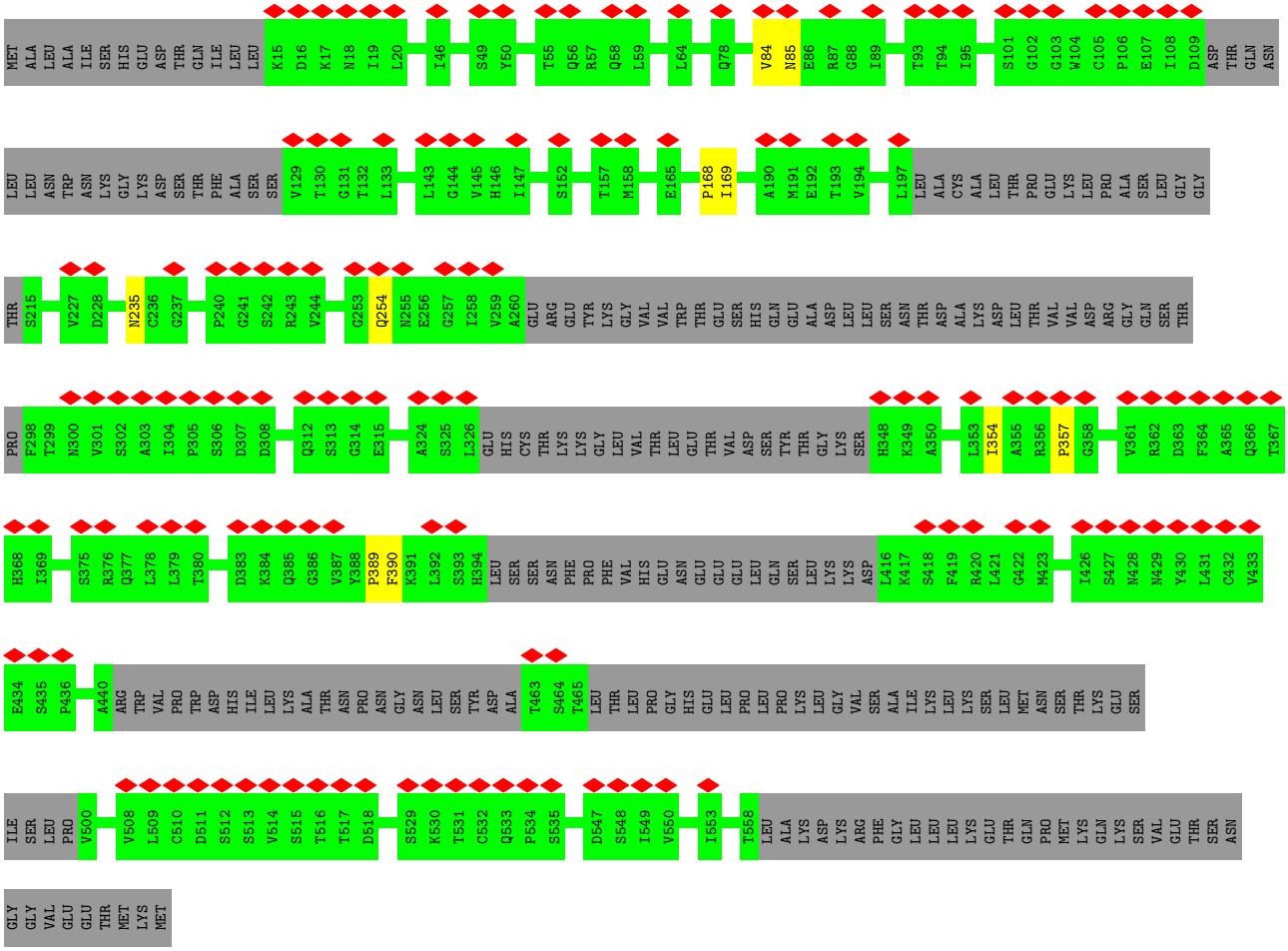
Chain S:





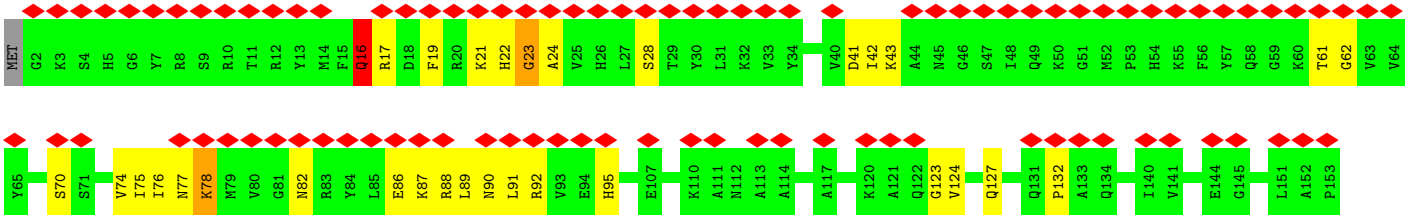
• Molecule 38: Probable metalloprotease ARX1

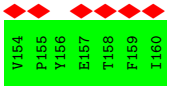
Chain u:



• Molecule 39: 60S ribosomal protein L21-A

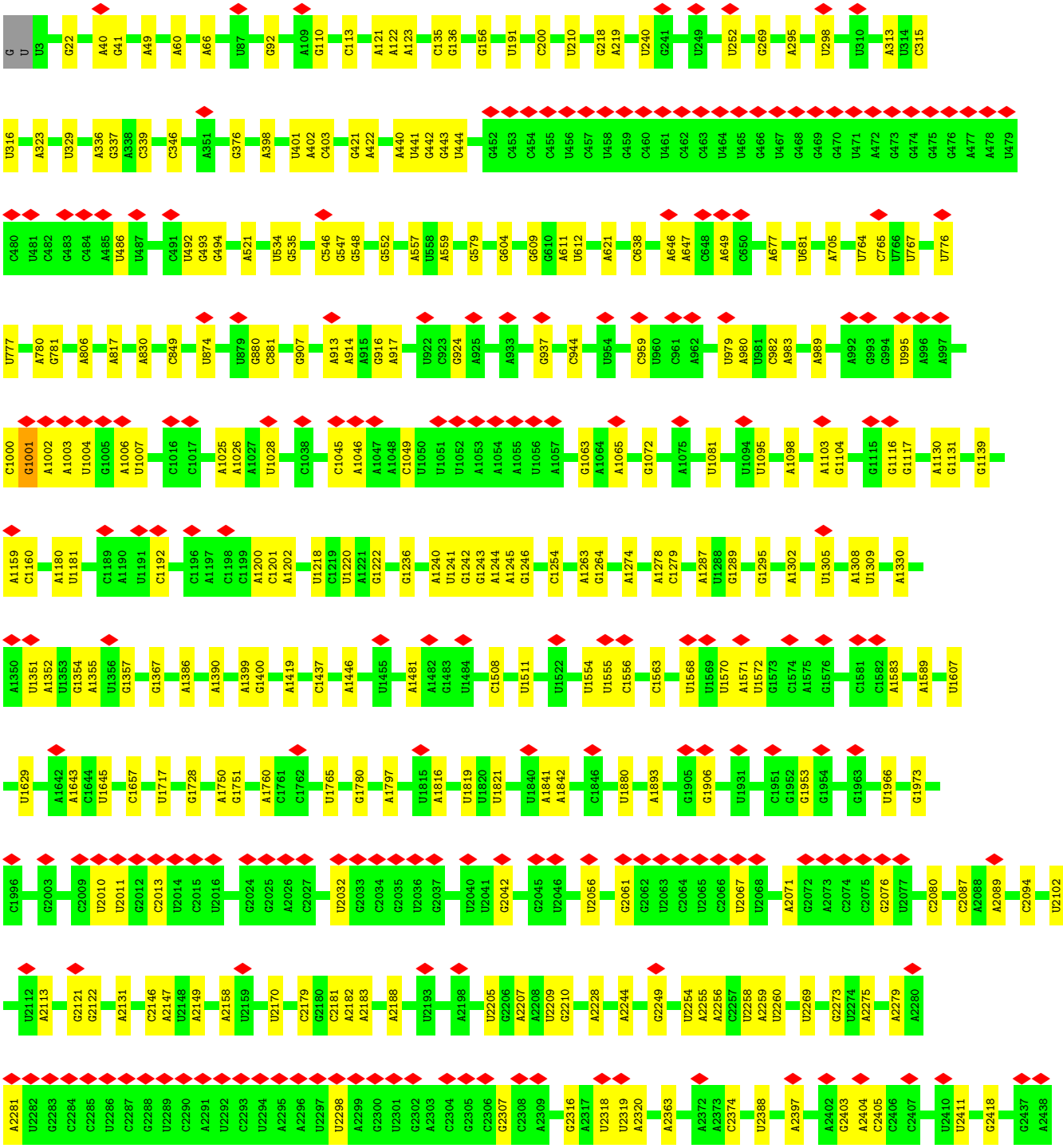
Chain T:

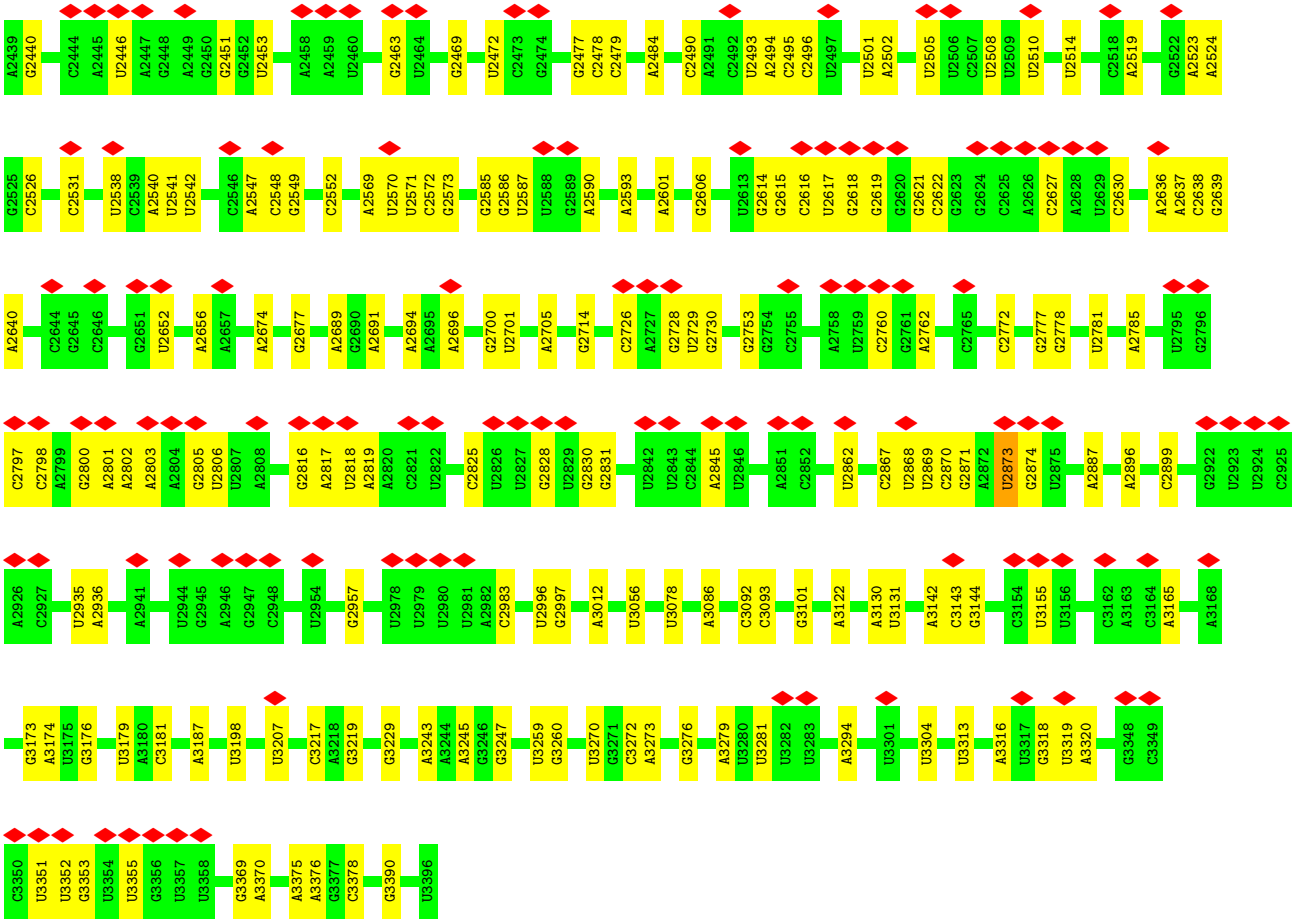




• Molecule 40: 25S ribosomal RNA

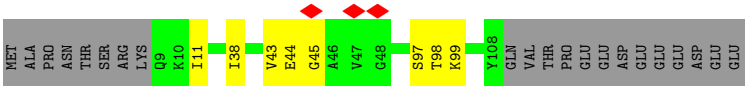
Chain x:





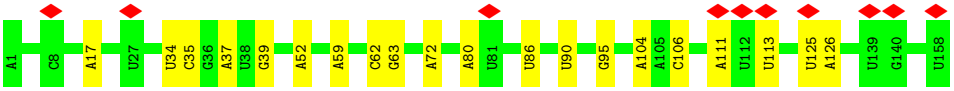
• Molecule 41: 60S ribosomal protein L22-A

Chain U:



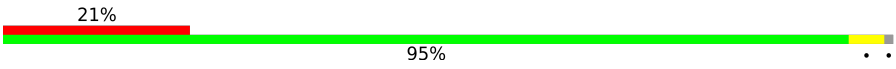
• Molecule 42: 5.8S ribosomal RNA

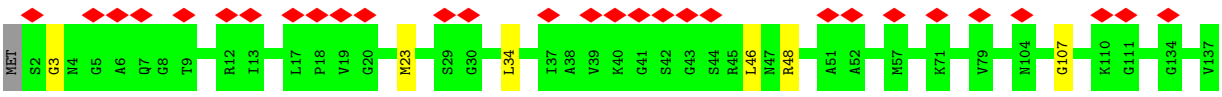
Chain y:



• Molecule 43: 60S ribosomal protein L23-A

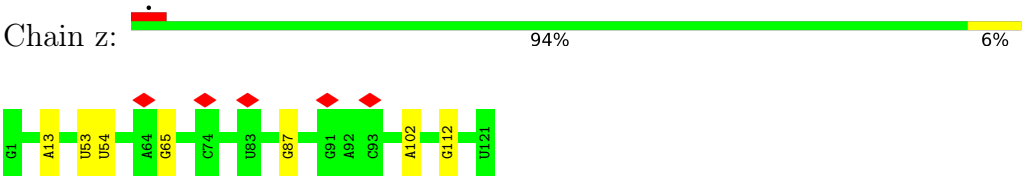
Chain V:





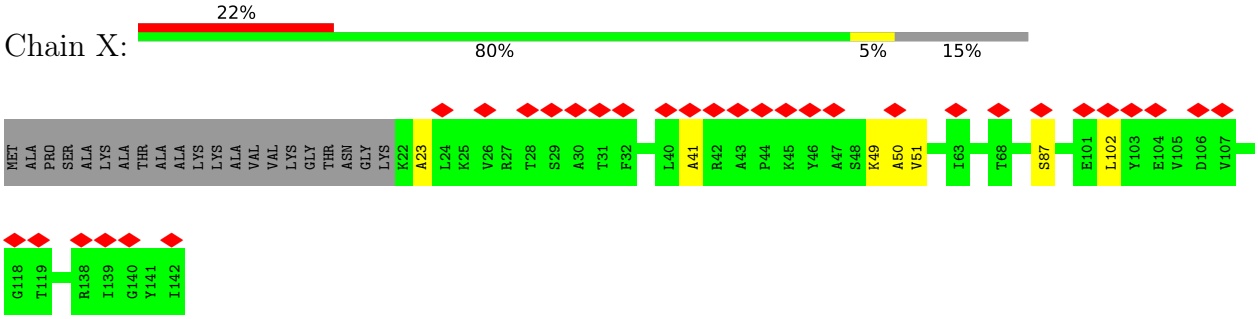
• Molecule 44: 5S ribosomal RNA

Chain z:



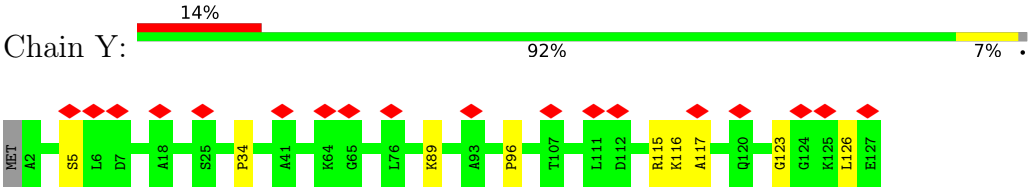
• Molecule 45: 60S ribosomal protein L25

Chain X:



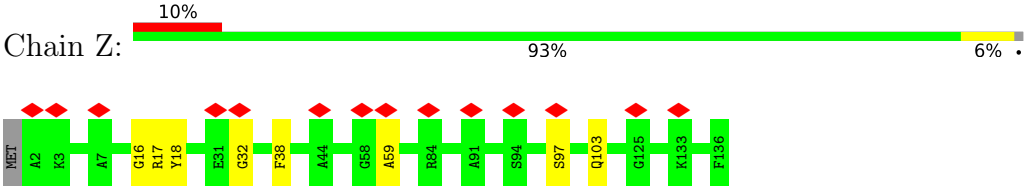
• Molecule 46: 60S ribosomal protein L26-A

Chain Y:



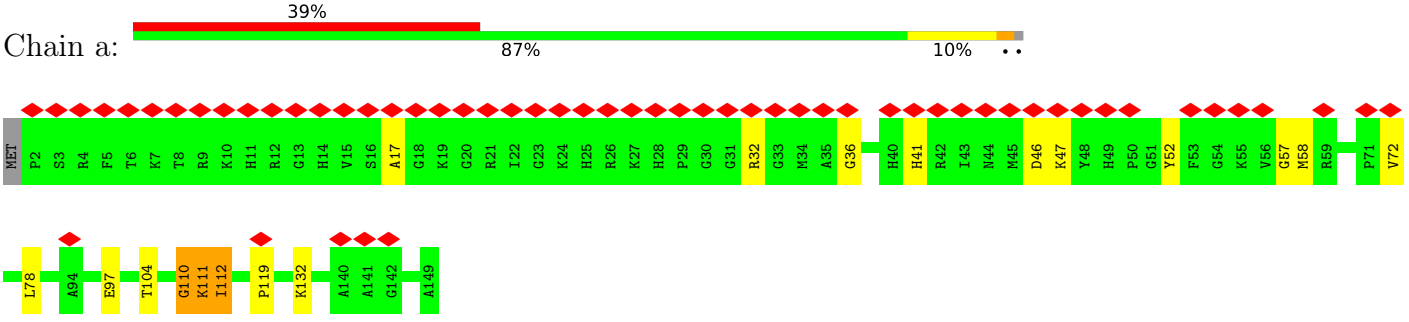
• Molecule 47: 60S ribosomal protein L27-A

Chain Z:



• Molecule 48: 60S ribosomal protein L28

Chain a:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15749	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	TVIPS TEMCAM-F816 (8k x 8k)	Depositor
Maximum map value	1.479	Depositor
Minimum map value	-0.721	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	827.6, 827.6, 827.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.069, 2.069, 2.069	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.35	1/1006 (0.1%)	0.47	0/1256
2	c	0.17	0/386	0.27	0/481
3	B	0.19	0/1542	0.36	0/1926
4	d	0.18	0/434	0.31	0/541
5	C	0.19	0/1442	0.37	1/1801 (0.1%)
6	e	0.17	0/506	0.32	0/631
7	D	0.18	0/1182	0.32	0/1476
8	f	0.49	1/422 (0.2%)	0.71	1/526 (0.2%)
9	E	0.55	1/620 (0.2%)	0.70	4/772 (0.5%)
10	g	0.18	0/446	0.32	0/556
11	F	0.18	0/886	0.32	0/1106
12	h	0.17	0/474	0.29	0/591
13	G	0.18	0/930	0.32	0/1161
14	i	0.18	0/394	0.31	0/491
15	H	0.17	0/762	0.30	0/951
16	j	0.57	1/346 (0.3%)	0.57	1/431 (0.2%)
17	I	0.18	0/866	0.31	0/1081
18	k	0.17	0/306	0.29	0/381
19	J	0.54	0/674	0.78	0/841
20	l	0.17	0/198	0.36	0/246
21	K	0.18	0/506	0.34	0/631
22	m	0.18	0/894	0.30	0/1116
23	L	0.18	0/770	0.35	0/961
24	n	0.18	0/846	0.31	0/1056
25	M	0.17	0/542	0.30	0/676
26	o	0.59	2/1386 (0.1%)	0.85	9/1731 (0.5%)
27	N	0.19	0/810	0.38	0/1011
28	p	0.18	0/362	0.30	0/451
29	O	0.20	0/786	0.47	1/981 (0.1%)
30	q	0.92	0/1950	0.88	0/2436
31	P	0.17	0/730	0.33	0/911
32	r	0.55	1/1276 (0.1%)	0.90	4/1553 (0.3%)
33	Q	0.17	0/738	0.30	0/921
34	s	0.29	1/8001 (0.0%)	0.49	8/9992 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	R	0.20	0/750	0.41	0/936
36	t	0.34	0/250	0.52	0/311
37	S	0.16	0/686	0.32	0/856
38	u	0.92	0/1483	0.86	1/1840 (0.1%)
39	T	0.44	1/634 (0.2%)	0.64	2/791 (0.3%)
40	x	0.20	5/81221 (0.0%)	0.74	168/126638 (0.1%)
41	U	0.18	0/398	0.31	0/496
42	y	0.13	0/3743	0.64	0/5828
43	V	0.22	0/542	0.35	0/676
44	z	0.13	0/2880	0.64	0/4487
45	X	0.17	0/482	0.29	0/601
46	Y	0.17	0/502	0.30	0/626
47	Z	0.18	0/538	0.31	0/671
48	a	0.80	3/590 (0.5%)	0.71	3/736 (0.4%)
All	All	0.28	17/128118 (0.0%)	0.68	203/187166 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
3	B	0	2
8	f	0	2
9	E	0	1
19	J	0	1
26	o	0	1
32	r	0	3
34	s	0	11
36	t	0	1
39	T	0	3
48	a	0	1
All	All	0	27

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	a	111	LYS	N-CA	14.13	1.74	1.46
48	a	110	GLY	C-N	10.00	1.57	1.34
9	E	67	GLY	CA-C	-9.76	1.36	1.51
16	j	39	TYR	C-O	-8.62	1.06	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	x	2638	C	O3'-P	-7.47	1.52	1.61

The worst 5 of 203 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
34	s	858	GLU	O-C-N	-21.28	88.65	122.70
40	x	440	A	O5'-P-OP1	-19.65	87.12	110.70
40	x	440	A	O5'-P-OP2	17.48	131.68	110.70
40	x	2638	C	P-O3'-C3'	-16.82	99.52	119.70
40	x	2873	U	C5'-C4'-O4'	-15.31	90.73	109.10

There are no chirality outliers.

5 of 27 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	198	LYS	Peptide
3	B	255	TRP	Peptide
3	B	256	HIS	Peptide
8	f	100	ILE	Mainchain
8	f	103	TYR	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1007	0	310	18	0
2	c	387	0	113	0	0
3	B	1543	0	433	4	0
4	d	435	0	114	0	0
5	C	1443	0	399	7	0
6	e	507	0	135	0	0
7	D	1183	0	325	1	0
8	f	423	0	117	0	0
9	E	622	0	160	1	0
10	g	447	0	121	0	0
11	F	887	0	241	3	0
12	h	475	0	118	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	G	931	0	242	1	0
14	i	395	0	109	0	0
15	H	763	0	215	3	0
16	j	347	0	104	0	0
17	I	867	0	230	2	0
18	k	307	0	79	0	0
19	J	675	0	191	11	0
20	l	199	0	47	0	0
21	K	507	0	140	1	0
22	m	895	0	257	0	0
23	L	771	0	199	4	0
24	n	847	0	224	0	0
25	M	543	0	145	2	0
26	o	1387	0	358	0	0
27	N	811	0	221	3	0
28	p	363	0	108	0	0
29	O	787	0	214	5	0
30	q	1951	0	540	0	0
31	P	731	0	197	4	0
32	r	1304	0	332	0	0
33	Q	739	0	205	1	0
34	s	8007	0	2136	0	0
35	R	751	0	203	14	0
36	t	251	0	68	0	0
37	S	687	0	175	3	0
38	u	1491	0	399	0	0
39	T	635	0	174	14	0
40	x	72570	0	36462	0	0
41	U	399	0	109	2	0
42	y	3350	0	1696	0	0
43	V	543	0	162	2	0
44	z	2576	0	1304	0	0
45	X	483	0	121	1	0
46	Y	503	0	134	1	0
47	Z	539	0	144	1	0
48	a	591	0	176	0	0
All	All	118855	0	50406	109	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 109 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:T:62:GLY:N	39:T:75:ILE:H	1.51	1.07
39:T:43:LYS:O	39:T:95:HIS:CA	2.03	1.06
35:R:158:GLU:O	35:R:162:ARG:N	1.90	1.03
39:T:62:GLY:CA	39:T:75:ILE:H	1.72	1.03
39:T:62:GLY:HA3	39:T:75:ILE:N	1.80	0.96

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	250/254 (98%)	156 (62%)	70 (28%)	24 (10%)	0 10
2	c	95/105 (90%)	84 (88%)	10 (10%)	1 (1%)	14 52
3	B	384/387 (99%)	294 (77%)	70 (18%)	20 (5%)	2 19
4	d	107/113 (95%)	88 (82%)	15 (14%)	4 (4%)	3 24
5	C	359/362 (99%)	254 (71%)	80 (22%)	25 (7%)	1 14
6	e	125/130 (96%)	99 (79%)	24 (19%)	2 (2%)	9 44
7	D	294/297 (99%)	229 (78%)	53 (18%)	12 (4%)	3 23
8	f	104/107 (97%)	78 (75%)	19 (18%)	7 (7%)	1 15
9	E	152/176 (86%)	113 (74%)	35 (23%)	4 (3%)	5 31
10	g	110/121 (91%)	78 (71%)	27 (24%)	5 (4%)	2 22
11	F	220/244 (90%)	181 (82%)	30 (14%)	9 (4%)	3 23
12	h	117/120 (98%)	92 (79%)	21 (18%)	4 (3%)	3 26
13	G	231/256 (90%)	180 (78%)	42 (18%)	9 (4%)	3 23
14	i	97/100 (97%)	78 (80%)	13 (13%)	6 (6%)	1 17
15	H	189/191 (99%)	147 (78%)	37 (20%)	5 (3%)	5 31
16	j	85/88 (97%)	53 (62%)	26 (31%)	6 (7%)	1 14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
17	I	215/217 (99%)	159 (74%)	48 (22%)	8 (4%)	3 24
18	k	75/78 (96%)	66 (88%)	8 (11%)	1 (1%)	12 48
19	J	167/174 (96%)	116 (70%)	29 (17%)	22 (13%)	0 5
20	l	48/51 (94%)	33 (69%)	11 (23%)	4 (8%)	1 12
21	K	125/165 (76%)	81 (65%)	27 (22%)	17 (14%)	0 4
22	m	222/245 (91%)	170 (77%)	44 (20%)	8 (4%)	3 25
23	L	191/199 (96%)	141 (74%)	39 (20%)	11 (6%)	1 18
24	n	210/236 (89%)	156 (74%)	48 (23%)	6 (3%)	4 29
25	M	134/138 (97%)	106 (79%)	22 (16%)	6 (4%)	2 22
26	o	345/647 (53%)	223 (65%)	72 (21%)	50 (14%)	0 4
27	N	201/204 (98%)	147 (73%)	44 (22%)	10 (5%)	2 20
28	p	89/92 (97%)	72 (81%)	14 (16%)	3 (3%)	3 26
29	O	195/199 (98%)	143 (73%)	39 (20%)	13 (7%)	1 15
30	q	486/515 (94%)	458 (94%)	22 (4%)	6 (1%)	13 50
31	P	181/184 (98%)	141 (78%)	35 (19%)	5 (3%)	5 30
32	r	277/767 (36%)	155 (56%)	57 (21%)	65 (24%)	0 1
33	Q	183/186 (98%)	143 (78%)	30 (16%)	10 (6%)	2 19
34	s	1991/4910 (40%)	1585 (80%)	229 (12%)	177 (9%)	1 11
35	R	186/189 (98%)	136 (73%)	44 (24%)	6 (3%)	4 26
36	t	61/199 (31%)	52 (85%)	7 (12%)	2 (3%)	4 26
37	S	170/172 (99%)	133 (78%)	31 (18%)	6 (4%)	3 25
38	u	357/593 (60%)	342 (96%)	6 (2%)	9 (2%)	5 32
39	T	157/160 (98%)	90 (57%)	46 (29%)	21 (13%)	0 5
41	U	98/121 (81%)	77 (79%)	17 (17%)	4 (4%)	3 23
43	V	134/137 (98%)	95 (71%)	37 (28%)	2 (2%)	10 46
45	X	119/142 (84%)	91 (76%)	23 (19%)	5 (4%)	3 22
46	Y	124/127 (98%)	91 (73%)	26 (21%)	7 (6%)	2 19
47	Z	133/136 (98%)	97 (73%)	30 (23%)	6 (4%)	2 22
48	a	146/149 (98%)	89 (61%)	40 (27%)	17 (12%)	0 6
All	All	9939/14383 (69%)	7592 (76%)	1697 (17%)	650 (6%)	2 16

5 of 650 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	ASP
1	A	128	ARG
1	A	133	TYR
1	A	135	ILE
1	A	137	ILE

5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
40	x	3393/3396 (99%)	376 (11%)	0
42	y	157/158 (99%)	20 (12%)	0
44	z	120/121 (99%)	7 (5%)	0
All	All	3670/3675 (99%)	403 (10%)	0

5 of 403 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
40	x	22	G
40	x	40	A
40	x	41	G
40	x	49	A
40	x	60	A

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

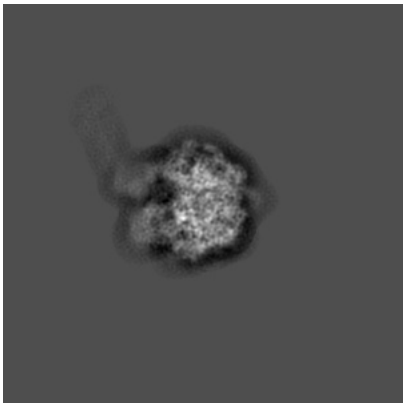
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-3199. These allow visual inspection of the internal detail of the map and identification of artifacts.

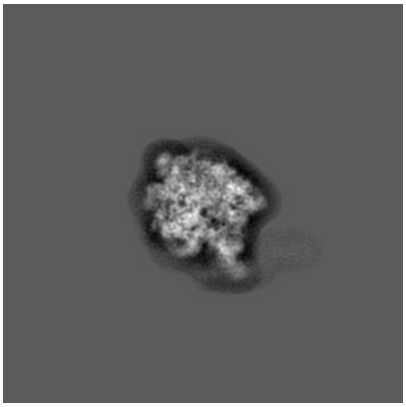
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

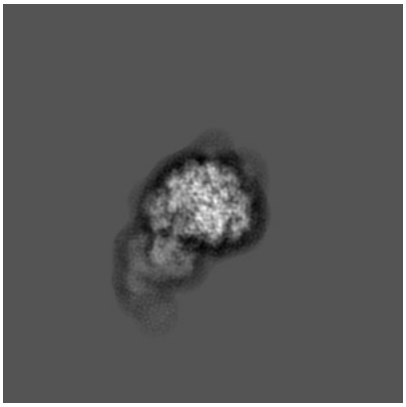
6.1.1 Primary map



X



Y

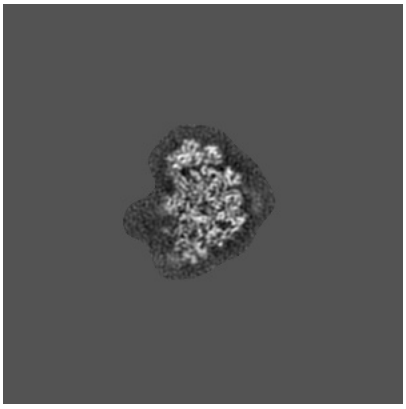


Z

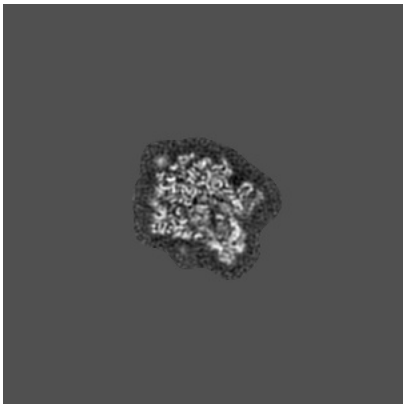
The images above show the map projected in three orthogonal directions.

6.2 Central slices

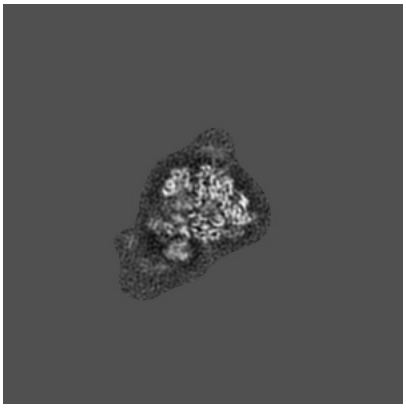
6.2.1 Primary map



X Index: 200



Y Index: 200

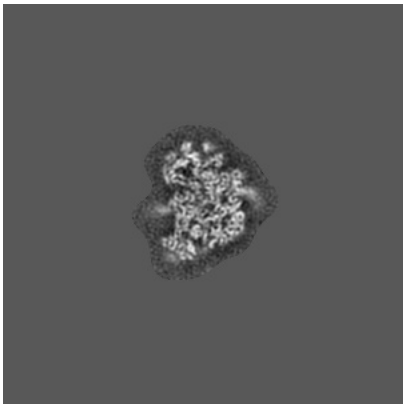


Z Index: 200

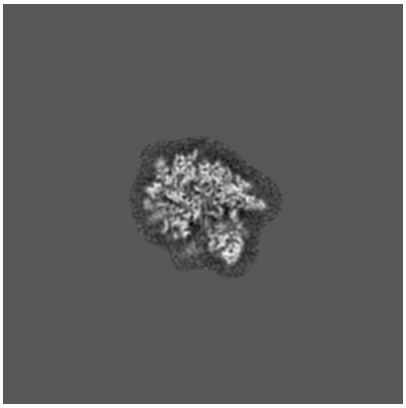
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

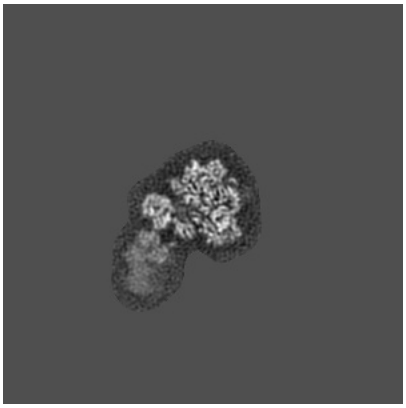
6.3.1 Primary map



X Index: 206



Y Index: 192

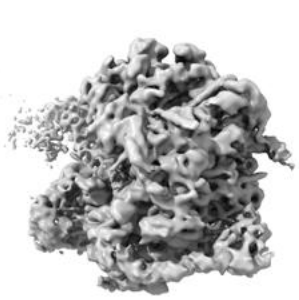


Z Index: 226

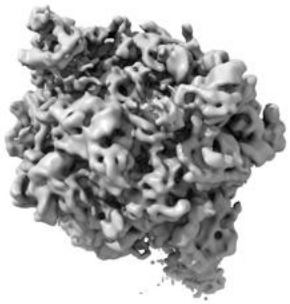
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

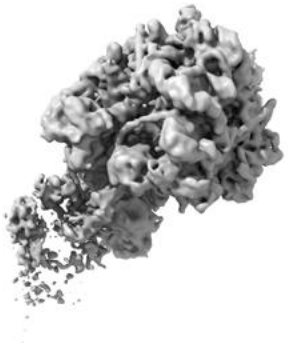
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

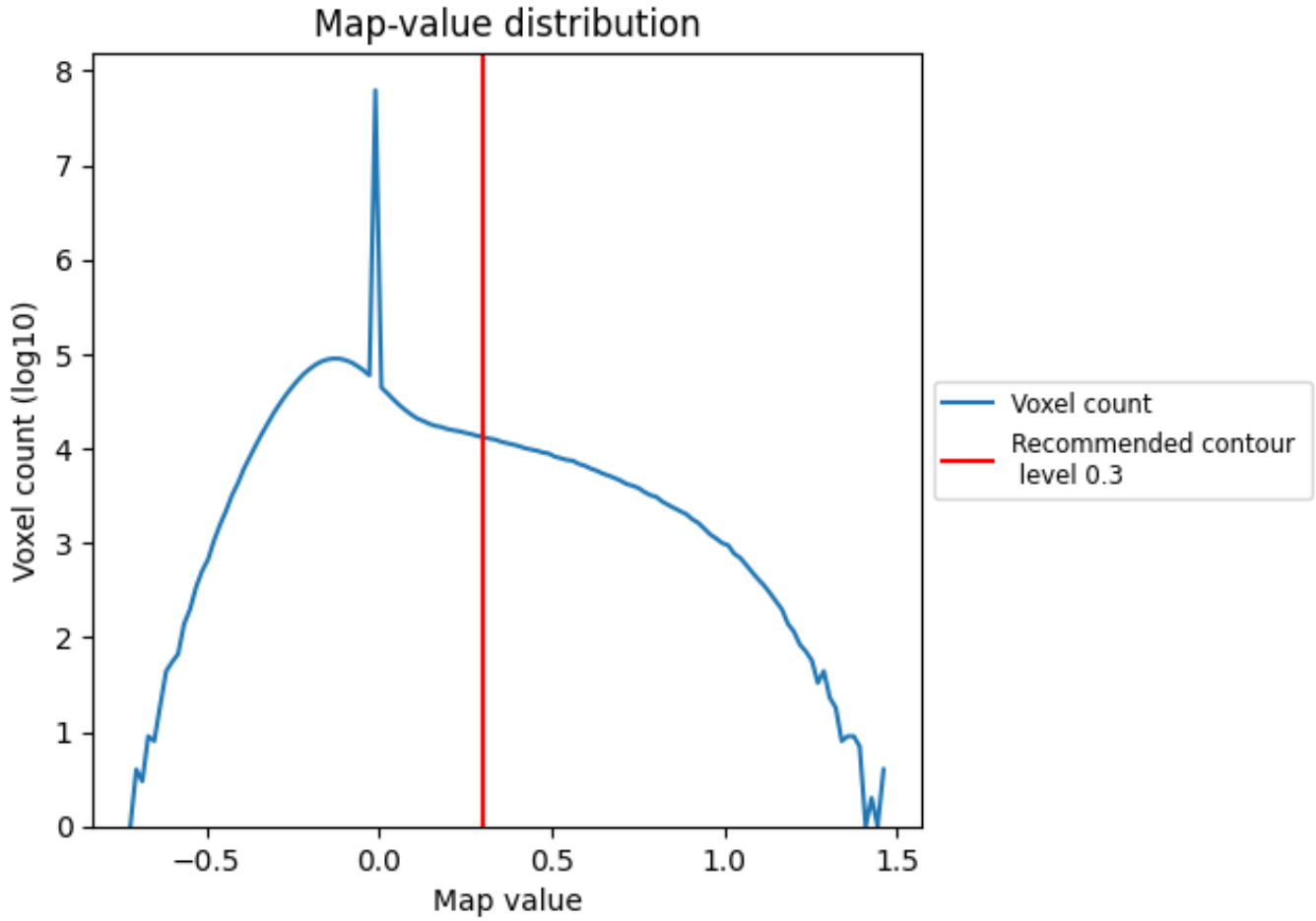
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

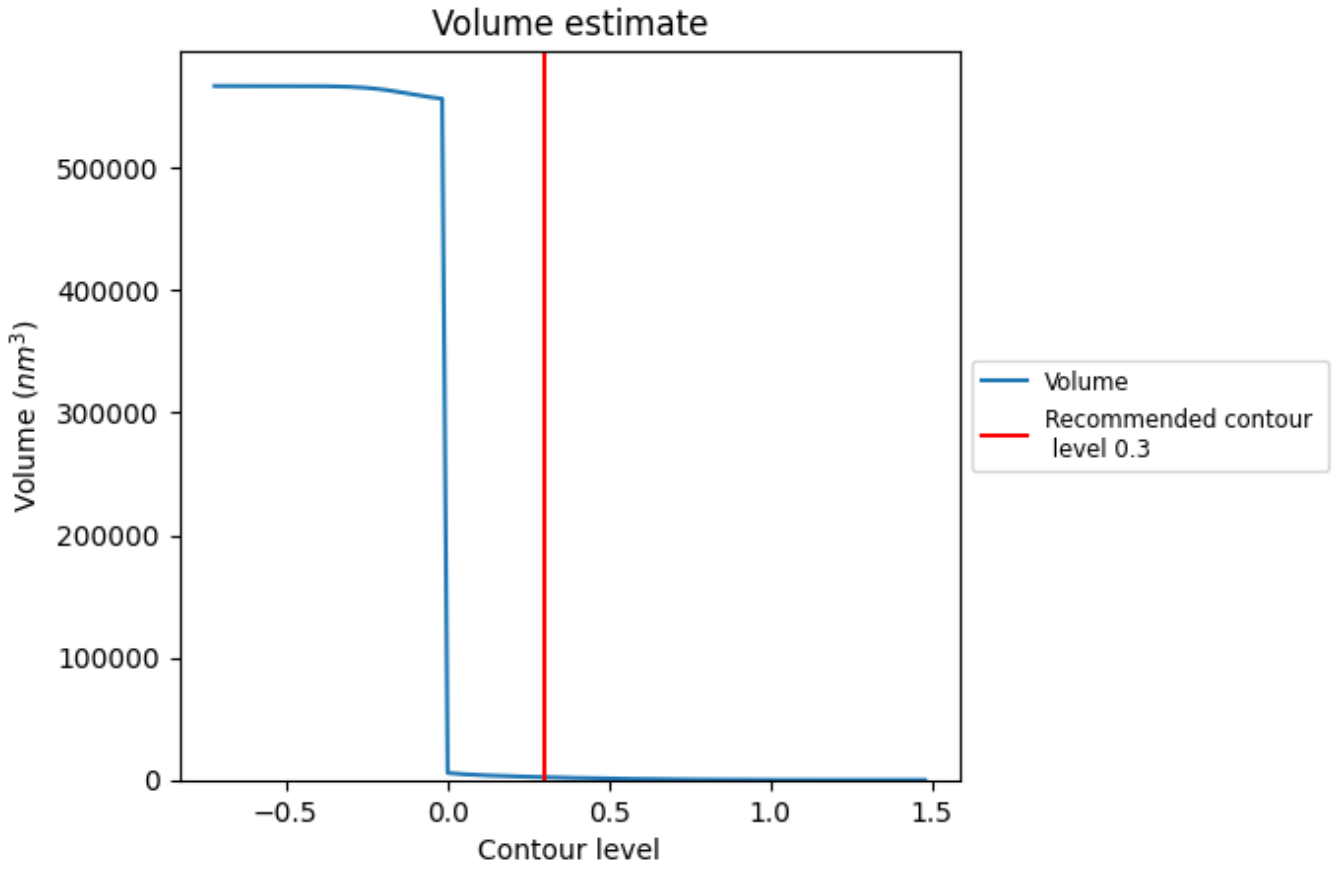
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

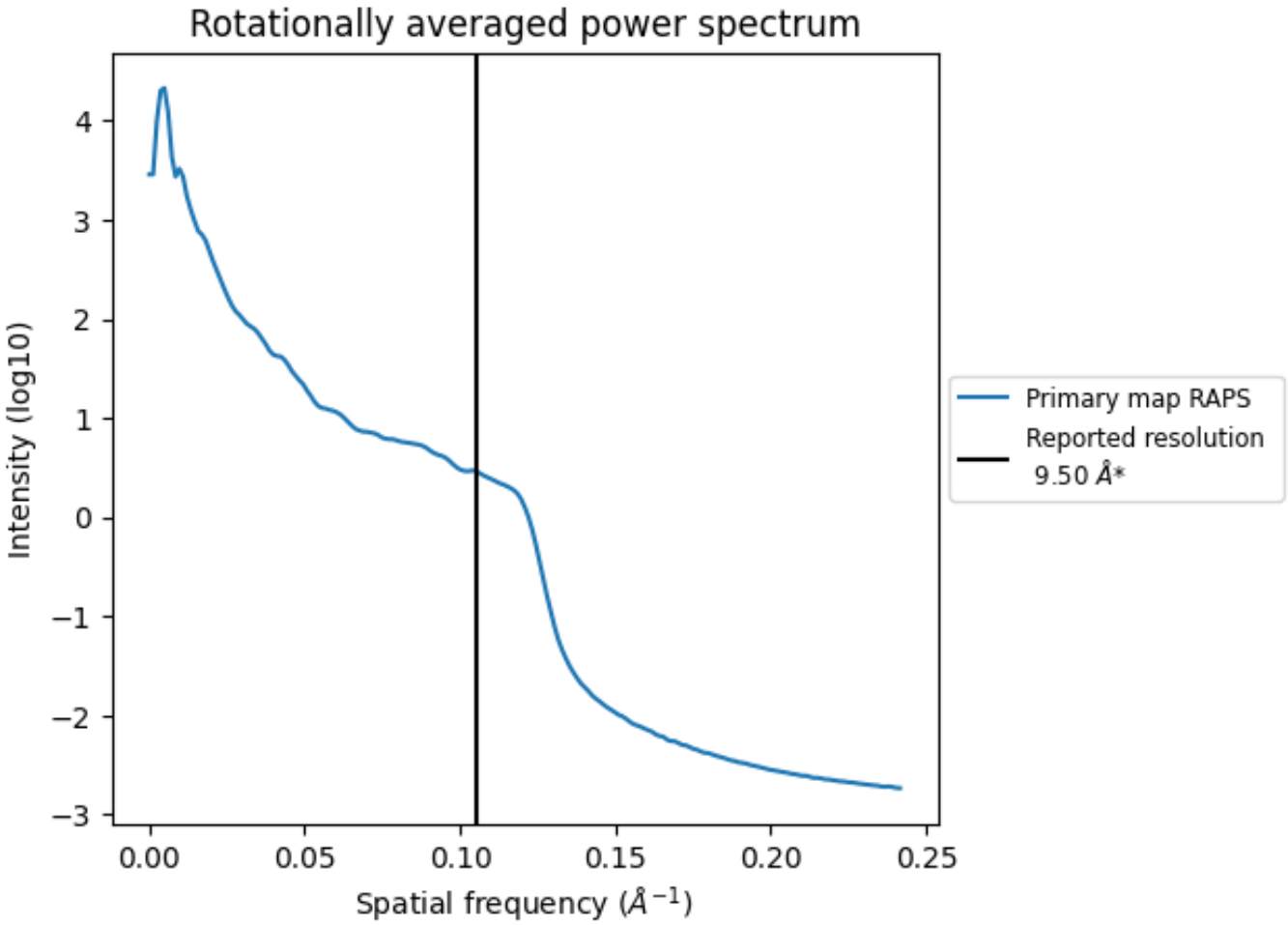
7.2 Volume estimate (i)



The volume at the recommended contour level is 2263 nm^3; this corresponds to an approximate mass of 2044 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.105 Å^{-1}

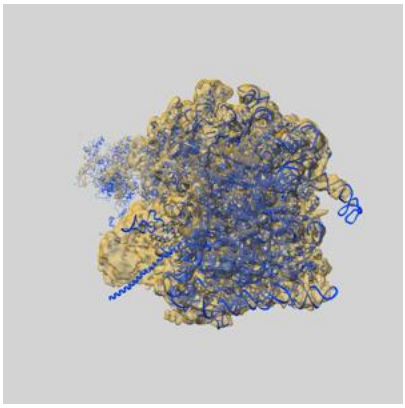
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

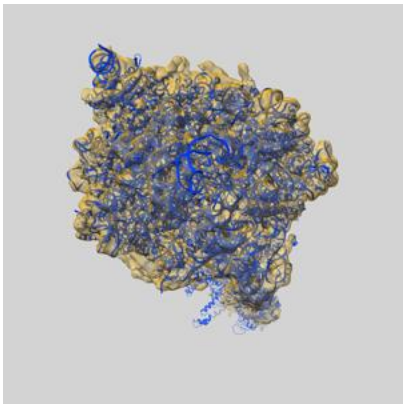
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-3199 and PDB model 5JCS. Per-residue inclusion information can be found in section 3 on page 12.

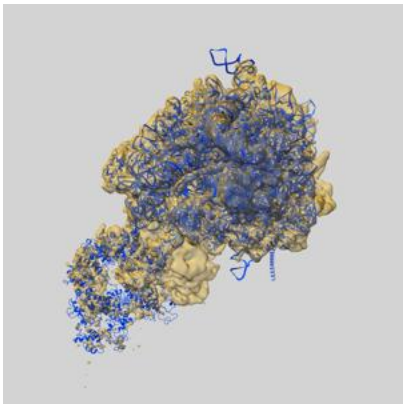
9.1 Map-model overlay



X



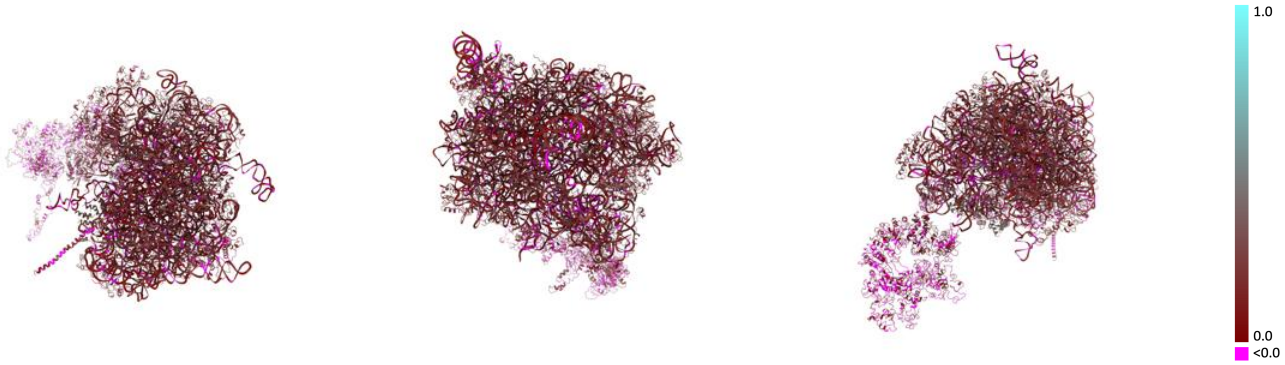
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

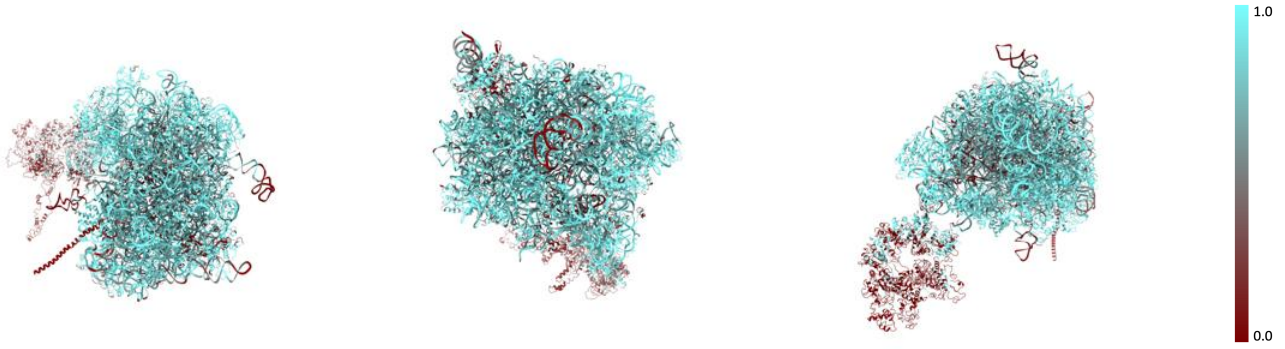
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

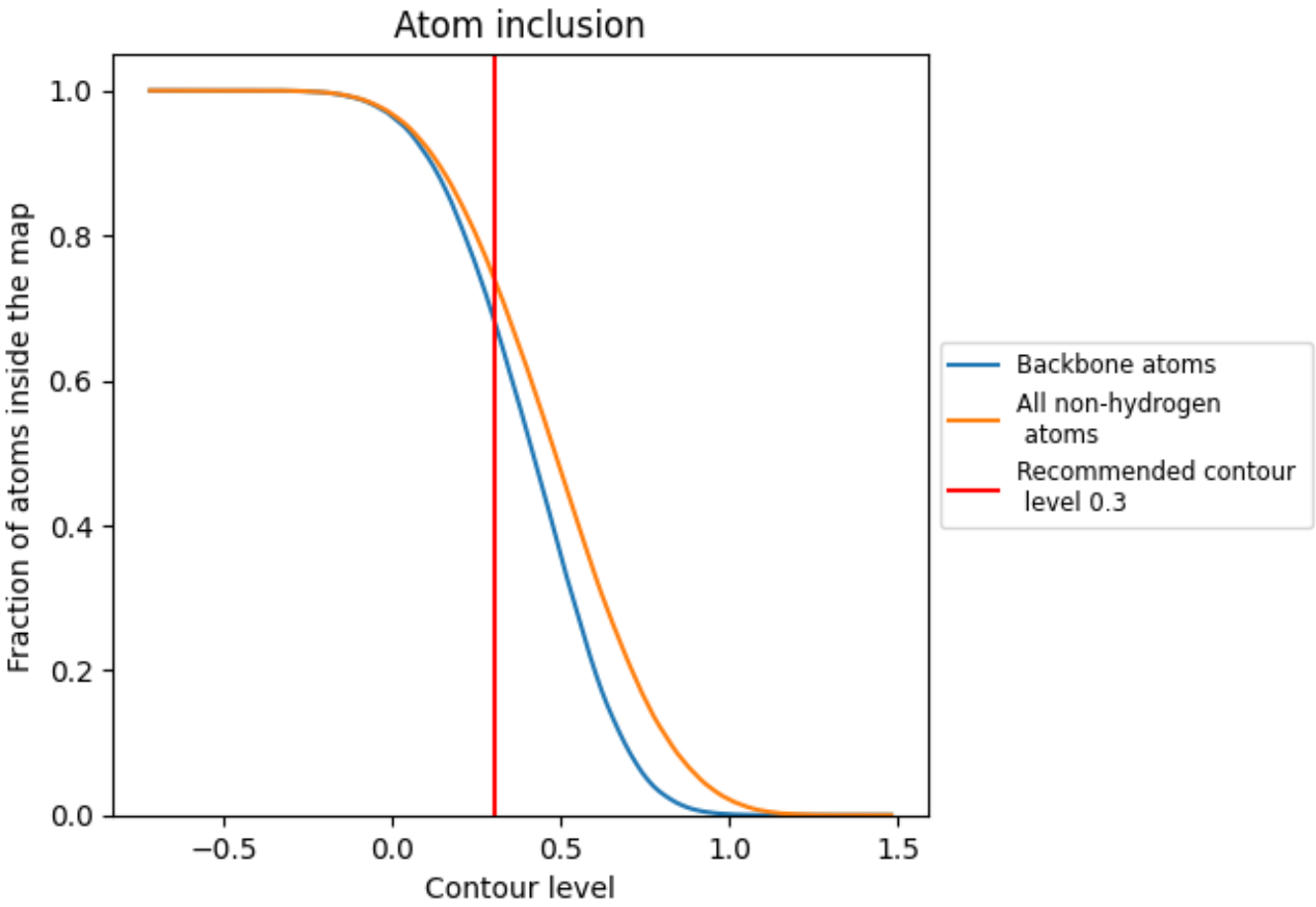
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).

9.4 Atom inclusion (i)



At the recommended contour level, 68% of all backbone atoms, 74% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7414	0.1460
A	0.5511	0.1300
B	0.7680	0.1560
C	0.6972	0.1620
D	0.8292	0.1880
E	0.8119	0.1930
F	0.8749	0.2170
G	0.7938	0.1700
H	0.8716	0.2110
I	0.1442	0.0270
J	0.9733	0.2200
K	0.7732	0.1550
L	0.8145	0.2240
M	0.8545	0.2100
N	0.7164	0.1600
O	0.7522	0.1850
P	0.7004	0.1780
Q	0.6292	0.1620
R	0.4967	0.1260
S	0.8603	0.2170
T	0.3449	0.0350
U	0.9223	0.2360
V	0.7274	0.1850
X	0.6832	0.1650
Y	0.8091	0.1760
Z	0.8534	0.1750
a	0.5787	0.1180
c	0.8346	0.2030
d	0.7770	0.1850
e	0.7101	0.1950
f	0.7707	0.1620
g	0.5347	0.1170
h	0.8695	0.2310
i	0.7519	0.1900
j	0.5591	0.1000

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Chain	Atom inclusion	Q-score
k	0.8827	0.2150
l	0.6432	0.1760
m	0.9352	0.1940
n	0.9516	0.2070
o	0.8745	0.2300
p	0.6419	0.1540
q	0.8606	0.1840
r	0.9716	0.3470
s	0.2121	0.0620
t	0.8127	0.1450
u	0.5513	0.1670
x	0.7877	0.1400
y	0.8107	0.1410
z	0.8855	0.1520