



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:48 PM UTC

PDB ID : 3JCK / pdb_00003jck
EMDB ID : EMD-6479
Title : Structure of the yeast 26S proteasome lid sub-complex
Authors : Herzik Jr., M.A.; Dambacher, C.M.; Worden, E.J.; Martin, A.; Lander, G.C.
Deposited on : 2015-12-20
Resolution : 3.50 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:

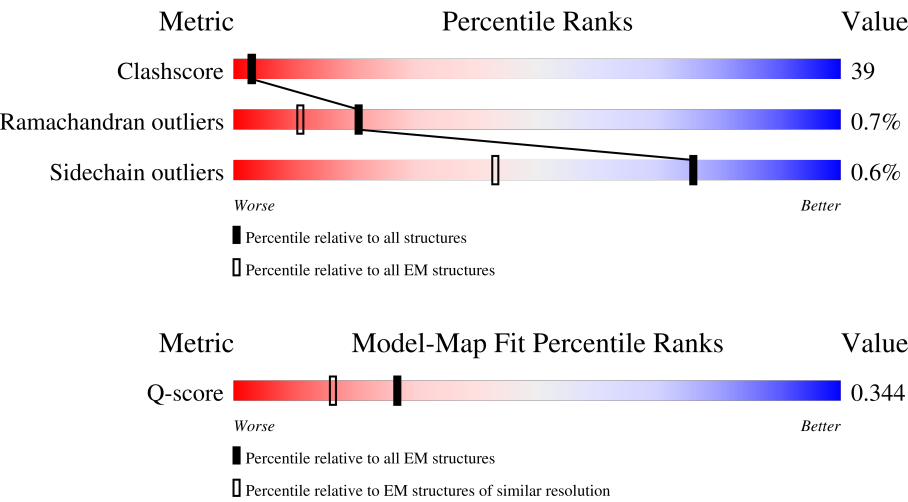
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.50 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.



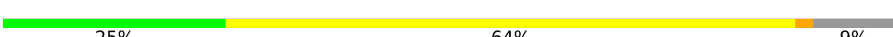
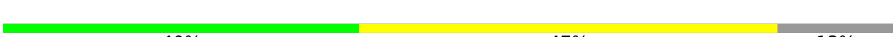
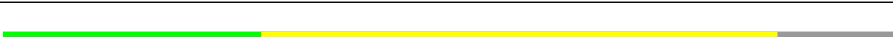
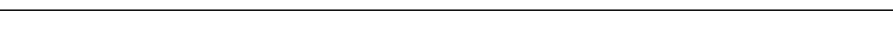
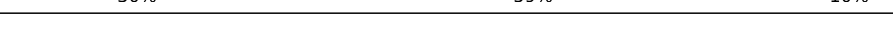
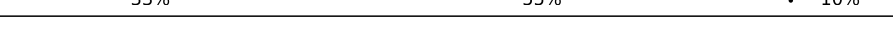
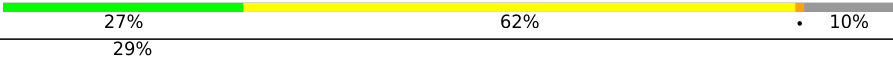
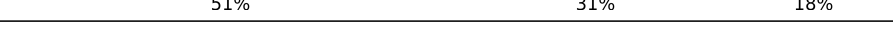
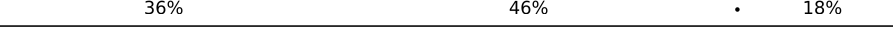
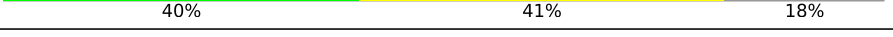
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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-A	438	
1	2-A	438	
1	3-A	438	
1	4-A	438	

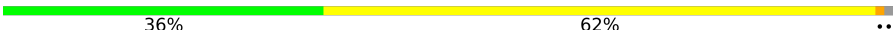
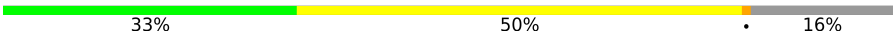
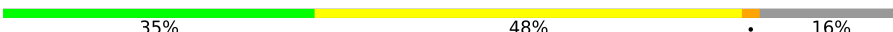
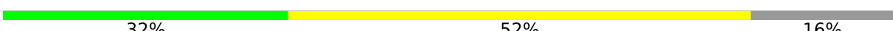
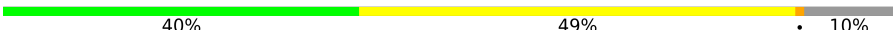
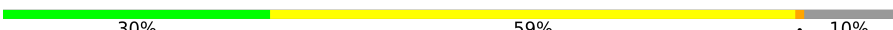
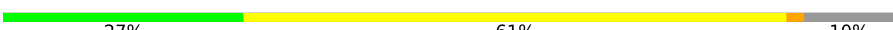
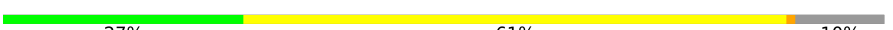
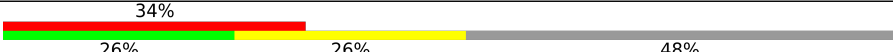
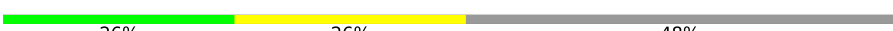
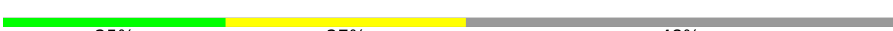
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Mol	Chain	Length	Quality of chain
1	5-A	438	
2	1-B	445	
2	2-B	445	
2	3-B	445	
2	4-B	445	
2	5-B	445	
3	1-C	434	
3	2-C	434	
3	3-C	434	
3	4-C	434	
3	5-C	434	
4	1-D	429	
4	2-D	429	
4	3-D	429	
4	4-D	429	
4	5-D	429	
5	1-E	338	
5	2-E	338	
5	3-E	338	
5	4-E	338	
5	5-E	338	
6	1-F	393	
6	2-F	393	
6	3-F	393	
6	4-F	393	

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Mol	Chain	Length	Quality of chain
6	5-F	393	
7	1-G	306	
7	2-G	306	
7	3-G	306	
7	4-G	306	
7	5-G	306	
8	1-H	274	
8	2-H	274	
8	3-H	274	
8	4-H	274	
8	5-H	274	
9	1-I	89	
9	2-I	89	
9	3-I	89	
9	4-I	89	
9	5-I	89	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 112285 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 26S proteasome regulatory subunit RPN3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1-A	397	Total	C	N	O	S	0	0
			3116	1991	528	583	14		
1	2-A	397	Total	C	N	O	S	0	0
			3116	1991	528	583	14		
1	3-A	397	Total	C	N	O	S	0	0
			3116	1991	528	583	14		
1	4-A	397	Total	C	N	O	S	0	0
			3116	1991	528	583	14		
1	5-A	397	Total	C	N	O	S	0	0
			3116	1991	528	583	14		

- Molecule 2 is a protein called 26S proteasome regulatory subunit RPN5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1-B	404	Total	C	N	O	S	0	0
			3323	2118	556	640	9		
2	2-B	404	Total	C	N	O	S	0	0
			3323	2118	556	640	9		
2	3-B	404	Total	C	N	O	S	0	0
			3323	2118	556	640	9		
2	4-B	404	Total	C	N	O	S	0	0
			3323	2118	556	640	9		
2	5-B	404	Total	C	N	O	S	0	0
			3323	2118	556	640	9		

- Molecule 3 is a protein called 26S proteasome regulatory subunit RPN6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1-C	378	Total	C	N	O	S	0	0
			3060	1959	499	587	15		
3	2-C	378	Total	C	N	O	S	0	0
			3060	1959	499	587	15		
3	3-C	378	Total	C	N	O	S	0	0
			3060	1959	499	587	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	4-C	378	Total	C	N	O	S	0	0
			3060	1959	499	587	15		
3	5-C	378	Total	C	N	O	S	0	0
			3060	1959	499	587	15		

- Molecule 4 is a protein called 26S proteasome regulatory subunit RPN7.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1-D	384	Total	C	N	O	S	0	0
			3084	1975	503	596	10		
4	2-D	384	Total	C	N	O	S	0	0
			3084	1975	503	596	10		
4	3-D	384	Total	C	N	O	S	0	0
			3084	1975	503	596	10		
4	4-D	384	Total	C	N	O	S	0	0
			3084	1975	503	596	10		
4	5-D	384	Total	C	N	O	S	0	0
			3084	1975	503	596	10		

- Molecule 5 is a protein called 26S proteasome regulatory subunit RPN8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1-E	277	Total	C	N	O	S	0	0
			2224	1414	382	422	6		
5	2-E	277	Total	C	N	O	S	0	0
			2224	1414	382	422	6		
5	3-E	277	Total	C	N	O	S	0	0
			2224	1414	382	422	6		
5	4-E	277	Total	C	N	O	S	0	0
			2224	1414	382	422	6		
5	5-E	277	Total	C	N	O	S	0	0
			2224	1414	382	422	6		

- Molecule 6 is a protein called 26S proteasome regulatory subunit RPN9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1-F	388	Total	C	N	O	S	0	0
			3186	2051	519	608	8		
6	2-F	388	Total	C	N	O	S	0	0
			3186	2051	519	608	8		
6	3-F	388	Total	C	N	O	S	0	0
			3186	2051	519	608	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	4-F	388	Total	C	N	O	S	0	0
			3186	2051	519	608	8		
6	5-F	388	Total	C	N	O	S	0	0
			3186	2051	519	608	8		

- Molecule 7 is a protein called Ubiquitin carboxyl-terminal hydrolase RPN11.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1-G	257	Total	C	N	O	S	0	0
			2036	1285	344	393	14		
7	2-G	257	Total	C	N	O	S	0	0
			2036	1285	344	393	14		
7	3-G	257	Total	C	N	O	S	0	0
			2036	1285	344	393	14		
7	4-G	257	Total	C	N	O	S	0	0
			2036	1285	344	393	14		
7	5-G	257	Total	C	N	O	S	0	0
			2036	1285	344	393	14		

- Molecule 8 is a protein called 26S proteasome regulatory subunit RPN12.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	1-H	246	Total	C	N	O	S	0	0
			2021	1305	321	391	4		
8	2-H	246	Total	C	N	O	S	0	0
			2021	1305	321	391	4		
8	3-H	246	Total	C	N	O	S	0	0
			2021	1305	321	391	4		
8	4-H	246	Total	C	N	O	S	0	0
			2021	1305	321	391	4		
8	5-H	246	Total	C	N	O	S	0	0
			2021	1305	321	391	4		

- Molecule 9 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	1-I	46	Total	C	N	O	0	0
			405	251	62	92		
9	2-I	46	Total	C	N	O	0	0
			405	251	62	92		
9	3-I	46	Total	C	N	O	0	0
			405	251	62	92		

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Mol	Chain	Residues	Atoms				AltConf	Trace
9	4-I	46	Total	C	N	O	0	0
			405	251	62	92		
9	5-I	46	Total	C	N	O	0	0
			405	251	62	92		

- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
10	1-G	1	Total	Zn	0
			1	1	
10	2-G	1	Total	Zn	0
			1	1	
10	3-G	1	Total	Zn	0
			1	1	
10	4-G	1	Total	Zn	0
			1	1	
10	5-G	1	Total	Zn	0
			1	1	

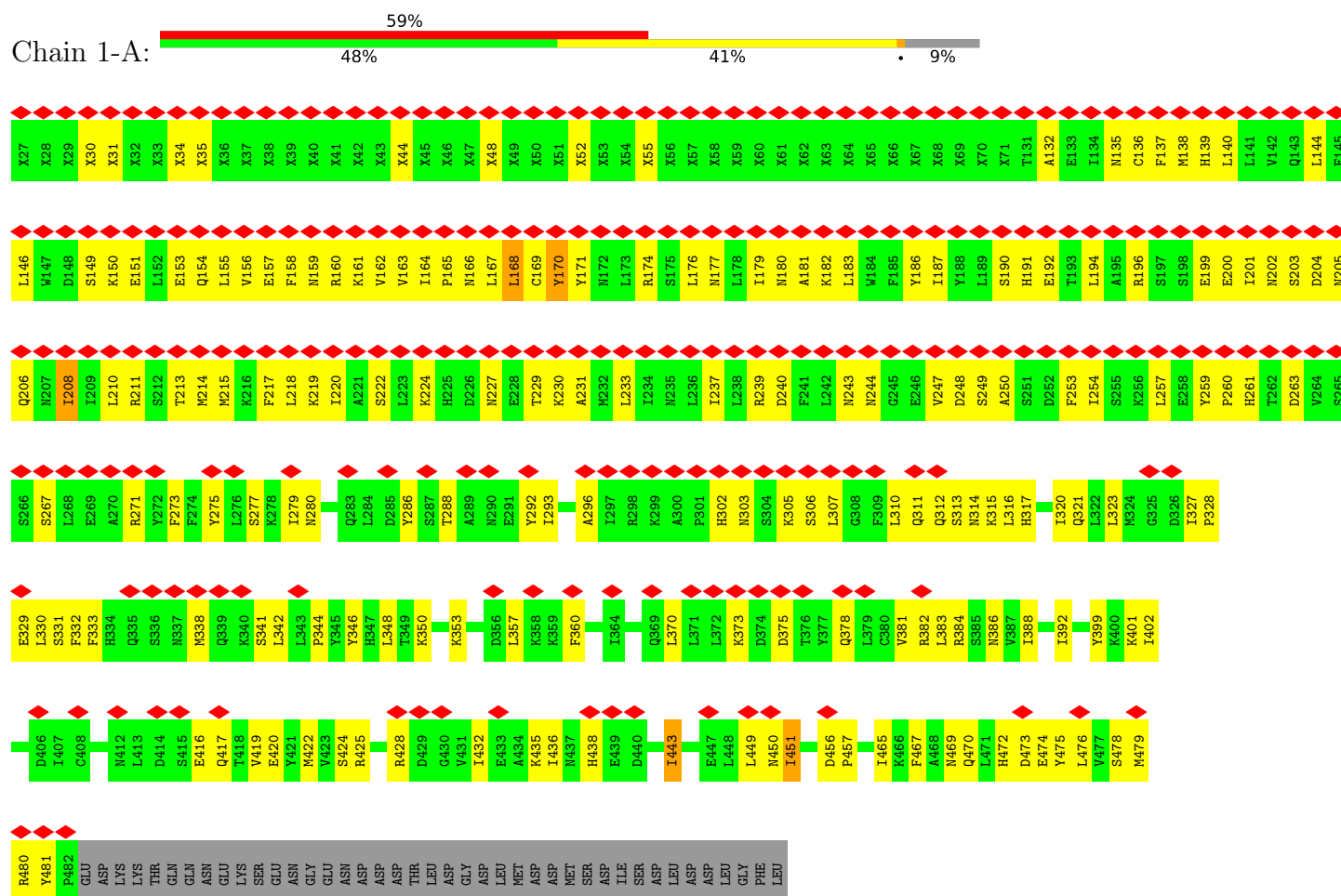
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		AltConf
11	1-B	1	Total	O	0
			1	1	
11	2-B	1	Total	O	0
			1	1	
11	3-B	1	Total	O	0
			1	1	
11	4-B	1	Total	O	0
			1	1	
11	5-B	1	Total	O	0
			1	1	

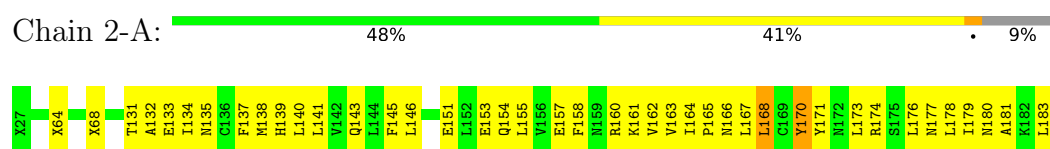
3 Residue-property plots

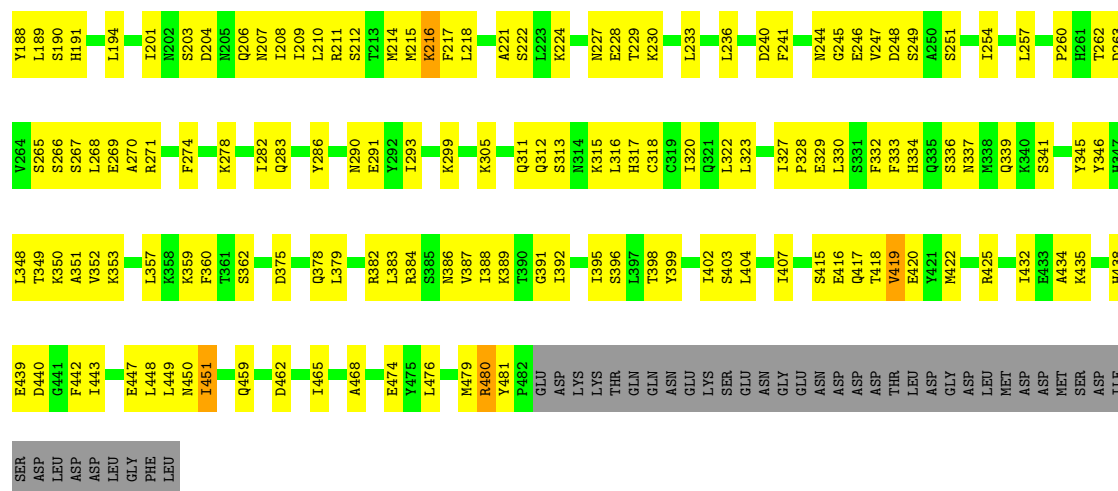
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 26S proteasome regulatory subunit RPN3



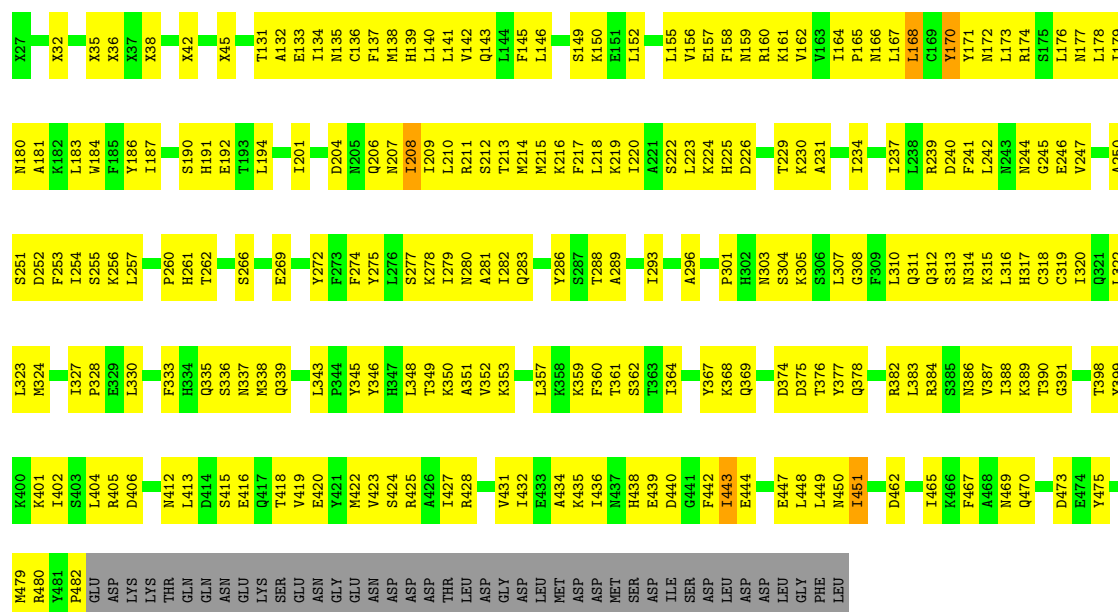
- Molecule 1: 26S proteasome regulatory subunit RPN3





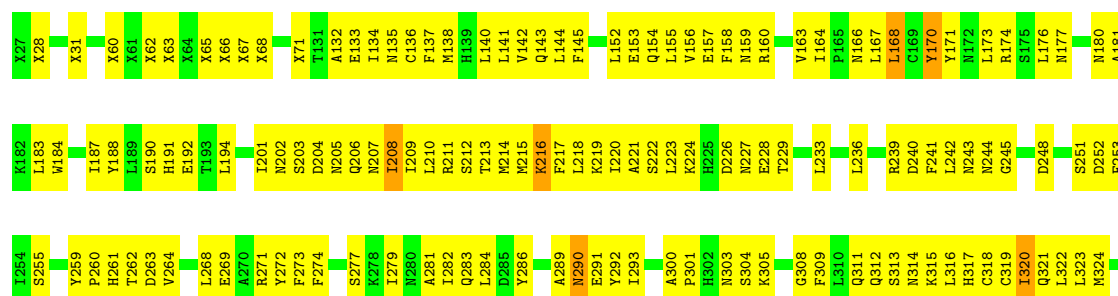
- Molecule 1: 26S proteasome regulatory subunit RPN3

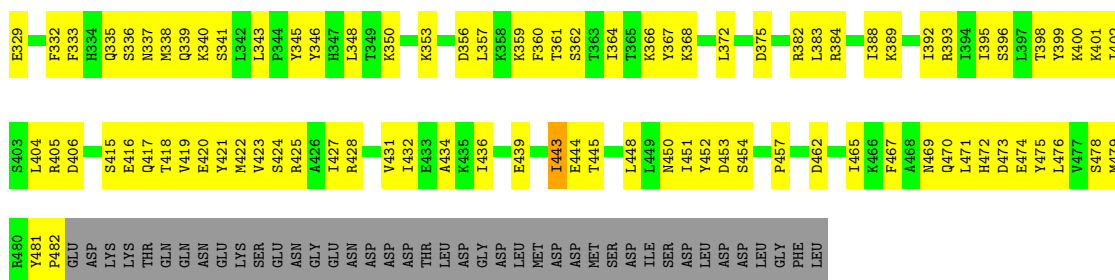
Chain 3-A: 39% 50% 9%



- Molecule 1: 26S proteasome regulatory subunit RPN3

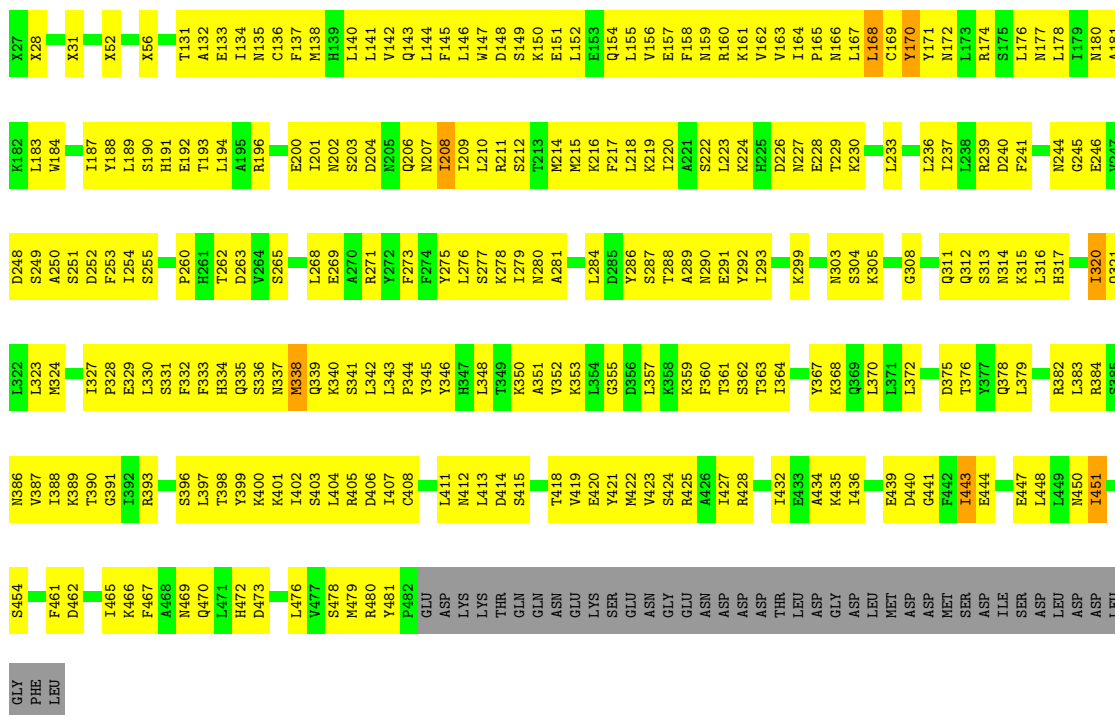
Chain 4-A: 39% 50% 9%





- Molecule 1: 26S proteasome regulatory subunit RPN3

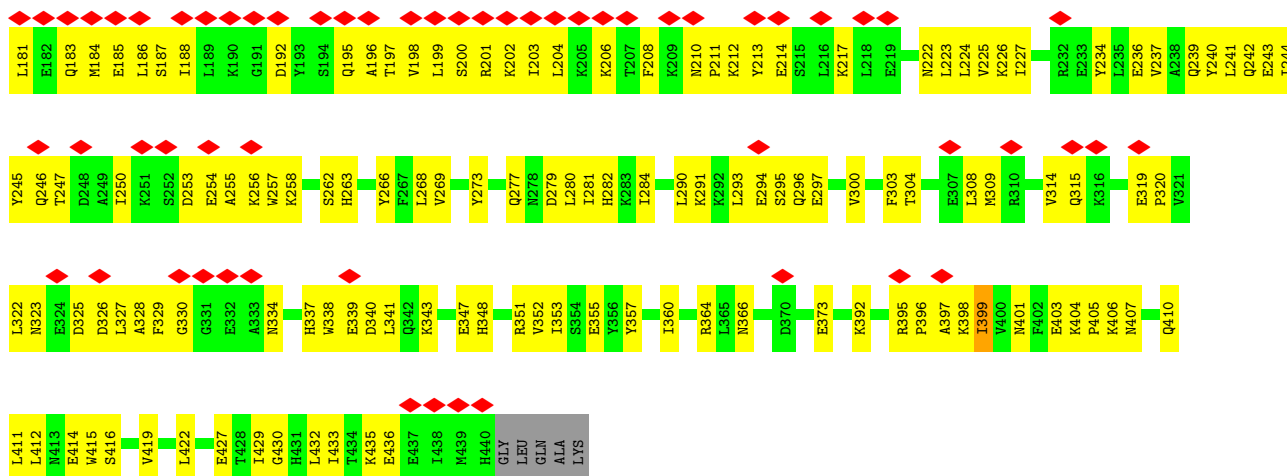
Chain 5-A: 33% 56% 9%



- Molecule 2: 26S proteasome regulatory subunit RPN5

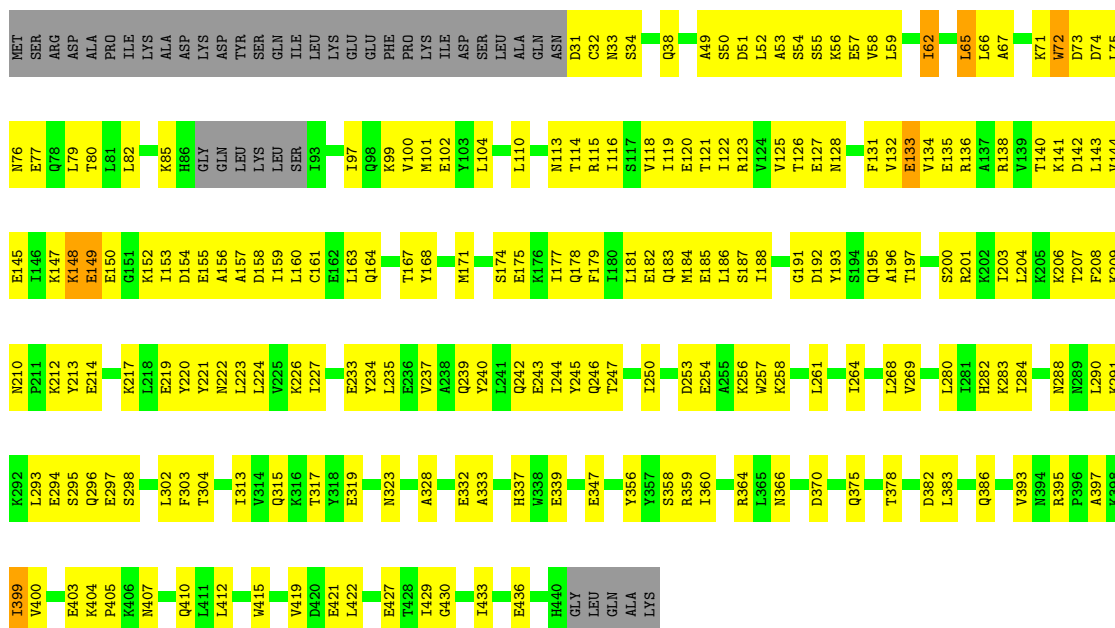
Chain 1-B: 37% 45% 52% 9%





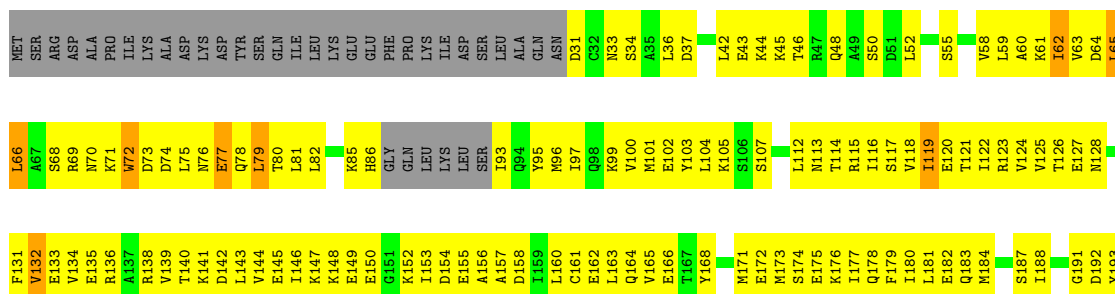
• Molecule 2: 26S proteasome regulatory subunit RPN5

Chain 2-B: 45% 44% 9%

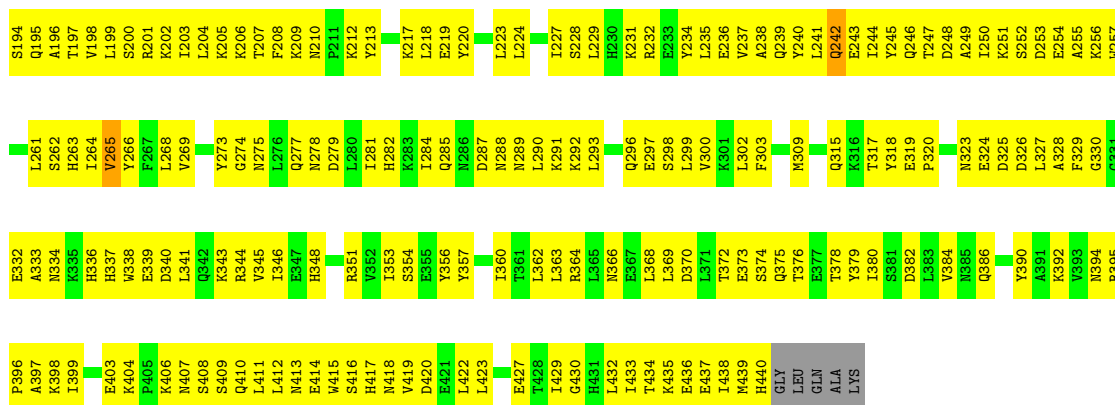


• Molecule 2: 26S proteasome regulatory subunit RPN5

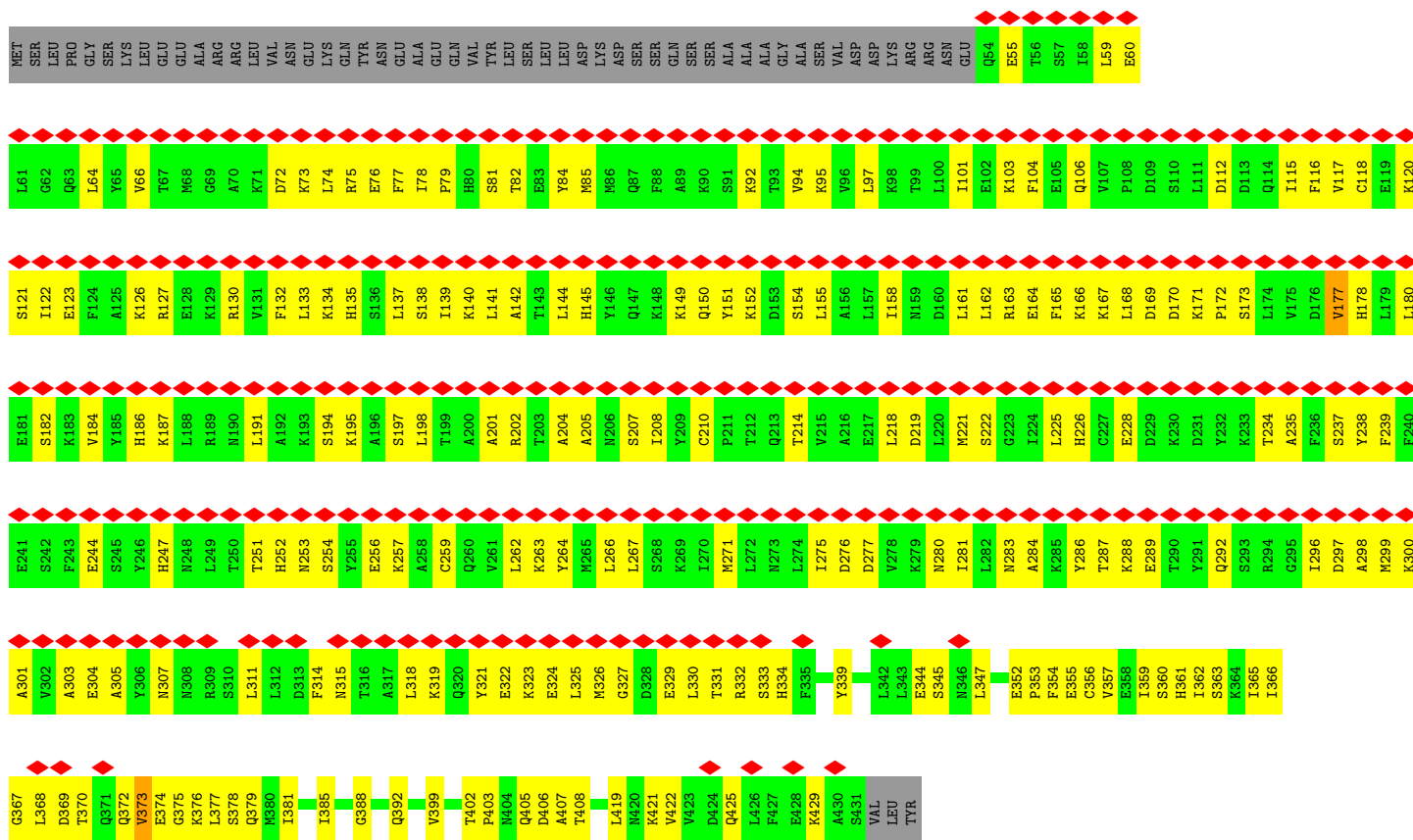
Chain 3-B: 24% 64% 9%



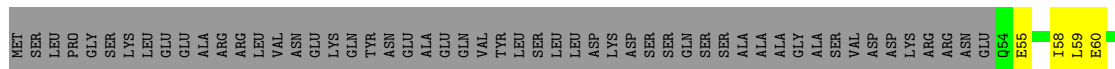


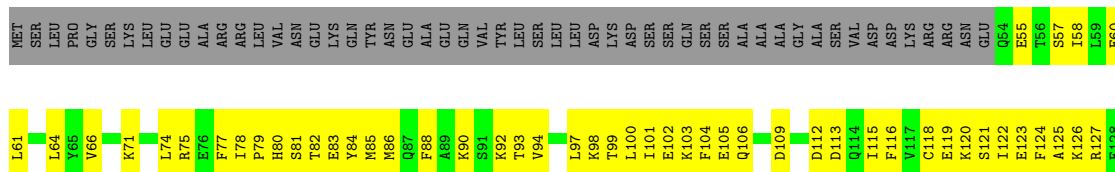


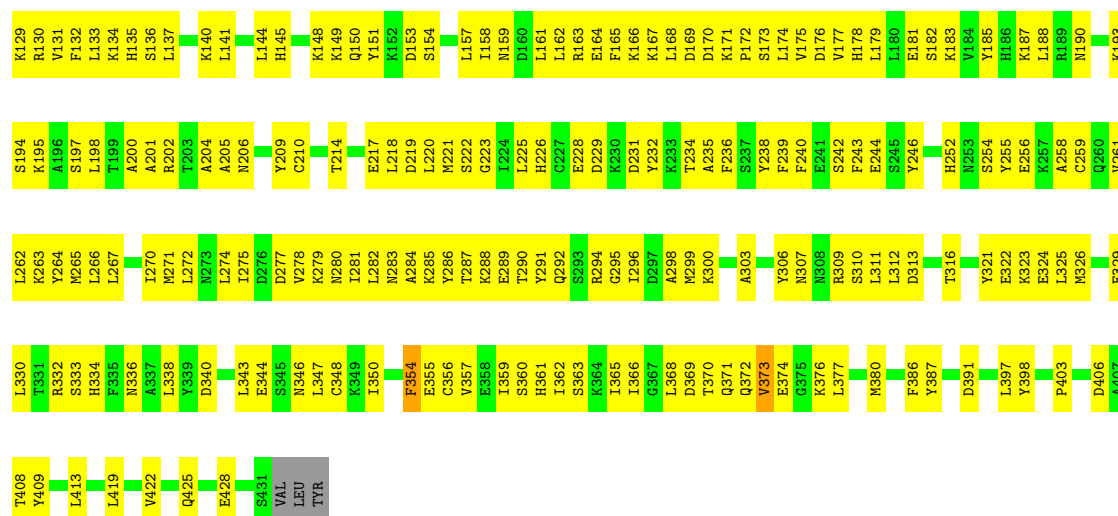
• Molecule 3: 26S proteasome regulatory subunit RPN6



• Molecule 3: 26S proteasome regulatory subunit RPN6

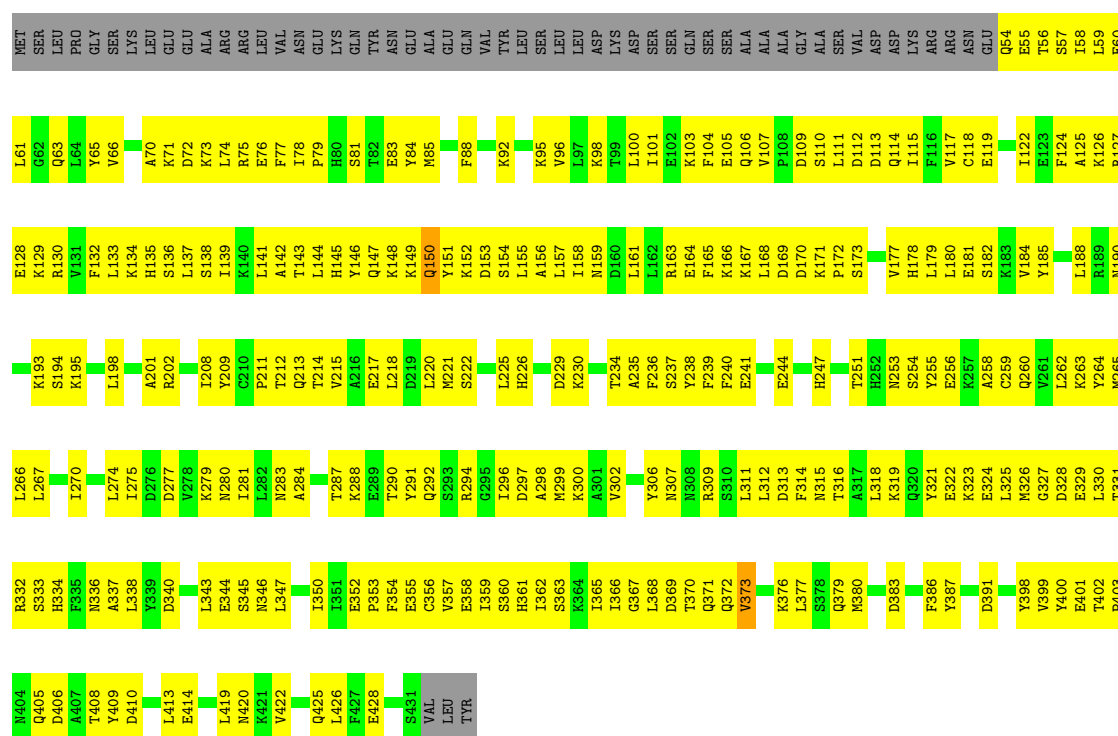






• Molecule 3: 26S proteasome regulatory subunit RPN6

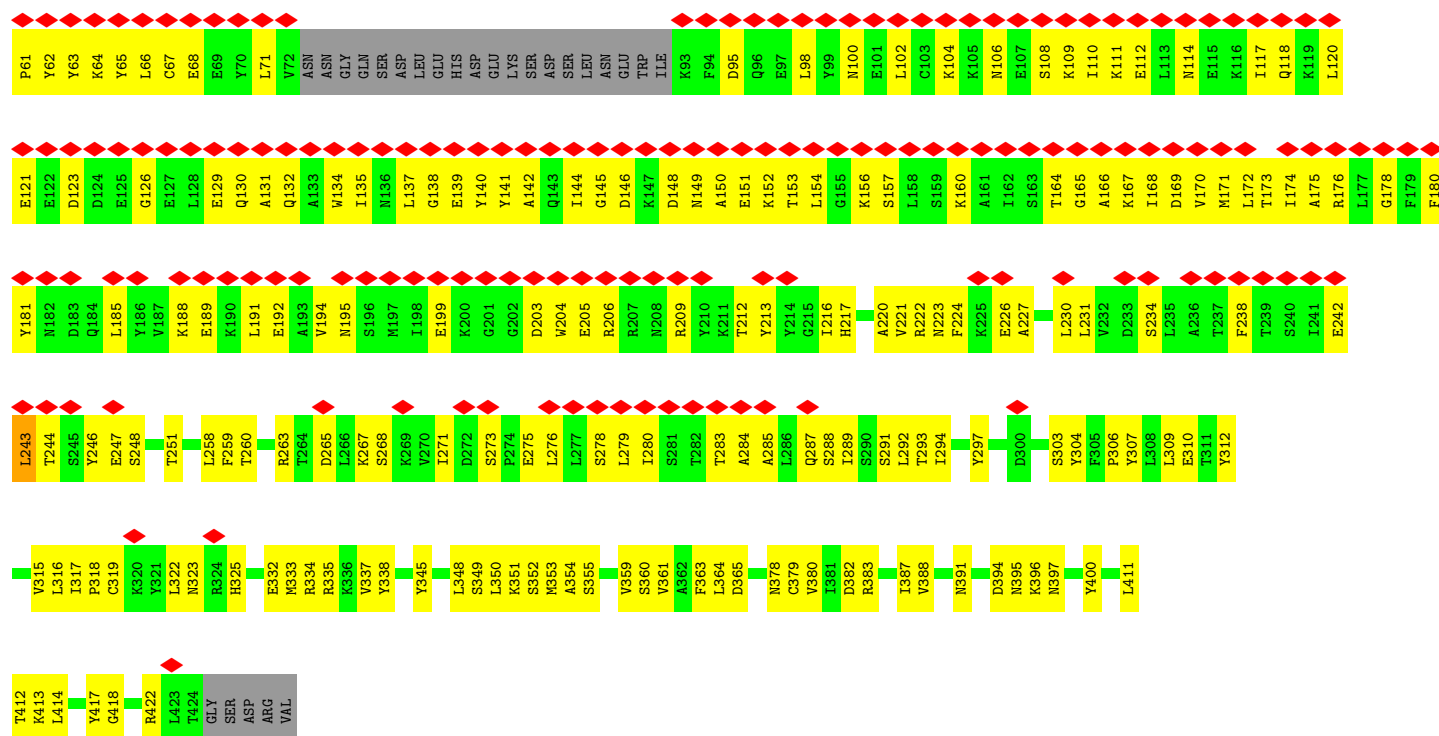
Chain 5-C: 29% 58% 13%



• Molecule 4: 26S proteasome regulatory subunit RPN7

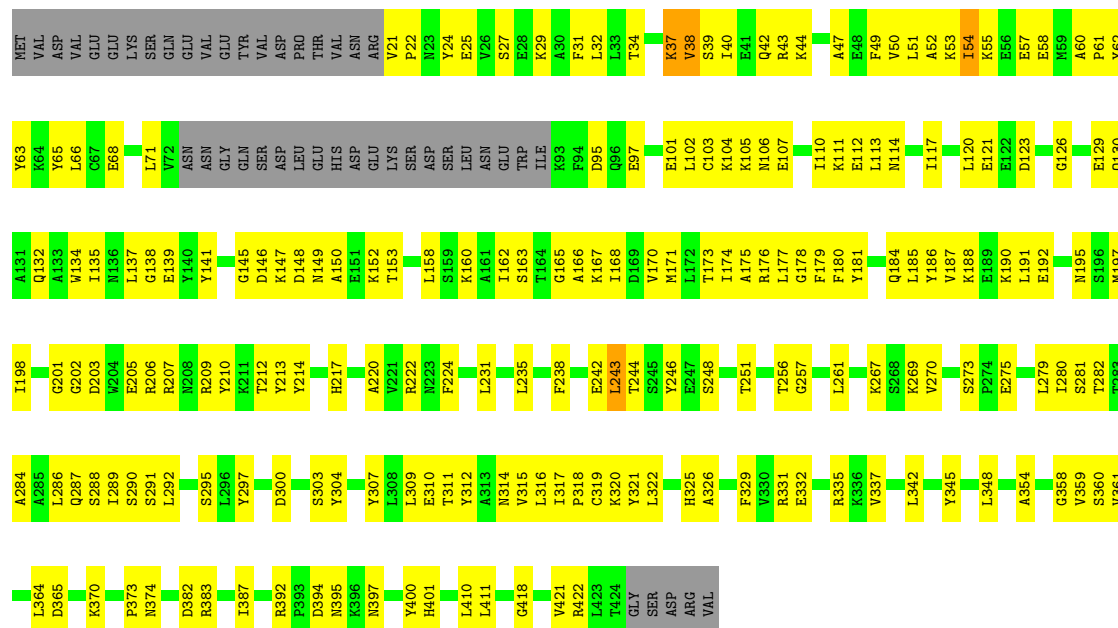
Chain 1-D: 40% 47% 48% 10%





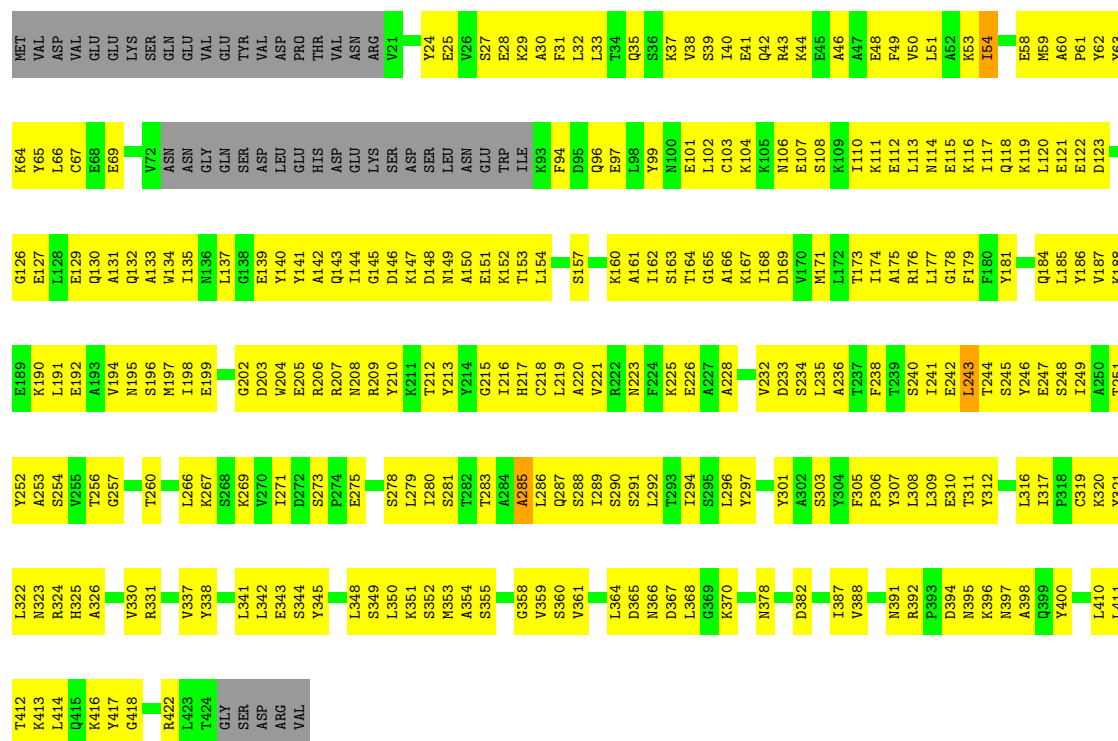
• Molecule 4: 26S proteasome regulatory subunit RPN7

Chain 2-D: 44% 45% 10%



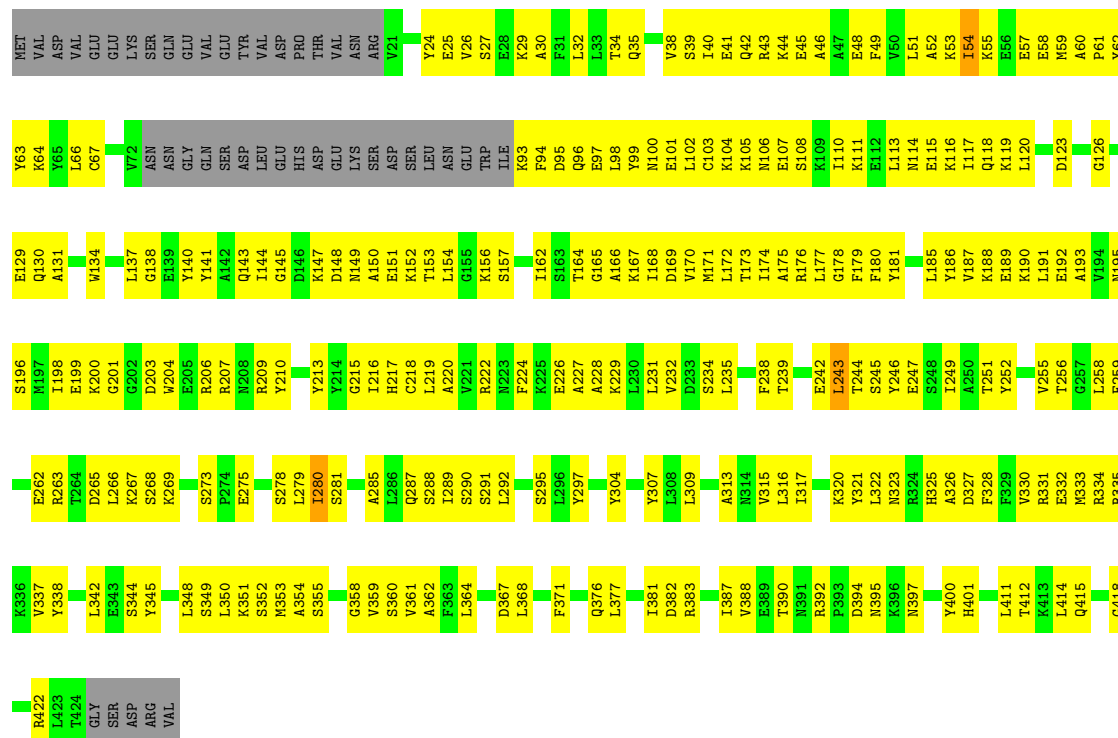
• Molecule 4: 26S proteasome regulatory subunit RPN7

Chain 3-D: 30% 59% 10%



- Molecule 4: 26S proteasome regulatory subunit RPN7

Chain 4-D: 33% 55% 10%



- Molecule 4: 26S proteasome regulatory subunit RPN7

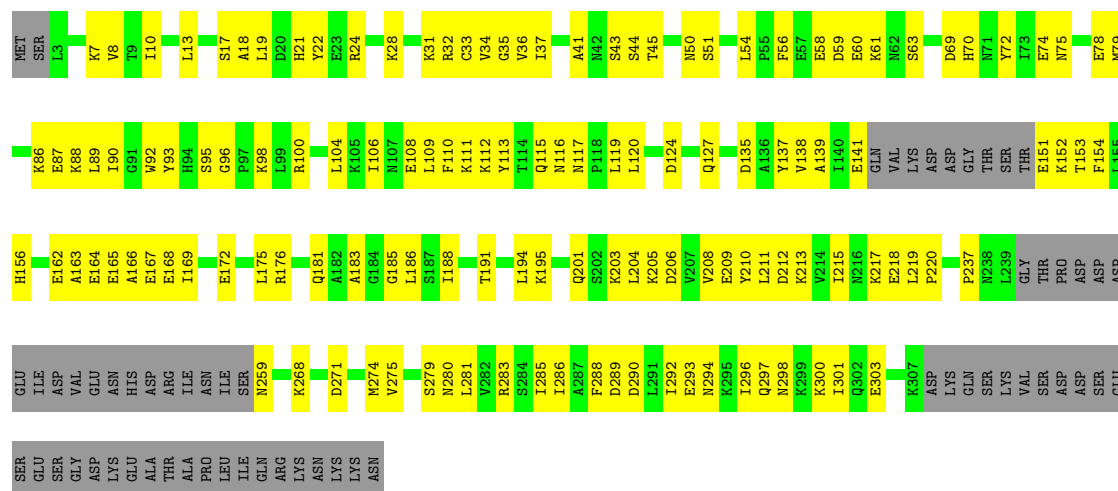
Response	Percentage
Doing a good job	27%
Not doing a good job	62%
Don't know	10%



Chain 1-E:

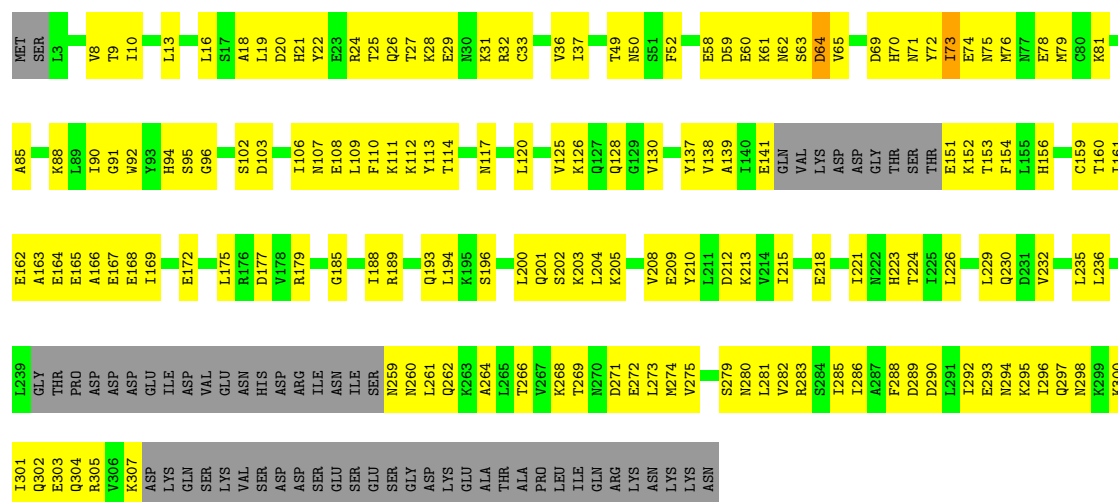


Chain 2-E:



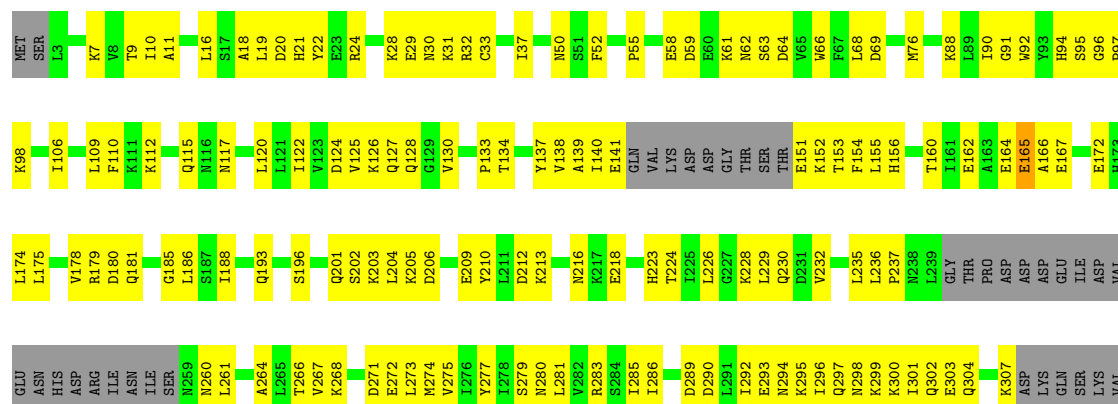
• Molecule 5: 26S proteasome regulatory subunit RPN8

Chain 3-E: 36% 46% 18%



• Molecule 5: 26S proteasome regulatory subunit RPN8

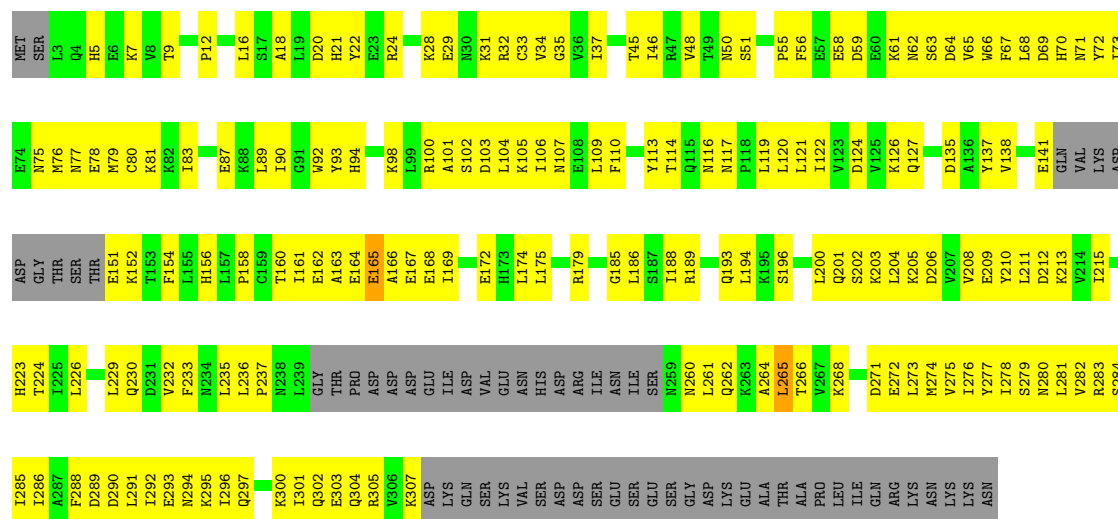
Chain 4-E: 40% 41% 18%



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

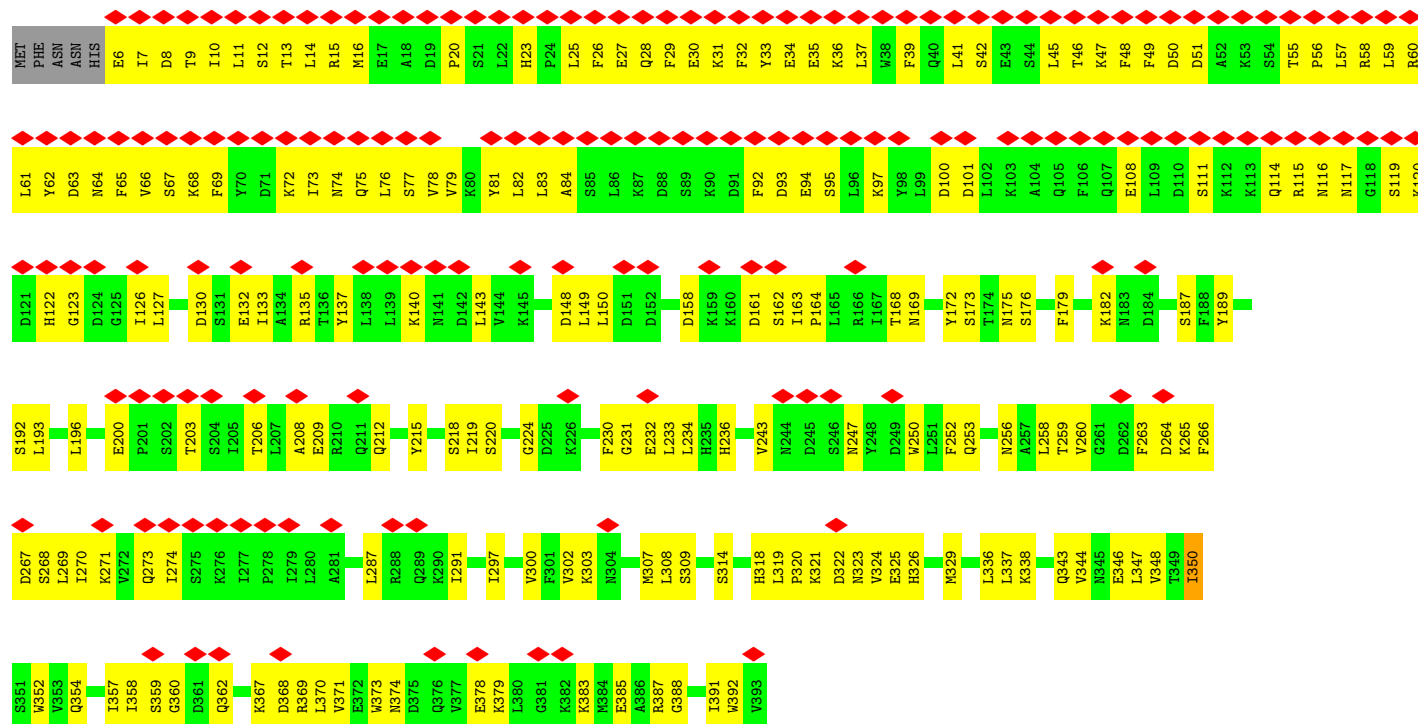
• Molecule 5: 26S proteasome regulatory subunit RPN8

Chain 5-E: 32% 50% 18%



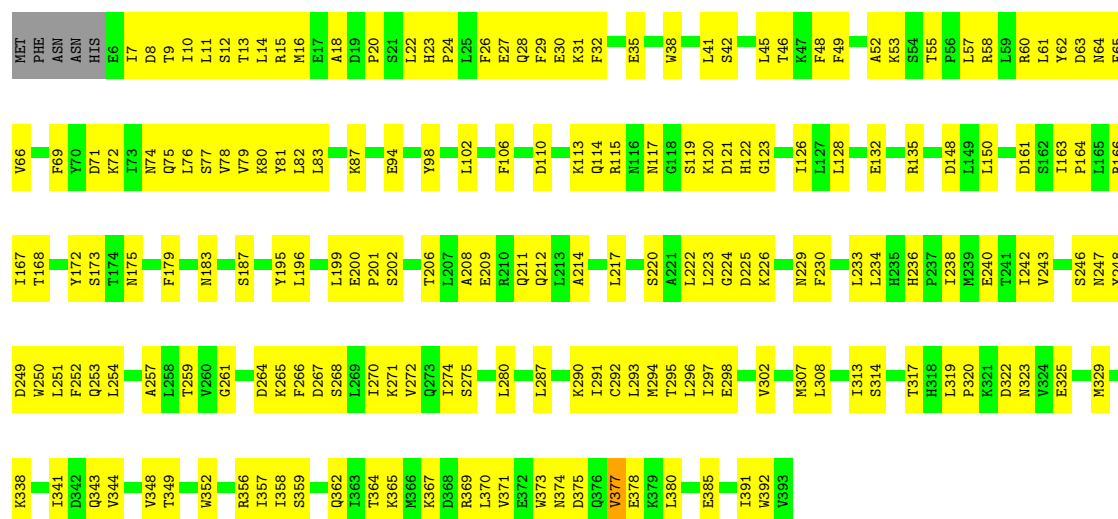
• Molecule 6: 26S proteasome regulatory subunit RPN9

Chain 1-F: 44% 48% 50%

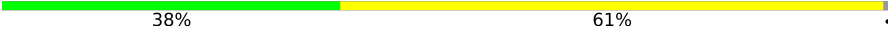


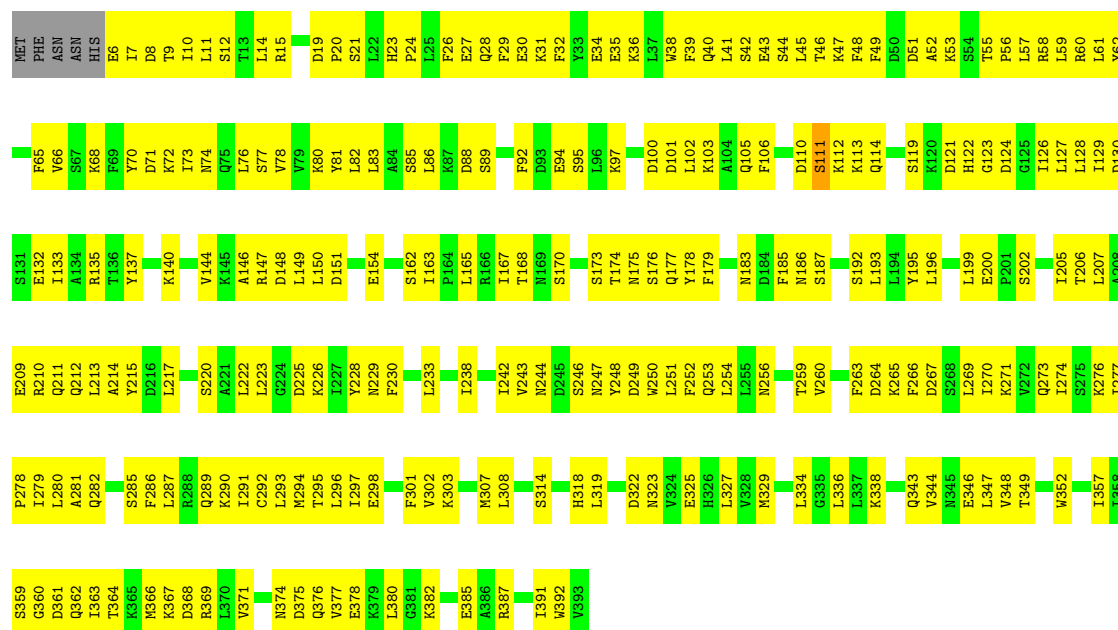
• Molecule 6: 26S proteasome regulatory subunit RPN9

Chain 2-F:  51% 48% .



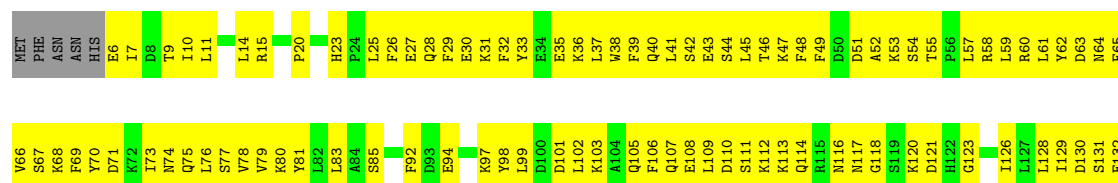
• Molecule 6: 26S proteasome regulatory subunit RPN9

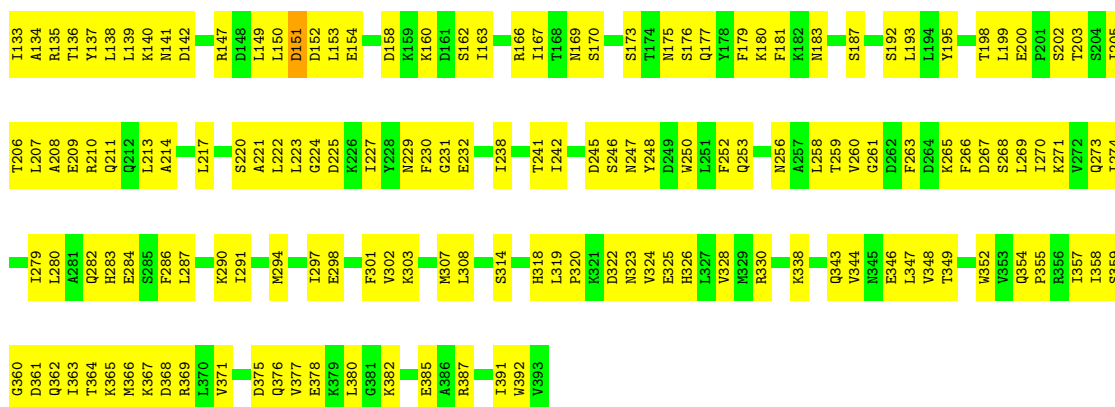
Chain 3-F:  38% 61% .



• Molecule 6: 26S proteasome regulatory subunit RPN9

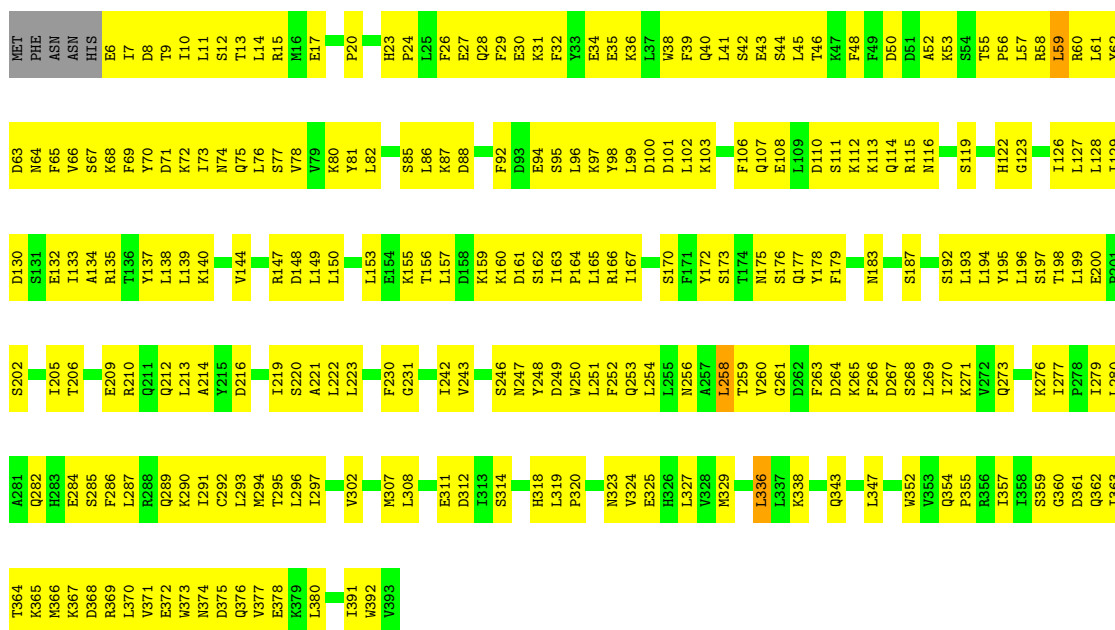
Chain 4-F:  37% 62% .





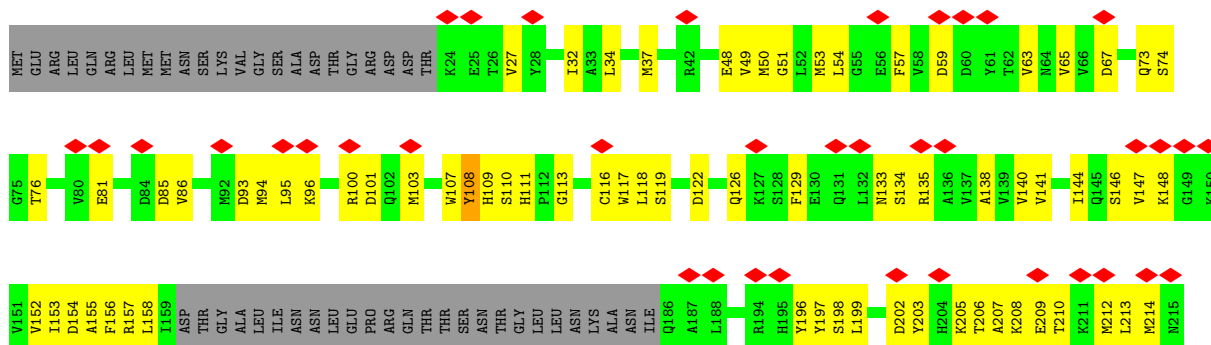
• Molecule 6: 26S proteasome regulatory subunit RPN9

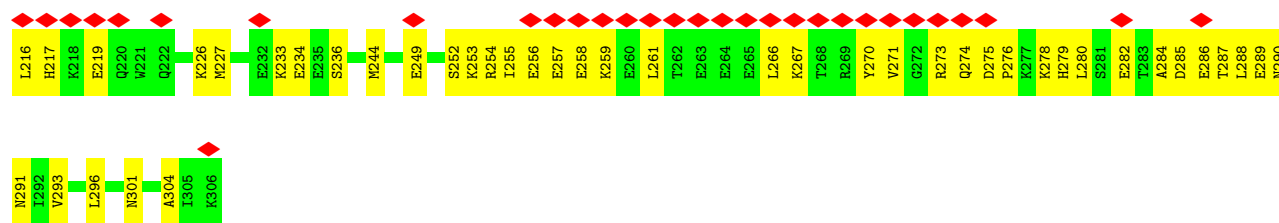
Chain 5-F: 36% 62% ..



• Molecule 7: Ubiquitin carboxyl-terminal hydrolase RPN11

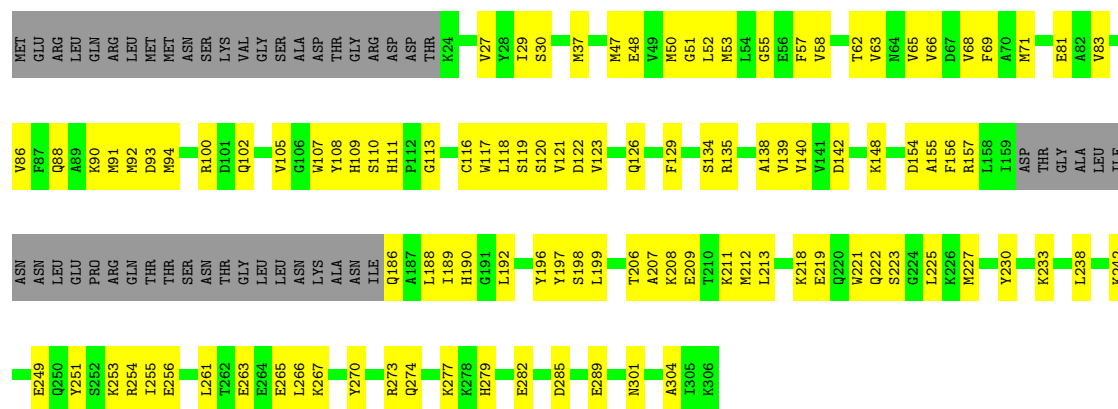
Chain 1-G: 23% 46% 38% 16%





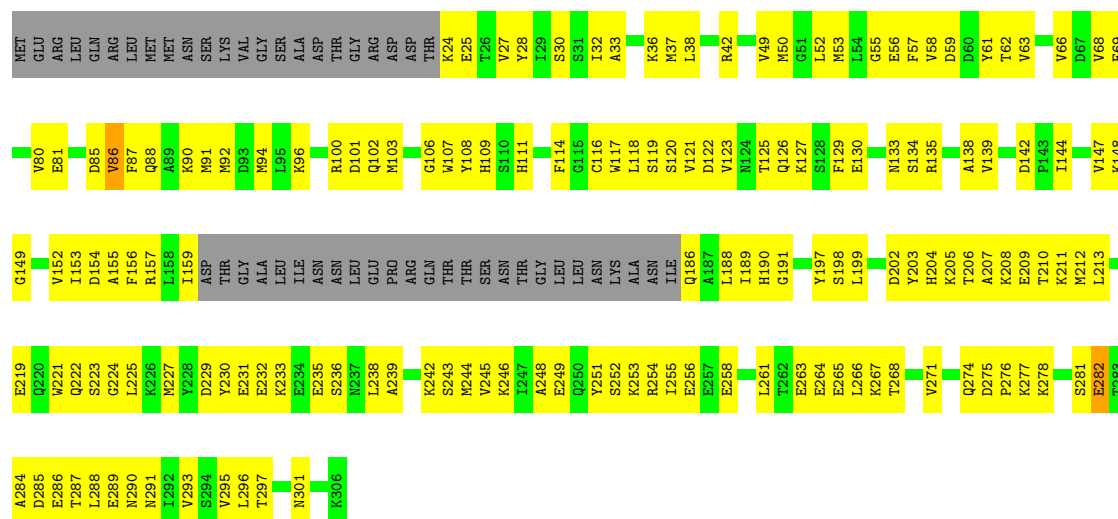
• Molecule 7: Ubiquitin carboxyl-terminal hydrolase RPN11

Chain 2-G: 49% 35% 16%



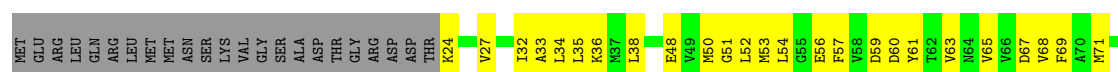
• Molecule 7: Ubiquitin carboxyl-terminal hydrolase RPN11

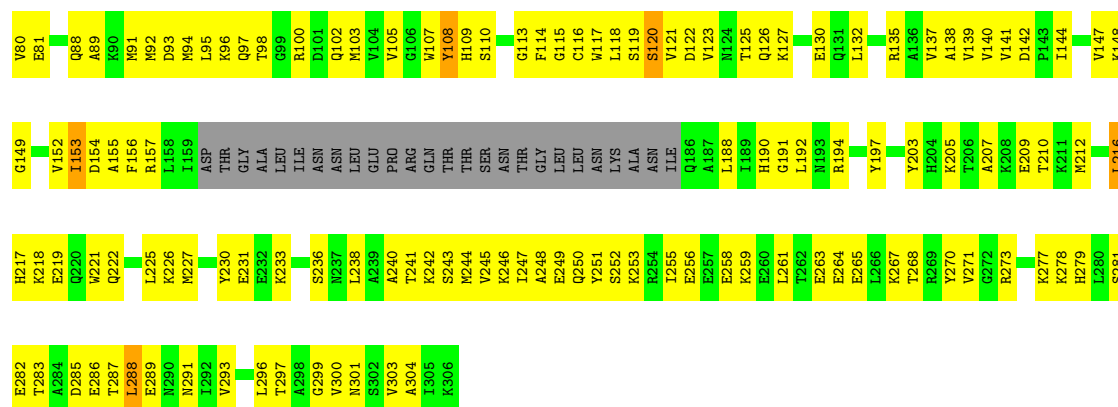
Chain 3-G: 33% 50% 16%



• Molecule 7: Ubiquitin carboxyl-terminal hydrolase RPN11

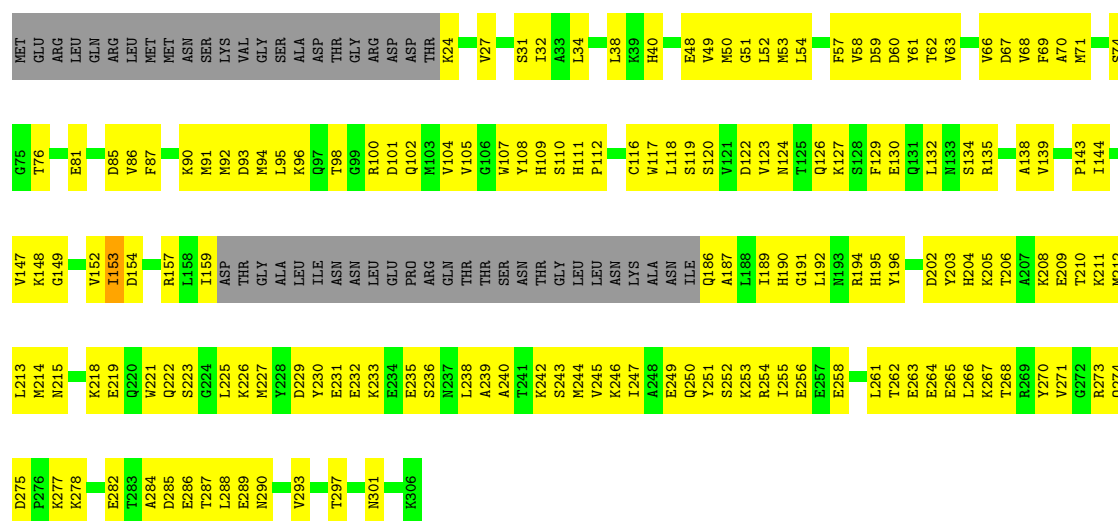
Chain 4-G: 35% 48% 16%





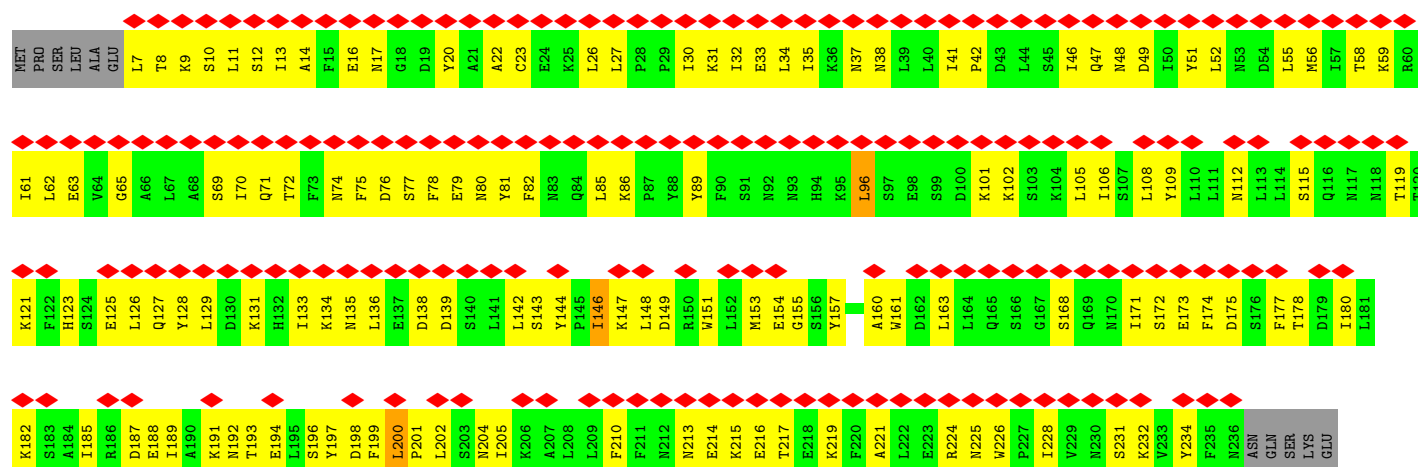
• Molecule 7: Ubiquitin carboxyl-terminal hydrolase RPN11

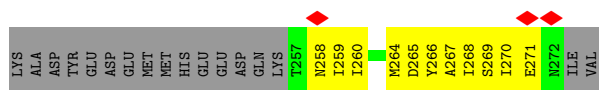
Chain 5-G: 32% 52% 16%



• Molecule 8: 26S proteasome regulatory subunit RPN12

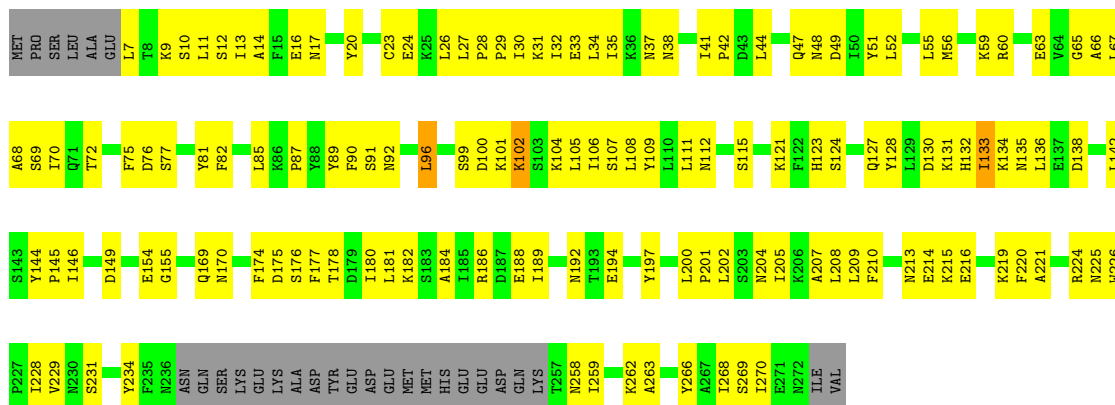
Chain 1-H: 36% 72% 53% 10%





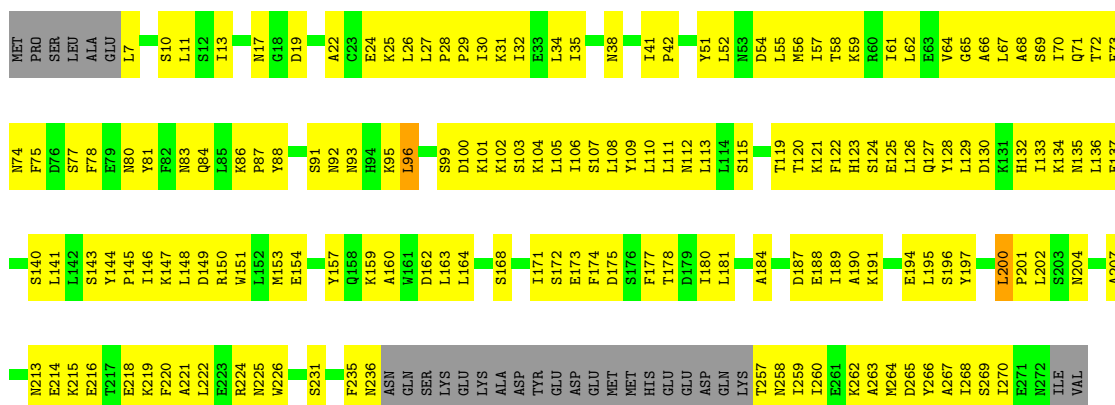
• Molecule 8: 26S proteasome regulatory subunit RPN12

Chain 2-H: 40% 49% 10%



• Molecule 8: 26S proteasome regulatory subunit RPN12

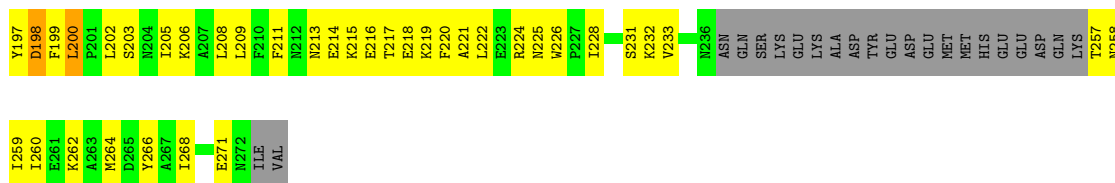
Chain 3-H: 30% 59% 10%



• Molecule 8: 26S proteasome regulatory subunit RPN12

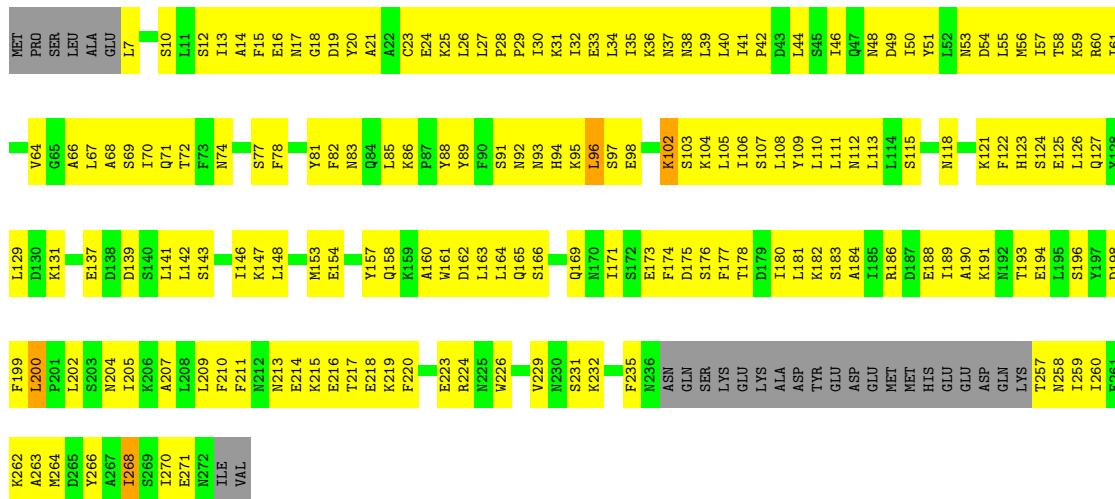
Chain 4-H: 27% 61% 10%





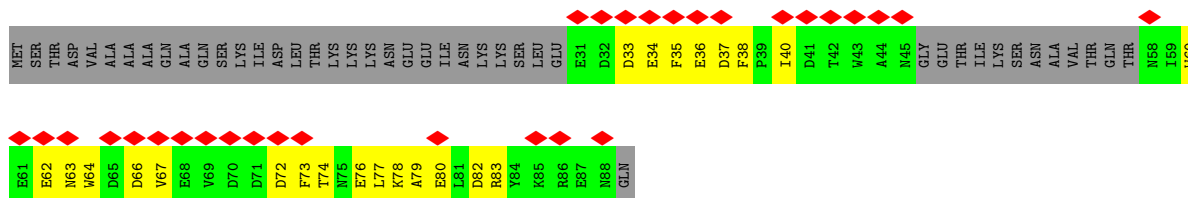
- Molecule 8: 26S proteasome regulatory subunit RPN12

Chain 5-H: 27% 61% 10%



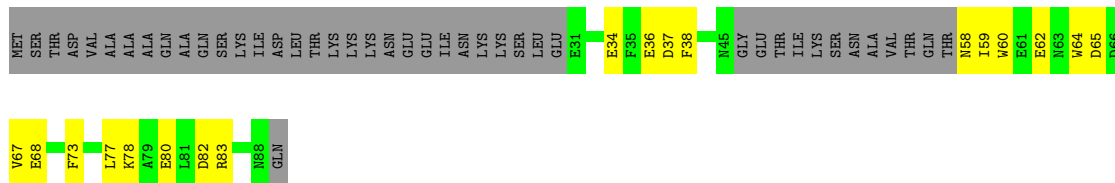
- Molecule 9: 26S proteasome complex subunit SEM1

Chain 1-I: 26% 34% 26% 48%



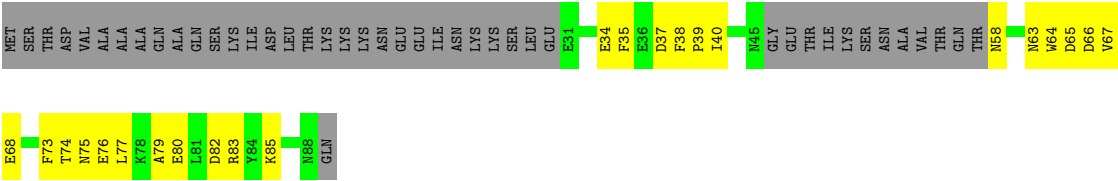
- Molecule 9: 26S proteasome complex subunit SEM1

Chain 2-I: 31% 20% 48%

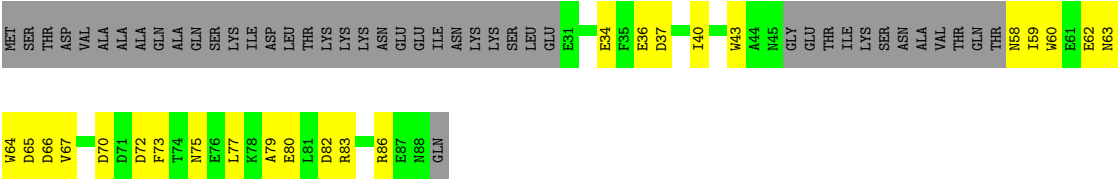
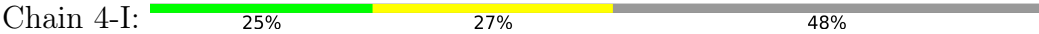


- Molecule 9: 26S proteasome complex subunit SEM1

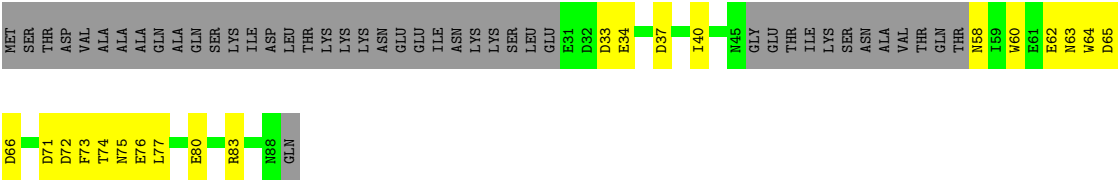
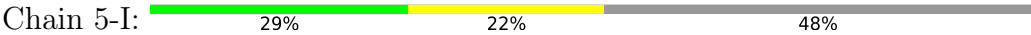
Chain 3-I: 26% 26% 48%



• Molecule 9: 26S proteasome complex subunit SEM1



• Molecule 9: 26S proteasome complex subunit SEM1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	109396	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	whole micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43.8	Depositor
Minimum defocus (nm)	1600	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	38168	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	0.247	Depositor
Minimum map value	-0.133	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.0642	Depositor
Map size ($\text{\AA}$)	209.59999, 209.59999, 209.59999	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.31, 1.31, 1.31	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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-A	0.34	0/2945	0.30	0/3976
1	2-A	0.34	0/2945	0.30	0/3976
1	3-A	0.34	0/2945	0.30	0/3976
1	4-A	0.34	0/2945	0.30	0/3976
1	5-A	0.34	0/2945	0.30	0/3976
2	1-B	0.39	0/3373	0.33	0/4550
2	2-B	0.39	0/3373	0.33	0/4550
2	3-B	0.39	0/3373	0.33	0/4550
2	4-B	0.39	0/3373	0.33	0/4550
2	5-B	0.39	0/3373	0.33	0/4550
3	1-C	0.29	0/3113	0.30	0/4193
3	2-C	0.29	0/3113	0.30	0/4193
3	3-C	0.29	0/3113	0.30	0/4193
3	4-C	0.29	0/3113	0.30	0/4193
3	5-C	0.29	0/3113	0.30	0/4193
4	1-D	0.37	0/3135	0.31	0/4227
4	2-D	0.37	0/3135	0.31	0/4227
4	3-D	0.37	0/3135	0.31	0/4227
4	4-D	0.37	0/3135	0.31	0/4227
4	5-D	0.37	0/3135	0.31	0/4227
5	1-E	0.38	0/2254	0.34	0/3042
5	2-E	0.38	0/2254	0.34	0/3042
5	3-E	0.38	0/2254	0.34	0/3042
5	4-E	0.38	0/2254	0.34	0/3042
5	5-E	0.38	0/2254	0.34	0/3042
6	1-F	0.38	0/3247	0.33	0/4380
6	2-F	0.38	0/3247	0.33	0/4380
6	3-F	0.38	0/3247	0.33	0/4380
6	4-F	0.38	0/3247	0.33	0/4380
6	5-F	0.38	0/3247	0.33	0/4380
7	1-G	0.38	0/2069	0.32	0/2786
7	2-G	0.38	0/2069	0.32	0/2786

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
7	3-G	0.38	0/2069	0.32	0/2786
7	4-G	0.38	0/2069	0.32	0/2786
7	5-G	0.38	0/2069	0.32	0/2786
8	1-H	0.28	0/2061	0.29	0/2785
8	2-H	0.28	0/2061	0.29	0/2785
8	3-H	0.28	0/2061	0.29	0/2785
8	4-H	0.28	0/2061	0.29	0/2785
8	5-H	0.28	0/2061	0.29	0/2785
9	1-I	0.29	0/414	0.28	0/562
9	2-I	0.29	0/414	0.28	0/562
9	3-I	0.29	0/414	0.28	0/562
9	4-I	0.29	0/414	0.28	0/562
9	5-I	0.29	0/414	0.28	0/562
All	All	0.35	0/113055	0.31	0/152505

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	4-A	0	1
3	4-C	0	1
3	5-C	0	1
4	5-D	0	1
7	1-G	0	1
7	4-G	0	1
All	All	0	6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	1-G	108	TYR	Peptide
1	4-A	261	HIS	Peptide
3	4-C	354	PHE	Peptide
7	4-G	108	TYR	Peptide
3	5-C	354	PHE	Peptide

5.2 Too-close contacts ⓘ

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-A	3116	0	2979	246	0
1	2-A	3116	0	2977	181	0
1	3-A	3116	0	2977	246	0
1	4-A	3116	0	2980	247	0
1	5-A	3116	0	2979	317	0
2	1-B	3323	0	3398	328	0
2	2-B	3323	0	3398	201	0
2	3-B	3323	0	3398	341	0
2	4-B	3323	0	3398	317	0
2	5-B	3323	0	3398	427	0
3	1-C	3060	0	3091	186	0
3	2-C	3060	0	3091	204	0
3	3-C	3060	0	3091	304	0
3	4-C	3060	0	3091	300	0
3	5-C	3060	0	3091	334	0
4	1-D	3084	0	3112	205	0
4	2-D	3084	0	3112	172	0
4	3-D	3084	0	3112	296	0
4	4-D	3084	0	3112	241	0
4	5-D	3084	0	3112	305	0
5	1-E	2224	0	2290	108	0
5	2-E	2224	0	2290	117	0
5	3-E	2224	0	2290	188	0
5	4-E	2224	0	2290	157	0
5	5-E	2224	0	2290	211	0
6	1-F	3186	0	3213	189	0
6	2-F	3186	0	3213	149	0
6	3-F	3186	0	3213	273	0
6	4-F	3186	0	3213	288	0
6	5-F	3186	0	3213	295	0
7	1-G	2036	0	2038	116	0
7	2-G	2036	0	2038	99	0
7	3-G	2036	0	2038	180	0
7	4-G	2036	0	2038	155	0
7	5-G	2036	0	2038	188	0
8	1-H	2021	0	2013	142	0
8	2-H	2021	0	2013	125	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	3-H	2021	0	2013	168	0
8	4-H	2021	0	2013	248	0
8	5-H	2021	0	2013	198	0
9	1-I	405	0	333	33	0
9	2-I	405	0	333	25	0
9	3-I	405	0	333	37	0
9	4-I	405	0	333	33	0
9	5-I	405	0	333	28	0
10	1-G	1	0	0	0	0
10	2-G	1	0	0	0	0
10	3-G	1	0	0	0	0
10	4-G	1	0	0	0	0
10	5-G	1	0	0	0	0
11	1-B	1	0	0	0	0
11	2-B	1	0	0	1	0
11	3-B	1	0	0	1	0
11	4-B	1	0	0	1	0
11	5-B	1	0	0	1	0
All	All	112285	0	112332	8710	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 39.

The worst 5 of 8710 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)
3:C:74:LEU:HD22	3:C:104:PHE:CE1	1.21	1.67
1:A:163:VAL:CG1	1:A:167:LEU:HD21	1.29	1.55
2:B:141:LYS:HD2	2:B:179:PHE:CD1	1.37	1.55
3:C:74:LEU:CD2	3:C:104:PHE:CE1	1.90	1.52
2:B:141:LYS:CD	2:B:179:PHE:CD1	1.99	1.44

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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-A	350/438 (80%)	316 (90%)	33 (9%)	1 (0%)	36	67
1	2-A	350/438 (80%)	306 (87%)	38 (11%)	6 (2%)	7	35
1	3-A	350/438 (80%)	305 (87%)	44 (13%)	1 (0%)	36	67
1	4-A	350/438 (80%)	308 (88%)	40 (11%)	2 (1%)	21	54
1	5-A	350/438 (80%)	310 (89%)	37 (11%)	3 (1%)	14	47
2	1-B	400/445 (90%)	353 (88%)	45 (11%)	2 (0%)	24	57
2	2-B	400/445 (90%)	348 (87%)	49 (12%)	3 (1%)	16	49
2	3-B	400/445 (90%)	355 (89%)	41 (10%)	4 (1%)	12	44
2	4-B	400/445 (90%)	333 (83%)	64 (16%)	3 (1%)	16	49
2	5-B	400/445 (90%)	349 (87%)	48 (12%)	3 (1%)	16	49
3	1-C	376/434 (87%)	344 (92%)	29 (8%)	3 (1%)	16	49
3	2-C	376/434 (87%)	323 (86%)	50 (13%)	3 (1%)	16	49
3	3-C	376/434 (87%)	323 (86%)	48 (13%)	5 (1%)	9	39
3	4-C	376/434 (87%)	333 (89%)	42 (11%)	1 (0%)	36	67
3	5-C	376/434 (87%)	325 (86%)	49 (13%)	2 (0%)	24	57
4	1-D	380/429 (89%)	337 (89%)	41 (11%)	2 (0%)	24	57
4	2-D	380/429 (89%)	341 (90%)	37 (10%)	2 (0%)	24	57
4	3-D	380/429 (89%)	334 (88%)	45 (12%)	1 (0%)	36	67
4	4-D	380/429 (89%)	337 (89%)	42 (11%)	1 (0%)	36	67
4	5-D	380/429 (89%)	342 (90%)	33 (9%)	5 (1%)	9	39
5	1-E	271/338 (80%)	243 (90%)	27 (10%)	1 (0%)	30	62
5	2-E	271/338 (80%)	247 (91%)	24 (9%)	0	100	100
5	3-E	271/338 (80%)	245 (90%)	23 (8%)	3 (1%)	11	43
5	4-E	271/338 (80%)	243 (90%)	27 (10%)	1 (0%)	30	62
5	5-E	271/338 (80%)	247 (91%)	22 (8%)	2 (1%)	18	51
6	1-F	386/393 (98%)	352 (91%)	33 (8%)	1 (0%)	36	67
6	2-F	386/393 (98%)	352 (91%)	33 (8%)	1 (0%)	36	67
6	3-F	386/393 (98%)	348 (90%)	37 (10%)	1 (0%)	36	67
6	4-F	386/393 (98%)	349 (90%)	36 (9%)	1 (0%)	36	67
6	5-F	386/393 (98%)	341 (88%)	42 (11%)	3 (1%)	16	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	1-G	253/306 (83%)	234 (92%)	19 (8%)	0	100	100
7	2-G	253/306 (83%)	227 (90%)	26 (10%)	0	100	100
7	3-G	253/306 (83%)	227 (90%)	23 (9%)	3 (1%)	10	41
7	4-G	253/306 (83%)	225 (89%)	23 (9%)	5 (2%)	6	32
7	5-G	253/306 (83%)	225 (89%)	26 (10%)	2 (1%)	16	49
8	1-H	242/274 (88%)	213 (88%)	27 (11%)	2 (1%)	16	49
8	2-H	242/274 (88%)	218 (90%)	21 (9%)	3 (1%)	10	41
8	3-H	242/274 (88%)	210 (87%)	31 (13%)	1 (0%)	30	62
8	4-H	242/274 (88%)	213 (88%)	25 (10%)	4 (2%)	7	35
8	5-H	242/274 (88%)	218 (90%)	22 (9%)	2 (1%)	16	49
9	1-I	42/89 (47%)	38 (90%)	4 (10%)	0	100	100
9	2-I	42/89 (47%)	35 (83%)	7 (17%)	0	100	100
9	3-I	42/89 (47%)	38 (90%)	4 (10%)	0	100	100
9	4-I	42/89 (47%)	37 (88%)	5 (12%)	0	100	100
9	5-I	42/89 (47%)	38 (90%)	4 (10%)	0	100	100
All	All	13500/15730 (86%)	11985 (89%)	1426 (11%)	89 (1%)	20	51

5 of 89 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	451	ILE
2	1-B	132	VAL
5	3-E	64	ASP
2	4-B	396	PRO
8	4-H	198	ASP

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-A	329/367 (90%)	324 (98%)	5 (2%)	57	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2-A	329/367 (90%)	324 (98%)	5 (2%)	57	71
1	3-A	329/367 (90%)	324 (98%)	5 (2%)	57	71
1	4-A	329/367 (90%)	324 (98%)	5 (2%)	57	71
1	5-A	329/367 (90%)	324 (98%)	5 (2%)	57	71
2	1-B	380/415 (92%)	374 (98%)	6 (2%)	55	70
2	2-B	380/415 (92%)	374 (98%)	6 (2%)	55	70
2	3-B	380/415 (92%)	374 (98%)	6 (2%)	55	70
2	4-B	380/415 (92%)	374 (98%)	6 (2%)	55	70
2	5-B	380/415 (92%)	374 (98%)	6 (2%)	55	70
3	1-C	343/391 (88%)	343 (100%)	0	100	100
3	2-C	343/391 (88%)	343 (100%)	0	100	100
3	3-C	343/391 (88%)	343 (100%)	0	100	100
3	4-C	343/391 (88%)	343 (100%)	0	100	100
3	5-C	343/391 (88%)	343 (100%)	0	100	100
4	1-D	336/379 (89%)	334 (99%)	2 (1%)	78	79
4	2-D	336/379 (89%)	334 (99%)	2 (1%)	78	79
4	3-D	336/379 (89%)	334 (99%)	2 (1%)	78	79
4	4-D	336/379 (89%)	334 (99%)	2 (1%)	78	79
4	5-D	336/379 (89%)	334 (99%)	2 (1%)	78	79
5	1-E	252/308 (82%)	252 (100%)	0	100	100
5	2-E	252/308 (82%)	252 (100%)	0	100	100
5	3-E	252/308 (82%)	252 (100%)	0	100	100
5	4-E	252/308 (82%)	252 (100%)	0	100	100
5	5-E	252/308 (82%)	252 (100%)	0	100	100
6	1-F	363/368 (99%)	363 (100%)	0	100	100
6	2-F	363/368 (99%)	363 (100%)	0	100	100
6	3-F	363/368 (99%)	363 (100%)	0	100	100
6	4-F	363/368 (99%)	363 (100%)	0	100	100
6	5-F	363/368 (99%)	363 (100%)	0	100	100
7	1-G	226/268 (84%)	226 (100%)	0	100	100
7	2-G	226/268 (84%)	226 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	3-G	226/268 (84%)	226 (100%)	0	100	100
7	4-G	226/268 (84%)	226 (100%)	0	100	100
7	5-G	226/268 (84%)	226 (100%)	0	100	100
8	1-H	230/256 (90%)	228 (99%)	2 (1%)	70	76
8	2-H	230/256 (90%)	228 (99%)	2 (1%)	70	76
8	3-H	230/256 (90%)	228 (99%)	2 (1%)	70	76
8	4-H	230/256 (90%)	228 (99%)	2 (1%)	70	76
8	5-H	230/256 (90%)	228 (99%)	2 (1%)	70	76
9	1-I	44/81 (54%)	44 (100%)	0	100	100
9	2-I	44/81 (54%)	44 (100%)	0	100	100
9	3-I	44/81 (54%)	44 (100%)	0	100	100
9	4-I	44/81 (54%)	44 (100%)	0	100	100
9	5-I	44/81 (54%)	44 (100%)	0	100	100
All	All	12515/14165 (88%)	12440 (99%)	75 (1%)	76	79

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	4-D	243	LEU
4	5-D	54	ILE
8	4-H	200	LEU
2	5-B	62	ILE
2	2-B	79	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 249 such sidechains are listed below:

Mol	Chain	Res	Type
1	3-A	337	ASN
4	5-D	323	ASN
6	3-F	283	HIS
4	5-D	96	GLN
6	5-F	75	GLN

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](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	4-A	1
1	5-A	1
1	1-A	1
1	2-A	1
1	3-A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
4	A	71:UNK	C	131:THR	N	12.75
5	A	71:UNK	C	131:THR	N	12.40
1	A	71:UNK	C	131:THR	N	10.10

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
2	A	71:UNK	C	131:THR	N	9.66
3	A	71:UNK	C	131:THR	N	9.19

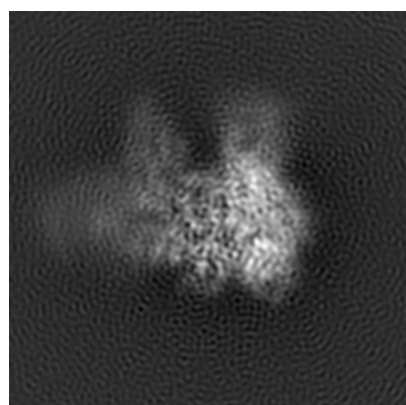
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6479. These allow visual inspection of the internal detail of the map and identification of artifacts.

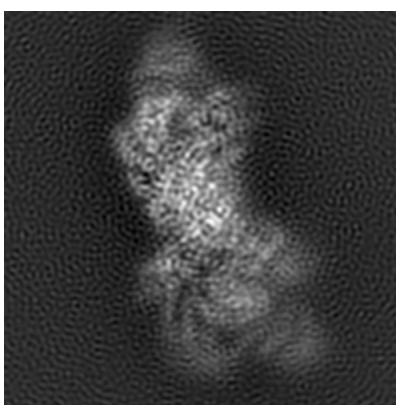
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

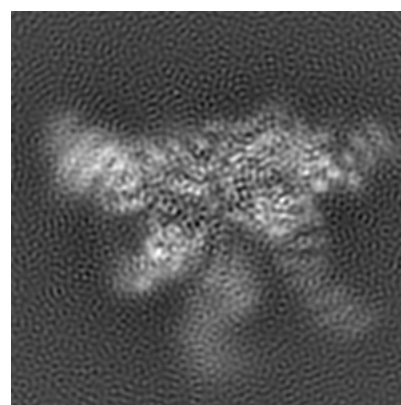
6.1.1 Primary map



X



Y

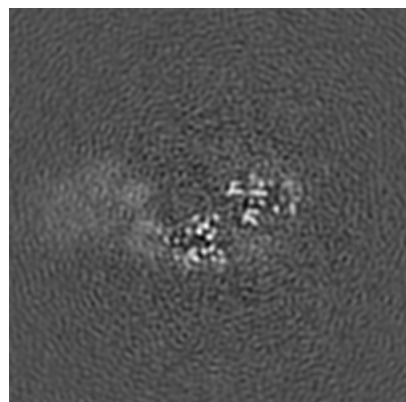


Z

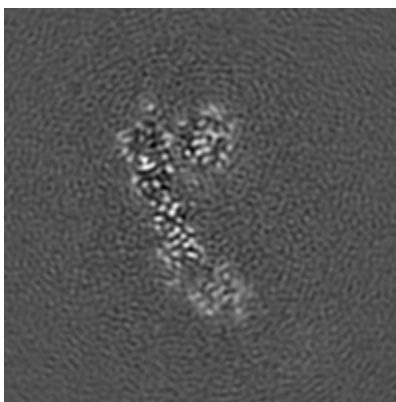
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

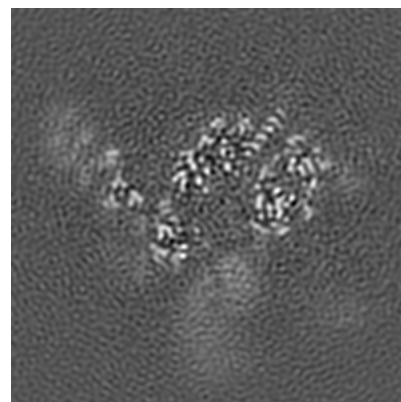
6.2.1 Primary map



X Index: 80



Y Index: 80

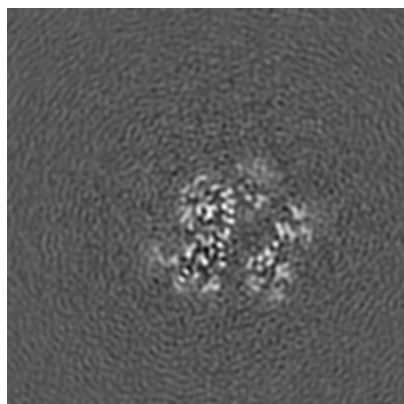


Z Index: 80

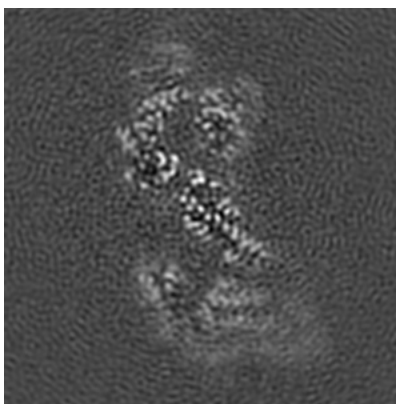
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

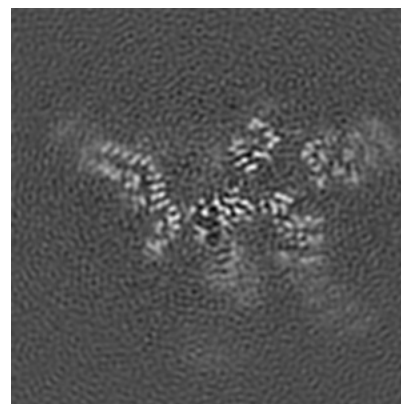
6.3.1 Primary map



X Index: 106



Y Index: 98

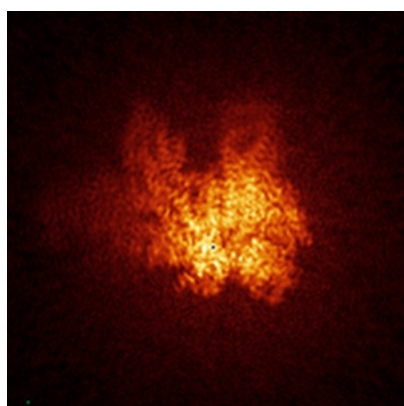


Z Index: 65

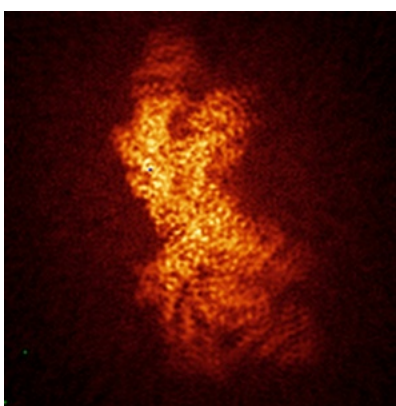
The images above show the largest variance slices of the map in three orthogonal directions.

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

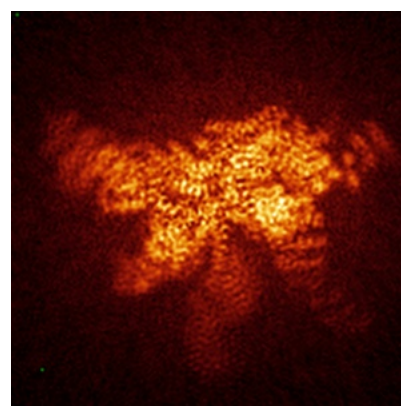
6.4.1 Primary map



X



Y

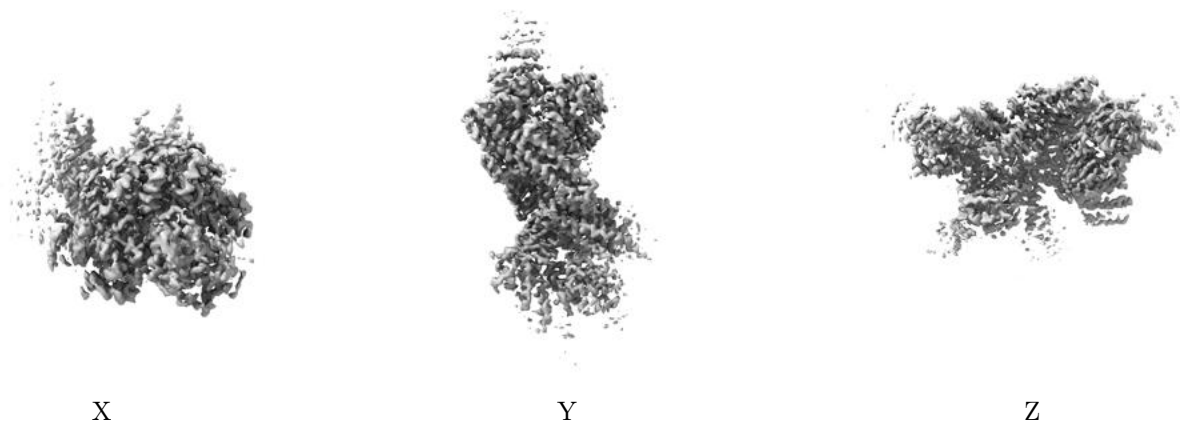


Z

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 0.0642. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

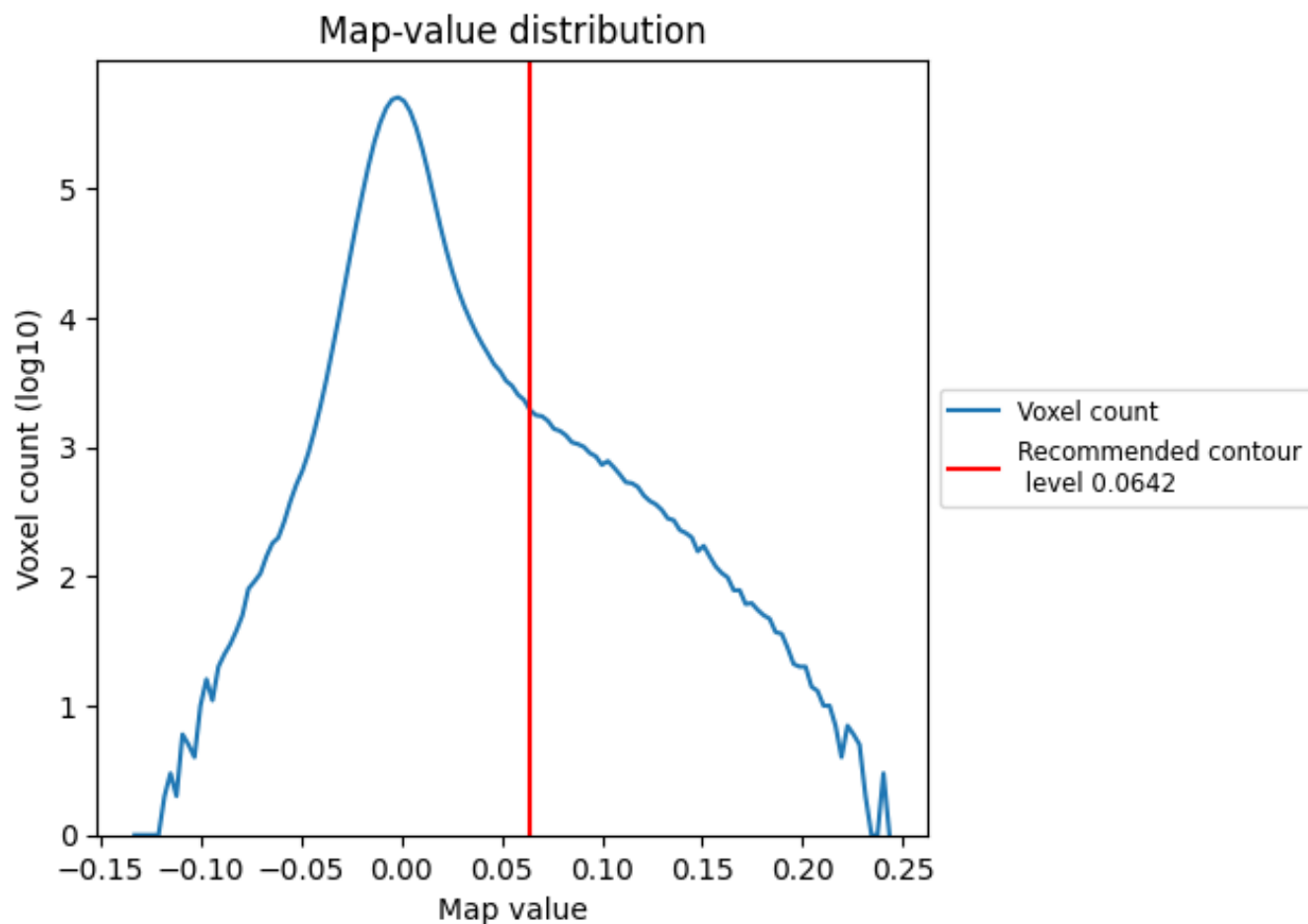
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

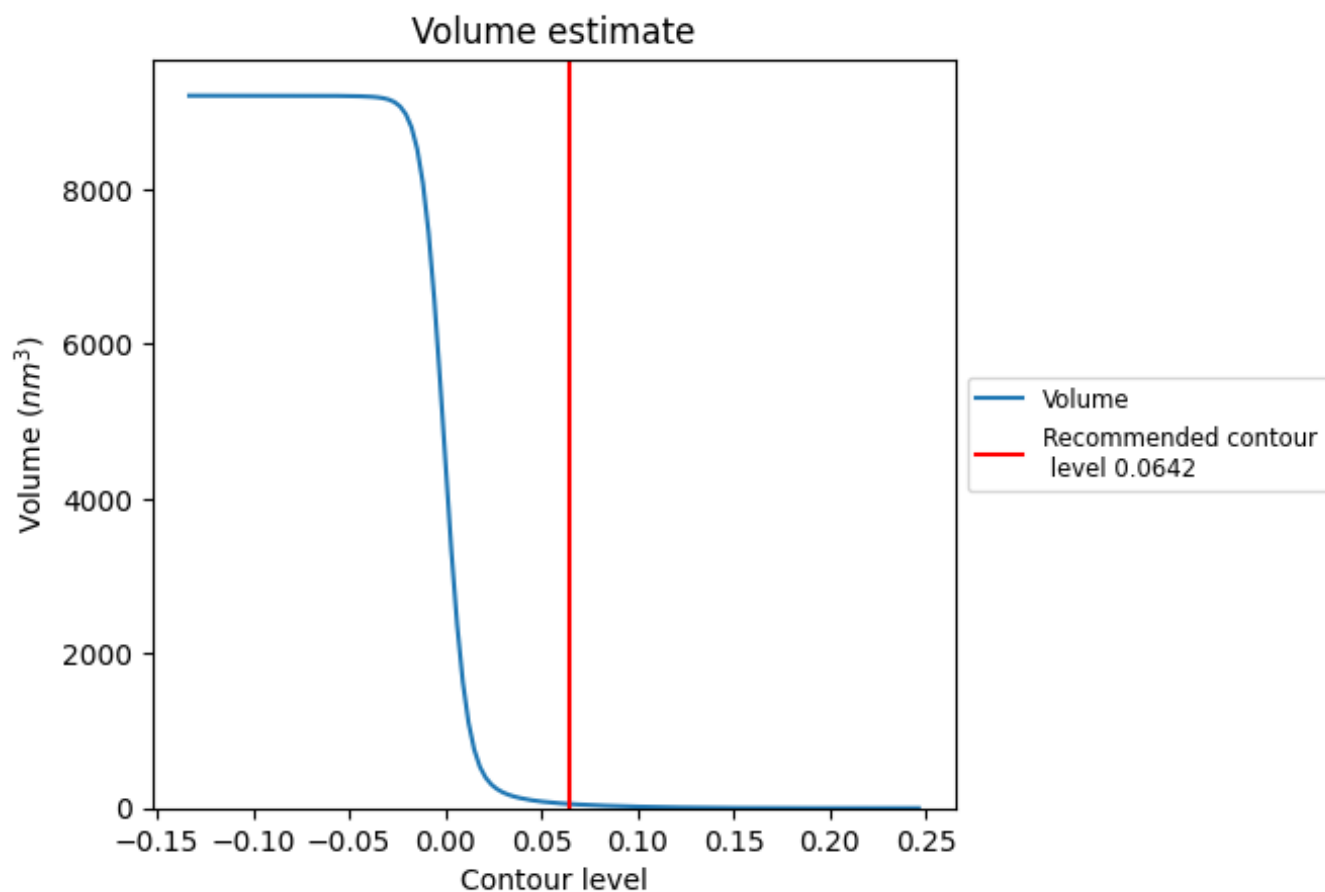
This section contains the results of statistical analysis of the map.

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.

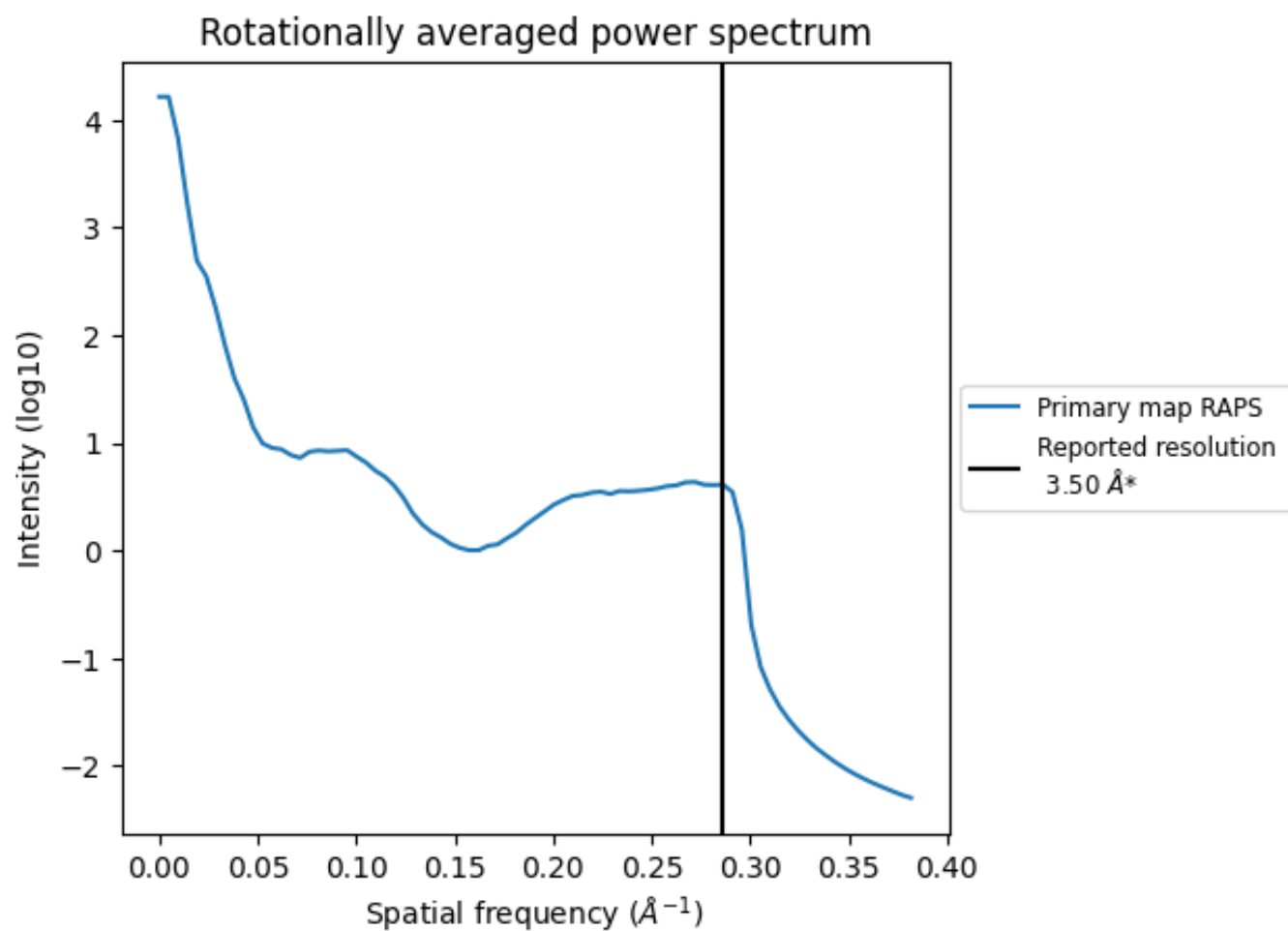
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 55 nm^3 ; this corresponds to an approximate mass of 49 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 ⓘ

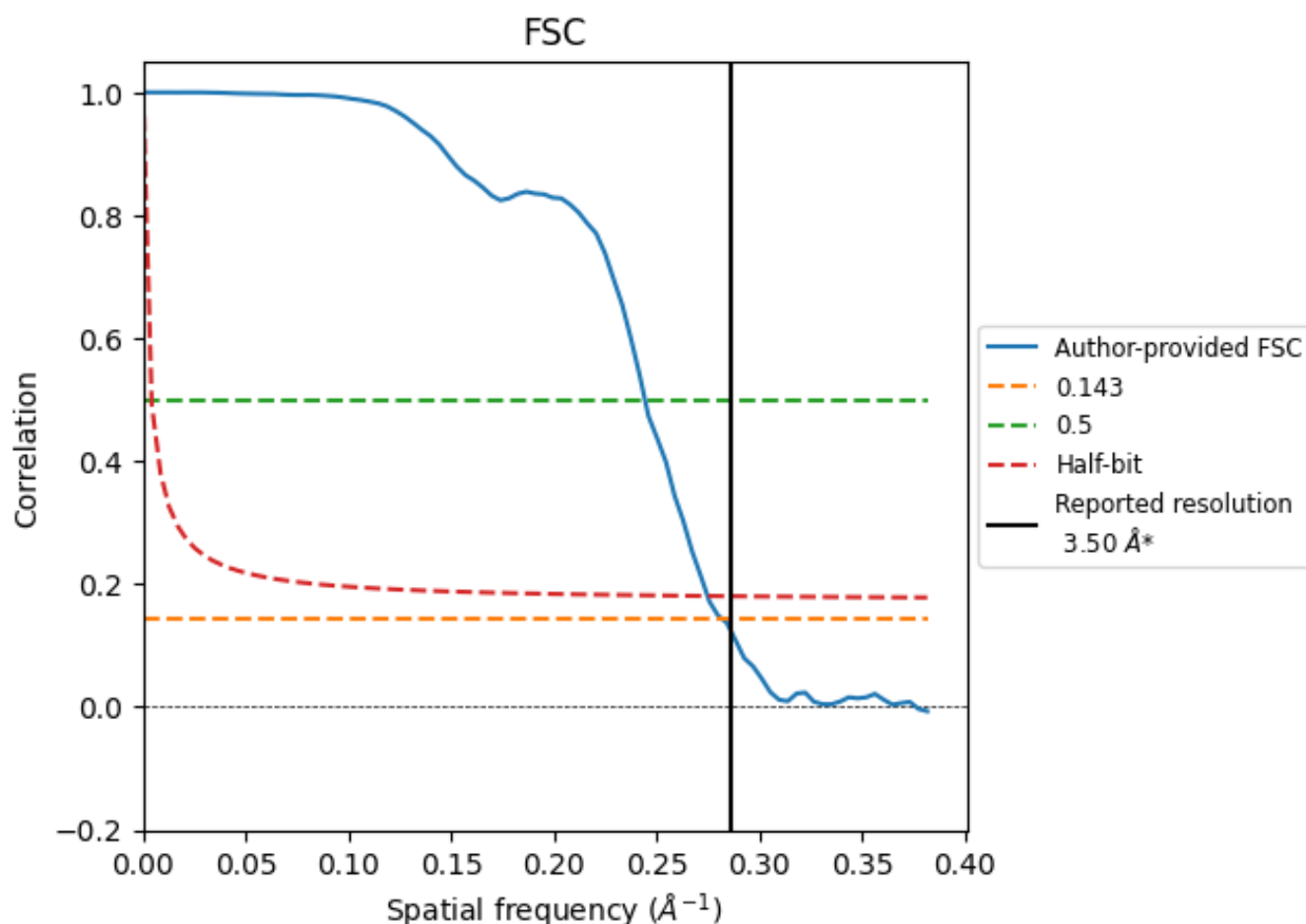


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

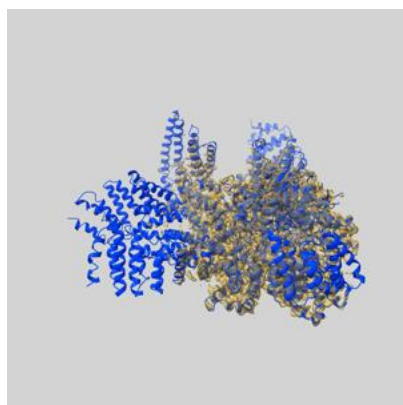
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.55	4.09	3.64
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

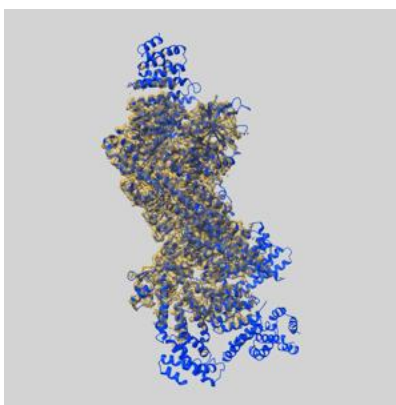
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6479 and PDB model 3JCK. Per-residue inclusion information can be found in section [3](#) on page [9](#).

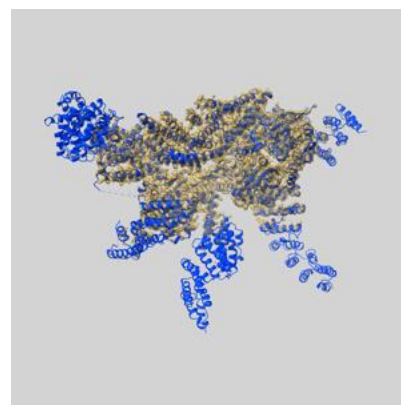
9.1 Map-model overlay [i](#)



X



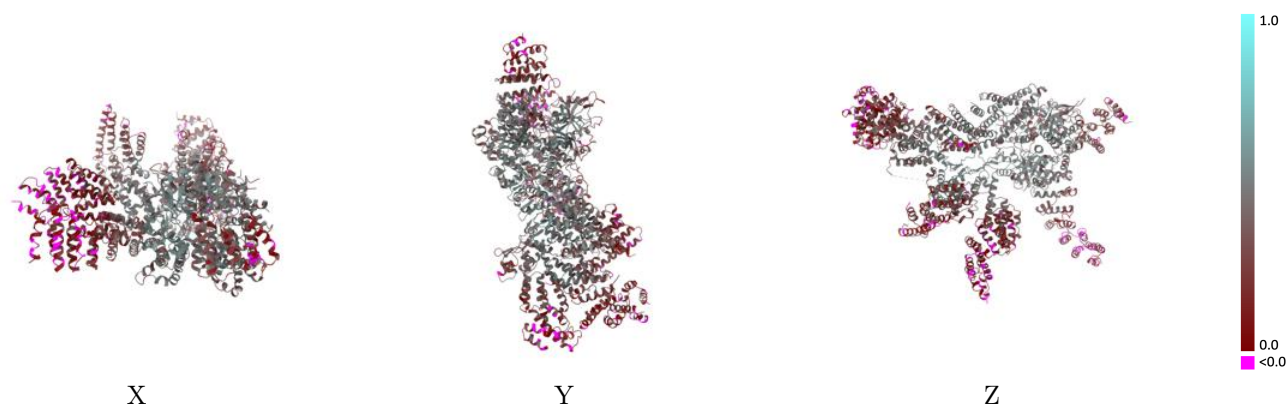
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0642 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](#)

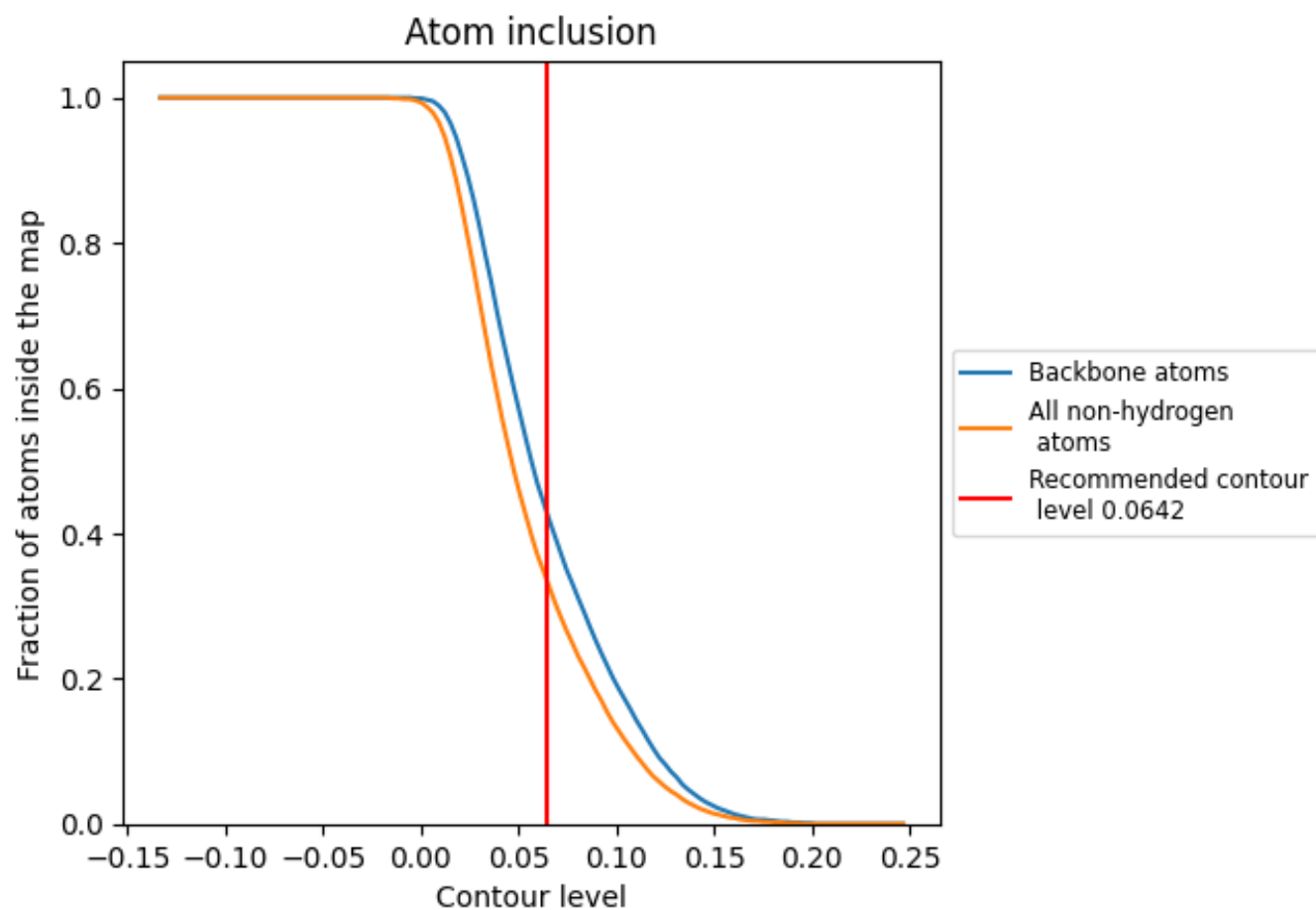


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 43% of all backbone atoms, 34% 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 (0.0642) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3370	0.3440
A	0.2830	0.3310
B	0.3790	0.3350
C	0.1760	0.2300
D	0.3630	0.3640
E	0.4660	0.4240
F	0.3990	0.3800
G	0.5170	0.4400
H	0.1830	0.2690
I	0.3100	0.3730

1.0

0.0

<0.0