



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 09:50 AM UTC

PDB ID : 5VFP / pdb_00005vfp
EMDB ID : EMD-8663
Title : Nucleotide-driven Triple-state Remodeling of the AAA-ATPase Channel in the Activated Human 26S Proteasome
Authors : Zhu, Y.; Wang, W.L.; Yu, D.; Ouyang, Q.; Lu, Y.; Mao, Y.
Deposited on : 2017-04-09
Resolution : 4.20 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:

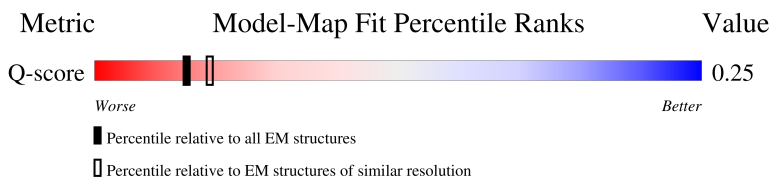
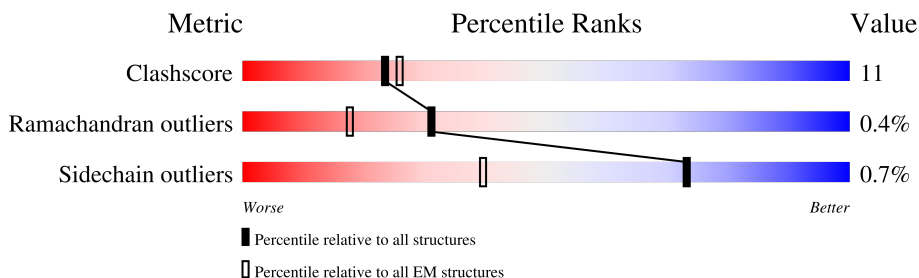
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 4.20 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	5410 (3.70 - 4.70)

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	G	240	<p>25% 85% 14%</p>
1	g	240	<p>40% 83% 16%</p>
2	H	232	<p>26% 76% 23%</p>
2	h	232	<p>42% 82% 18%</p>

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Mol	Chain	Length	Quality of chain
3	I	250	42% 81% 18%
3	i	250	49% 76% 24%
4	J	243	46% 86% 12%
4	j	243	42% 81% 18%
5	K	234	41% 71% 24%
5	k	234	37% 77% 21%
6	L	238	29% 78% 22%
6	l	238	32% 84% 16%
7	M	245	29% 75% 22%
7	m	245	41% 72% 26%
8	N	191	13% 83% 16%
8	n	191	12% 83% 16%
9	O	220	22% 80% 19%
9	o	220	25% 81% 19%
10	P	204	15% 83% 17%
10	p	204	16% 85% 15%
11	Q	199	27% 78% 22%
11	q	199	19% 79% 21%
12	R	201	17% 85% 15%
12	r	201	13% 84% 16%
13	S	213	23% 85% 15%
13	s	213	19% 84% 16%
14	T	215	14% 83% 17%
14	t	215	16% 80% 19%
15	U	911	59% 60% 28% 12%

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Mol	Chain	Length	Quality of chain
16	V	480	81% 64% 33% ..
17	W	456	74% 65% 35% .
18	Y	378	63% 68% 31% .
19	Z	286	72% 75% 23% .
20	a	373	80% 68% 31% .
21	b	191	87% 69% 30% ..
22	c	287	63% 69% 27% ..
23	d	257	90% 68% 31% .
24	e	70	51% 30% 27% 43%
25	X	380	72% 77% 22% .
26	A	399	58% 71% 24% 5%
27	B	389	71% 75% 20% 5%
28	C	392	67% 73% 19% 7%
29	D	380	72% 73% 26% .
30	E	375	61% 81% 19%
31	F	396	56% 75% 19% 5%
32	f	908	68% 40% 33% 24%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
34	AGS	E	401	-	-	X	-

2 Entry composition [i](#)

There are 34 unique types of molecules in this entry. The entry contains 101342 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 alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	G	239	Total	C	N	O	S	0	0
			1820	1157	304	346	13		
1	g	240	Total	C	N	O	S	0	0
			1826	1160	305	348	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	H	230	Total	C	N	O	S	0	0
			1688	1070	284	329	5		
2	h	232	Total	C	N	O	S	0	0
			1708	1081	289	333	5		

- Molecule 3 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	I	248	Total	C	N	O	S	0	0
			1895	1195	324	368	8		
3	i	250	Total	C	N	O	S	0	0
			1912	1204	329	371	8		

- Molecule 4 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	J	239	Total	C	N	O	S	0	0
			1704	1056	308	335	5		
4	j	239	Total	C	N	O	S	0	0
			1704	1056	308	335	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	K	228	1729	1086	284	349	10	0	0
5	k	228	1722	1080	284	348	10	0	0

- Molecule 6 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	L	238	1850	1159	334	346	11	0	0
6	l	238	1850	1159	334	346	11	0	0

- Molecule 7 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	M	240	1856	1178	314	353	11	0	0
7	m	240	1856	1178	314	353	11	0	0

- Molecule 8 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	N	191	1430	893	245	280	12	0	0
8	n	191	1430	893	245	280	12	0	0

- Molecule 9 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	O	220	1643	1033	280	318	12	0	0
9	o	220	1643	1033	280	318	12	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	P	204	1585	1010	262	294	19	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	p	204	1585	1010	262	294	19	0	0

- Molecule 11 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	Q	199	1570	1006	265	290	9	0	0
11	q	199	1570	1006	265	290	9	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	R	201	1548	974	273	292	9	0	0
12	r	201	1548	974	273	292	9	0	0

- Molecule 13 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	S	213	1641	1036	282	313	10	0	0
13	s	213	1641	1036	282	313	10	0	0

- Molecule 14 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	T	215	1667	1052	285	318	12	0	0
14	t	215	1667	1052	285	318	12	0	0

- Molecule 15 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	U	806	6287	3990	1075	1178	44	0	0

- Molecule 16 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	V	473	3808	2418	676	700	14	0	0

- Molecule 17 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	W	456	3703	2339	635	704	25	0	0

- Molecule 18 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	Y	378	3115	1987	533	578	17	0	0

- Molecule 19 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	Z	286	2281	1457	392	427	5	0	0

- Molecule 20 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	a	373	2995	1911	510	559	15	0	0

- Molecule 21 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	b	191	1458	910	261	279	8	0	0

- Molecule 22 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	c	278	2187	1389	374	406	18	0	0

- Molecule 23 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	257	Total	C	N	O	S	0	0
			2116	1371	346	390	9		

- Molecule 24 is a protein called sem1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	40	Total	C	N	O	S	0	0
			334	200	55	77	2		

- Molecule 25 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	380	Total	C	N	O	S	0	0
			3009	1918	509	570	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	380	Total	C	N	O	S	0	0
			2893	1817	515	543	18		

- Molecule 27 is a protein called 26S proteasome regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B	370	Total	C	N	O	S	0	0
			2806	1763	478	553	12		

- Molecule 28 is a protein called 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	C	363	Total	C	N	O	S	0	0
			2859	1804	513	525	17		

- Molecule 29 is a protein called 26S proteasome regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	D	380	Total	C	N	O	S	0	0
			3040	1923	524	580	13		

- Molecule 30 is a protein called 26S proteasome regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	E	375	2860	1796	512	536	16	0	0

- Molecule 31 is a protein called 26S proteasome regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	F	376	2859	1802	496	546	15	0	0

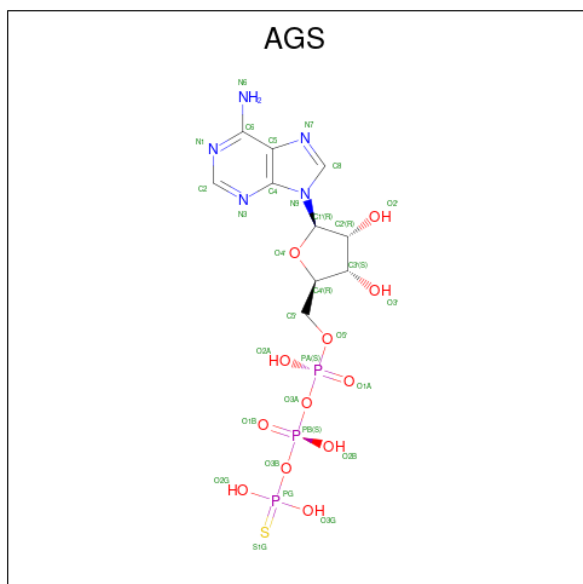
- Molecule 32 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	f	689	5319	3343	904	1037	35	0	0

- Molecule 33 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
33	c	1	1	1	0

- Molecule 34 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).



Mol	Chain	Residues	Atoms						AltConf
			Total	C	N	O	P	S	
34	A	1	31	10	5	12	3	1	0

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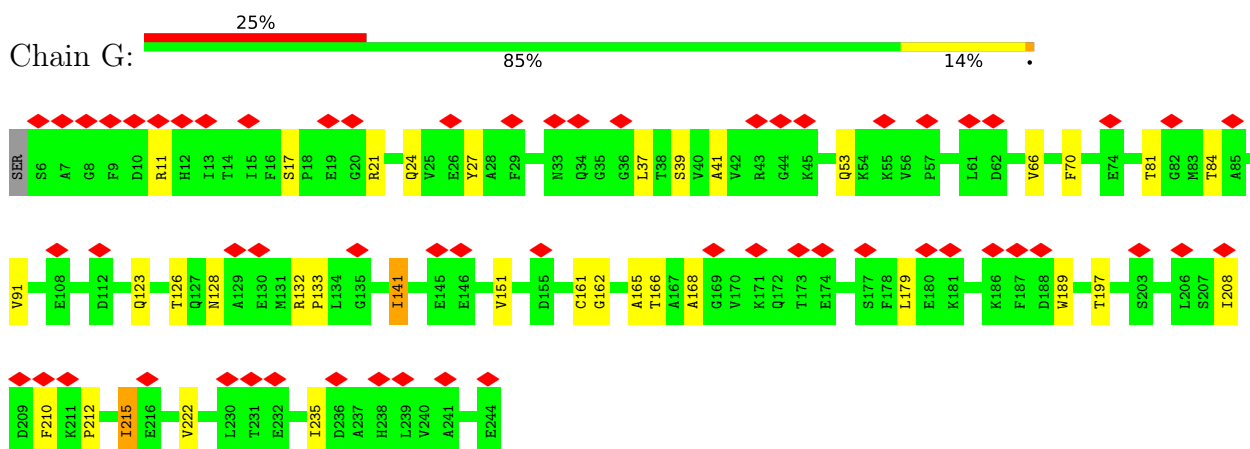
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Mol	Chain	Residues	Atoms						AltConf
			Total	C	N	O	P	S	
34	D	1	Total 31	10	5	12	3	1	0
34	E	1	Total 31	10	5	12	3	1	0
34	F	1	Total 31	10	5	12	3	1	0

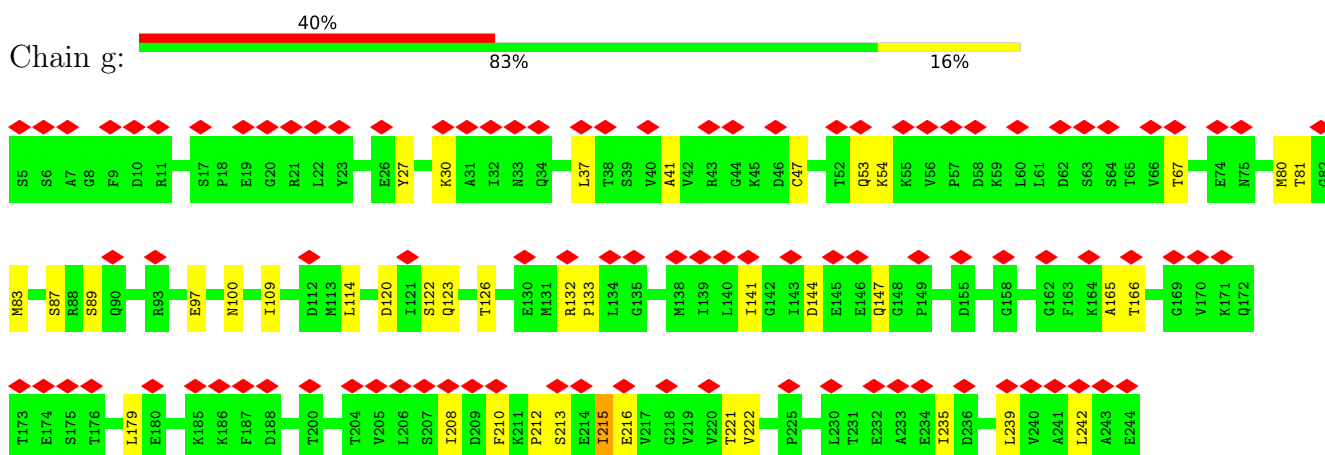
3 Residue-property plots [i](#)

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

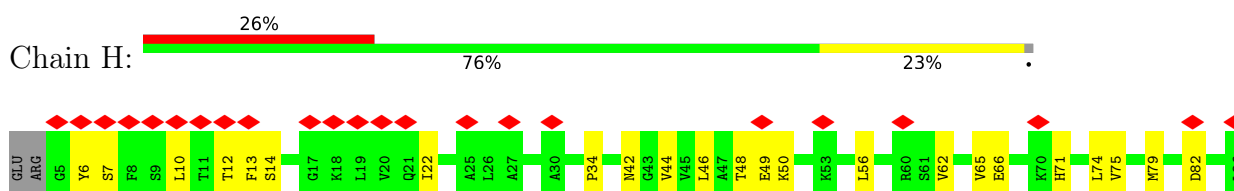
- Molecule 1: Proteasome subunit alpha type-6

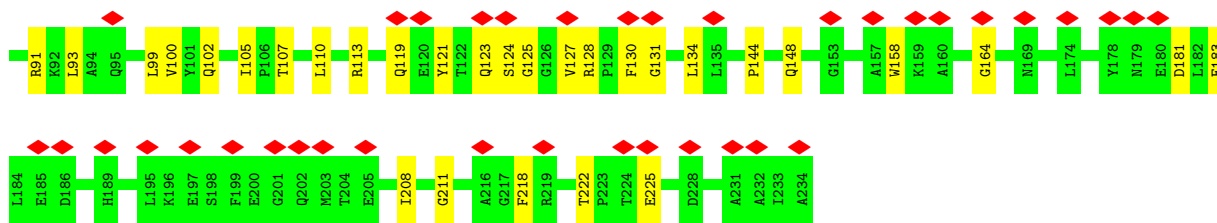


- Molecule 1: Proteasome subunit alpha type-6

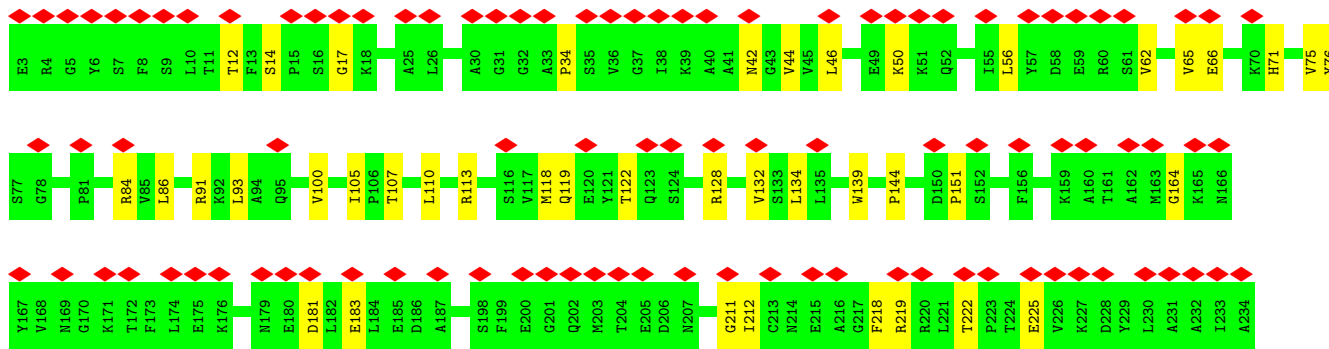
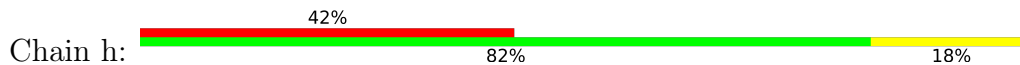


- Molecule 2: Proteasome subunit alpha type-2

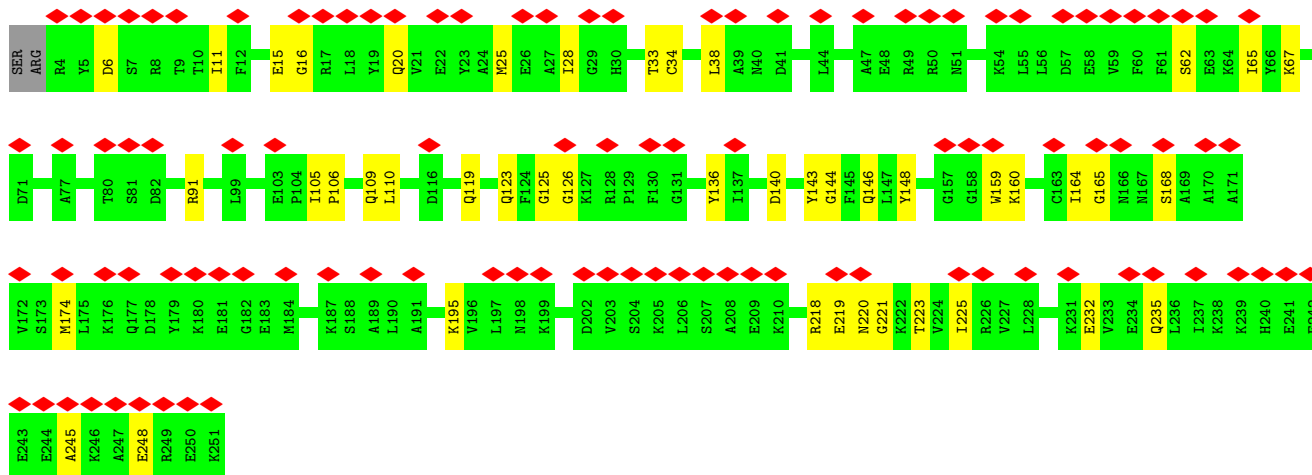
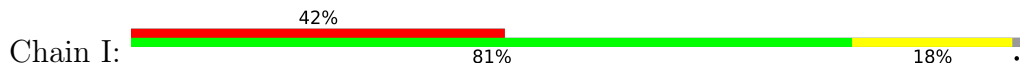




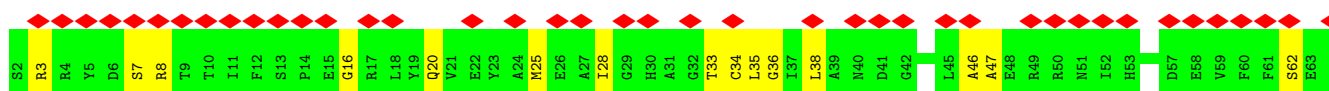
• Molecule 2: Proteasome subunit alpha type-2

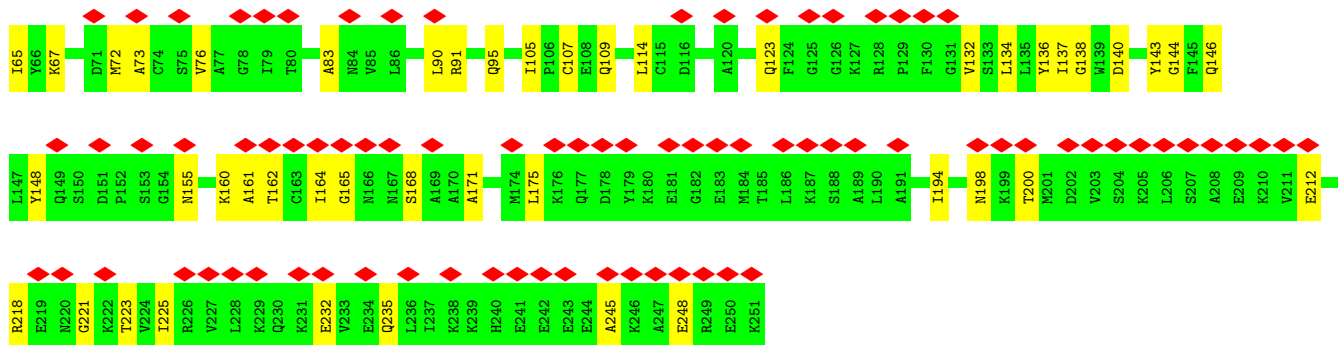


• Molecule 3: Proteasome subunit alpha type-4

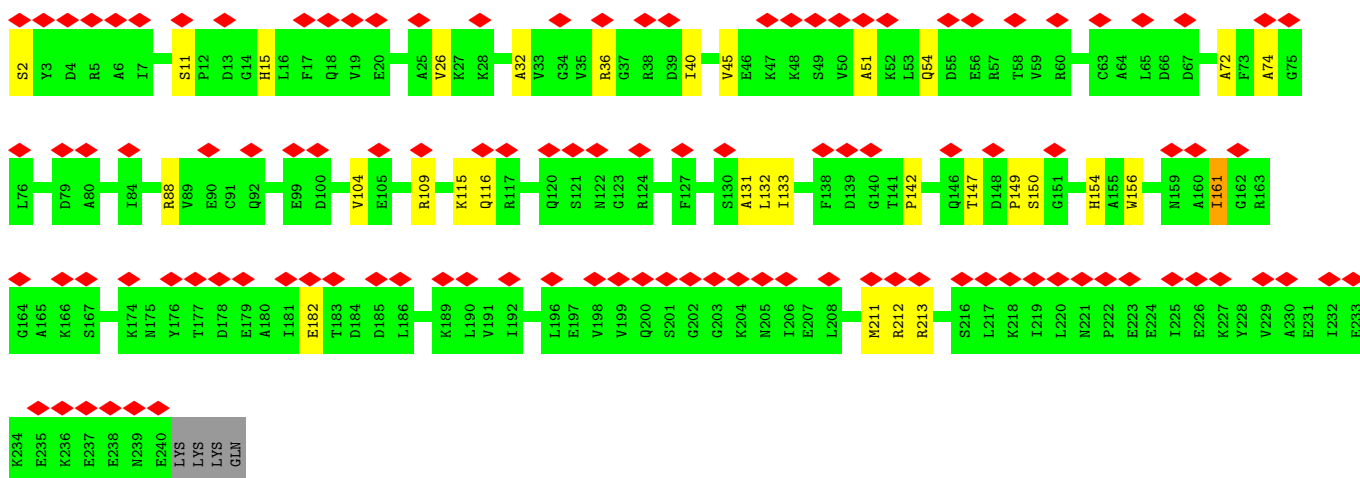
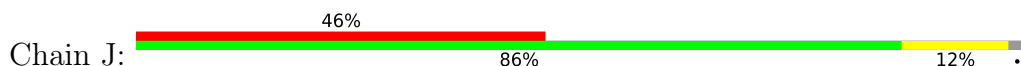


• Molecule 3: Proteasome subunit alpha type-4

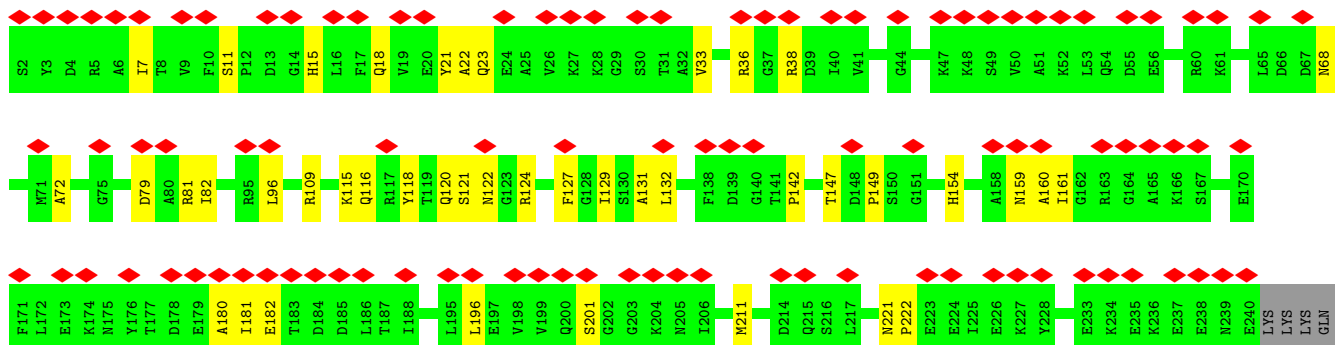
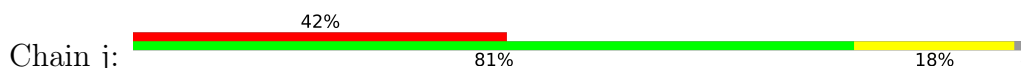




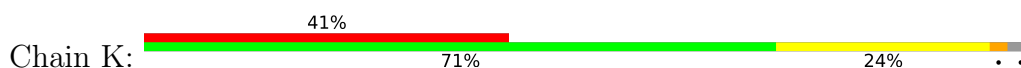
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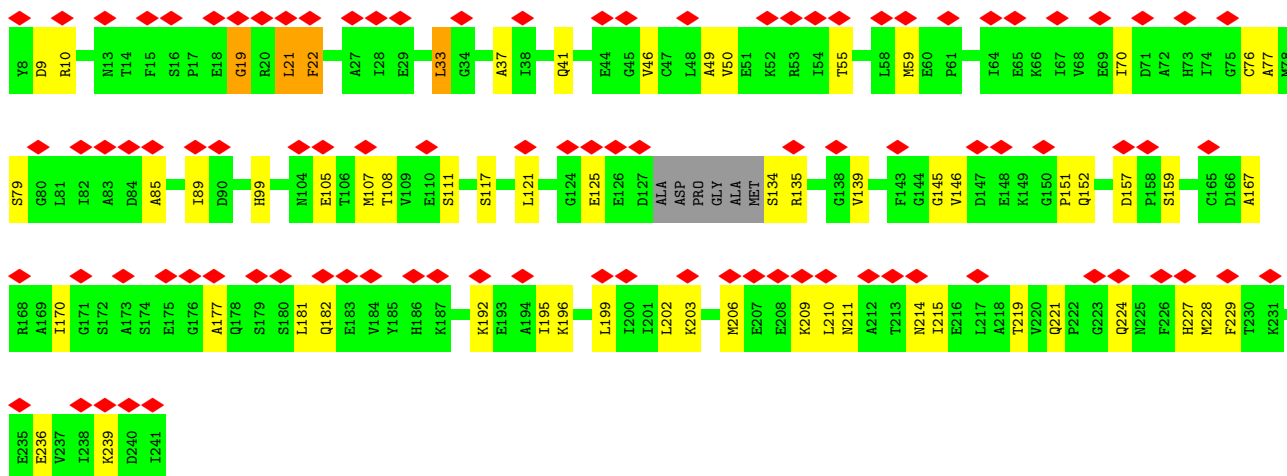


• Molecule 4: Proteasome subunit alpha type-7

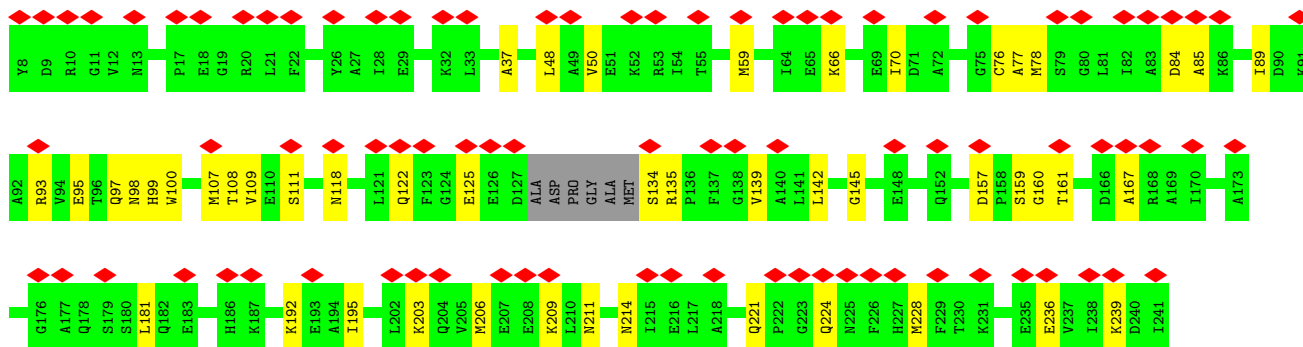
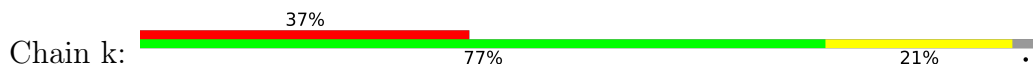


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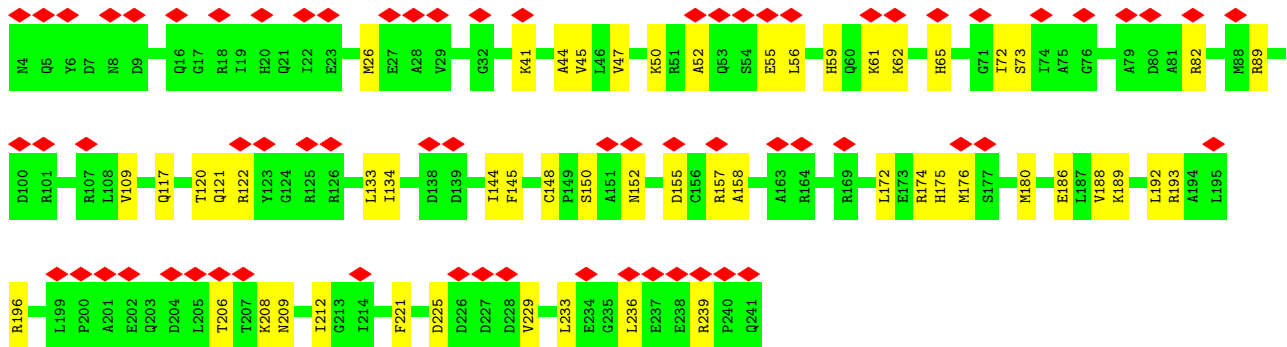
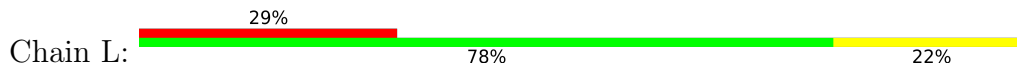




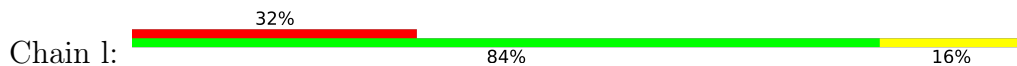
• Molecule 5: Proteasome subunit alpha type-5

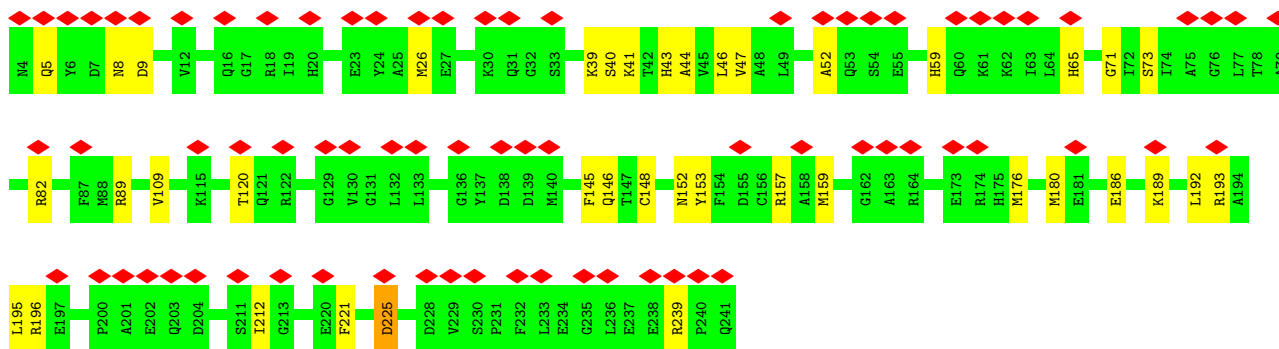


• Molecule 6: Proteasome subunit alpha type-1

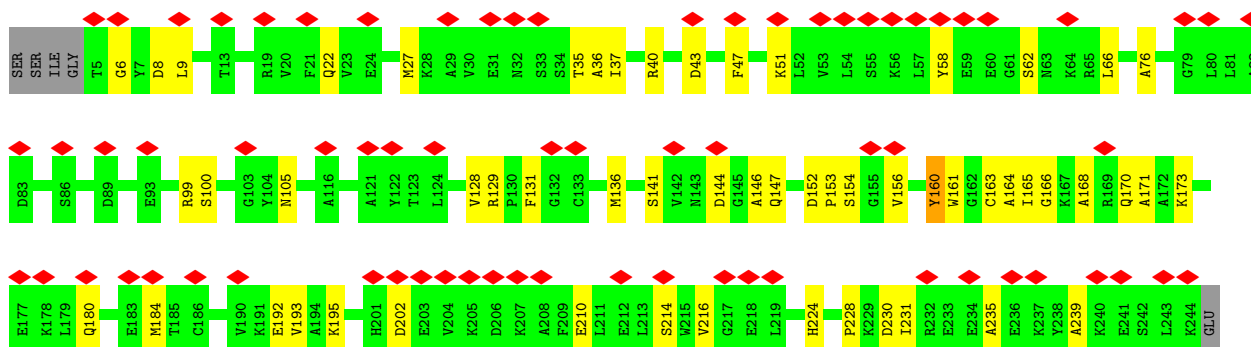
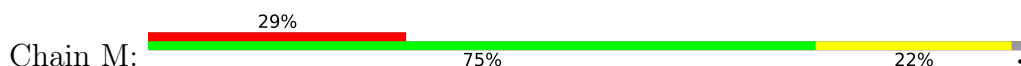


• Molecule 6: Proteasome subunit alpha type-1

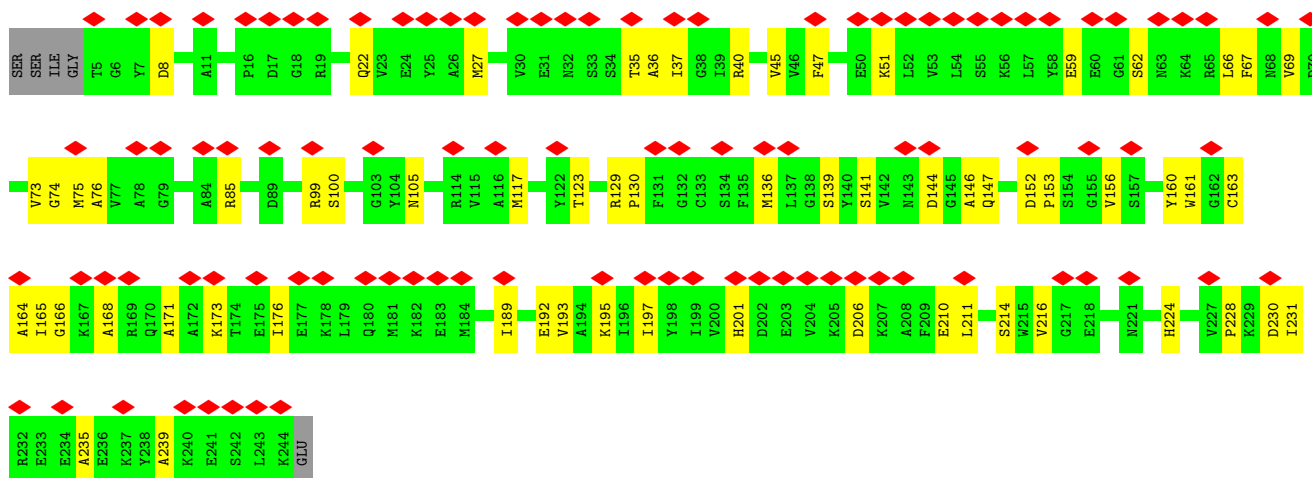




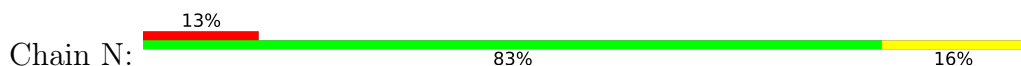
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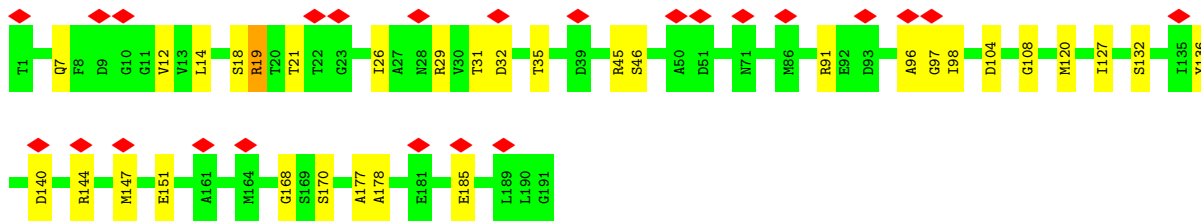


• Molecule 7: Proteasome subunit alpha type-3

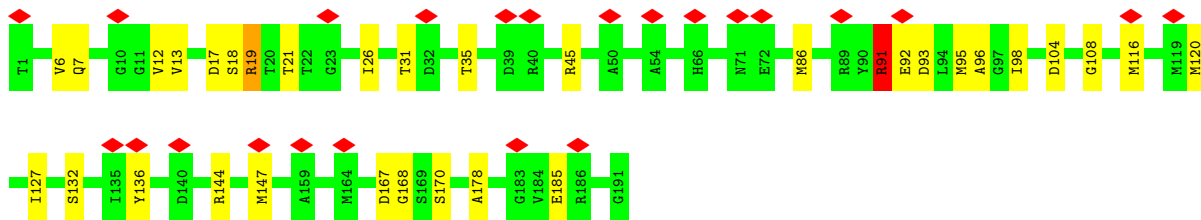
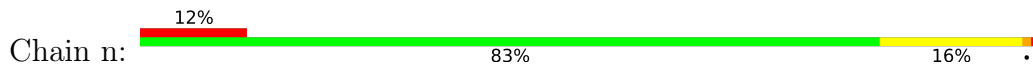


• Molecule 8: Proteasome subunit beta type-6

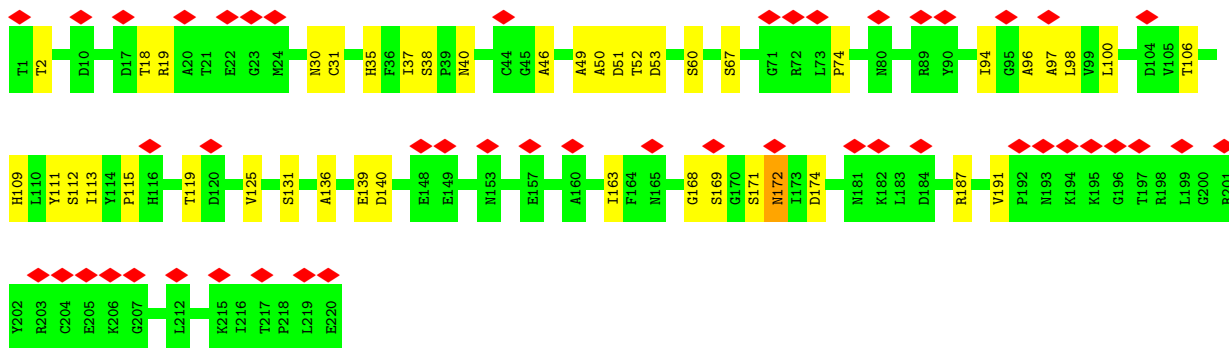
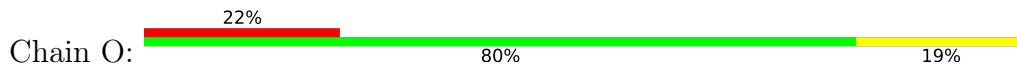




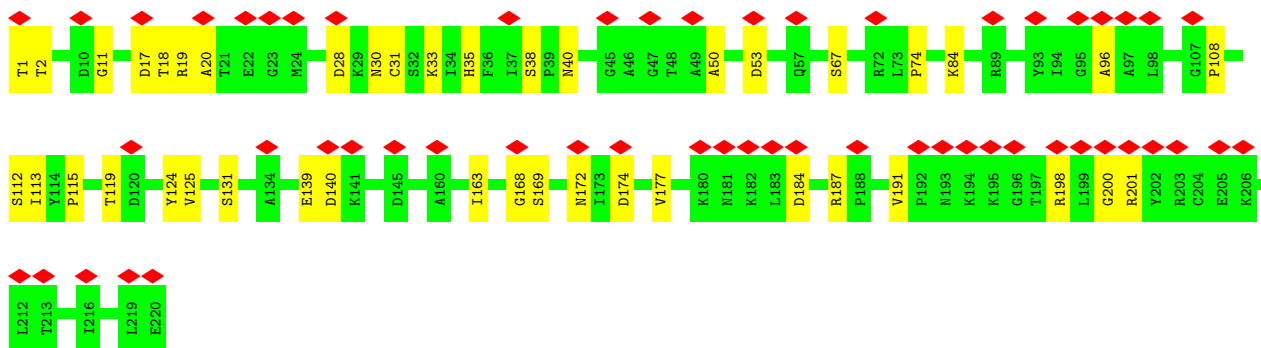
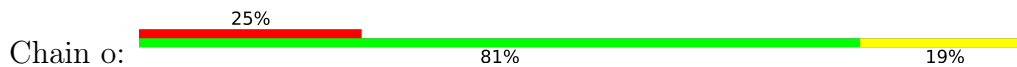
• Molecule 8: Proteasome subunit beta type-6



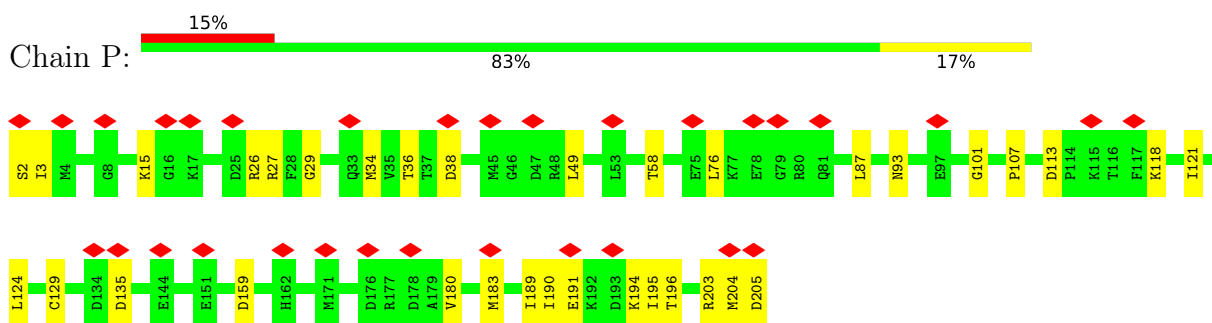
• Molecule 9: Proteasome subunit beta type-7



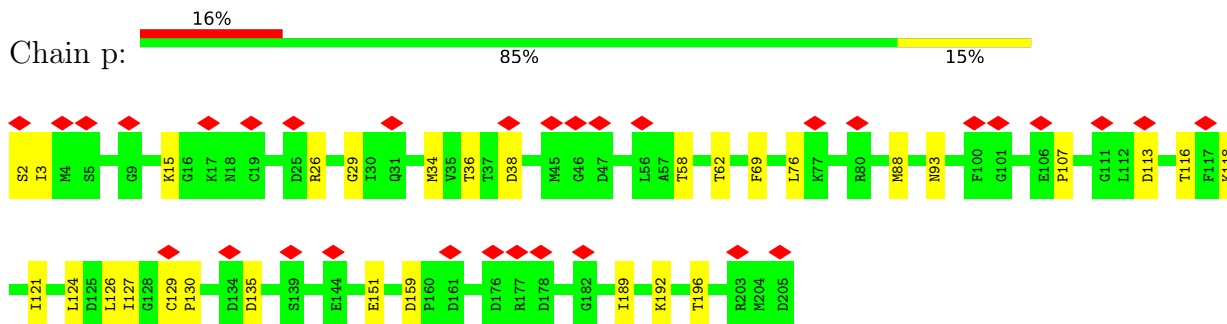
• Molecule 9: Proteasome subunit beta type-7



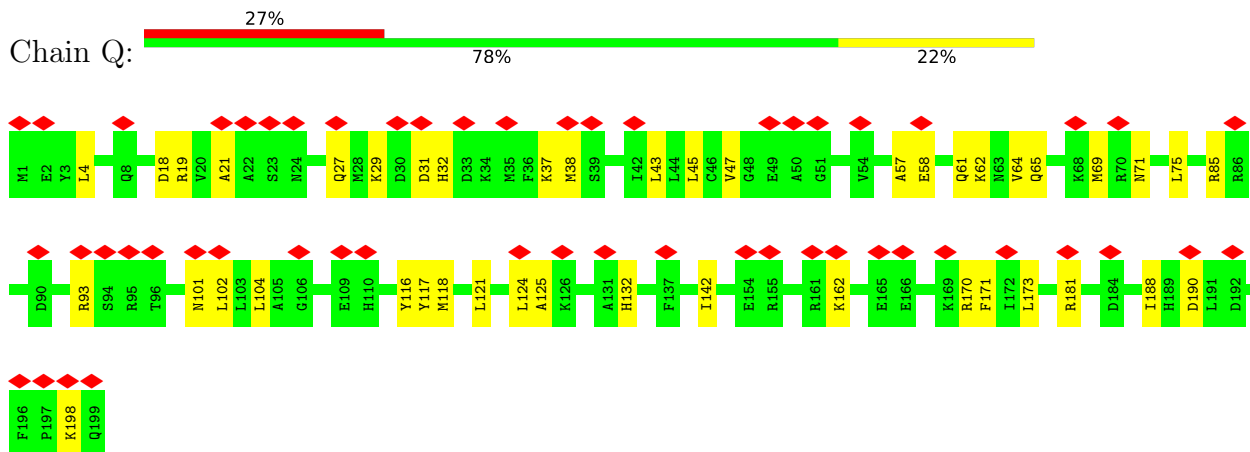
• Molecule 10: Proteasome subunit beta type-3



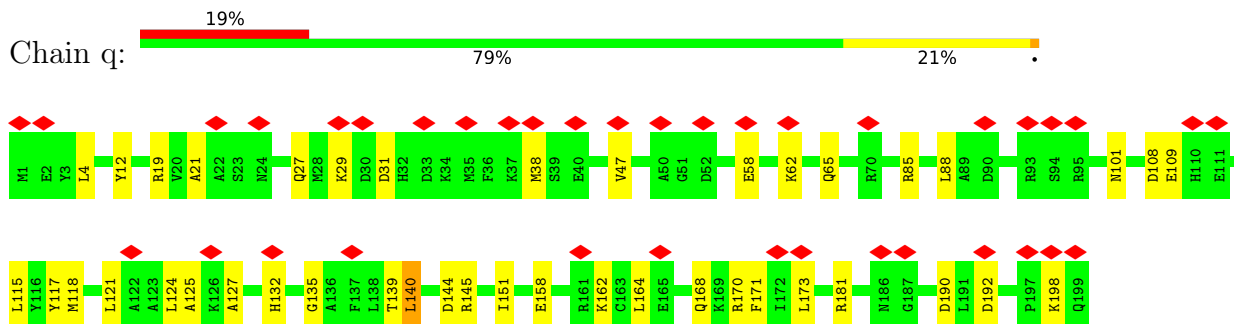
- Molecule 10: Proteasome subunit beta type-3



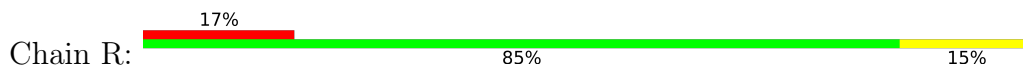
- Molecule 11: Proteasome subunit beta type-2

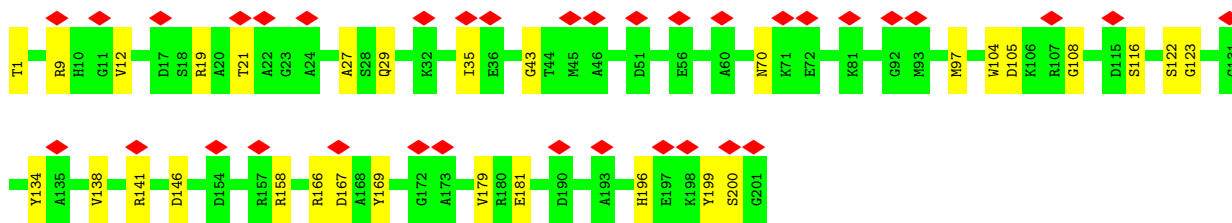


- Molecule 11: Proteasome subunit beta type-2

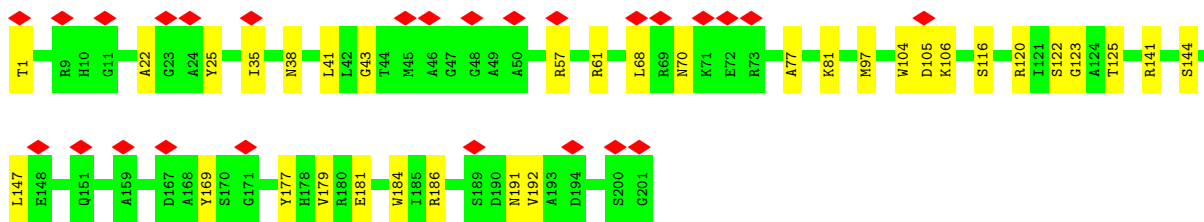
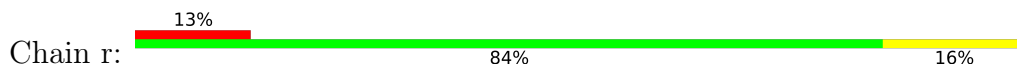


- Molecule 12: Proteasome subunit beta type-5

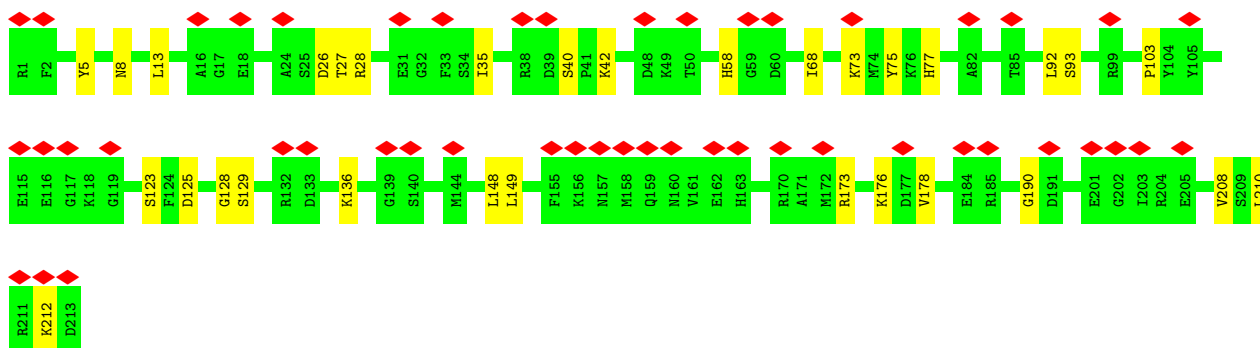
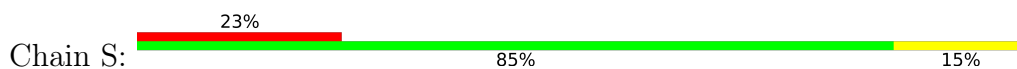




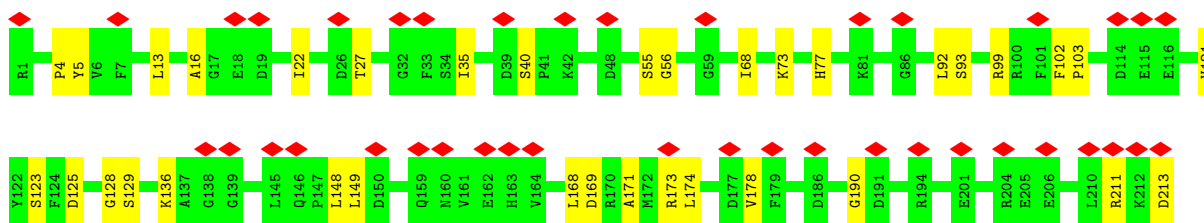
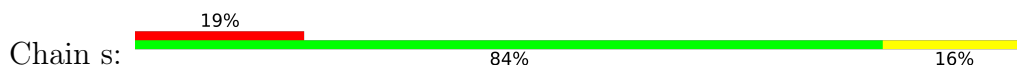
- Molecule 12: Proteasome subunit beta type-5



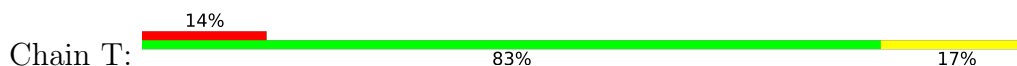
- Molecule 13: Proteasome subunit beta type-1

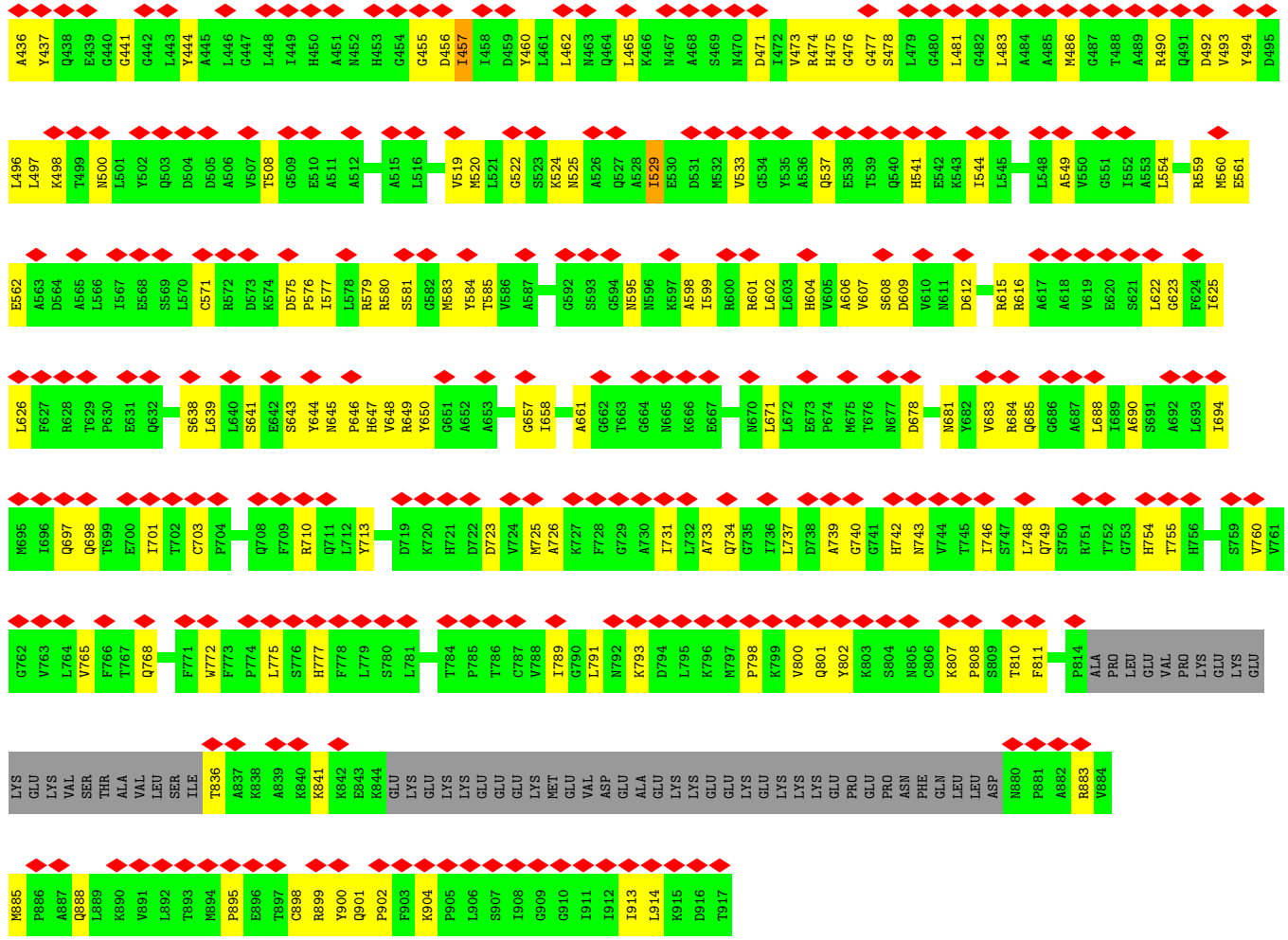


- Molecule 13: Proteasome subunit beta type-1

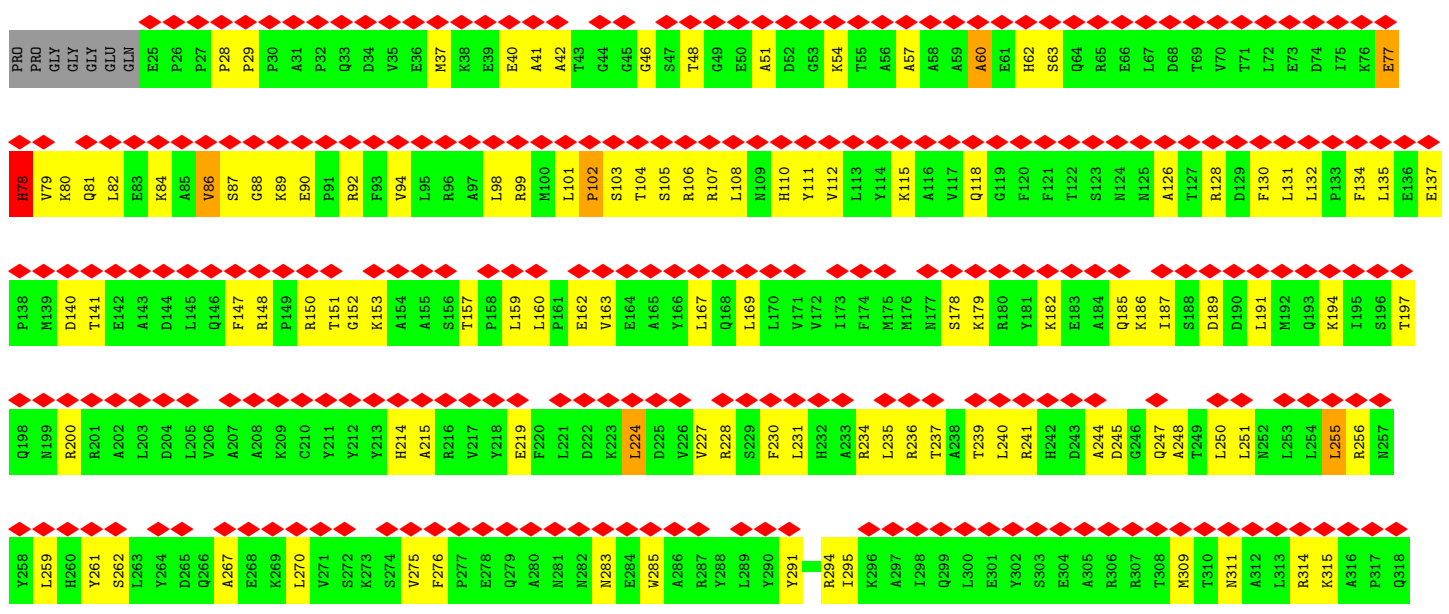
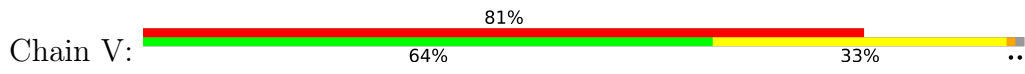


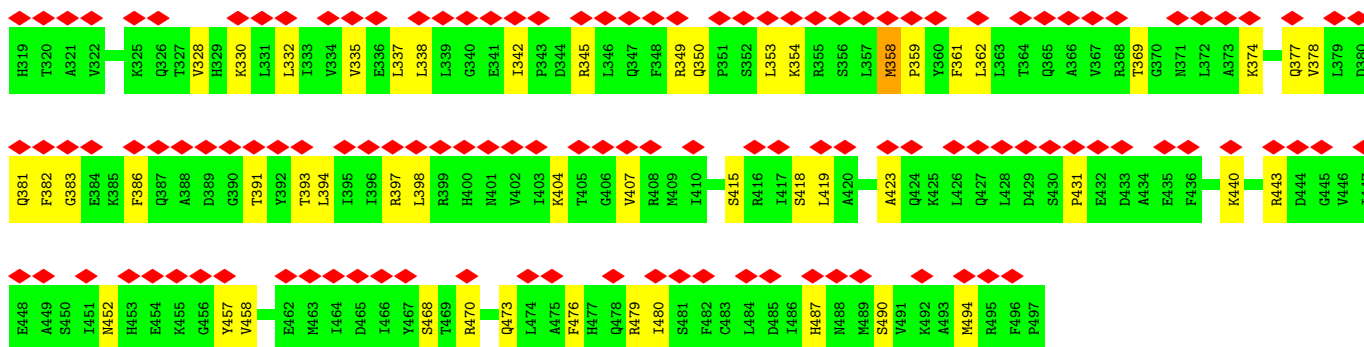
- Molecule 14: Proteasome subunit beta type-4



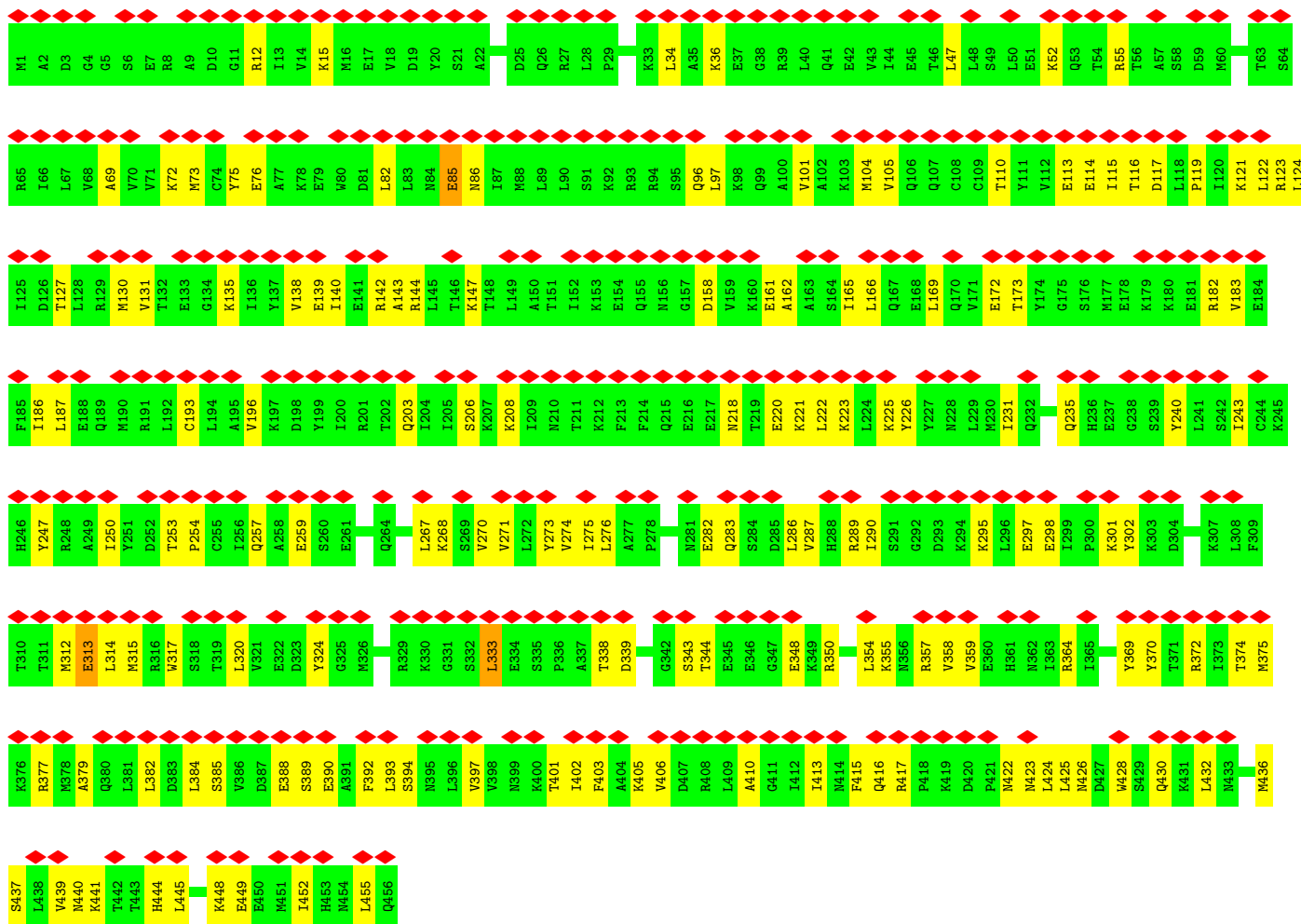
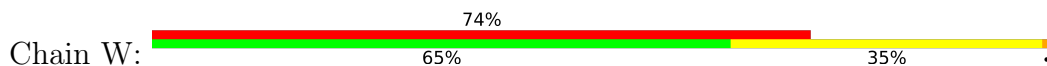


● Molecule 16: 26S proteasome non-ATPase regulatory subunit 3



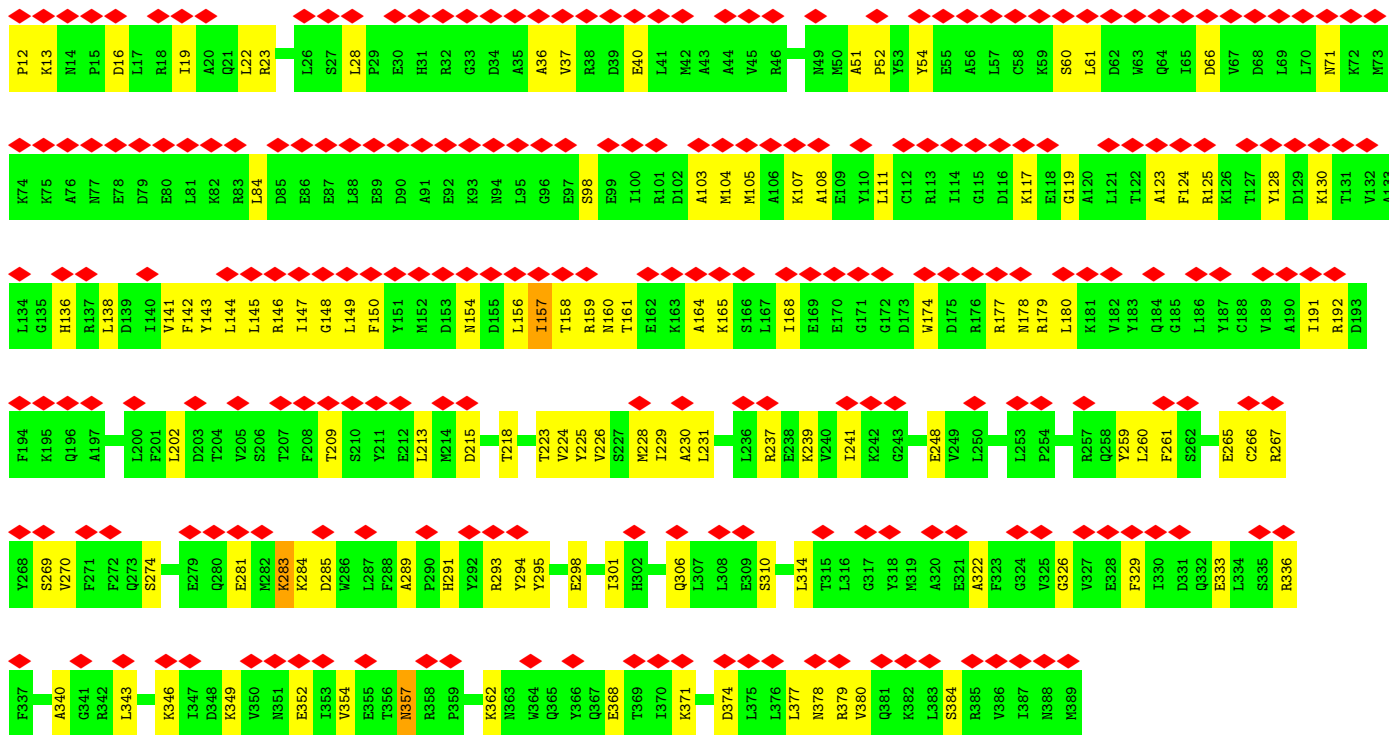


• Molecule 17: 26S proteasome non-ATPase regulatory subunit 12

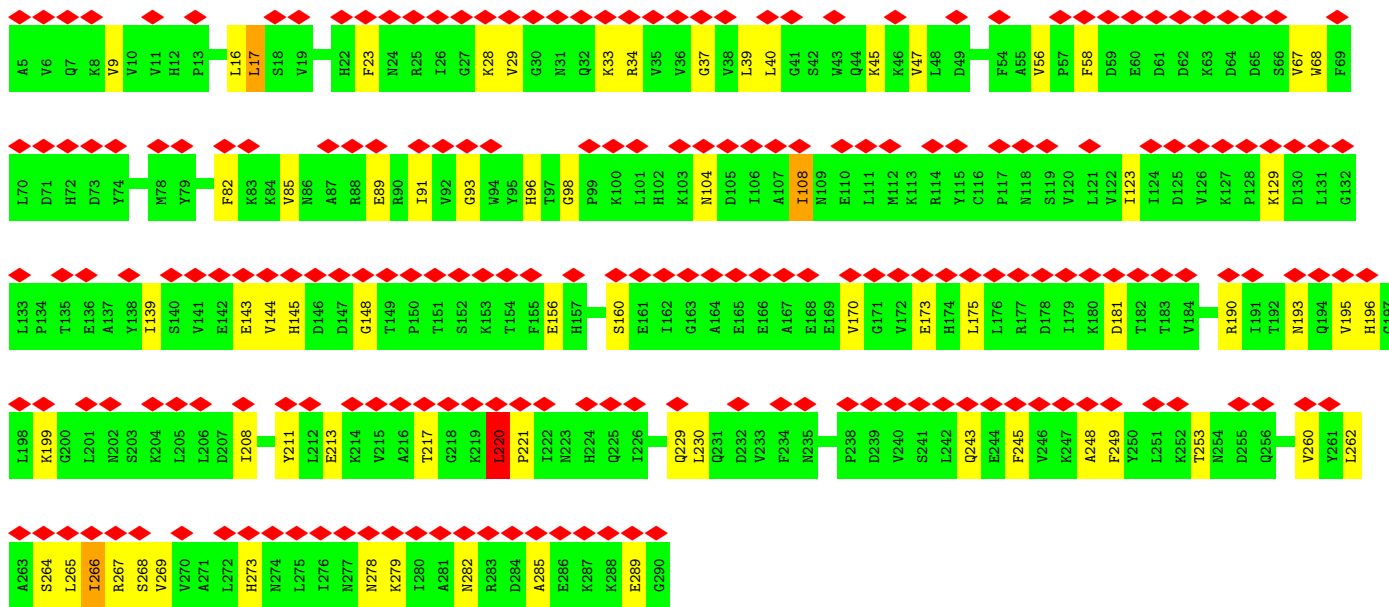
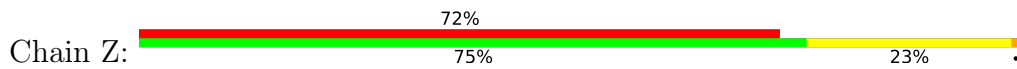


• Molecule 18: 26S proteasome non-ATPase regulatory subunit 6

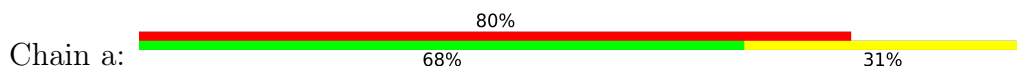


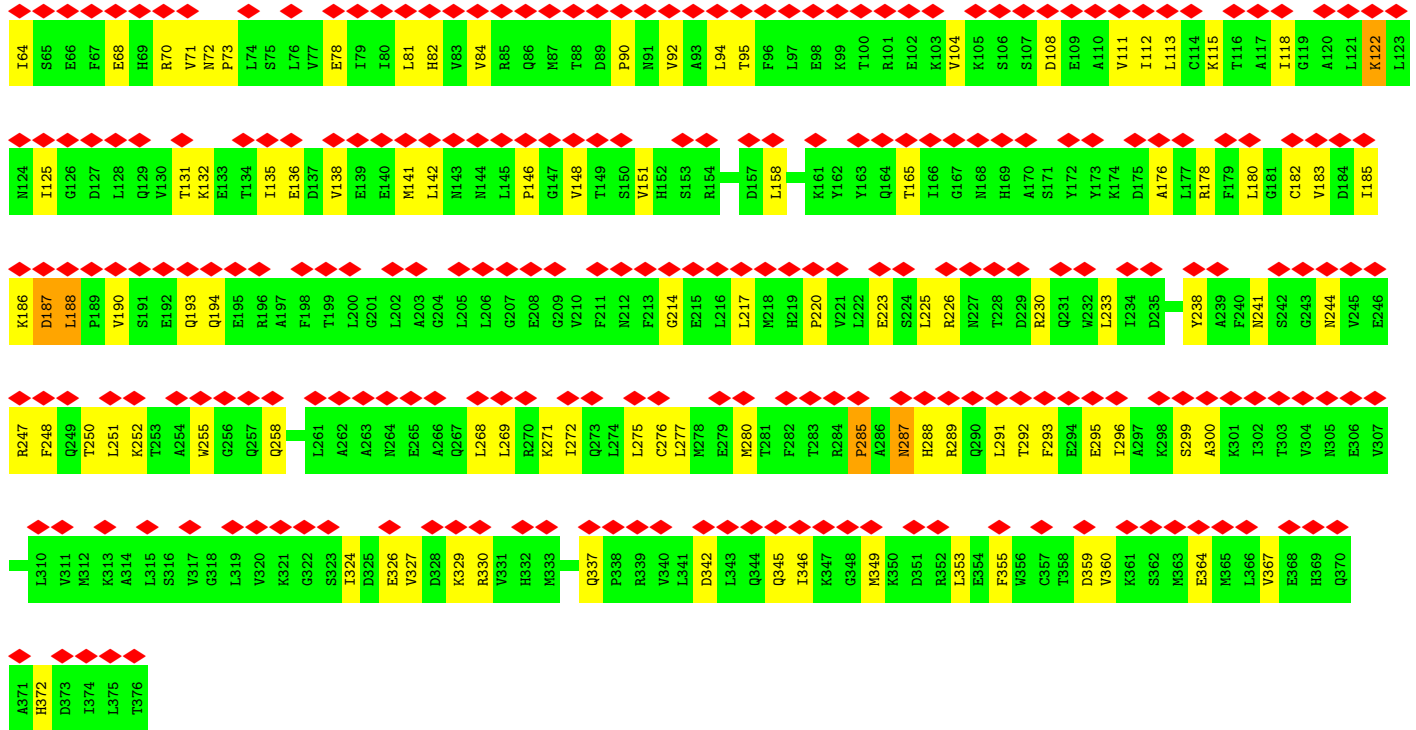


• Molecule 19: 26S proteasome non-ATPase regulatory subunit 7

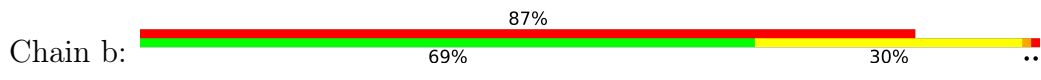


• Molecule 20: 26S proteasome non-ATPase regulatory subunit 13

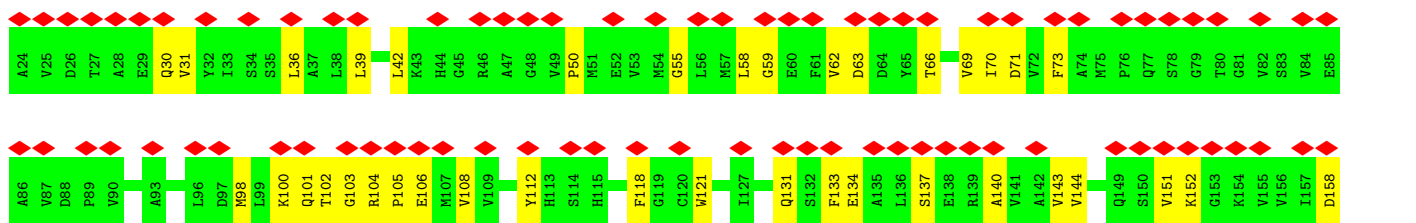


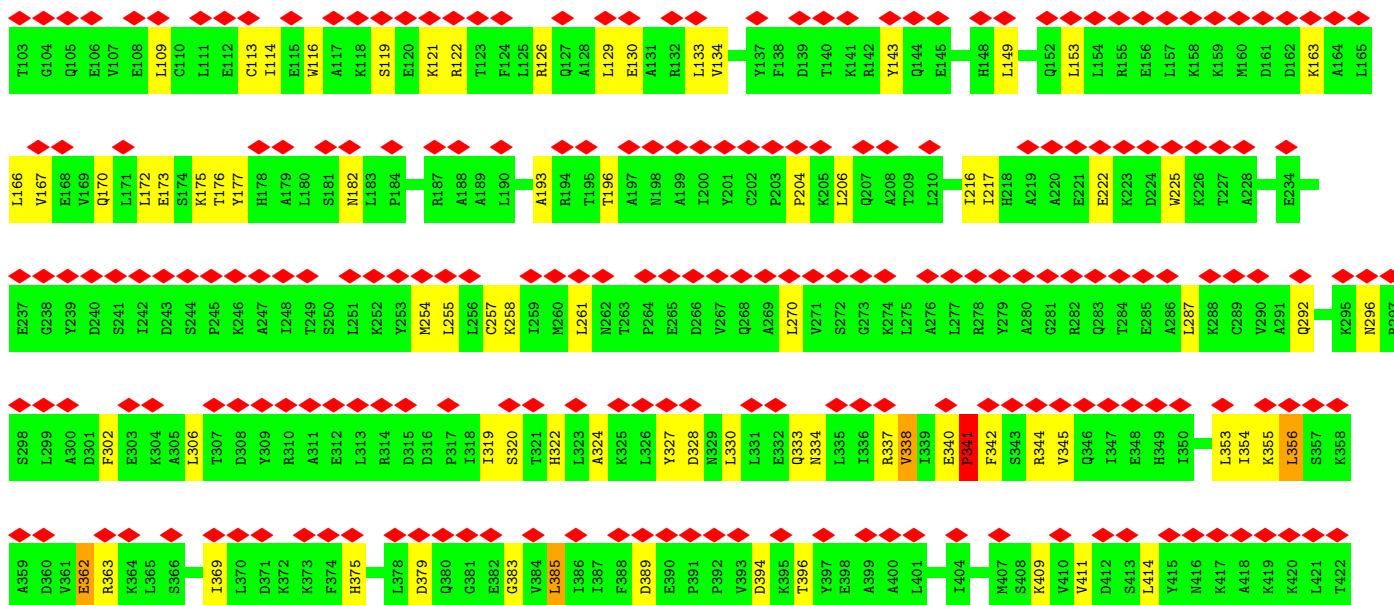


• Molecule 21: 26S proteasome non-ATPase regulatory subunit 4

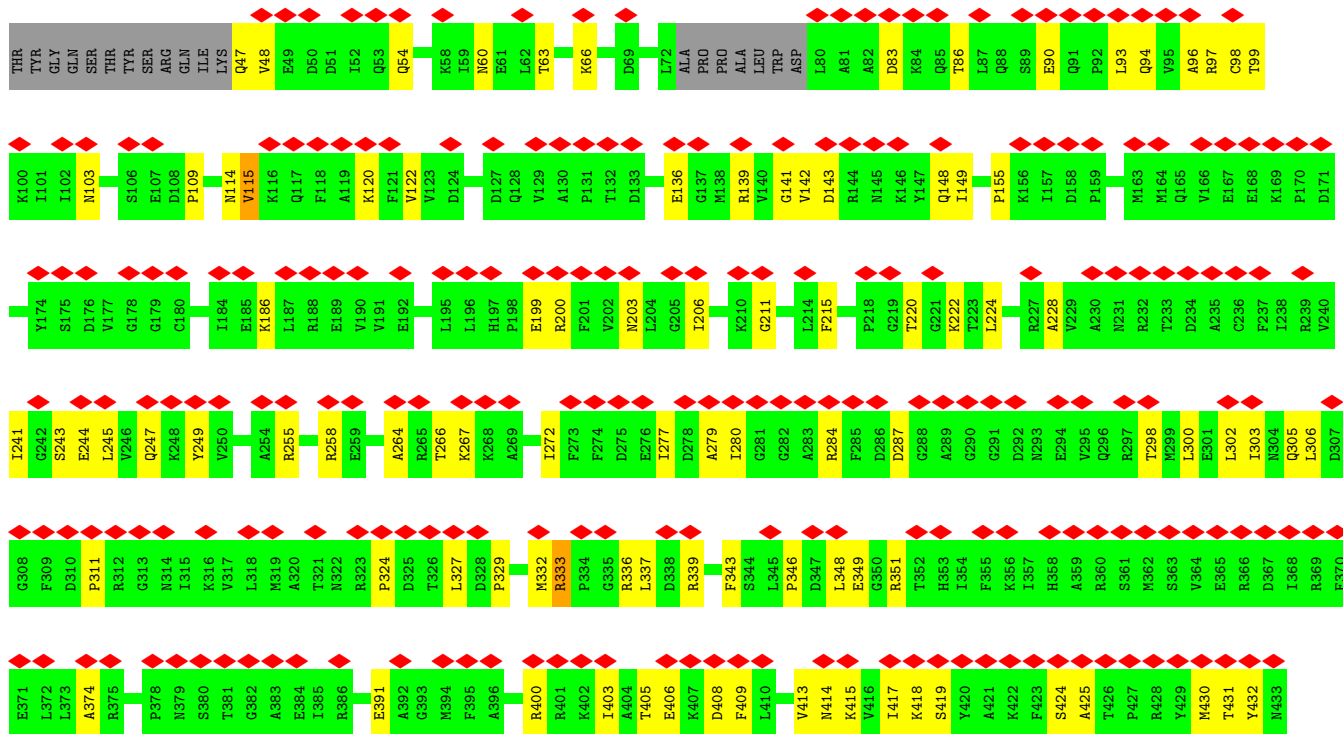


• Molecule 22: 26S proteasome non-ATPase regulatory subunit 14

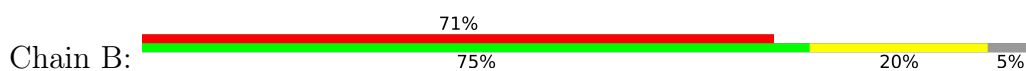


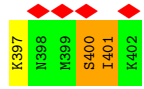


• Molecule 26: 26S proteasome regulatory subunit 7

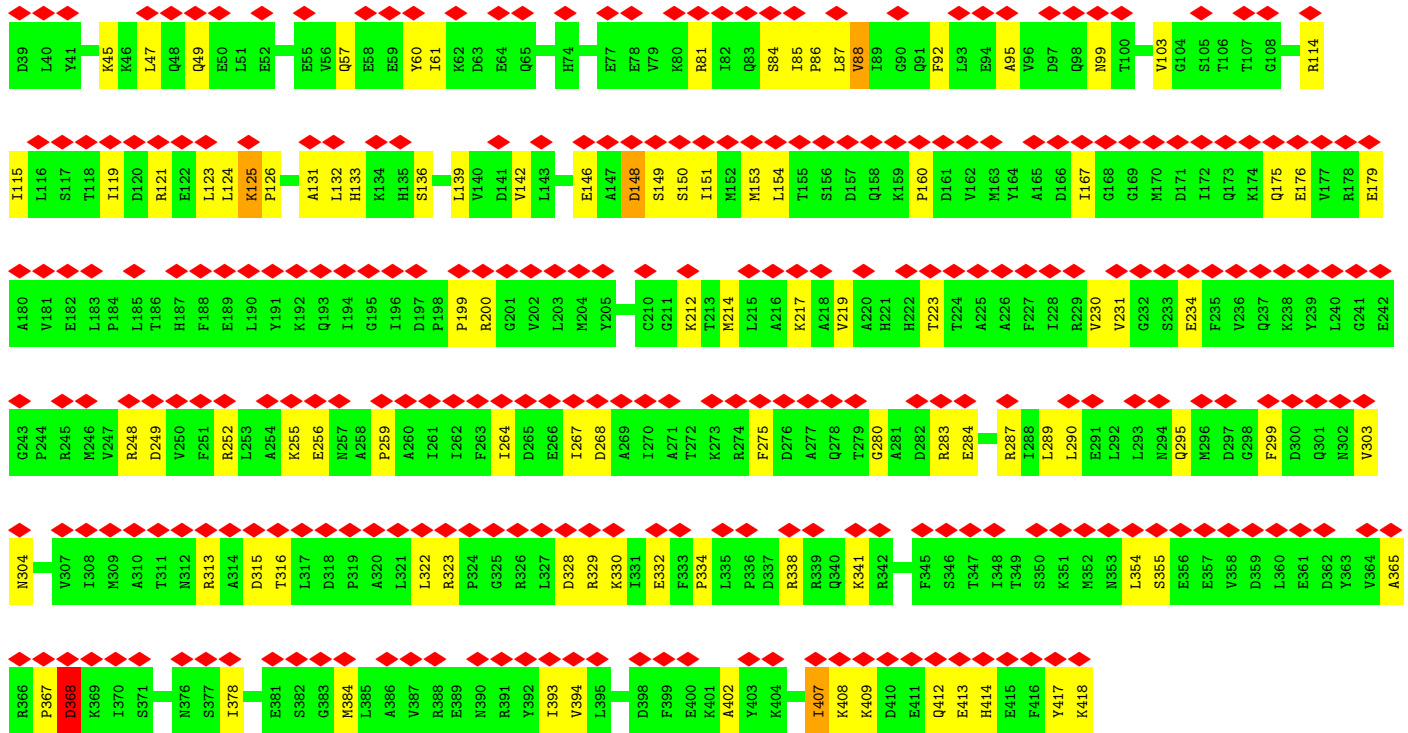
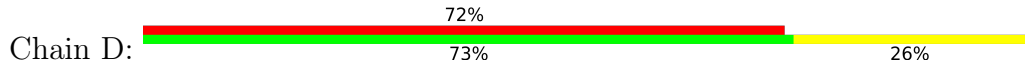


• Molecule 27: 26S proteasome regulatory subunit 4

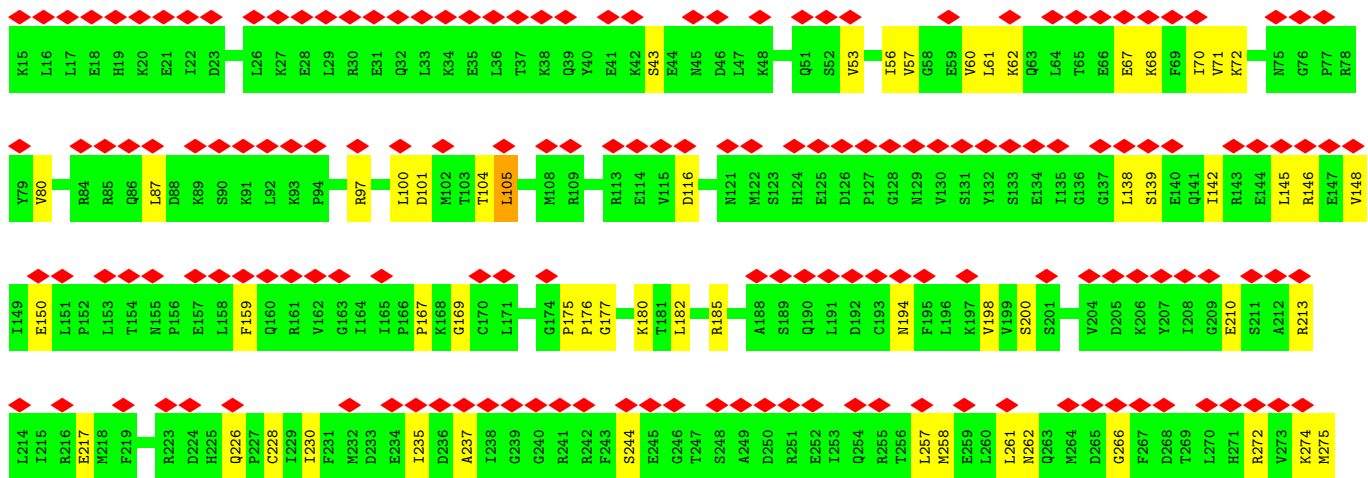
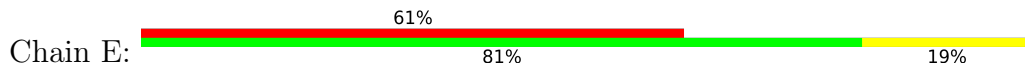


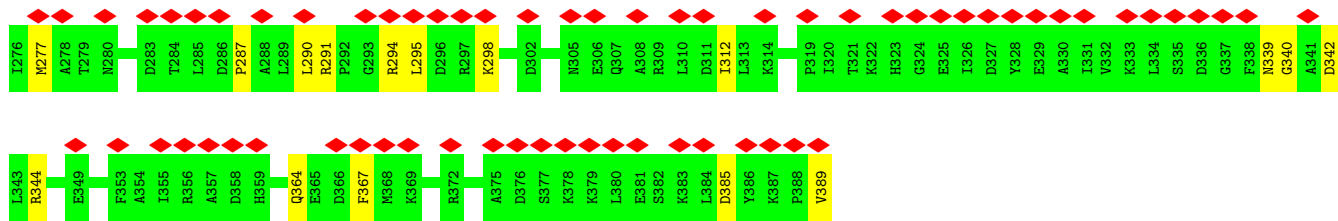


• Molecule 29: 26S proteasome regulatory subunit 6B

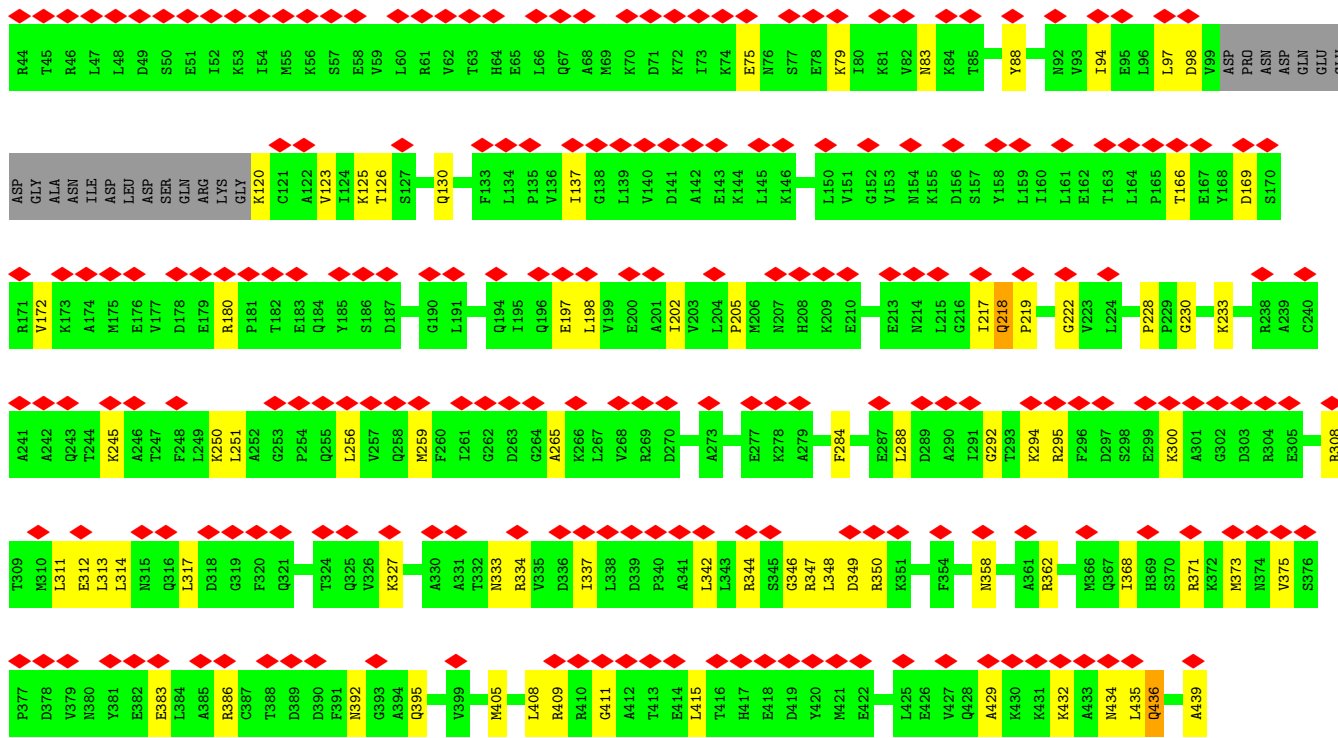
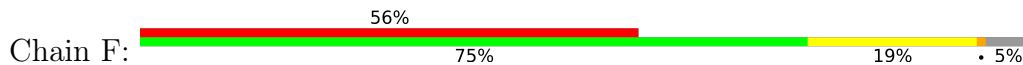


• Molecule 30: 26S proteasome regulatory subunit 10B

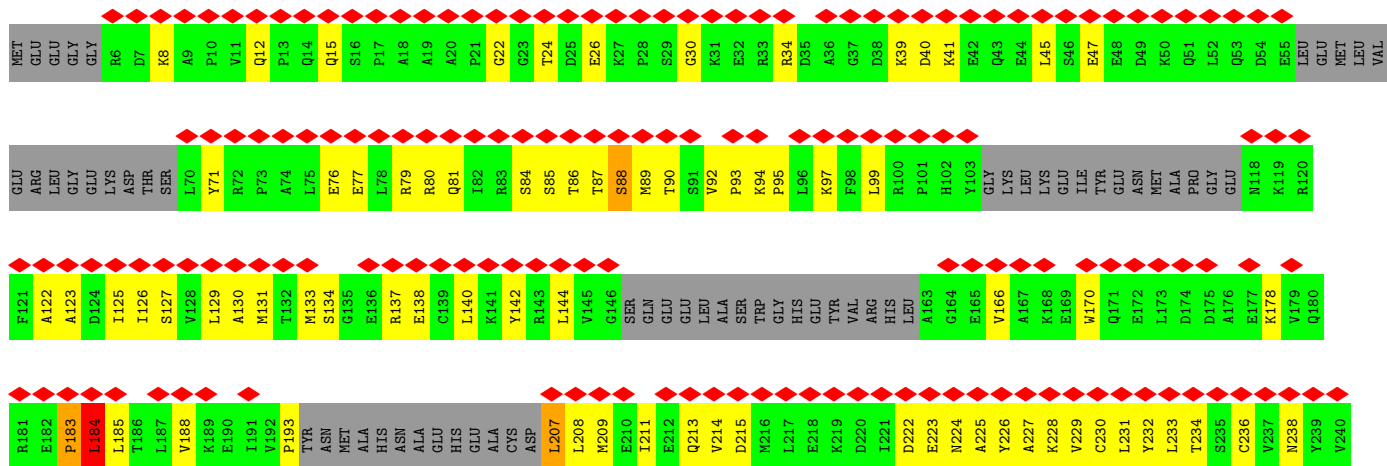
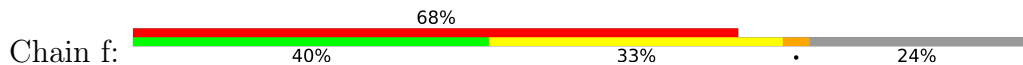




• Molecule 31: 26S proteasome regulatory subunit 6A



• Molecule 32: 26S proteasome non-ATPase regulatory subunit 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	66246	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	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	0.023	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (Å)	420.0, 420.0, 420.0	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.75, 0.75, 0.75	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AGS, 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	G	0.31	0/1853	0.65	0/2515
1	g	0.29	0/1859	0.61	0/2523
2	H	0.31	0/1723	0.63	3/2346 (0.1%)
2	h	0.26	0/1743	0.53	0/2372
3	I	0.32	0/1925	0.68	0/2606
3	i	0.30	0/1942	0.66	0/2628
4	J	0.32	0/1728	0.66	2/2358 (0.1%)
4	j	0.29	0/1728	0.60	0/2358
5	K	0.30	0/1755	0.72	4/2375 (0.2%)
5	k	0.29	0/1747	0.57	0/2364
6	L	0.32	0/1885	0.59	0/2552
6	l	0.30	0/1885	0.58	2/2552 (0.1%)
7	M	0.31	0/1891	0.63	2/2552 (0.1%)
7	m	0.29	0/1891	0.61	2/2552 (0.1%)
8	N	0.32	0/1454	0.57	0/1967
8	n	0.31	0/1454	0.61	2/1967 (0.1%)
9	O	0.30	0/1670	0.57	0/2265
9	o	0.31	0/1670	0.54	0/2265
10	P	0.29	0/1614	0.52	0/2177
10	p	0.29	0/1614	0.52	0/2177
11	Q	0.34	0/1603	0.62	0/2174
11	q	0.36	0/1603	0.64	0/2174
12	R	0.31	0/1579	0.50	0/2134
12	r	0.30	0/1579	0.49	0/2134
13	S	0.30	0/1671	0.52	2/2253 (0.1%)
13	s	0.31	0/1671	0.54	2/2253 (0.1%)
14	T	0.32	0/1700	0.56	0/2305
14	t	0.30	0/1700	0.56	2/2305 (0.1%)
15	U	0.29	0/6396	0.70	3/8646 (0.0%)
16	V	0.36	1/3883 (0.0%)	0.84	10/5247 (0.2%)
17	W	0.31	0/3751	0.80	3/5042 (0.1%)
18	Y	0.32	0/3173	0.76	0/4273

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	Z	0.32	0/2324	0.77	0/3150
20	a	0.30	0/3053	0.74	2/4133 (0.0%)
21	b	0.29	0/1478	0.75	5/2001 (0.2%)
22	c	0.32	0/2226	0.79	2/3007 (0.1%)
23	d	0.31	0/2162	0.83	4/2919 (0.1%)
24	e	0.35	0/338	0.94	0/450
25	X	0.29	0/3053	0.68	0/4115
26	A	0.30	0/2939	0.68	0/3970
27	B	0.28	0/2844	0.70	3/3846 (0.1%)
28	C	0.29	0/2896	0.73	6/3895 (0.2%)
29	D	0.33	0/3090	0.84	13/4168 (0.3%)
30	E	0.27	0/2904	0.62	0/3924
31	F	0.29	0/2897	0.75	9/3912 (0.2%)
32	f	0.33	1/5393 (0.0%)	0.87	19/7271 (0.3%)
All	All	0.31	2/102937 (0.0%)	0.69	102/139172 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	1
1	g	0	1
3	I	0	1
4	J	0	1
4	j	0	1
5	K	0	4
7	M	0	1
8	n	0	1
9	O	0	1
15	U	0	2
16	V	0	3
19	Z	0	2
20	a	0	2
21	b	0	1
23	d	0	2
25	X	0	2
26	A	0	1
28	C	0	2
29	D	0	6
All	All	0	35

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	V	358	MET	C-N	6.66	1.39	1.33
32	f	494	ARG	CA-C	5.23	1.59	1.52

The worst 5 of 102 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	D	368	ASP	CA-C-N	10.80	141.14	121.70
29	D	368	ASP	C-N-CA	10.80	141.14	121.70
32	f	488	ALA	N-CA-C	10.54	122.85	111.36
5	K	21	LEU	CA-C-N	9.27	138.39	121.70
5	K	21	LEU	C-N-CA	9.27	138.39	121.70

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	222	VAL	Peptide
3	I	6	ASP	Peptide
4	J	2	SER	Peptide
5	K	19	GLY	Peptide
5	K	9	ASP	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1820	0	1791	21	0
1	g	1826	0	1796	23	0
2	H	1688	0	1575	33	0
2	h	1708	0	1594	25	0
3	I	1895	0	1833	26	0
3	i	1912	0	1851	35	0
4	J	1704	0	1517	19	0
4	j	1704	0	1517	29	0
5	K	1729	0	1680	40	0
5	k	1722	0	1673	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	L	1850	0	1822	39	0
6	l	1850	0	1822	29	0
7	M	1856	0	1814	40	0
7	m	1856	0	1814	40	0
8	N	1430	0	1398	20	0
8	n	1430	0	1398	20	0
9	O	1643	0	1644	25	0
9	o	1643	0	1644	25	0
10	P	1585	0	1598	24	0
10	p	1585	0	1598	24	0
11	Q	1570	0	1547	33	0
11	q	1570	0	1547	28	0
12	R	1548	0	1499	20	0
12	r	1548	0	1499	23	0
13	S	1641	0	1618	17	0
13	s	1641	0	1618	18	0
14	T	1667	0	1628	22	0
14	t	1667	0	1628	27	0
15	U	6287	0	6338	164	0
16	V	3808	0	3855	119	0
17	W	3703	0	3822	116	0
18	Y	3115	0	3120	89	0
19	Z	2281	0	2312	53	0
20	a	2995	0	3012	95	0
21	b	1458	0	1505	39	0
22	c	2187	0	2214	56	0
23	d	2116	0	2146	53	0
24	e	334	0	294	17	0
25	X	3009	0	3113	54	0
26	A	2893	0	2843	75	0
27	B	2806	0	2770	47	0
28	C	2859	0	2971	45	0
29	D	3040	0	3076	58	0
30	E	2860	0	2828	53	0
31	F	2859	0	2853	50	0
32	f	5319	0	5329	469	0
33	c	1	0	0	0	0
34	A	31	0	12	3	0
34	D	31	0	12	3	0
34	E	31	0	12	16	0
34	F	31	0	12	4	0
All	All	101342	0	100412	2212	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 11.

The worst 5 of 2212 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)
30:E:340:GLY:HA3	34:E:401:AGS:N7	1.32	1.37
32:f:796:LEU:O	32:f:799:VAL:HG22	1.30	1.31
32:f:753:ALA:O	32:f:754:LYS:HE2	1.27	1.25
32:f:494:ARG:HD3	32:f:496:ASP:OD1	1.26	1.24
32:f:742:ALA:HA	32:f:745:LEU:CD2	1.66	1.23

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	G	237/240 (99%)	210 (89%)	27 (11%)	0	100	100
1	g	238/240 (99%)	218 (92%)	20 (8%)	0	100	100
2	H	228/232 (98%)	213 (93%)	15 (7%)	0	100	100
2	h	230/232 (99%)	226 (98%)	4 (2%)	0	100	100
3	I	246/250 (98%)	226 (92%)	19 (8%)	1 (0%)	30	66
3	i	248/250 (99%)	227 (92%)	20 (8%)	1 (0%)	30	66
4	J	237/243 (98%)	218 (92%)	19 (8%)	0	100	100
4	j	237/243 (98%)	216 (91%)	20 (8%)	1 (0%)	30	66
5	K	224/234 (96%)	205 (92%)	18 (8%)	1 (0%)	30	66
5	k	224/234 (96%)	206 (92%)	18 (8%)	0	100	100
6	L	236/238 (99%)	225 (95%)	11 (5%)	0	100	100
6	l	236/238 (99%)	224 (95%)	12 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	M	238/245 (97%)	221 (93%)	17 (7%)	0	100	100
7	m	238/245 (97%)	222 (93%)	16 (7%)	0	100	100
8	N	189/191 (99%)	180 (95%)	8 (4%)	1 (0%)	24	62
8	n	189/191 (99%)	178 (94%)	8 (4%)	3 (2%)	7	37
9	O	218/220 (99%)	207 (95%)	11 (5%)	0	100	100
9	o	218/220 (99%)	207 (95%)	11 (5%)	0	100	100
10	P	202/204 (99%)	193 (96%)	9 (4%)	0	100	100
10	p	202/204 (99%)	190 (94%)	12 (6%)	0	100	100
11	Q	197/199 (99%)	178 (90%)	19 (10%)	0	100	100
11	q	197/199 (99%)	177 (90%)	20 (10%)	0	100	100
12	R	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
12	r	199/201 (99%)	189 (95%)	10 (5%)	0	100	100
13	S	211/213 (99%)	205 (97%)	6 (3%)	0	100	100
13	s	211/213 (99%)	204 (97%)	7 (3%)	0	100	100
14	T	213/215 (99%)	206 (97%)	7 (3%)	0	100	100
14	t	213/215 (99%)	204 (96%)	9 (4%)	0	100	100
15	U	798/911 (88%)	721 (90%)	77 (10%)	0	100	100
16	V	471/480 (98%)	411 (87%)	55 (12%)	5 (1%)	11	45
17	W	454/456 (100%)	400 (88%)	51 (11%)	3 (1%)	18	54
18	Y	376/378 (100%)	325 (86%)	48 (13%)	3 (1%)	16	52
19	Z	284/286 (99%)	246 (87%)	35 (12%)	3 (1%)	11	45
20	a	371/373 (100%)	331 (89%)	39 (10%)	1 (0%)	36	71
21	b	189/191 (99%)	170 (90%)	17 (9%)	2 (1%)	11	45
22	c	274/287 (96%)	235 (86%)	38 (14%)	1 (0%)	30	66
23	d	255/257 (99%)	219 (86%)	35 (14%)	1 (0%)	30	66
24	e	36/70 (51%)	29 (81%)	7 (19%)	0	100	100
25	X	378/380 (100%)	341 (90%)	35 (9%)	2 (0%)	24	62
26	A	376/399 (94%)	327 (87%)	45 (12%)	4 (1%)	11	45
27	B	366/389 (94%)	322 (88%)	42 (12%)	2 (0%)	24	62
28	C	359/392 (92%)	320 (89%)	36 (10%)	3 (1%)	16	52
29	D	378/380 (100%)	323 (85%)	49 (13%)	6 (2%)	7	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	E	373/375 (100%)	340 (91%)	33 (9%)	0	100	100
31	F	372/396 (94%)	337 (91%)	33 (9%)	2 (0%)	24	62
32	f	669/908 (74%)	579 (86%)	82 (12%)	8 (1%)	10	42
All	All	12934/13558 (95%)	11738 (91%)	1142 (9%)	54 (0%)	31	66

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	V	78	HIS
16	V	262	SER
17	W	314	LEU
18	Y	283	LYS
18	Y	284	LYS

5.3.2 Protein sidechains [i](#)

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	G	192/205 (94%)	189 (98%)	3 (2%)	55	69
1	g	193/205 (94%)	191 (99%)	2 (1%)	68	75
2	H	162/190 (85%)	160 (99%)	2 (1%)	63	73
2	h	164/190 (86%)	164 (100%)	0	100	100
3	I	191/210 (91%)	190 (100%)	1 (0%)	81	81
3	i	193/210 (92%)	193 (100%)	0	100	100
4	J	152/207 (73%)	151 (99%)	1 (1%)	76	78
4	j	152/207 (73%)	151 (99%)	1 (1%)	76	78
5	K	187/196 (95%)	186 (100%)	1 (0%)	81	81
5	k	186/196 (95%)	186 (100%)	0	100	100
6	L	198/204 (97%)	198 (100%)	0	100	100
6	l	198/204 (97%)	198 (100%)	0	100	100
7	M	192/202 (95%)	192 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	m	192/202 (95%)	192 (100%)	0	100	100
8	N	148/148 (100%)	148 (100%)	0	100	100
8	n	148/148 (100%)	148 (100%)	0	100	100
9	O	177/181 (98%)	177 (100%)	0	100	100
9	o	177/181 (98%)	177 (100%)	0	100	100
10	P	172/173 (99%)	172 (100%)	0	100	100
10	p	172/173 (99%)	172 (100%)	0	100	100
11	Q	164/170 (96%)	164 (100%)	0	100	100
11	q	164/170 (96%)	161 (98%)	3 (2%)	51	66
12	R	153/156 (98%)	153 (100%)	0	100	100
12	r	153/156 (98%)	153 (100%)	0	100	100
13	S	174/178 (98%)	174 (100%)	0	100	100
13	s	174/178 (98%)	174 (100%)	0	100	100
14	T	175/178 (98%)	175 (100%)	0	100	100
14	t	175/178 (98%)	175 (100%)	0	100	100
15	U	685/779 (88%)	679 (99%)	6 (1%)	70	75
16	V	410/414 (99%)	405 (99%)	5 (1%)	63	73
17	W	416/416 (100%)	412 (99%)	4 (1%)	68	75
18	Y	334/334 (100%)	332 (99%)	2 (1%)	78	80
19	Z	257/257 (100%)	252 (98%)	5 (2%)	50	66
20	a	333/333 (100%)	331 (99%)	2 (1%)	78	80
21	b	167/167 (100%)	165 (99%)	2 (1%)	63	73
22	c	243/252 (96%)	241 (99%)	2 (1%)	73	77
23	d	231/231 (100%)	229 (99%)	2 (1%)	70	75
24	e	38/38 (100%)	38 (100%)	0	100	100
25	X	327/327 (100%)	321 (98%)	6 (2%)	51	66
26	A	298/343 (87%)	297 (100%)	1 (0%)	86	84
27	B	300/345 (87%)	300 (100%)	0	100	100
28	C	315/340 (93%)	312 (99%)	3 (1%)	68	75
29	D	333/333 (100%)	331 (99%)	2 (1%)	78	80
30	E	298/329 (91%)	293 (98%)	5 (2%)	53	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	F	296/340 (87%)	295 (100%)	1 (0%)	86	84
32	f	580/763 (76%)	564 (97%)	16 (3%)	38	59
All	All	10739/11537 (93%)	10661 (99%)	78 (1%)	73	78

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	E	105	LEU
32	f	403	LYS
30	E	257	LEU
32	f	337	LEU
32	f	641	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 151 such sidechains are listed below:

Mol	Chain	Res	Type
25	X	329	ASN
32	f	213	GLN
26	A	296	GLN
29	D	133	HIS
32	f	650	GLN

5.3.3 RNA [i](#)

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, 1 is monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	AGS	F	501	-	32,33,33	1.01	2 (6%)	45,52,52	1.24	2 (4%)
34	AGS	E	401	-	32,33,33	0.94	2 (6%)	45,52,52	0.90	2 (4%)
34	AGS	D	501	-	32,33,33	0.75	2 (6%)	45,52,52	1.11	3 (6%)
34	AGS	A	501	-	32,33,33	0.78	2 (6%)	45,52,52	0.98	2 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	AGS	F	501	-	-	6/21/38/38	0/3/3/3
34	AGS	E	401	-	-	6/21/38/38	0/3/3/3
34	AGS	D	501	-	-	8/21/38/38	0/3/3/3
34	AGS	A	501	-	-	5/21/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	E	401	AGS	PA-O3A	-3.47	1.55	1.59
34	F	501	AGS	PB-O3B	-3.28	1.56	1.59
34	F	501	AGS	PB-O3A	-3.16	1.56	1.59
34	D	501	AGS	PB-O3B	-2.88	1.56	1.59
34	E	401	AGS	PB-O3A	-2.33	1.57	1.59

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	F	501	AGS	PB-O3B-PG	-5.95	111.39	133.17
34	D	501	AGS	PB-O3B-PG	-5.72	112.25	133.17
34	A	501	AGS	PB-O3B-PG	-4.36	117.21	133.17
34	E	401	AGS	PB-O3B-PG	-3.84	119.12	133.17
34	E	401	AGS	O3A-PA-O1A	-2.70	102.58	110.70

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

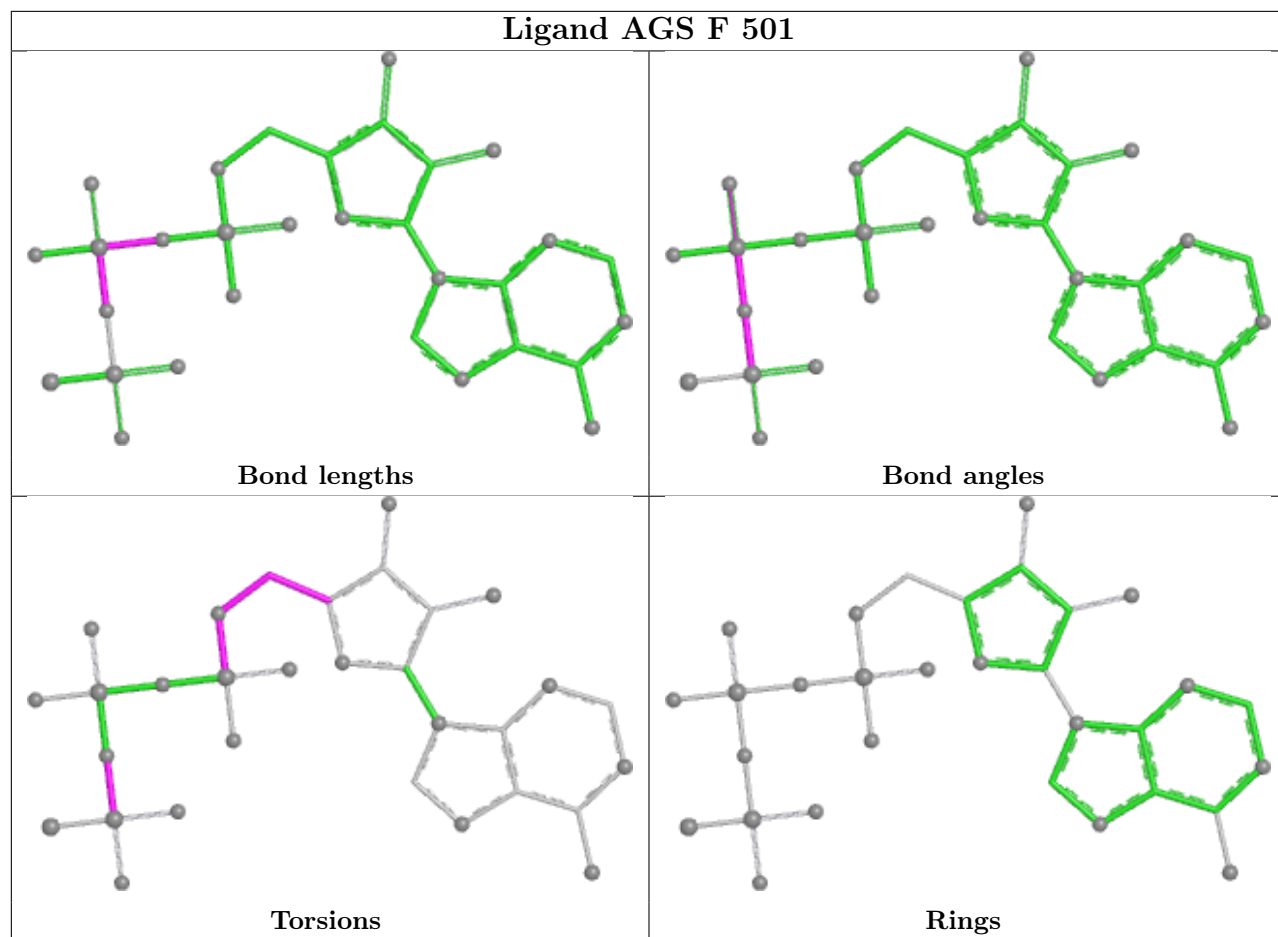
Mol	Chain	Res	Type	Atoms
34	A	501	AGS	C5'-O5'-PA-O1A
34	D	501	AGS	C5'-O5'-PA-O1A
34	D	501	AGS	C5'-O5'-PA-O3A
34	E	401	AGS	PB-O3B-PG-O2G
34	E	401	AGS	C5'-O5'-PA-O1A

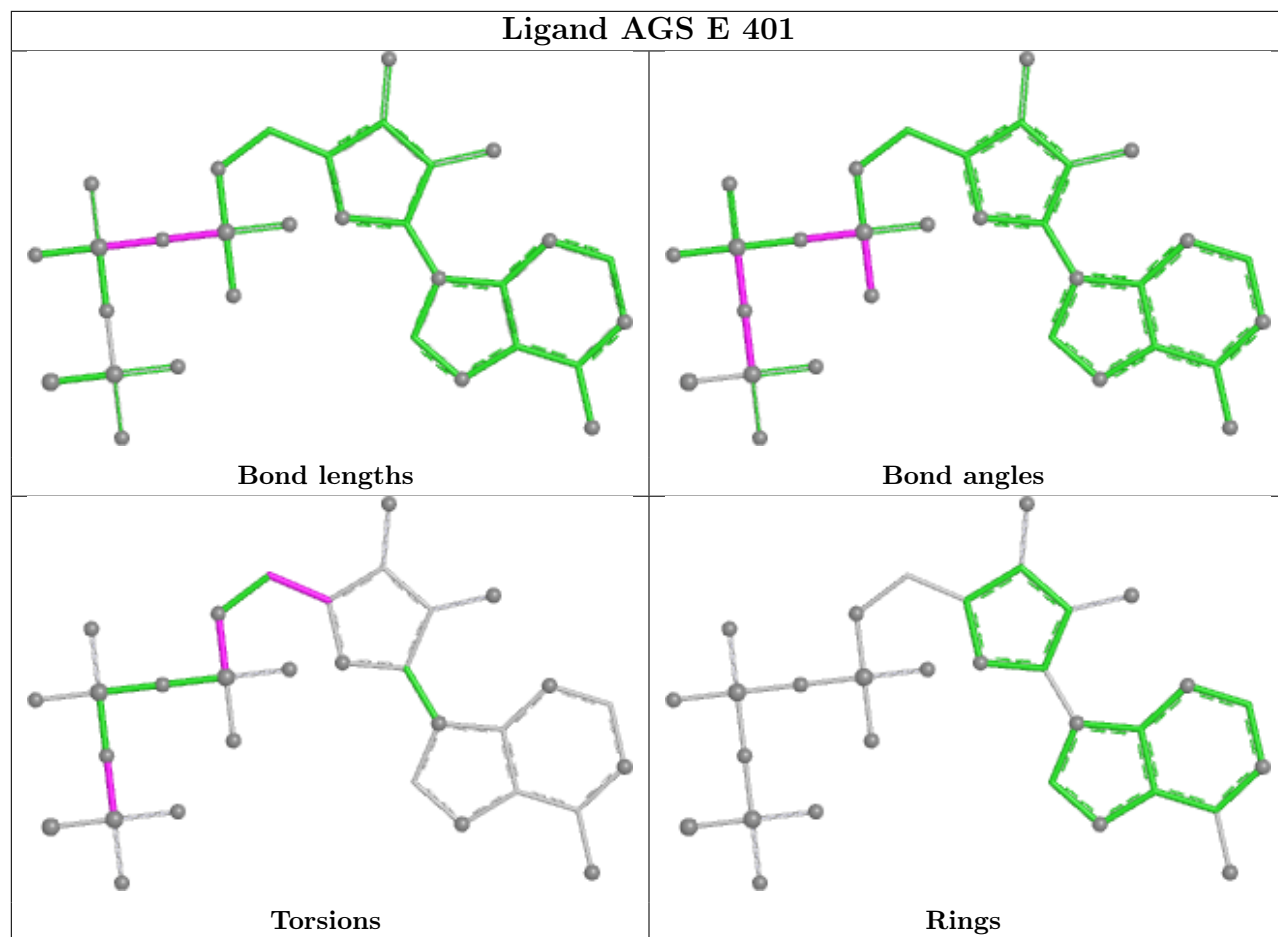
There are no ring outliers.

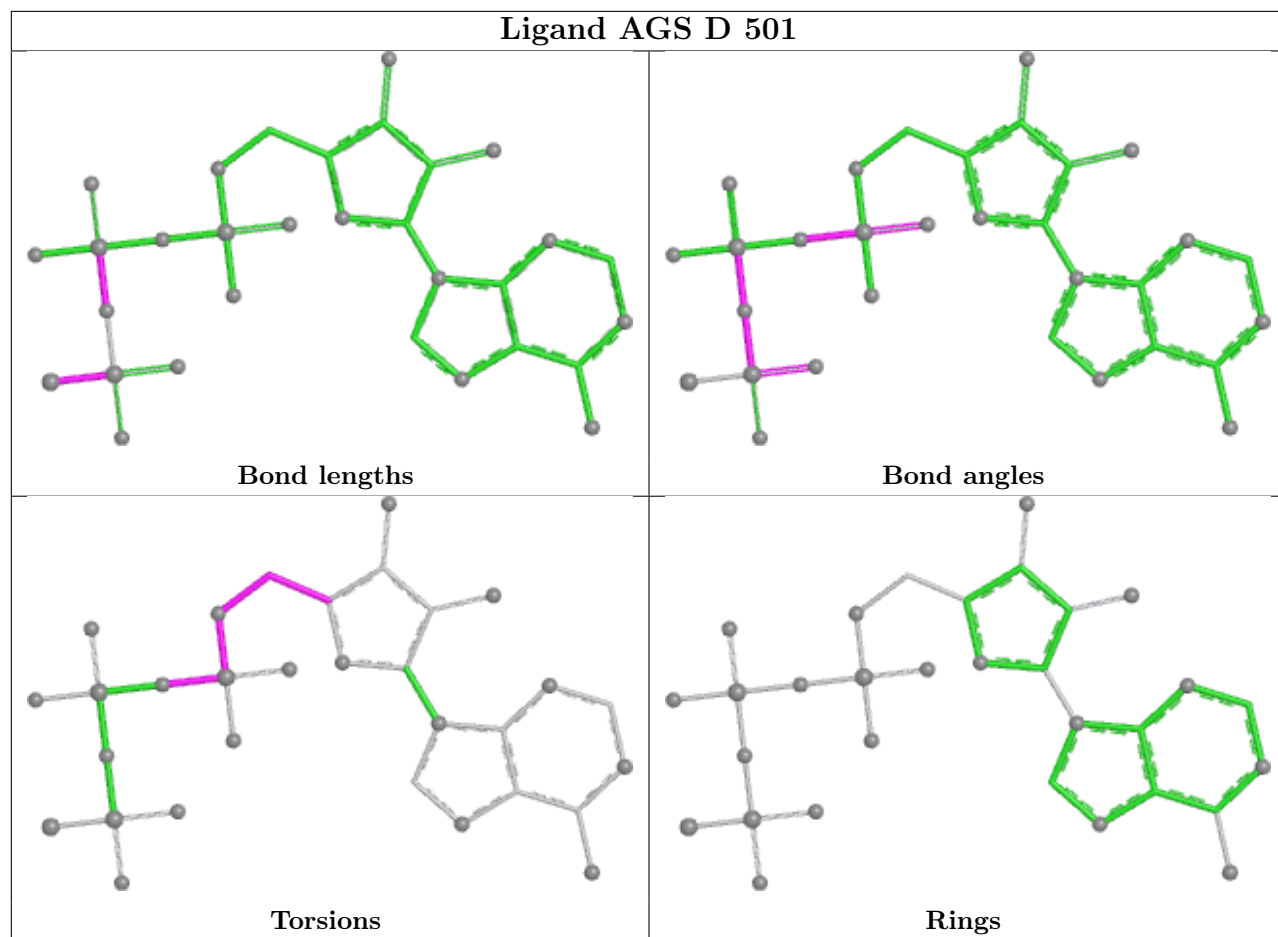
4 monomers are involved in 26 short contacts:

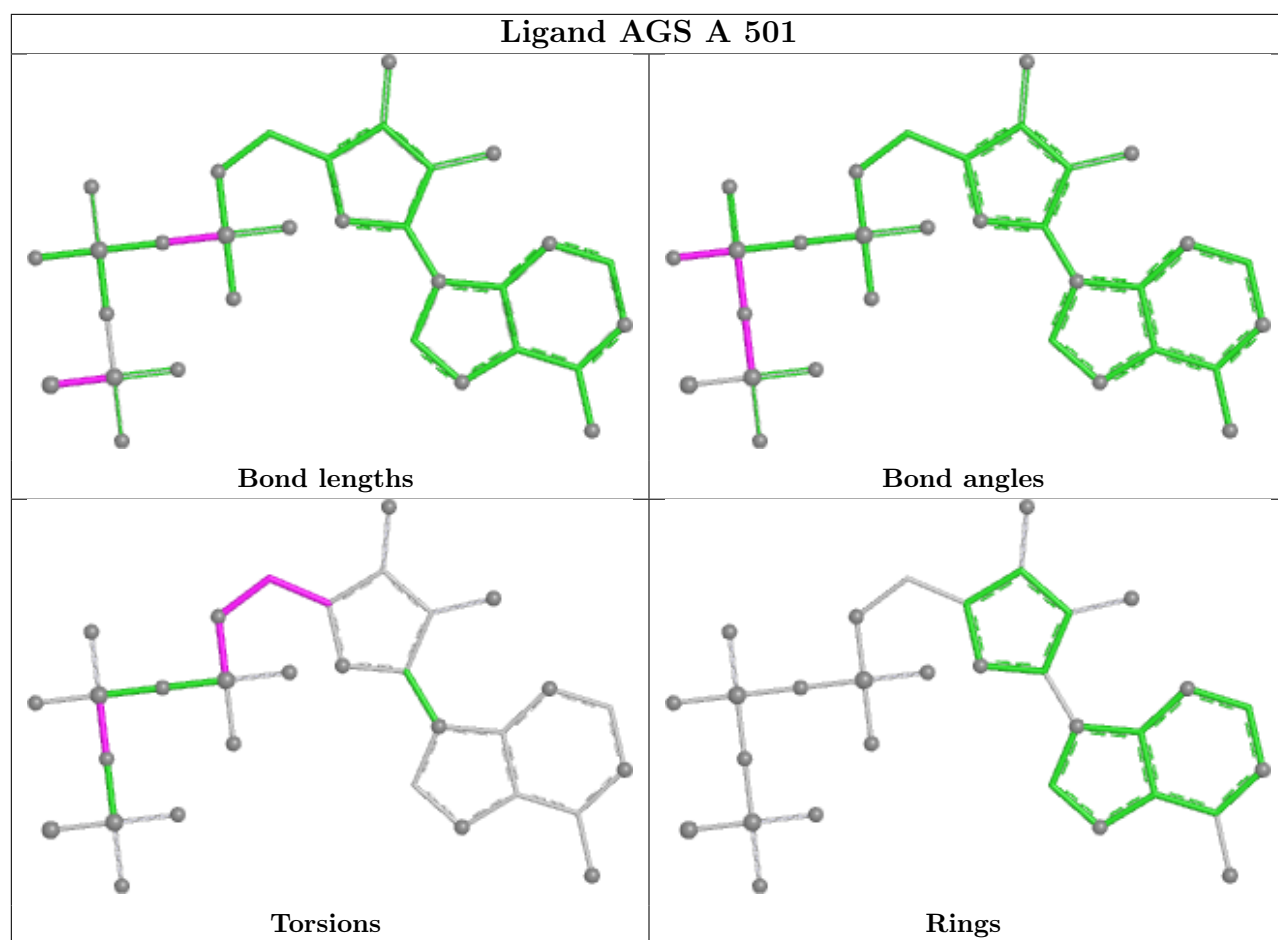
Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	F	501	AGS	4	0
34	E	401	AGS	16	0
34	D	501	AGS	3	0
34	A	501	AGS	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









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.

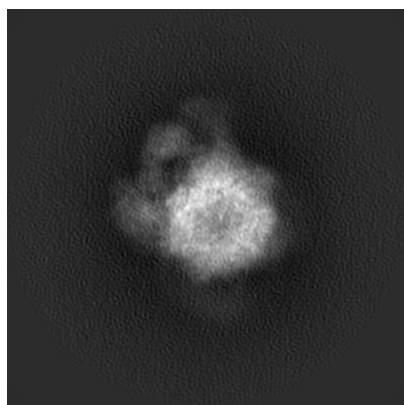
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8663. These allow visual inspection of the internal detail of the map and identification of artifacts.

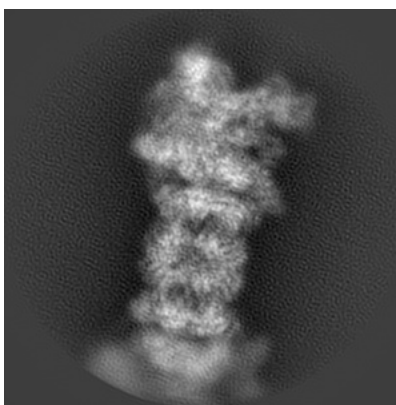
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

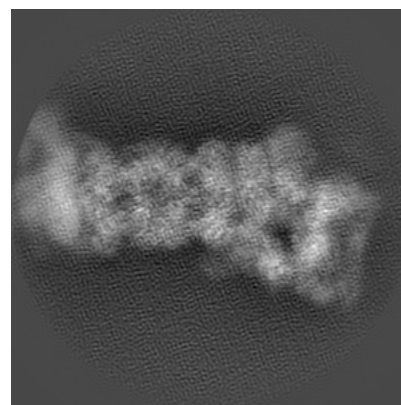
6.1.1 Primary map



X



Y

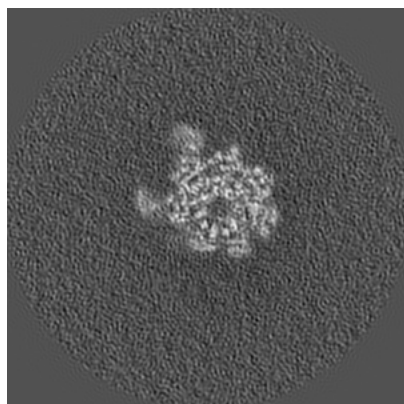


Z

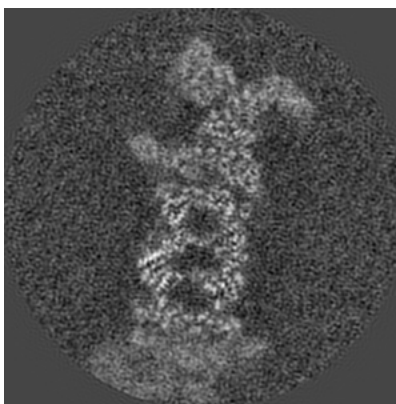
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

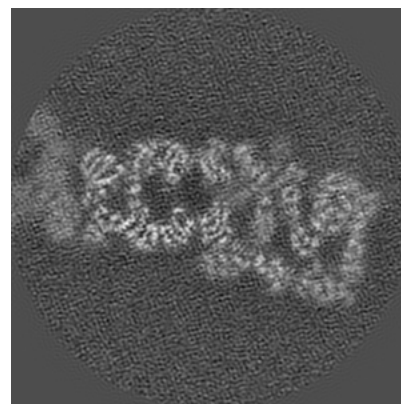
6.2.1 Primary map



X Index: 280



Y Index: 280

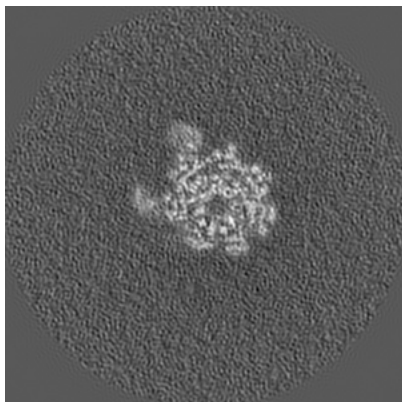


Z Index: 280

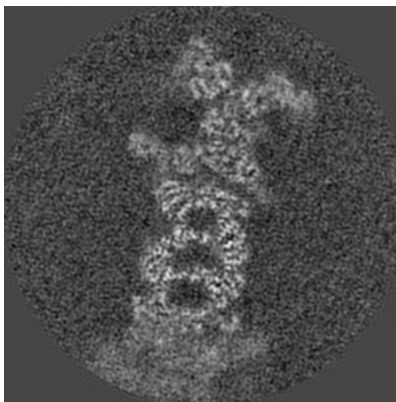
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

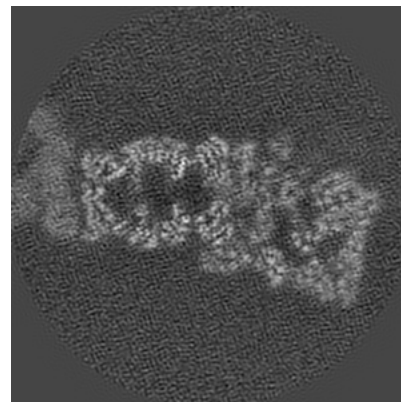
6.3.1 Primary map



X Index: 281



Y Index: 277

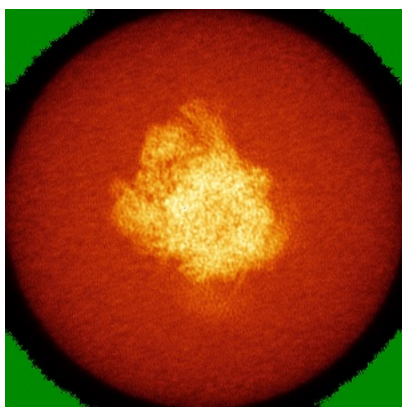


Z Index: 275

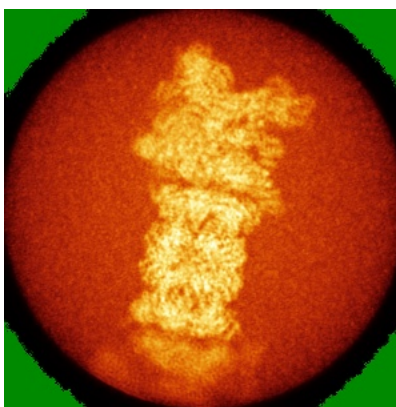
The images above show the largest variance slices of the map in three orthogonal directions.

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

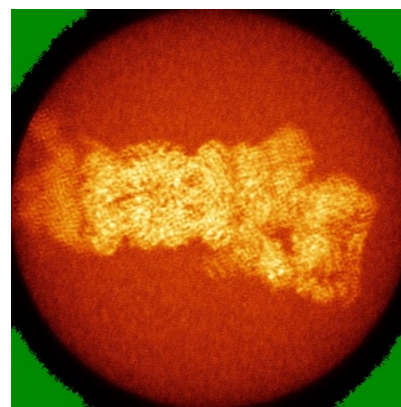
6.4.1 Primary map



X



Y

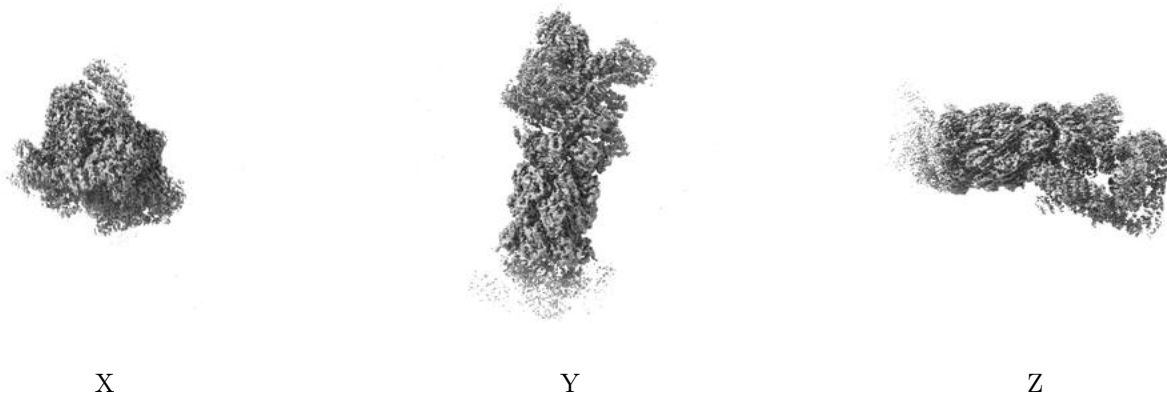


Z

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

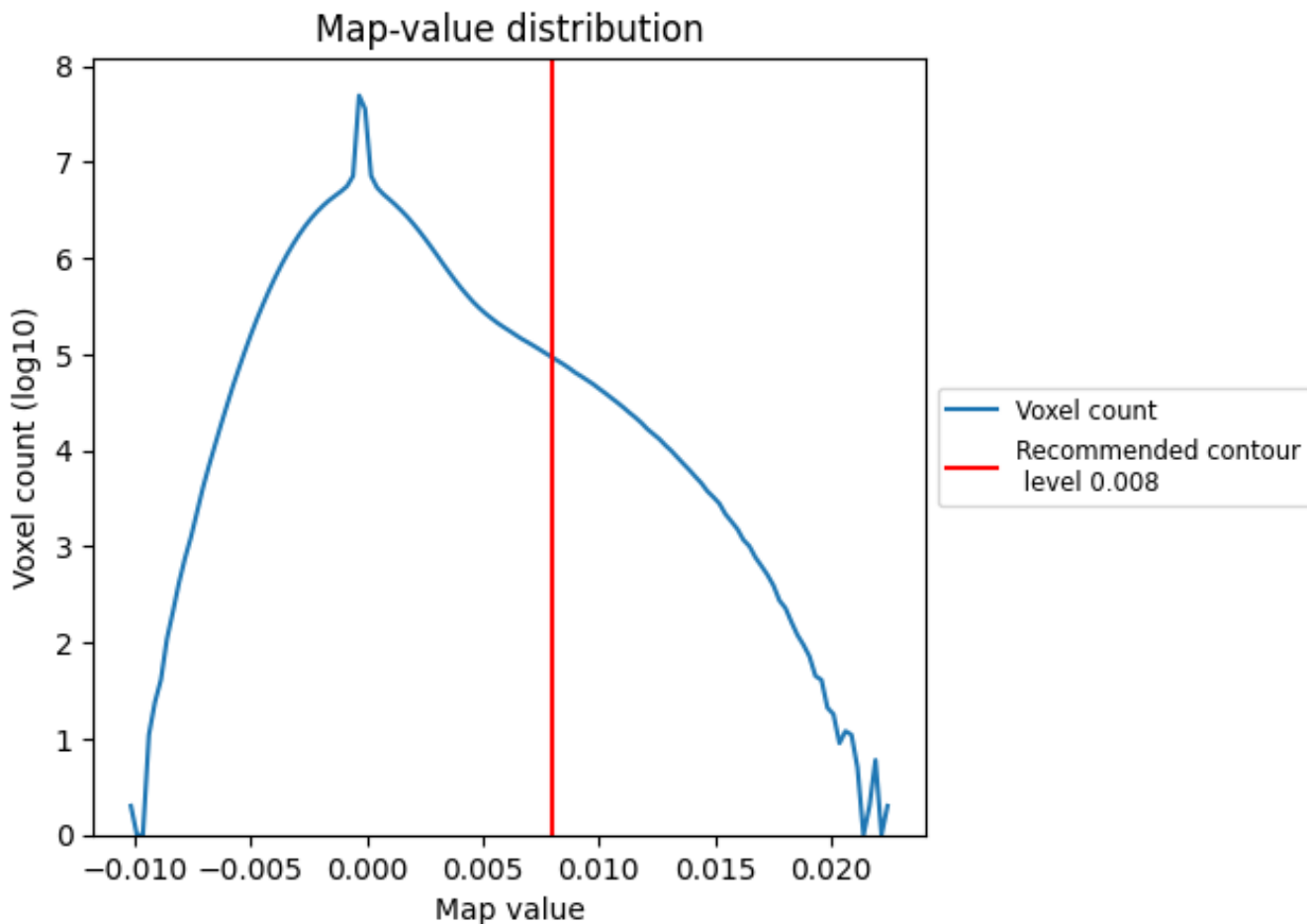
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

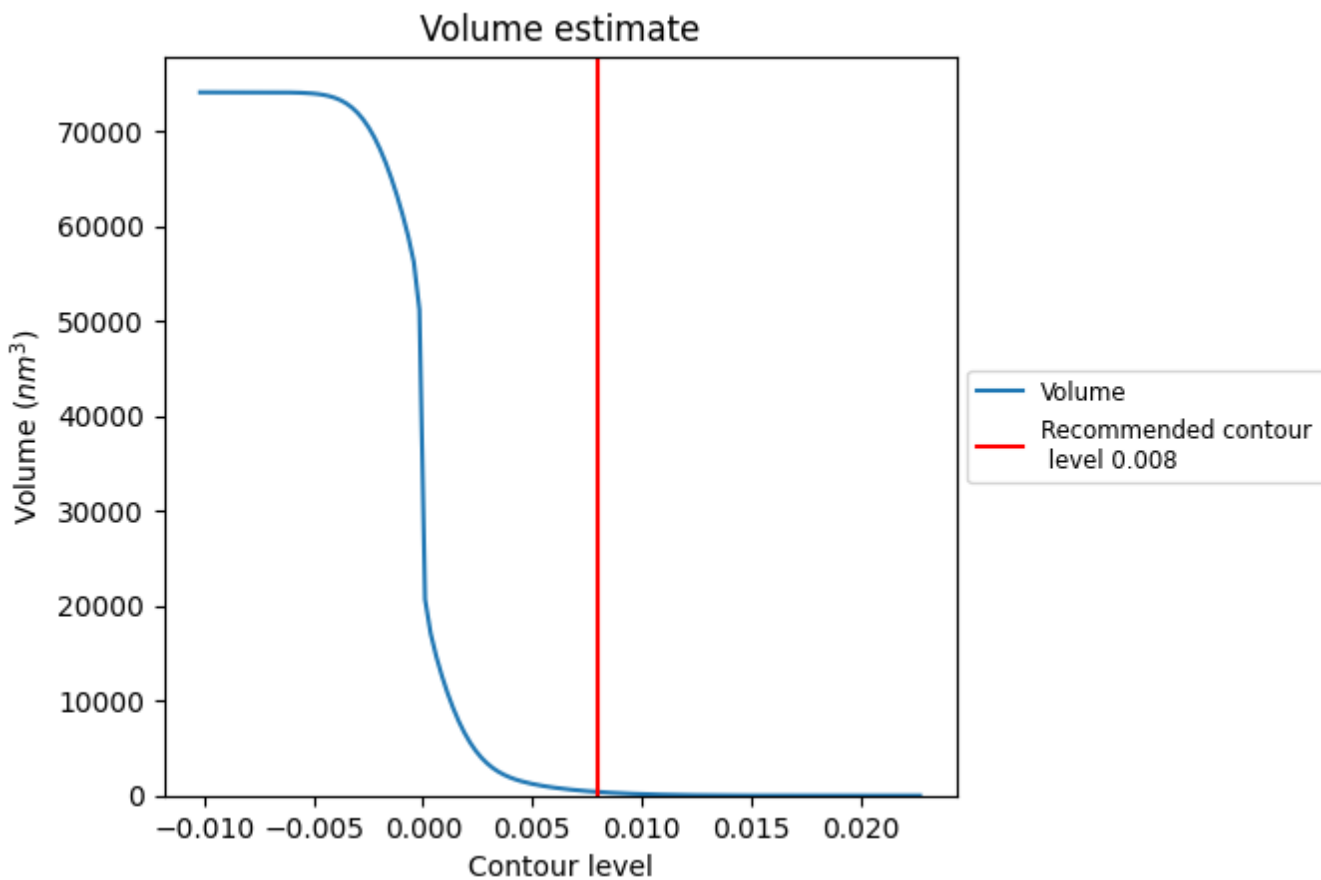
This section contains the results of statistical analysis of the map.

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.

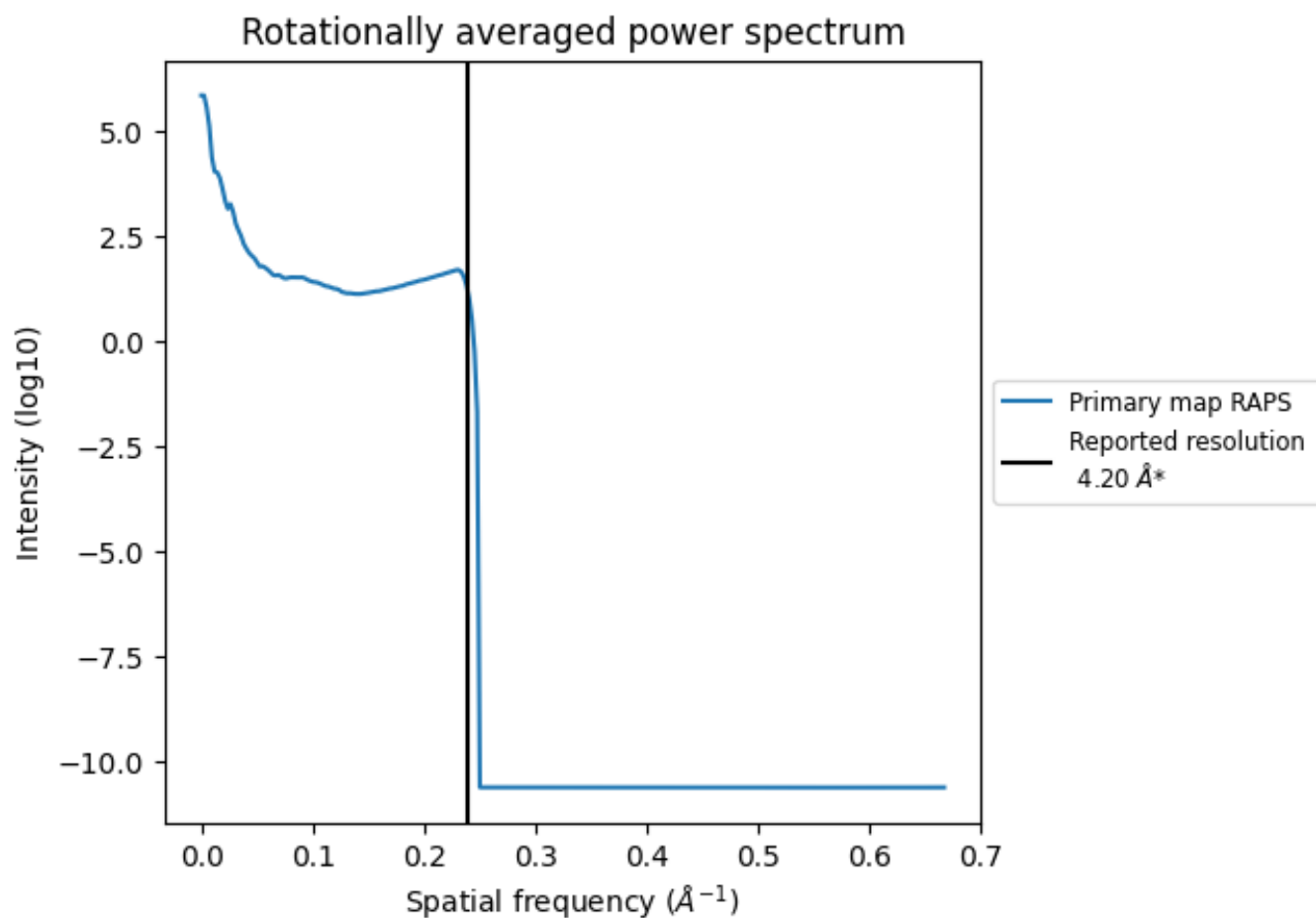
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 381 nm³; this corresponds to an approximate mass of 344 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

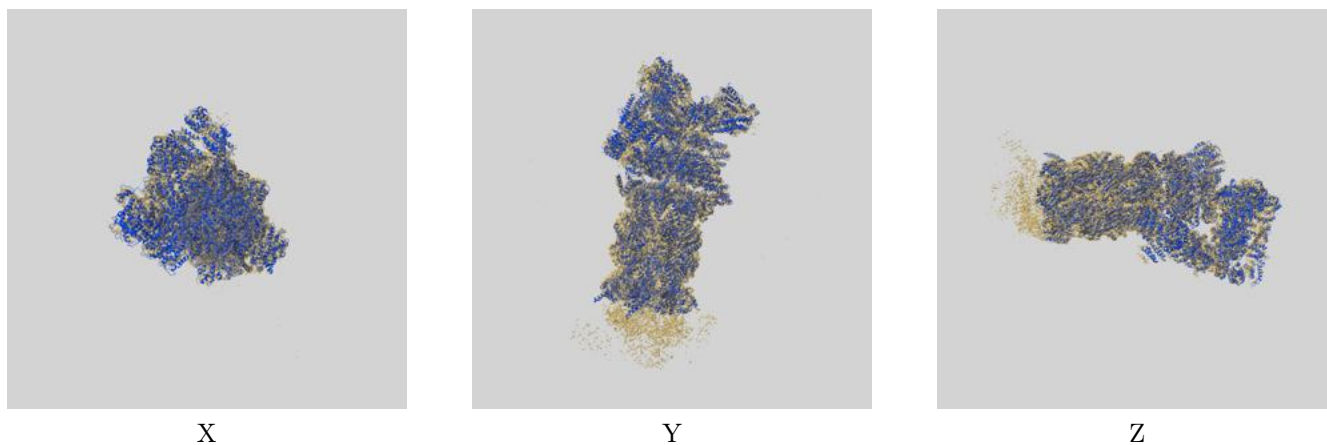
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

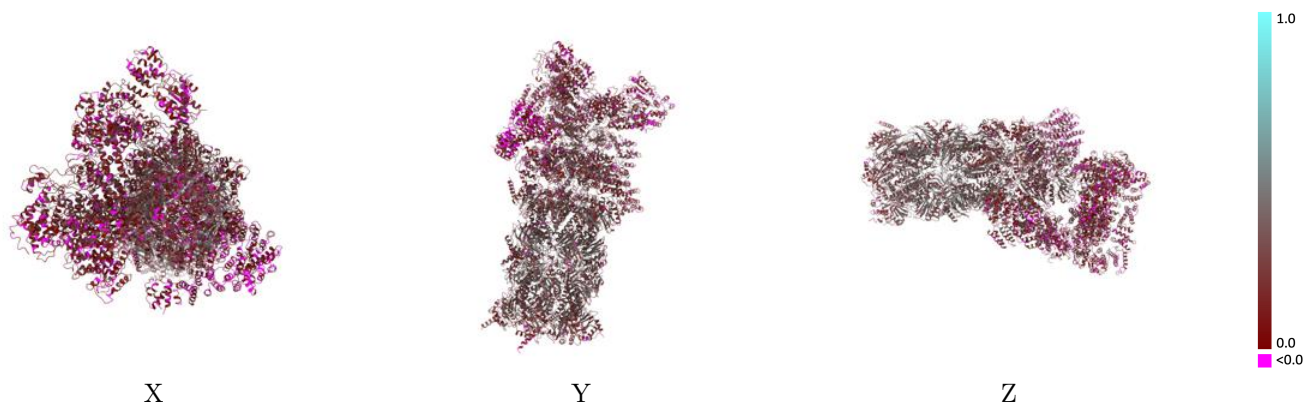
This section contains information regarding the fit between EMDB map EMD-8663 and PDB model 5VFP. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



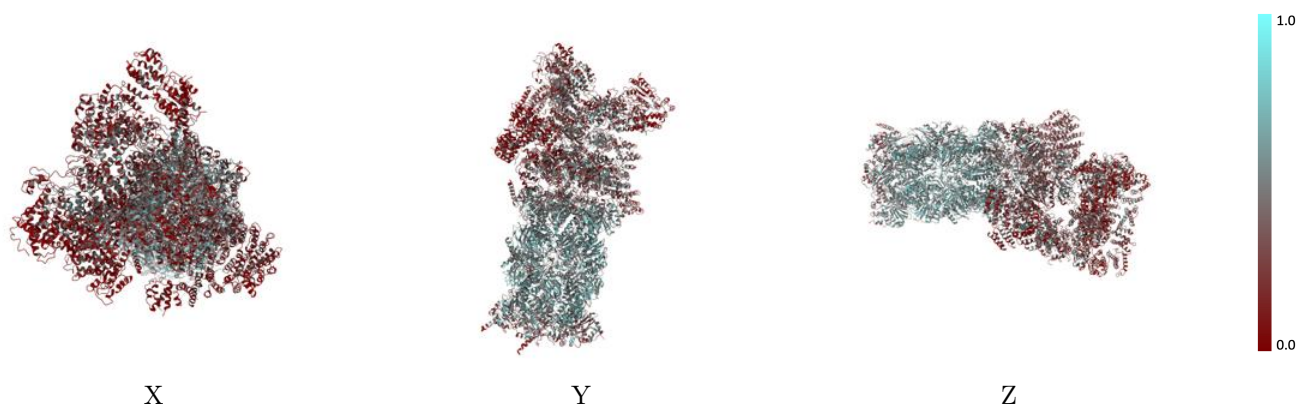
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



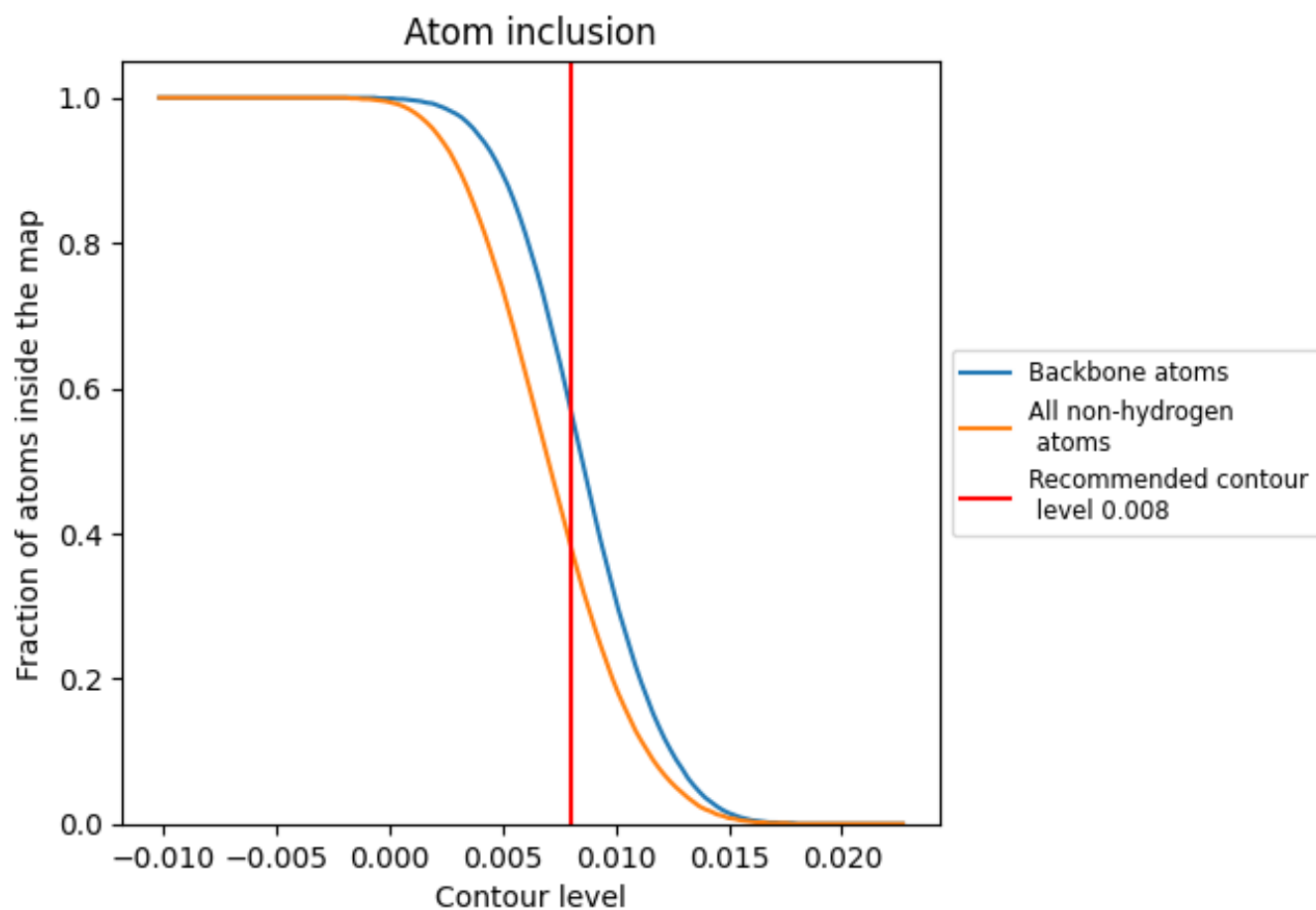
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 57% of all backbone atoms, 38% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3840	 0.2500
A	 0.3480	 0.2590
B	 0.2810	 0.2520
C	 0.2830	 0.2300
D	 0.2940	 0.2570
E	 0.3560	 0.2650
F	 0.3600	 0.2590
G	 0.5150	 0.3320
H	 0.5350	 0.3240
I	 0.4580	 0.2840
J	 0.4330	 0.2700
K	 0.4490	 0.2760
L	 0.5040	 0.3020
M	 0.5070	 0.3020
N	 0.6130	 0.3610
O	 0.5520	 0.3400
P	 0.5710	 0.3530
Q	 0.5420	 0.3170
R	 0.5980	 0.3540
S	 0.5440	 0.3410
T	 0.5950	 0.3570
U	 0.3000	 0.1860
V	 0.2060	 0.1670
W	 0.2570	 0.1650
X	 0.2740	 0.2240
Y	 0.3160	 0.1800
Z	 0.2810	 0.1930
a	 0.2280	 0.1600
b	 0.1570	 0.1470
c	 0.3050	 0.1920
d	 0.1330	 0.1380
e	 0.1790	 0.1800
f	 0.1530	 0.0730
g	 0.4370	 0.2810
h	 0.4470	 0.2890



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Chain	Atom inclusion	Q-score
i	 0.4190	 0.2660
j	 0.4480	 0.2800
k	 0.4550	 0.2810
l	 0.5090	 0.2900
m	 0.4570	 0.2710
n	 0.6040	 0.3600
o	 0.5340	 0.3320
p	 0.5670	 0.3490
q	 0.5730	 0.3350
r	 0.6060	 0.3570
s	 0.5740	 0.3460
t	 0.6140	 0.3510