



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 11:52 PM UTC

PDB ID : 7QYA / pdb_00007qya
EMDB ID : EMD-14210
Title : Proteasome-ZFAND5 Complex Z-B state
Authors : Zhu, Y.; Lu, Y.
Deposited on : 2022-01-27
Resolution : 4.80 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

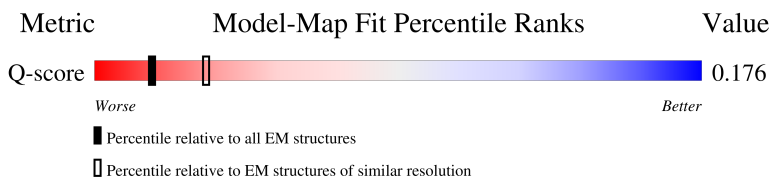
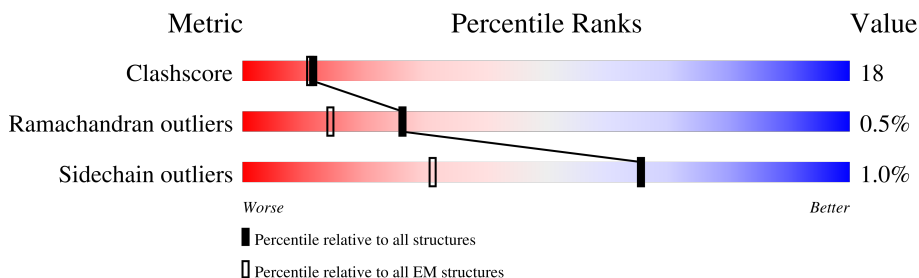
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

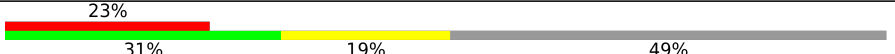
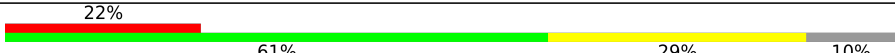
The reported resolution of this entry is 4.80 Å.

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	1575 (4.30 - 5.30)

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	376	
2	b	377	
3	c	309	
4	d	349	

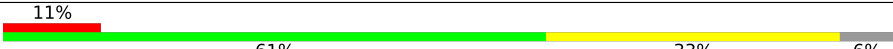
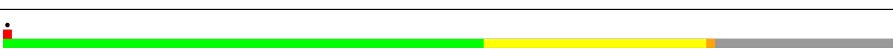
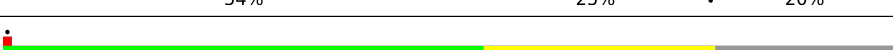
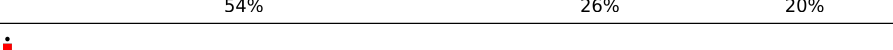
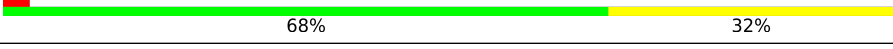
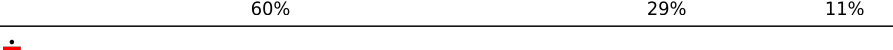
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Mol	Chain	Length	Quality of chain
5	e	70	
6	f	908	
7	U	953	
8	V	533	
9	W	456	
10	X	422	
11	Y	389	
12	Z	324	
13	A	433	
14	B	440	
15	C	398	
16	D	418	
17	E	403	
18	F	439	
19	G	245	
19	g	245	
20	H	233	
20	h	233	
21	I	260	
21	i	260	
22	J	247	
22	j	247	
23	K	240	
23	k	240	
24	L	268	

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Mol	Chain	Length	Quality of chain
24	l	268	
25	M	254	
25	m	254	
26	N	238	
26	n	238	
27	O	276	
27	o	276	
28	P	204	
28	p	204	
29	Q	201	
29	q	201	
30	R	262	
30	r	262	
31	S	240	
31	s	240	
32	T	263	
32	t	263	

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 101325 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 26S proteasome non-ATPase regulatory subunit 13.

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

- Molecule 2 is a protein called 26S proteasome non-ATPase regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	191	Total	C	N	O	S	0	0
			1457	910	260	279	8		

- Molecule 3 is a protein called 26S proteasome non-ATPase regulatory subunit 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	278	Total	C	N	O	S	0	0
			2186	1389	373	406	18		

- Molecule 4 is a protein called 26S proteasome non-ATPase regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	257	Total	C	N	O	S	0	0
			2115	1371	345	390	9		

- Molecule 5 is a protein called 26S proteasome complex subunit SEM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	40	Total	C	N	O	S	0	0
			333	200	54	77	2		

- Molecule 6 is a protein called 26S proteasome non-ATPase regulatory subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	689	Total	C	N	O	S	0	0
			5318	3343	903	1037	35		

- Molecule 7 is a protein called 26S proteasome non-ATPase regulatory subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	U	806	Total	C	N	O	S	0	0
			6286	3990	1074	1178	44		

- Molecule 8 is a protein called 26S proteasome non-ATPase regulatory subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	473	Total	C	N	O	S	0	0
			3807	2418	675	700	14		

- Molecule 9 is a protein called 26S proteasome non-ATPase regulatory subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	W	456	Total	C	N	O	S	0	0
			3702	2339	634	704	25		

- Molecule 10 is a protein called 26S proteasome non-ATPase regulatory subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	X	380	Total	C	N	O	S	0	0
			3008	1918	508	570	12		

- Molecule 11 is a protein called 26S proteasome non-ATPase regulatory subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Y	378	Total	C	N	O	S	0	0
			3114	1987	532	578	17		

- Molecule 12 is a protein called 26S proteasome non-ATPase regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Z	286	Total	C	N	O	S	0	0
			2280	1457	391	427	5		

- Molecule 13 is a protein called 26S protease regulatory subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A	380	Total	C	N	O	S	0	0
			2892	1817	514	543	18		

- Molecule 14 is a protein called 26S protease regulatory subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	B	370	Total	C	N	O	S	0	0
			2805	1763	477	553	12		

- Molecule 15 is a protein called Isoform 2 of 26S proteasome regulatory subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	C	363	Total	C	N	O	S	0	0
			2858	1804	512	525	17		

- Molecule 16 is a protein called 26S protease regulatory subunit 6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	D	380	Total	C	N	O	S	0	0
			3039	1923	523	580	13		

- Molecule 17 is a protein called 26S proteasome regulatory subunit 10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	E	375	Total	C	N	O	S	0	0
			2859	1796	511	536	16		

- Molecule 18 is a protein called 26S protease regulatory subunit 6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	F	376	Total	C	N	O	S	0	0
			2858	1802	495	546	15		

- Molecule 19 is a protein called Proteasome subunit alpha type-6.

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

- Molecule 20 is a protein called Proteasome subunit alpha type-2.

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

- Molecule 21 is a protein called Proteasome subunit alpha type-4.

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

- Molecule 22 is a protein called Proteasome subunit alpha type-7.

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

- Molecule 23 is a protein called Proteasome subunit alpha type-5.

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

- Molecule 24 is a protein called Isoform Long of Proteasome subunit alpha type-1.

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

- Molecule 25 is a protein called Proteasome subunit alpha type-3.

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

- Molecule 26 is a protein called Proteasome subunit beta type-6.

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

- Molecule 27 is a protein called Proteasome subunit beta type-7.

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

- Molecule 28 is a protein called Proteasome subunit beta type-3.

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

- Molecule 29 is a protein called Proteasome subunit beta type-2.

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

- Molecule 30 is a protein called Proteasome subunit beta type-5.

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

- Molecule 31 is a protein called Proteasome subunit beta type-1.

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

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

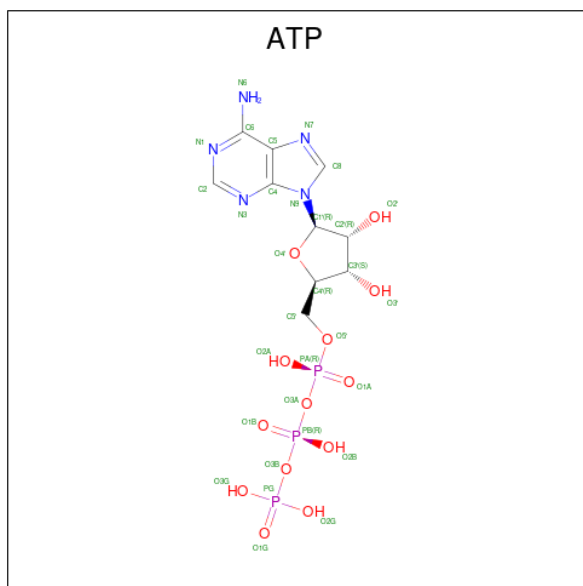
- Molecule 32 is a protein called Proteasome subunit beta type-4.

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

- Molecule 33 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 34 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
34	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
34	D	1	Total	C	N	O	P	0
			31	10	5	13	3	

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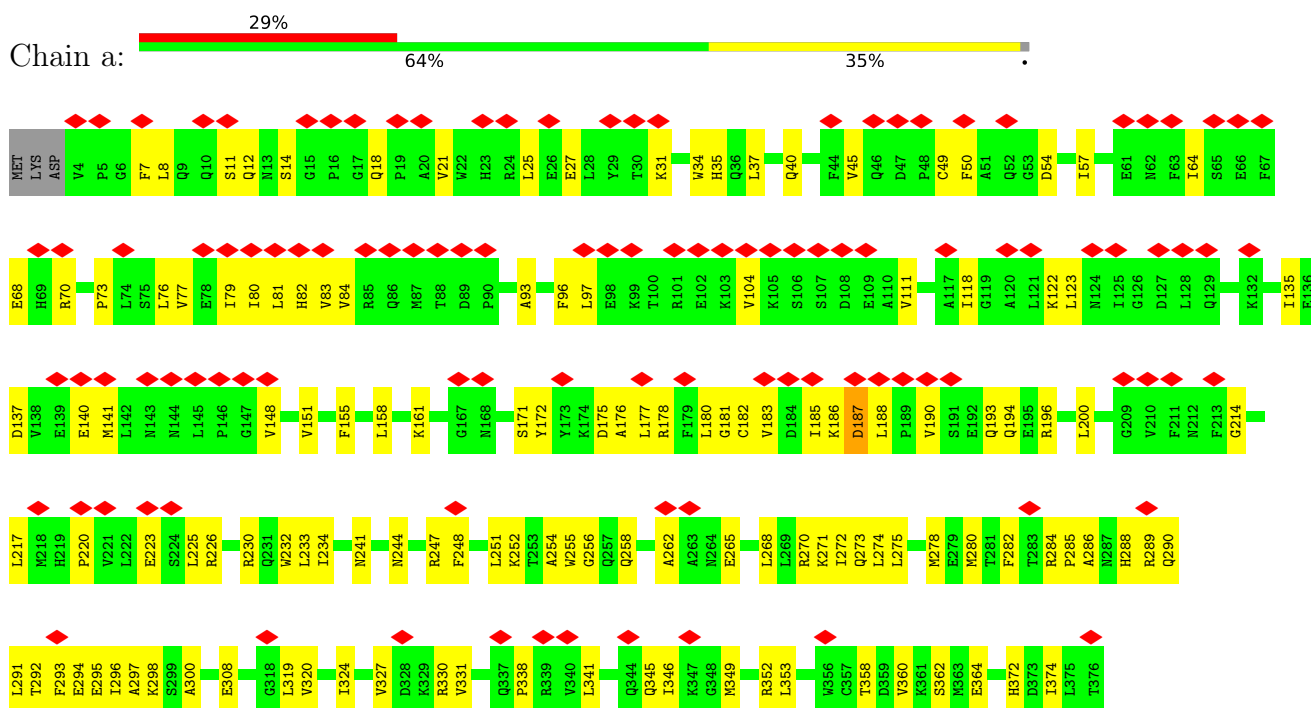
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Mol	Chain	Residues	Atoms					AltConf
34	E	1	Total	C	N	O	P	0
			31	10	5	13	3	
34	F	1	Total	C	N	O	P	0
			31	10	5	13	3	

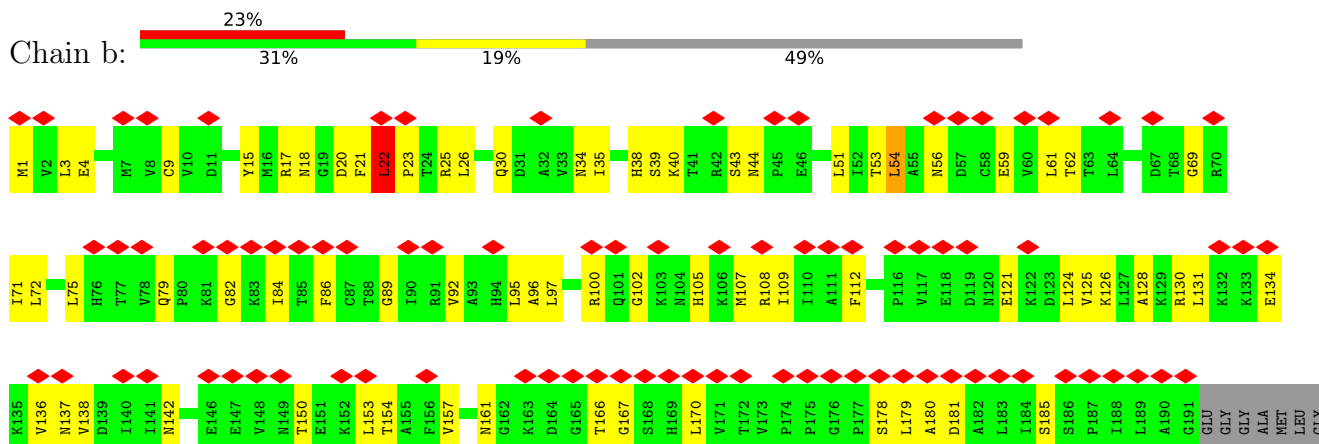
3 Residue-property plots

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

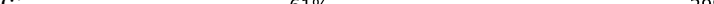
- Molecule 1: 26S proteasome non-ATPase regulatory subunit 13

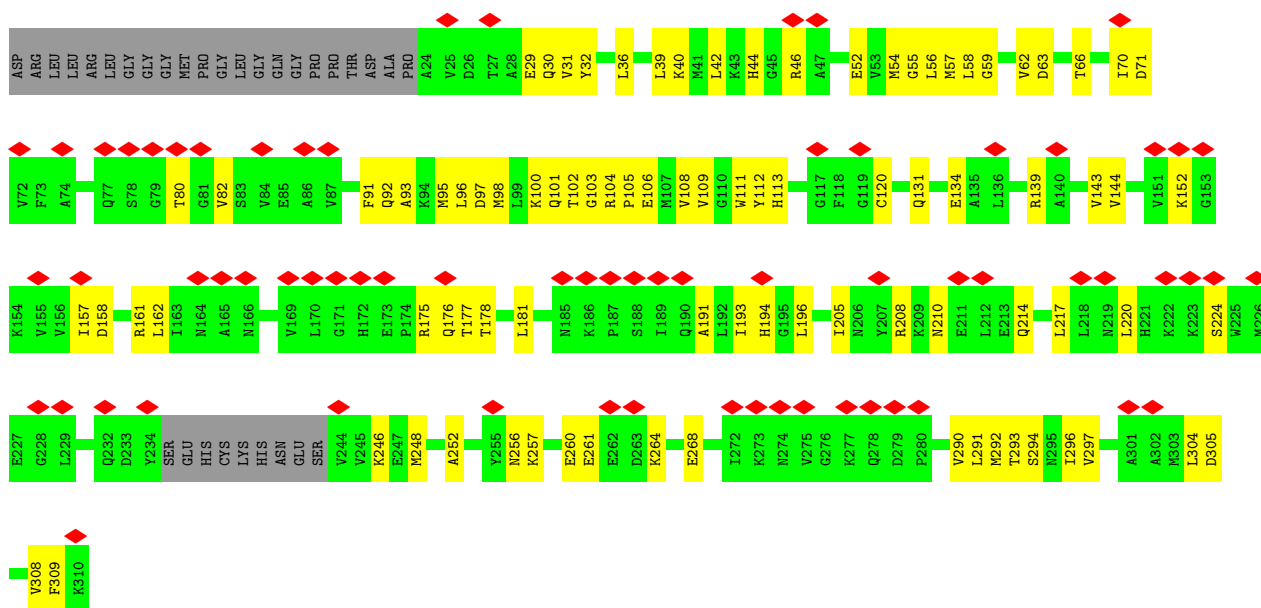


- Molecule 2: 26S proteasome non-ATPase regulatory subunit 4

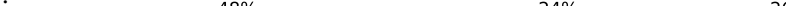


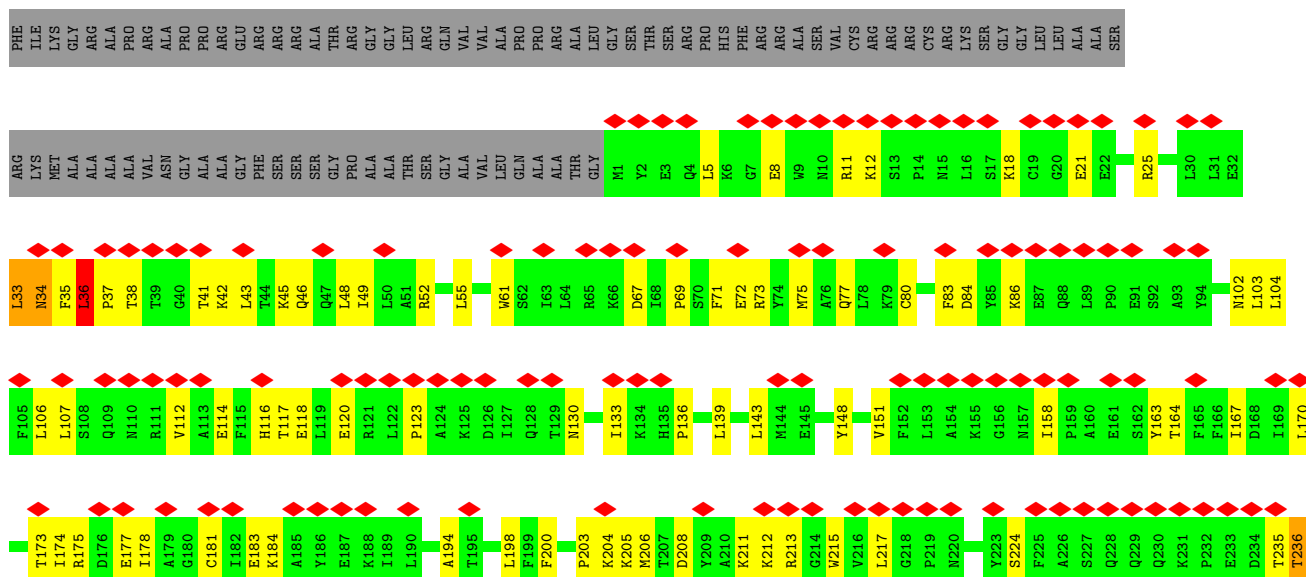
- Molecule 3: 26S proteasome non-ATPase regulatory subunit 14

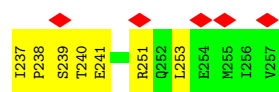
Chain c: 



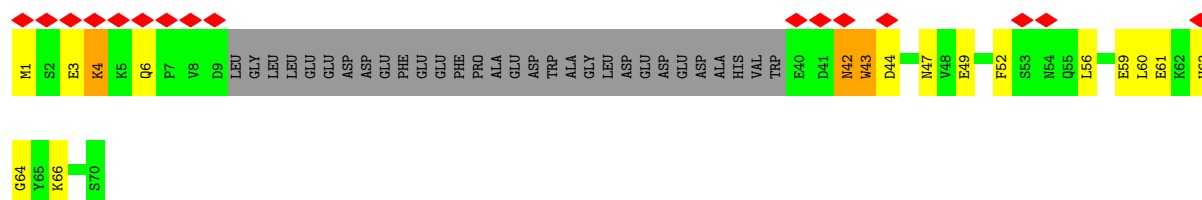
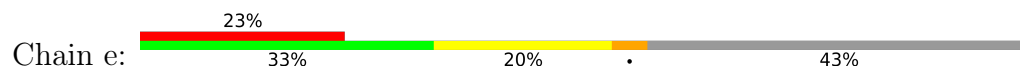
- Molecule 4: 26S proteasome non-ATPase regulatory subunit 8

Chain d: 

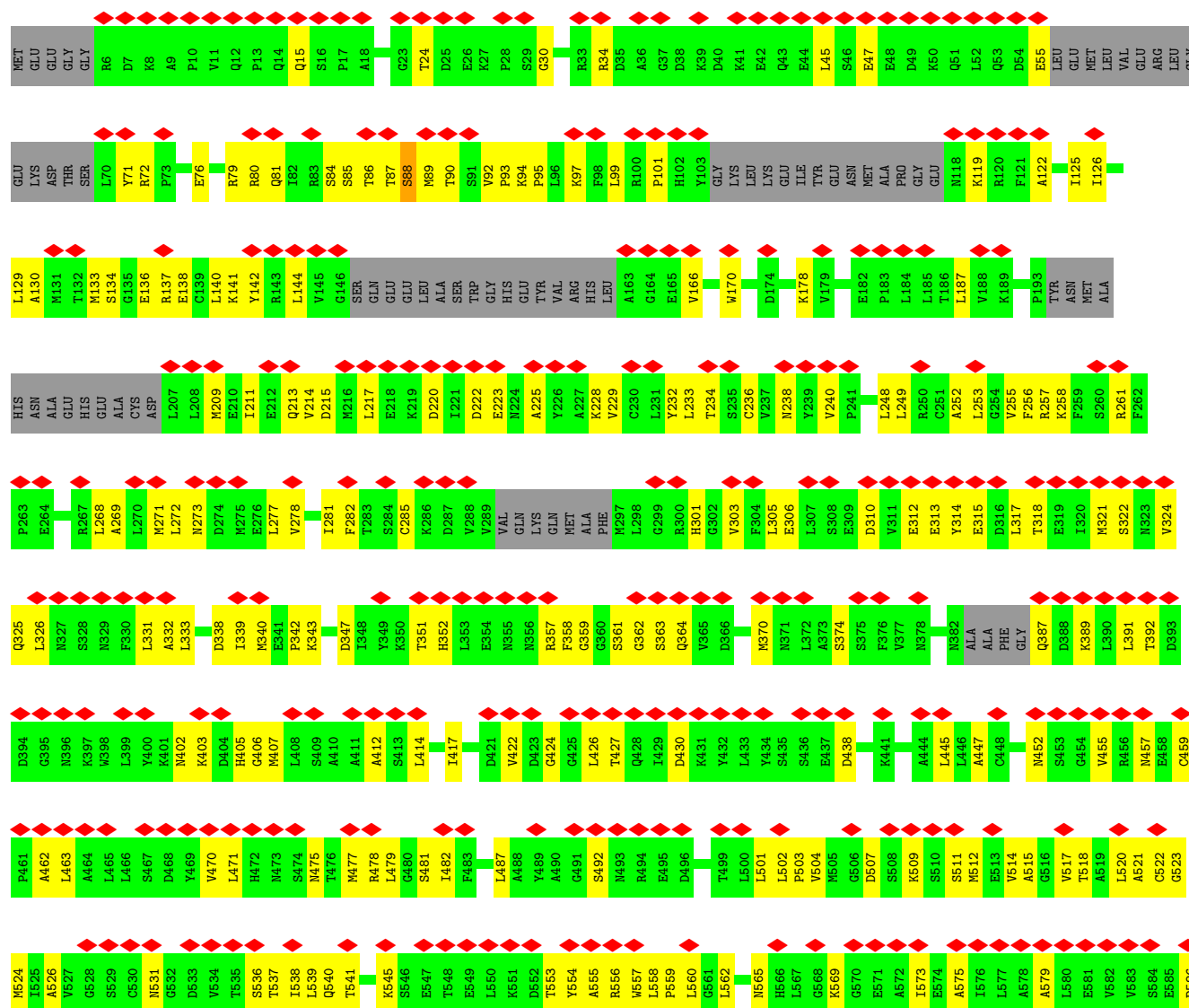
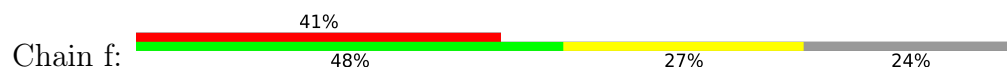


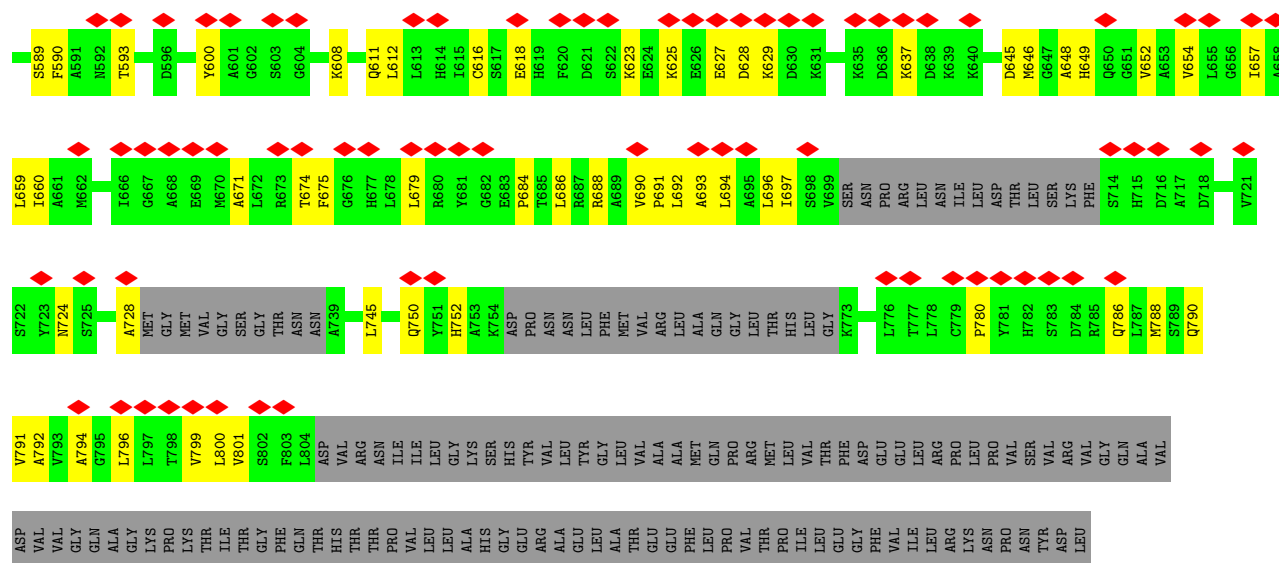


• Molecule 5: 26S proteasome complex subunit SEM1

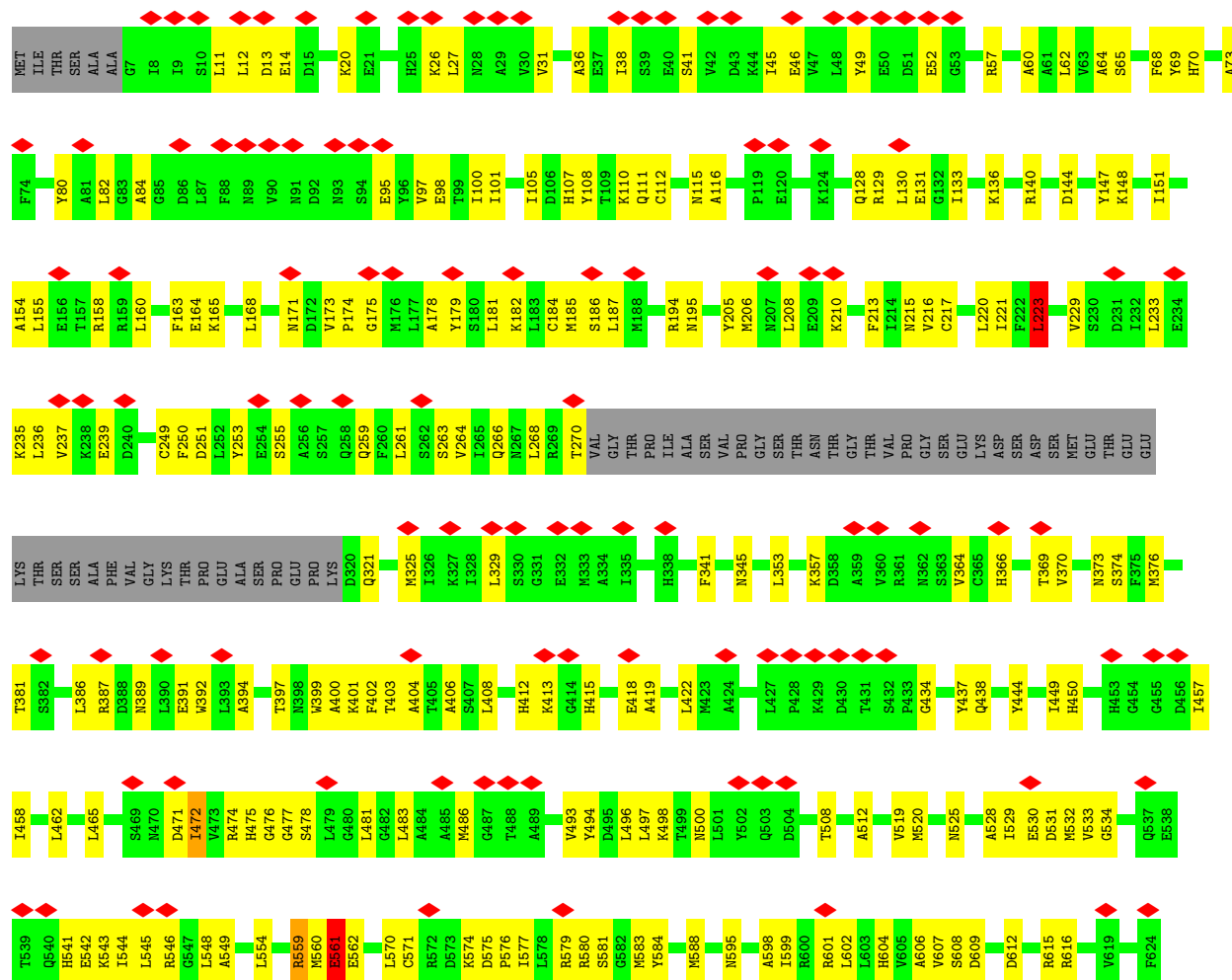


• Molecule 6: 26S proteasome non-ATPase regulatory subunit 2



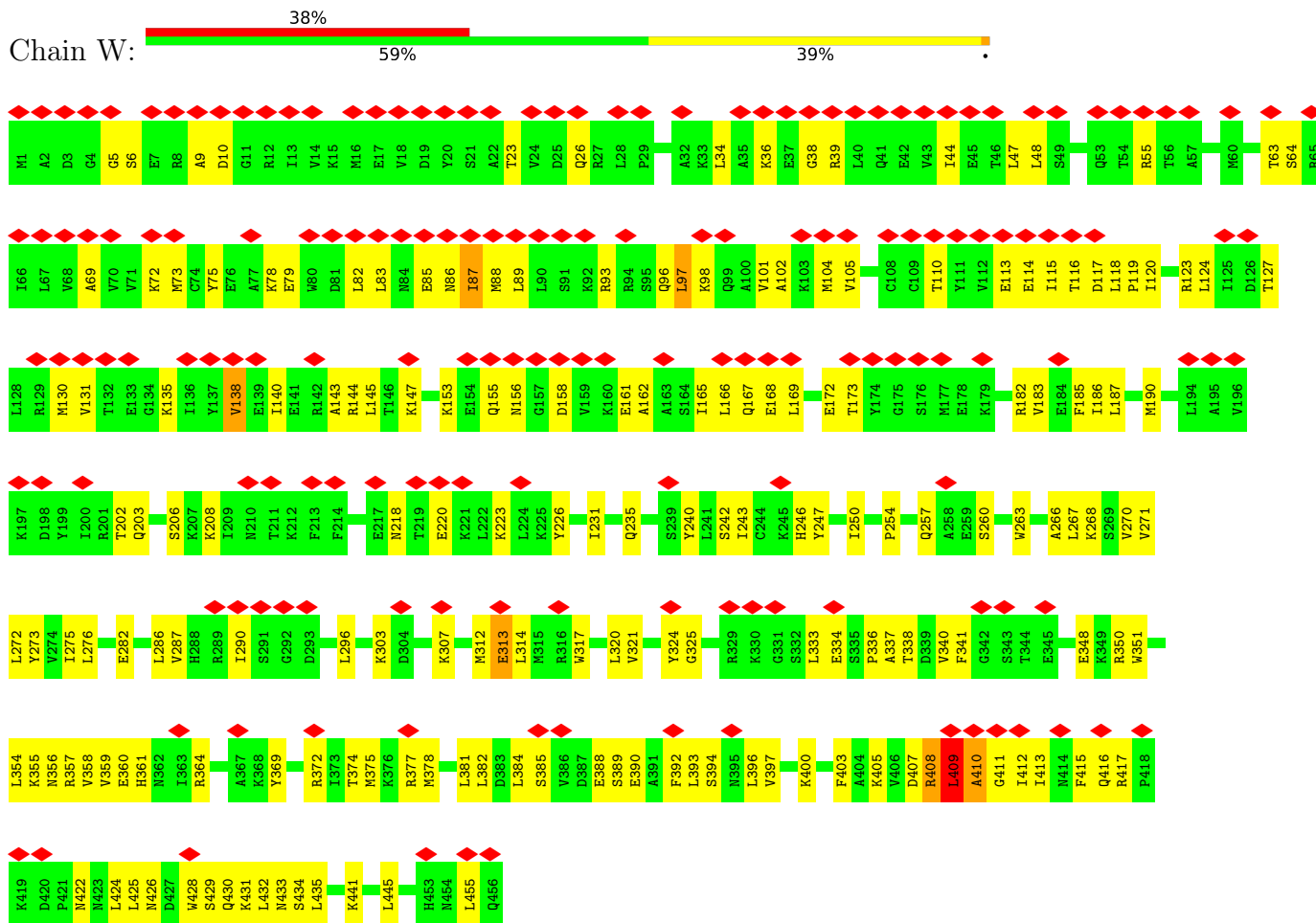


• Molecule 7: 26S proteasome non-ATPase regulatory subunit 1

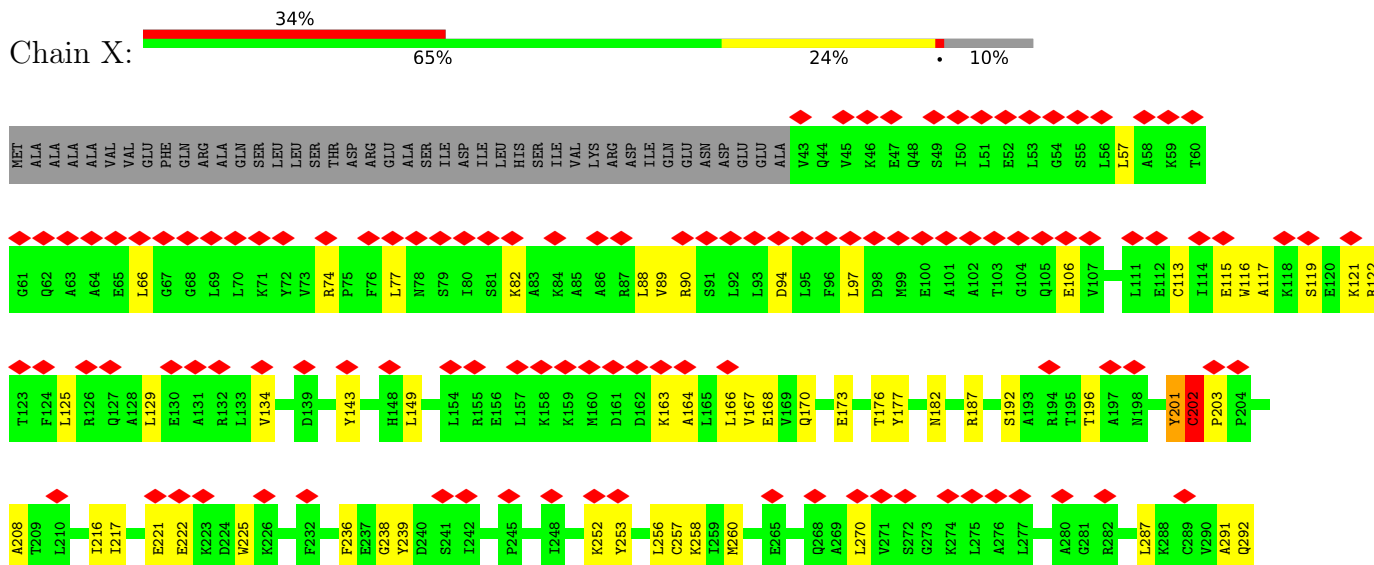


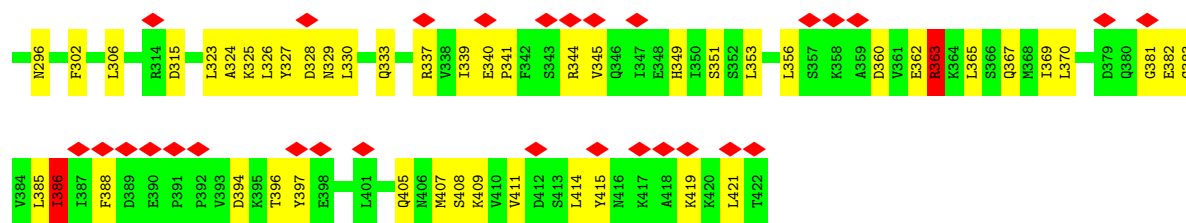
ASP
ASP
ASP
SER
PHE
PRO

- Molecule 9: 26S proteasome non-ATPase regulatory subunit 12

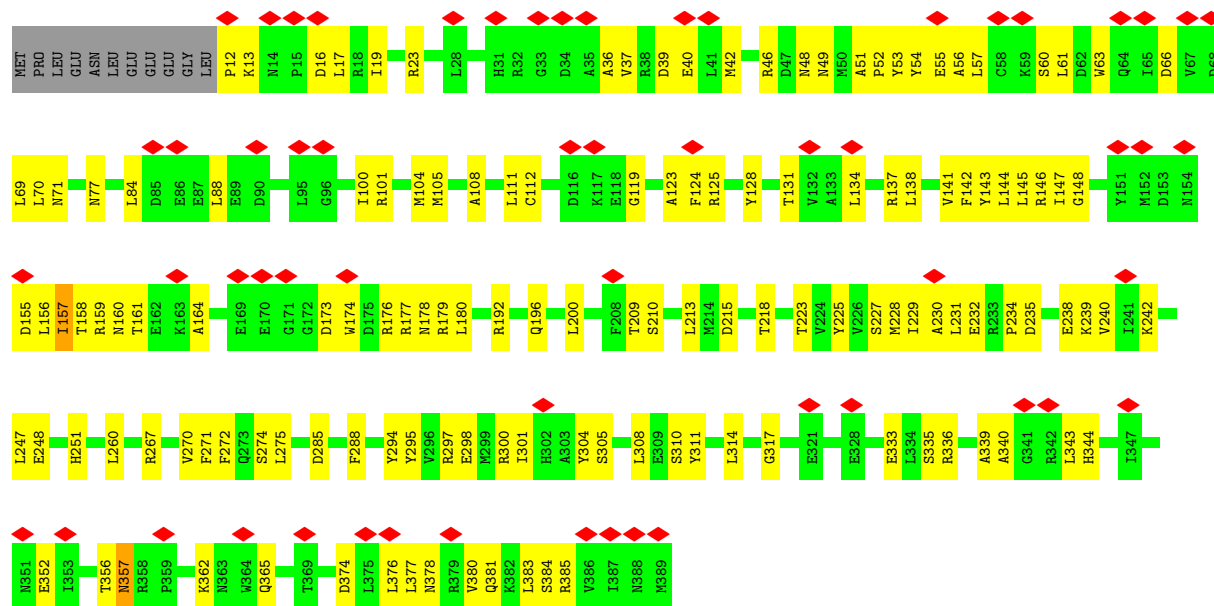


- Molecule 10: 26S proteasome non-ATPase regulatory subunit 11

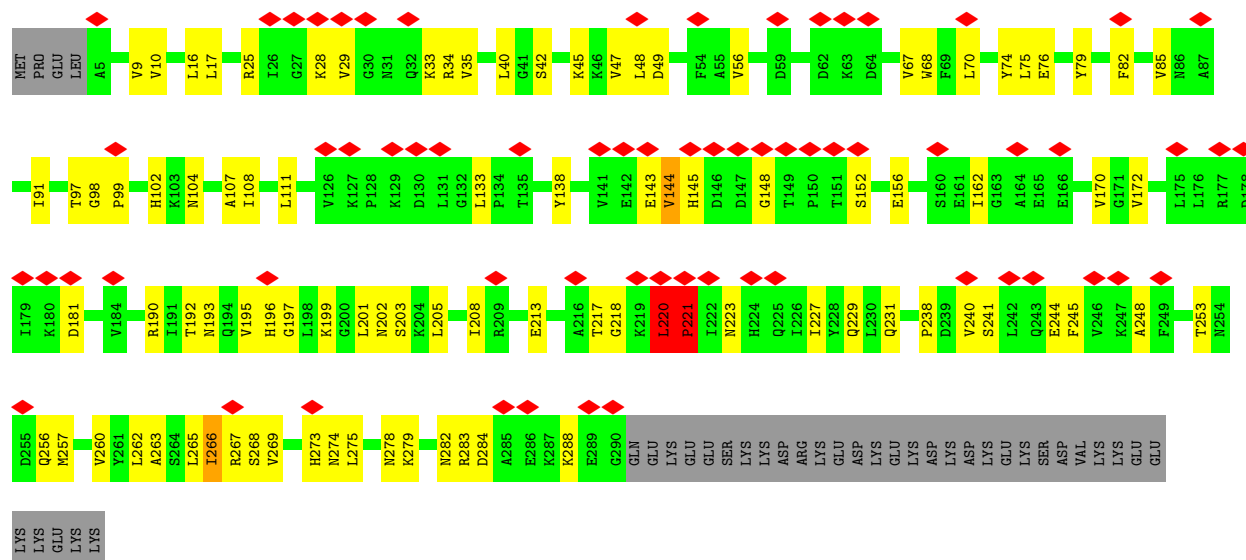




• Molecule 11: 26S proteasome non-ATPase regulatory subunit 6



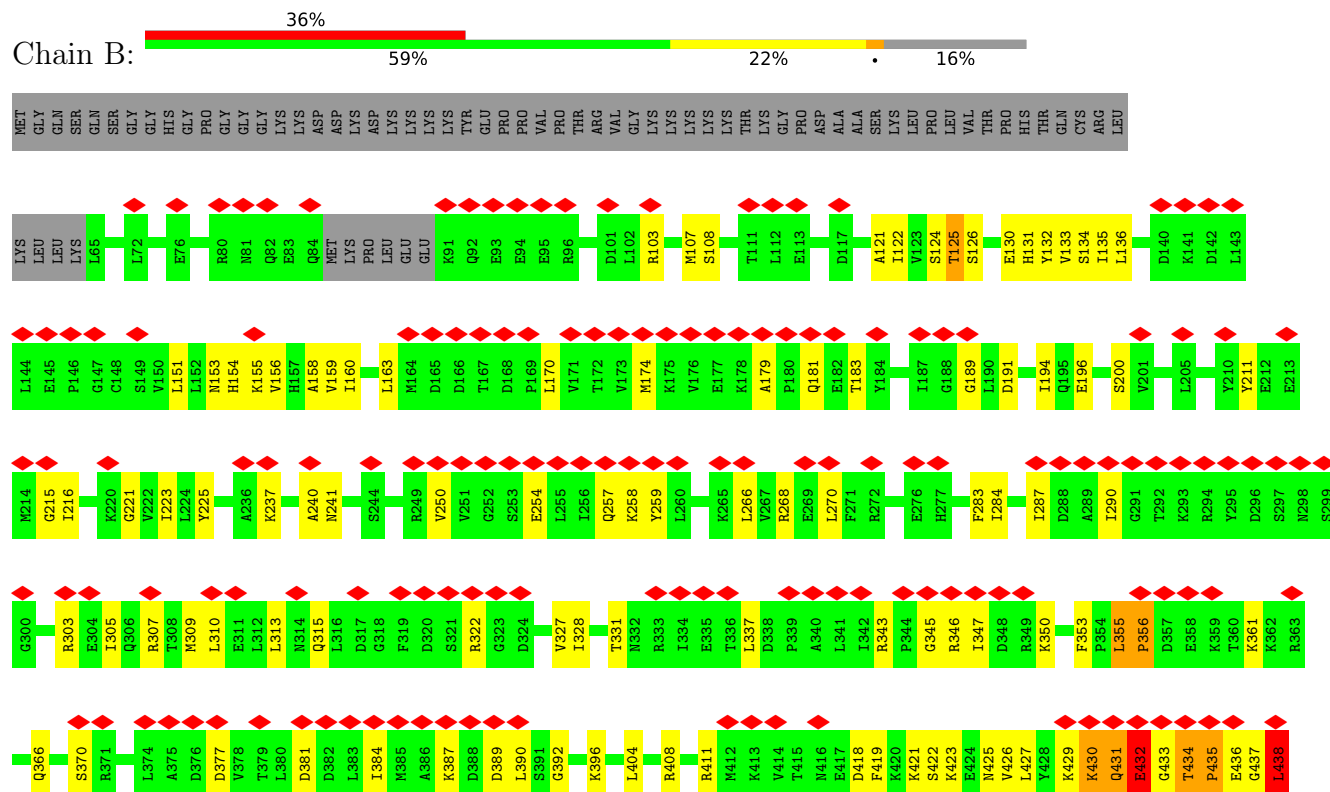
• Molecule 12: 26S proteasome non-ATPase regulatory subunit 7



Chain A:

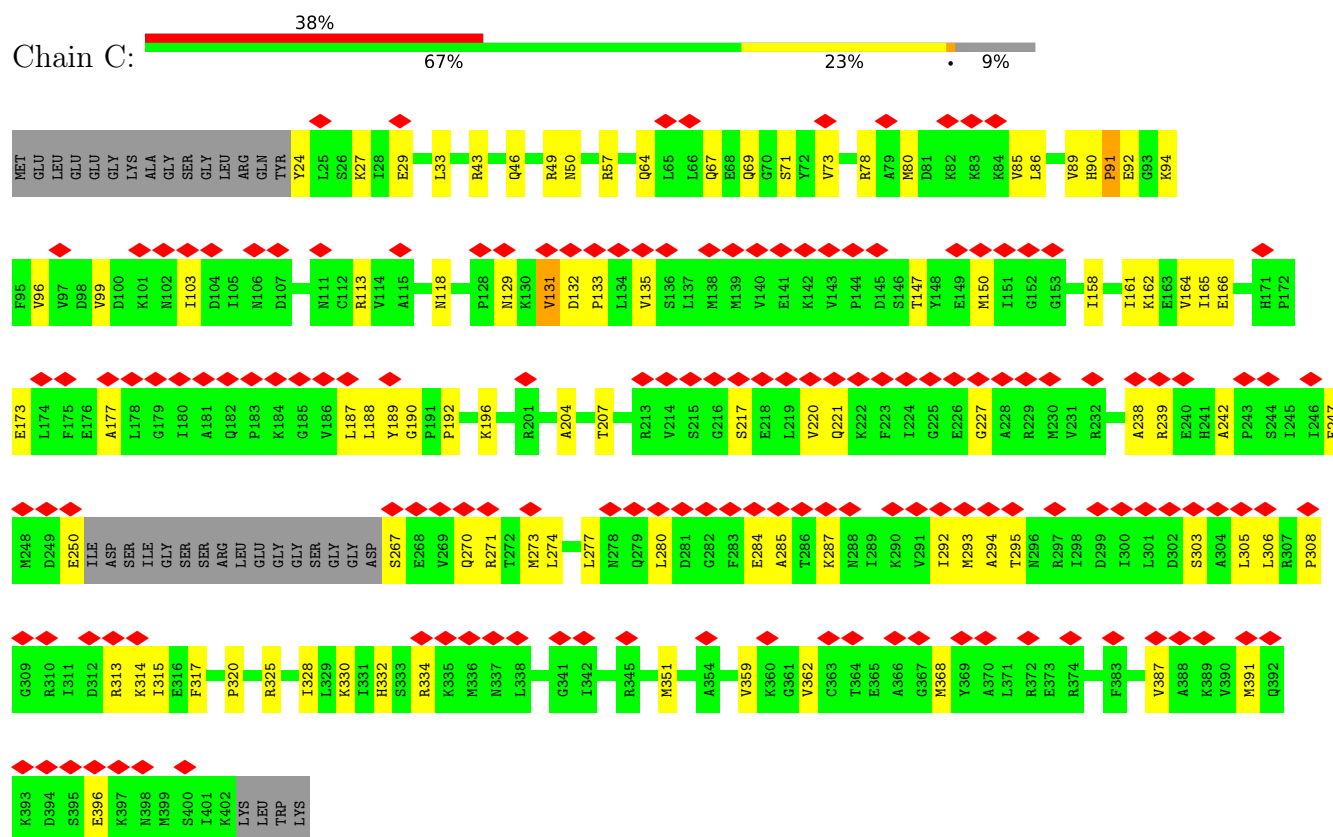


Chain B:

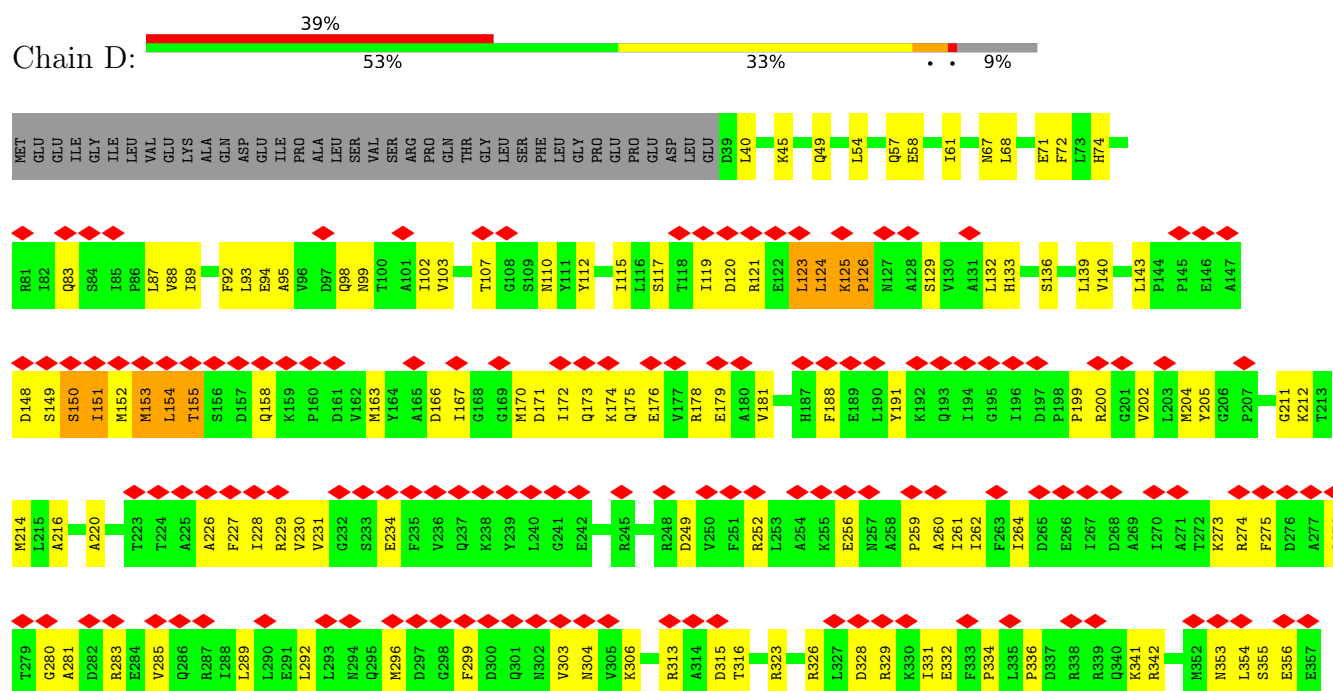


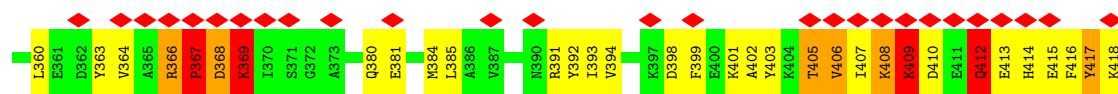


- Molecule 15: Isoform 2 of 26S proteasome regulatory subunit 8

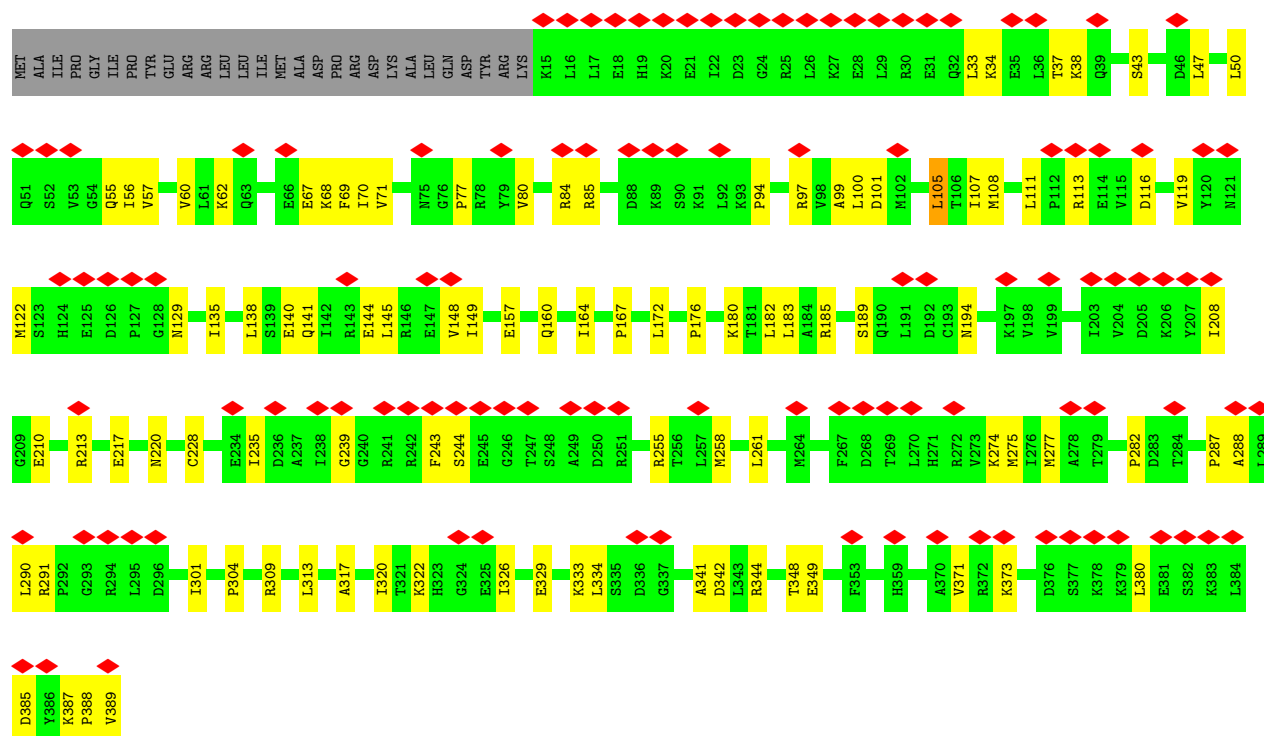


- Molecule 16: 26S protease regulatory subunit 6B

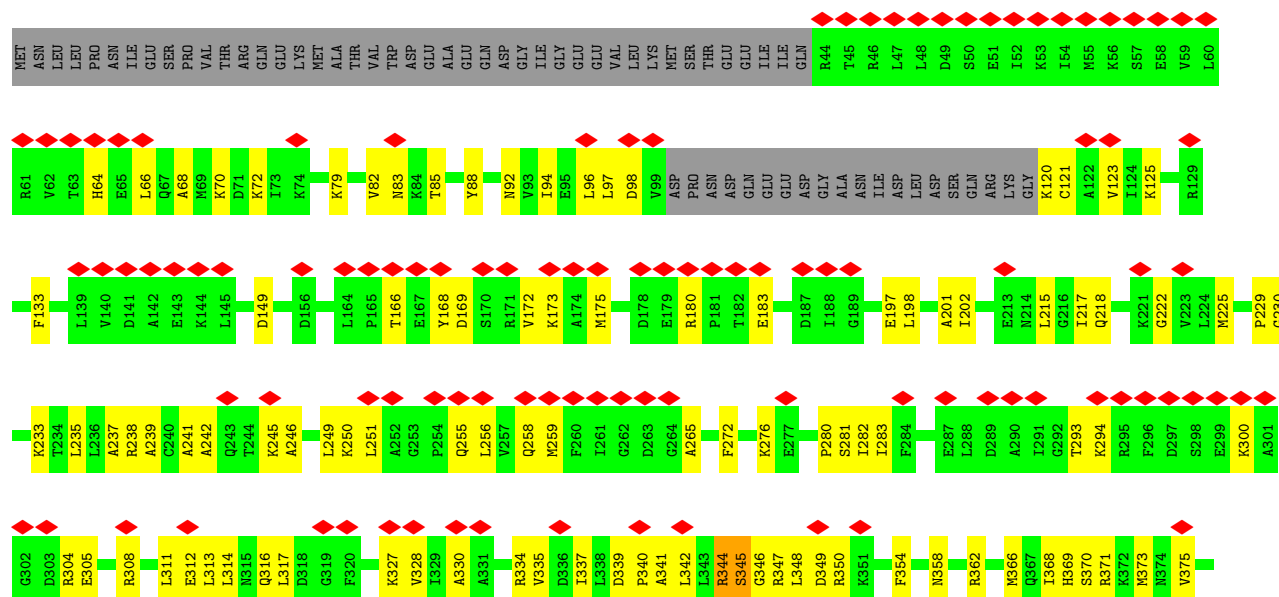


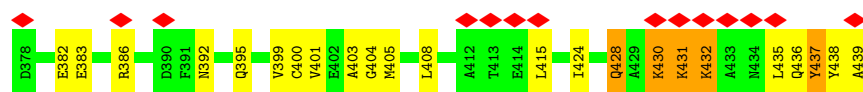


• Molecule 17: 26S proteasome regulatory subunit 10B

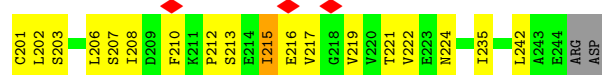


• Molecule 18: 26S protease regulatory subunit 6A

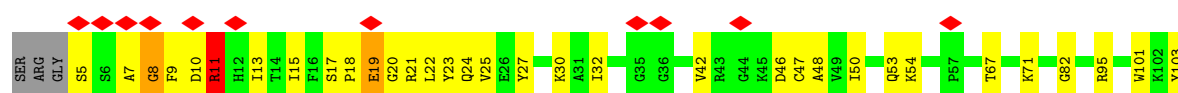




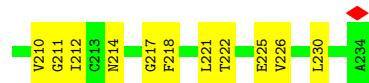
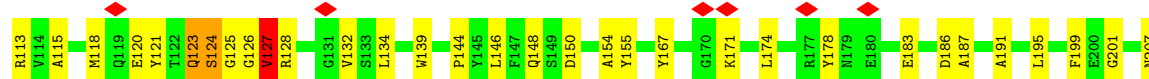
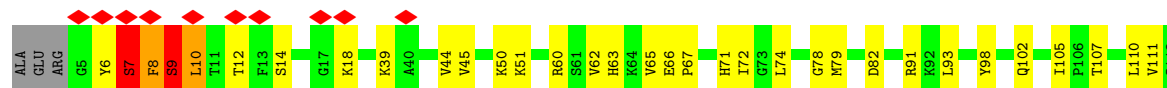
- Molecule 19: Proteasome subunit alpha type-6



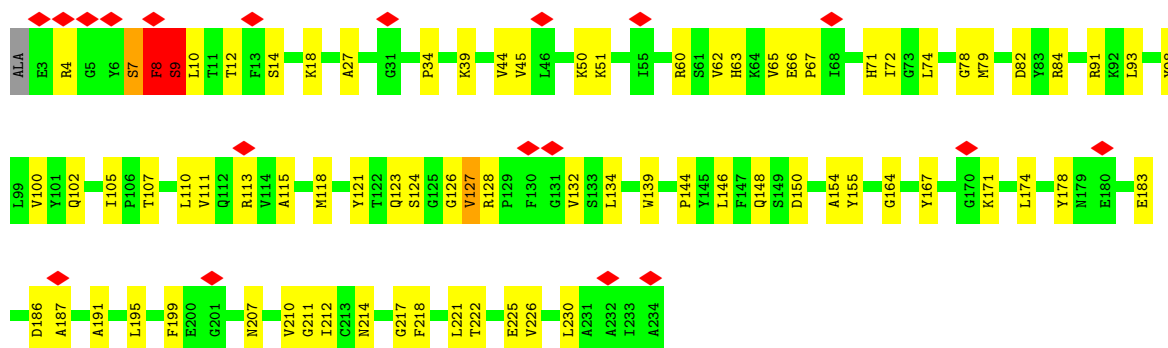
- Molecule 19: Proteasome subunit alpha type-6



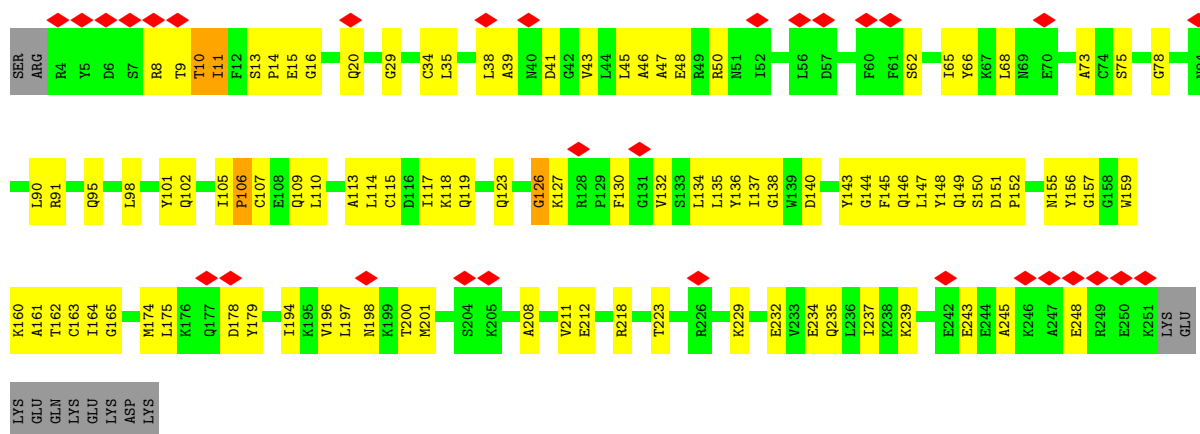
- Molecule 20: Proteasome subunit alpha type-2



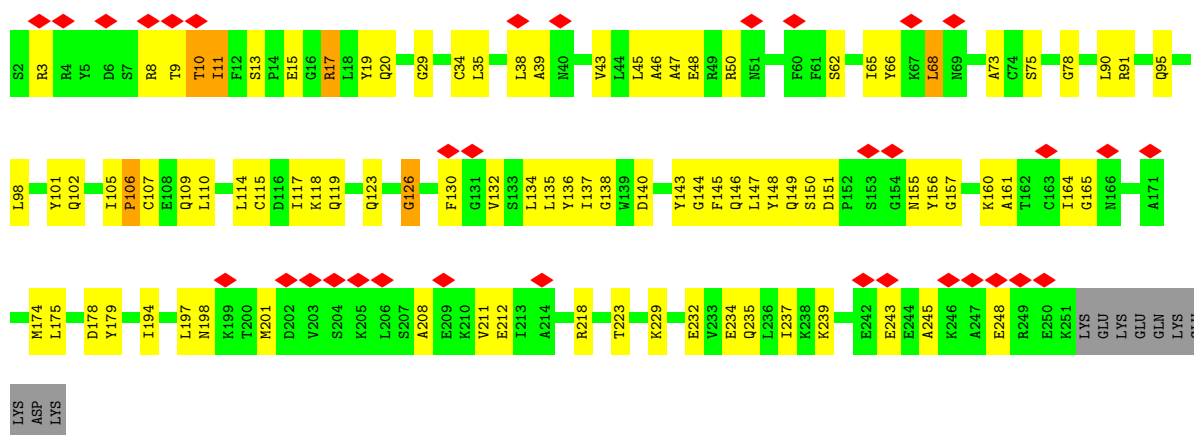
- Molecule 20: Proteasome subunit alpha type-2



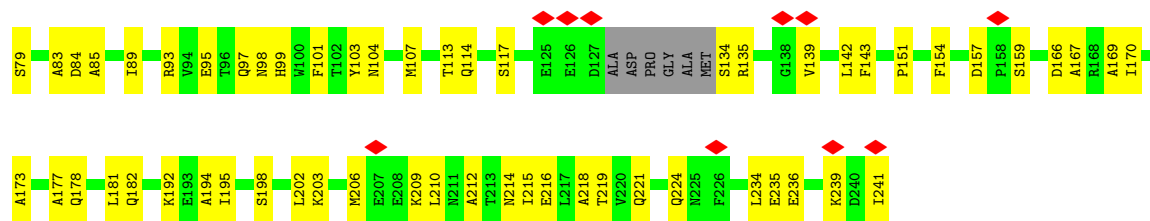
• Molecule 21: Proteasome subunit alpha type-4



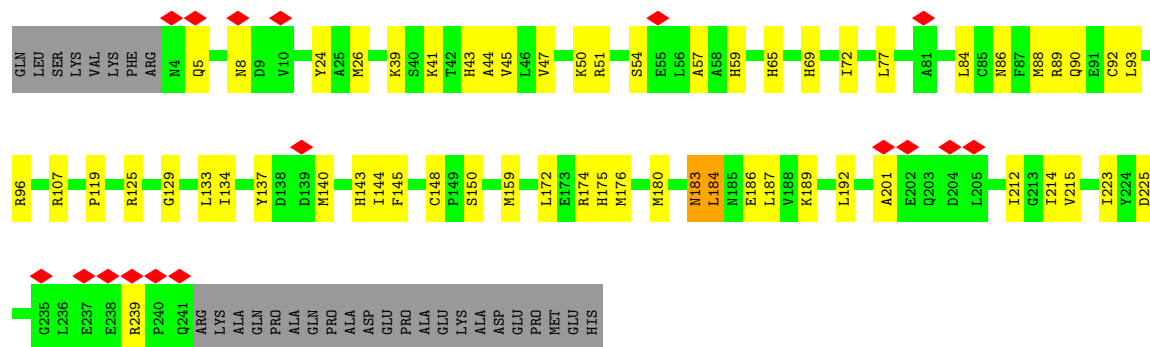
• Molecule 21: Proteasome subunit alpha type-4



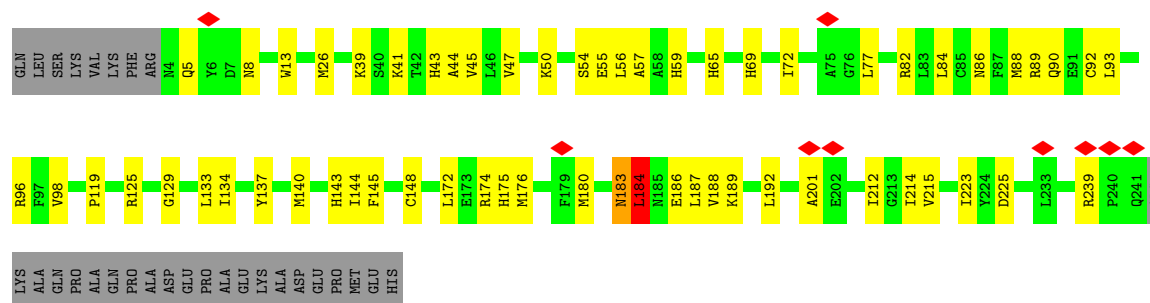
• Molecule 22: Proteasome subunit alpha type-7



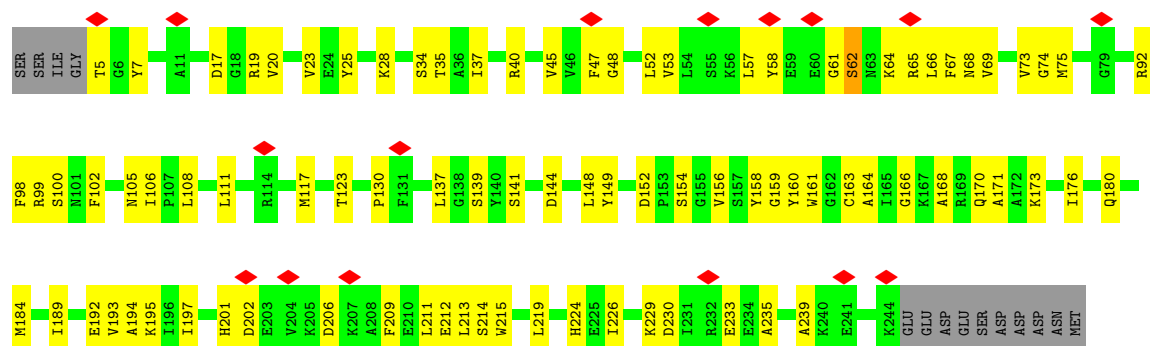
• Molecule 24: Isoform Long of Proteasome subunit alpha type-1



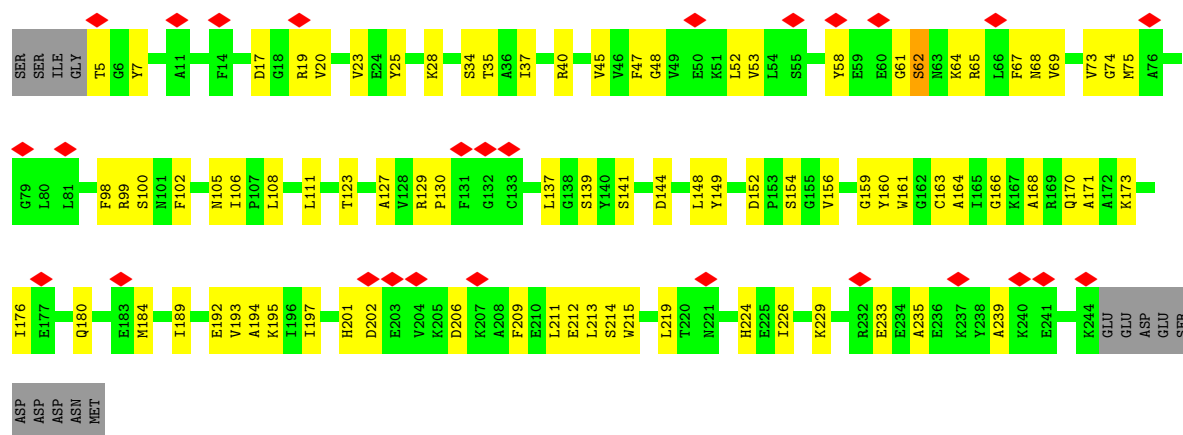
• Molecule 24: Isoform Long of Proteasome subunit alpha type-1



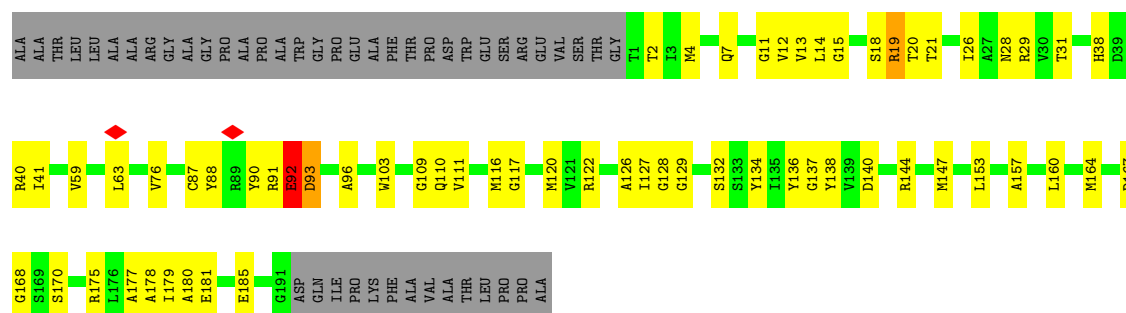
• Molecule 25: Proteasome subunit alpha type-3



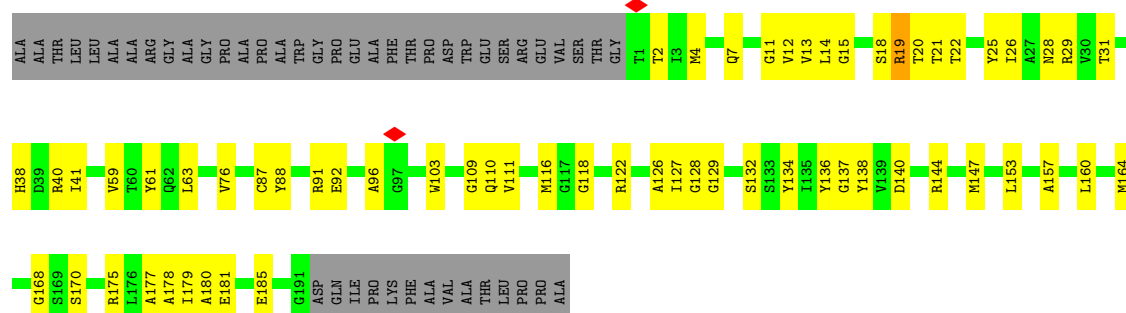
Chain m:



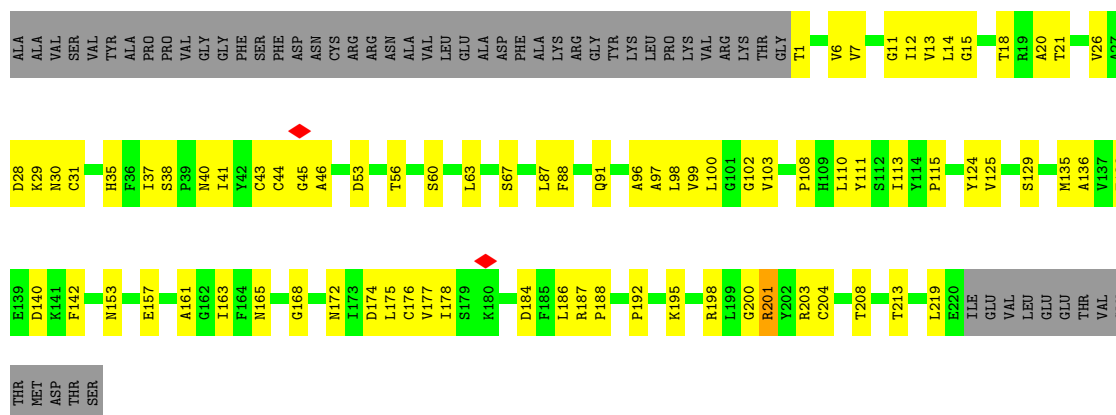
Chain N: 54% 25% 20%



Chain n:

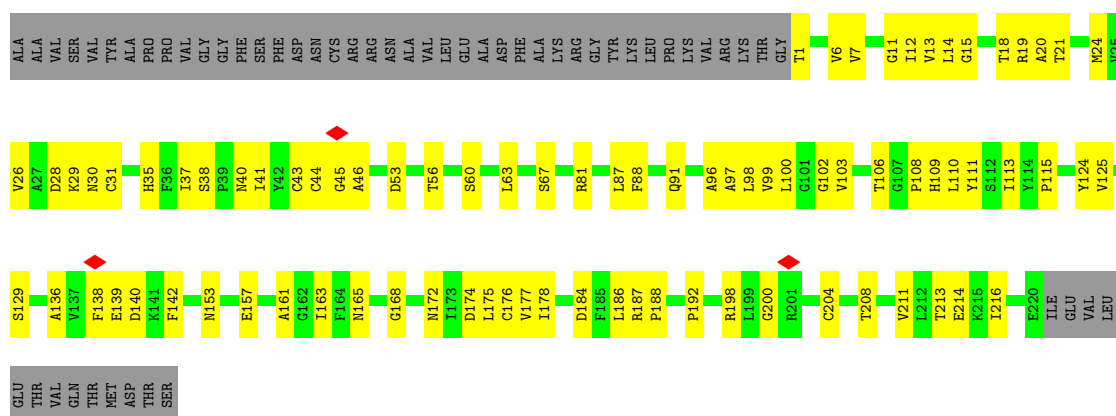


Chain O:



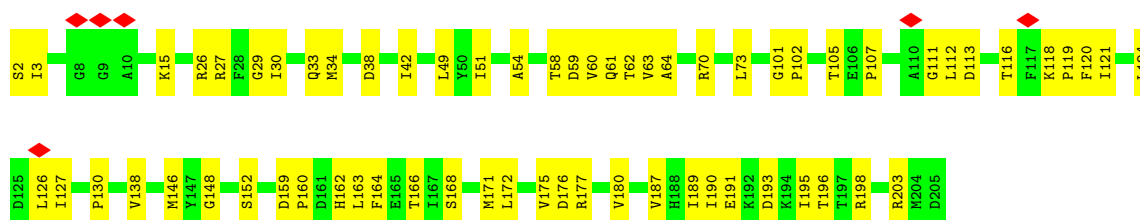
• Molecule 27: Proteasome subunit beta type-7

Chain o: 50% 30% 20%



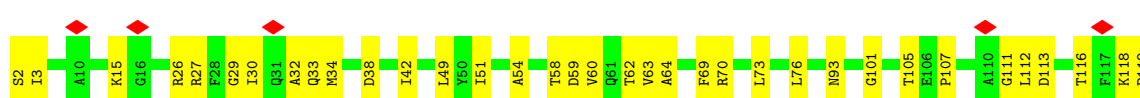
• Molecule 28: Proteasome subunit beta type-3

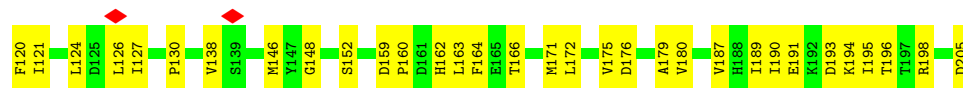
Chain P: 68% 32%



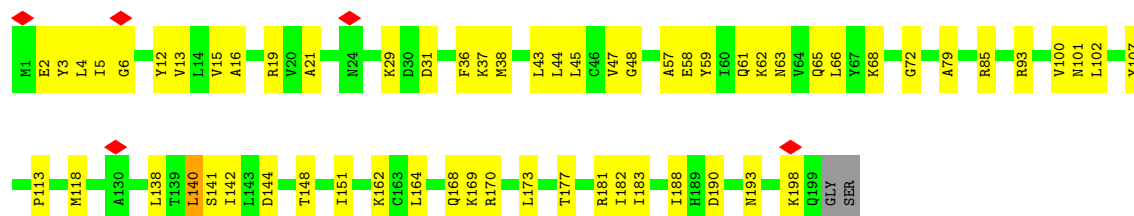
• Molecule 28: Proteasome subunit beta type-3

Chain p: 67% 33%

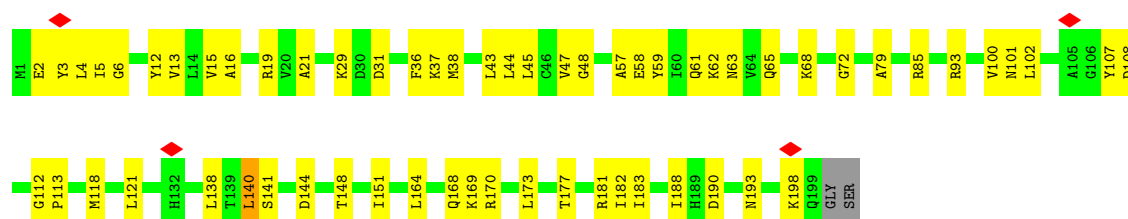




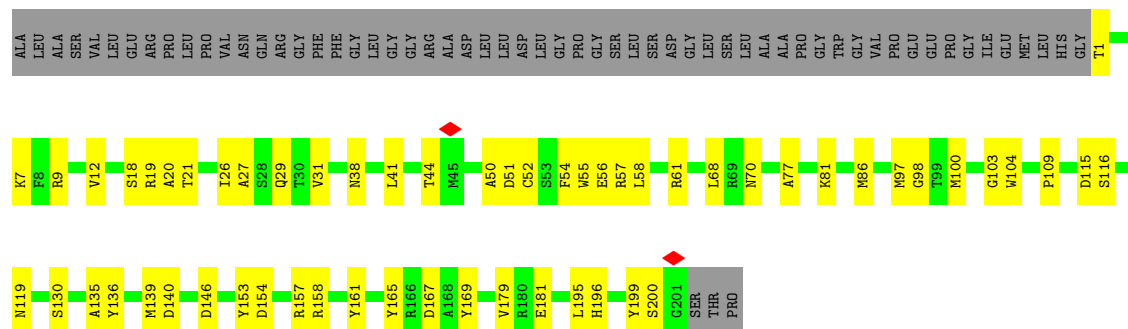
- Molecule 29: Proteasome subunit beta type-2



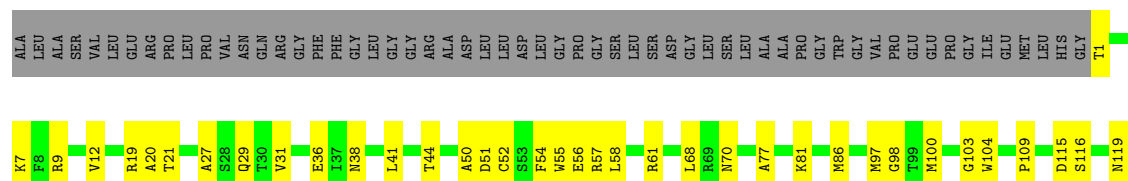
- Molecule 29: Proteasome subunit beta type-2

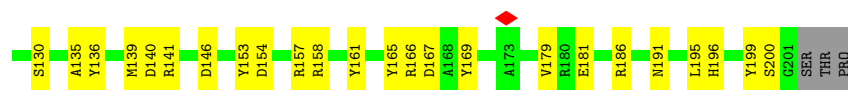


- Molecule 30: Proteasome subunit beta type-5

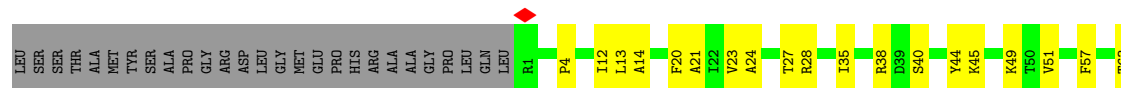


- Molecule 30: Proteasome subunit beta type-5

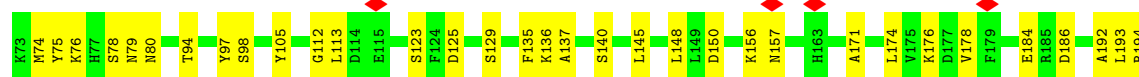
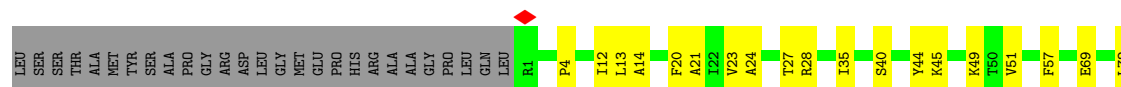




• Molecule 31: Proteasome subunit beta type-1



• Molecule 31: Proteasome subunit beta type-1

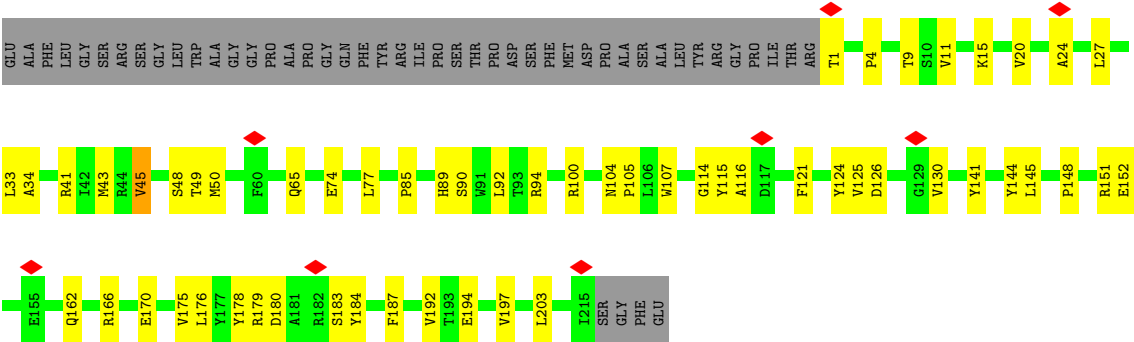


• Molecule 32: Proteasome subunit beta type-4



• Molecule 32: Proteasome subunit beta type-4





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34075	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 ($e^-/\text{\AA}^2$)	46.6	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.095	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.032	Depositor
Map size (Å)	438.4, 438.4, 438.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.37, 1.37, 1.37	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, 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	a	0.26	0/3053	0.69	0/4133
2	b	0.26	0/1477	0.68	2/1999 (0.1%)
3	c	0.27	0/2225	0.71	0/3005
4	d	0.29	0/2161	0.79	6/2917 (0.2%)
5	e	0.34	0/337	0.94	1/448 (0.2%)
6	f	0.29	0/5392	0.76	7/7269 (0.1%)
7	U	0.27	1/6395 (0.0%)	0.66	5/8645 (0.1%)
8	V	0.30	0/3882	0.76	6/5245 (0.1%)
9	W	0.27	0/3750	0.74	5/5040 (0.1%)
10	X	0.26	0/3052	0.69	4/4113 (0.1%)
11	Y	0.28	0/3171	0.70	0/4269
12	Z	0.30	0/2323	0.80	8/3148 (0.3%)
13	A	0.24	0/2938	0.63	3/3968 (0.1%)
14	B	0.23	0/2843	0.75	6/3844 (0.2%)
15	C	0.25	0/2895	0.65	1/3893 (0.0%)
16	D	0.28	0/3089	0.79	8/4166 (0.2%)
17	E	0.24	0/2903	0.58	0/3922
18	F	0.24	0/2896	0.59	0/3910
19	G	0.29	0/1853	0.64	4/2515 (0.2%)
19	g	0.25	0/1859	0.65	3/2523 (0.1%)
20	H	0.25	0/1723	0.63	4/2346 (0.2%)
20	h	0.25	0/1743	0.62	4/2372 (0.2%)
21	I	0.25	0/1925	0.69	6/2606 (0.2%)
21	i	0.25	0/1942	0.64	4/2628 (0.2%)
22	J	0.25	0/1728	0.60	1/2358 (0.0%)
22	j	0.24	0/1728	0.57	1/2358 (0.0%)
23	K	0.26	0/1755	0.62	1/2375 (0.0%)
23	k	0.25	0/1747	0.62	2/2364 (0.1%)
24	L	0.25	0/1885	0.59	2/2552 (0.1%)
24	l	0.25	0/1885	0.59	2/2552 (0.1%)
25	M	0.25	0/1891	0.61	2/2552 (0.1%)
25	m	0.25	0/1891	0.61	2/2552 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
26	N	0.24	0/1454	0.60	0/1967
26	n	0.25	0/1454	0.58	0/1967
27	O	0.23	0/1670	0.57	1/2265 (0.0%)
27	o	0.23	0/1670	0.57	1/2265 (0.0%)
28	P	0.24	0/1614	0.50	0/2177
28	p	0.24	0/1614	0.50	0/2177
29	Q	0.27	0/1603	0.59	0/2174
29	q	0.27	0/1603	0.59	0/2174
30	R	0.25	0/1579	0.49	0/2134
30	r	0.25	0/1579	0.49	0/2134
31	S	0.24	0/1671	0.54	0/2253
31	s	0.24	0/1671	0.54	0/2253
32	T	0.25	0/1700	0.53	1/2305 (0.0%)
32	t	0.25	0/1700	0.53	1/2305 (0.0%)
All	All	0.26	1/102919 (0.0%)	0.65	104/139137 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	U	773	PHE	C-N	5.87	1.39	1.34

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	B	434	THR	CA-C-N	14.60	138.09	119.84
14	B	434	THR	C-N-CA	14.60	138.09	119.84
16	D	366	ARG	CA-C-N	14.30	137.72	119.84
16	D	366	ARG	C-N-CA	14.30	137.72	119.84
12	Z	220	LEU	CA-C-N	9.39	131.58	119.84

There are no chirality outliers.

There are no planarity outliers.

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	2995	0	3012	110	0
2	b	1457	0	1501	77	0
3	c	2186	0	2210	67	0
4	d	2115	0	2142	72	0
5	e	333	0	290	31	0
6	f	5318	0	5328	208	0
7	U	6286	0	6336	213	0
8	V	3807	0	3854	196	0
9	W	3702	0	3818	183	0
10	X	3008	0	3112	106	0
11	Y	3114	0	3117	108	0
12	Z	2280	0	2308	91	0
13	A	2892	0	2842	83	0
14	B	2805	0	2769	110	0
15	C	2858	0	2970	90	0
16	D	3039	0	3075	209	0
17	E	2859	0	2827	89	0
18	F	2858	0	2851	161	0
19	G	1820	0	1791	105	0
19	g	1826	0	1796	107	0
20	H	1688	0	1575	70	0
20	h	1708	0	1594	64	0
21	I	1895	0	1833	79	0
21	i	1912	0	1851	107	0
22	J	1704	0	1517	54	0
22	j	1704	0	1517	54	0
23	K	1729	0	1680	82	0
23	k	1722	0	1673	96	0
24	L	1850	0	1822	50	0
24	l	1850	0	1822	51	0
25	M	1856	0	1814	65	0
25	m	1856	0	1814	62	0
26	N	1430	0	1398	49	0
26	n	1430	0	1396	69	0
27	O	1643	0	1644	64	0
27	o	1643	0	1644	60	0
28	P	1585	0	1598	47	0
28	p	1585	0	1598	50	0
29	Q	1570	0	1547	46	0
29	q	1570	0	1547	41	0
30	R	1548	0	1499	43	0
30	r	1548	0	1499	45	0
31	S	1641	0	1618	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	s	1641	0	1618	47	0
32	T	1667	0	1628	45	0
32	t	1667	0	1628	42	0
33	c	1	0	0	0	0
34	A	31	0	12	4	0
34	D	31	0	12	2	0
34	E	31	0	12	6	0
34	F	31	0	12	2	0
All	All	101325	0	100371	3568	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 18.

The worst 5 of 3568 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)
26:n:88:TYR:HA	26:n:91:ARG:CD	1.22	1.69
16:D:403:TYR:CD2	16:D:407:ILE:CD1	1.85	1.59
15:C:73:VAL:CG1	15:C:90:HIS:CE1	1.88	1.52
16:D:403:TYR:CG	16:D:407:ILE:HD11	1.02	1.52
16:D:403:TYR:CG	16:D:407:ILE:CD1	1.89	1.49

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	a	371/376 (99%)	334 (90%)	36 (10%)	1 (0%)	36	71
2	b	189/377 (50%)	165 (87%)	23 (12%)	1 (0%)	24	63
3	c	274/309 (89%)	230 (84%)	44 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	d	255/349 (73%)	220 (86%)	32 (12%)	3 (1%)	10	42
5	e	36/70 (51%)	27 (75%)	8 (22%)	1 (3%)	4	24
6	f	669/908 (74%)	582 (87%)	86 (13%)	1 (0%)	48	83
7	U	798/953 (84%)	721 (90%)	76 (10%)	1 (0%)	48	83
8	V	471/533 (88%)	400 (85%)	70 (15%)	1 (0%)	43	78
9	W	454/456 (100%)	392 (86%)	58 (13%)	4 (1%)	14	49
10	X	378/422 (90%)	336 (89%)	38 (10%)	4 (1%)	11	45
11	Y	376/389 (97%)	329 (88%)	47 (12%)	0	100	100
12	Z	284/324 (88%)	245 (86%)	37 (13%)	2 (1%)	18	55
13	A	376/433 (87%)	328 (87%)	46 (12%)	2 (0%)	24	63
14	B	366/440 (83%)	324 (88%)	36 (10%)	6 (2%)	7	37
15	C	359/398 (90%)	317 (88%)	40 (11%)	2 (1%)	21	58
16	D	378/418 (90%)	324 (86%)	41 (11%)	13 (3%)	3	20
17	E	373/403 (93%)	330 (88%)	43 (12%)	0	100	100
18	F	372/439 (85%)	329 (88%)	41 (11%)	2 (0%)	24	63
19	G	237/245 (97%)	204 (86%)	29 (12%)	4 (2%)	7	35
19	g	238/245 (97%)	207 (87%)	28 (12%)	3 (1%)	9	41
20	H	228/233 (98%)	213 (93%)	12 (5%)	3 (1%)	9	41
20	h	230/233 (99%)	213 (93%)	14 (6%)	3 (1%)	9	41
21	I	246/260 (95%)	220 (89%)	22 (9%)	4 (2%)	7	37
21	i	248/260 (95%)	222 (90%)	24 (10%)	2 (1%)	16	52
22	J	237/247 (96%)	219 (92%)	17 (7%)	1 (0%)	30	67
22	j	237/247 (96%)	221 (93%)	16 (7%)	0	100	100
23	K	224/240 (93%)	202 (90%)	22 (10%)	0	100	100
23	k	224/240 (93%)	202 (90%)	22 (10%)	0	100	100
24	L	236/268 (88%)	223 (94%)	13 (6%)	0	100	100
24	l	236/268 (88%)	223 (94%)	13 (6%)	0	100	100
25	M	238/254 (94%)	218 (92%)	20 (8%)	0	100	100
25	m	238/254 (94%)	218 (92%)	20 (8%)	0	100	100
26	N	189/238 (79%)	174 (92%)	13 (7%)	2 (1%)	11	45
26	n	189/238 (79%)	176 (93%)	12 (6%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	O	218/276 (79%)	208 (95%)	10 (5%)	0	100	100
27	o	218/276 (79%)	207 (95%)	11 (5%)	0	100	100
28	P	202/204 (99%)	193 (96%)	9 (4%)	0	100	100
28	p	202/204 (99%)	193 (96%)	9 (4%)	0	100	100
29	Q	197/201 (98%)	179 (91%)	18 (9%)	0	100	100
29	q	197/201 (98%)	179 (91%)	18 (9%)	0	100	100
30	R	199/262 (76%)	188 (94%)	11 (6%)	0	100	100
30	r	199/262 (76%)	188 (94%)	11 (6%)	0	100	100
31	S	211/240 (88%)	203 (96%)	8 (4%)	0	100	100
31	s	211/240 (88%)	203 (96%)	8 (4%)	0	100	100
32	T	213/263 (81%)	200 (94%)	13 (6%)	0	100	100
32	t	213/263 (81%)	200 (94%)	13 (6%)	0	100	100
All	All	12934/14859 (87%)	11629 (90%)	1238 (10%)	67 (0%)	26	63

5 of 67 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	b	23	PRO
4	d	34	ASN
9	W	410	ALA
10	X	363	ARG
10	X	386	ILE

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	333/336 (99%)	333 (100%)	0	100	100
2	b	166/312 (53%)	164 (99%)	2 (1%)	63	73
3	c	243/267 (91%)	242 (100%)	1 (0%)	84	83
4	d	230/293 (78%)	228 (99%)	2 (1%)	70	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	e	37/63 (59%)	35 (95%)	2 (5%)	20	42
6	f	579/763 (76%)	577 (100%)	2 (0%)	86	84
7	U	685/816 (84%)	678 (99%)	7 (1%)	68	76
8	V	409/459 (89%)	401 (98%)	8 (2%)	48	66
9	W	415/416 (100%)	411 (99%)	4 (1%)	68	76
10	X	326/362 (90%)	322 (99%)	4 (1%)	63	73
11	Y	333/344 (97%)	331 (99%)	2 (1%)	78	81
12	Z	257/295 (87%)	254 (99%)	3 (1%)	63	73
13	A	297/372 (80%)	296 (100%)	1 (0%)	86	84
14	B	300/385 (78%)	294 (98%)	6 (2%)	48	66
15	C	314/346 (91%)	313 (100%)	1 (0%)	86	84
16	D	332/366 (91%)	319 (96%)	13 (4%)	28	50
17	E	298/353 (84%)	297 (100%)	1 (0%)	86	84
18	F	296/379 (78%)	290 (98%)	6 (2%)	48	66
19	G	192/209 (92%)	185 (96%)	7 (4%)	31	52
19	g	193/209 (92%)	187 (97%)	6 (3%)	35	56
20	H	162/190 (85%)	157 (97%)	5 (3%)	35	56
20	h	164/190 (86%)	159 (97%)	5 (3%)	36	57
21	I	191/220 (87%)	189 (99%)	2 (1%)	68	76
21	i	193/220 (88%)	190 (98%)	3 (2%)	55	69
22	J	152/210 (72%)	152 (100%)	0	100	100
22	j	152/210 (72%)	151 (99%)	1 (1%)	76	79
23	K	187/202 (93%)	182 (97%)	5 (3%)	39	60
23	k	186/202 (92%)	182 (98%)	4 (2%)	45	64
24	L	198/229 (86%)	198 (100%)	0	100	100
24	l	198/229 (86%)	197 (100%)	1 (0%)	81	82
25	M	192/211 (91%)	192 (100%)	0	100	100
25	m	192/211 (91%)	192 (100%)	0	100	100
26	N	148/180 (82%)	146 (99%)	2 (1%)	59	71
26	n	148/180 (82%)	147 (99%)	1 (1%)	76	79
27	O	177/227 (78%)	176 (99%)	1 (1%)	78	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	o	177/227 (78%)	177 (100%)	0	100	100
28	P	172/173 (99%)	172 (100%)	0	100	100
28	p	172/173 (99%)	172 (100%)	0	100	100
29	Q	164/171 (96%)	163 (99%)	1 (1%)	78	81
29	q	164/171 (96%)	163 (99%)	1 (1%)	78	81
30	R	153/201 (76%)	153 (100%)	0	100	100
30	r	153/201 (76%)	153 (100%)	0	100	100
31	S	174/198 (88%)	174 (100%)	0	100	100
31	s	174/198 (88%)	174 (100%)	0	100	100
32	T	175/214 (82%)	175 (100%)	0	100	100
32	t	175/214 (82%)	175 (100%)	0	100	100
All	All	10728/12597 (85%)	10618 (99%)	110 (1%)	65	76

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	D	415	GLU
19	G	224	ASN
29	q	140	LEU
21	i	11	ILE
18	F	198	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 166 such sidechains are listed below:

Mol	Chain	Res	Type
24	L	8	ASN
23	k	114	GLN
25	M	110	HIS
19	g	224	ASN
24	l	90	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 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	ATP	E	401	-	32,33,33	2.65	3 (9%)	48,52,52	0.44	0
34	ATP	D	501	-	32,33,33	2.60	1 (3%)	48,52,52	0.44	0
34	ATP	A	501	-	32,33,33	2.60	1 (3%)	48,52,52	0.52	0
34	ATP	F	501	-	32,33,33	2.60	1 (3%)	48,52,52	0.57	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	ATP	E	401	-	-	7/22/38/38	0/3/3/3
34	ATP	D	501	-	-	6/22/38/38	0/3/3/3
34	ATP	A	501	-	-	7/22/38/38	0/3/3/3
34	ATP	F	501	-	-	9/22/38/38	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	D	501	ATP	PG-O1G	14.44	1.95	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	F	501	ATP	PG-O1G	14.38	1.95	1.50
34	A	501	ATP	PG-O1G	14.37	1.95	1.50
34	E	401	ATP	PG-O1G	14.35	1.95	1.50
34	E	401	ATP	PB-O3A	-2.76	1.56	1.59

There are no bond angle outliers.

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

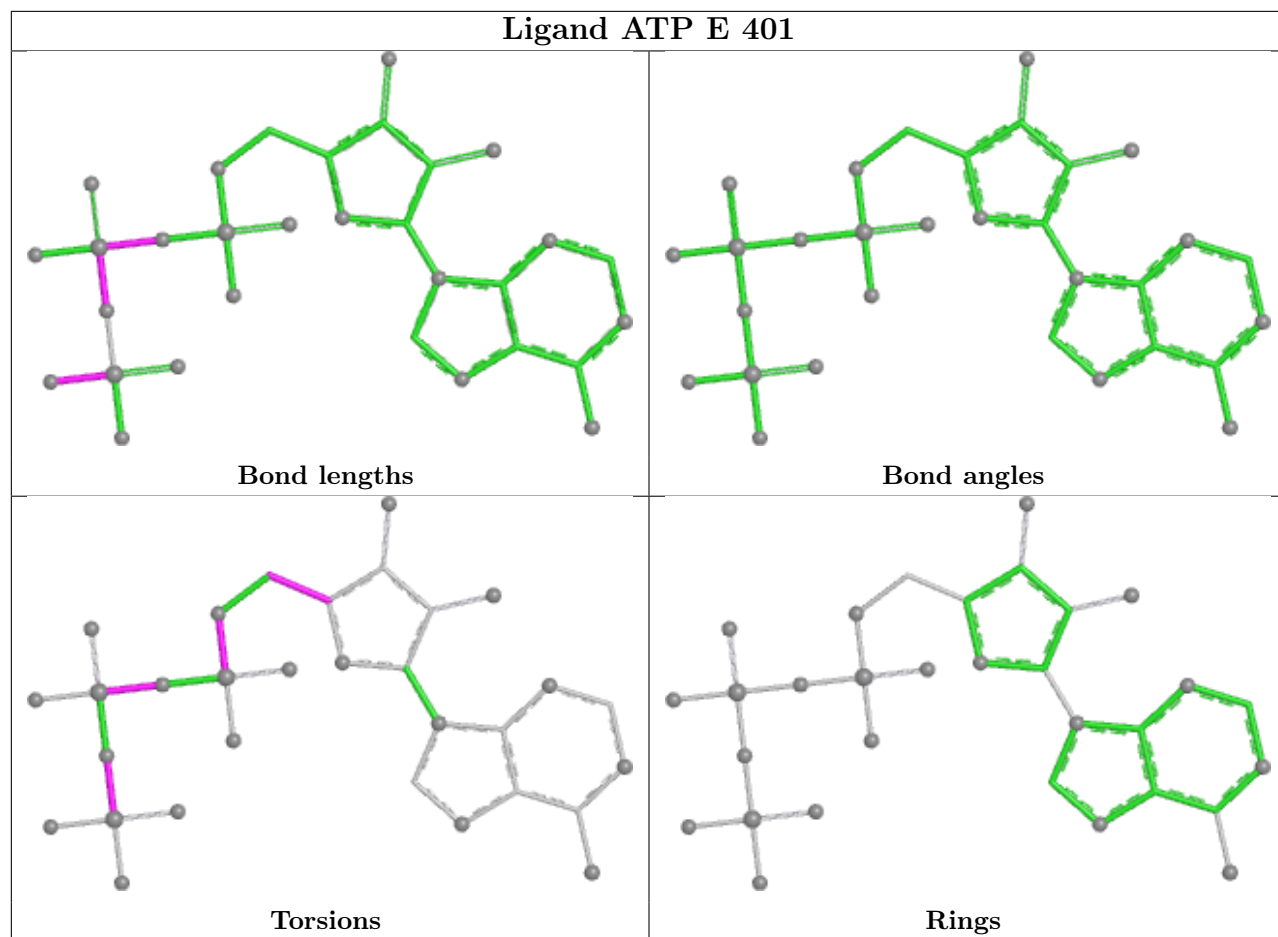
Mol	Chain	Res	Type	Atoms
34	A	501	ATP	C5'-O5'-PA-O1A
34	A	501	ATP	C5'-O5'-PA-O3A
34	D	501	ATP	C5'-O5'-PA-O1A
34	E	401	ATP	PB-O3B-PG-O2G
34	E	401	ATP	PB-O3B-PG-O3G

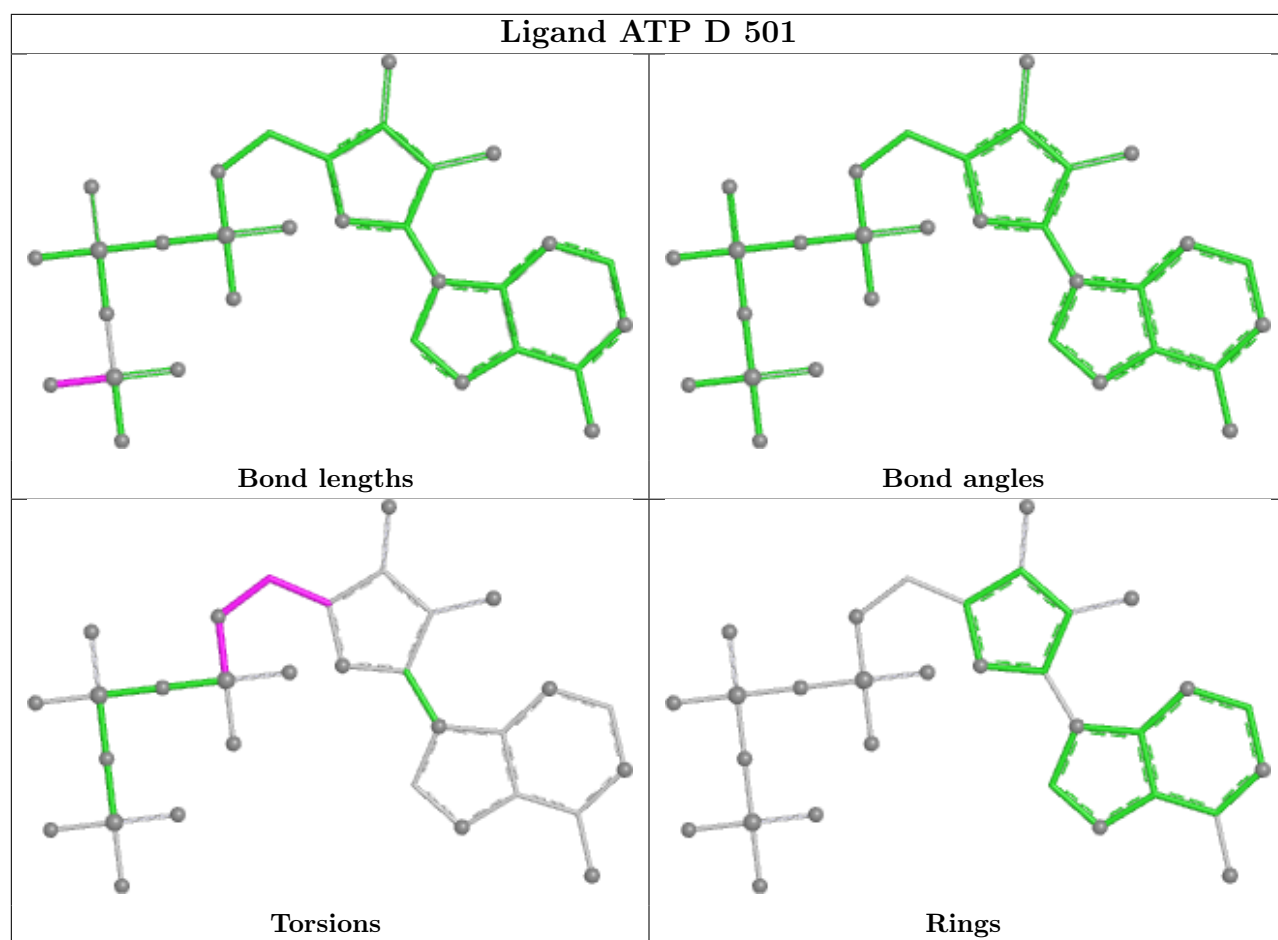
There are no ring outliers.

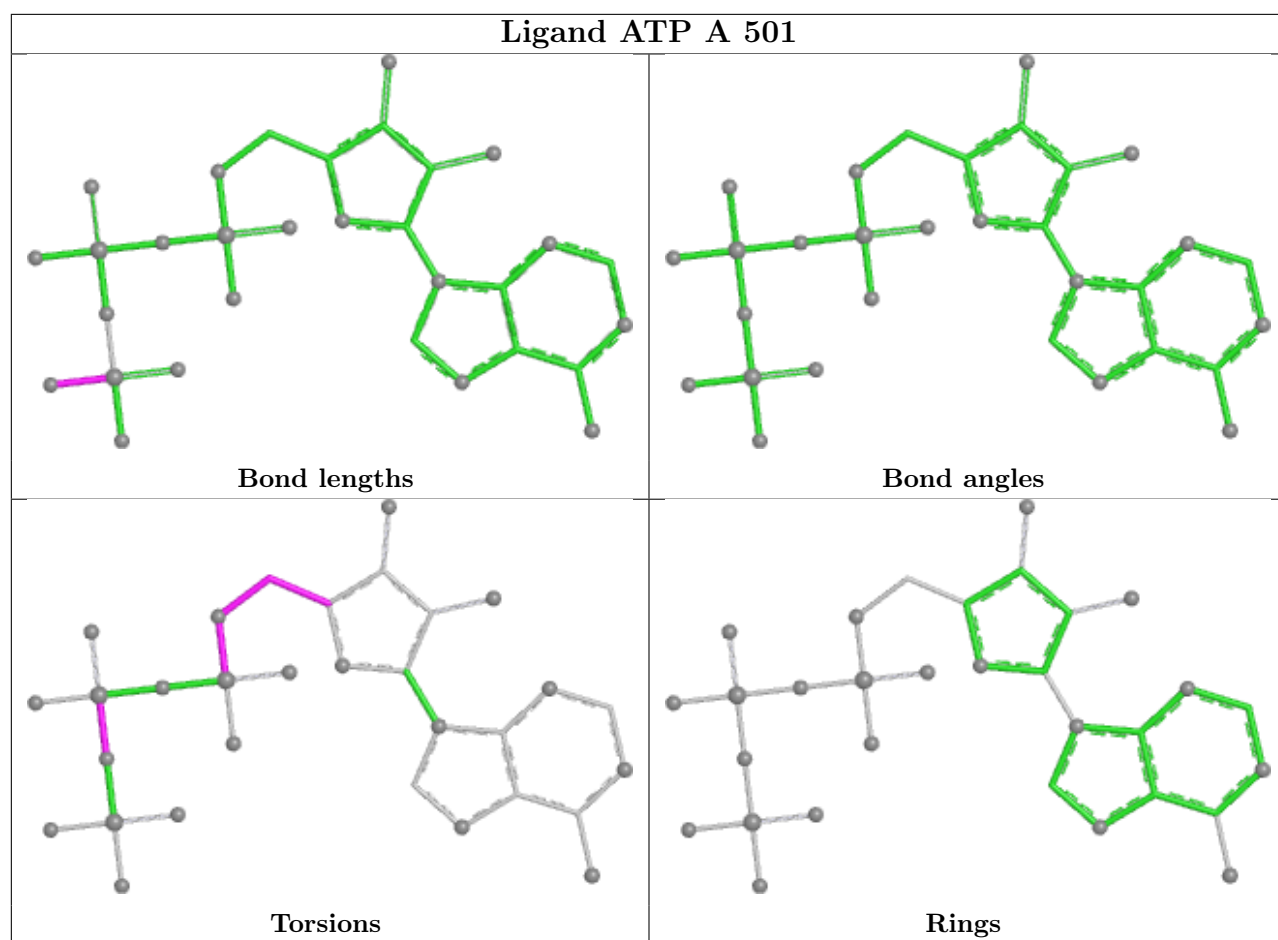
4 monomers are involved in 14 short contacts:

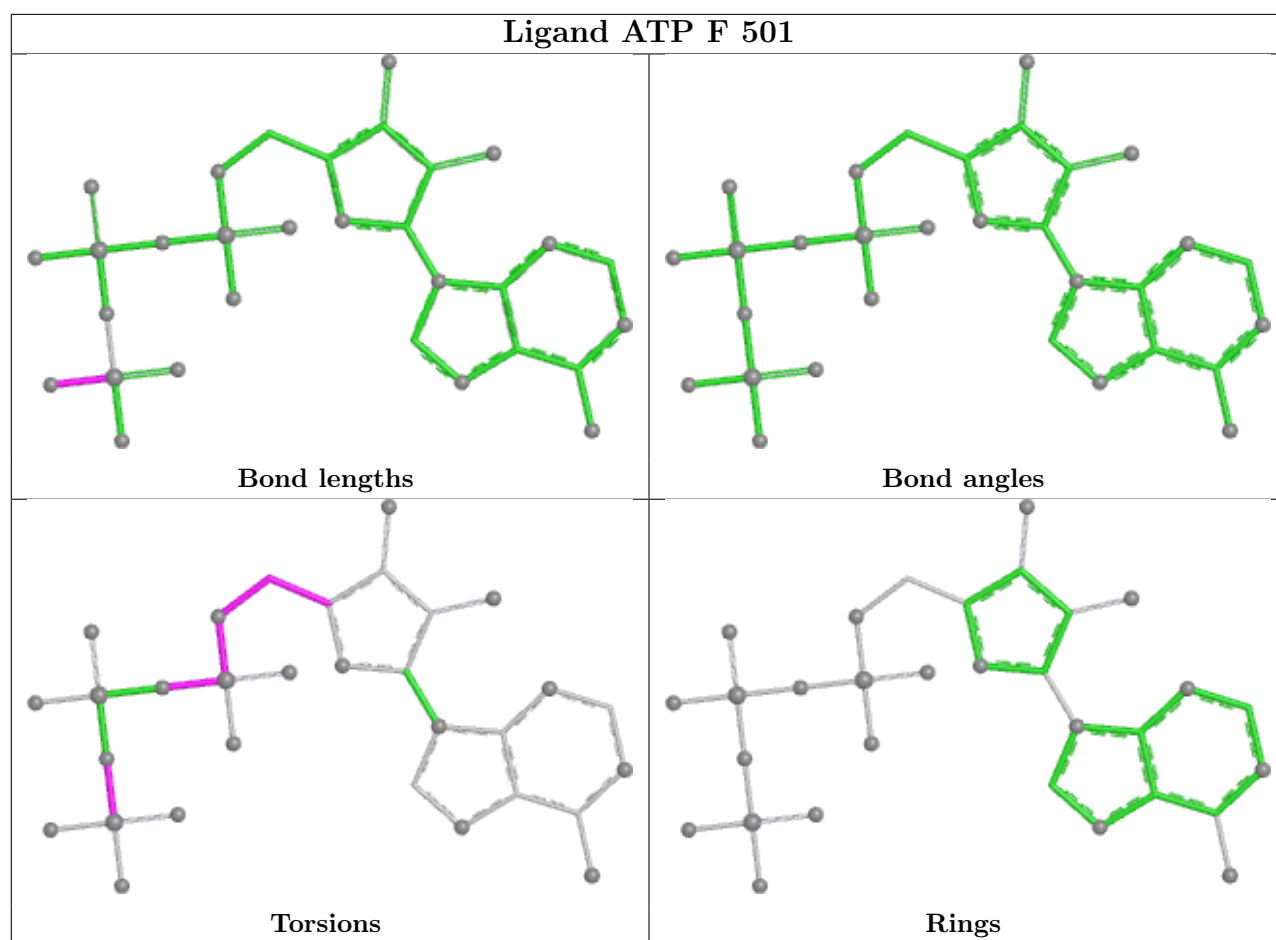
Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	E	401	ATP	6	0
34	D	501	ATP	2	0
34	A	501	ATP	4	0
34	F	501	ATP	2	0

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.

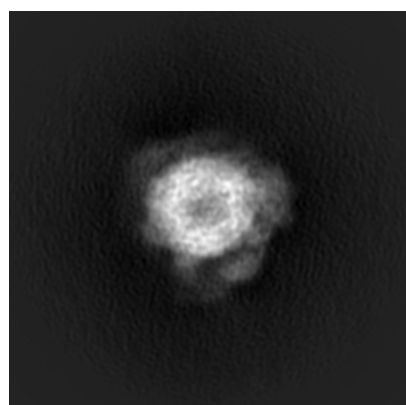
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14210. These allow visual inspection of the internal detail of the map and identification of artifacts.

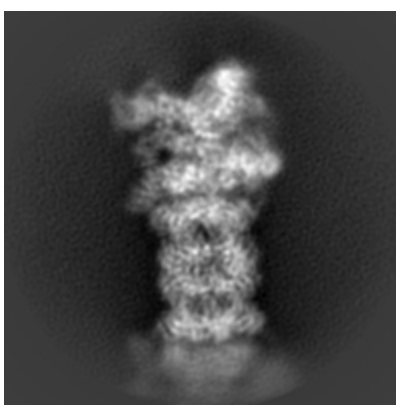
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

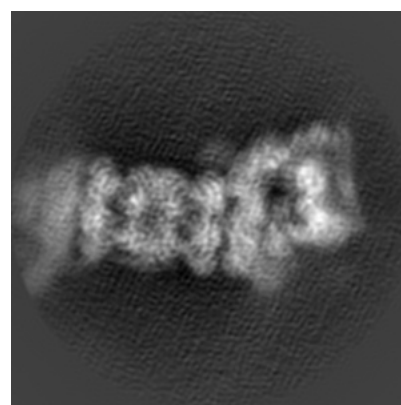
6.1.1 Primary map



X



Y

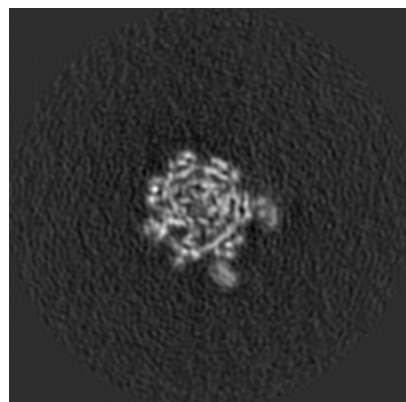


Z

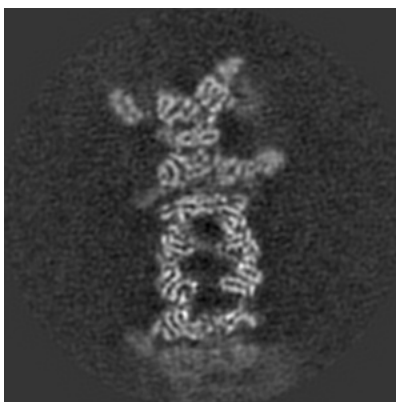
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

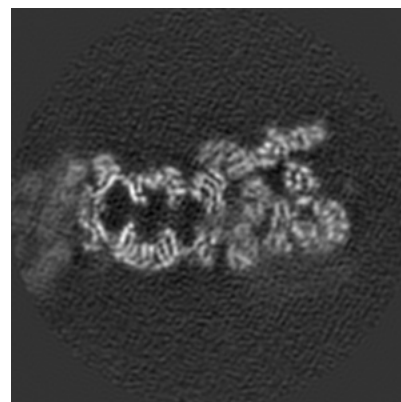
6.2.1 Primary map



X Index: 160



Y Index: 160

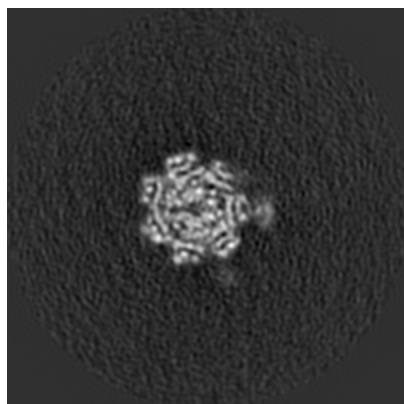


Z Index: 160

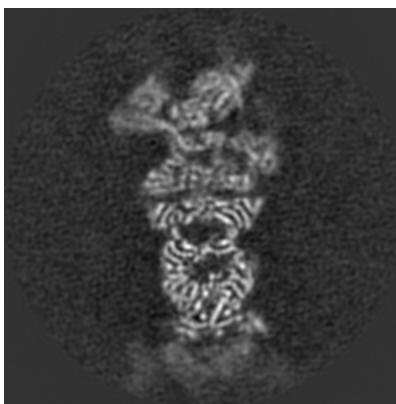
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

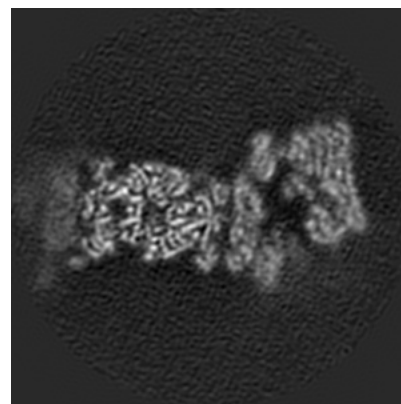
6.3.1 Primary map



X Index: 156



Y Index: 140

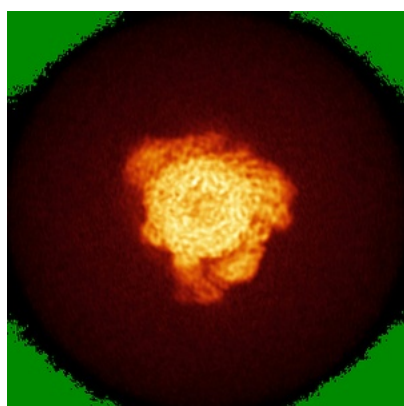


Z Index: 181

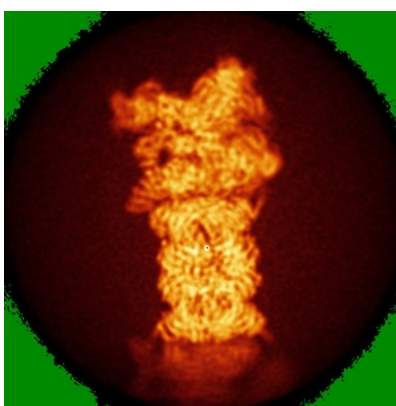
The images above show the largest variance slices of the map in three orthogonal directions.

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

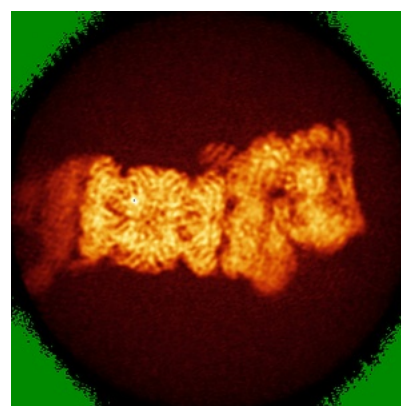
6.4.1 Primary map



X



Y

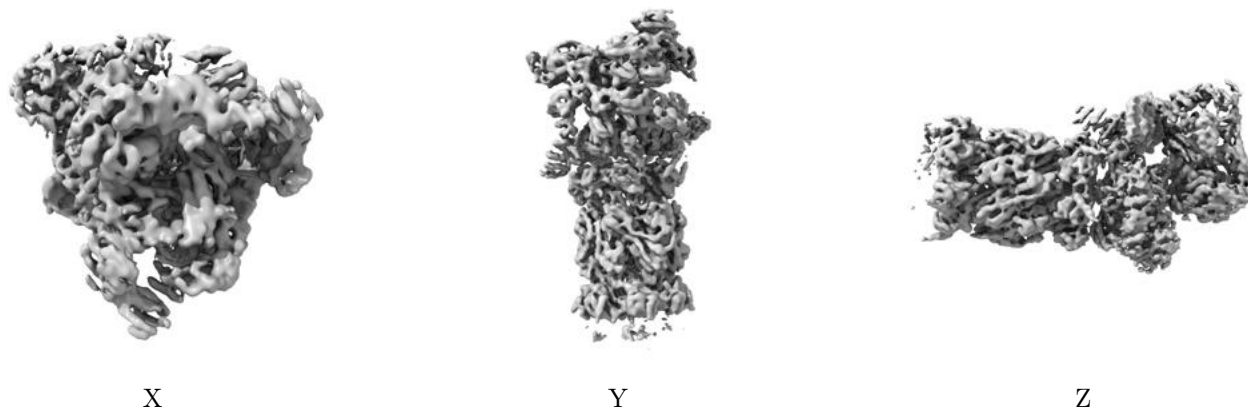


Z

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

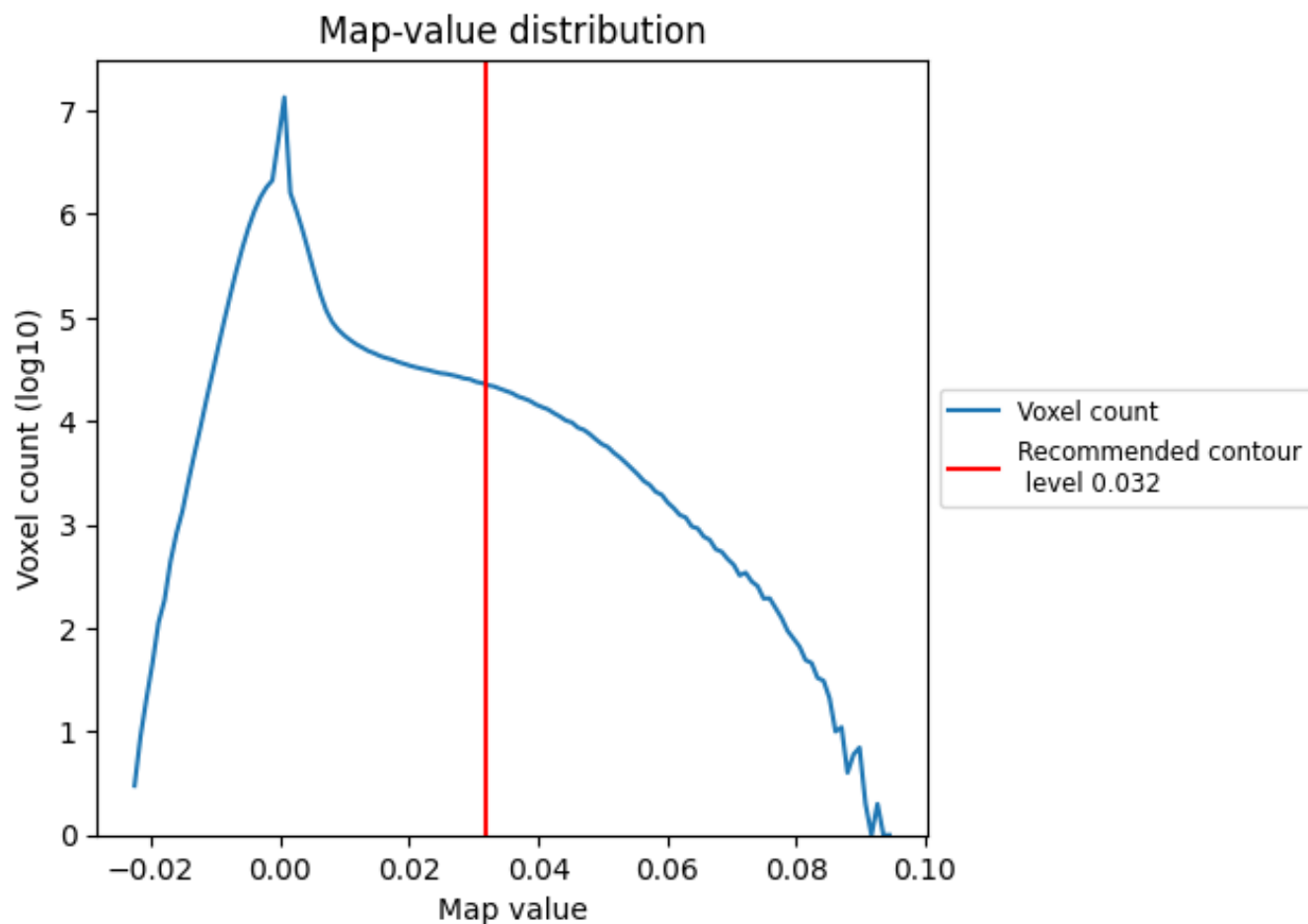
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

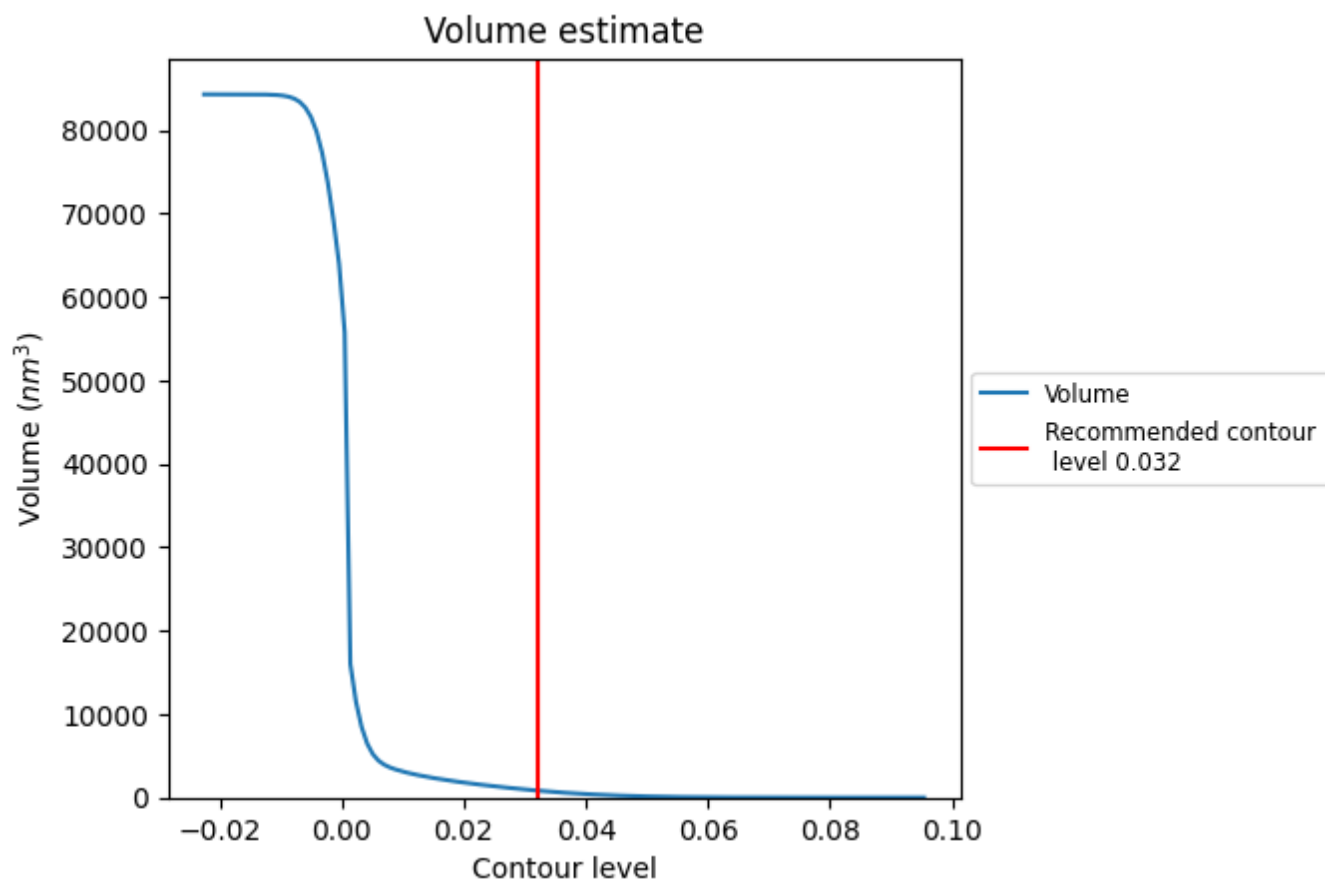
This section contains the results of statistical analysis of the map.

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.

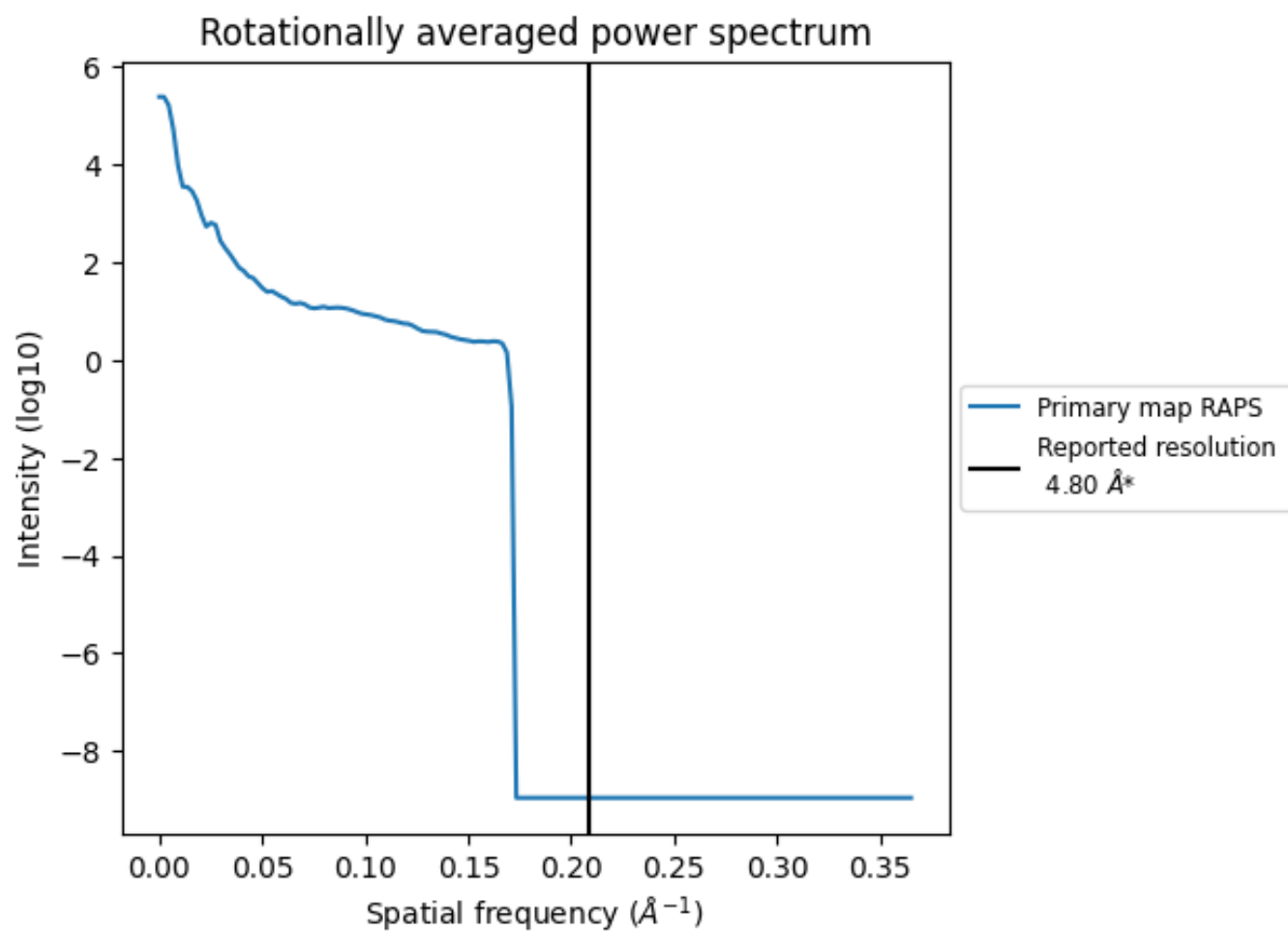
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 840 nm³; this corresponds to an approximate mass of 759 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 0.208 Å⁻¹

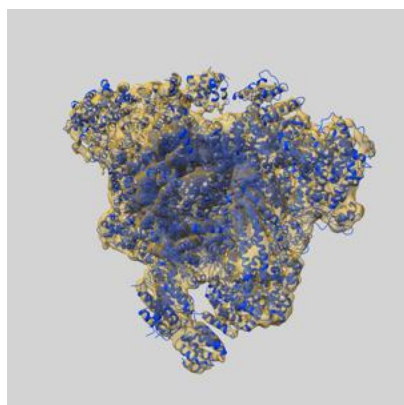
8 Fourier-Shell correlation

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

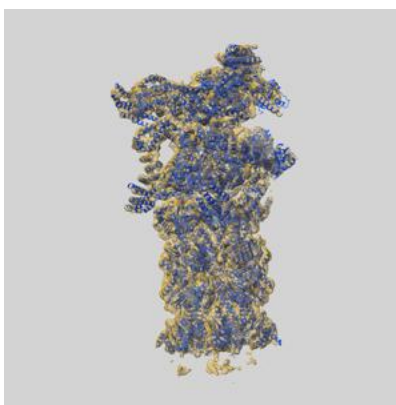
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14210 and PDB model 7QYA. Per-residue inclusion information can be found in section [3](#) on page [12](#).

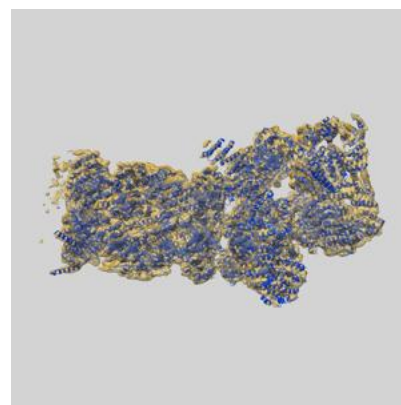
9.1 Map-model overlay [i](#)



X



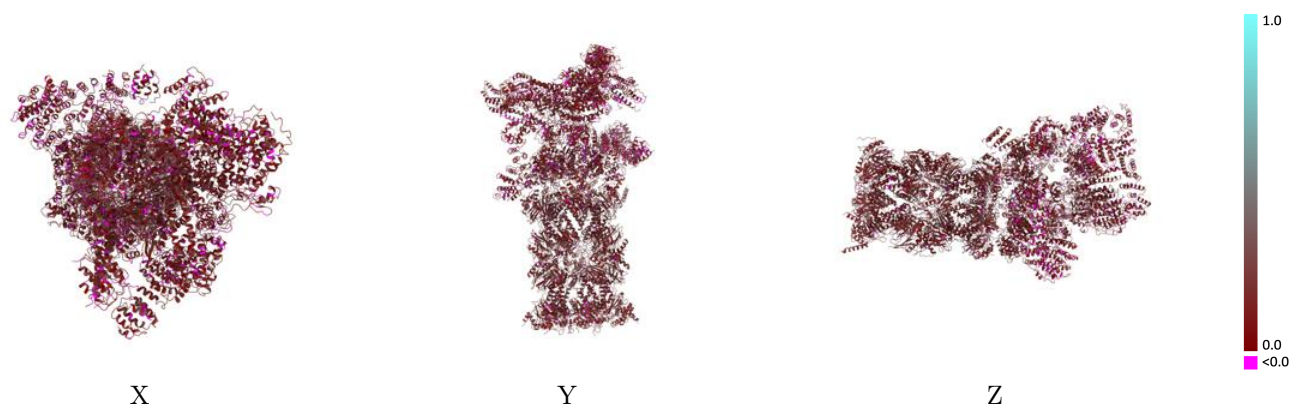
Y



Z

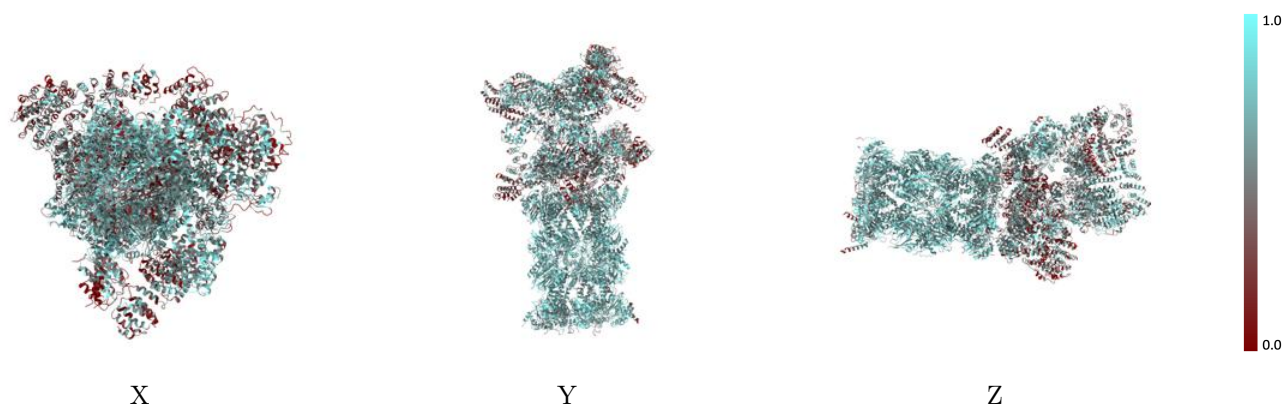
The images above show the 3D surface view of the map at the recommended contour level 0.032 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



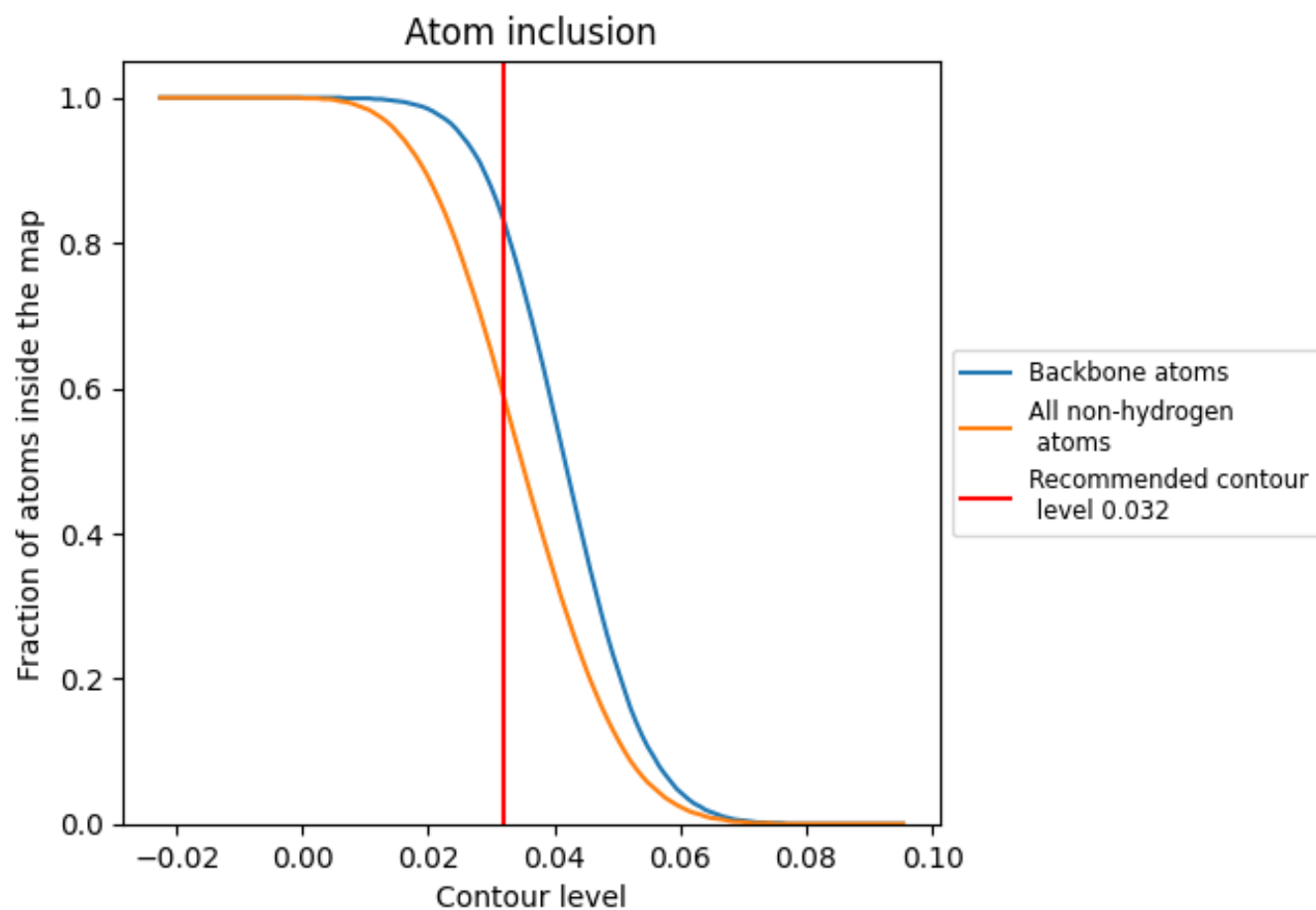
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.032).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 59% 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 (0.032) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5870	 0.1760
A	 0.5090	 0.1800
B	 0.4240	 0.1710
C	 0.4500	 0.1670
D	 0.4330	 0.1680
E	 0.5330	 0.1740
F	 0.5370	 0.1730
G	 0.6810	 0.1990
H	 0.6750	 0.1950
I	 0.6250	 0.1920
J	 0.6850	 0.2140
K	 0.6280	 0.1850
L	 0.6960	 0.1940
M	 0.6800	 0.1930
N	 0.7300	 0.2040
O	 0.7310	 0.2110
P	 0.7010	 0.1940
Q	 0.7130	 0.2050
R	 0.7460	 0.2070
S	 0.7100	 0.2060
T	 0.7440	 0.2160
U	 0.6130	 0.1570
V	 0.4190	 0.1360
W	 0.4870	 0.1530
X	 0.4800	 0.1620
Y	 0.6400	 0.1500
Z	 0.5610	 0.1580
a	 0.5330	 0.1520
b	 0.4190	 0.1420
c	 0.5770	 0.1560
d	 0.4090	 0.1400
e	 0.4470	 0.0890
f	 0.3630	 0.1210
g	 0.6560	 0.2010
h	 0.6560	 0.2010



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Chain	Atom inclusion	Q-score
i	 0.6210	 0.1940
j	 0.6430	 0.1980
k	 0.6560	 0.1980
l	 0.6960	 0.2070
m	 0.6580	 0.1830
n	 0.7470	 0.2070
o	 0.7390	 0.2140
p	 0.7060	 0.1930
q	 0.7240	 0.2090
r	 0.7580	 0.2070
s	 0.7290	 0.2110
t	 0.7330	 0.2130