



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 01:31 AM UTC

PDB ID : 6J30 / pdb_00006j30
EMDB ID : EMD-9773
Title : yeast proteasome in Ub-engaged state (C2)
Authors : Cong, Y.
Deposited on : 2019-01-03
Resolution : 4.50 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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

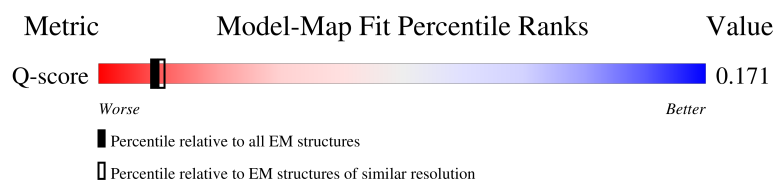
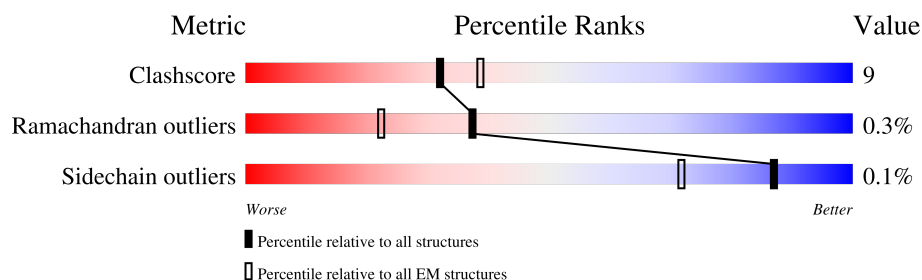
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

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 $\leq 5\%$. 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	1	215	11% 73% 18% 9%
1	b	215	10% 71% 20% 9%
2	2	261	13% 70% 16% 13%
2	i	261	9% 69% 18% 13%

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Mol	Chain	Length	Quality of chain
3	3	205	
3	h	205	
4	4	198	
4	g	198	
5	5	287	
5	f	287	
6	6	241	
6	e	241	
7	7	266	
7	a	266	
8	A	252	
8	c	252	
9	B	250	
9	j	250	
10	C	258	
10	d	258	
11	D	254	
11	n	254	
12	E	260	
12	m	260	
13	F	234	
13	l	234	
14	G	288	
14	k	288	
15	H	467	

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Mol	Chain	Length	Quality of chain
16	I	437	
17	J	405	
18	K	428	
19	L	437	
20	M	434	
21	N	945	
22	O	393	
23	P	445	
24	Q	434	
25	R	429	
26	S	523	
27	T	274	
28	U	338	
29	V	306	
30	W	268	
31	X	156	
32	Y	89	
33	Z	993	

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 106227 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 Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	196	Total	C	N	O	S	0	0
			1512	955	250	300	7		
1	b	196	Total	C	N	O	S	0	0
			1512	955	250	300	7		

- Molecule 2 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	226	Total	C	N	O	S	0	0
			1719	1082	298	332	7		
2	i	226	Total	C	N	O	S	0	0
			1719	1082	298	332	7		

- Molecule 3 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	204	Total	C	N	O	S	0	0
			1581	1010	258	305	8		
3	h	204	Total	C	N	O	S	0	0
			1581	1010	258	305	8		

- Molecule 4 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	195	Total	C	N	O	S	0	0
			1561	992	264	299	6		
4	g	195	Total	C	N	O	S	0	0
			1561	992	264	299	6		

- Molecule 5 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	212	Total	C	N	O	S	0	0
			1644	1045	280	312	7		
5	f	212	Total	C	N	O	S	0	0
			1644	1045	280	312	7		

- Molecule 6 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	222	Total	C	N	O	S	0	0
			1757	1115	303	335	4		
6	e	222	Total	C	N	O	S	0	0
			1757	1115	303	335	4		

- Molecule 7 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	229	Total	C	N	O	S	0	0
			1790	1133	306	344	7		
7	a	232	Total	C	N	O	S	0	0
			1815	1148	311	349	7		

- Molecule 8 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	241	Total	C	N	O	S	0	0
			1907	1214	320	365	8		
8	c	241	Total	C	N	O	S	0	0
			1907	1214	320	365	8		

- Molecule 9 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	250	Total	C	N	O	S	0	0
			1915	1219	315	377	4		
9	j	250	Total	C	N	O	S	0	0
			1915	1219	315	377	4		

- Molecule 10 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	244	Total	C	N	O	S	0	0
			1904	1201	321	379	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	d	244	Total	C	N	O	S	0	0
			1904	1201	321	379	3		

- Molecule 11 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	240	Total	C	N	O	S	0	0
			1881	1176	329	372	4		
11	n	240	Total	C	N	O	S	0	0
			1881	1176	329	372	4		

- Molecule 12 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	242	Total	C	N	O	S	0	0
			1861	1162	314	378	7		
12	m	242	Total	C	N	O	S	0	0
			1861	1162	314	378	7		

- Molecule 13 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	233	Total	C	N	O	S	0	0
			1795	1129	312	350	4		
13	l	231	Total	C	N	O	S	0	0
			1773	1114	307	348	4		

- Molecule 14 is a protein called Probable proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	243	Total	C	N	O	S	0	0
			1892	1203	329	356	4		
14	k	243	Total	C	N	O	S	0	0
			1892	1203	329	356	4		

- Molecule 15 is a protein called 26S proteasome regulatory subunit 7 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	355	Total	C	N	O	S	0	0
			2787	1755	500	515	17		

- Molecule 16 is a protein called 26S proteasome regulatory subunit 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	362	Total	C	N	O	S	0	0
			2822	1773	471	563	15		

- Molecule 17 is a protein called 26S proteasome regulatory subunit 8 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	373	Total	C	N	O	S	0	0
			2928	1837	527	547	17		

- Molecule 18 is a protein called 26S proteasome regulatory subunit 6B homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	381	Total	C	N	O	S	0	0
			3019	1898	530	581	10		

- Molecule 19 is a protein called 26S proteasome subunit RPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	371	Total	C	N	O	S	0	0
			2937	1852	519	554	12		

- Molecule 20 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	367	Total	C	N	O	S	0	0
			2866	1799	503	553	11		

- Molecule 21 is a protein called 26S proteasome regulatory subunit RPN2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	849	Total	C	N	O	S	0	0
			6562	4174	1099	1261	28		

- Molecule 22 is a protein called 26S proteasome regulatory subunit RPN9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	387	Total	C	N	O	S	0	0
			3182	2047	520	606	9		

- Molecule 23 is a protein called 26S proteasome regulatory subunit RPN5.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	432	Total	C	N	O	S	0	0
			3545	2260	592	684	9		

- Molecule 24 is a protein called 26S proteasome regulatory subunit RPN6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Q	431	Total	C	N	O	S	0	0
			3471	2205	574	676	16		

- Molecule 25 is a protein called 26S proteasome regulatory subunit RPN7.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	R	400	Total	C	N	O	S	0	0
			3218	2051	527	630	10		

- Molecule 26 is a protein called 26S proteasome regulatory subunit RPN3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	475	Total	C	N	O	S	0	0
			3894	2488	653	738	15		

- Molecule 27 is a protein called 26S proteasome regulatory subunit RPN12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	272	Total	C	N	O	S	0	0
			2235	1432	355	441	7		

- Molecule 28 is a protein called 26S proteasome regulatory subunit RPN8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	262	Total	C	N	O	S	0	0
			2118	1348	362	402	6		

- Molecule 29 is a protein called Ubiquitin carboxyl-terminal hydrolase RPN11.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	284	Total	C	N	O	S	0	0
			2236	1405	381	436	14		

- Molecule 30 is a protein called 26S proteasome regulatory subunit RPN10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	197	Total	C	N	O	S	0	0
			1534	962	269	300	3		

- Molecule 31 is a protein called 26S proteasome regulatory subunit RPN13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	111	Total	C	N	O	S	0	0
			906	586	148	169	3		

- Molecule 32 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Y	27	Total	C	N	O	0	0
			236	143	39	54		

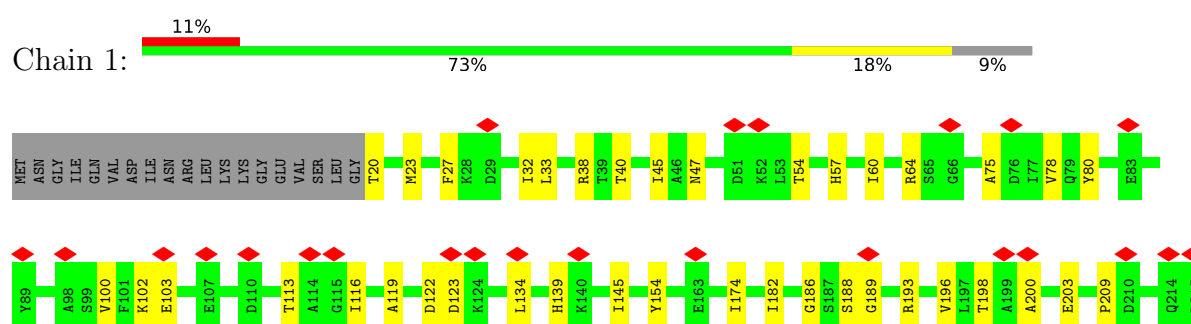
- Molecule 33 is a protein called 26S proteasome regulatory subunit RPN1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	813	Total	C	N	O	S	0	0
			6290	3995	1029	1237	29		

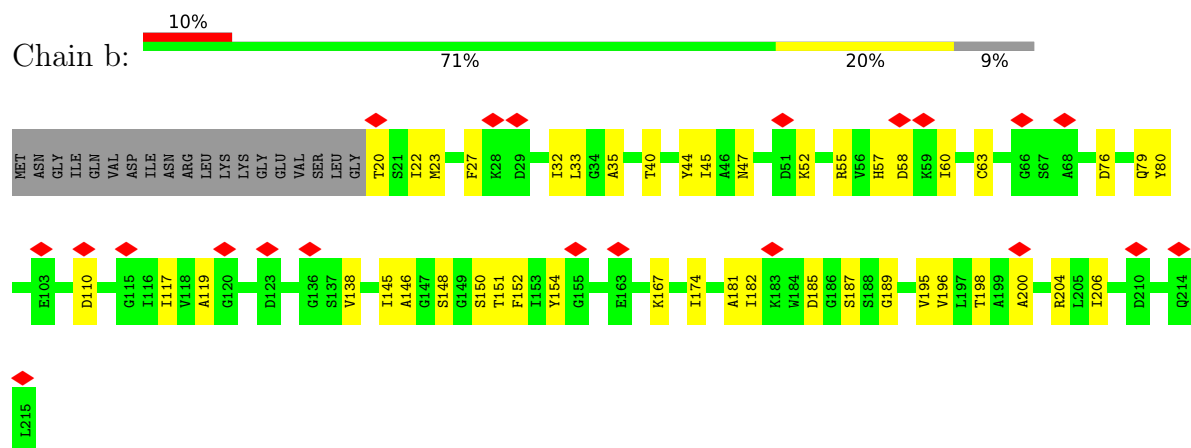
3 Residue-property plots

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.

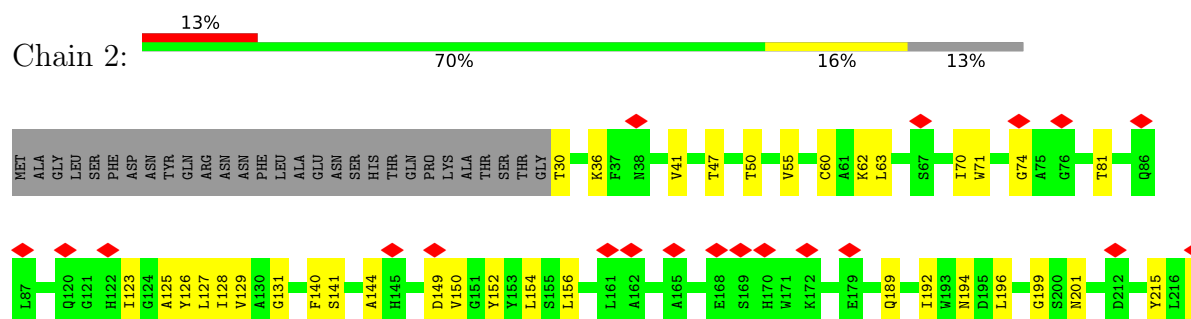
- Molecule 1: Proteasome subunit beta type-1

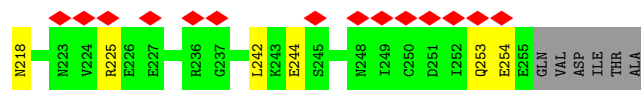


- Molecule 1: Proteasome subunit beta type-1

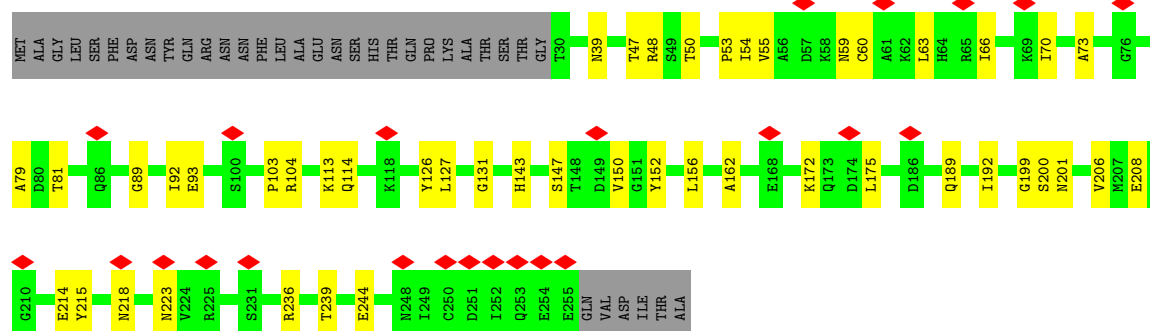


- Molecule 2: Proteasome subunit beta type-2

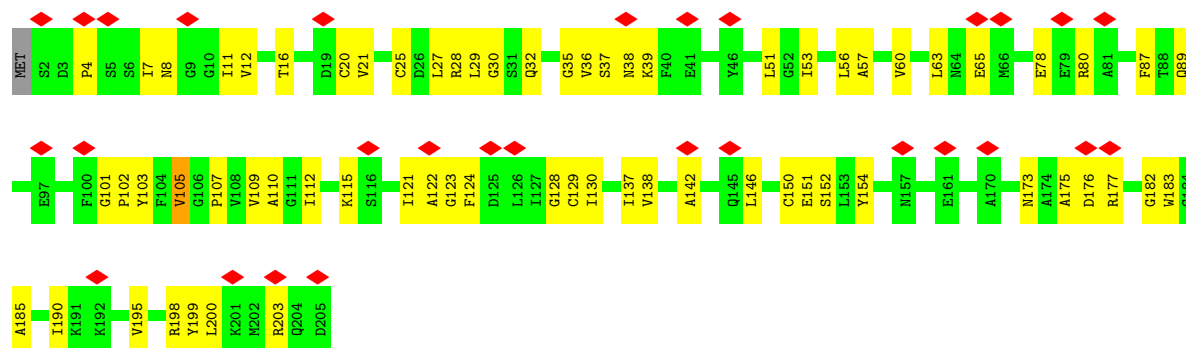




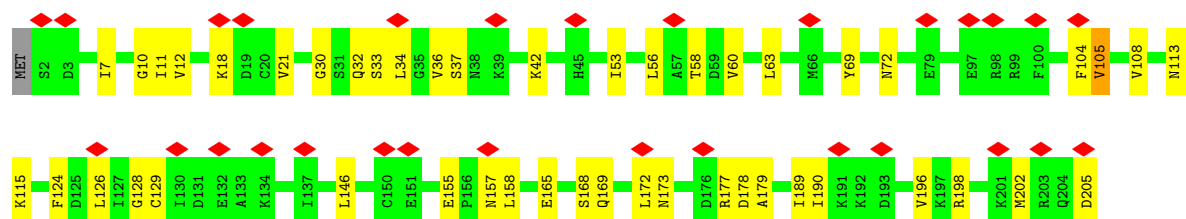
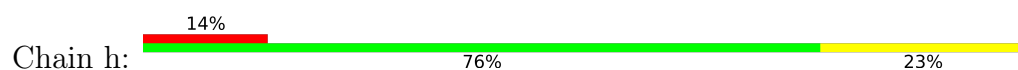
• Molecule 2: Proteasome subunit beta type-2



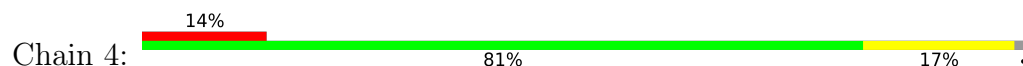
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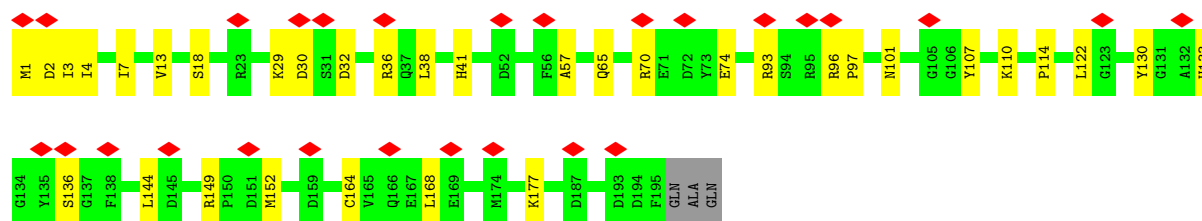


• Molecule 3: Proteasome subunit beta type-3

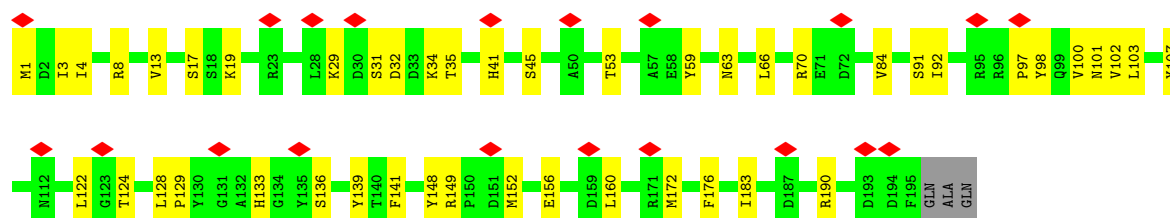
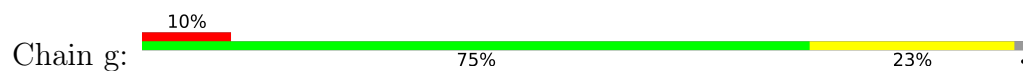


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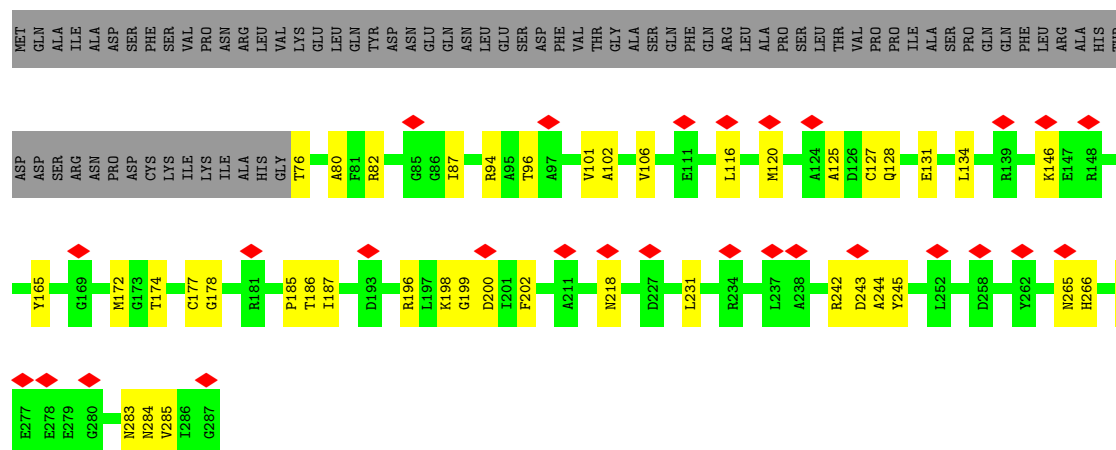




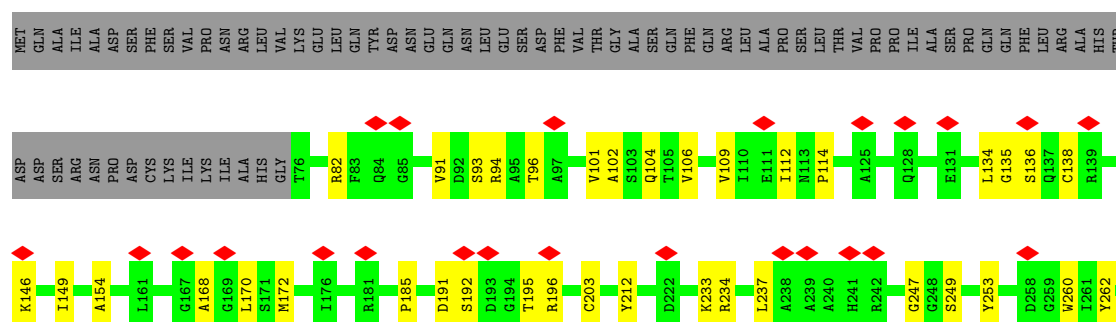
• Molecule 4: Proteasome subunit beta type-4

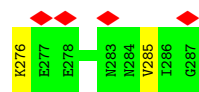


• Molecule 5: Proteasome subunit beta type-5

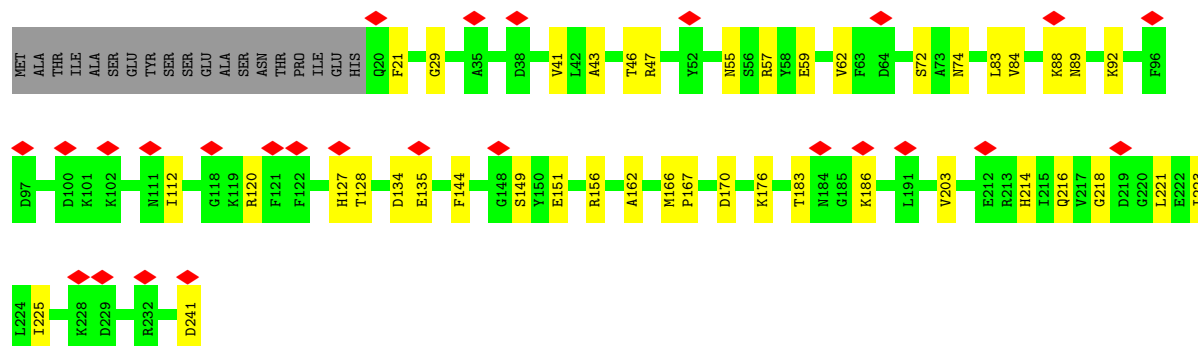
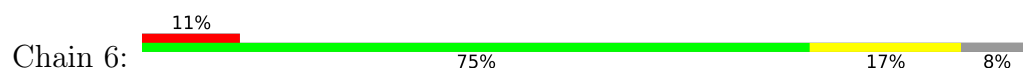


• Molecule 5: Proteasome subunit beta type-5

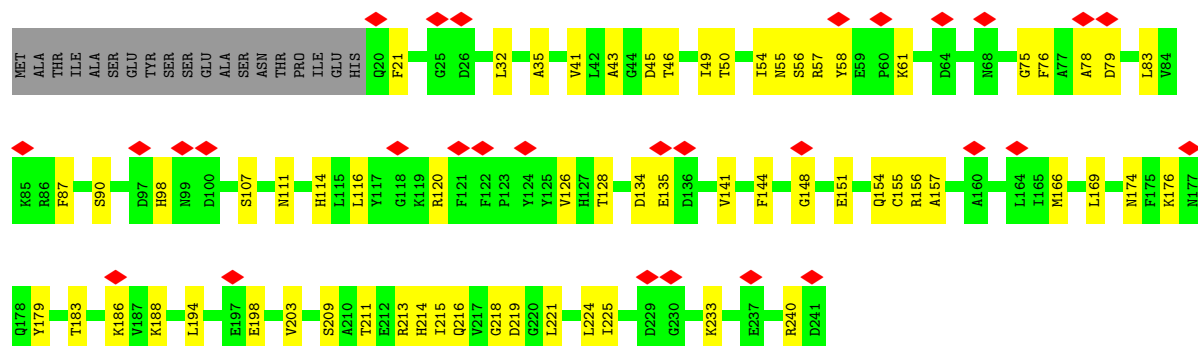




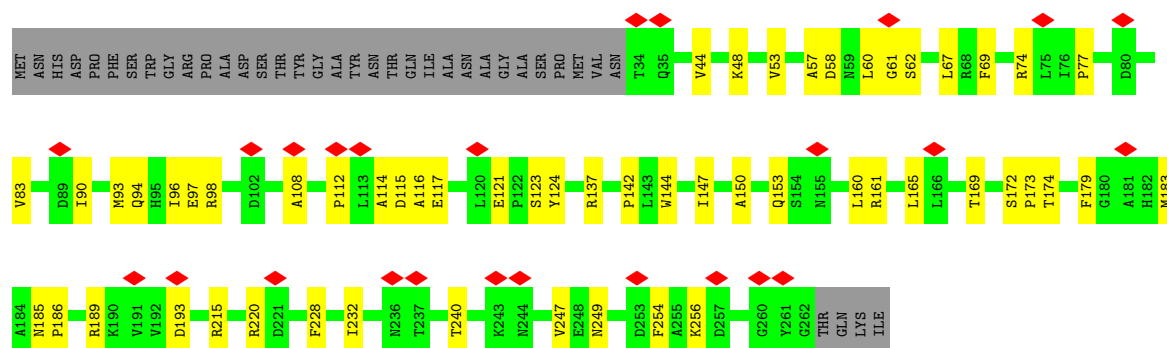
- Molecule 6: Proteasome subunit beta type-6



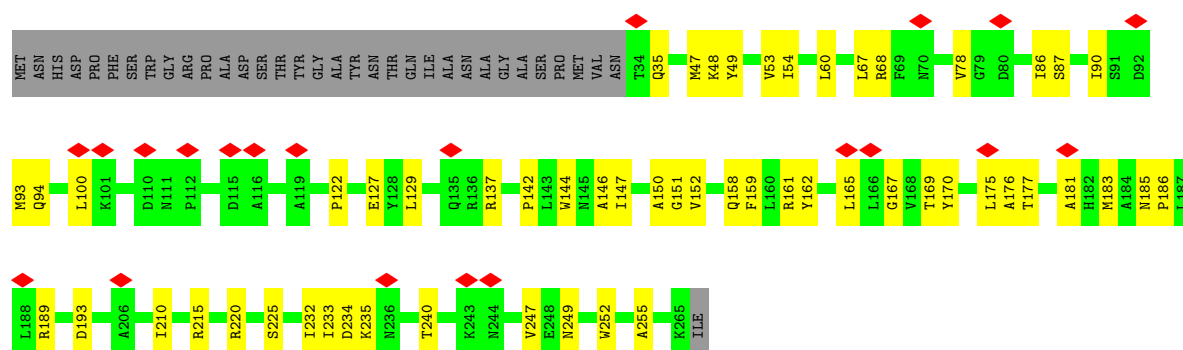
- Molecule 6: Proteasome subunit beta type-6



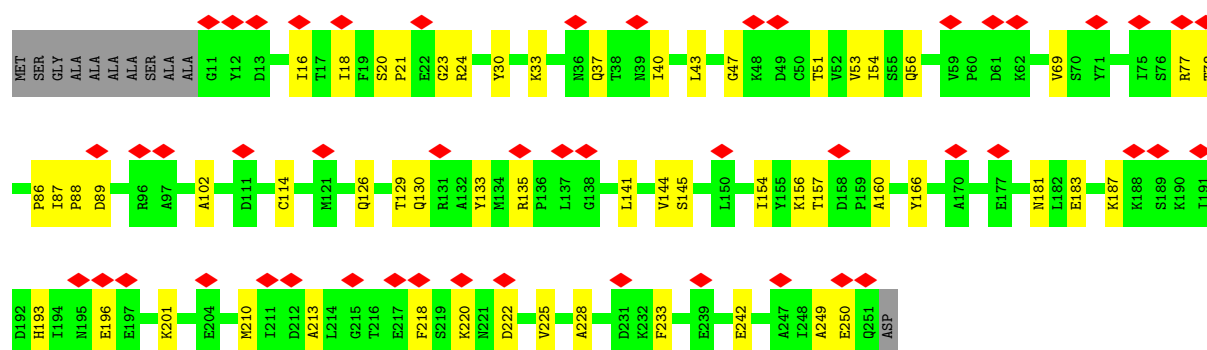
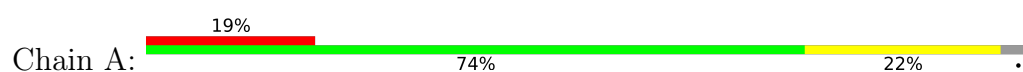
- Molecule 7: Proteasome subunit beta type-7



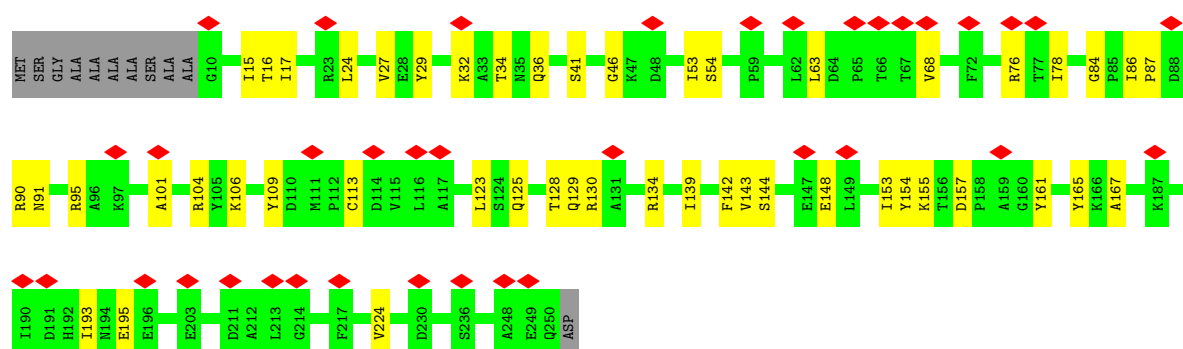
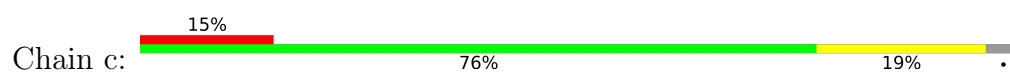
- Molecule 7: Proteasome subunit beta type-7



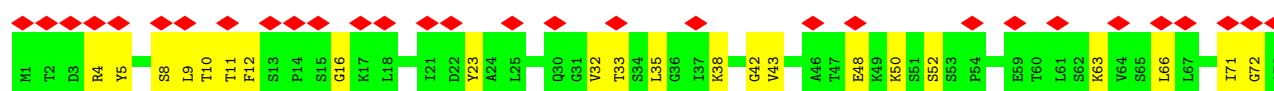
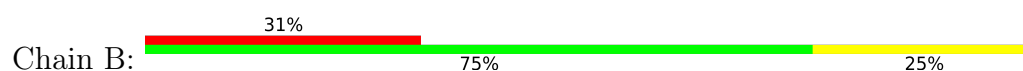
• Molecule 8: Proteasome subunit alpha type-1

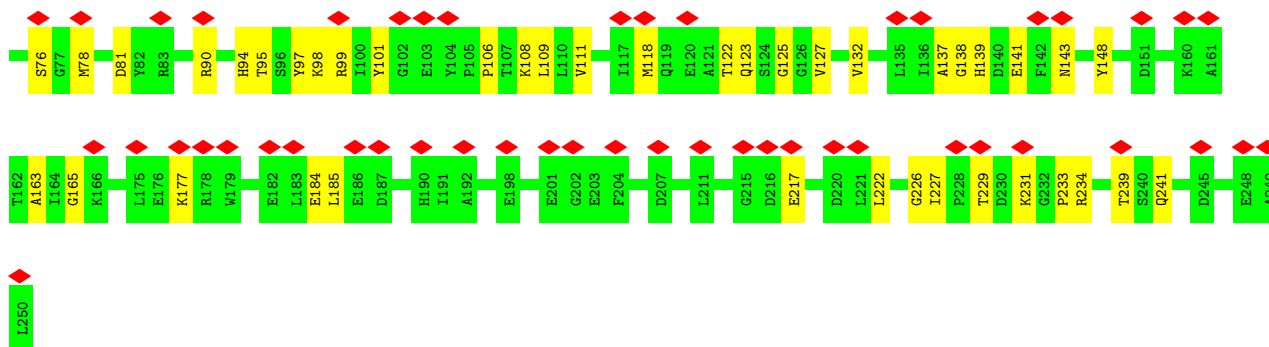


• Molecule 8: Proteasome subunit alpha type-1

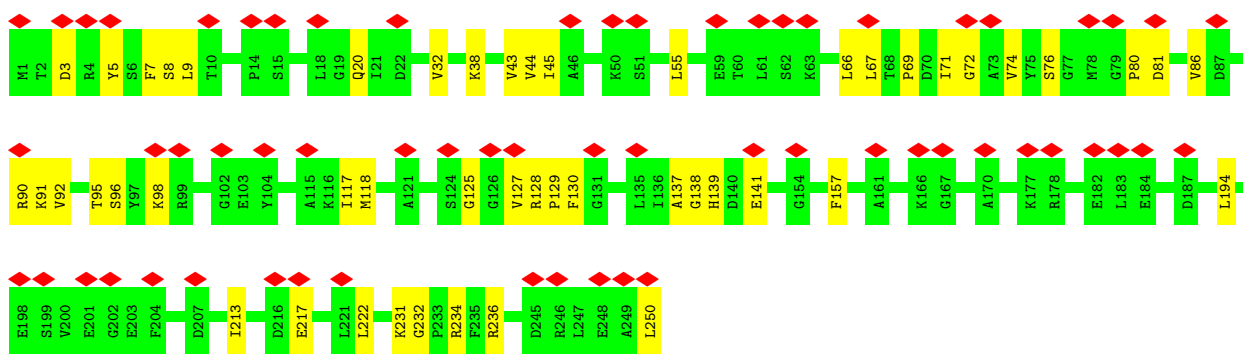
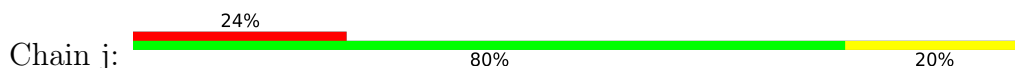


• Molecule 9: Proteasome subunit alpha type-2

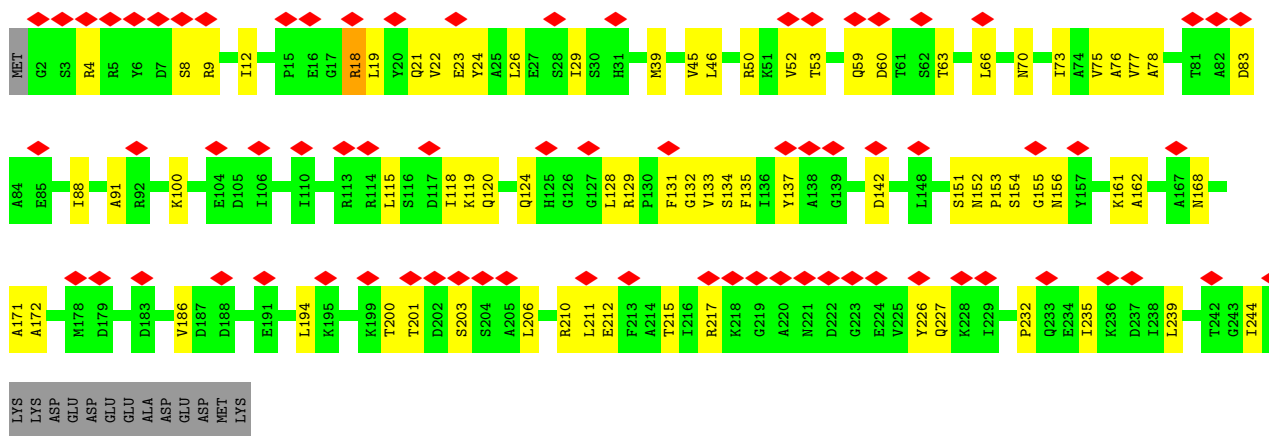




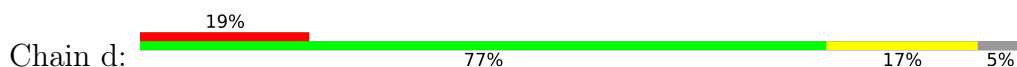
• Molecule 9: Proteasome subunit alpha type-2

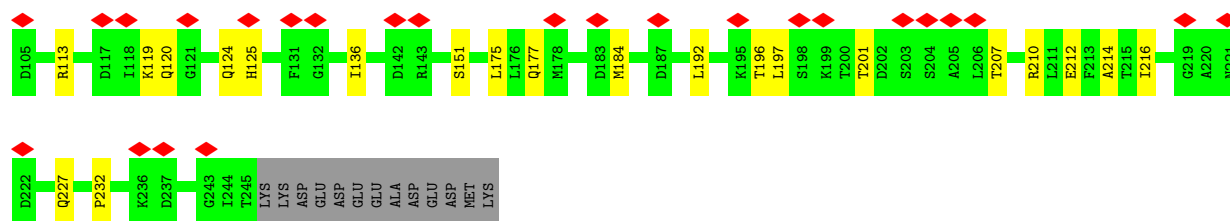


• Molecule 10: Proteasome subunit alpha type-3

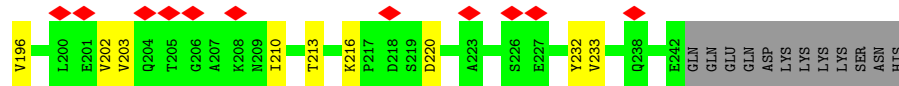
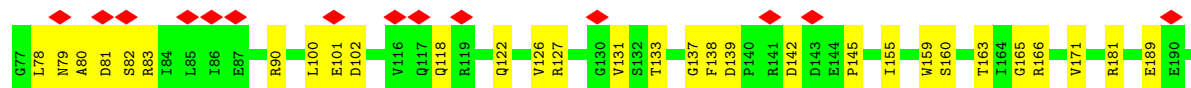
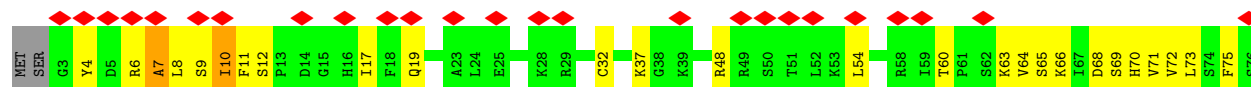


• Molecule 10: Proteasome subunit alpha type-3

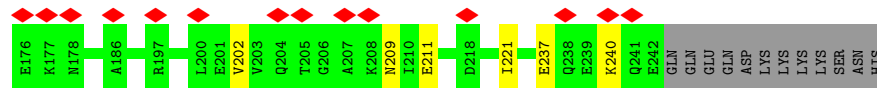
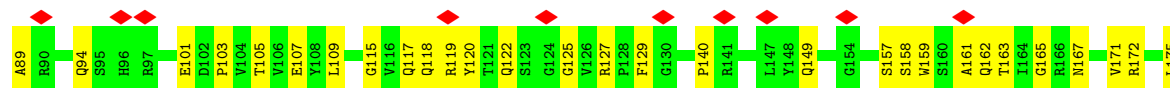
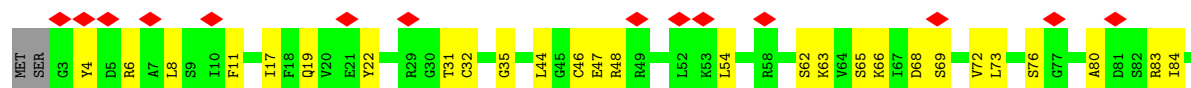




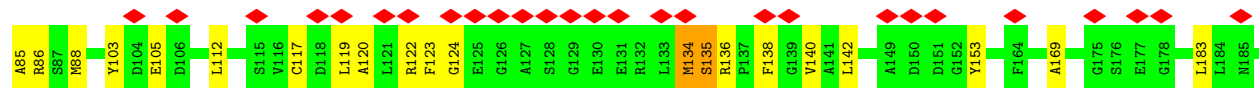
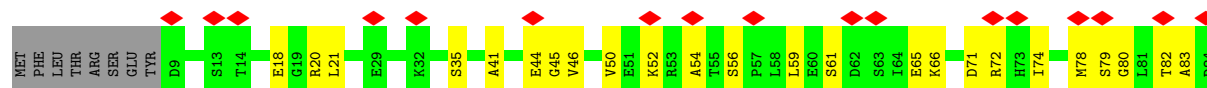
• Molecule 11: Proteasome subunit alpha type-4

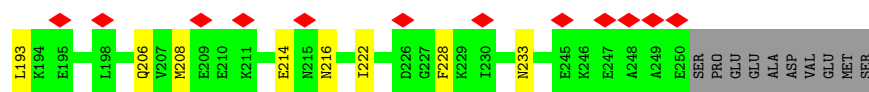


• Molecule 11: Proteasome subunit alpha type-4

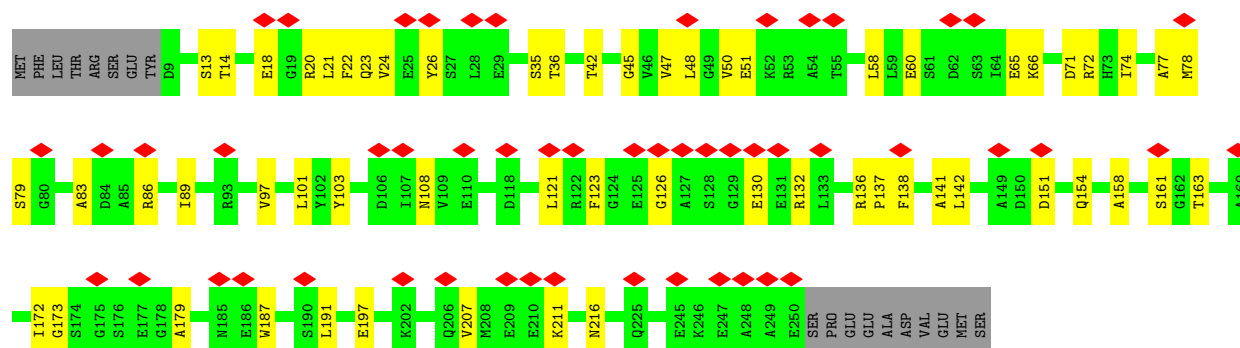


• Molecule 12: Proteasome subunit alpha type-5

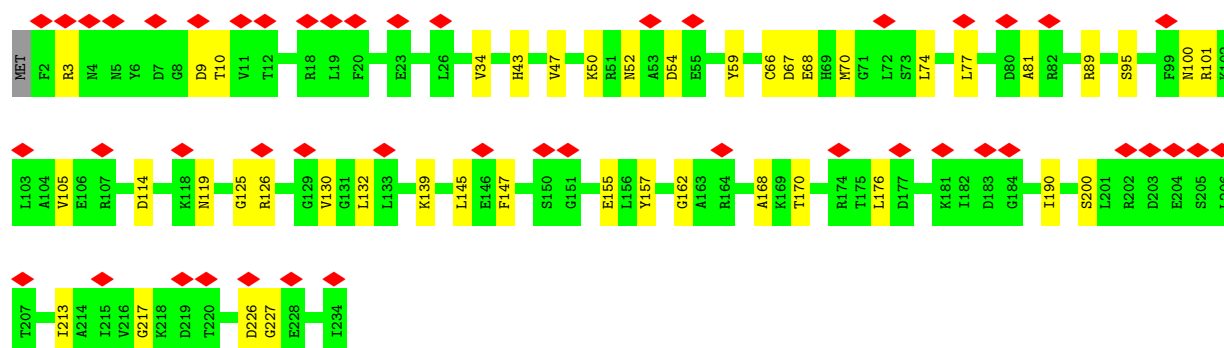
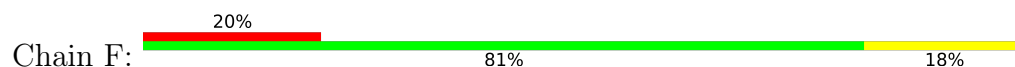




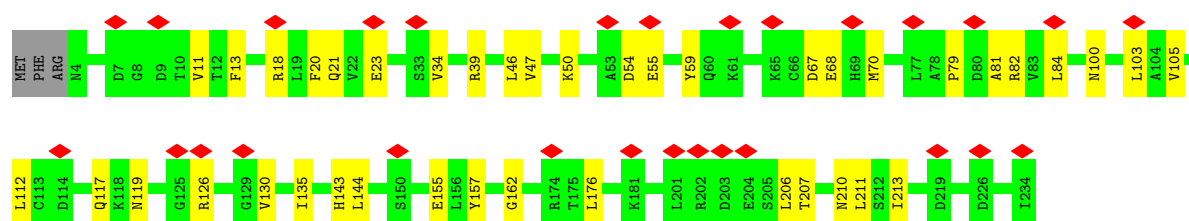
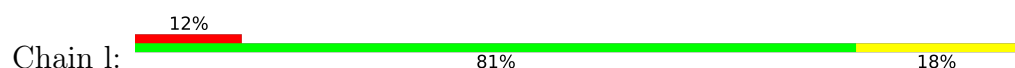
• Molecule 12: Proteasome subunit alpha type-5



• Molecule 13: Proteasome subunit alpha type-6

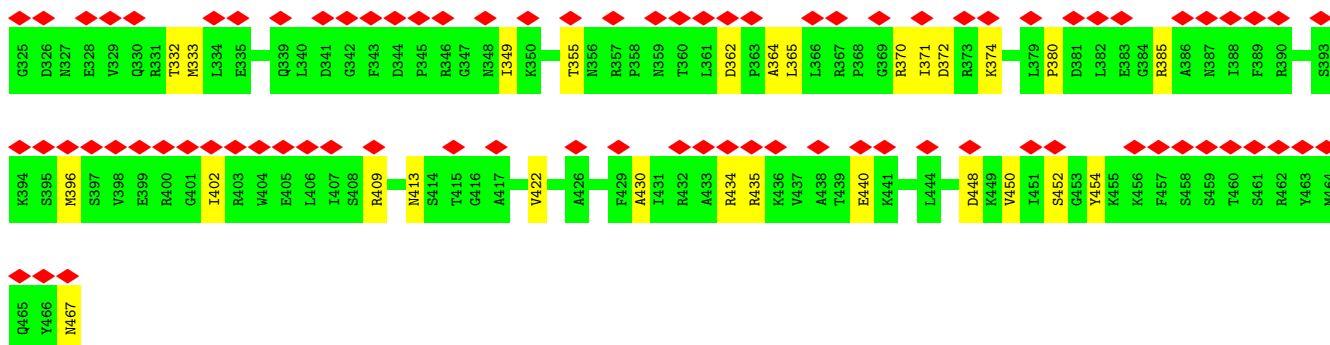


• Molecule 13: Proteasome subunit alpha type-6

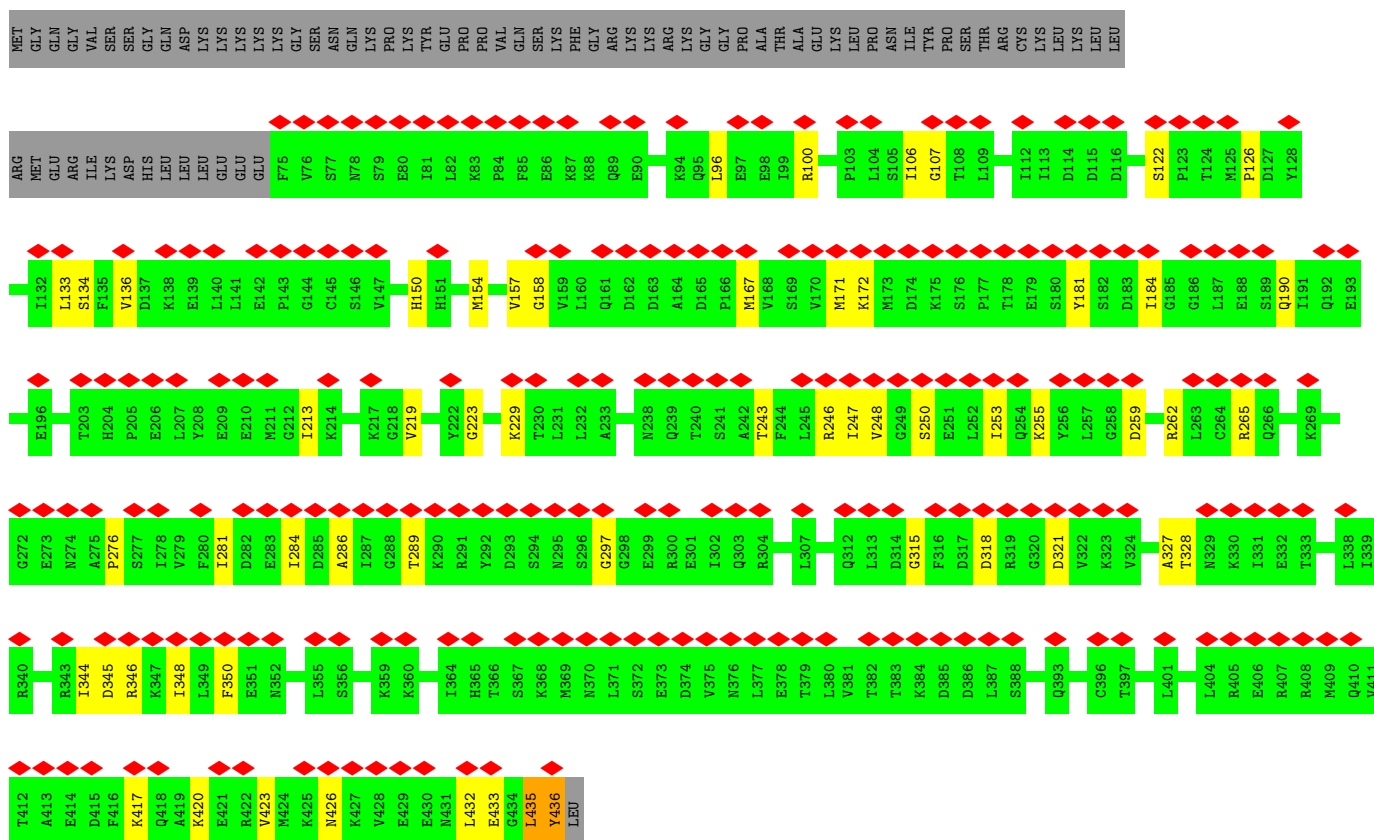


• Molecule 14: Probable proteasome subunit alpha type-7

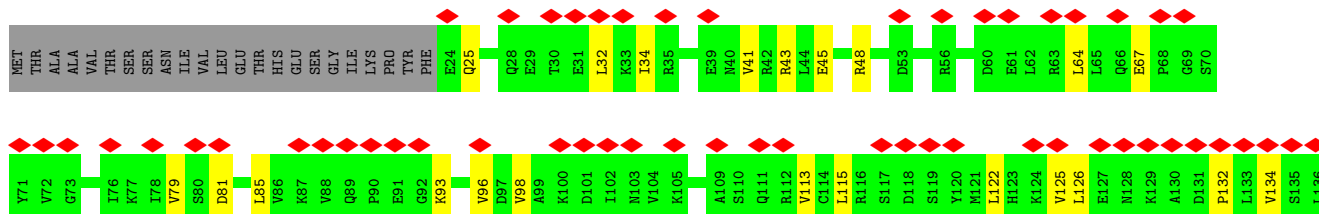
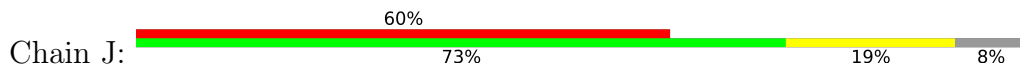


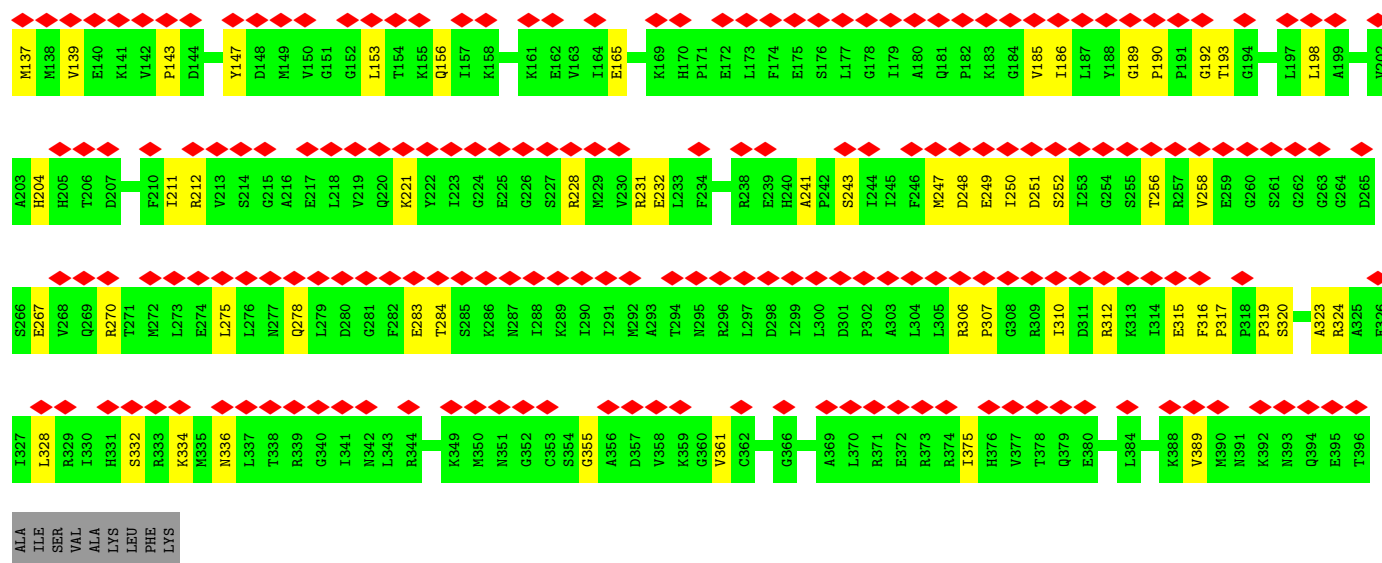


- Molecule 16: 26S proteasome regulatory subunit 4 homolog

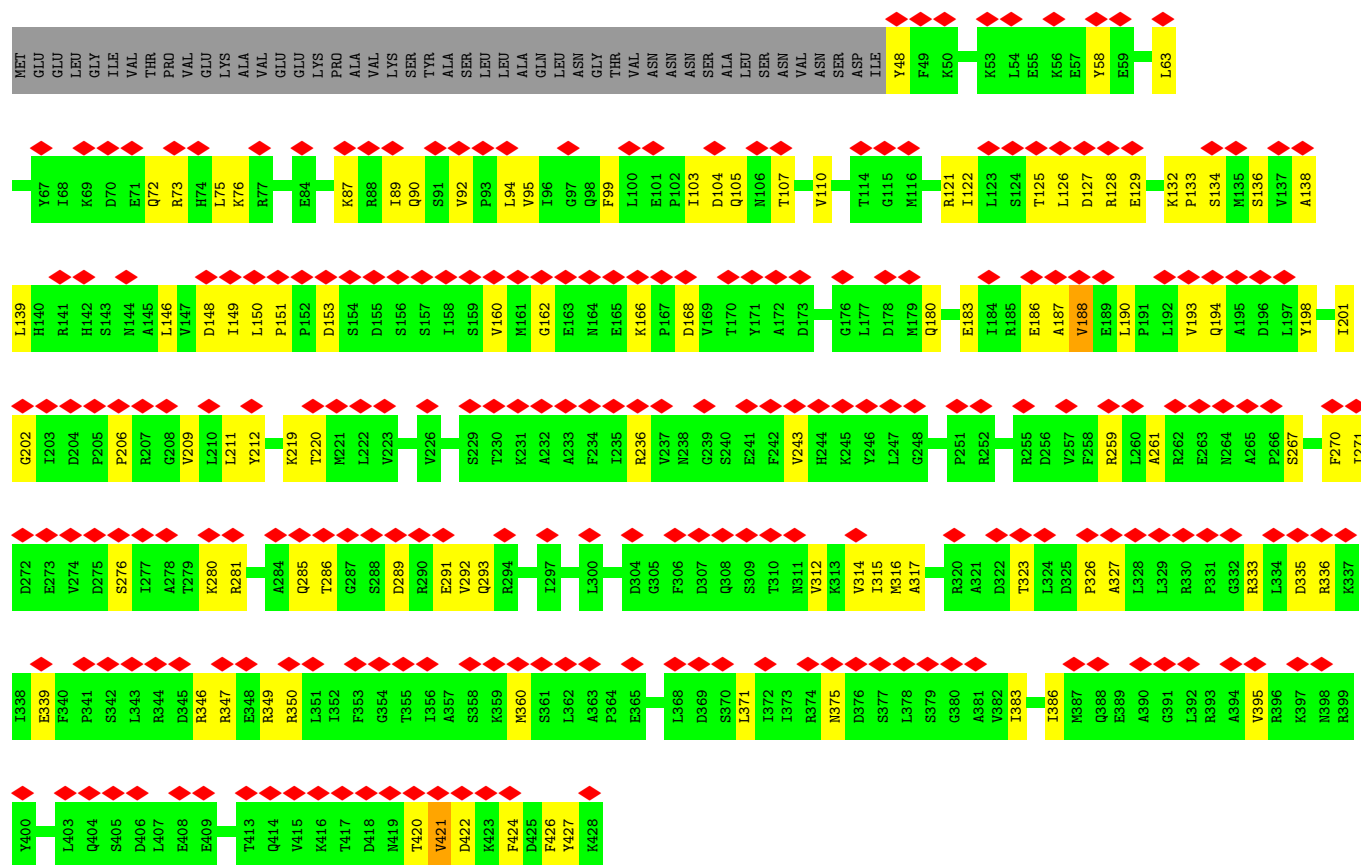


- Molecule 17: 26S proteasome regulatory subunit 8 homolog



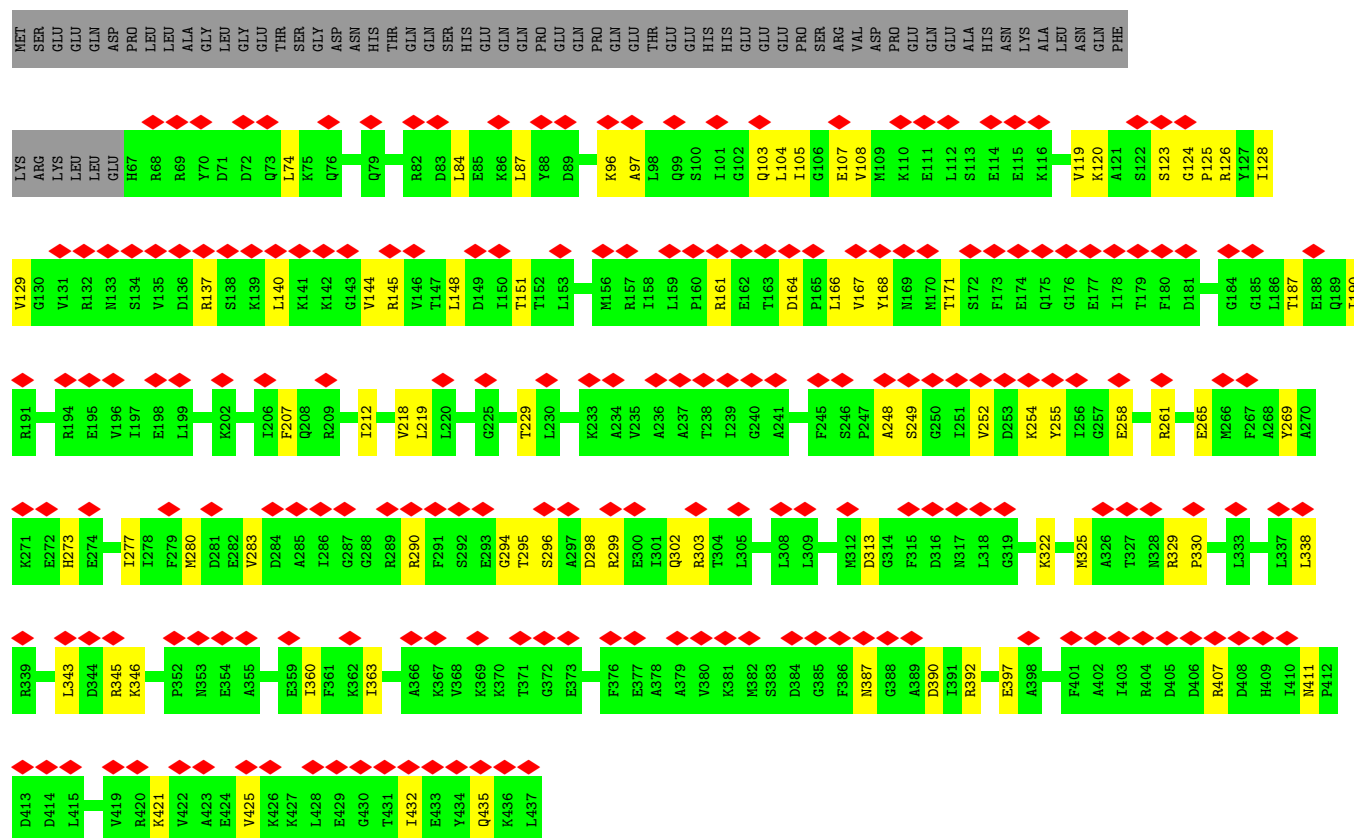


• Molecule 18: 26S proteasome regulatory subunit 6B homolog

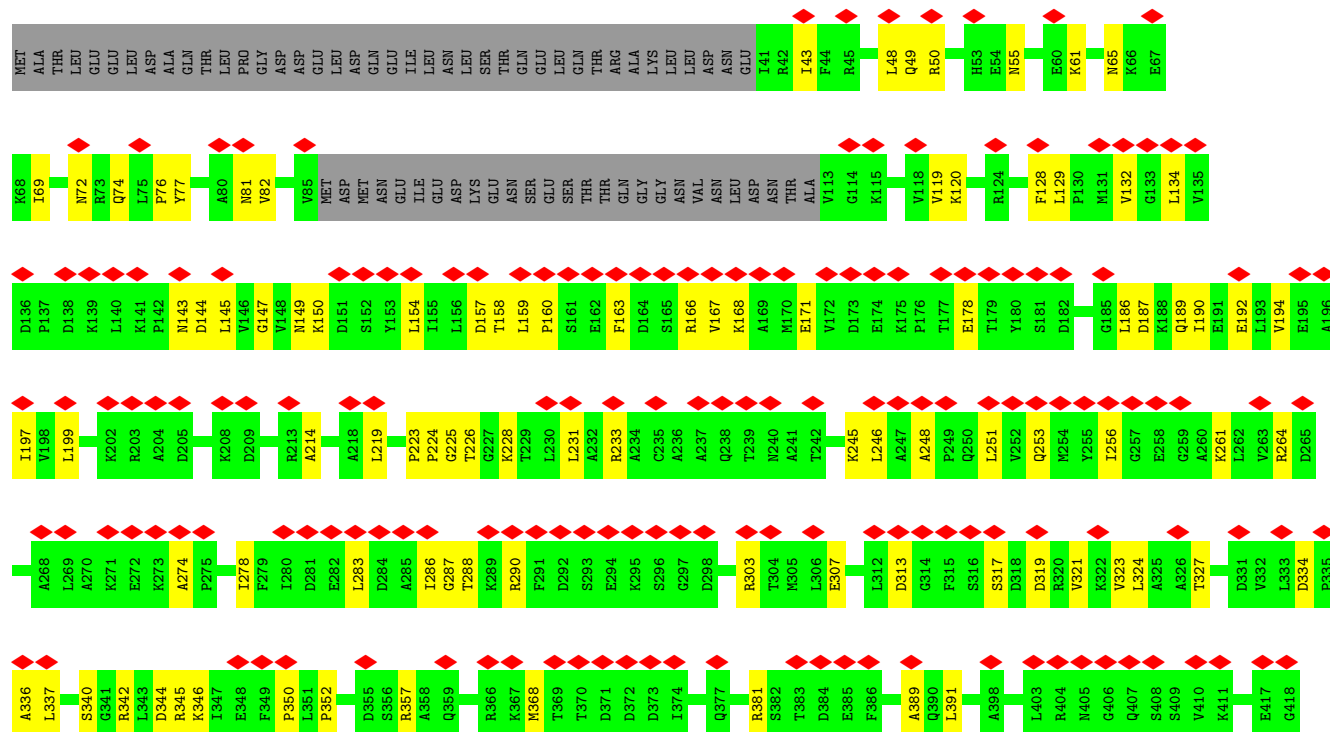


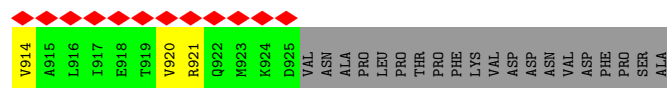
• Molecule 19: 26S proteasome subunit RPT4



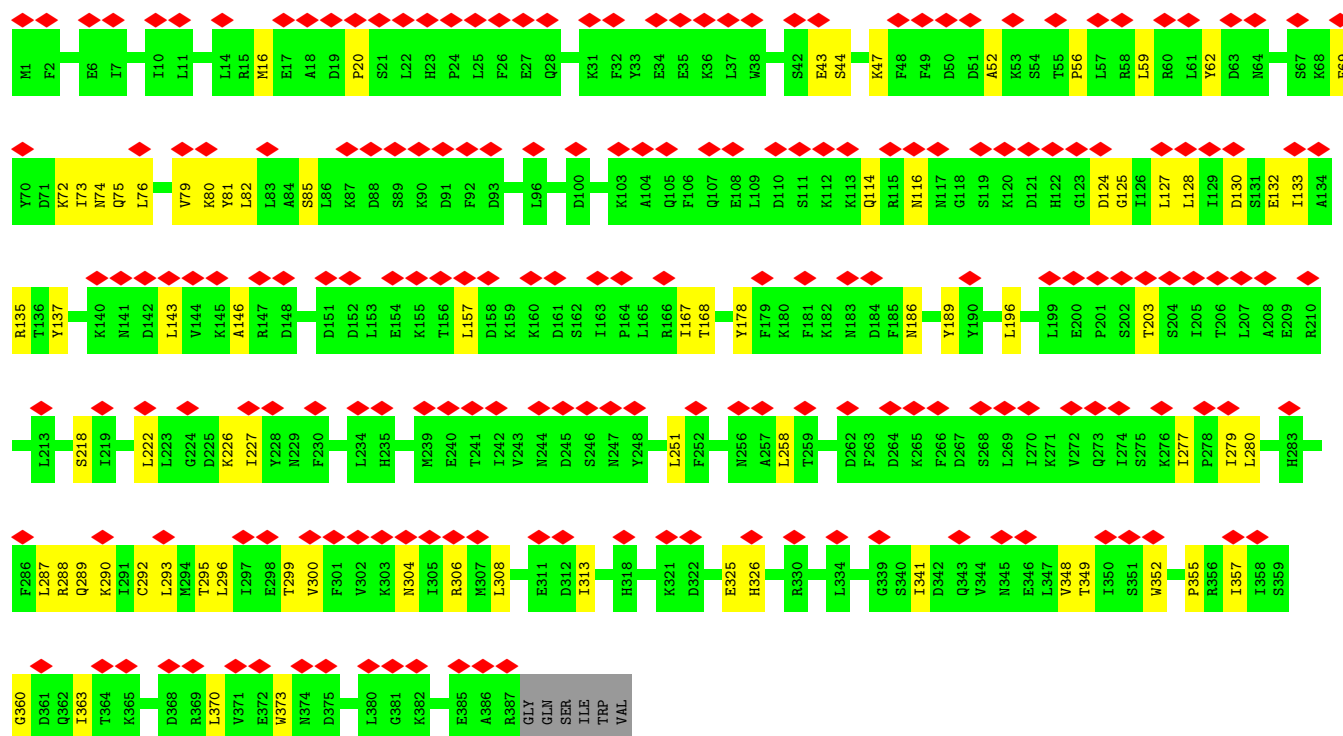
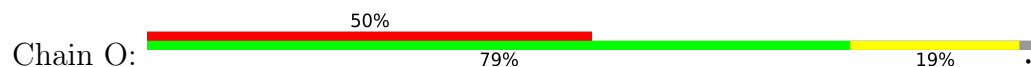


• Molecule 20: 26S proteasome regulatory subunit 6A

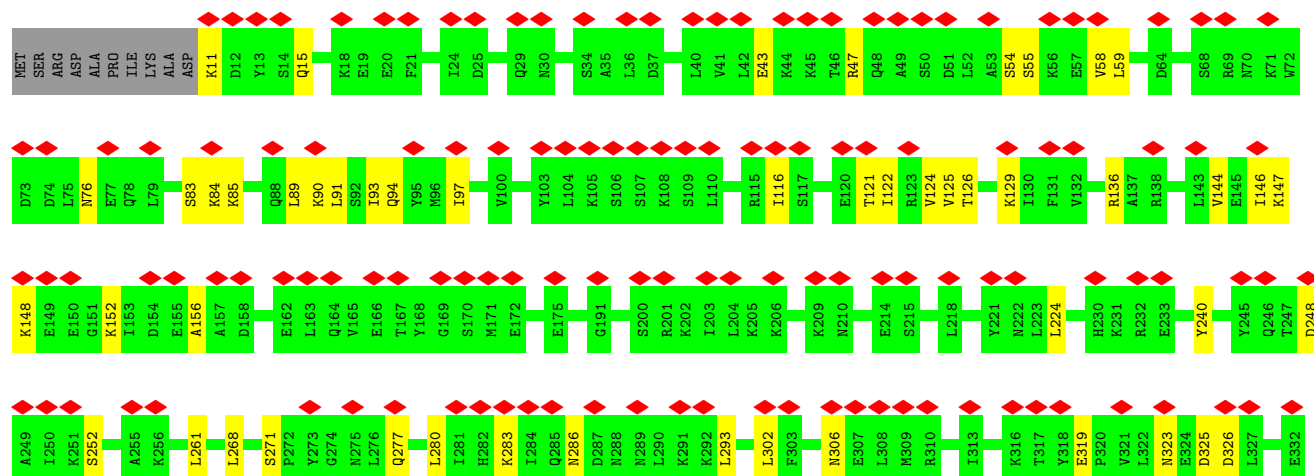
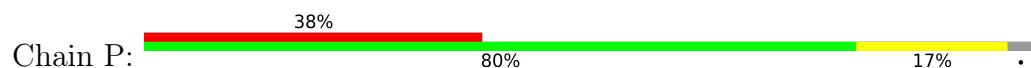


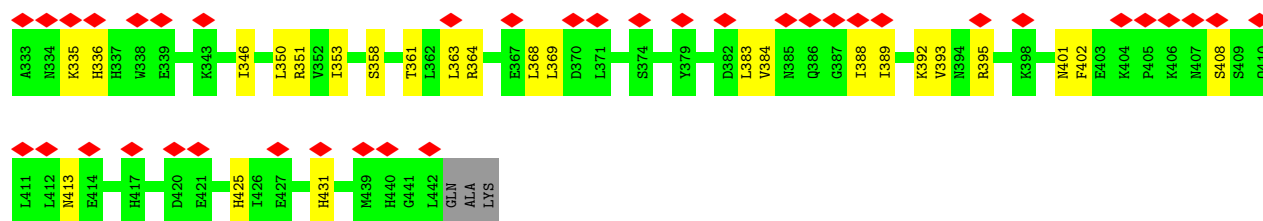


• Molecule 22: 26S proteasome regulatory subunit RPN9

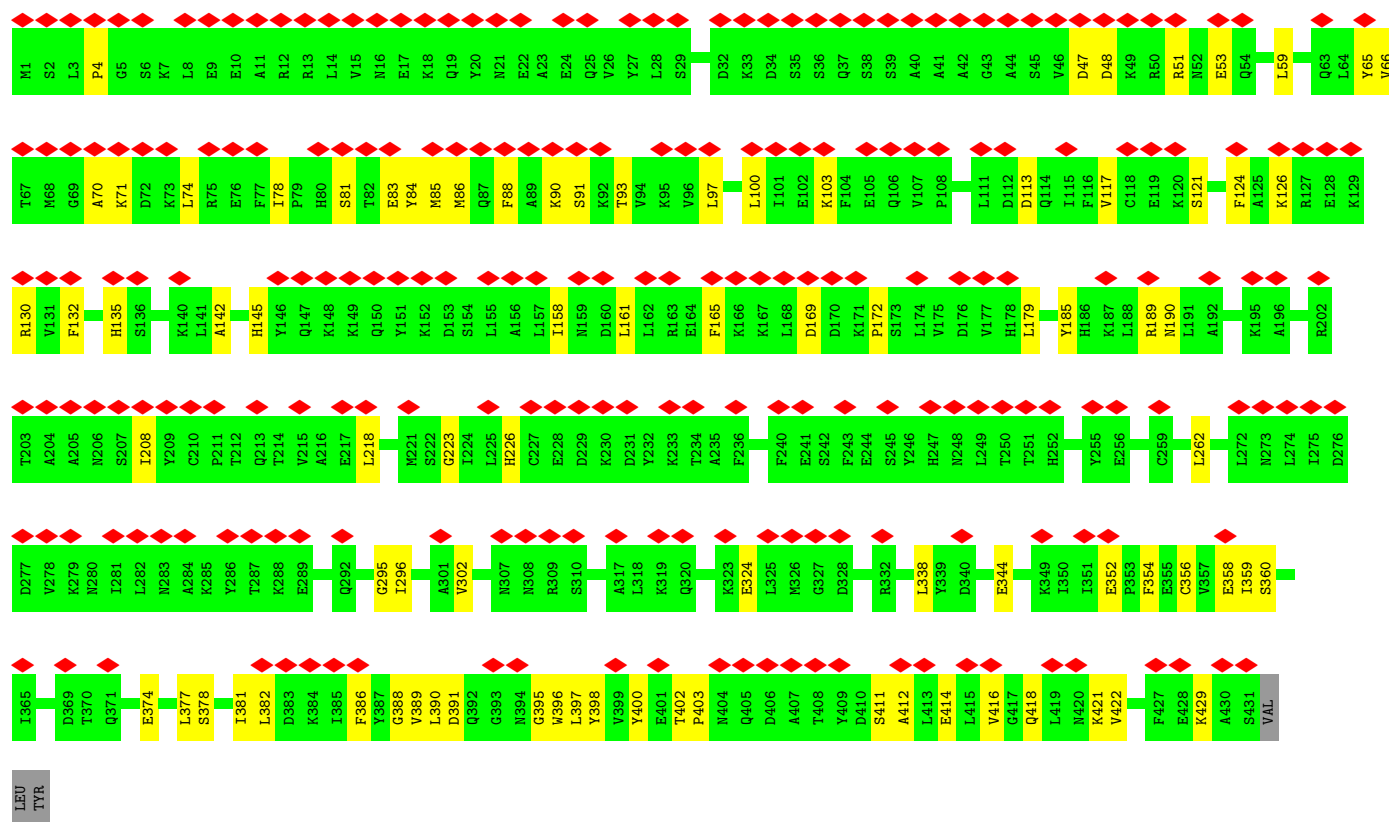
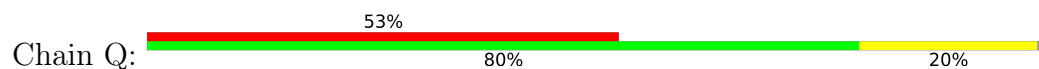


• Molecule 23: 26S proteasome regulatory subunit RPN5

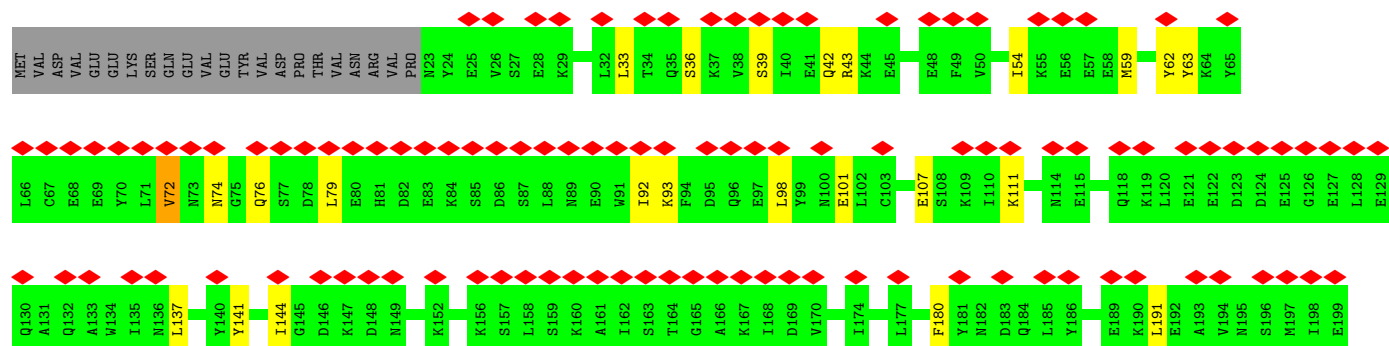
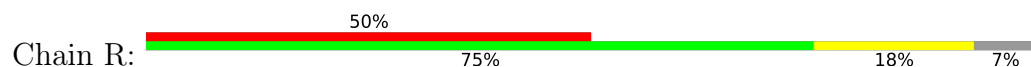


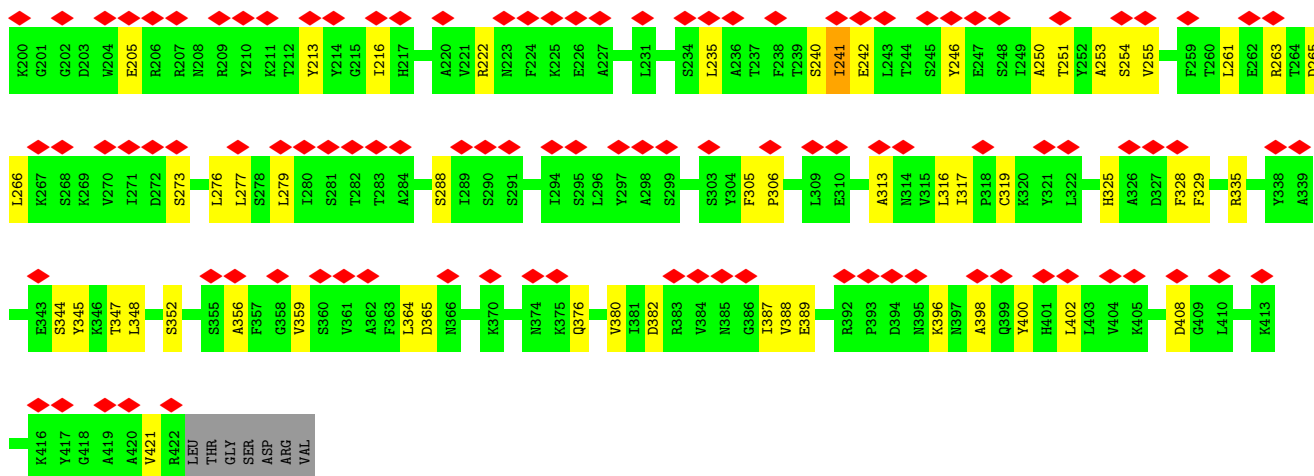


• Molecule 24: 26S proteasome regulatory subunit RPN6



• Molecule 25: 26S proteasome regulatory subunit RPN7

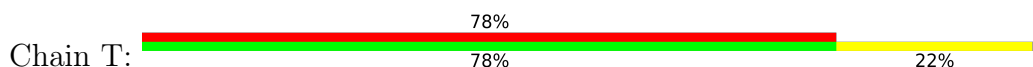


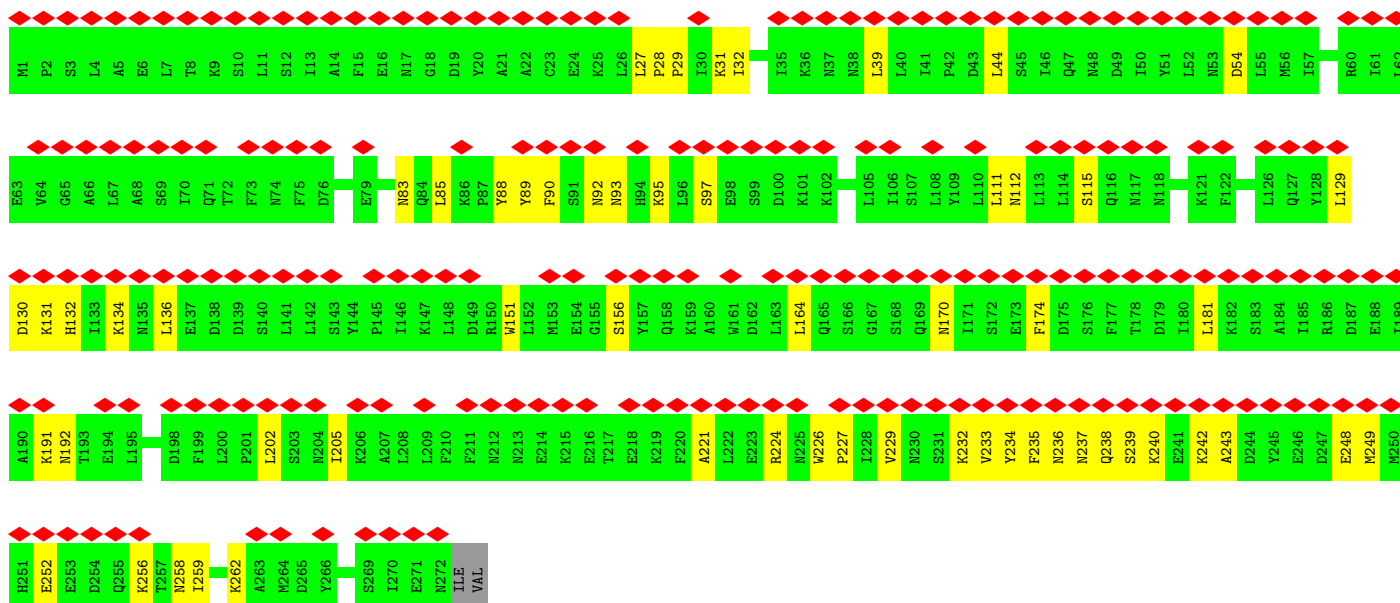


• Molecule 26: 26S proteasome regulatory subunit RPN3

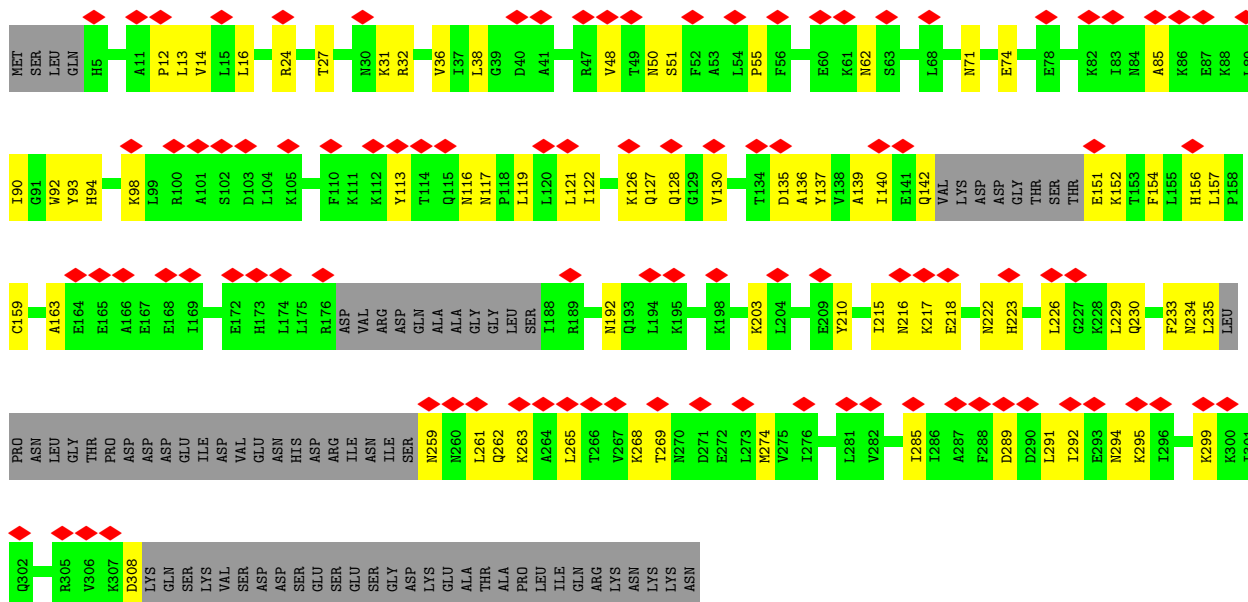


• Molecule 27: 26S proteasome regulatory subunit RPN12

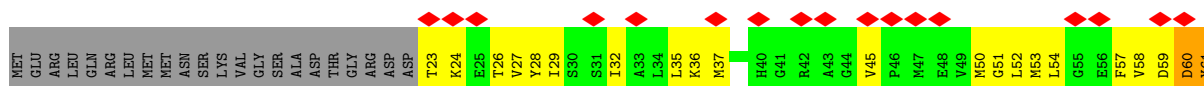


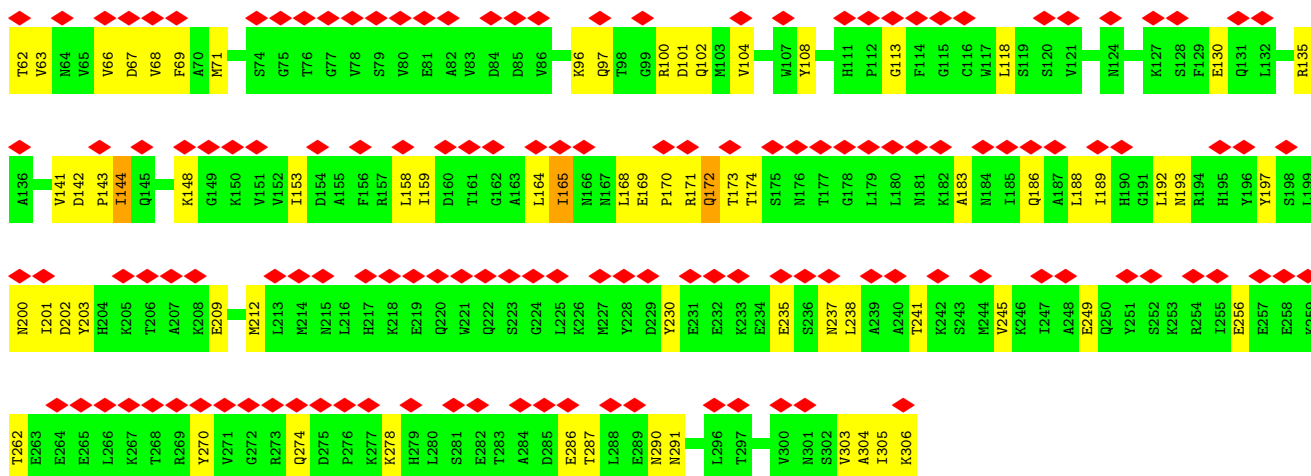


• Molecule 28: 26S proteasome regulatory subunit RPN8

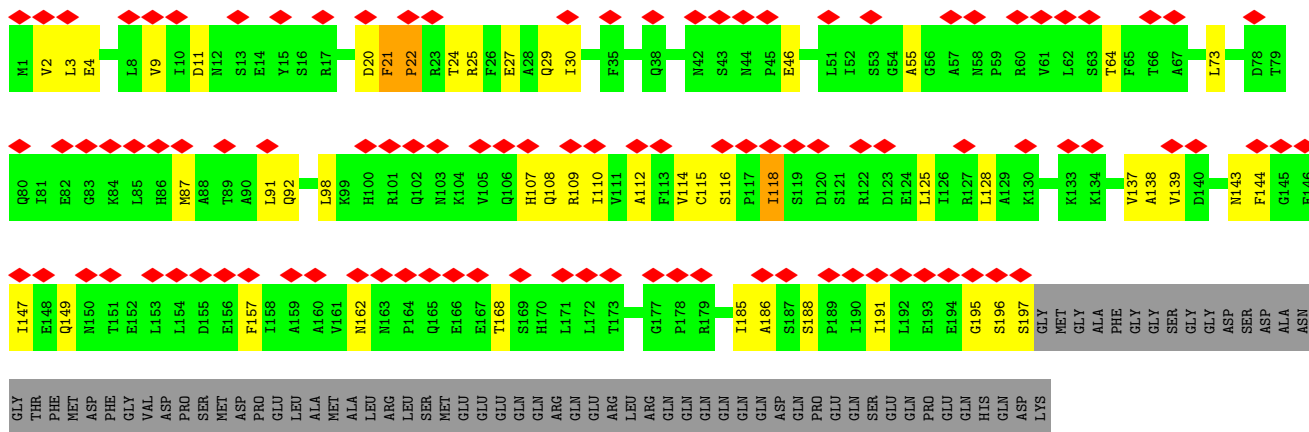
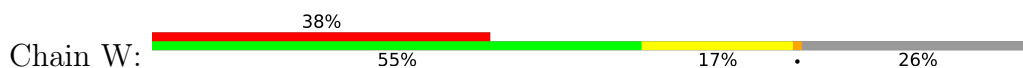


• Molecule 29: Ubiquitin carboxyl-terminal hydrolase RPN11

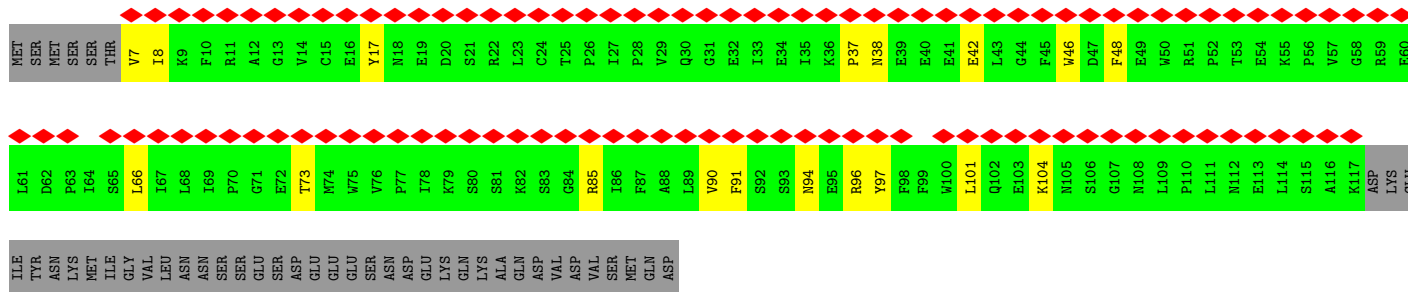




• Molecule 30: 26S proteasome regulatory subunit RPN10



• Molecule 31: 26S proteasome regulatory subunit RPN13



• Molecule 32: 26S proteasome complex subunit SEM1



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

GLU E62 E63 E64 V67 E68 E69 D70 D71 D72 F73 T74 N75 E76 L77 R86 E87 R88

• Molecule 33: 26S proteasome regulatory subunit RPN1

Chain Z: 64% 65% 17% 18%

MET VAL ASP GLU ASP ASP ASP LYS LYS GLN THR THR ILE ASP GLU GLN SER SER LEU THR LYS LYS ASN PRO ASP ASP THR TRP LYS LYS THR ASP L49 E50 E51 E52 E53 E54 E55 E56 E57 E58 E59 D60

S61 S62 S63 S64 S65 S66 S67 L68 M69 M70 M71 M72 M73 M74 M75 M76 M77 M78 M79 M80 S81 S82 S83 S84 S85 S86 S87 S88 S89 S90 S91 S92 S93 S94 S95 S96 S97 S98 S99 S100 S101 S102 S103 S104 S105 S106 S107 S108 S109 S110 S111 S112 S113 S114 S115 S116 S117 S118 S119 S120

L121 L122 L123 L124 L125 L126 L127 E128 M129 M130 M131 M132 M133 M134 M135 M136 M137 M138 M139 M140 M141 S142 D143 D144 D145 F146 F147 F148 F149 G150 H151 E152 Y153 I154 R155 R156 R157 R158 R159 R160 R161 R162 R163 R164 R165 R166 R167 R168 R169 R170 R171 R172 A173 E174 E175 E176 E177 E178 E179 E180 G181

S182 K183 S184 D185 G186 S187 A188 A189 T190 T191 T192 T193 T194 T195 T196 T197 T198 T199 T200 T201 C202 L203 L204 L205 D206 D207 Y210 F211 L212 K213 H214 N215 Y216 G217 E218 D219 D220 D221 D222 D223 D224 D225 D226 D227 D228 D229 D230 D231 D232 D233 D234 V237 D238 D239 E240 N241 F242 Q243 R244

V245 C246 Q247 Y248 A251 C252 C253 P254 P255 L256 P257 P258 P259 E260 D261 V262 A263 F264 L265 K266 T267 A268 Y269 S270 T271 Y272 L273 H274 Q275 T279 I282 A283 A285 A286 V287 R287 L288 G289 E290 E291 D292 M293 I294 V297 F298 D299 A300 T301 S302 D303 P304 V305 M306 H307 K308 Q309

Y312 I313 L314 A315 A316 A317 K318 T319 S320 F321 E322 Y323 E324 G325 Q327 D328 I329 I330 G331 N332 G333 K334 L335 S336 E337 H338 F339 L340 Y341 L342 A343 K344 E345 N347 L348 T349 G350 P351 K352 V353 E354 E355 D356 Y357 Y358 K359 S360 H361 L362 D363 N364 S365 K366 S367 V368 F369 S370

S371 A372 G373 L374 D375 S376 A377 Q378 M379 N380 L381 A382 S383 N387 G388 F389 Y394 C395 L396 D397 K398 L399 I400 V401 D402 M403 D404 M405 A406 Y407 Y408 K409 T410 K411 G412 G413 G414 M415 A418 V419 I422 G423 S424 I425 Y426 Q427 M428 M429 L430 D431 G432 L433 Q434 Q435 L436 D437

K438 Y439 L440 Y441 V442 D443 E444 E445 E446 V447 K448 A449 A450 A451 L452 L453 G454 G455 G456 I457 S458 A459 S460 G461 V462 H463 D464 G465 A466 V467 E468 A469 A470 L471 L472 L473 L474 Q475 D476 Y477 Y478 T479 M480 D482 T483 K484 I485 S486 S487 A488 L491 G492 A496 F497 S500 K501

N502 D503 E504 V505 L506 L507 L508 L509 L510 P511 I512 A513 A514 S515 S516 D517 L518 P519 I520 E521 T522 A523 A524 M525 A526 S527 L528 S529 L530 A531 H532 V533 F534 V535 G536 T537 C538 N539 G540 D541 I542 T543 T544 S545 I546 M547 Y548 N549 T550 L551 E552 R553 T554 A555 I556 E557 L558 K559 T560 D561

W562 V563 R564 F565 L566 A567 L568 A569 L570 G571 L572 L573 Y574 M575 G576 Q577 G578 E579 Q580 V581 D582 D583 V584 L585 E586 T587 I588 S589 A590 I591 E592 H593 P594 M595 T596 S597 A598 I599 E600 V601 L602 V603 G604 C606 A607 Y608 T609 G610 T611 G612 D613 V614 L615 L616 I617 Q618 D619 L620 L621

H622 R623 L624 T625 PRO LYS ASN VAL LYS GLY GLU GLU ASP ALA ASP GLU GLU THR THR ALA GLY GLN THR ASN SER ILE SER ASP PHE LEU GLY GLU GLN VAL ASN GLU PRO THR LYS LYS T596 S597 A598 I599 E600 V601 L602 V603 G604 C606 A607 Y608 T609 G610 T611 G612 D613 V614 L615 L616 I617 Q618 D619 L620 L621



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	40585	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.122	Depositor
Minimum map value	-1.006	Depositor
Average map value	0.011	Depositor
Map value standard deviation	0.088	Depositor
Recommended contour level	0.686	Depositor
Map size (Å)	474.47998, 474.47998, 474.47998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.318, 1.318, 1.318	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	1	0.06	0/1541	0.21	0/2087
1	b	0.06	0/1541	0.21	0/2087
2	2	0.06	0/1750	0.21	0/2373
2	i	0.06	0/1750	0.20	0/2373
3	3	0.07	0/1611	0.24	0/2174
3	h	0.07	0/1611	0.24	0/2174
4	4	0.07	0/1589	0.24	0/2142
4	g	0.07	0/1589	0.23	0/2142
5	5	0.07	0/1681	0.22	0/2274
5	f	0.07	0/1681	0.21	0/2274
6	6	0.07	0/1795	0.23	0/2420
6	e	0.07	0/1795	0.23	0/2420
7	7	0.08	0/1821	0.24	0/2470
7	a	0.08	0/1846	0.25	0/2503
8	A	0.07	0/1945	0.22	0/2634
8	c	0.08	0/1945	0.23	0/2634
9	B	0.08	0/1952	0.28	0/2642
9	j	0.07	0/1952	0.23	0/2642
10	C	0.07	0/1934	0.24	0/2618
10	d	0.08	0/1934	0.27	0/2618
11	D	0.09	0/1910	0.28	0/2586
11	n	0.08	0/1910	0.24	0/2586
12	E	0.06	0/1886	0.21	0/2541
12	m	0.07	0/1886	0.23	0/2541
13	F	0.07	0/1823	0.24	0/2463
13	l	0.07	0/1800	0.22	0/2433
14	G	0.07	0/1932	0.22	0/2609
14	k	0.08	0/1932	0.22	0/2609
15	H	0.09	0/2834	0.28	0/3816
16	I	0.08	0/2860	0.27	0/3856
17	J	0.09	0/2964	0.28	0/3981
18	K	0.10	0/3062	0.34	0/4132
19	L	0.09	0/2981	0.29	0/4008
20	M	0.21	1/2903 (0.0%)	0.29	0/3909

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
21	N	0.10	0/6670	0.29	0/9023
22	O	0.07	0/3243	0.25	0/4374
23	P	0.07	0/3599	0.23	0/4854
24	Q	0.08	0/3527	0.25	0/4748
25	R	0.08	0/3272	0.28	0/4412
26	S	0.09	0/3966	0.35	3/5355 (0.1%)
27	T	0.11	0/2279	0.36	0/3077
28	U	0.08	0/2146	0.28	0/2893
29	V	0.10	0/2271	0.33	0/3064
30	W	0.16	0/1557	0.32	0/2111
31	X	0.07	0/931	0.23	0/1262
32	Y	0.10	0/239	0.33	0/322
33	Z	0.11	1/6404 (0.0%)	0.26	0/8686
All	All	0.09	2/108050 (0.0%)	0.26	3/145952 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	M	274	ALA	C-N	10.45	1.58	1.33
33	Z	468	GLU	C-N	6.49	1.49	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	S	477	VAL	N-CA-C	12.68	123.19	111.91
26	S	477	VAL	CA-C-N	-7.12	113.00	123.11
26	S	477	VAL	C-N-CA	-7.12	113.00	123.11

There are no chirality outliers.

There are no planarity outliers.

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	1	1512	0	1478	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	1512	0	1478	32	0
2	2	1719	0	1716	31	0
2	i	1719	0	1716	36	0
3	3	1581	0	1571	49	0
3	h	1581	0	1571	33	0
4	4	1561	0	1569	22	0
4	g	1561	0	1569	30	0
5	5	1644	0	1592	34	0
5	f	1644	0	1592	28	0
6	6	1757	0	1708	31	0
6	e	1757	0	1708	46	0
7	7	1790	0	1790	42	0
7	a	1815	0	1818	40	0
8	A	1907	0	1901	38	0
8	c	1907	0	1901	41	0
9	B	1915	0	1929	45	0
9	j	1915	0	1929	34	0
10	C	1904	0	1901	66	0
10	d	1904	0	1901	36	0
11	D	1881	0	1892	56	0
11	n	1881	0	1892	50	0
12	E	1861	0	1836	38	0
12	m	1861	0	1836	45	0
13	F	1795	0	1797	28	0
13	l	1773	0	1775	28	0
14	G	1892	0	1883	36	0
14	k	1892	0	1883	32	0
15	H	2787	0	2851	57	0
16	I	2822	0	2870	46	0
17	J	2928	0	3057	59	0
18	K	3019	0	3084	74	0
19	L	2937	0	3011	58	0
20	M	2866	0	2938	71	0
21	N	6562	0	6625	124	0
22	O	3182	0	3207	50	0
23	P	3545	0	3629	52	0
24	Q	3471	0	3495	57	0
25	R	3218	0	3216	50	0
26	S	3894	0	3938	58	0
27	T	2235	0	2207	56	0
28	U	2118	0	2177	66	0
29	V	2236	0	2242	85	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	W	1534	0	1542	30	0
31	X	906	0	888	14	0
32	Y	236	0	203	4	0
33	Z	6290	0	6236	102	0
All	All	106227	0	106548	1836	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 9.

The worst 5 of 1836 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)
10:C:18:ARG:NE	10:C:23:GLU:HG2	1.67	1.09
29:V:59:ASP:O	29:V:60:ASP:HB2	1.56	1.05
10:C:18:ARG:CZ	10:C:23:GLU:HG2	1.91	0.98
28:U:152:LYS:HE3	28:U:154:PHE:CE1	1.99	0.96
10:C:18:ARG:NE	10:C:23:GLU:CG	2.31	0.93

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	1	194/215 (90%)	188 (97%)	6 (3%)	0	100	100
1	b	194/215 (90%)	186 (96%)	8 (4%)	0	100	100
2	2	224/261 (86%)	214 (96%)	10 (4%)	0	100	100
2	i	224/261 (86%)	220 (98%)	4 (2%)	0	100	100
3	3	202/205 (98%)	195 (96%)	6 (3%)	1 (0%)	24	63
3	h	202/205 (98%)	193 (96%)	8 (4%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	4	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
4	g	193/198 (98%)	189 (98%)	4 (2%)	0	100	100
5	5	210/287 (73%)	206 (98%)	4 (2%)	0	100	100
5	f	210/287 (73%)	204 (97%)	6 (3%)	0	100	100
6	6	220/241 (91%)	211 (96%)	9 (4%)	0	100	100
6	e	220/241 (91%)	211 (96%)	9 (4%)	0	100	100
7	7	227/266 (85%)	214 (94%)	13 (6%)	0	100	100
7	a	230/266 (86%)	223 (97%)	7 (3%)	0	100	100
8	A	239/252 (95%)	230 (96%)	9 (4%)	0	100	100
8	c	239/252 (95%)	228 (95%)	11 (5%)	0	100	100
9	B	248/250 (99%)	237 (96%)	11 (4%)	0	100	100
9	j	248/250 (99%)	232 (94%)	16 (6%)	0	100	100
10	C	242/258 (94%)	231 (96%)	11 (4%)	0	100	100
10	d	242/258 (94%)	229 (95%)	13 (5%)	0	100	100
11	D	238/254 (94%)	225 (94%)	11 (5%)	2 (1%)	16	53
11	n	238/254 (94%)	227 (95%)	11 (5%)	0	100	100
12	E	240/260 (92%)	229 (95%)	9 (4%)	2 (1%)	16	53
12	m	240/260 (92%)	228 (95%)	12 (5%)	0	100	100
13	F	231/234 (99%)	217 (94%)	14 (6%)	0	100	100
13	l	229/234 (98%)	227 (99%)	2 (1%)	0	100	100
14	G	241/288 (84%)	232 (96%)	9 (4%)	0	100	100
14	k	241/288 (84%)	236 (98%)	5 (2%)	0	100	100
15	H	351/467 (75%)	313 (89%)	38 (11%)	0	100	100
16	I	360/437 (82%)	324 (90%)	36 (10%)	0	100	100
17	J	371/405 (92%)	350 (94%)	19 (5%)	2 (0%)	24	63
18	K	379/428 (89%)	336 (89%)	40 (11%)	3 (1%)	16	53
19	L	369/437 (84%)	338 (92%)	31 (8%)	0	100	100
20	M	363/434 (84%)	329 (91%)	32 (9%)	2 (1%)	21	58
21	N	843/945 (89%)	783 (93%)	56 (7%)	4 (0%)	24	63
22	O	385/393 (98%)	345 (90%)	40 (10%)	0	100	100
23	P	430/445 (97%)	381 (89%)	49 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	Q	429/434 (99%)	394 (92%)	35 (8%)	0	100	100
25	R	398/429 (93%)	354 (89%)	41 (10%)	3 (1%)	16	53
26	S	473/523 (90%)	454 (96%)	18 (4%)	1 (0%)	43	77
27	T	270/274 (98%)	228 (84%)	42 (16%)	0	100	100
28	U	254/338 (75%)	244 (96%)	8 (3%)	2 (1%)	16	53
29	V	282/306 (92%)	239 (85%)	36 (13%)	7 (2%)	4	26
30	W	195/268 (73%)	177 (91%)	14 (7%)	4 (2%)	5	30
31	X	109/156 (70%)	96 (88%)	13 (12%)	0	100	100
32	Y	25/89 (28%)	20 (80%)	5 (20%)	0	100	100
33	Z	807/993 (81%)	747 (93%)	60 (7%)	0	100	100
All	All	13392/15139 (88%)	12503 (93%)	855 (6%)	34 (0%)	37	71

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	D	7	ALA
11	D	10	ILE
18	K	292	VAL
18	K	421	VAL
21	N	903	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain 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 sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	162/178 (91%)	162 (100%)	0	100	100
1	b	162/178 (91%)	162 (100%)	0	100	100
2	2	185/214 (86%)	185 (100%)	0	100	100
2	i	185/214 (86%)	185 (100%)	0	100	100
3	3	172/173 (99%)	172 (100%)	0	100	100
3	h	172/173 (99%)	172 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	4	173/175 (99%)	173 (100%)	0	100	100
4	g	173/175 (99%)	173 (100%)	0	100	100
5	5	169/235 (72%)	169 (100%)	0	100	100
5	f	169/235 (72%)	169 (100%)	0	100	100
6	6	185/201 (92%)	185 (100%)	0	100	100
6	e	185/201 (92%)	185 (100%)	0	100	100
7	7	195/224 (87%)	195 (100%)	0	100	100
7	a	198/224 (88%)	198 (100%)	0	100	100
8	A	206/210 (98%)	206 (100%)	0	100	100
8	c	206/210 (98%)	206 (100%)	0	100	100
9	B	209/209 (100%)	209 (100%)	0	100	100
9	j	209/209 (100%)	209 (100%)	0	100	100
10	C	203/216 (94%)	202 (100%)	1 (0%)	81	81
10	d	203/216 (94%)	203 (100%)	0	100	100
11	D	212/226 (94%)	212 (100%)	0	100	100
11	n	212/226 (94%)	212 (100%)	0	100	100
12	E	198/215 (92%)	198 (100%)	0	100	100
12	m	198/215 (92%)	198 (100%)	0	100	100
13	F	192/193 (100%)	192 (100%)	0	100	100
13	l	190/193 (98%)	190 (100%)	0	100	100
14	G	201/239 (84%)	201 (100%)	0	100	100
14	k	201/239 (84%)	201 (100%)	0	100	100
15	H	303/399 (76%)	303 (100%)	0	100	100
16	I	319/385 (83%)	317 (99%)	2 (1%)	78	80
17	J	325/352 (92%)	325 (100%)	0	100	100
18	K	334/374 (89%)	334 (100%)	0	100	100
19	L	317/377 (84%)	317 (100%)	0	100	100
20	M	315/375 (84%)	315 (100%)	0	100	100
21	N	713/797 (90%)	710 (100%)	3 (0%)	84	82
22	O	363/368 (99%)	363 (100%)	0	100	100
23	P	405/415 (98%)	405 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	Q	388/391 (99%)	388 (100%)	0	100	100
25	R	351/379 (93%)	351 (100%)	0	100	100
26	S	447/489 (91%)	446 (100%)	1 (0%)	87	85
27	T	254/256 (99%)	254 (100%)	0	100	100
28	U	241/308 (78%)	240 (100%)	1 (0%)	84	82
29	V	249/268 (93%)	249 (100%)	0	100	100
30	W	171/230 (74%)	171 (100%)	0	100	100
31	X	101/144 (70%)	101 (100%)	0	100	100
32	Y	26/81 (32%)	26 (100%)	0	100	100
33	Z	692/850 (81%)	692 (100%)	0	100	100
All	All	11639/13054 (89%)	11631 (100%)	8 (0%)	87	88

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	U	151	GLU
26	S	477	VAL
21	N	510	HIS
21	N	231	ASN
21	N	512	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 162 such sidechains are listed below:

Mol	Chain	Res	Type
24	Q	425	GLN
29	V	195	HIS
26	S	20	HIS
26	S	438	HIS
31	X	38	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 oligosaccharides 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.

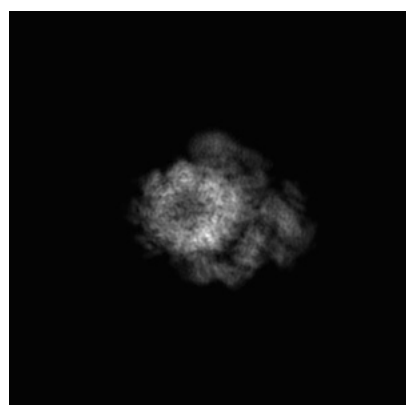
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9773. These allow visual inspection of the internal detail of the map and identification of artifacts.

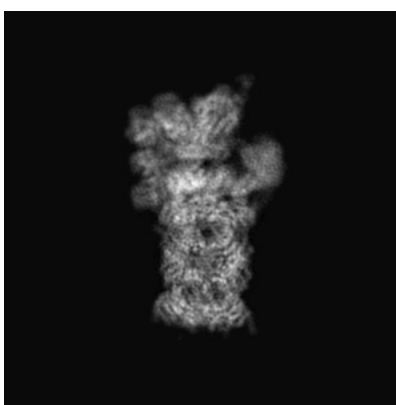
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

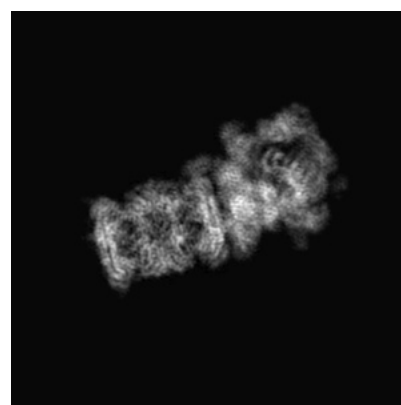
6.1.1 Primary map



X



Y

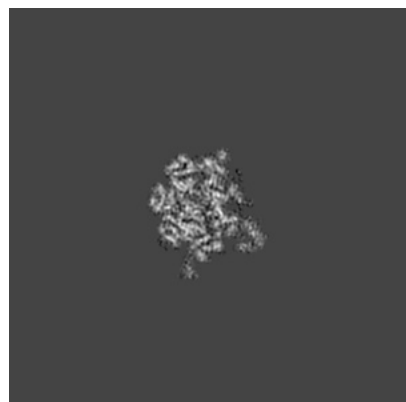


Z

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

6.2 Central slices [i](#)

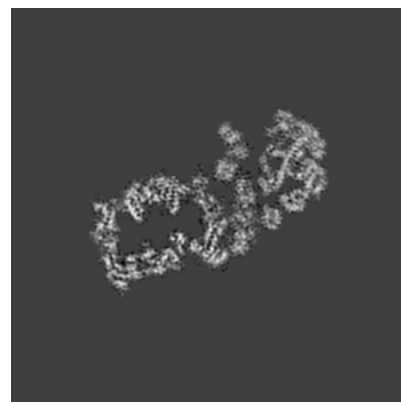
6.2.1 Primary map



X Index: 180



Y Index: 180

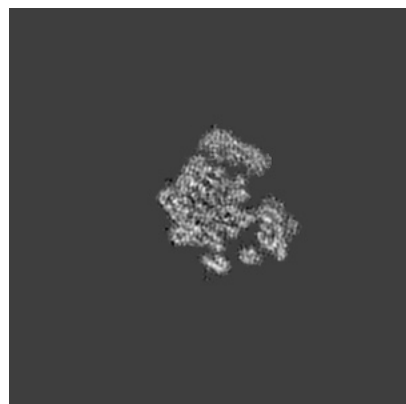


Z Index: 180

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

6.3 Largest variance slices [i](#)

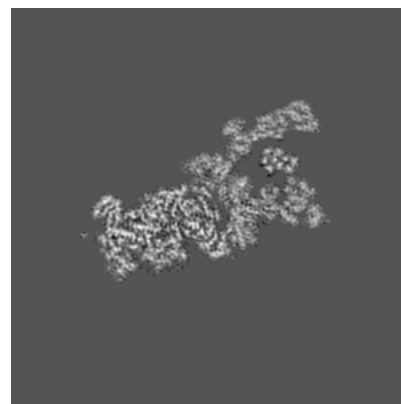
6.3.1 Primary map



X Index: 206



Y Index: 178

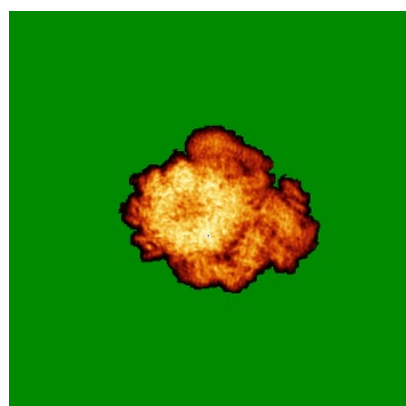


Z Index: 159

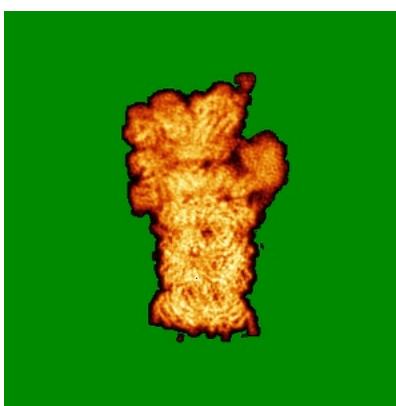
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

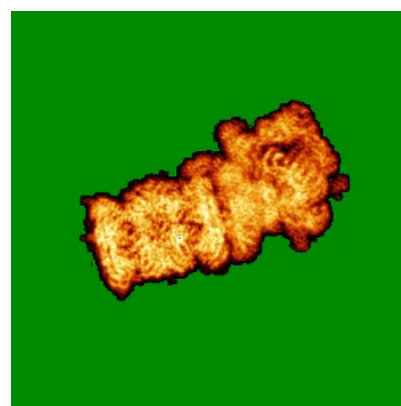
6.4.1 Primary map



X



Y

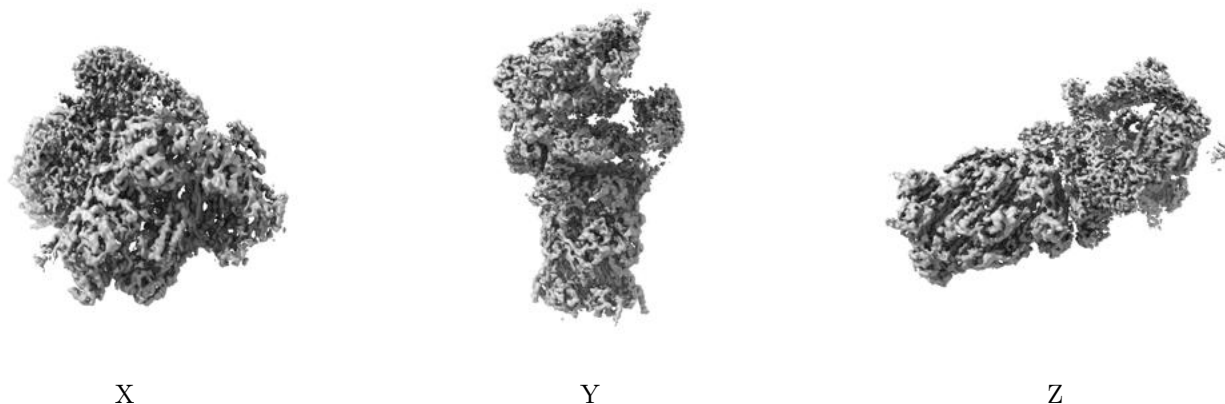


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.686. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

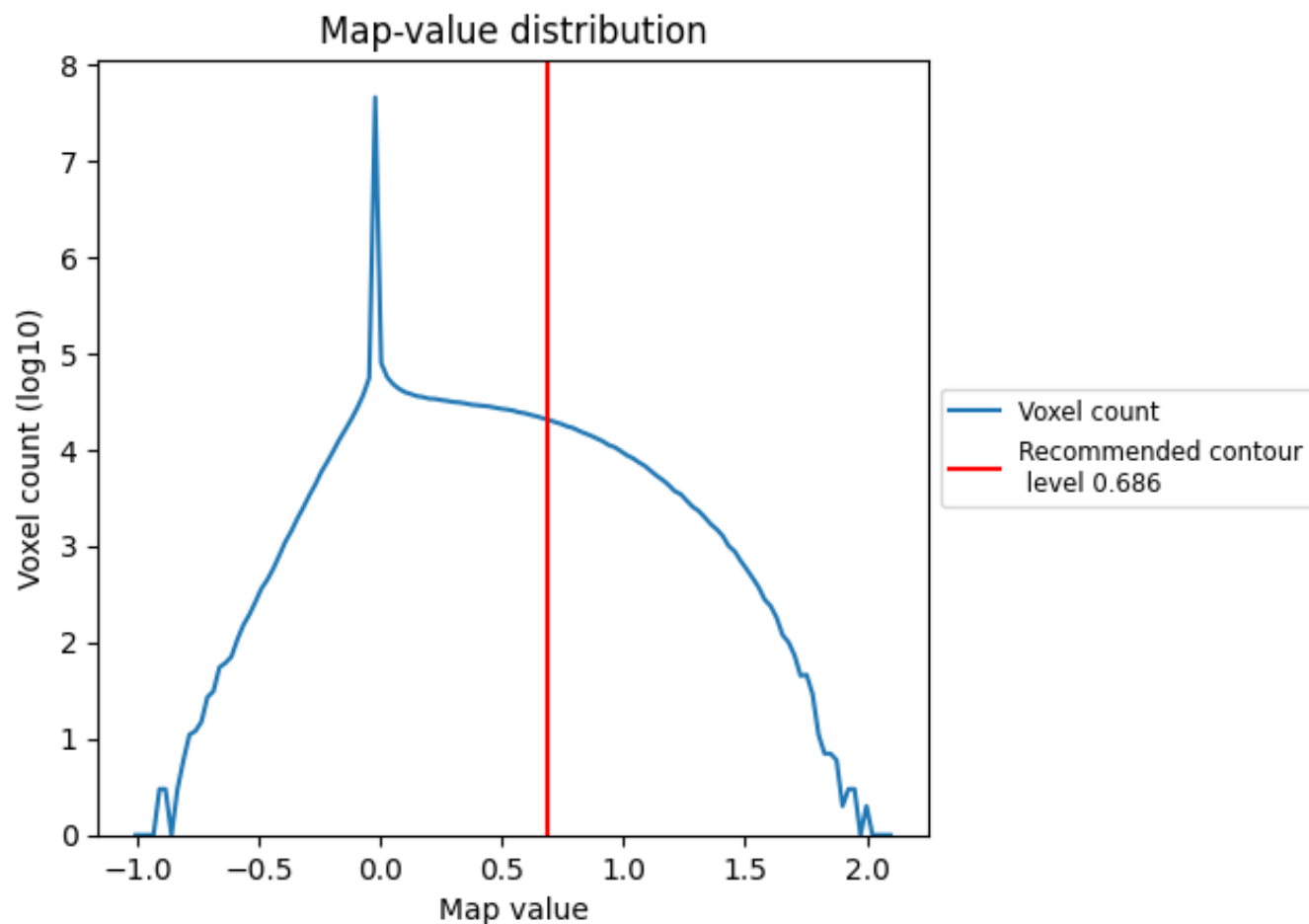
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

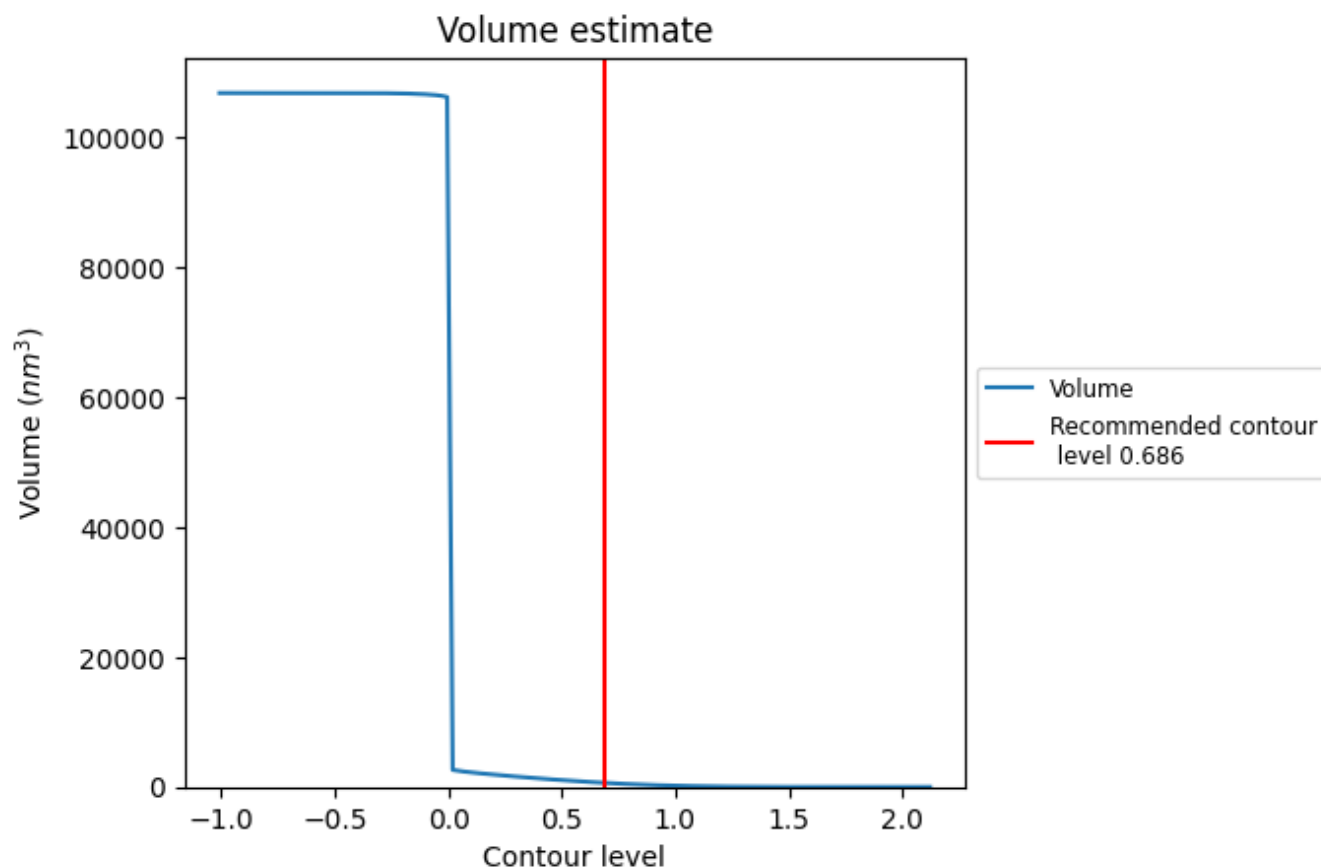
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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.

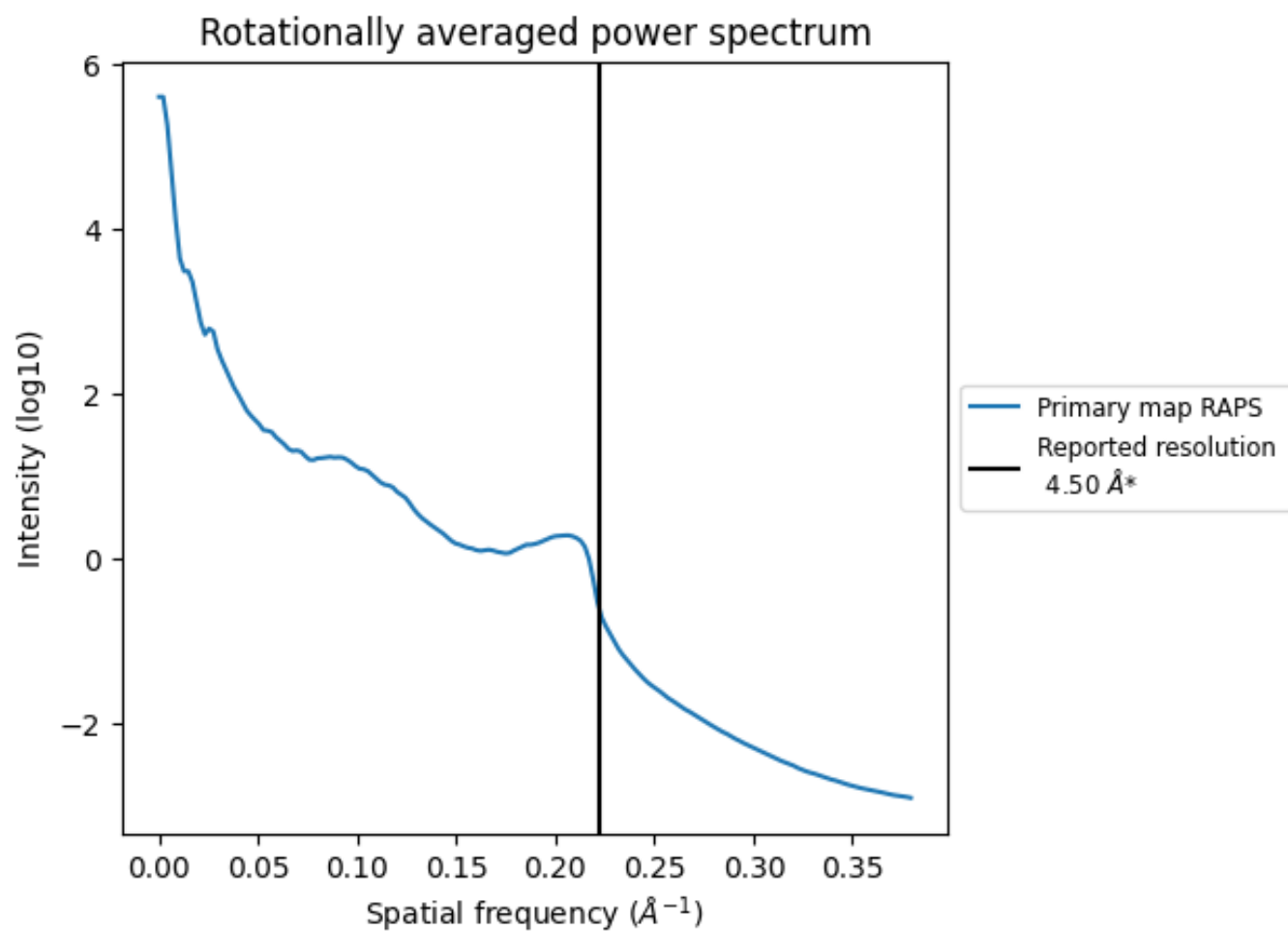
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 636 nm^3 ; this corresponds to an approximate mass of 574 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.222 $\text{\AA}^{-1}$

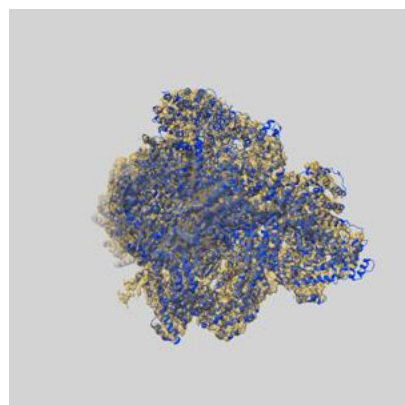
8 Fourier-Shell correlation

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

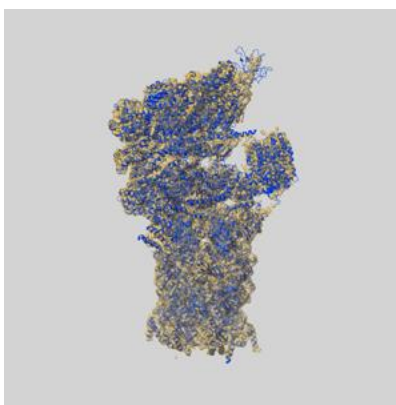
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9773 and PDB model 6J30. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

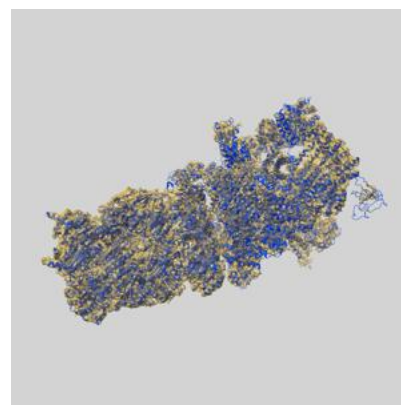
9.1 Map-model overlay [i](#)



X



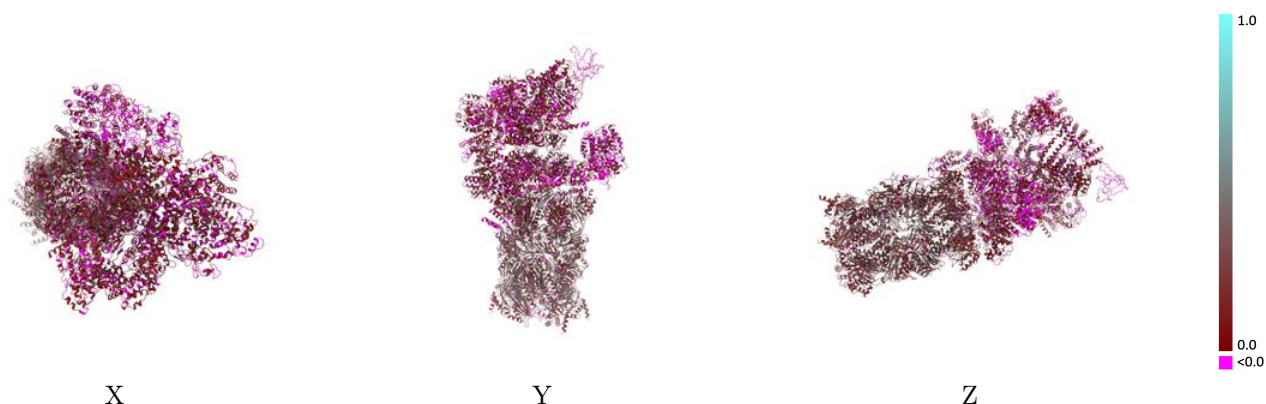
Y



Z

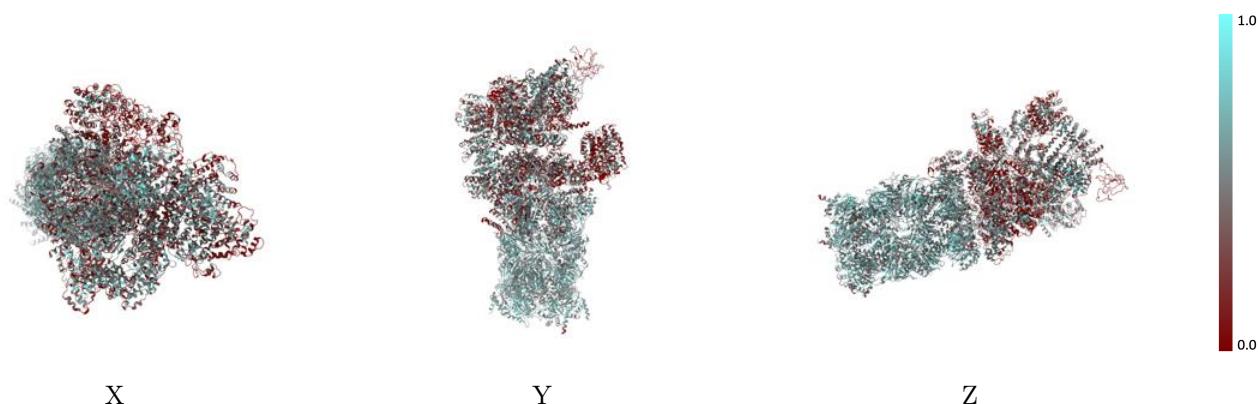
The images above show the 3D surface view of the map at the recommended contour level 0.686 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



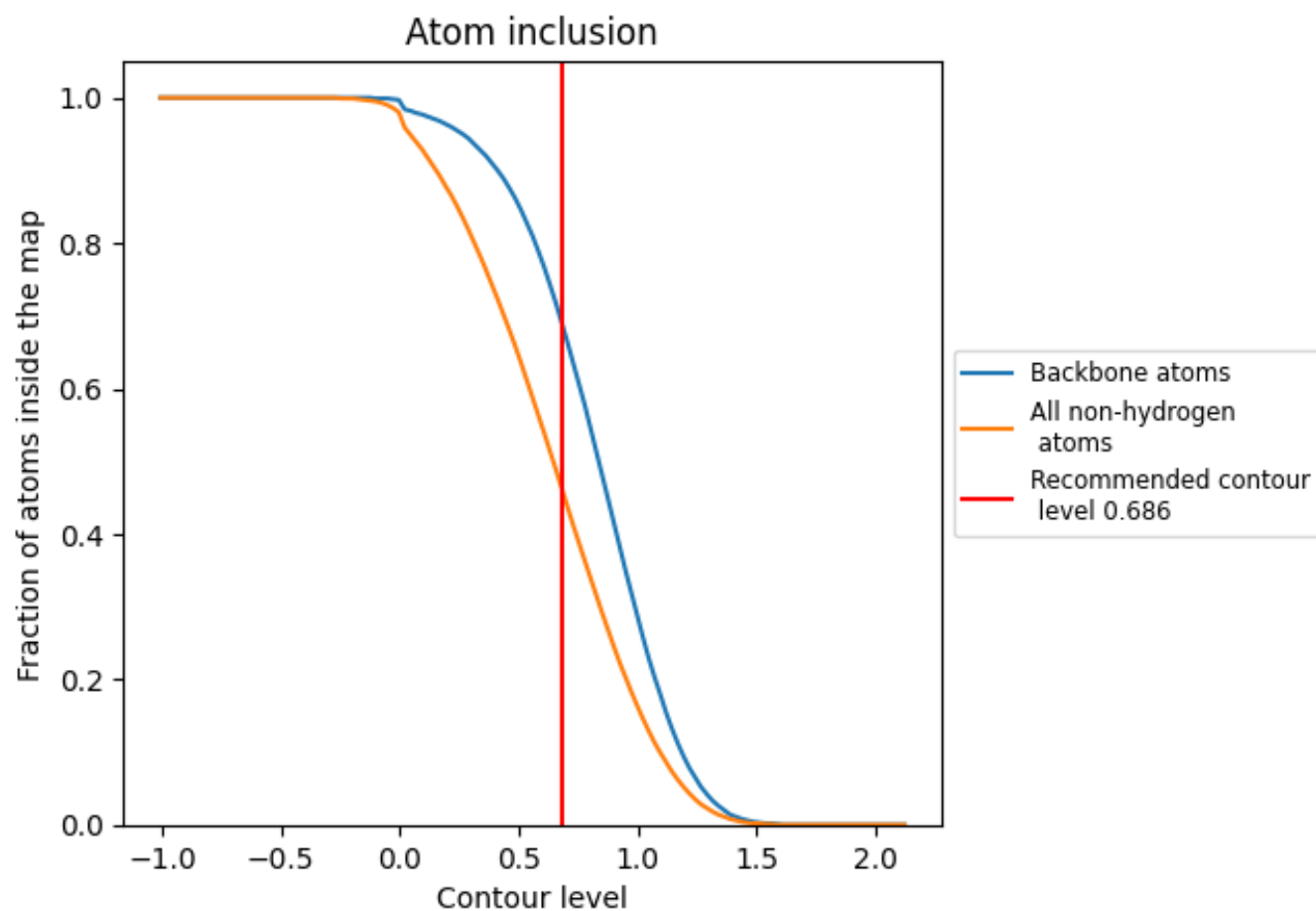
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 [i](#)



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 (0.686).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 46% 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 (0.686) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4570	 0.1710
1	 0.6120	 0.2860
2	 0.5980	 0.2640
3	 0.5810	 0.2540
4	 0.6020	 0.2560
5	 0.6020	 0.2670
6	 0.6060	 0.2690
7	 0.6100	 0.2740
A	 0.5450	 0.2310
B	 0.4860	 0.2040
C	 0.5090	 0.1880
D	 0.5520	 0.2190
E	 0.5460	 0.2210
F	 0.5650	 0.2210
G	 0.5700	 0.2380
H	 0.3540	 0.1410
I	 0.3080	 0.1020
J	 0.2950	 0.1080
K	 0.3320	 0.1150
L	 0.3820	 0.1520
M	 0.3840	 0.1380
N	 0.4490	 0.1330
O	 0.4020	 0.1020
P	 0.4490	 0.1250
Q	 0.3680	 0.1110
R	 0.3890	 0.0980
S	 0.3390	 0.1080
T	 0.2080	 0.0490
U	 0.4530	 0.1550
V	 0.3640	 0.1150
W	 0.3950	 0.0980
X	 0.0290	 -0.0290
Y	 0.5000	 0.1450
Z	 0.2140	 0.0320
a	 0.6110	 0.2860



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Chain	Atom inclusion	Q-score
b	 0.6070	 0.2680
c	 0.5950	 0.2280
d	 0.5640	 0.2290
e	 0.5980	 0.2550
f	 0.6230	 0.2740
g	 0.6050	 0.2700
h	 0.5840	 0.2840
i	 0.5960	 0.2760
j	 0.5500	 0.2170
k	 0.5990	 0.2380
l	 0.6180	 0.2470
m	 0.5550	 0.2150
n	 0.5830	 0.2290