



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 04:59 AM UTC

PDB ID : 5GJQ / pdb_00005gjQ
EMDB ID : EMD-9511
Title : Structure of the human 26S proteasome bound to USP14-UbA1
Authors : Huang, X.L.; Luan, B.; Wu, J.P.; Shi, Y.G.
Deposited on : 2016-07-01
Resolution : 4.35 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:

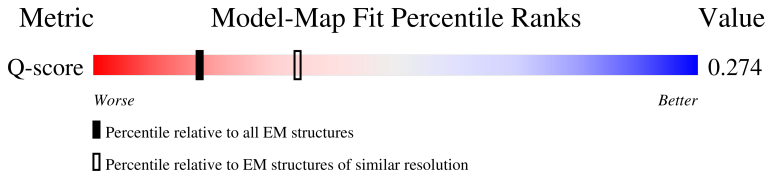
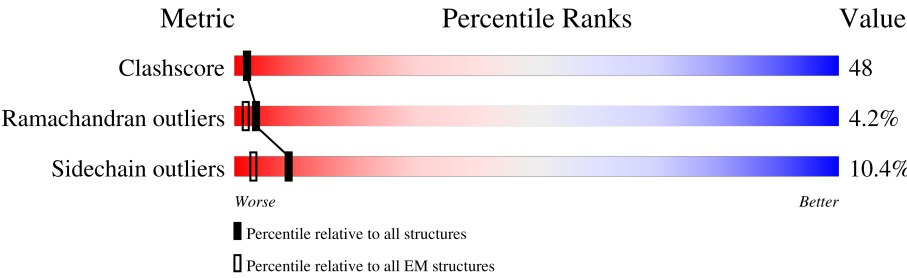
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 4.35 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.



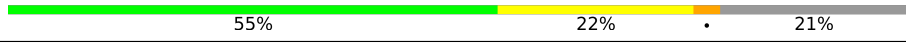
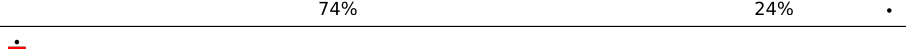
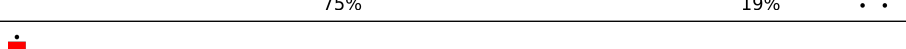
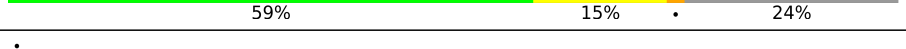
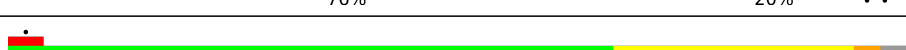
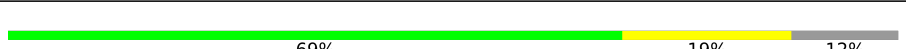
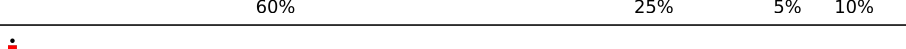
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3796 (3.85 - 4.85)

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	a	239	
1	o	239	
2	B	246	
2	h	246	

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Mol	Chain	Length	Quality of chain
3	b	277	
3	p	277	
4	C	234	
4	i	234	
5	c	205	
5	q	205	
6	D	261	
6	j	261	
7	d	201	
7	r	201	
8	E	248	
8	k	248	
9	e	263	
9	s	263	
10	F	241	
10	l	241	
11	f	241	
11	t	241	
12	G	263	
12	m	263	
13	g	264	
13	u	264	
14	H	433	
15	I	440	
16	J	406	

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Mol	Chain	Length	Quality of chain
17	K	418	
18	L	389	
19	M	439	
20	N	953	
21	X	255	
21	n	255	
22	O	376	
23	P	456	
24	Q	422	
25	R	389	
26	S	534	
27	T	350	
28	U	324	
29	V	310	
30	W	377	
31	Y	70	
32	Z	908	
33	x	494	
34	y	76	

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
35	ADP	H	501	-	-	X	-
35	ADP	K	501	-	-	X	-

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 98461 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	202	Total	C	N	O	S	0	0
			1509	945	258	294	12		
1	o	202	Total	C	N	O	S	0	0
			1509	945	258	294	12		

- Molecule 2 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	244	Total	C	N	O	S	0	0
			1845	1171	309	352	13		
2	h	244	Total	C	N	O	S	0	0
			1853	1177	311	352	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	220	Total	C	N	O	S	0	0
			1643	1033	280	318	12		
3	p	220	Total	C	N	O	S	0	0
			1643	1033	280	318	12		

- Molecule 4 is a protein called Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	233	Total	C	N	O	S	0	0
			1707	1081	287	334	5		
4	i	231	Total	C	N	O	S	0	0
			1744	1112	290	336	6		

- Molecule 5 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	204	Total	C	N	O	S	0	0
			1585	1010	262	294	19		
5	q	204	Total	C	N	O	S	0	0
			1585	1010	262	294	19		

- Molecule 6 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	250	Total	C	N	O	S	0	0
			1912	1204	329	371	8		
6	j	250	Total	C	N	O	S	0	0
			1913	1203	330	372	8		

- Molecule 7 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	d	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		
7	r	199	Total	C	N	O	S	0	0
			1570	1006	265	290	9		

- Molecule 8 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	243	Total	C	N	O	S	0	0
			1724	1068	312	339	5		
8	k	243	Total	C	N	O	S	0	0
			1691	1051	309	327	4		

- Molecule 9 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	e	201	Total	C	N	O	S	0	0
			1548	974	273	292	9		
9	s	201	Total	C	N	O	S	0	0
			1551	977	273	292	9		

- Molecule 10 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	234	Total	C	N	O	S	0	0
			1766	1108	290	357	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	l	234	Total	C	N	O	S	0	0
			1726	1107	291	317	11		

- Molecule 11 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	f	213	Total	C	N	O	S	0	0
			1641	1036	282	313	10		
11	t	213	Total	C	N	O	S	0	0
			1644	1039	282	313	10		

- Molecule 12 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	238	Total	C	N	O	S	0	0
			1850	1159	334	346	11		
12	m	238	Total	C	N	O	S	0	0
			1850	1159	334	346	11		

- Molecule 13 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	g	216	Total	C	N	O	S	0	0
			1672	1055	286	319	12		
13	u	217	Total	C	N	O	S	0	0
			1678	1058	290	318	12		

- Molecule 14 is a protein called 26S protease regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	380	Total	C	N	O	S	0	0
			2879	1809	513	539	18		

- Molecule 15 is a protein called 26S protease regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	359	Total	C	N	O	S	0	0
			2720	1708	465	535	12		

- Molecule 16 is a protein called 26S protease regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	358	Total	C	N	O	S	0	0
			2820	1780	506	518	16		

- Molecule 17 is a protein called 26S protease regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	380	Total	C	N	O	S	0	0
			3039	1923	524	579	13		

- Molecule 18 is a protein called 26S protease regulatory subunit 10B.

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

- Molecule 19 is a protein called 26S protease regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	376	Total	C	N	O	S	0	0
			2858	1802	496	545	15		

- Molecule 20 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	823	Total	C	N	O	S	0	0
			5462	3499	933	1012	18		

- Molecule 21 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	n	243	Total	C	N	O	S	0	0
			1873	1189	317	356	11		
21	X	243	Total	C	N	O	S	0	0
			1873	1189	317	356	11		

- Molecule 22 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	372	Total	C	N	O	S	0	0
			2372	1518	405	438	11		

- Molecule 23 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	413	Total	C	N	O	S	0	0
			2828	1819	489	514	6		

- Molecule 24 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Q	421	Total	C	N	O	S	0	0
			2948	1864	509	567	8		

- Molecule 25 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	R	376	Total	C	N	O	S	0	0
			2767	1794	461	503	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	395	Total	C	N	O	S	0	0
			2600	1662	463	472	3		

- Molecule 27 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	258	Total	C	N	O	S	0	0
			1702	1102	280	315	5		

- Molecule 28 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	283	Total	C	N	O	S	0	0
			2131	1370	369	388	4		

- Molecule 29 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	257	Total	C	N	O	S	0	0
			2011	1276	341	377	17		

- Molecule 30 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	193	Total	C	N	O	S	0	0
			1300	818	228	250	4		

- Molecule 31 is a protein called 26S proteasome complex subunit DSS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	Y	59	Total	C	N	O	0	0
			308	184	60	64		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Z	732	Total	C	N	O	0	0
			3608	2144	732	732		

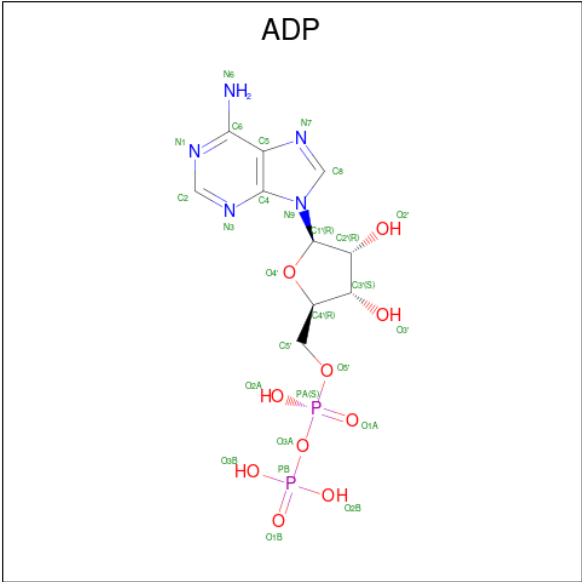
- Molecule 33 is a protein called Ubiquitin carboxyl-terminal hydrolase 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	x	355	Total	C	N	O	S	0	0
			2810	1782	470	538	20		

- Molecule 34 is a protein called Polyubiquitin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	y	76	Total	C	N	O	S	0	0
			601	378	105	117	1		

- Molecule 35 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

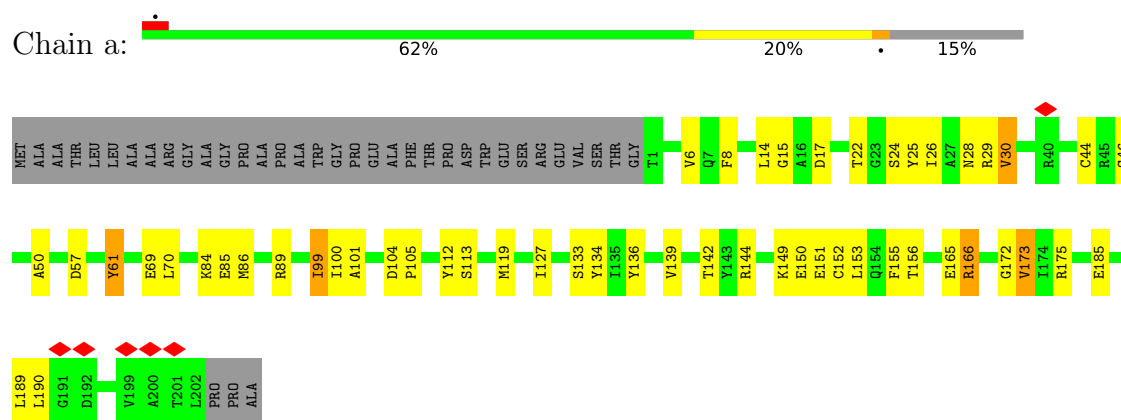


Mol	Chain	Residues	Atoms					AltConf
35	H	1	Total	C	N	O	P	0
			27	10	5	10	2	
35	I	1	Total	C	N	O	P	0
			27	10	5	10	2	
35	J	1	Total	C	N	O	P	0
			27	10	5	10	2	
35	K	1	Total	C	N	O	P	0
			27	10	5	10	2	
35	L	1	Total	C	N	O	P	0
			27	10	5	10	2	
35	M	1	Total	C	N	O	P	0
			27	10	5	10	2	

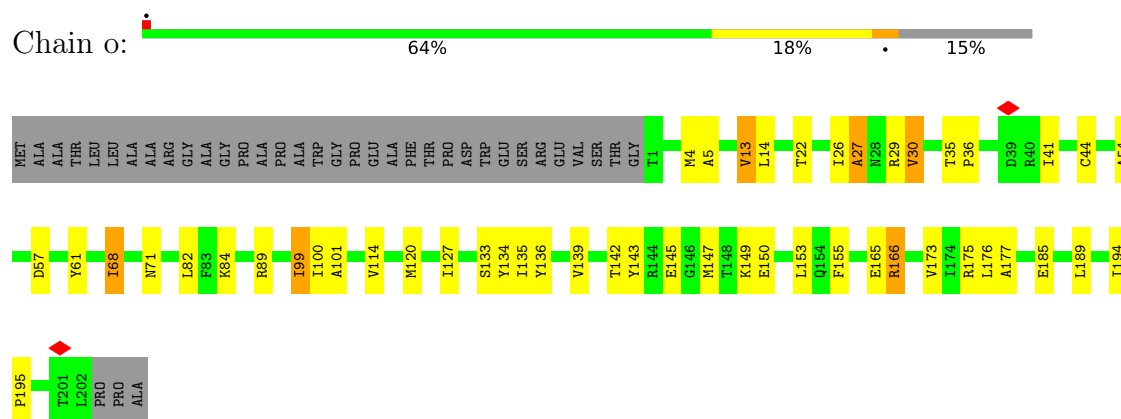
3 Residue-property plots [i](#)

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.

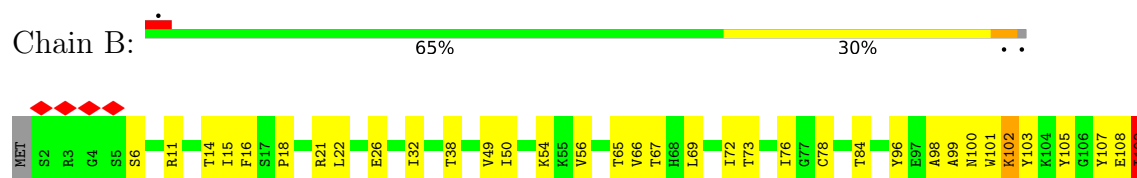
- Molecule 1: Proteasome subunit beta type-6

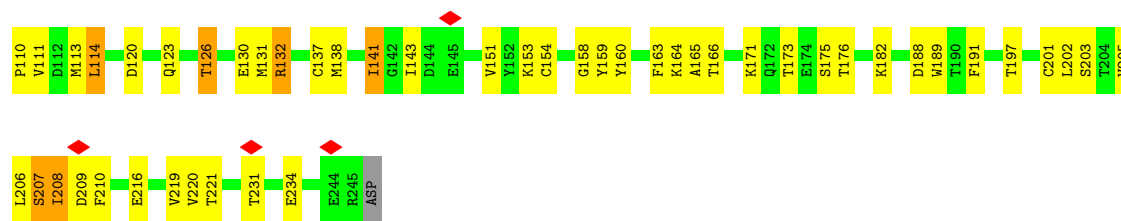


- Molecule 1: Proteasome subunit beta type-6

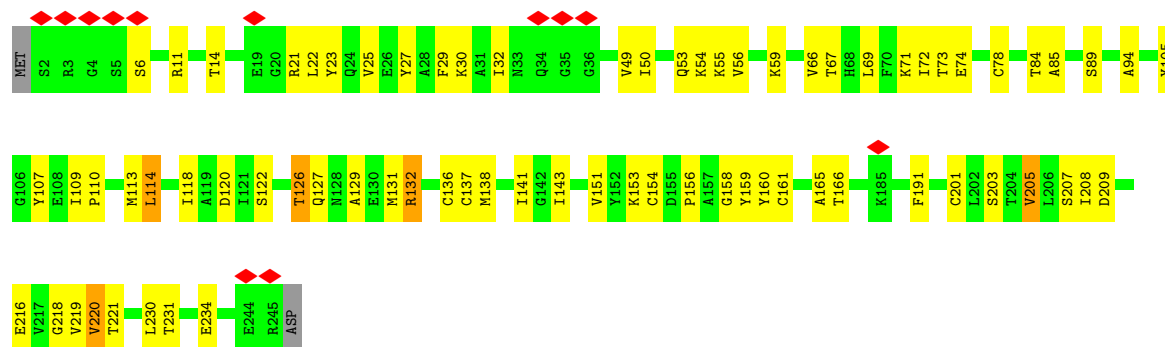


- Molecule 2: Proteasome subunit alpha type-6

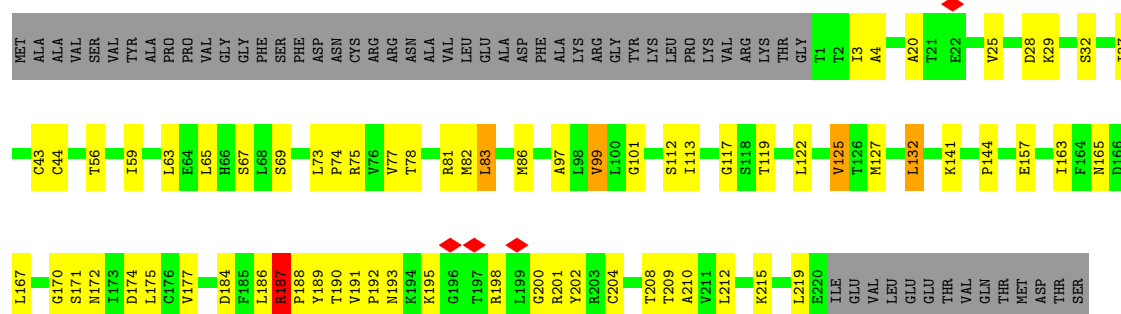




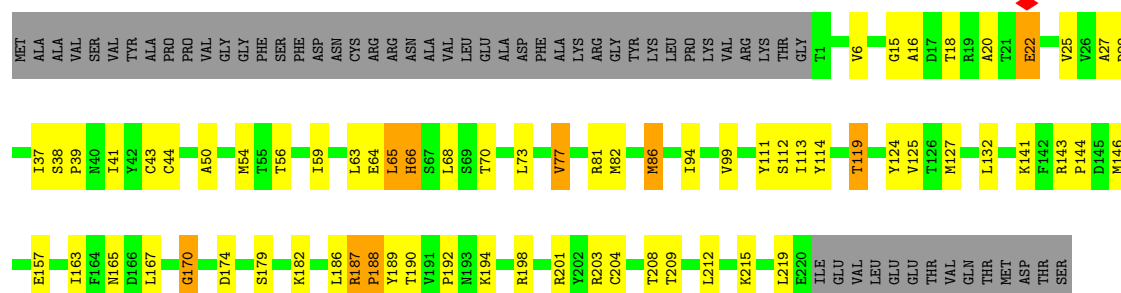
• Molecule 2: Proteasome subunit alpha type-6



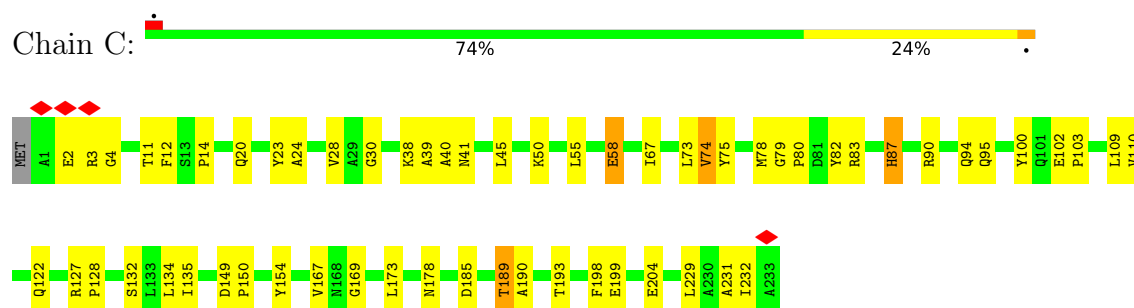
• Molecule 3: Proteasome subunit beta type-7



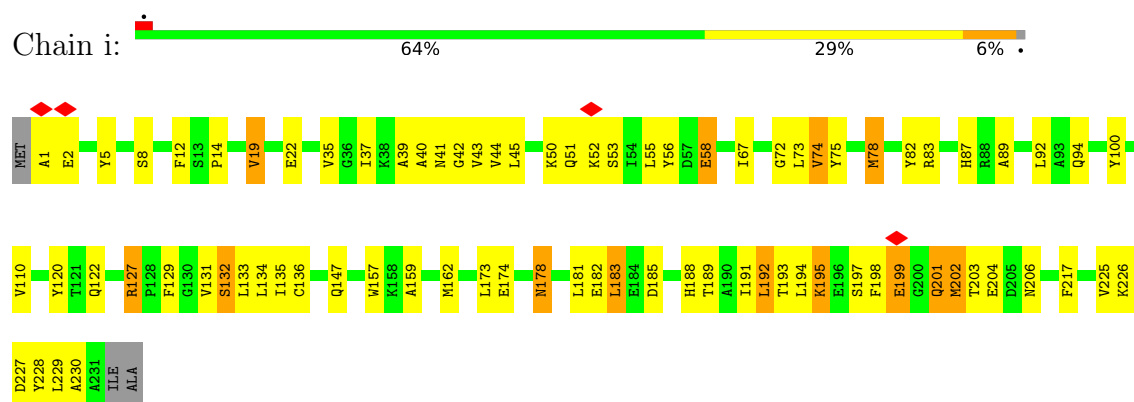
• Molecule 3: Proteasome subunit beta type-7



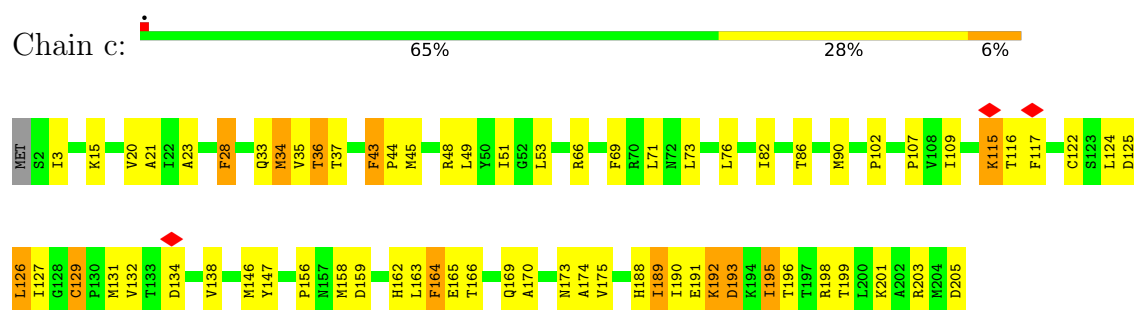
- Molecule 4: Proteasome subunit alpha type-2



- Molecule 4: Proteasome subunit alpha type-2



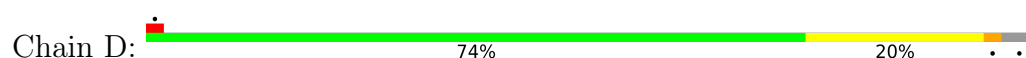
- Molecule 5: Proteasome subunit beta type-3

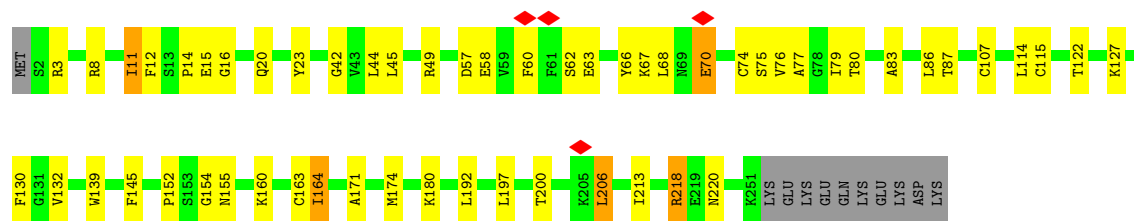


- Molecule 5: Proteasome subunit beta type-3

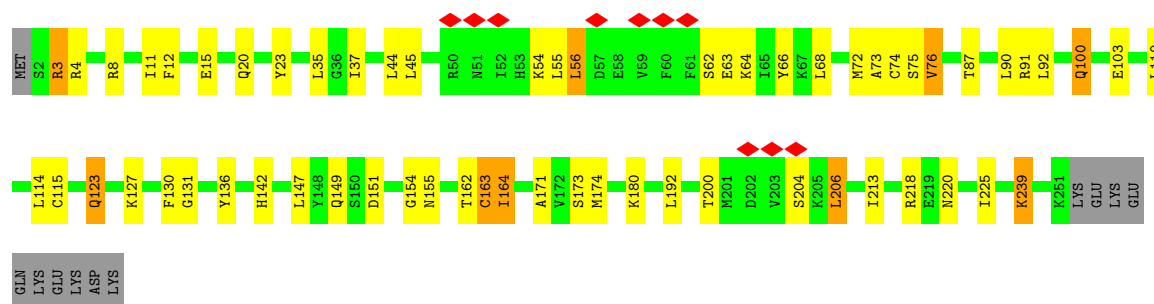


- Molecule 6: Proteasome subunit alpha type-4

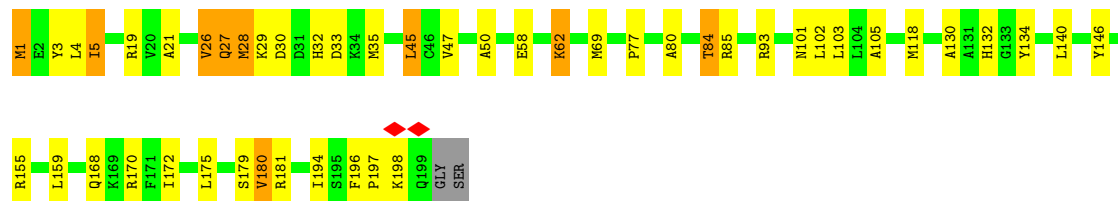
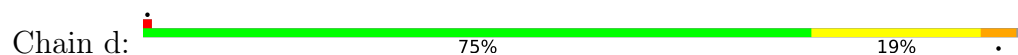




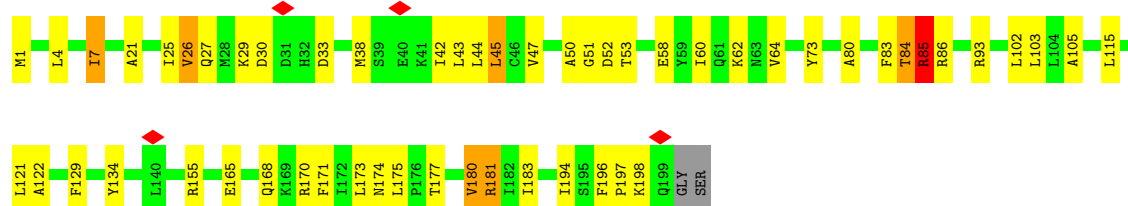
• Molecule 6: Proteasome subunit alpha type-4



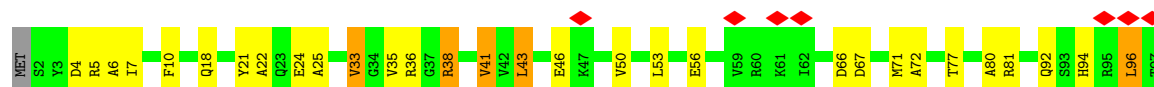
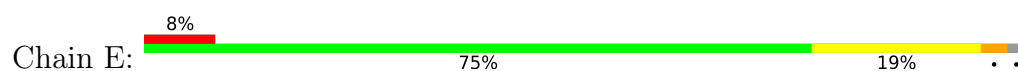
• Molecule 7: Proteasome subunit beta type-2

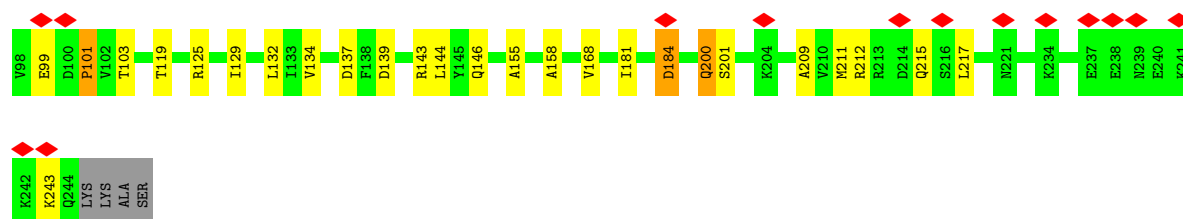


• Molecule 7: Proteasome subunit beta type-2

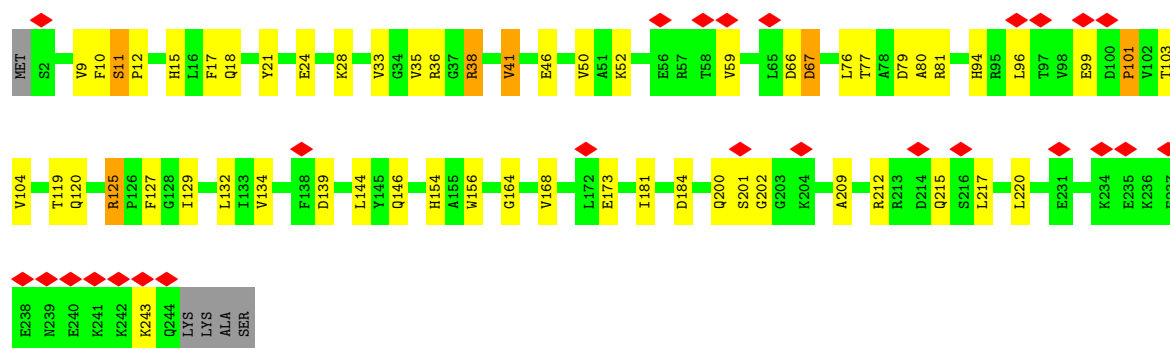
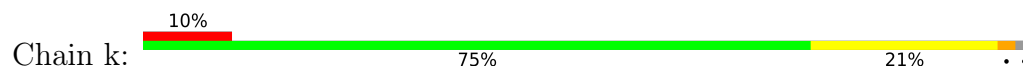


• Molecule 8: Proteasome subunit alpha type-7

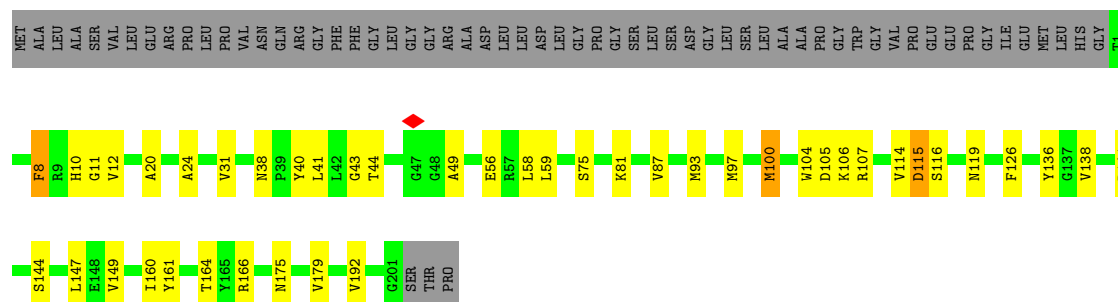




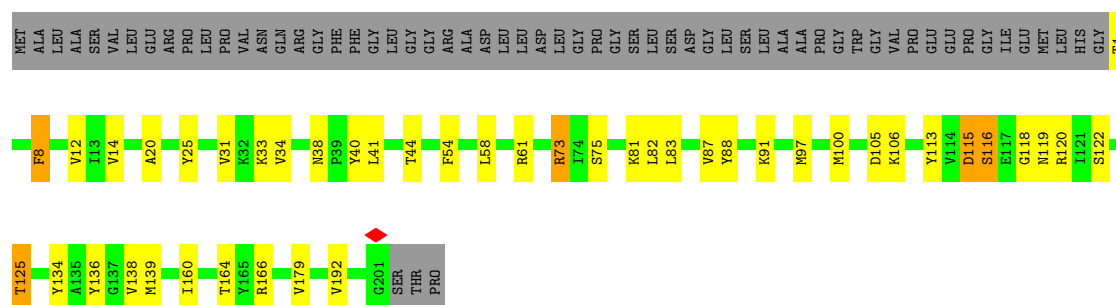
- Molecule 8: Proteasome subunit alpha type-7



- Molecule 9: Proteasome subunit beta type-5

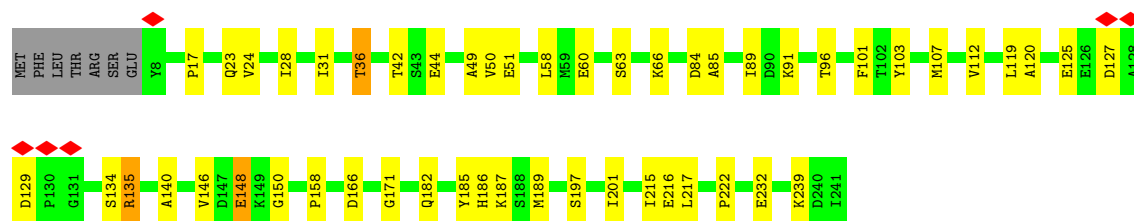


- Molecule 9: Proteasome subunit beta type-5



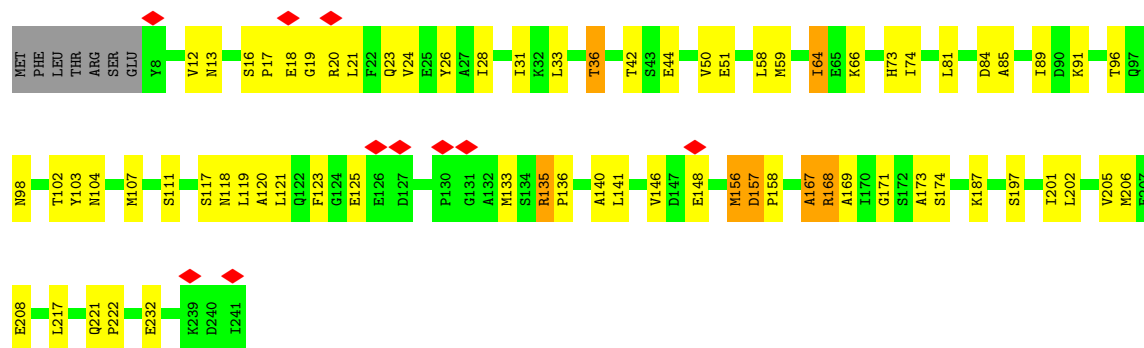
- Molecule 10: Proteasome subunit alpha type-5

Chain F:  76% 20% ..



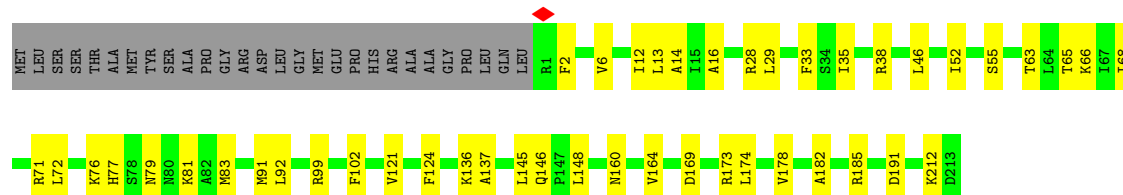
• Molecule 10: Proteasome subunit alpha type-5

Chain l:  68% 27% ..



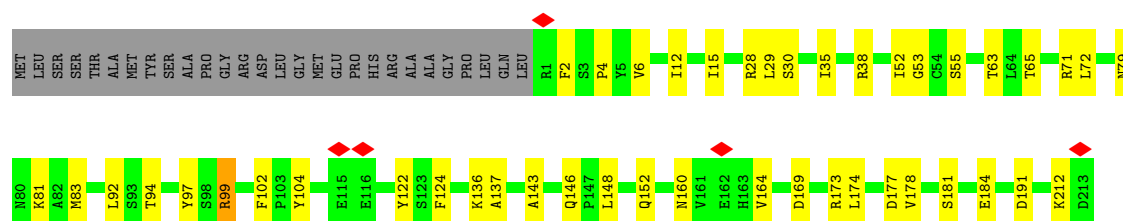
• Molecule 11: Proteasome subunit beta type-1

Chain f:  69% 19% 12%



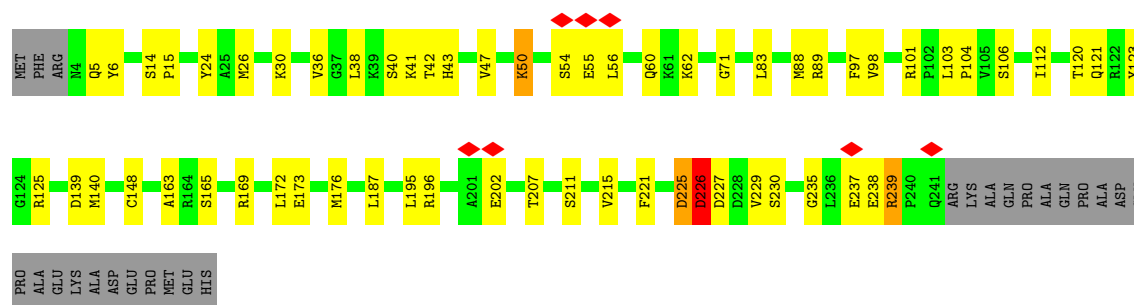
• Molecule 11: Proteasome subunit beta type-1

Chain t:  70% 18% 12%

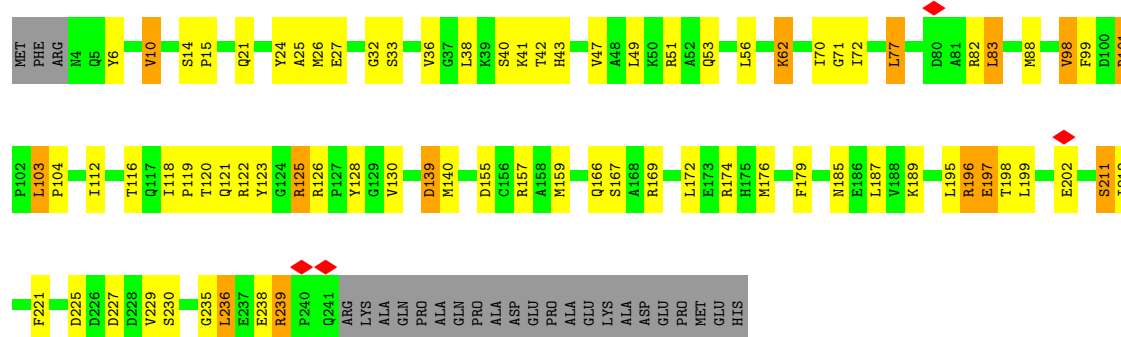


• Molecule 12: Proteasome subunit alpha type-1

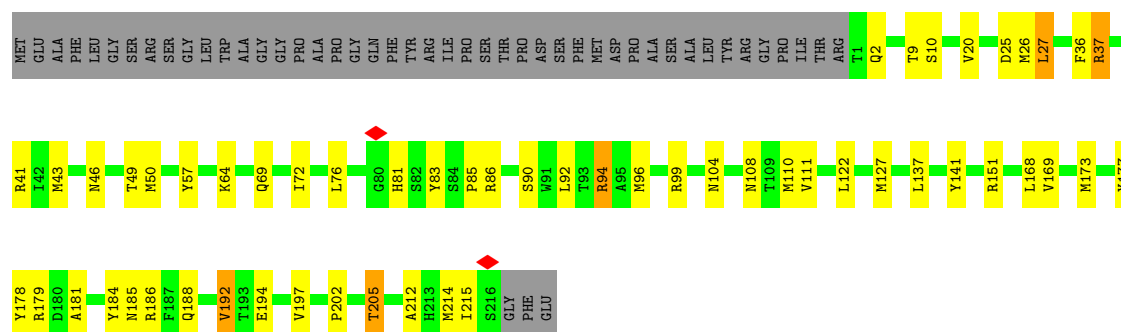
Chain G:  67% 22% 10%



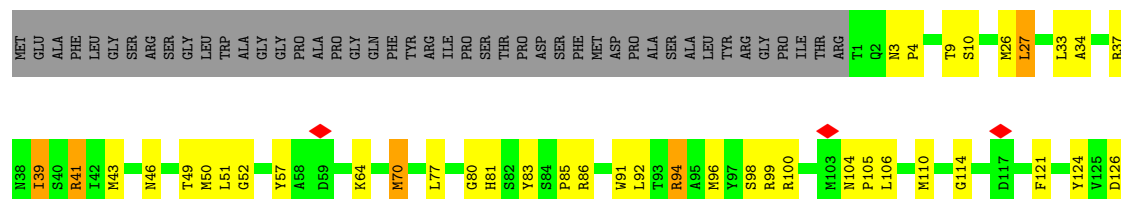
- Molecule 12: Proteasome subunit alpha type-1



- Molecule 13: Proteasome subunit beta type-4

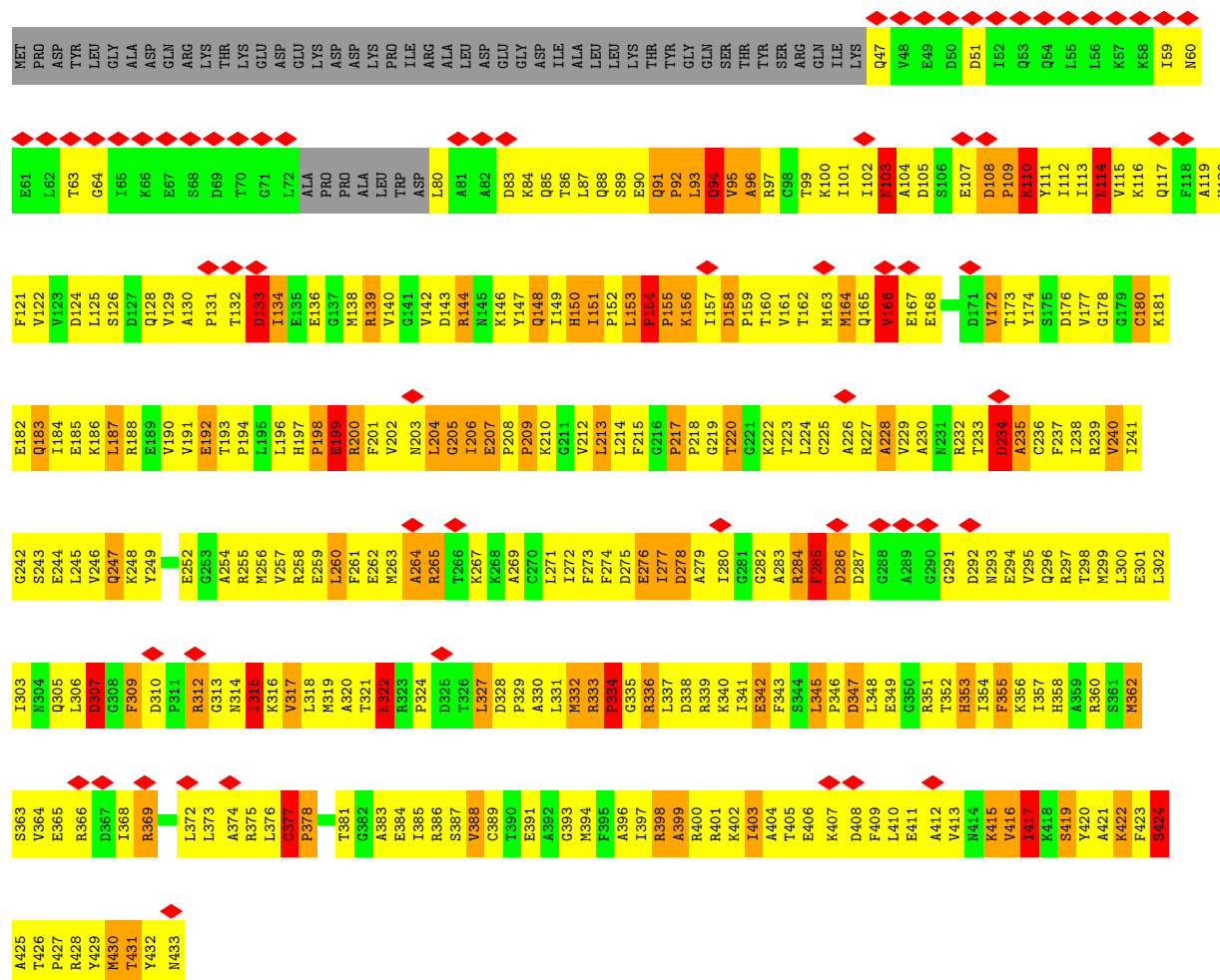
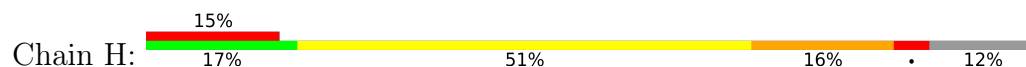


- Molecule 13: Proteasome subunit beta type-4

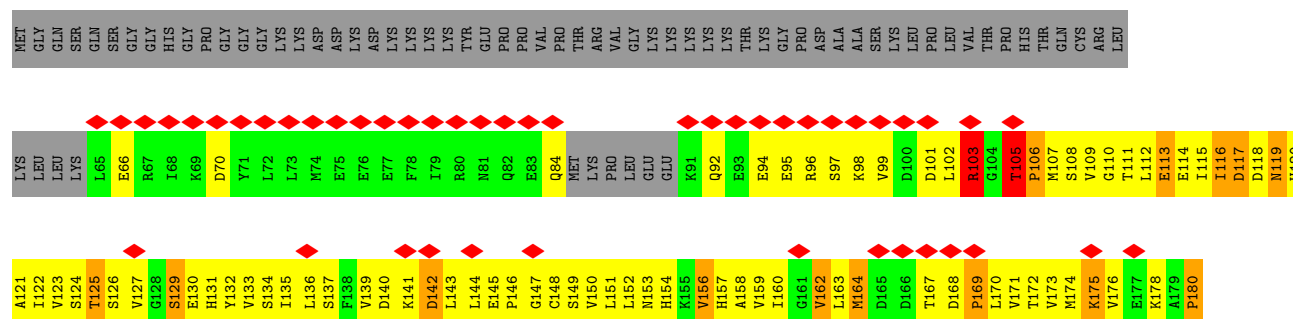
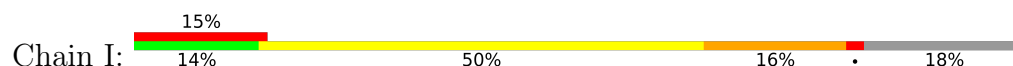


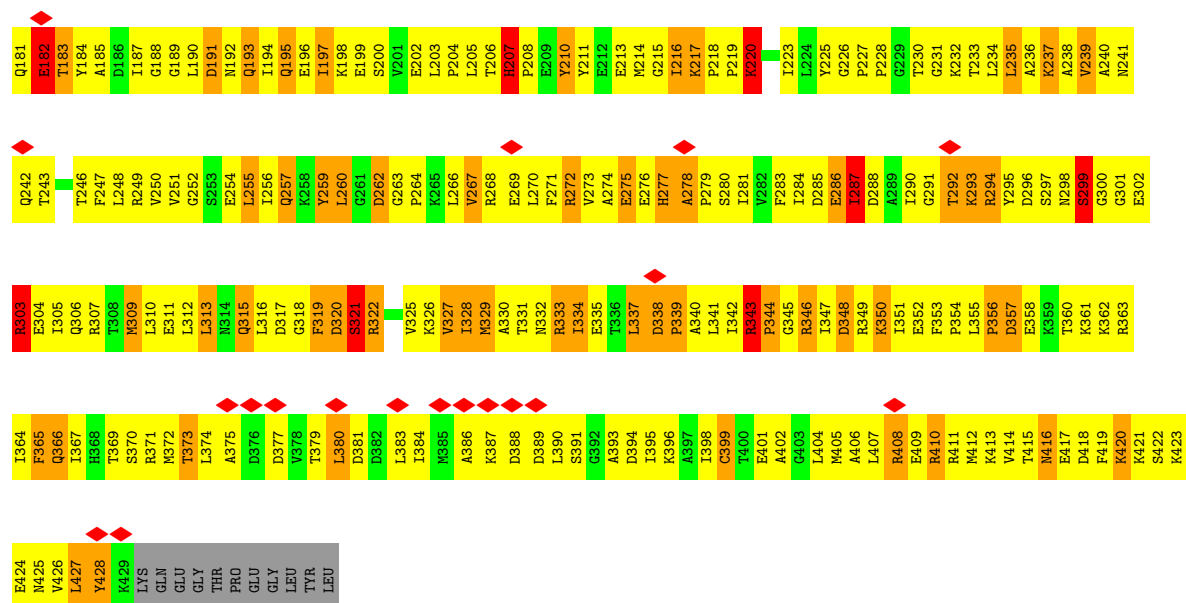


• Molecule 14: 26S protease regulatory subunit 7

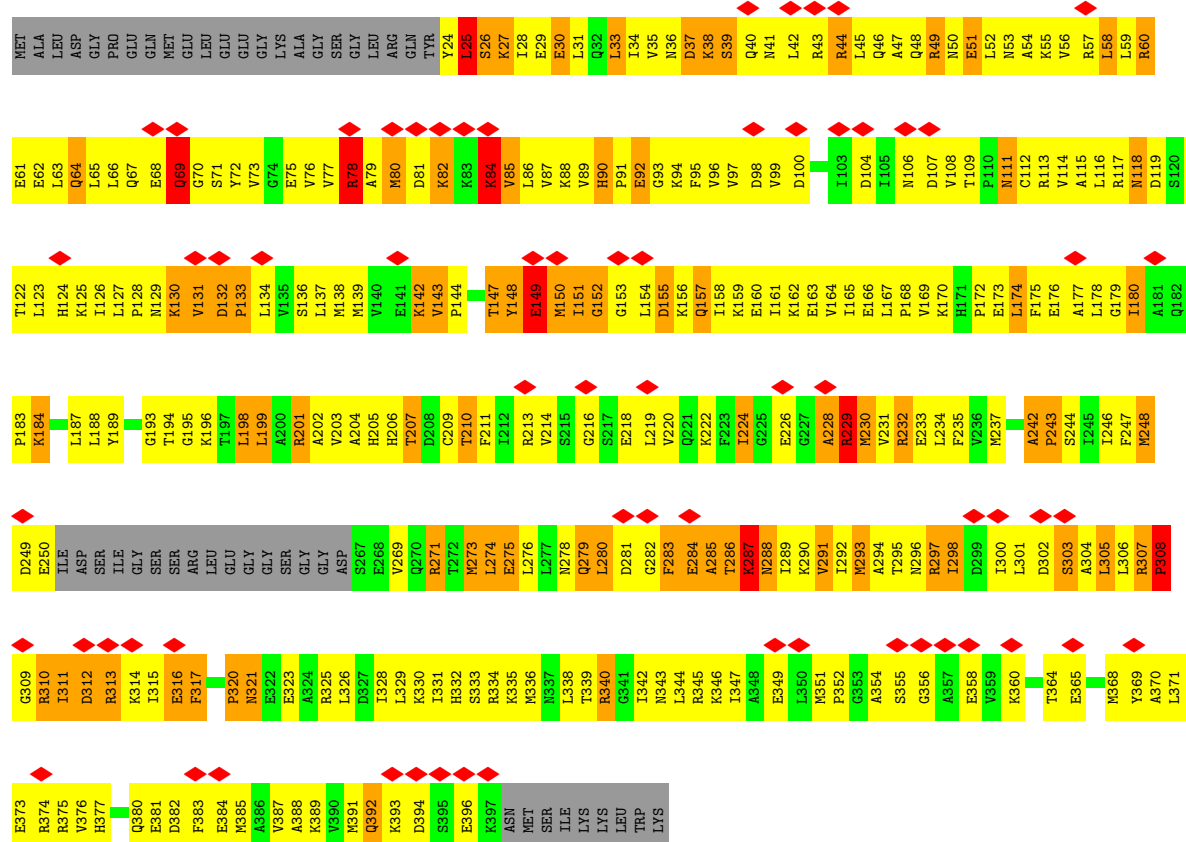
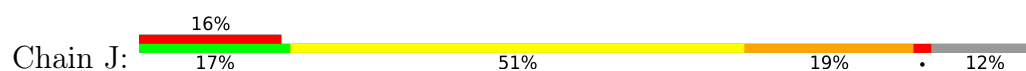


• Molecule 15: 26S protease regulatory subunit 4

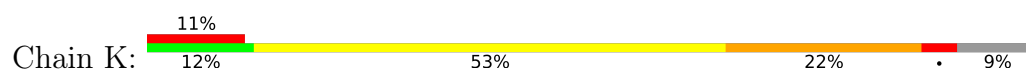


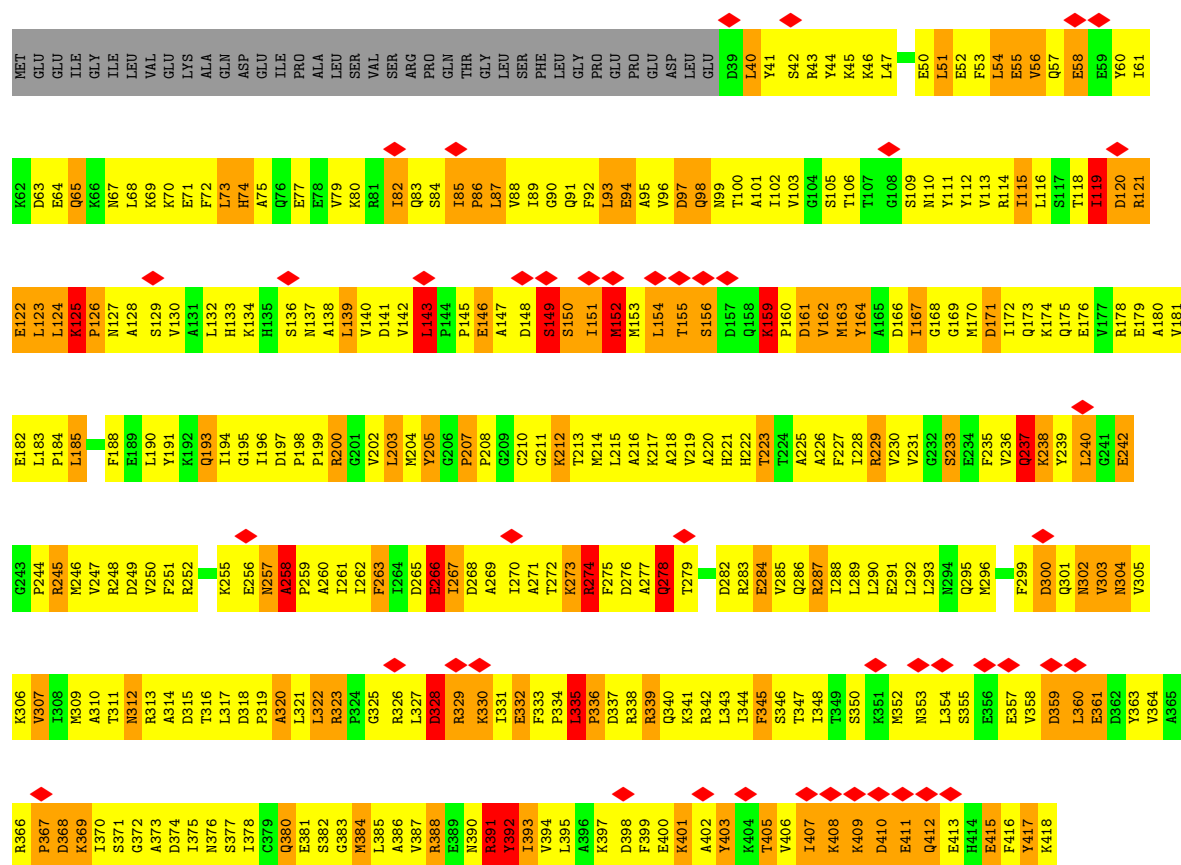


• Molecule 16: 26S protease regulatory subunit 8

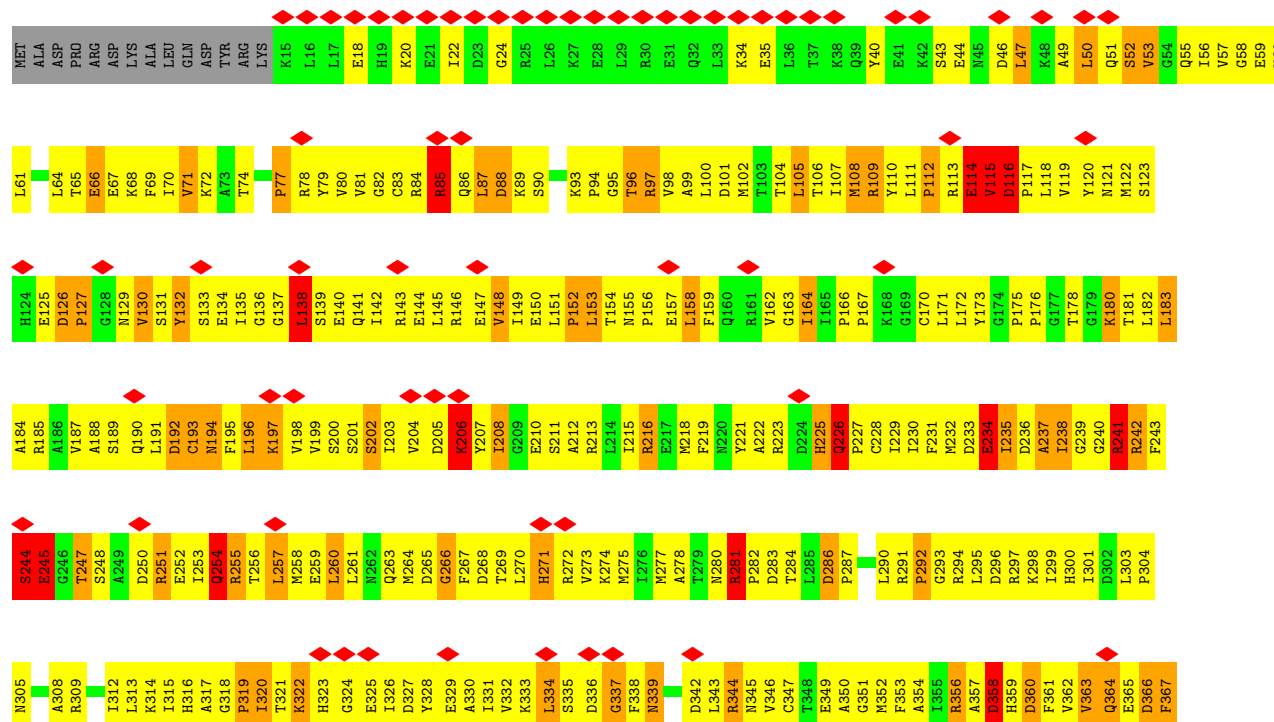
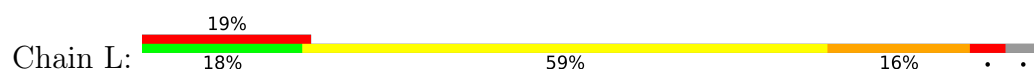


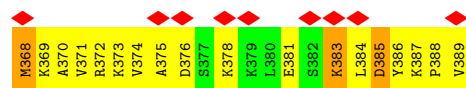
• Molecule 17: 26S protease regulatory subunit 6B



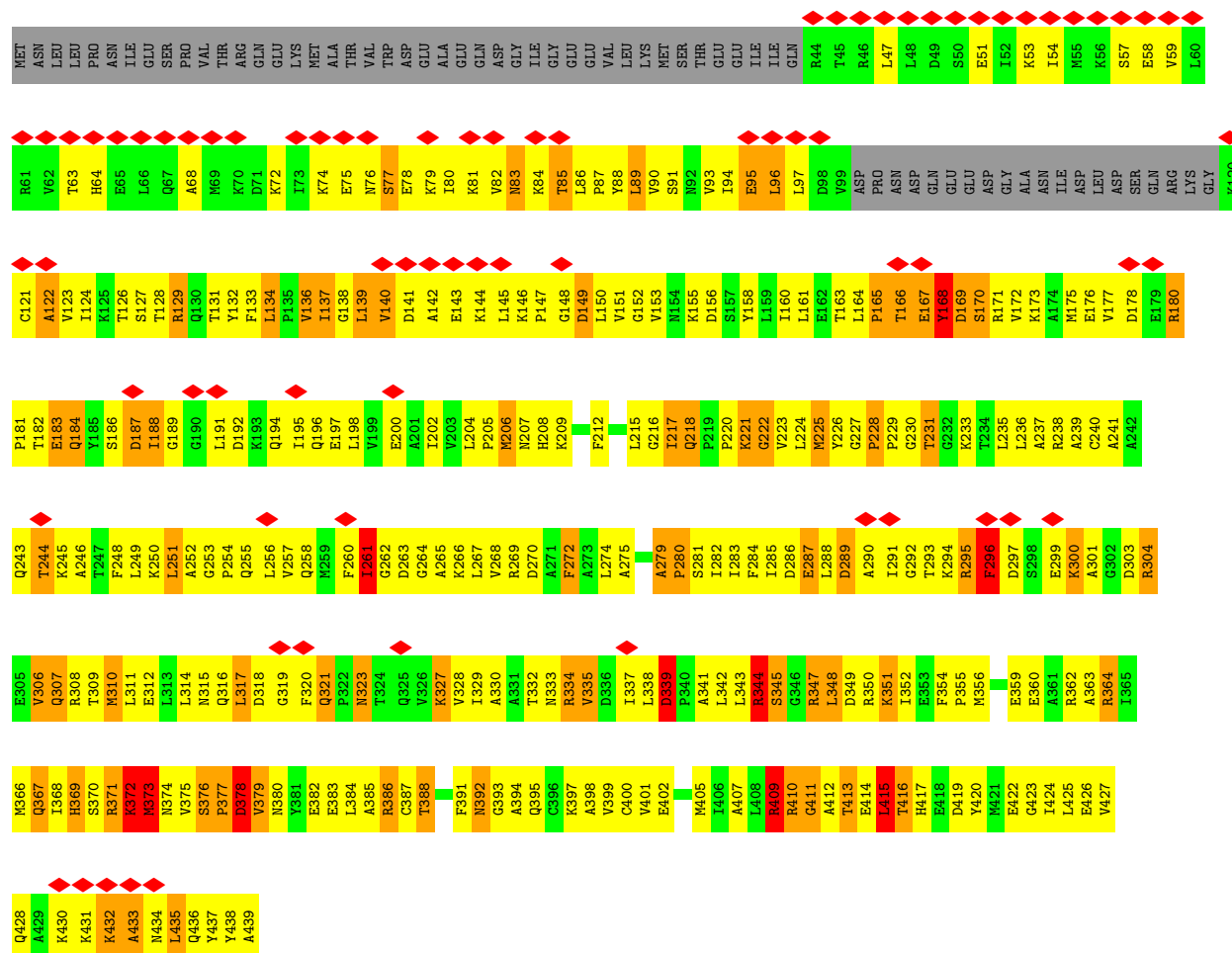
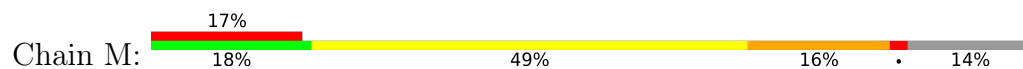


• Molecule 18: 26S protease regulatory subunit 10B

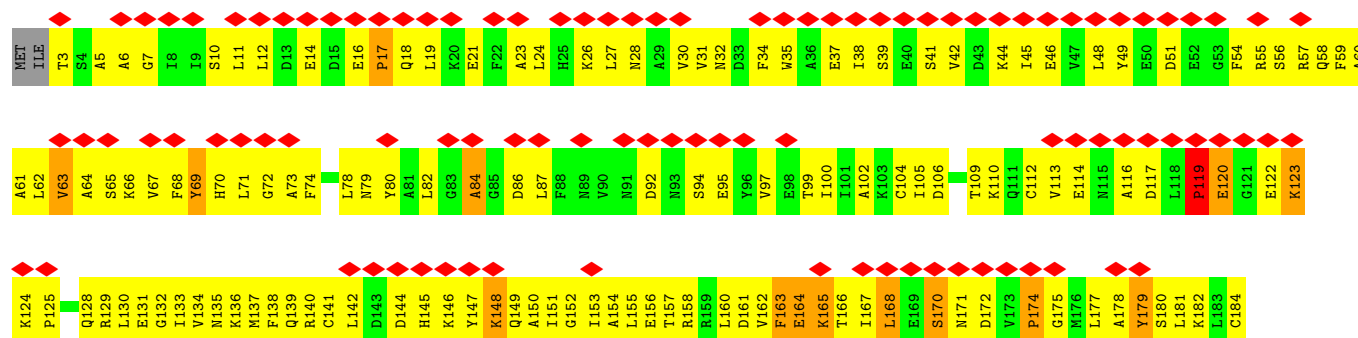


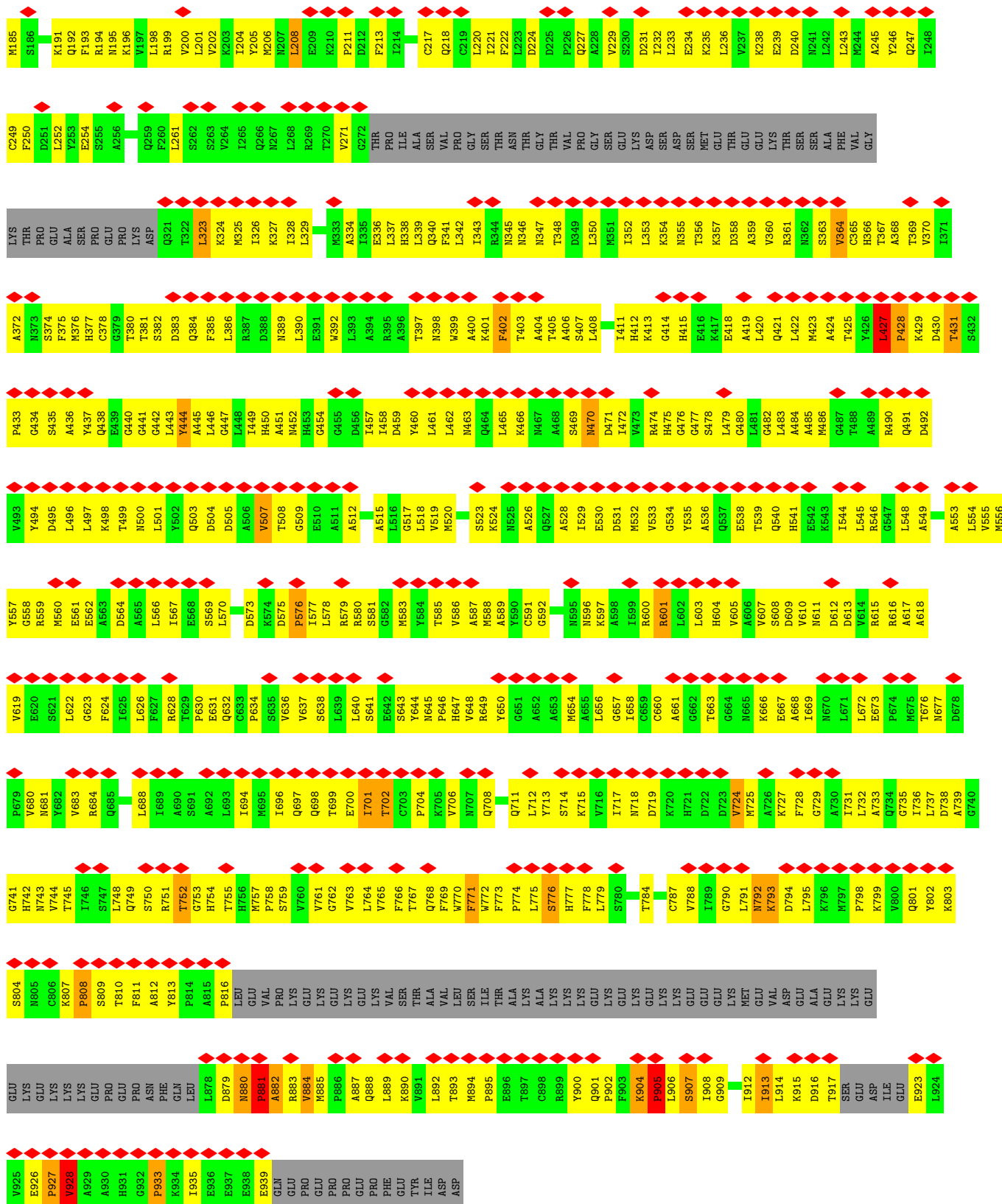


• Molecule 19: 26S protease regulatory subunit 6A



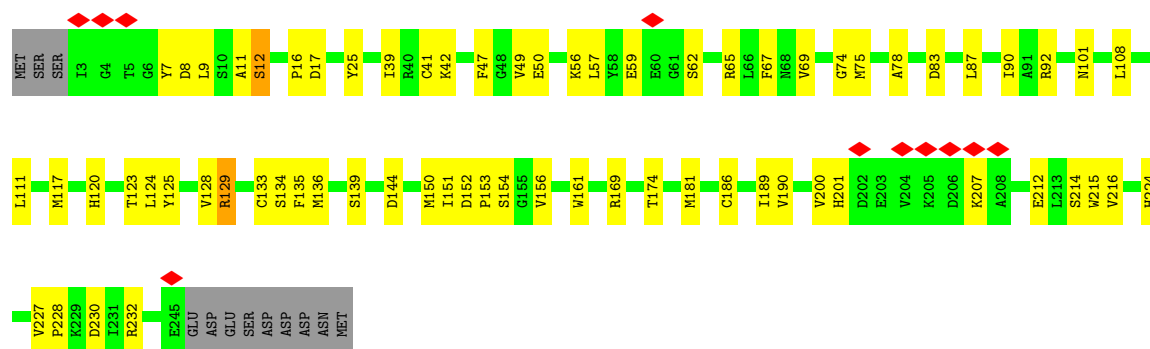
• Molecule 20: 26S proteasome non-ATPase regulatory subunit 1





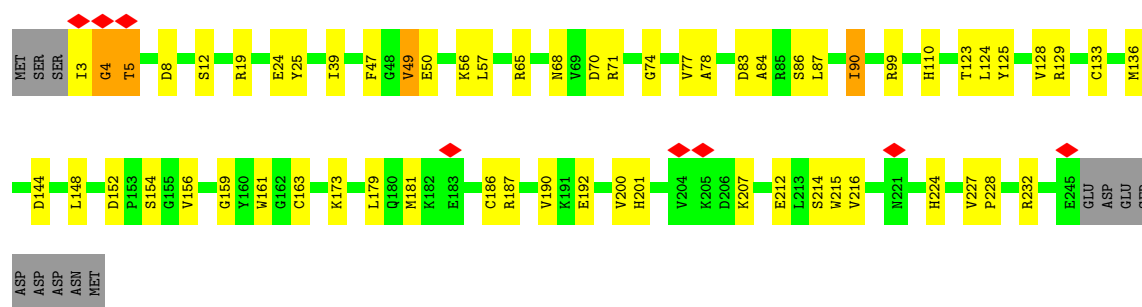
- Molecule 21: Proteasome subunit alpha type-3





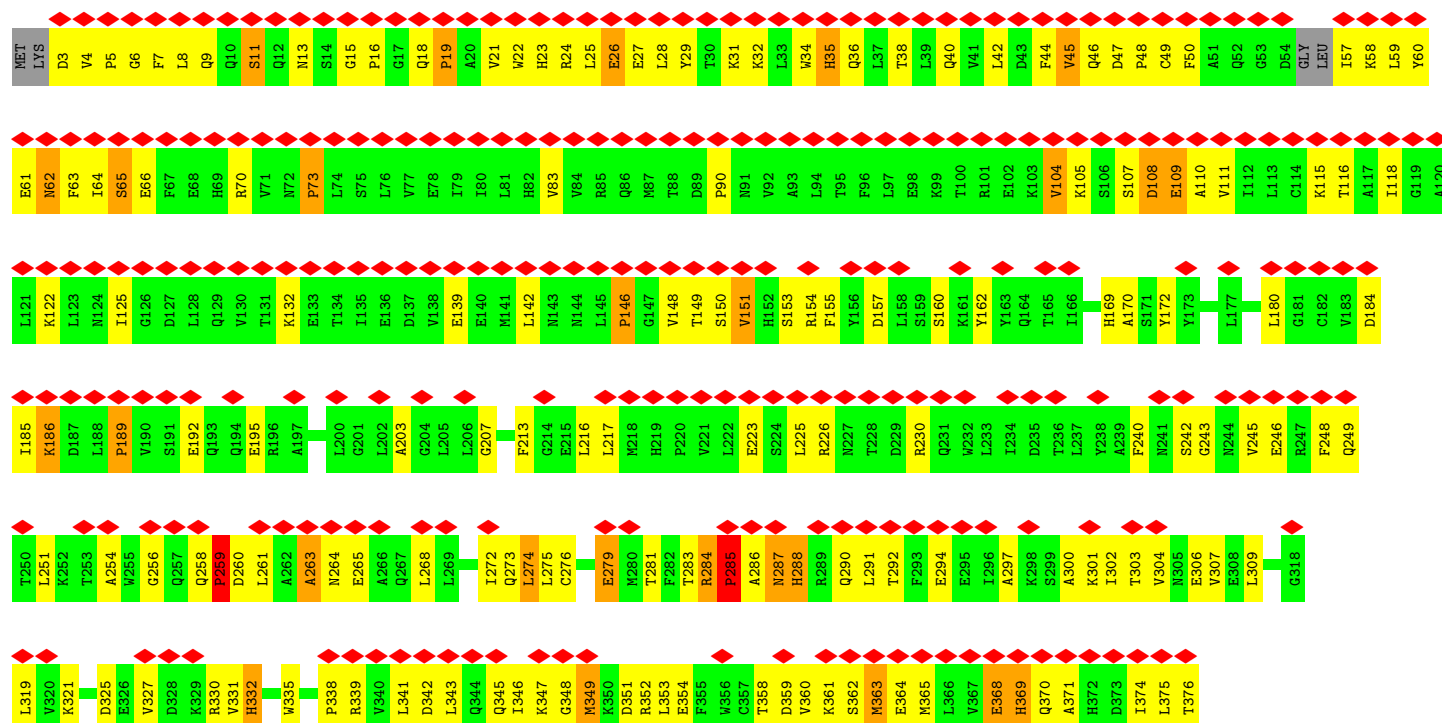
• Molecule 21: Proteasome subunit alpha type-3

Chain X: 71% 22% 5%

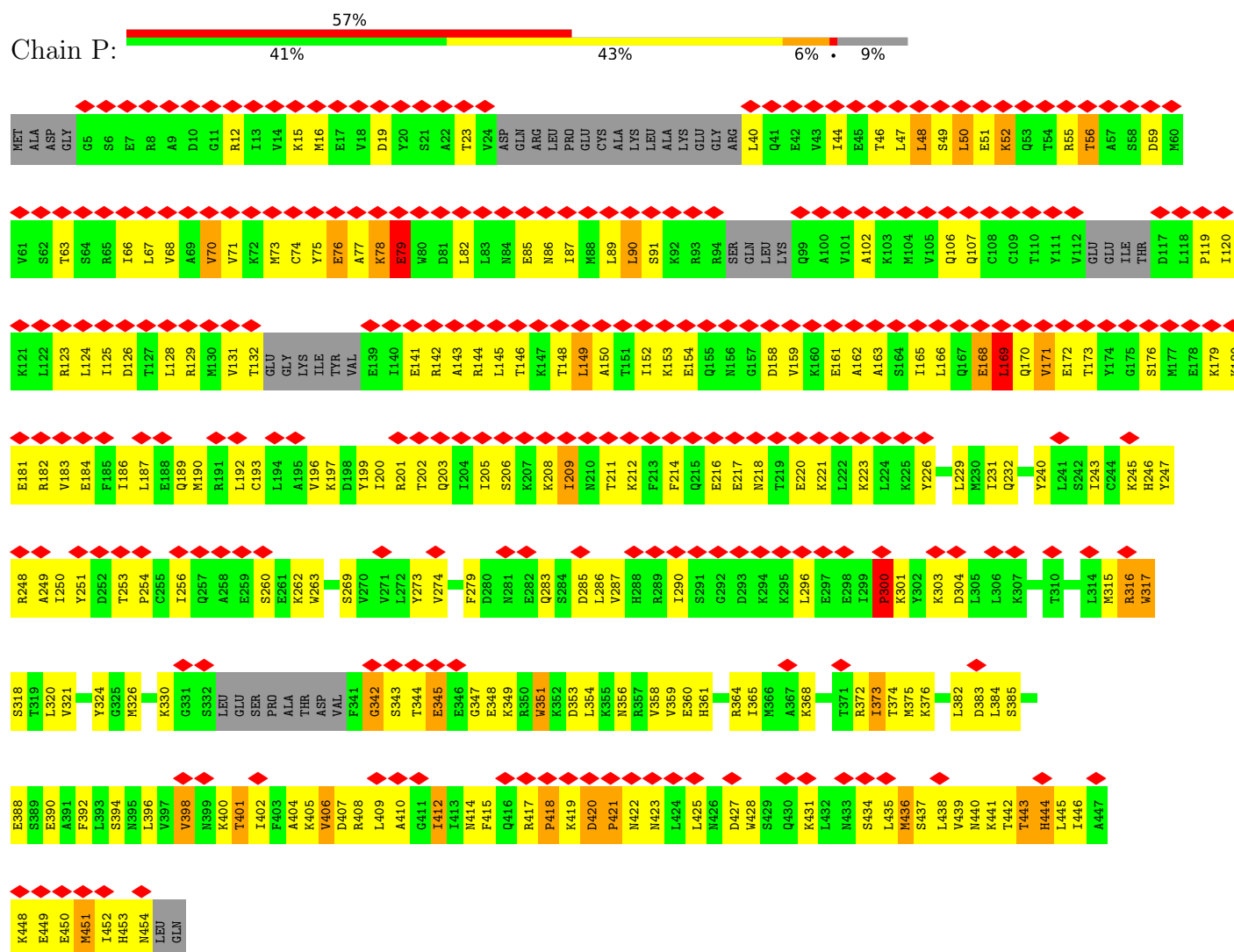


• Molecule 22: 26S proteasome non-ATPase regulatory subunit 13

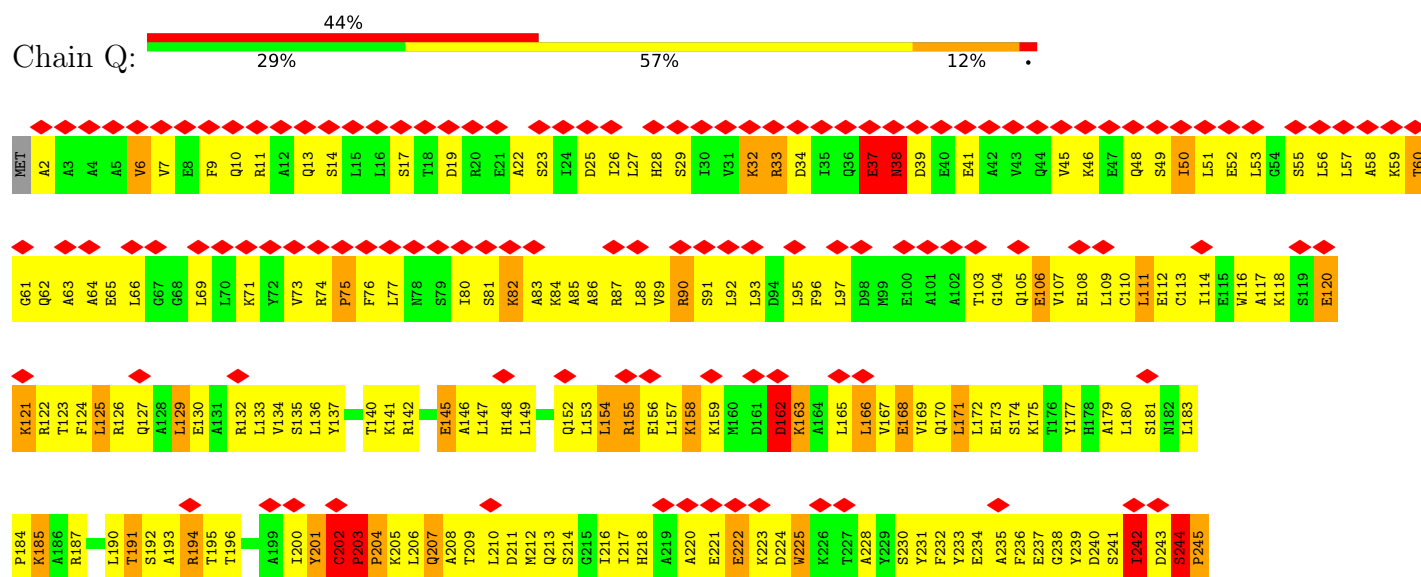
Chain O: 73% 52% 40% 7%

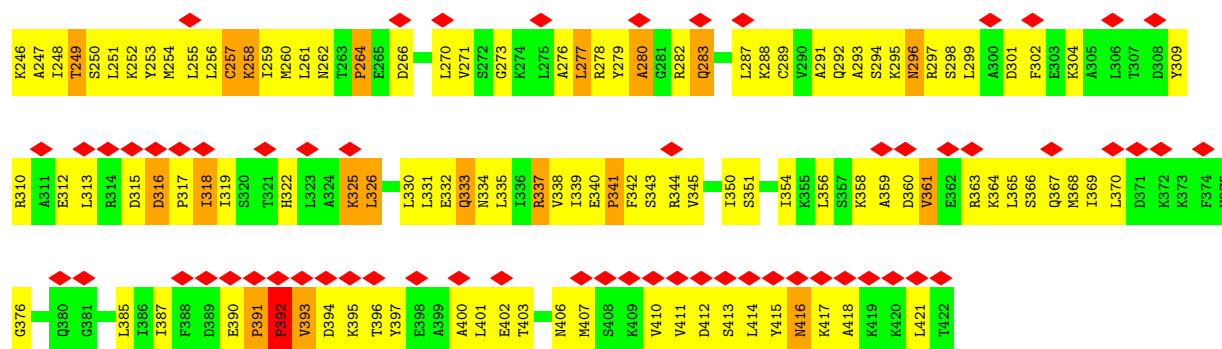


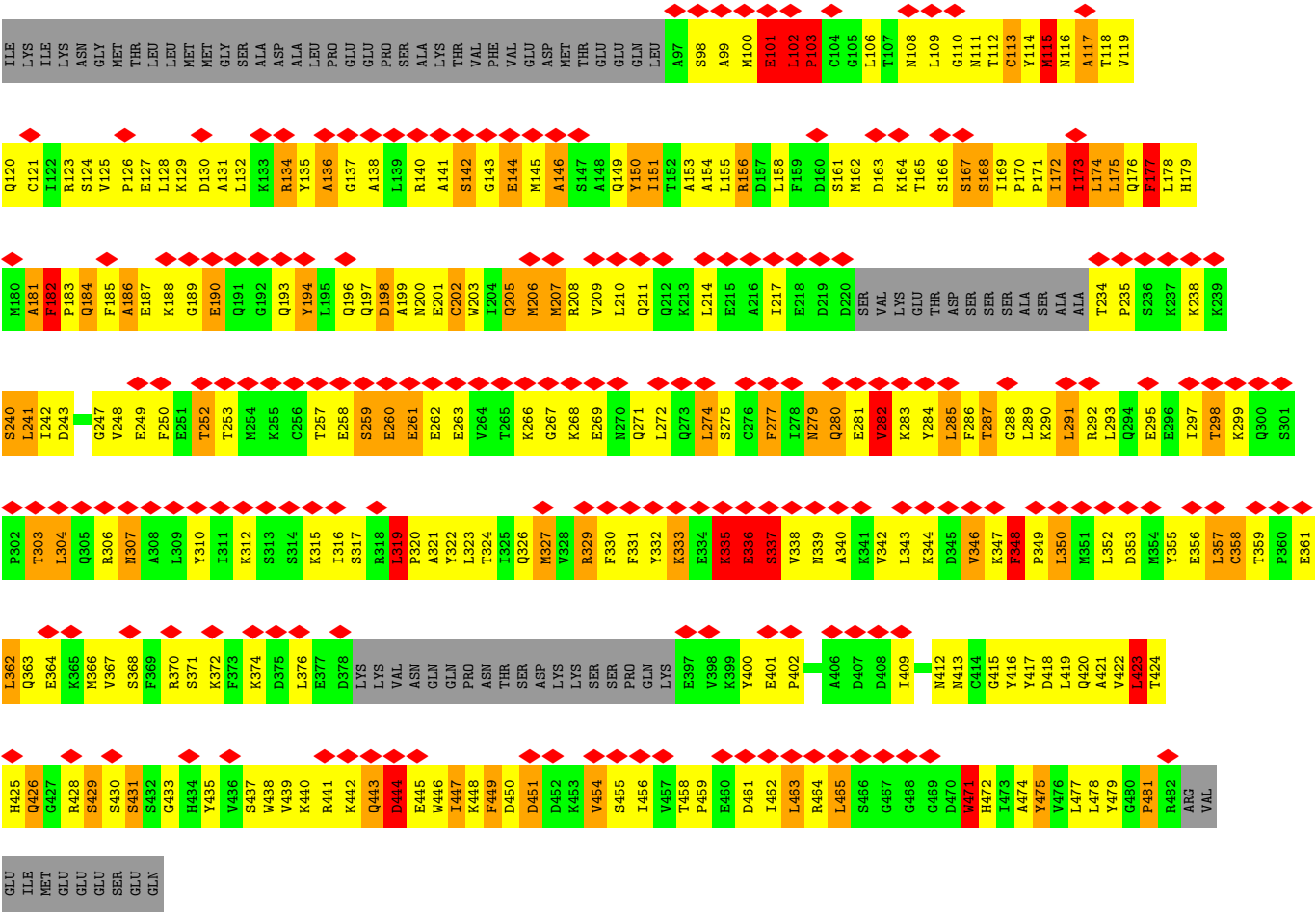
• Molecule 23: 26S proteasome non-ATPase regulatory subunit 12



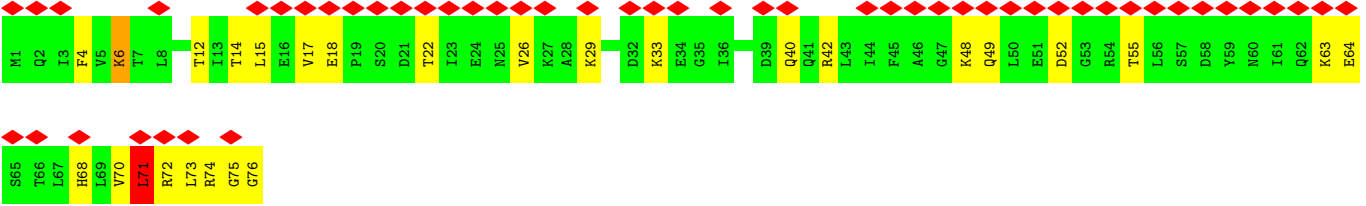
• Molecule 24: 26S proteasome non-ATPase regulatory subunit 11







● Molecule 34: Polyubiquitin-B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	141293	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	37	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.171	Depositor
Minimum map value	-0.078	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.033	Depositor
Map size (Å)	547.84, 547.84, 547.84	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	1.39	9/1535 (0.6%)	1.24	3/2078 (0.1%)
1	o	1.47	16/1535 (1.0%)	1.27	0/2078
2	B	1.07	1/1878 (0.1%)	1.11	7/2549 (0.3%)
2	h	1.27	5/1886 (0.3%)	1.17	3/2557 (0.1%)
3	b	1.27	6/1670 (0.4%)	1.26	4/2265 (0.2%)
3	p	1.37	12/1670 (0.7%)	1.32	10/2265 (0.4%)
4	C	1.03	3/1742 (0.2%)	1.08	0/2372
4	i	1.38	9/1780 (0.5%)	1.25	4/2417 (0.2%)
5	c	1.38	12/1614 (0.7%)	1.24	3/2177 (0.1%)
5	q	1.53	14/1614 (0.9%)	1.35	5/2177 (0.2%)
6	D	1.02	2/1942 (0.1%)	1.06	2/2628 (0.1%)
6	j	1.25	9/1943 (0.5%)	1.19	3/2629 (0.1%)
7	d	1.25	6/1603 (0.4%)	1.19	2/2174 (0.1%)
7	r	1.48	12/1603 (0.7%)	1.28	2/2174 (0.1%)
8	E	1.03	0/1748	1.05	0/2386
8	k	1.22	3/1716 (0.2%)	1.22	2/2347 (0.1%)
9	e	1.35	4/1579 (0.3%)	1.20	2/2134 (0.1%)
9	s	1.34	3/1582 (0.2%)	1.20	1/2138 (0.0%)
10	F	1.00	1/1794 (0.1%)	1.08	4/2430 (0.2%)
10	l	1.22	8/1753 (0.5%)	1.22	2/2346 (0.1%)
11	f	1.32	2/1671 (0.1%)	1.20	0/2253
11	t	1.41	6/1674 (0.4%)	1.27	1/2257 (0.0%)
12	G	1.00	1/1885 (0.1%)	1.07	1/2552 (0.0%)
12	m	1.21	4/1885 (0.2%)	1.16	10/2552 (0.4%)
13	g	1.30	9/1705 (0.5%)	1.18	0/2312
13	u	1.35	7/1711 (0.4%)	1.25	3/2319 (0.1%)
14	H	1.11	12/2925 (0.4%)	1.24	16/3952 (0.4%)
15	I	1.07	6/2756 (0.2%)	1.20	14/3727 (0.4%)
16	J	1.01	3/2857 (0.1%)	1.11	6/3844 (0.2%)
17	K	1.02	3/3089 (0.1%)	1.15	17/4168 (0.4%)
18	L	1.08	6/2904 (0.2%)	1.23	18/3924 (0.5%)
19	M	0.98	2/2896 (0.1%)	1.13	13/3912 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
20	N	0.53	2/5520 (0.0%)	0.83	8/7446 (0.1%)
21	X	1.02	2/1908 (0.1%)	1.03	1/2575 (0.0%)
21	n	1.19	6/1908 (0.3%)	1.13	1/2575 (0.0%)
22	O	0.81	3/2387 (0.1%)	0.99	8/3211 (0.2%)
23	P	0.74	1/2857 (0.0%)	0.92	9/3855 (0.2%)
24	Q	0.87	2/2981 (0.1%)	1.01	13/4045 (0.3%)
25	R	0.86	3/2817 (0.1%)	1.01	12/3811 (0.3%)
26	S	0.80	1/2623 (0.0%)	0.97	4/3545 (0.1%)
27	T	0.79	0/1716	0.90	3/2310 (0.1%)
28	U	0.75	1/2167 (0.0%)	0.92	1/2936 (0.0%)
29	V	0.77	0/2047	0.94	3/2763 (0.1%)
30	W	0.71	1/1312 (0.1%)	1.05	6/1769 (0.3%)
31	Y	0.93	1/307 (0.3%)	1.38	4/424 (0.9%)
32	Z	0.54	1/3603 (0.0%)	0.88	7/5005 (0.1%)
33	x	0.86	1/2860 (0.0%)	1.27	32/3852 (0.8%)
34	y	0.78	0/603	1.06	2/811 (0.2%)
All	All	1.07	221/99761 (0.2%)	1.12	272/135026 (0.2%)

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
3	b	0	2
4	i	0	1
6	j	0	1
7	r	0	1
14	H	0	1
15	I	0	4
16	J	0	1
17	K	0	1
18	L	0	4
19	M	0	2
20	N	0	3
22	O	0	2
23	P	0	2
24	Q	0	6
25	R	0	5
27	T	0	1
28	U	0	1
29	V	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
30	W	0	7
31	Y	0	2
32	Z	0	7
34	y	0	2
All	All	0	59

The worst 5 of 221 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	L	116	ASP	N-CA	-14.43	1.25	1.46
11	t	53	GLY	CA-C	12.10	1.60	1.52
1	o	13	VAL	C-O	-11.33	1.12	1.24
18	L	115	VAL	CA-CB	-10.51	1.40	1.54
24	Q	163	LYS	N-CA	-10.49	1.32	1.46

The worst 5 of 272 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	L	115	VAL	CA-C-N	-18.51	76.64	121.80
18	L	115	VAL	C-N-CA	-18.51	76.64	121.80
18	L	115	VAL	O-C-N	13.97	140.04	122.57
22	O	62	ASN	O-C-N	-13.79	103.88	122.36
14	H	336	ARG	NE-CZ-NH1	-11.96	109.54	121.50

There are no chirality outliers.

5 of 59 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	H	154	PRO	Peptide
15	I	105	THR	Peptide
15	I	137	SER	Peptide
15	I	299	SER	Mainchain
3	b	187	ARG	Mainchain,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	a	1509	0	1473	49	0
1	o	1509	0	1473	37	0
2	B	1845	0	1805	101	0
2	h	1853	0	1827	64	0
3	b	1643	0	1644	73	0
3	p	1643	0	1644	48	0
4	C	1707	0	1591	57	0
4	i	1744	0	1693	97	0
5	c	1585	0	1598	45	0
5	q	1585	0	1598	46	0
6	D	1912	0	1851	48	0
6	j	1913	0	1848	54	0
7	d	1570	0	1547	40	0
7	r	1570	0	1547	39	0
8	E	1724	0	1525	47	0
8	k	1691	0	1468	53	0
9	e	1548	0	1499	32	0
9	s	1551	0	1508	39	0
10	F	1766	0	1714	39	0
10	l	1726	0	1722	74	0
11	f	1641	0	1618	34	0
11	t	1644	0	1627	39	0
12	G	1850	0	1822	57	0
12	m	1850	0	1822	84	0
13	g	1672	0	1630	48	0
13	u	1678	0	1640	60	0
14	H	2879	0	2812	691	0
15	I	2720	0	2685	816	0
16	J	2820	0	2927	744	0
17	K	3039	0	3072	954	0
18	L	2860	0	2827	749	0
19	M	2858	0	2852	634	0
20	N	5462	0	4587	744	0
21	X	1873	0	1832	59	0
21	n	1873	0	1832	48	0
22	O	2372	0	1859	182	0
23	P	2828	0	2378	334	0
24	Q	2948	0	2659	515	0
25	R	2767	0	2471	435	0
26	S	2600	0	2160	286	0
27	T	1702	0	1373	187	0
28	U	2131	0	2038	366	0
29	V	2011	0	1980	311	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	W	1300	0	1134	209	0
31	Y	308	0	140	18	0
32	Z	3608	0	1688	215	0
33	x	2810	0	2763	378	0
34	y	601	0	630	30	0
35	H	27	0	12	9	0
35	I	27	0	12	7	0
35	J	27	0	12	8	0
35	K	27	0	12	21	0
35	L	27	0	12	5	0
35	M	27	0	12	4	0
All	All	98461	0	91505	9109	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 48.

The worst 5 of 9109 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)
28:U:23:PHE:CE2	28:U:126:VAL:HG11	1.18	1.67
20:N:35:TRP:CH2	26:S:273:LYS:HE2	1.19	1.67
17:K:41:TYR:CE2	20:N:155:LEU:HD23	1.21	1.63
14:H:111:TYR:CE2	14:H:125:LEU:CD2	1.77	1.62
14:H:111:TYR:CE2	14:H:125:LEU:HD22	1.31	1.60

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	a	200/239 (84%)	195 (98%)	4 (2%)	1 (0%)	24 62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	o	200/239 (84%)	195 (98%)	4 (2%)	1 (0%)	24	62
2	B	242/246 (98%)	228 (94%)	9 (4%)	5 (2%)	5	30
2	h	242/246 (98%)	230 (95%)	12 (5%)	0	100	100
3	b	218/277 (79%)	210 (96%)	7 (3%)	1 (0%)	24	62
3	p	218/277 (79%)	207 (95%)	9 (4%)	2 (1%)	14	49
4	C	231/234 (99%)	204 (88%)	24 (10%)	3 (1%)	9	41
4	i	229/234 (98%)	202 (88%)	24 (10%)	3 (1%)	9	41
5	c	202/205 (98%)	189 (94%)	11 (5%)	2 (1%)	12	47
5	q	202/205 (98%)	188 (93%)	11 (5%)	3 (2%)	8	38
6	D	248/261 (95%)	236 (95%)	11 (4%)	1 (0%)	30	66
6	j	248/261 (95%)	233 (94%)	12 (5%)	3 (1%)	10	43
7	d	197/201 (98%)	186 (94%)	10 (5%)	1 (0%)	24	62
7	r	197/201 (98%)	186 (94%)	9 (5%)	2 (1%)	12	47
8	E	241/248 (97%)	223 (92%)	12 (5%)	6 (2%)	4	26
8	k	241/248 (97%)	224 (93%)	11 (5%)	6 (2%)	4	26
9	e	199/263 (76%)	195 (98%)	4 (2%)	0	100	100
9	s	199/263 (76%)	191 (96%)	8 (4%)	0	100	100
10	F	232/241 (96%)	216 (93%)	14 (6%)	2 (1%)	14	49
10	l	232/241 (96%)	215 (93%)	15 (6%)	2 (1%)	14	49
11	f	211/241 (88%)	205 (97%)	6 (3%)	0	100	100
11	t	211/241 (88%)	202 (96%)	9 (4%)	0	100	100
12	G	236/263 (90%)	223 (94%)	10 (4%)	3 (1%)	9	41
12	m	236/263 (90%)	222 (94%)	10 (4%)	4 (2%)	7	35
13	g	214/264 (81%)	203 (95%)	10 (5%)	1 (0%)	24	62
13	u	215/264 (81%)	205 (95%)	9 (4%)	1 (0%)	24	62
14	H	376/433 (87%)	254 (68%)	81 (22%)	41 (11%)	0	6
15	I	355/440 (81%)	264 (74%)	63 (18%)	28 (8%)	1	10
16	J	354/406 (87%)	253 (72%)	68 (19%)	33 (9%)	0	8
17	K	378/418 (90%)	260 (69%)	73 (19%)	45 (12%)	0	4
18	L	373/389 (96%)	268 (72%)	69 (18%)	36 (10%)	0	7
19	M	372/439 (85%)	257 (69%)	72 (19%)	43 (12%)	0	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	N	815/953 (86%)	610 (75%)	176 (22%)	29 (4%)	2	20
21	X	241/255 (94%)	233 (97%)	5 (2%)	3 (1%)	10	43
21	n	241/255 (94%)	232 (96%)	7 (3%)	2 (1%)	16	52
22	O	368/376 (98%)	292 (79%)	55 (15%)	21 (6%)	1	14
23	P	401/456 (88%)	333 (83%)	55 (14%)	13 (3%)	3	21
24	Q	419/422 (99%)	324 (77%)	67 (16%)	28 (7%)	1	12
25	R	374/389 (96%)	292 (78%)	60 (16%)	22 (6%)	1	14
26	S	389/534 (73%)	332 (85%)	42 (11%)	15 (4%)	2	19
27	T	254/350 (73%)	191 (75%)	44 (17%)	19 (8%)	1	10
28	U	279/324 (86%)	224 (80%)	42 (15%)	13 (5%)	2	16
29	V	253/310 (82%)	210 (83%)	32 (13%)	11 (4%)	2	17
30	W	191/377 (51%)	143 (75%)	38 (20%)	10 (5%)	1	15
31	Y	55/70 (79%)	36 (66%)	12 (22%)	7 (13%)	0	4
32	Z	722/908 (80%)	560 (78%)	113 (16%)	49 (7%)	1	12
33	x	349/494 (71%)	245 (70%)	62 (18%)	42 (12%)	0	4
34	y	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
All	All	13374/15440 (87%)	11297 (84%)	1514 (11%)	563 (4%)	3	17

5 of 563 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	F	120	ALA
12	G	238	GLU
14	H	95	VAL
14	H	108	ASP
14	H	109	PRO

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	a	155/181 (86%)	147 (95%)	8 (5%)	21	43
1	o	155/181 (86%)	148 (96%)	7 (4%)	24	46
2	B	193/210 (92%)	182 (94%)	11 (6%)	18	41
2	h	195/210 (93%)	183 (94%)	12 (6%)	16	38
3	b	177/228 (78%)	168 (95%)	9 (5%)	21	43
3	p	177/228 (78%)	167 (94%)	10 (6%)	19	41
4	C	163/191 (85%)	154 (94%)	9 (6%)	19	42
4	i	177/191 (93%)	163 (92%)	14 (8%)	11	32
5	c	172/174 (99%)	160 (93%)	12 (7%)	14	36
5	q	172/174 (99%)	160 (93%)	12 (7%)	14	36
6	D	193/221 (87%)	181 (94%)	12 (6%)	16	38
6	j	193/221 (87%)	180 (93%)	13 (7%)	15	37
7	d	164/171 (96%)	156 (95%)	8 (5%)	22	44
7	r	164/171 (96%)	155 (94%)	9 (6%)	19	42
8	E	152/211 (72%)	136 (90%)	16 (10%)	6	22
8	k	142/211 (67%)	134 (94%)	8 (6%)	19	41
9	e	153/202 (76%)	148 (97%)	5 (3%)	33	55
9	s	154/202 (76%)	148 (96%)	6 (4%)	28	50
10	F	190/203 (94%)	185 (97%)	5 (3%)	40	60
10	l	191/203 (94%)	183 (96%)	8 (4%)	26	48
11	f	174/199 (87%)	167 (96%)	7 (4%)	28	49
11	t	175/199 (88%)	168 (96%)	7 (4%)	28	49
12	G	198/224 (88%)	189 (96%)	9 (4%)	24	46
12	m	198/224 (88%)	182 (92%)	16 (8%)	11	31
13	g	175/215 (81%)	165 (94%)	10 (6%)	18	41
13	u	175/215 (81%)	166 (95%)	9 (5%)	21	43
14	H	292/372 (78%)	232 (80%)	60 (20%)	1	8
15	I	291/385 (76%)	228 (78%)	63 (22%)	1	6
16	J	310/352 (88%)	241 (78%)	69 (22%)	1	6
17	K	333/366 (91%)	260 (78%)	73 (22%)	1	6
18	L	298/341 (87%)	237 (80%)	61 (20%)	1	8
19	M	296/379 (78%)	239 (81%)	57 (19%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	N	377/816 (46%)	344 (91%)	33 (9%)	9	29
21	X	193/212 (91%)	185 (96%)	8 (4%)	27	49
21	n	193/212 (91%)	182 (94%)	11 (6%)	18	41
22	O	144/336 (43%)	122 (85%)	22 (15%)	3	13
23	P	202/416 (49%)	178 (88%)	24 (12%)	5	19
24	Q	249/362 (69%)	205 (82%)	44 (18%)	2	11
25	R	226/344 (66%)	199 (88%)	27 (12%)	5	19
26	S	163/460 (35%)	155 (95%)	8 (5%)	22	44
27	T	109/294 (37%)	91 (84%)	18 (16%)	2	12
28	U	212/295 (72%)	188 (89%)	24 (11%)	5	20
29	V	219/268 (82%)	188 (86%)	31 (14%)	3	15
30	W	109/312 (35%)	102 (94%)	7 (6%)	16	38
31	Y	4/63 (6%)	4 (100%)	0	100	100
33	x	305/439 (70%)	250 (82%)	55 (18%)	2	10
34	y	68/68 (100%)	63 (93%)	5 (7%)	13	34
All	All	9120/12352 (74%)	8168 (90%)	952 (10%)	9	23

5 of 952 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	L	226	GLN
21	X	90	ILE
12	m	236	LEU
30	W	23	PRO
33	x	471	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 167 such sidechains are listed below:

Mol	Chain	Res	Type
25	R	280	GLN
29	V	298	GLN
7	r	61	GLN
28	U	102	HIS
33	x	176	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	GLZ	y	76	34	3,3,3	0.85	0	1,2,2	0.34	0

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	GLZ	y	76	34	-	0/0/1/1	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	y	76	GLZ	1	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

6 ligands are modelled in this entry.

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
35	ADP	K	501	-	28,29,29	1.71	6 (21%)	43,45,45	2.42	18 (41%)
35	ADP	M	501	-	28,29,29	1.95	7 (25%)	43,45,45	1.91	13 (30%)
35	ADP	J	501	-	28,29,29	1.64	8 (28%)	43,45,45	2.56	15 (34%)
35	ADP	L	401	-	28,29,29	1.58	4 (14%)	43,45,45	2.14	14 (32%)
35	ADP	H	501	-	28,29,29	2.20	7 (25%)	43,45,45	2.79	21 (48%)
35	ADP	I	501	-	28,29,29	2.15	7 (25%)	43,45,45	1.87	9 (20%)

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
35	ADP	K	501	-	-	3/16/32/32	0/3/3/3
35	ADP	M	501	-	-	5/16/32/32	0/3/3/3
35	ADP	J	501	-	-	5/16/32/32	0/3/3/3
35	ADP	L	401	-	-	2/16/32/32	0/3/3/3
35	ADP	H	501	-	-	1/16/32/32	0/3/3/3
35	ADP	I	501	-	-	3/16/32/32	0/3/3/3

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	I	501	ADP	C5-C4	7.56	1.52	1.39
35	H	501	ADP	PA-O3A	7.35	1.67	1.59
35	M	501	ADP	PA-O3A	5.87	1.65	1.59
35	L	401	ADP	C5-C4	5.08	1.48	1.39
35	M	501	ADP	C5-C4	4.97	1.47	1.39

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	H	501	ADP	C5-C4-N3	-7.39	116.54	126.72
35	K	501	ADP	C5-C4-N3	-6.72	117.47	126.72
35	J	501	ADP	C5-C4-N3	-6.55	117.70	126.72
35	L	401	ADP	C5-C4-N3	-6.00	118.46	126.72
35	H	501	ADP	C3'-C2'-C1'	5.98	112.77	101.46

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

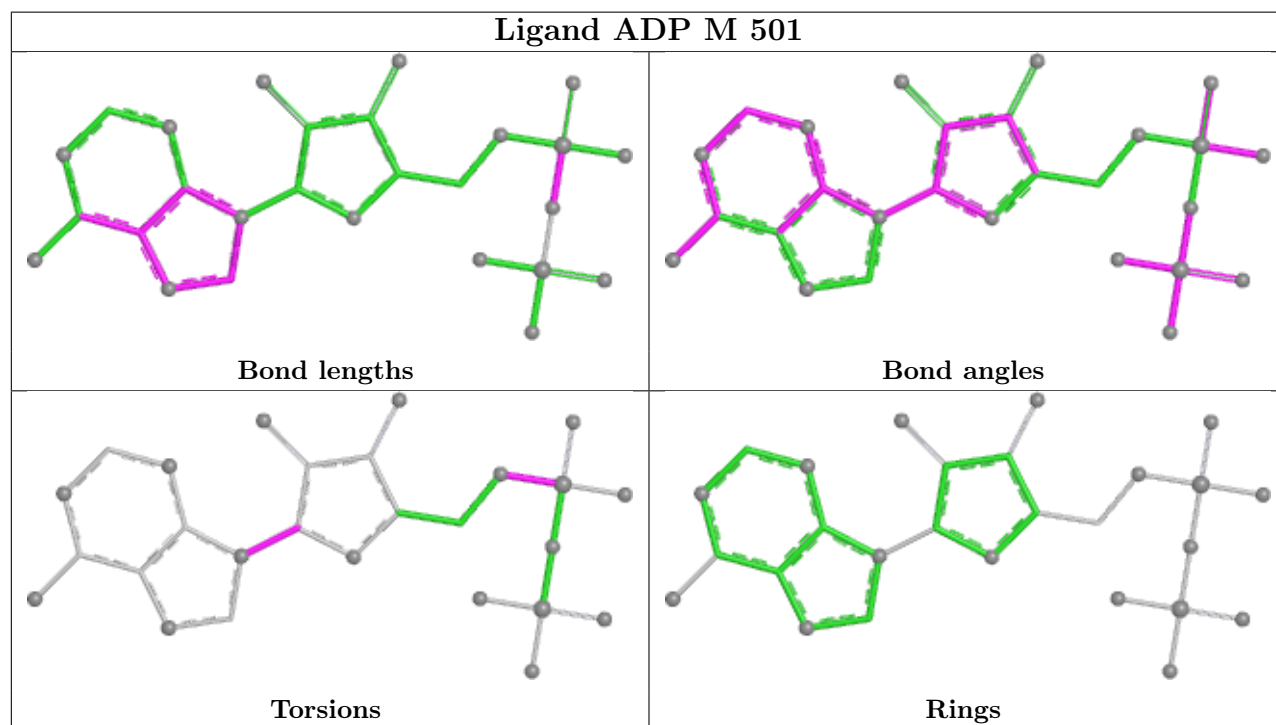
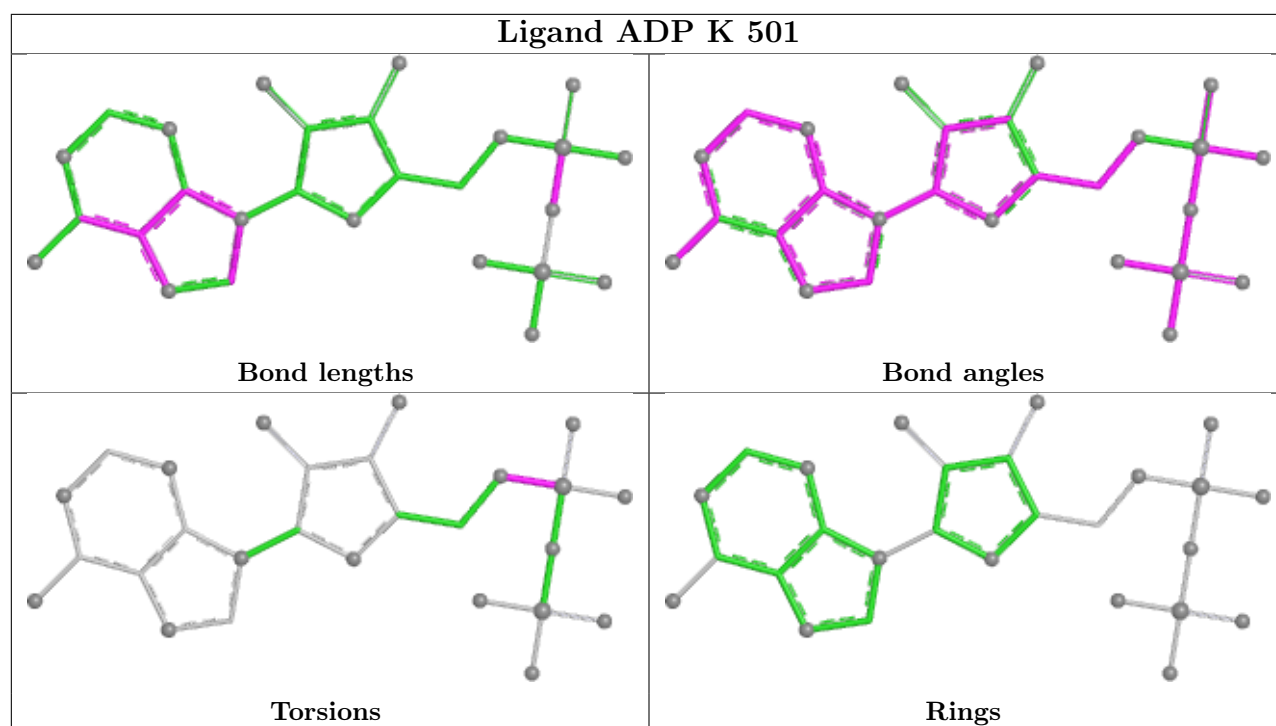
Mol	Chain	Res	Type	Atoms
35	J	501	ADP	C5'-O5'-PA-O1A
35	J	501	ADP	C5'-O5'-PA-O2A
35	J	501	ADP	C5'-O5'-PA-O3A
35	J	501	ADP	O4'-C4'-C5'-O5'
35	K	501	ADP	C5'-O5'-PA-O1A

There are no ring outliers.

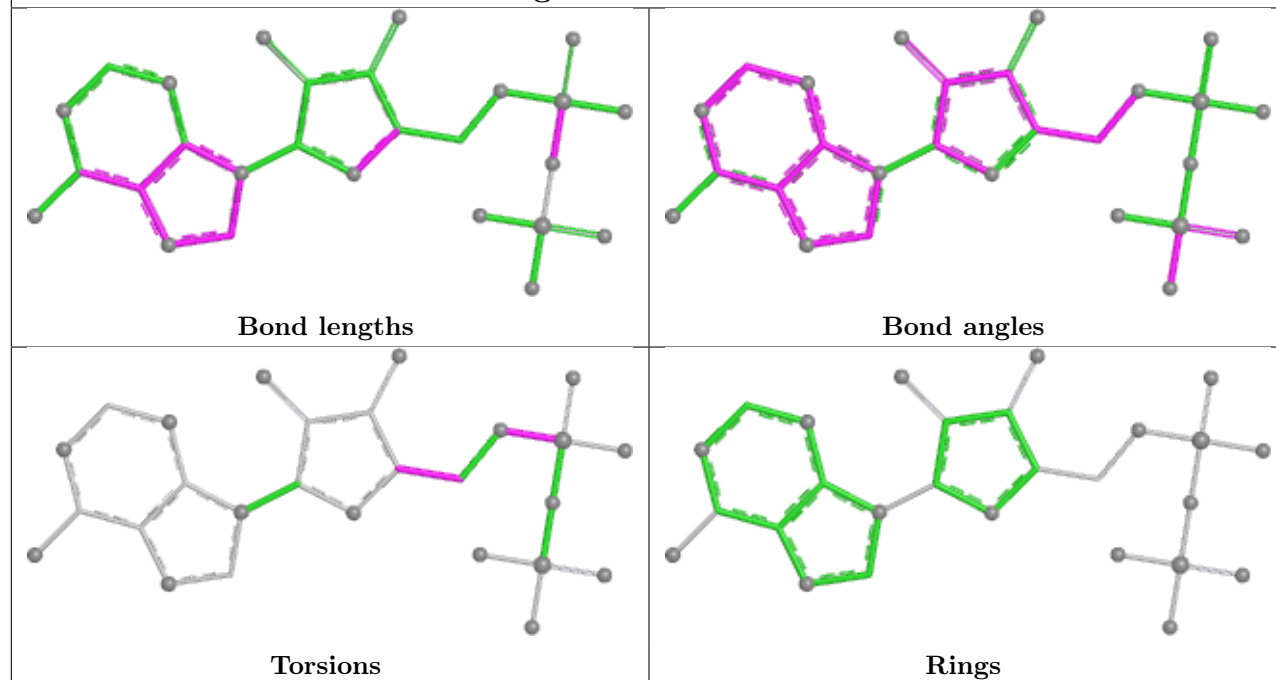
6 monomers are involved in 54 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	K	501	ADP	21	0
35	M	501	ADP	4	0
35	J	501	ADP	8	0
35	L	401	ADP	5	0
35	H	501	ADP	9	0
35	I	501	ADP	7	0

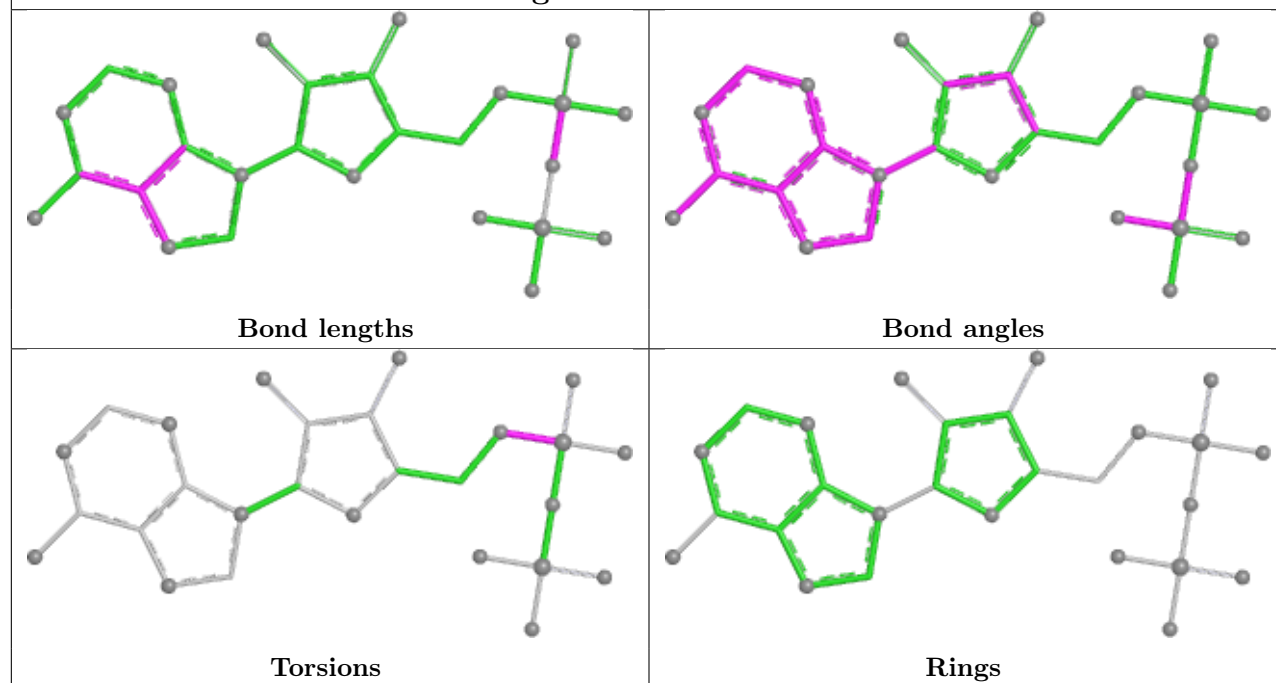
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

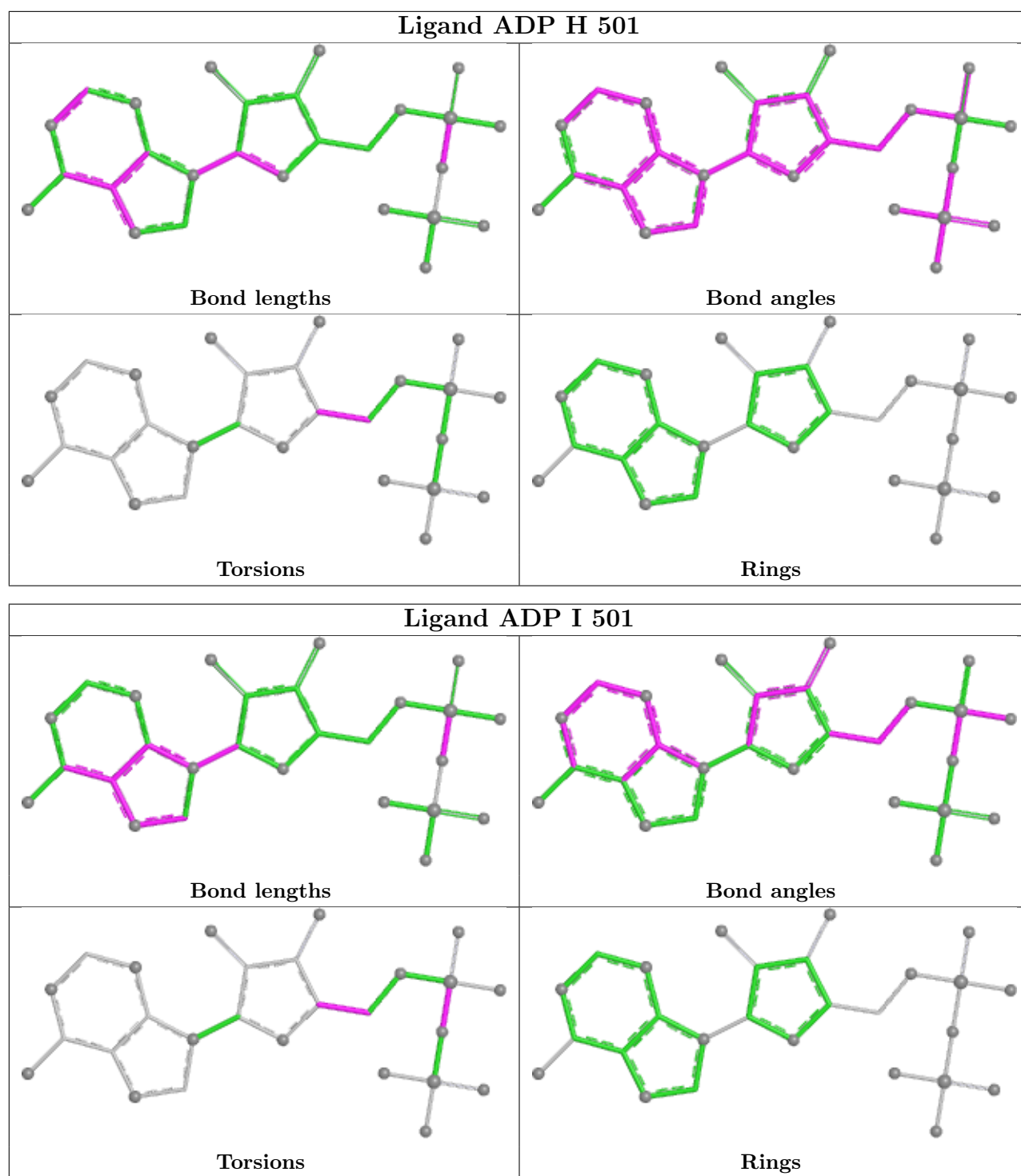


Ligand ADP J 501



Ligand ADP L 401





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

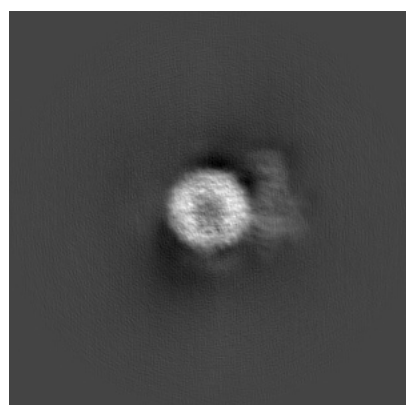
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9511. These allow visual inspection of the internal detail of the map and identification of artifacts.

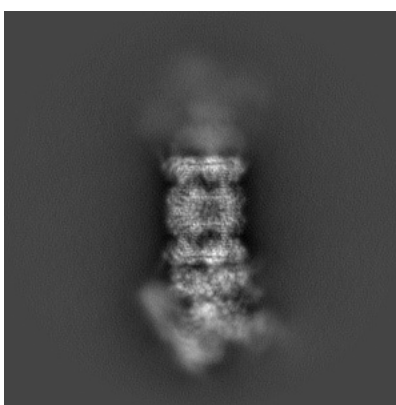
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

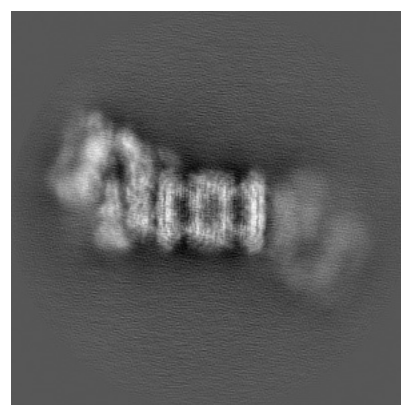
6.1.1 Primary map



X



Y

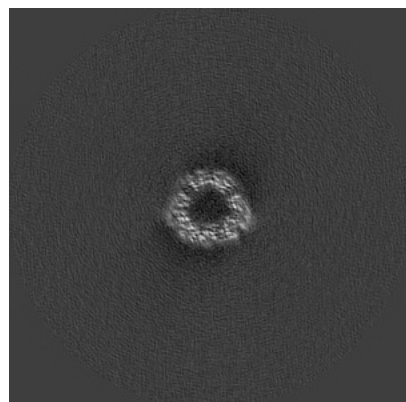


Z

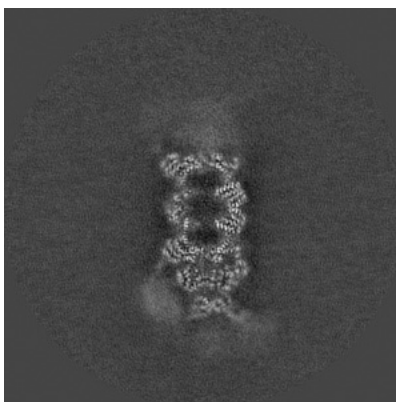
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

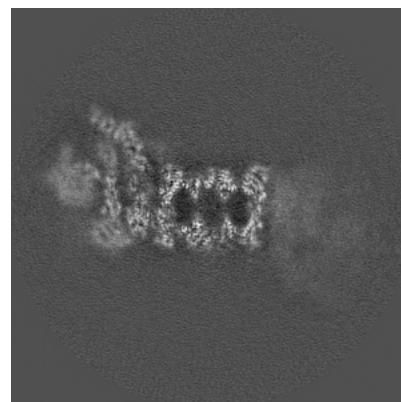
6.2.1 Primary map



X Index: 256



Y Index: 256

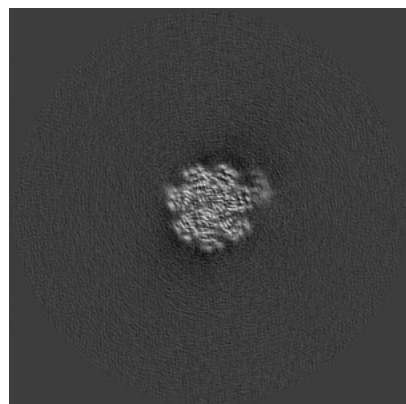


Z Index: 256

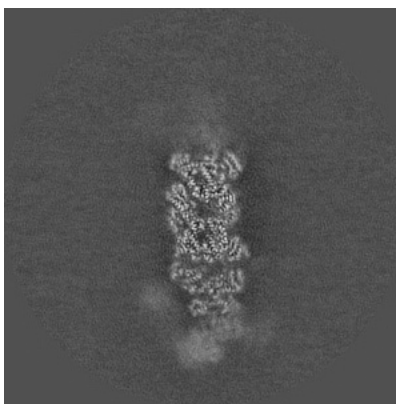
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

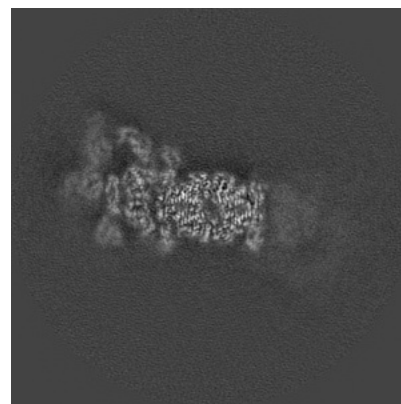
6.3.1 Primary map



X Index: 202



Y Index: 278

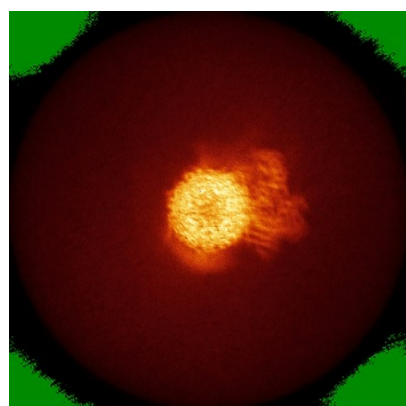


Z Index: 280

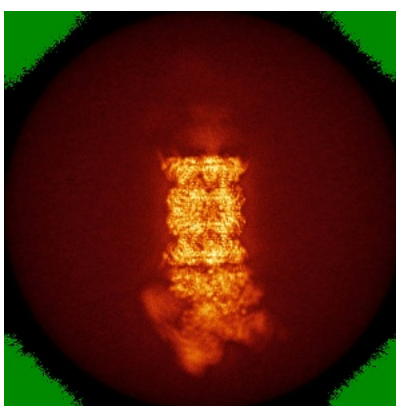
The images above show the largest variance slices of the map in three orthogonal directions.

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

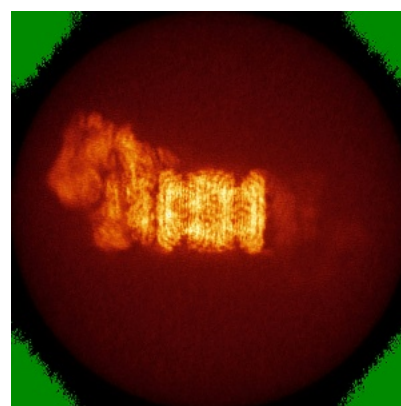
6.4.1 Primary map



X



Y

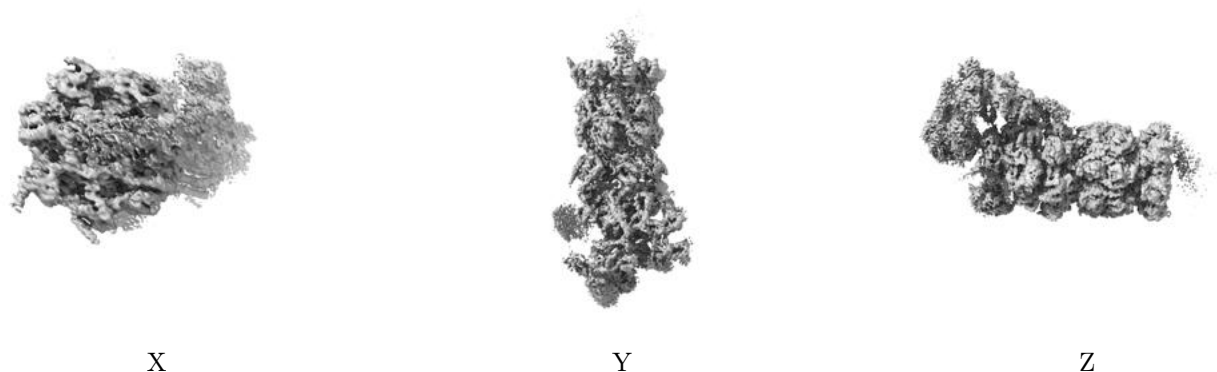


Z

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

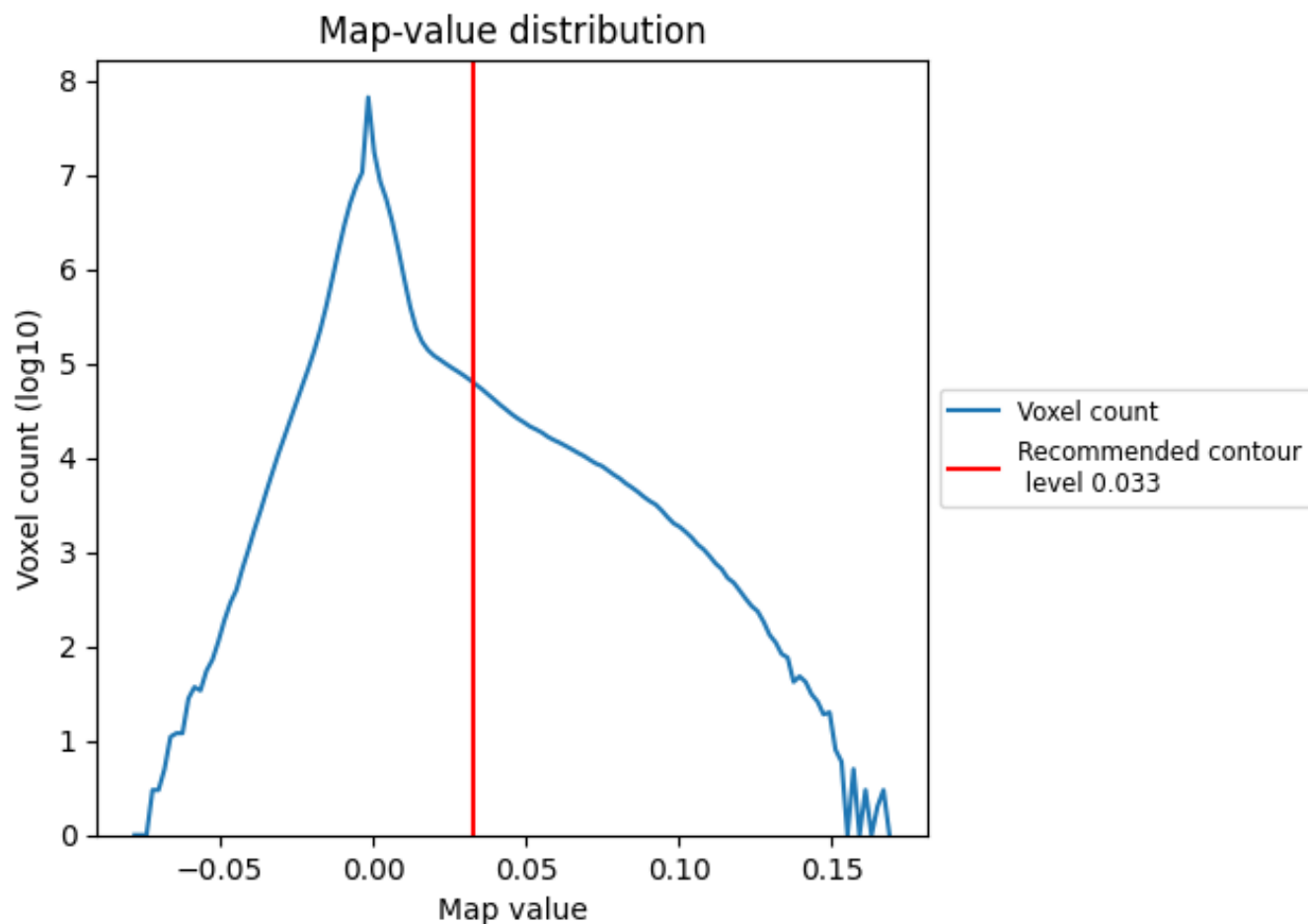
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

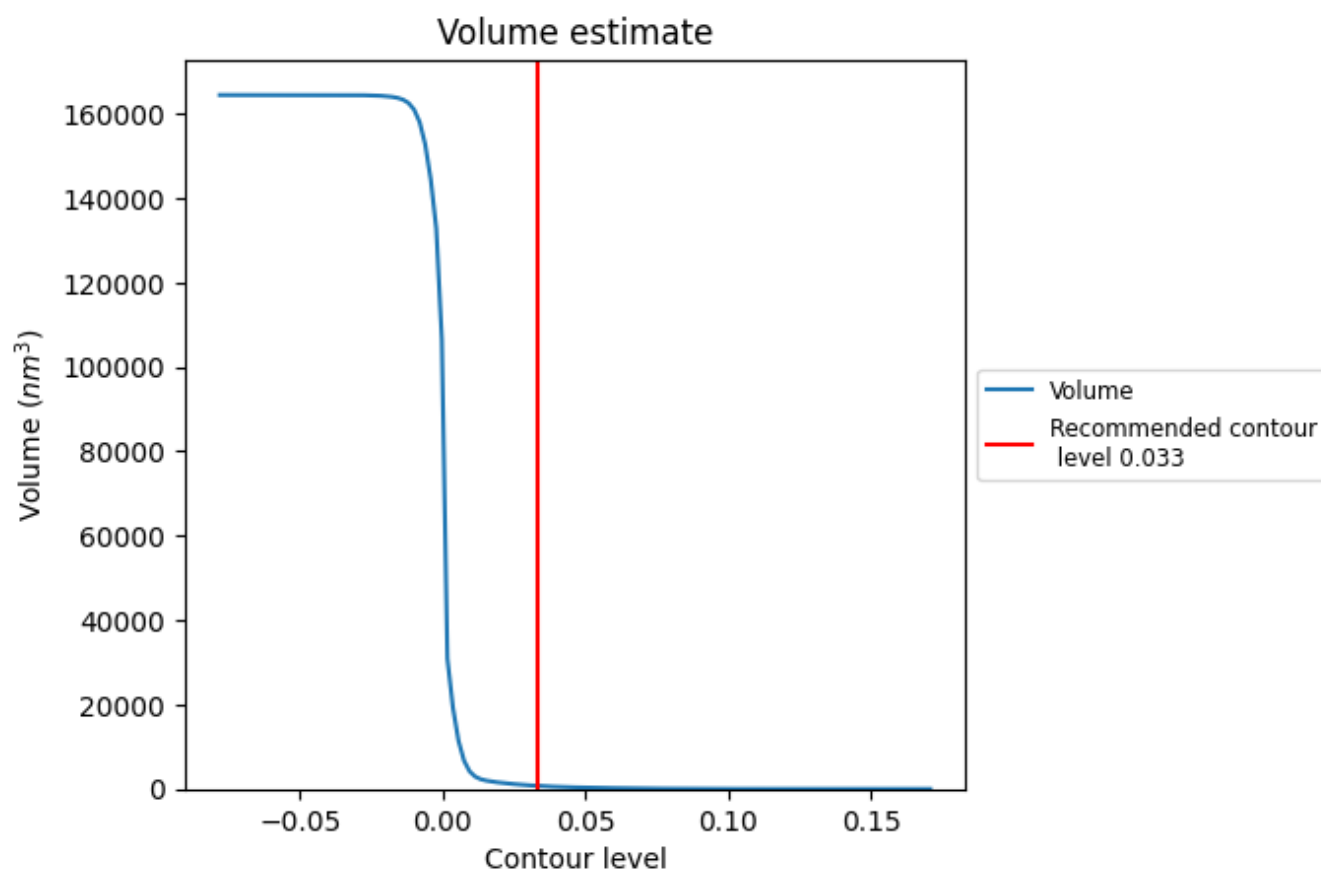
This section contains the results of statistical analysis of the map.

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.

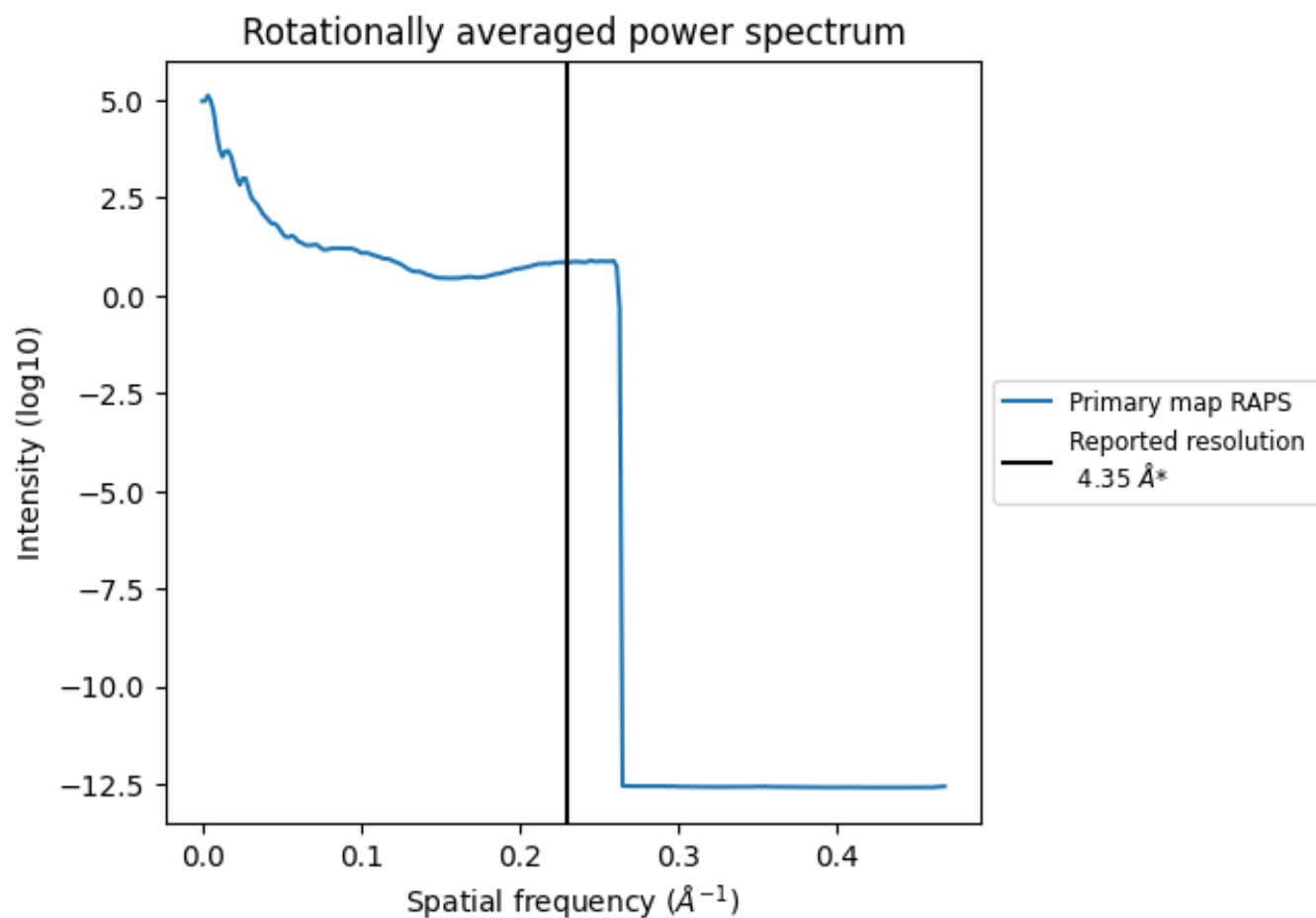
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 752 nm^3 ; this corresponds to an approximate mass of 679 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 0.230 $\text{\AA}^{-1}$

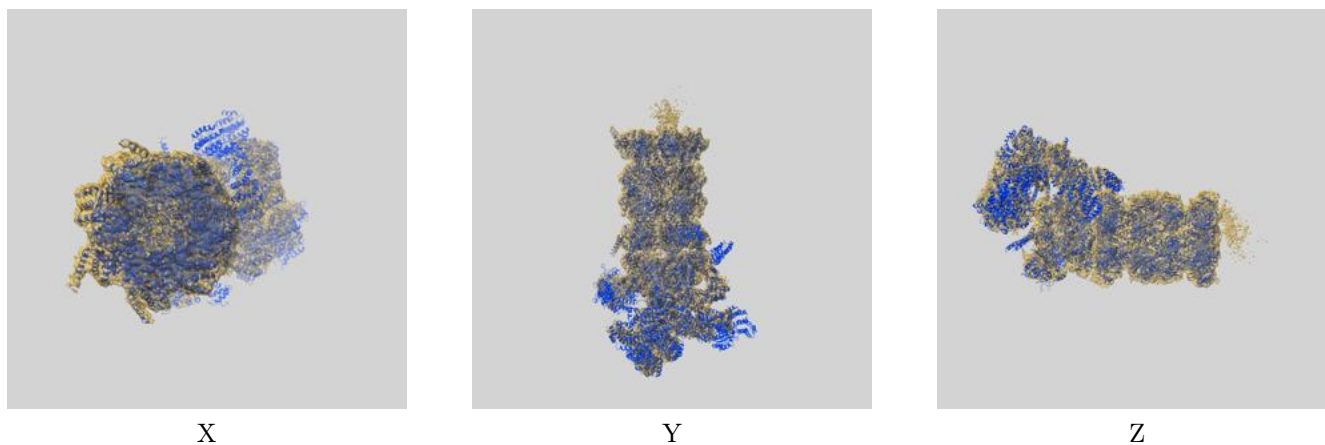
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

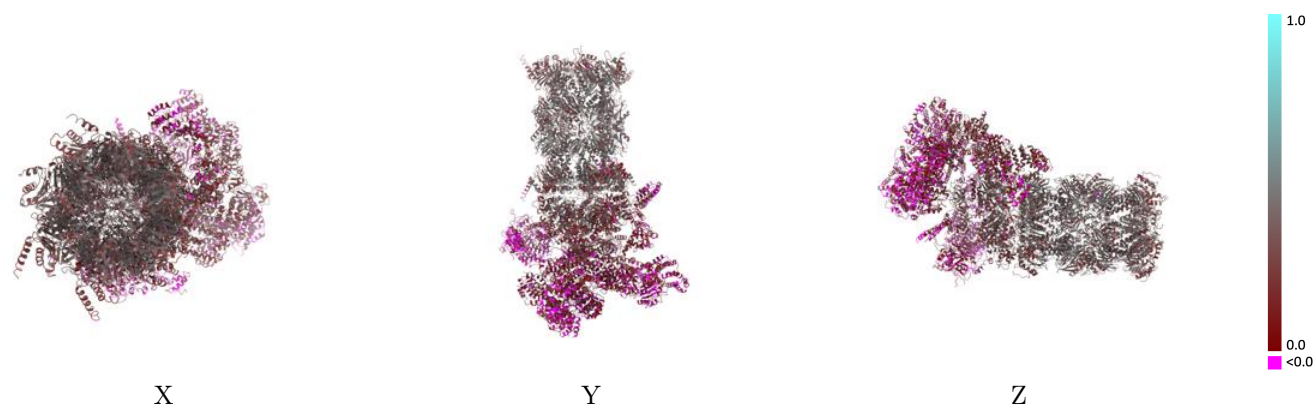
This section contains information regarding the fit between EMDB map EMD-9511 and PDB model 5GJQ. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



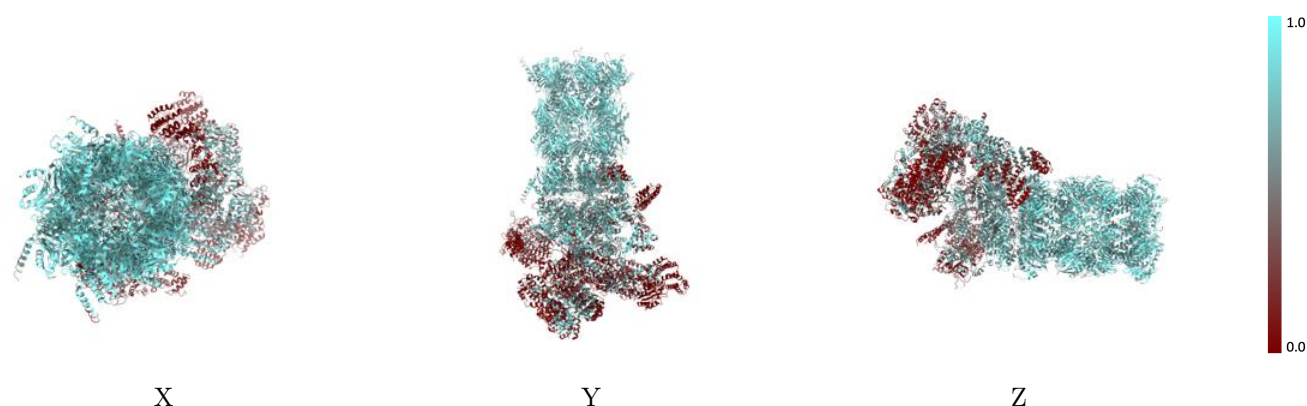
The images above show the 3D surface view of the map at the recommended contour level 0.033 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



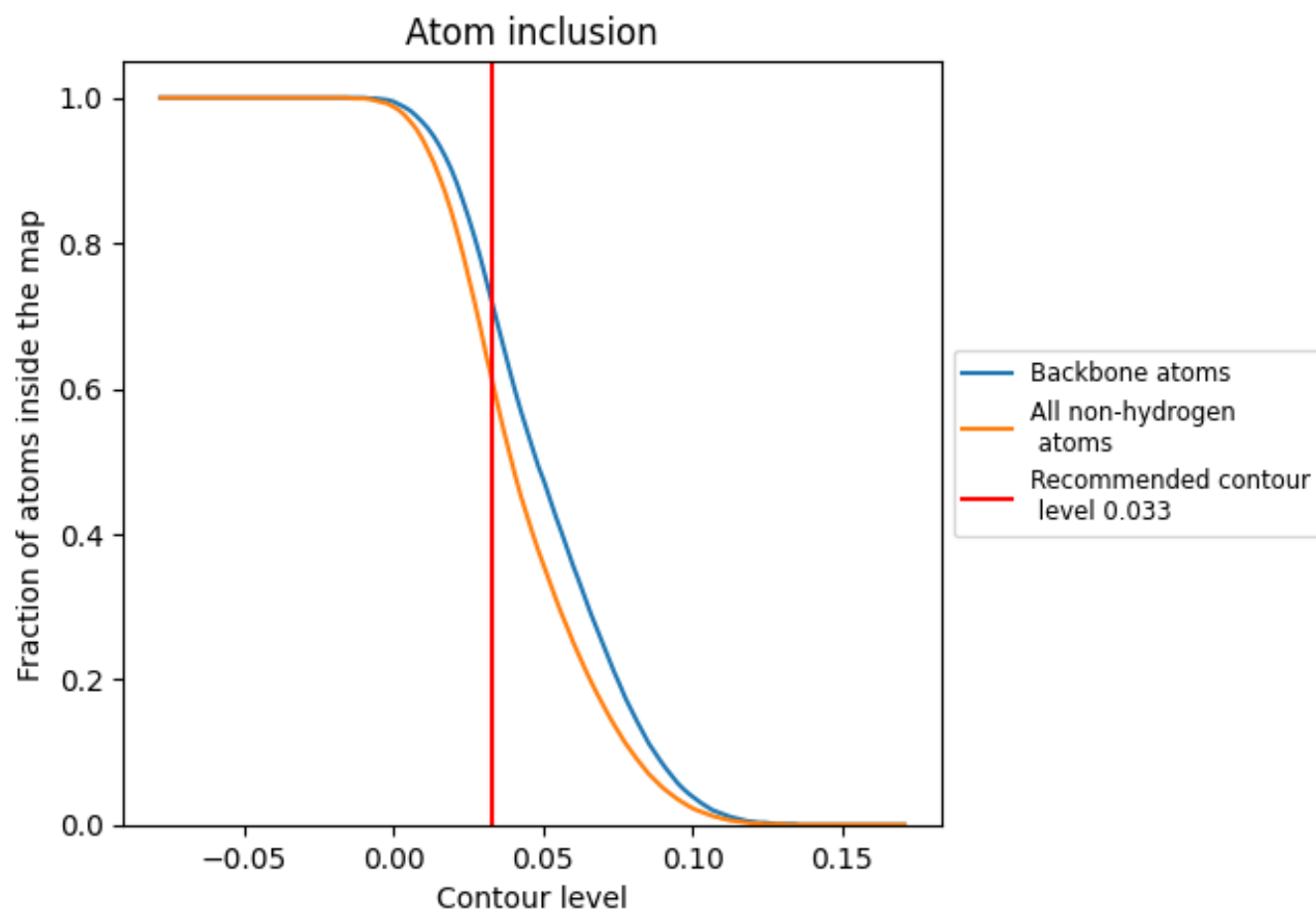
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.033).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 61% 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 (0.033) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6090	 0.2740
B	 0.7940	 0.3520
C	 0.8170	 0.3590
D	 0.8030	 0.3480
E	 0.7650	 0.3130
F	 0.7880	 0.3570
G	 0.8010	 0.3490
H	 0.6430	 0.3090
I	 0.6240	 0.3070
J	 0.6240	 0.2940
K	 0.6550	 0.2840
L	 0.6180	 0.2840
M	 0.6230	 0.2930
N	 0.3860	 0.0710
O	 0.2560	 0.1060
P	 0.3280	 0.1410
Q	 0.4820	 0.2210
R	 0.5940	 0.2160
S	 0.2860	 0.1500
T	 0.1910	 0.1140
U	 0.2700	 0.1230
V	 0.3090	 0.1700
W	 0.0050	 0.0270
X	 0.8120	 0.3640
Y	 0.2760	 0.2040
Z	 0.0790	 0.0230
a	 0.8080	 0.3870
b	 0.8040	 0.3810
c	 0.8050	 0.3870
d	 0.8300	 0.3760
e	 0.8260	 0.3890
f	 0.8470	 0.3860
g	 0.8620	 0.4020
h	 0.7820	 0.3800
i	 0.7940	 0.3970



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Chain	Atom inclusion	Q-score
j	 0.7640	 0.3570
k	 0.7650	 0.3420
l	 0.7860	 0.3670
m	 0.8120	 0.3770
n	 0.7870	 0.3670
o	 0.8400	 0.3930
p	 0.8350	 0.3940
q	 0.8350	 0.4030
r	 0.8140	 0.3910
s	 0.8590	 0.3920
t	 0.8000	 0.3950
u	 0.8160	 0.3960
x	 0.3770	 0.1260
y	 0.2700	 0.0860