



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 06:01 AM UTC

PDB ID : 3JCO / pdb_00003jco
EMDB ID : EMD-6574
Title : Structure of yeast 26S proteasome in M1 state derived from Titan dataset
Authors : Luan, B.; Huang, X.L.; Wu, J.P.; Shi, Y.G.; Wang, F.
Deposited on : 2016-01-06
Resolution : 4.80 Å(reported)
Based on initial model : 4CR4

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

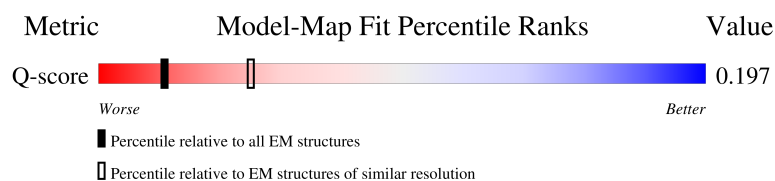
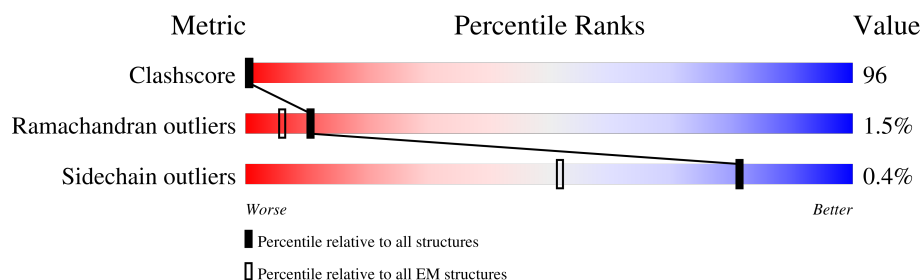
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

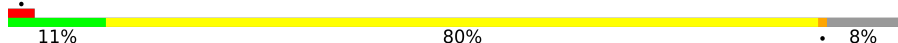
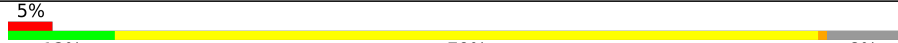
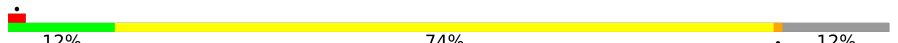
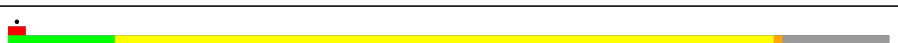
The reported resolution of this entry is 4.80 Å.

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.



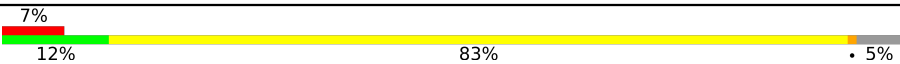
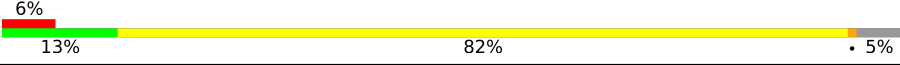
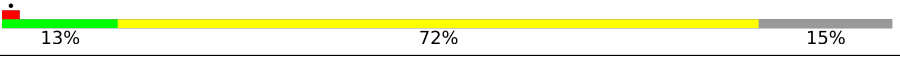
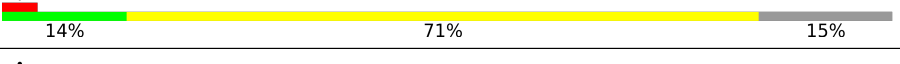
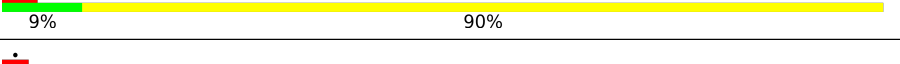
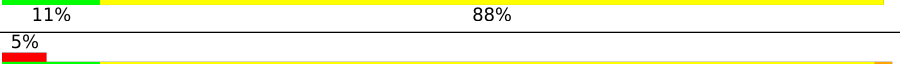
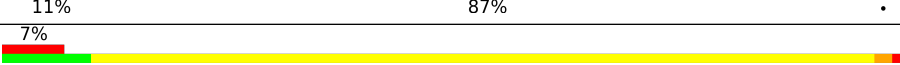
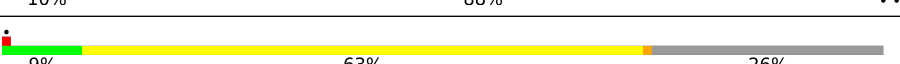
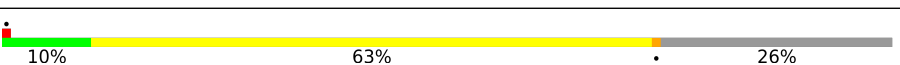
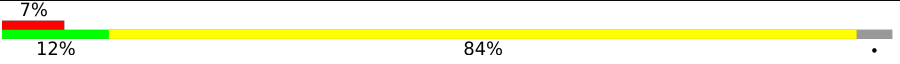
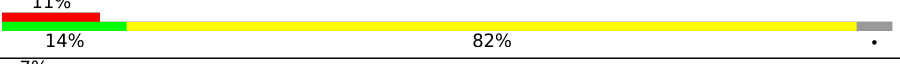
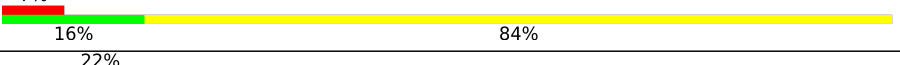
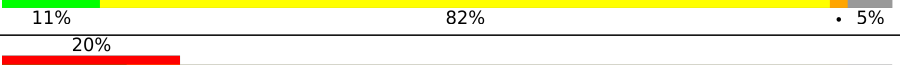
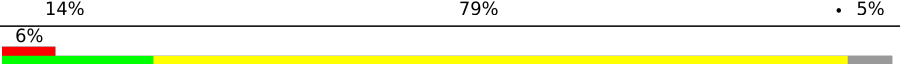
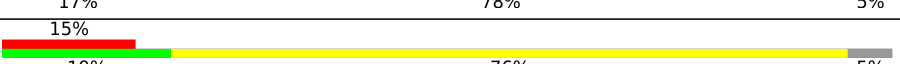
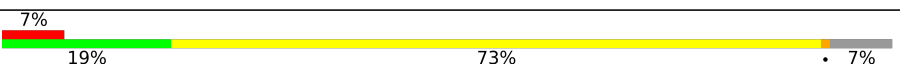
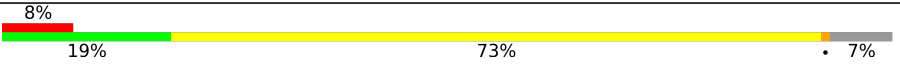
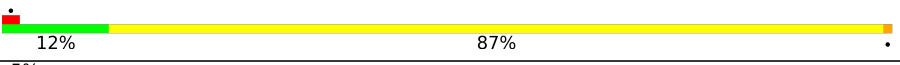
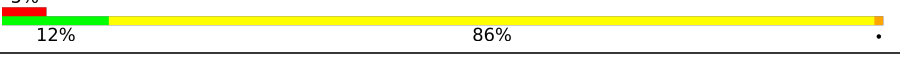
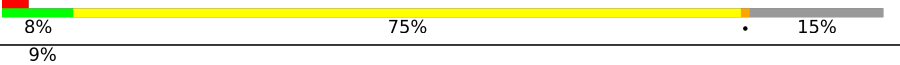
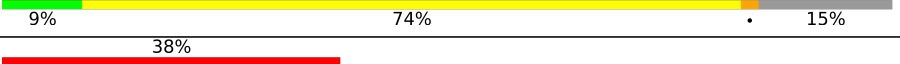
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1575 (4.30 - 5.30)

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	1	241	 11% 80% 8%
1	8	241	 5% 12% 79% 8%
2	2	266	 12% 74% 12%
2	9	266	 12% 74% 12%

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Mol	Chain	Length	Quality of chain
3	3	215	
3	h	215	
4	4	261	
4	i	261	
5	5	205	
5	j	205	
6	6	198	
6	k	198	
7	7	287	
7	l	287	
8	A	252	
8	a	252	
9	B	250	
9	b	250	
10	C	258	
10	c	258	
11	D	254	
11	d	254	
12	E	260	
12	e	260	
13	F	234	
13	f	234	
14	G	288	
14	g	288	
15	H	467	

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

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 104317 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	1	222	Total	C	N	O	S	0	0
			1757	1115	303	335	4		
1	8	222	Total	C	N	O	S	0	0
			1757	1115	303	335	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	233	Total	C	N	O	S	0	0
			1824	1154	312	351	7		
2	9	233	Total	C	N	O	S	0	0
			1824	1154	312	351	7		

- Molecule 3 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	205	Total	C	N	O	S	0	0
			1574	995	261	311	7		
3	h	205	Total	C	N	O	S	0	0
			1574	995	261	311	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	222	Total	C	N	O	S	0	0
			1684	1061	293	323	7		
4	i	222	Total	C	N	O	S	0	0
			1684	1061	293	323	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	204	Total	C	N	O	S	0	0
			1581	1010	258	305	8		
5	j	204	Total	C	N	O	S	0	0
			1581	1010	258	305	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	198	Total	C	N	O	S	0	0
			1585	1005	269	305	6		
6	k	198	Total	C	N	O	S	0	0
			1585	1005	269	305	6		

- Molecule 7 is a protein called Proteasome subunit beta type-5.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	243	Total	C	N	O	S	0	0
			1921	1221	322	370	8		
8	a	243	Total	C	N	O	S	0	0
			1921	1221	322	370	8		

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	241	Total	C	N	O	S	0	0
			1890	1181	331	374	4		
11	d	241	Total	C	N	O	S	0	0
			1890	1181	331	374	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	233	Total	C	N	O	S	0	0
			1795	1129	312	350	4		
13	f	233	Total	C	N	O	S	0	0
			1795	1129	312	350	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	244	Total	C	N	O	S	0	0
			1896	1205	330	357	4		
14	g	244	Total	C	N	O	S	0	0
			1896	1205	330	357	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	356	Total	C	N	O	S	0	0
			2771	1744	496	516	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	325	Total	C	N	O	S	0	0
			2513	1573	424	503	13		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	361	Total	C	N	O	S	0	0
			2849	1788	506	545	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	358	Total	C	N	O	S	0	0
			2829	1782	501	534	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	357	Total	C	N	O	S	0	0
			2754	1723	473	548	10		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	376	Total	C	N	O	S	0	0
			3083	1991	497	586	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	431	Total	C	N	O	S	0	0
			3470	2210	585	667	8		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	439	Total	C	N	O	S	0	0
			3357	2136	569	635	17		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	267	Total	C	N	O	S	0	0
			2201	1410	350	435	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	254	Total	C	N	O	S	0	0
			2034	1291	350	387	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	245	Total	C	N	O	S	0	0
			1912	1206	322	371	13		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	127	Total	C	N	O	S	0	0
			1032	664	169	195	4		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Y	34	Total	C	N	O	0	0
			243	146	45	52		

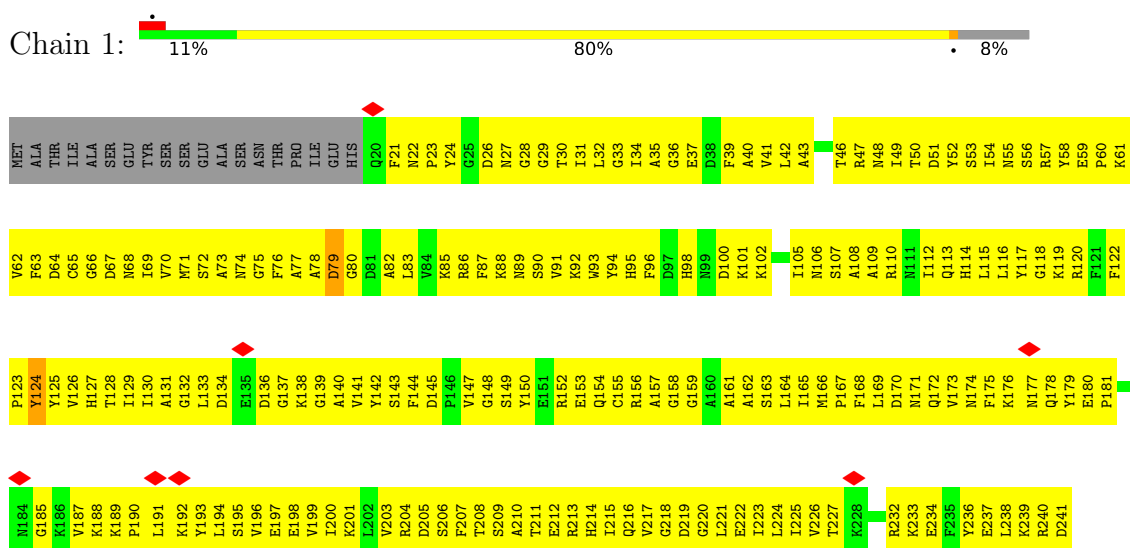
- Molecule 33 is a protein called 26S proteasome regulatory subunit RPN1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	763	Total	C	N	O	S	0	0
			5894	3744	966	1156	28		

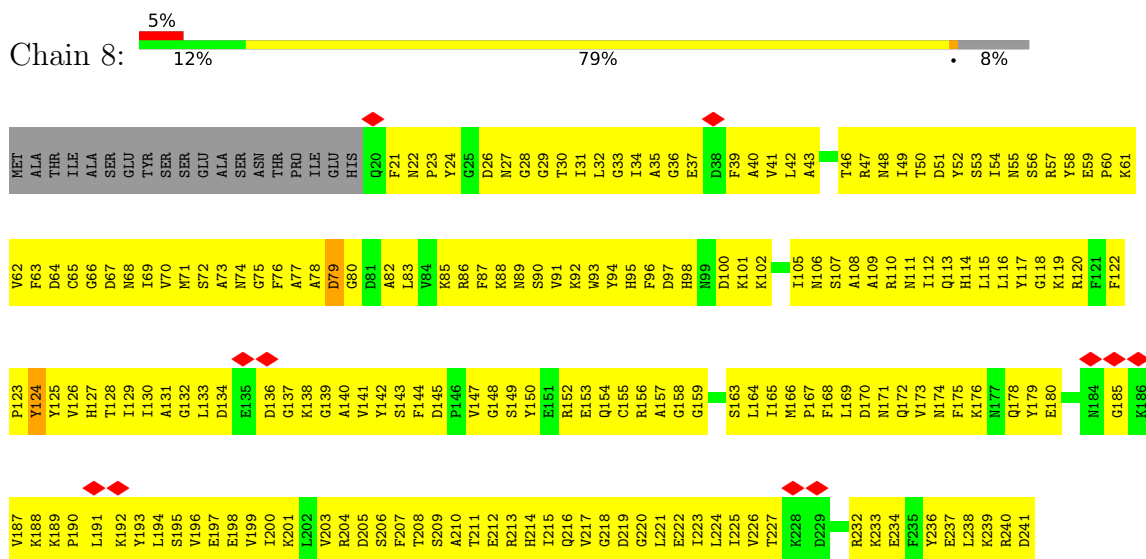
3 Residue-property plots

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

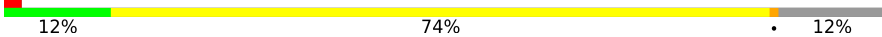
• Molecule 1: Proteasome subunit beta type-6

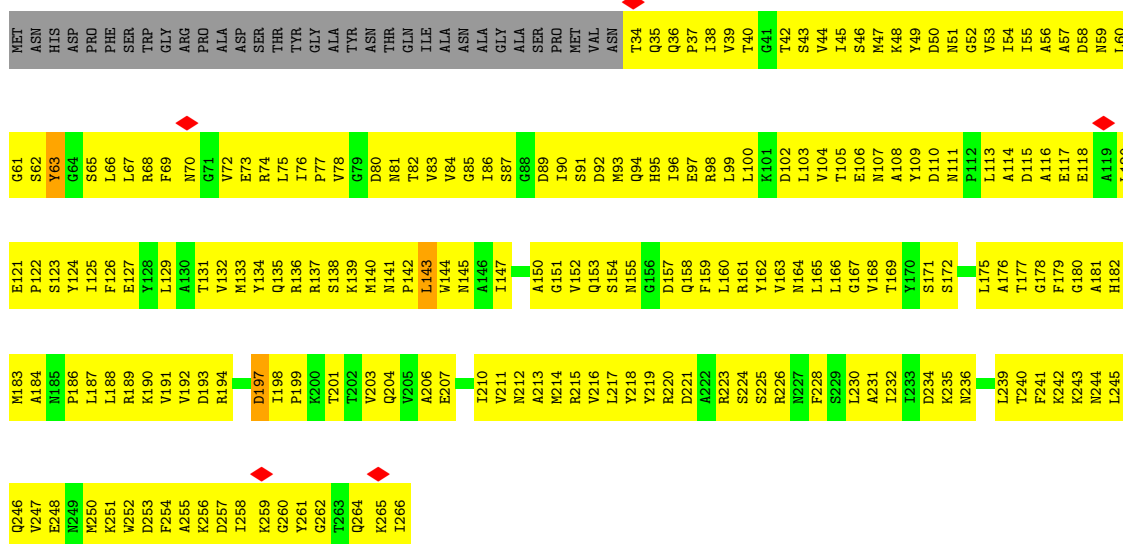


• Molecule 1: Proteasome subunit beta type-6

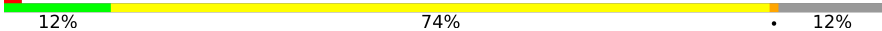


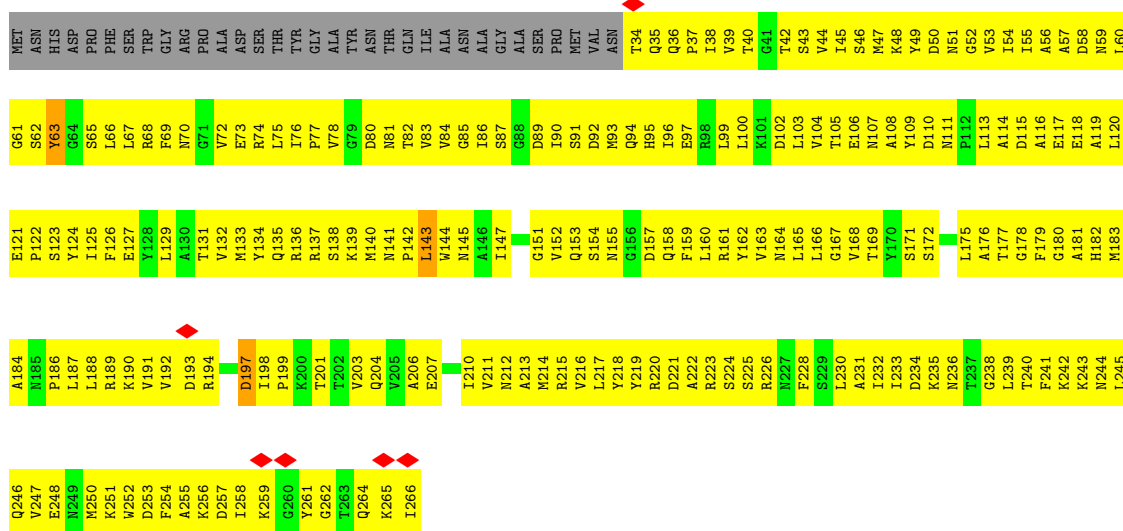
• Molecule 2: Proteasome subunit beta type-7

Chain 2:  12% 74% 12%

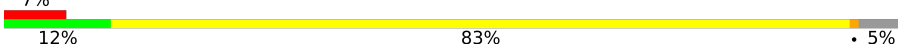


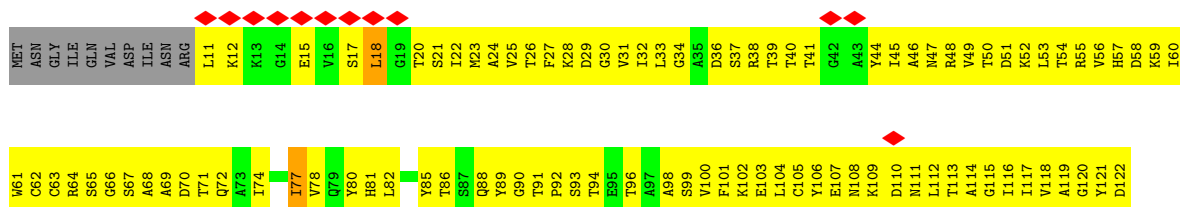
• Molecule 2: Proteasome subunit beta type-7

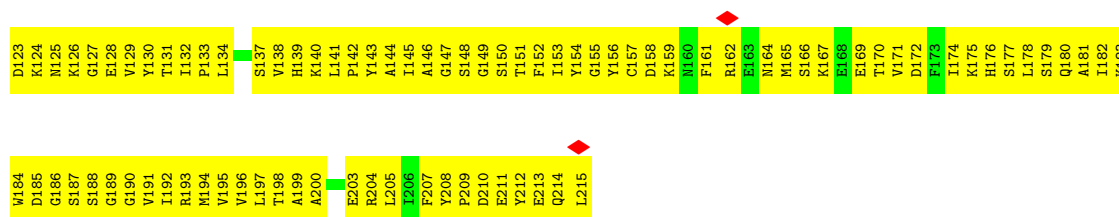
Chain 9:  12% 74% 12%



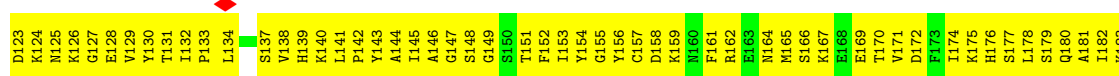
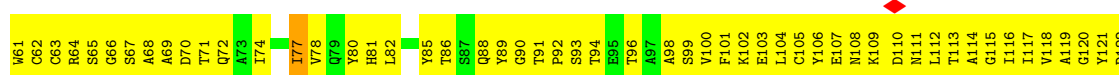
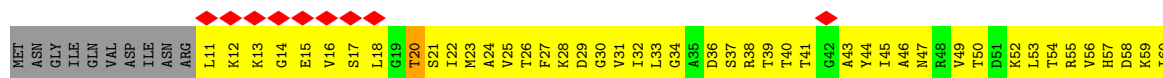
• Molecule 3: Proteasome subunit beta type-1

Chain 3:  7% 12% 83% 5%

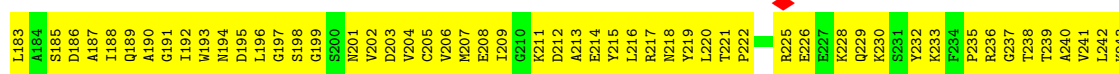
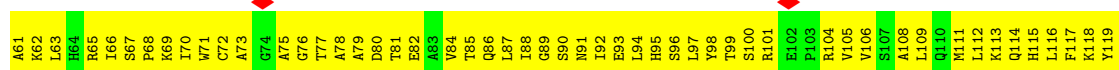
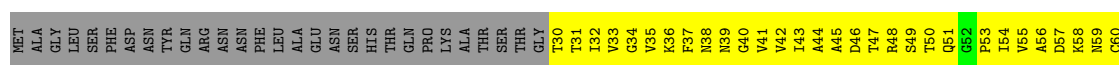




• Molecule 3: Proteasome subunit beta type-1



• Molecule 4: Proteasome subunit beta type-2

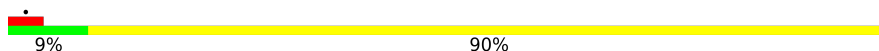


• Molecule 4: Proteasome subunit beta type-2



MET	ALA	GLY	LEU	SER	PHE	ASP	ASN	TYR	GLN	ARG	ASN	PHE	LEU	ALA	GLU	ASN	SER	HIS	THR	GLN	PRO	LYS	ALA	THR	SER	THR	THR	GLY	T30	T31	I32	V33	G34	K36	F37	N38	N39	G40	V41	V42	I43	A44	A45	D46	T47	R48	S49	T50	Q51	G52	P53	I54	V55	A56	D57	K58	N59	C60																																					
A61	K62	L63	H64	R65	I66	S67	P68	K69	L70	I71	C72	A73	G74	A75	G76	T77	A78	A79	D80	T81	E82	A83	V84	T85	Q86	L87	I88	G89	S90	N91	I92	E93	L94	H95	S96	L97	Y98	T99	S100	R101	E102	P103	R104	V105	V106	S107	A108	L109	Q110	M111	L112	K113	Q114	H115	L116	F117	K118	Y119	Q120																																				
G121	H122	I123	G124	A125	L126	L127	V128	A129	A130	G131	V132	D133	P134	T135	G136	S137	H138	L139	F140	S141	I142	H143	A144	H145	G146	S147	T148	D149	V150	G151	Y152	L153	L156	G157	S158	G159	S160	L161	A162	A163	M164	A165	V166	L167	E168	S169	H170	N171	K172	Q173	D174	L175	T176	K177	E178	E179	A180	I181																																					
K182	L183	A184	S185	D186	A187	I188	Q189	A190	G191	I192	W193	N194	D195	L196	G197	S198	G199	S200	N201	V202	D203	V204	C205	V206	H207	E208	L209	G210	K211	D212	A213	E214	V215	L216	R217	N218	Y219	L220	T221	P222	R225	E226	E227	K228	Q229	K230	S231	Y232	K233	P234	P235	R236	G237	T238	T239	A240	V241	L242																																					
K243	E244	S245	L246	V247	N248	L249	C250	D251	I252	G253	G254	V255	L256	G257	S258	T259	A260	N261	V262	D263	V264	C265	V266	H267	E268	L269	G270	K271	D272	A273	E274	V275	L276	R277	N278	Y279	L280	T281	P282	R285	E286	E287	K288	Q289	K290	S291	Y292	K293	P294	P295	R296	G297	T298	T299	A300	N301	V302	D303	V304	C305	V306	H307	E308	L309	G310	K311	D312	A313	E314	V315	L316	R317	N318	Y319	L320	T321	P322	R325	E326	E327	K328	Q329	K330	S331	Y332	K333	P334	P335	R336	G337	T338	T339	A340	V341	L342
K343	E344	S345	L346	V347	N348	L349	C350	D351	I352	G353	G354	V355	L356	G357	S358	T359	A360	N361	V362	D363	V364	C365	V366	H367	E368	L369	G370	K371	D372	A373	E374	V375	L376	R377	N378	Y379	L380	T381	P382	R385	E386	E387	K388	Q389	K390	S391	Y392	K393	P394	P395	R396	G397	T398	T399	A400	N401	V402	D403	V404	C405	V406	H407	E408	L409	G410	K411	D412	A413	E414	V415	L416	R417	N418	Y419	L420	T421	P422	R425	E426	E427	K428	Q429	K430	S431	Y432	K433	P434	P435	R436	G437	T438	T439	A440	V441	L442

• Molecule 5: Proteasome subunit beta type-3

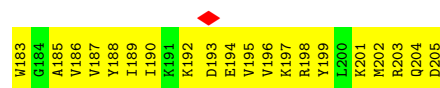
Chain 5:  9% 90%

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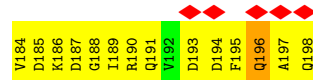
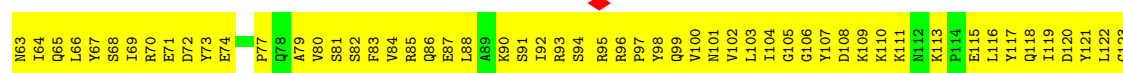
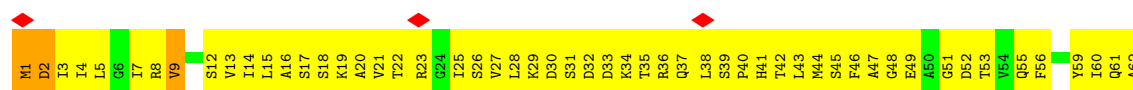
• Molecule 5: Proteasome subunit beta type-3

Chain j:  11% 88%

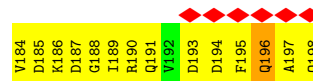
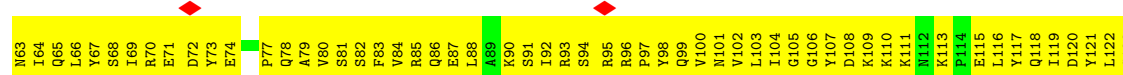
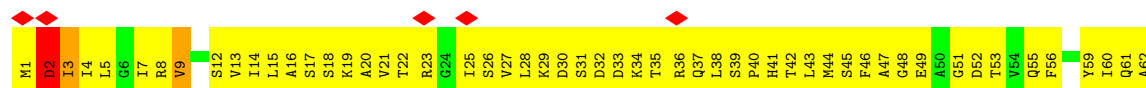
MET	S2	D3	P4		I7	N8	G9	G10	I11	V12	V13	A14	M15	T16	G17	K18	D19	C20	V21	A22	T23	A24	C25	D26	R27	L28	L29	G30	S31	Q32	S33	L34	G35	V36	S37	N38	F39	G40	E41	K42	I43	F44	H45	Y46	G47	H48	V49	F50	L51	G52	I53	T54	G55	L56	A57	T58	D59	V60	T61
	T62	L63	N64	E65	M66	R67	R68	Y69	K70	T71	N72	L73	W74	K75	L76	E77	E78	E79	R80	A81	E82	E83	P84	E85	T86	F87	T88	Q89	L90	V91	S94	L95	Y96	E97	R98	R99	F100	G101	P102	I103	F104	G105	T106	P107	V108	V109	A110	G111	I112	N113	S114	K115	S116	G117	K118	P119	F120	V121	
G123	F124	D125	L126	I127	G128	C129	I130	D131	E132	A133	K134	D135	F136	I137	V138	S139	G140	T141	A142	S143	D144	Q145	L146	F147	G148	M149	C150	E151	S152	L153	Y154	E155	P156	N157	L158	E159	P160	G161	D162	L163	F164	E165	T166	I167	S168	Q169	A170	L171	L172	N173	A174	A175	D176	R177	D178	A179	L180	S181	I182



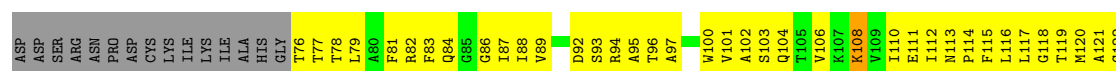
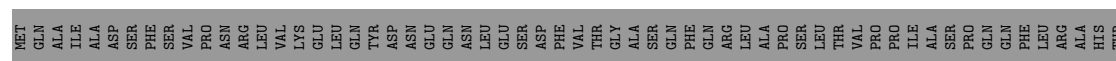
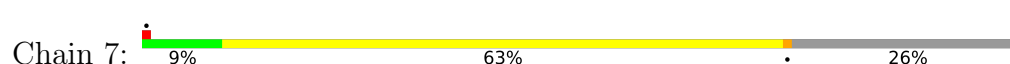
• Molecule 6: Proteasome subunit beta type-4



• Molecule 6: Proteasome subunit beta type-4

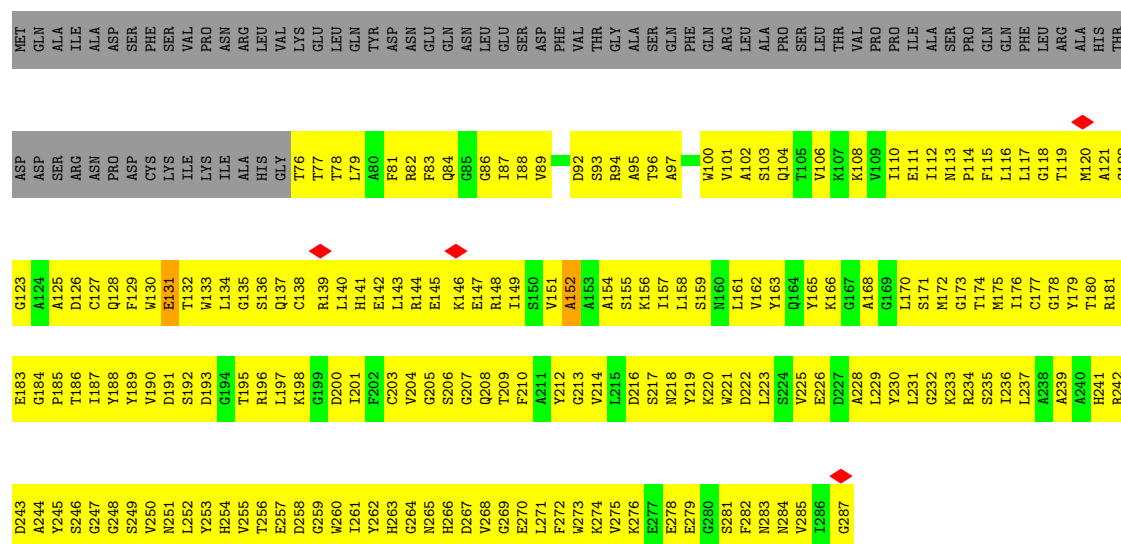
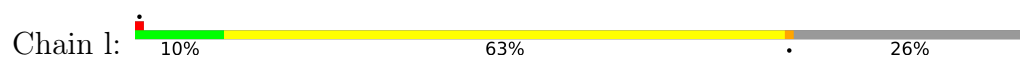


• Molecule 7: Proteasome subunit beta type-5

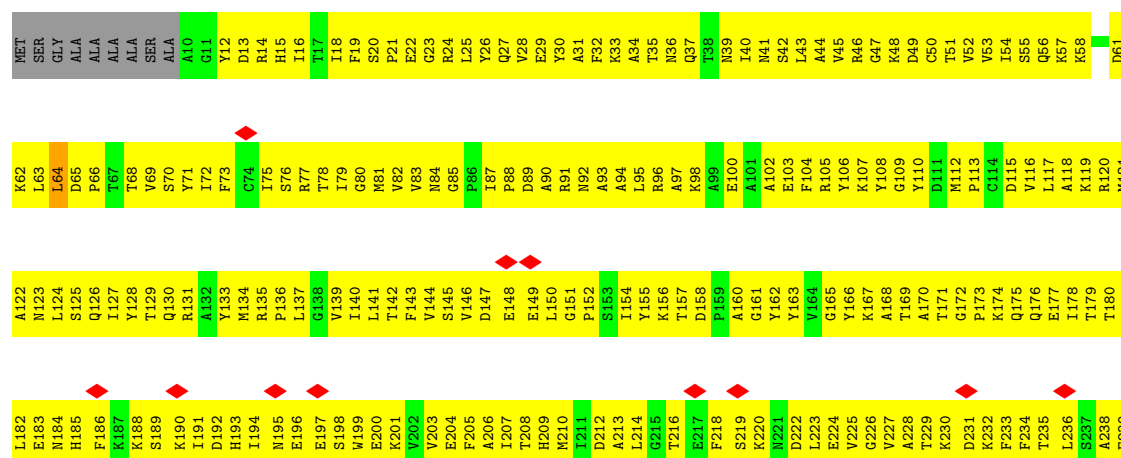




• Molecule 7: Proteasome subunit beta type-5

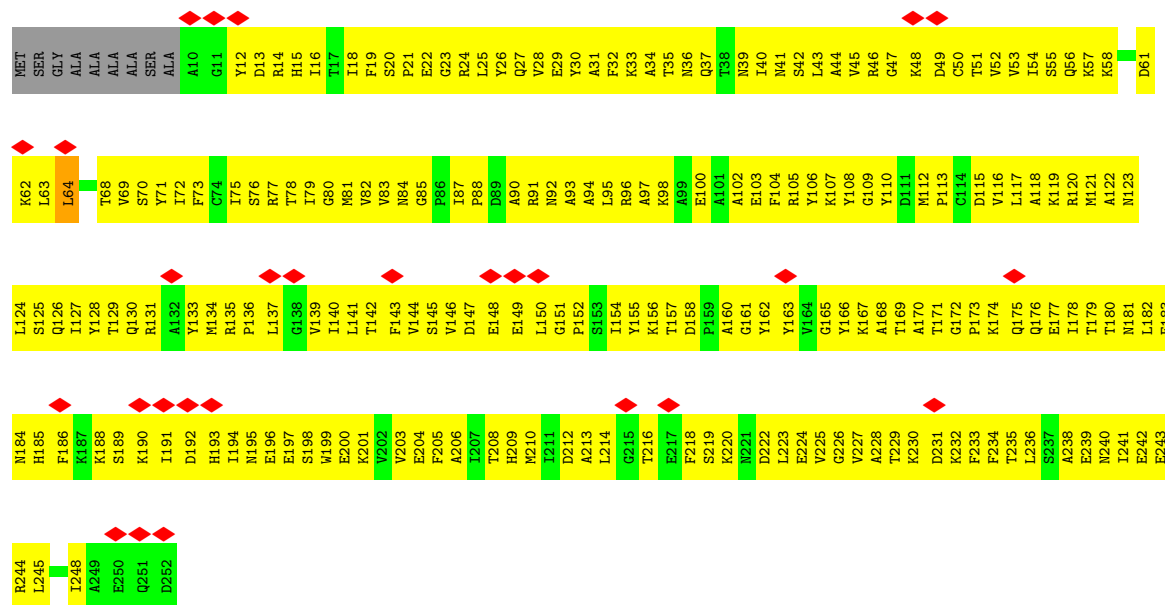


• Molecule 8: Proteasome subunit alpha type-1

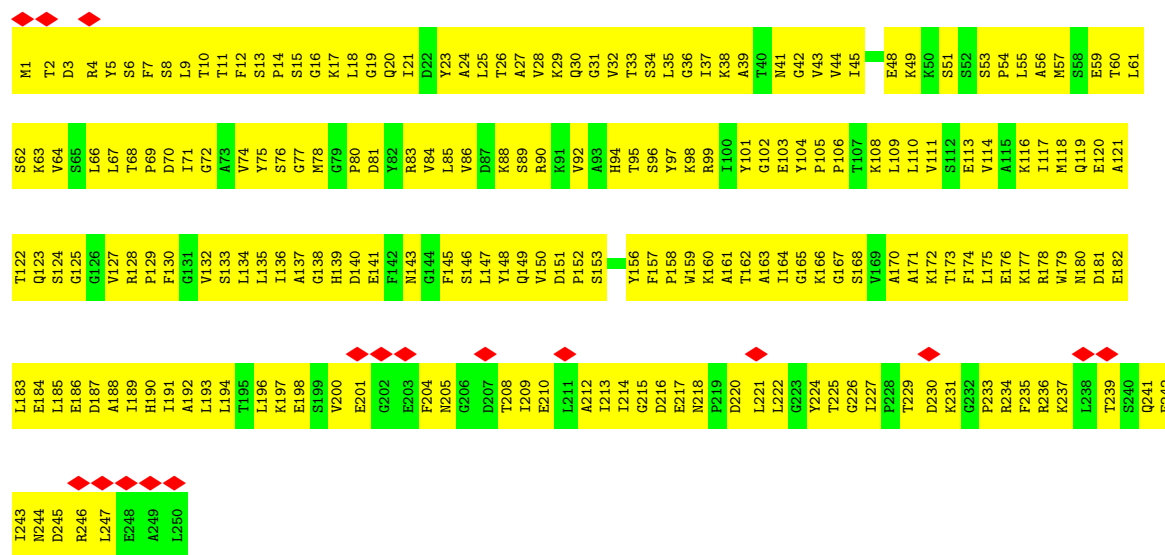




• Molecule 8: Proteasome subunit alpha type-1

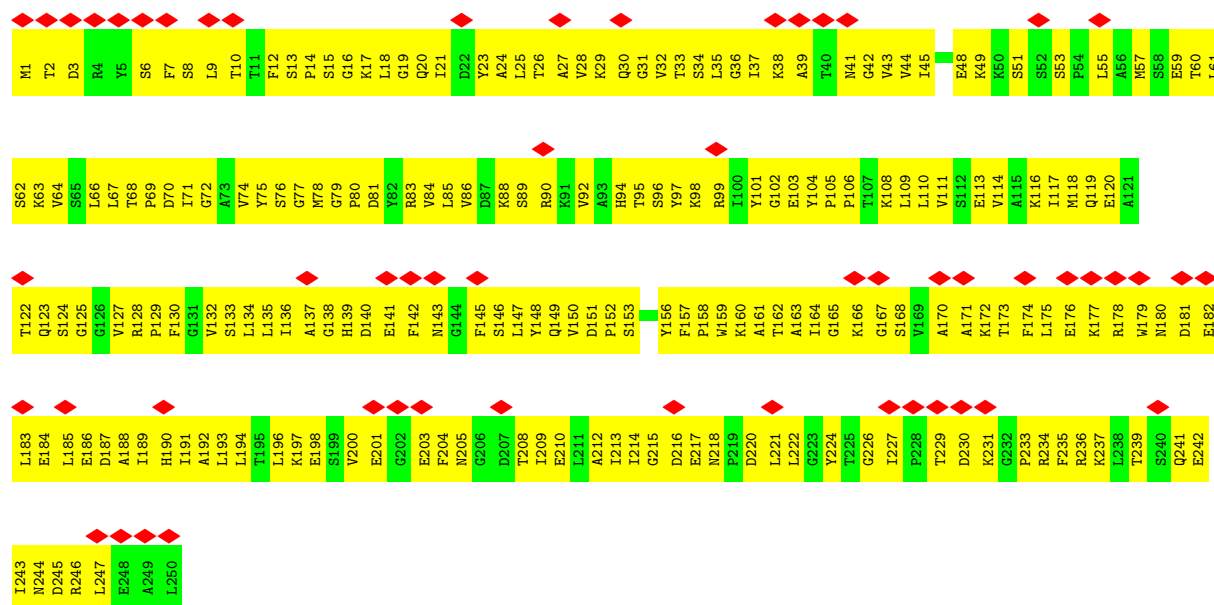


• Molecule 9: Proteasome subunit alpha type-2

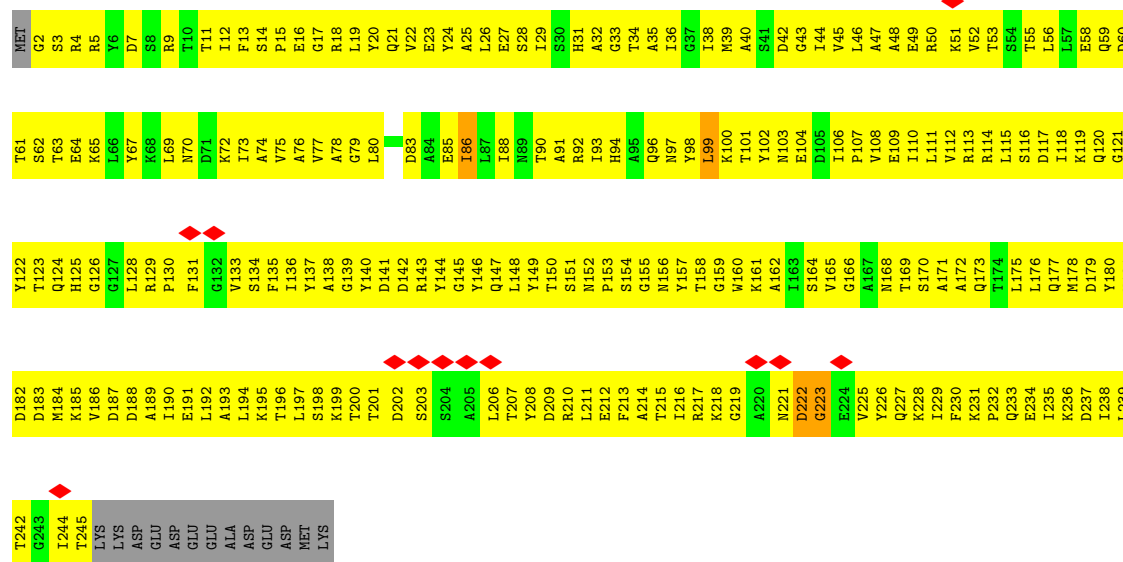


• Molecule 9: Proteasome subunit alpha type-2

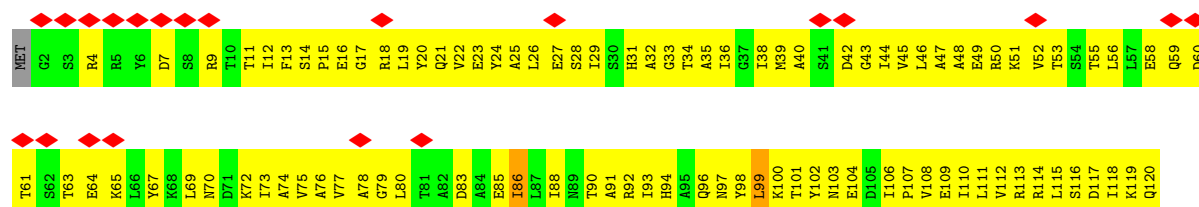




• Molecule 10: Proteasome subunit alpha type-3

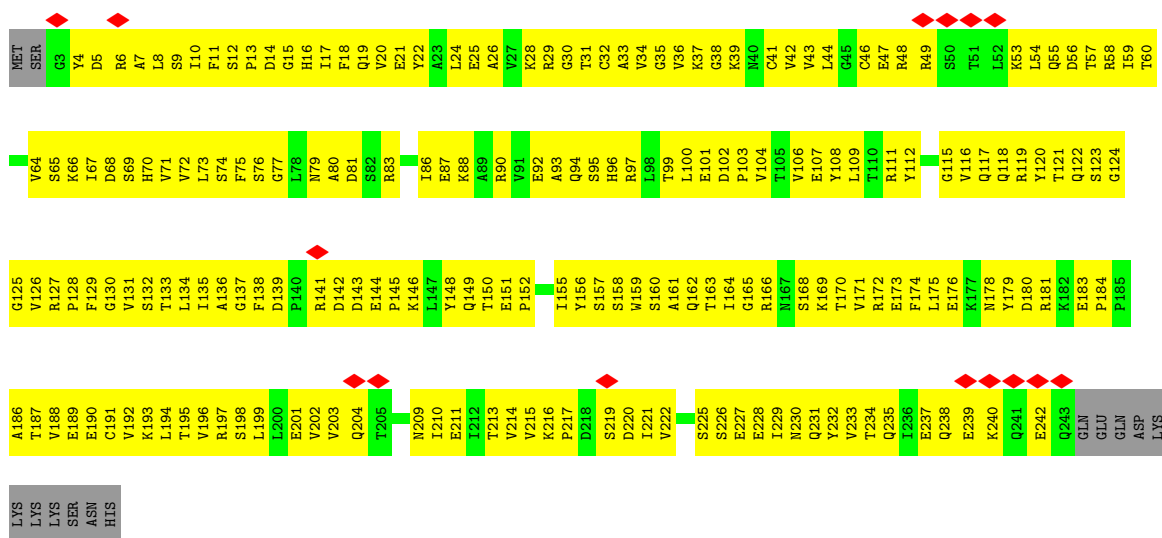


• Molecule 10: Proteasome subunit alpha type-3

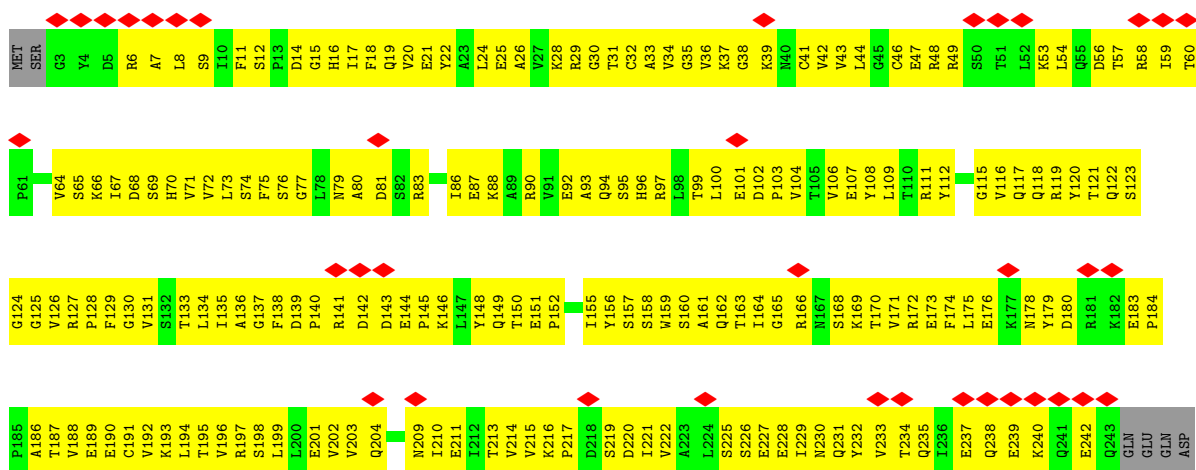




• Molecule 11: Proteasome subunit alpha type-4



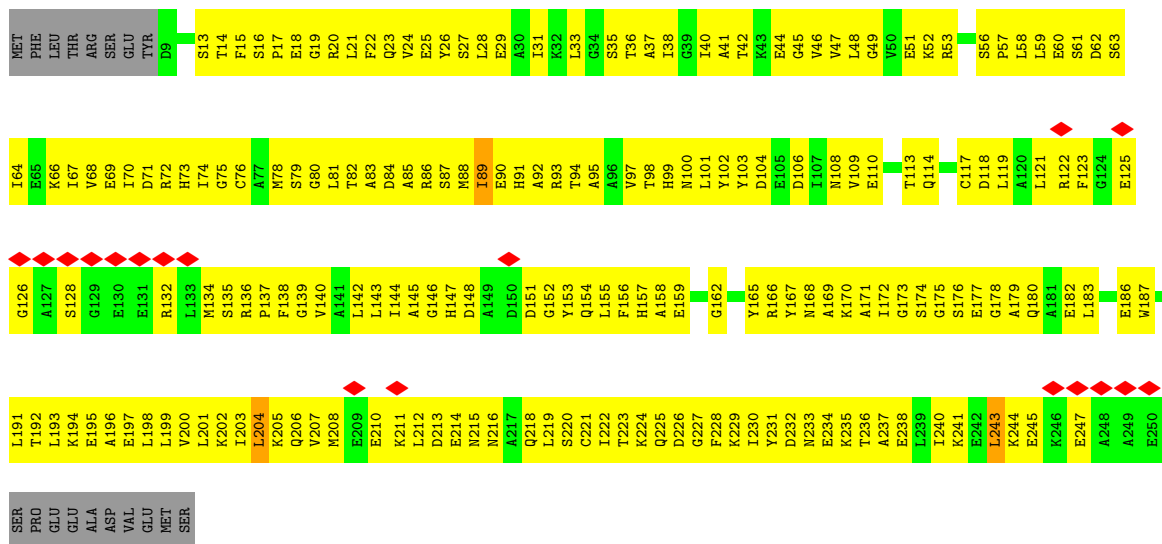
• Molecule 11: Proteasome subunit alpha type-4



LYS
LYS
LYS
LYS
SER
ASN
HIS

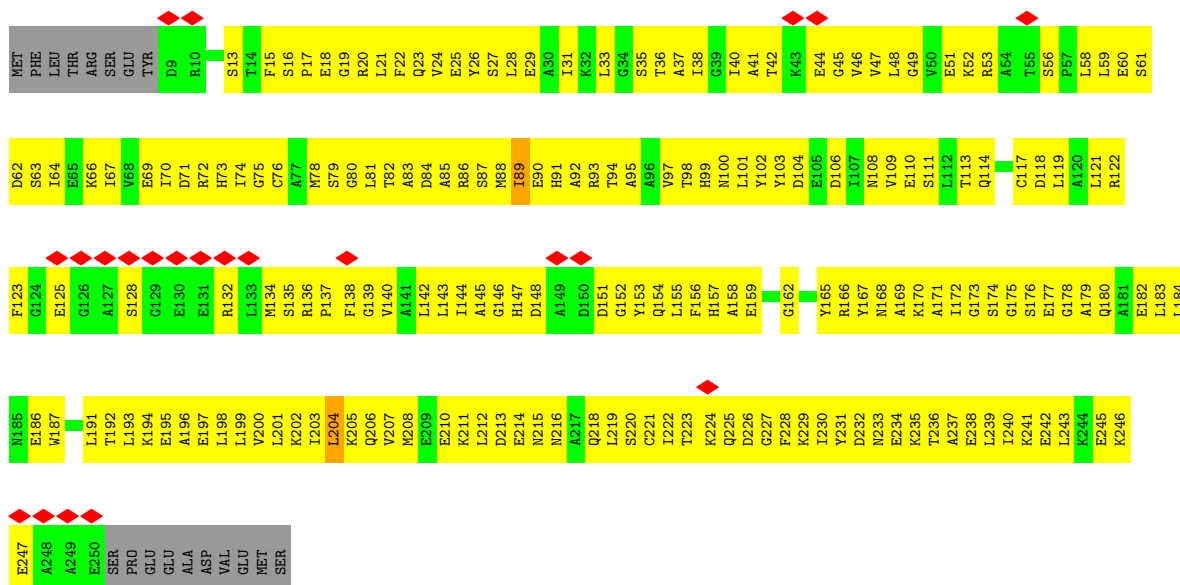
• Molecule 12: Proteasome subunit alpha type-5

Chain E: 



• Molecule 12: Proteasome subunit alpha type-5

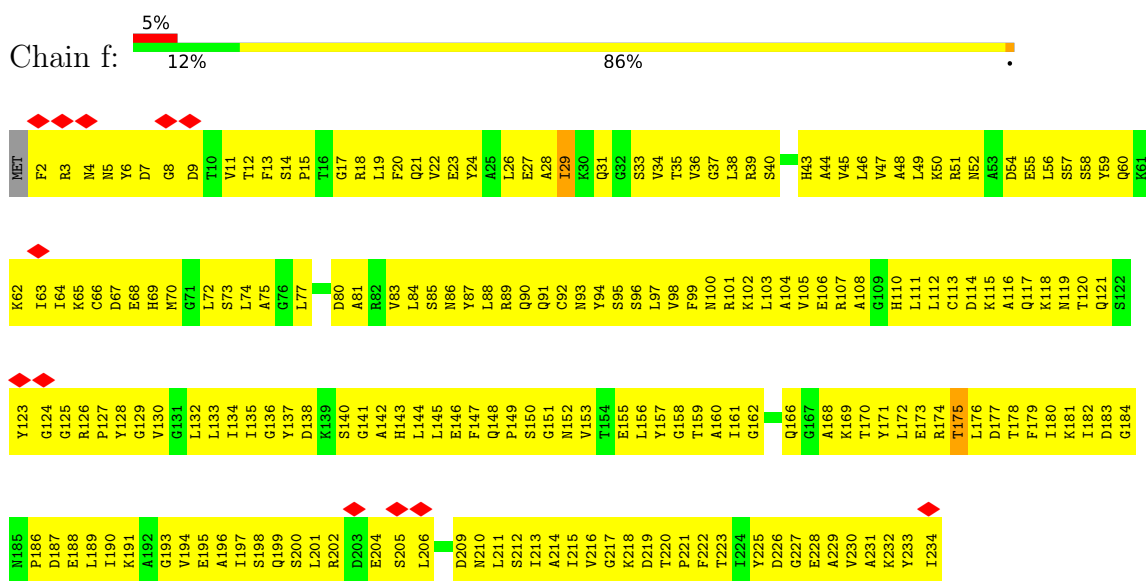
Chain e: 



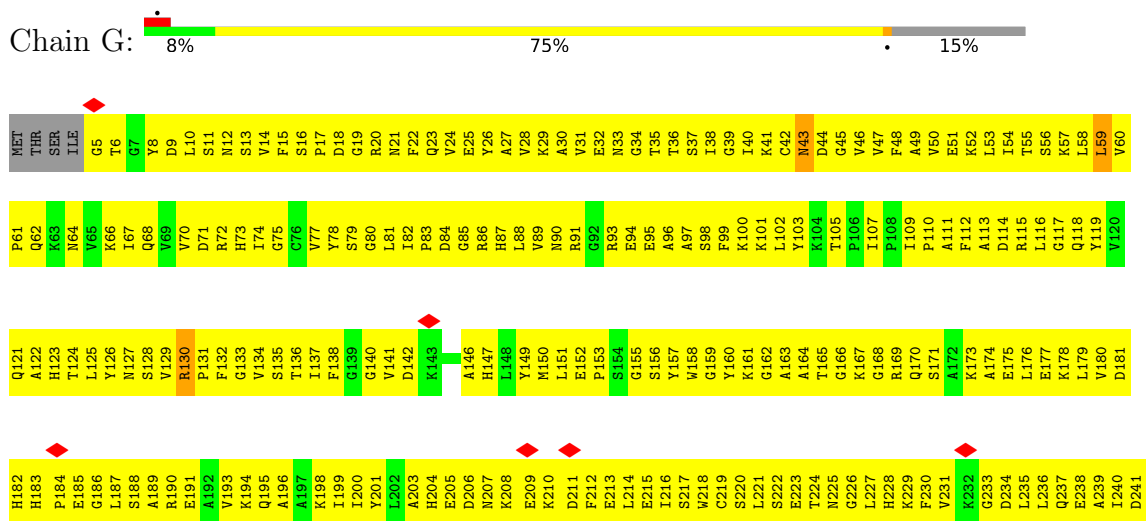
• Molecule 13: Proteasome subunit alpha type-6

Chain F: 

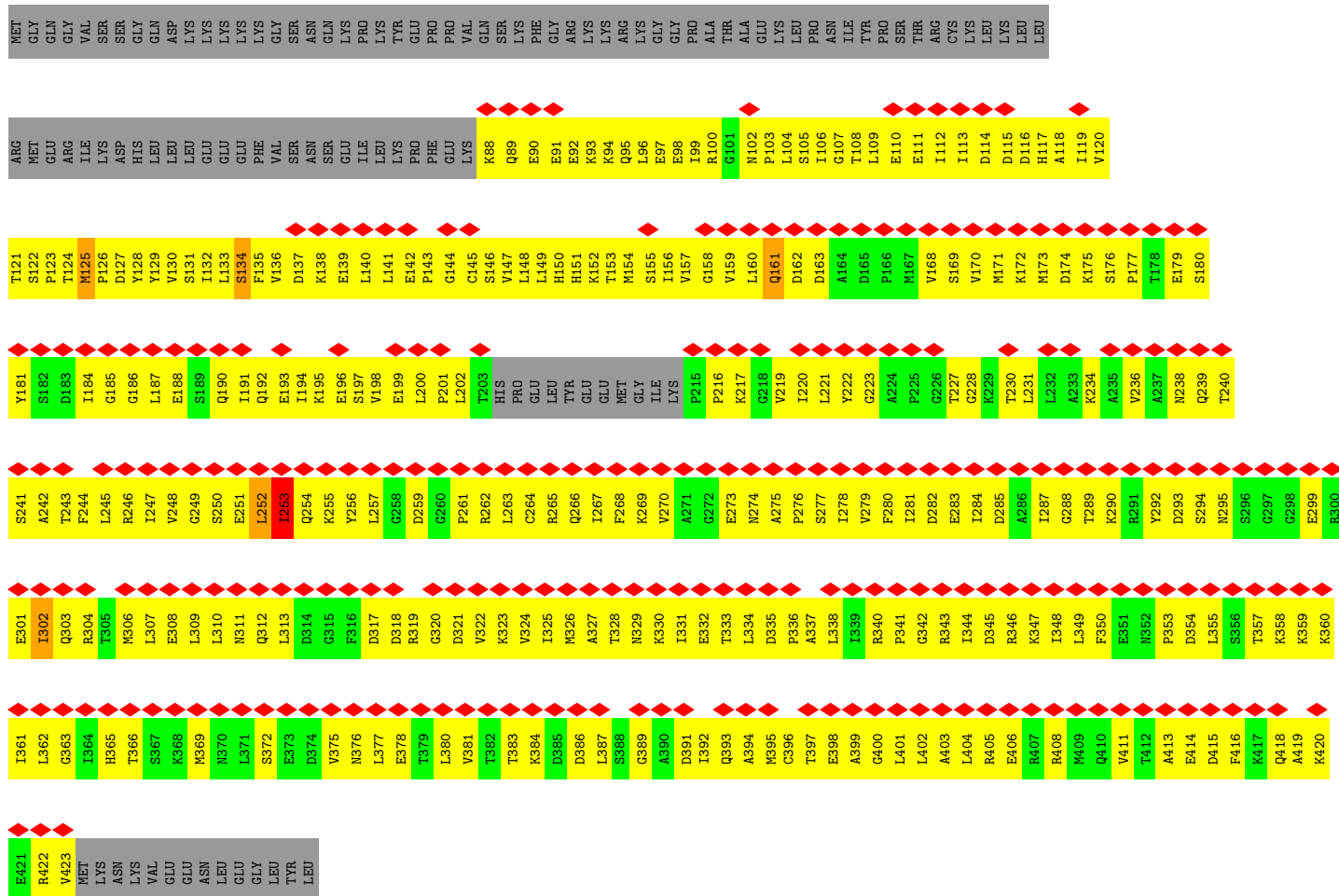
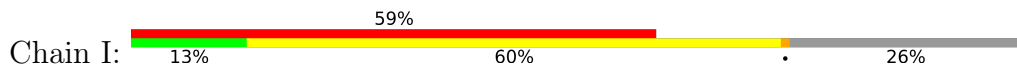
- Molecule 13: Proteasome subunit alpha type-6



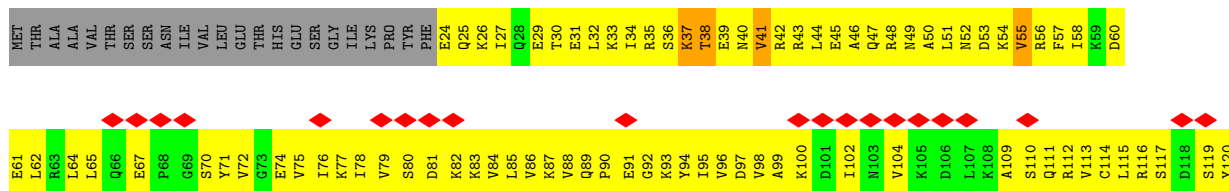
- Molecule 14: Probable proteasome subunit alpha type-7

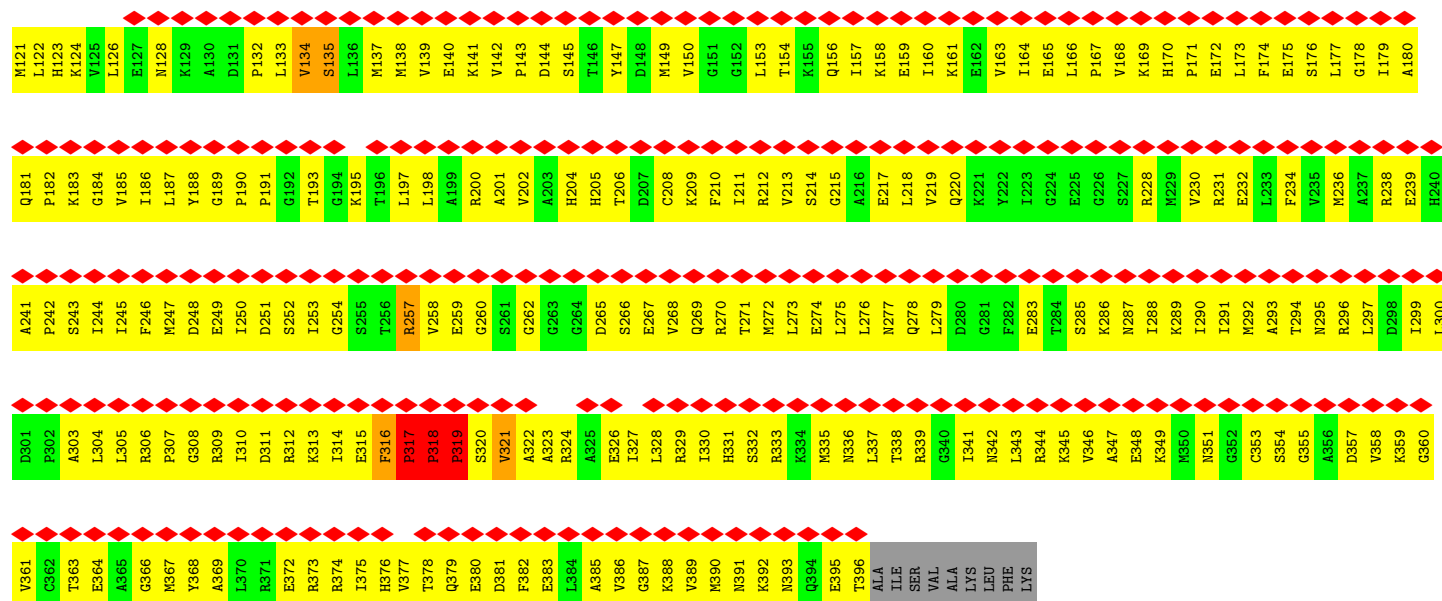


- Molecule 16: 26S protease regulatory subunit 4 homolog



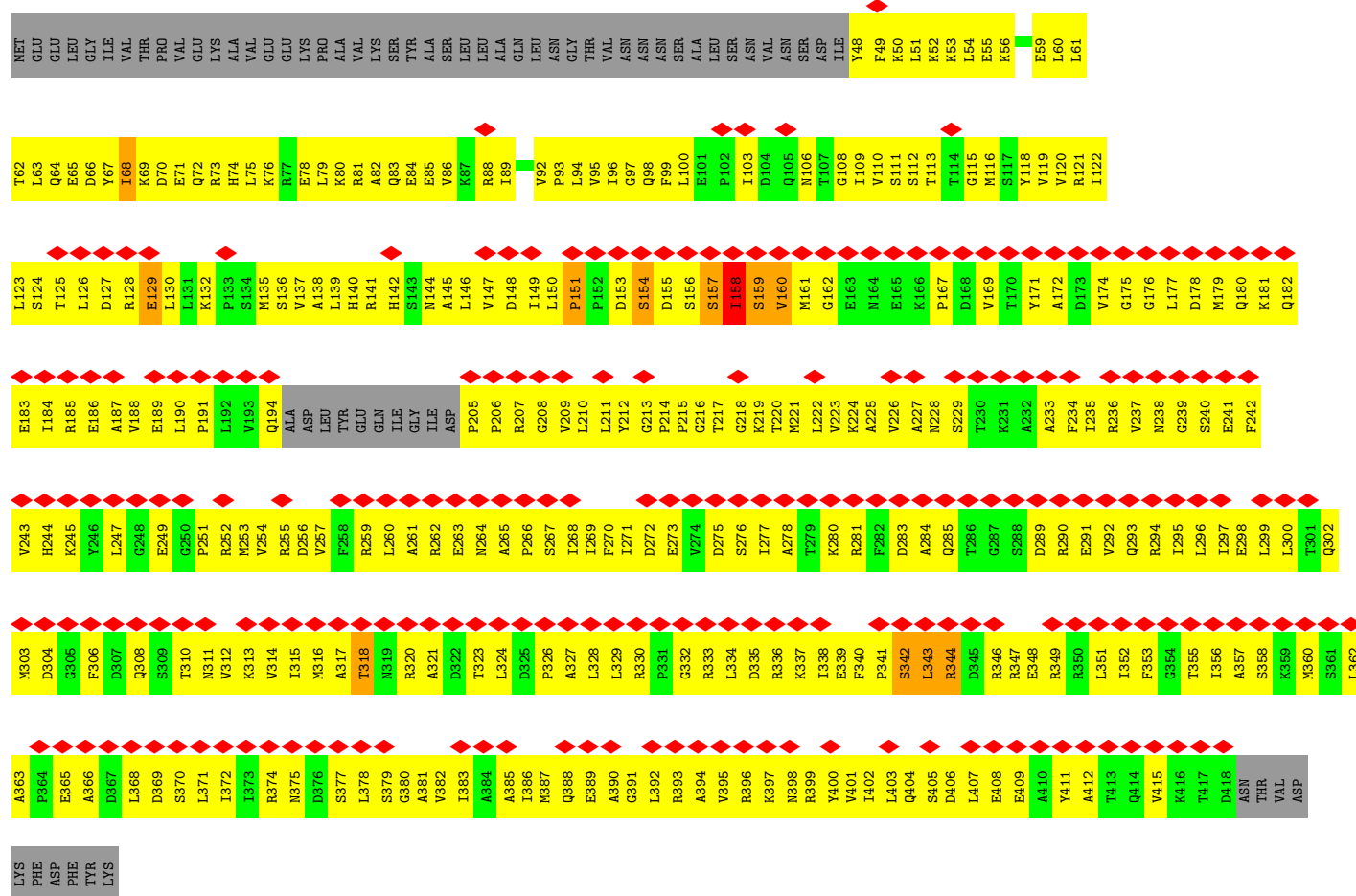
- Molecule 17: 26S protease regulatory subunit 8 homolog



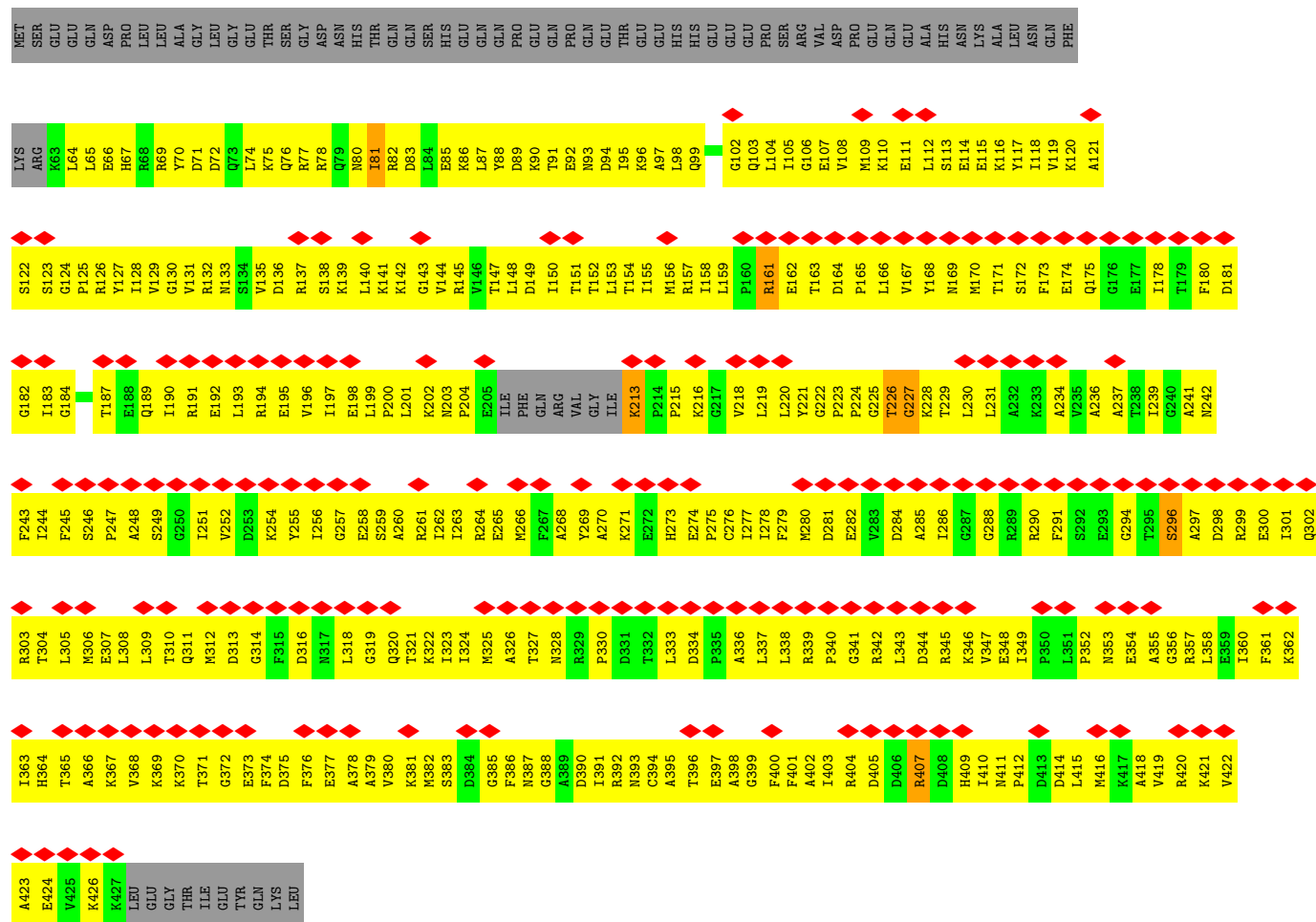
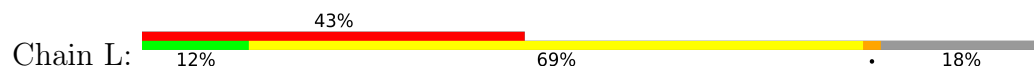


• Molecule 18: 26S protease regulatory subunit 6B homolog

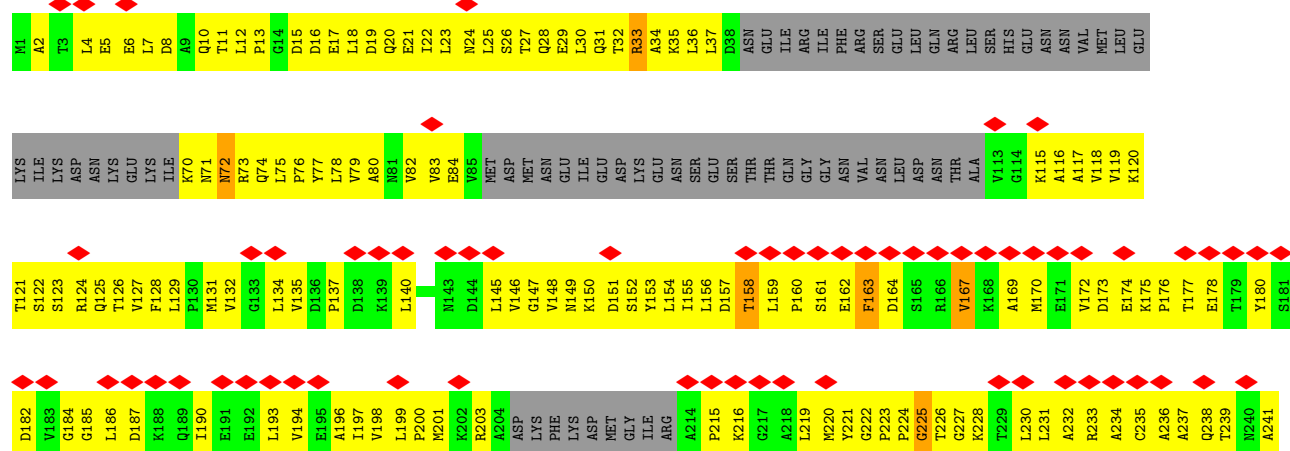
Chain K: 15% 54% 67% 16%



• Molecule 19: 26S protease subunit RPT4



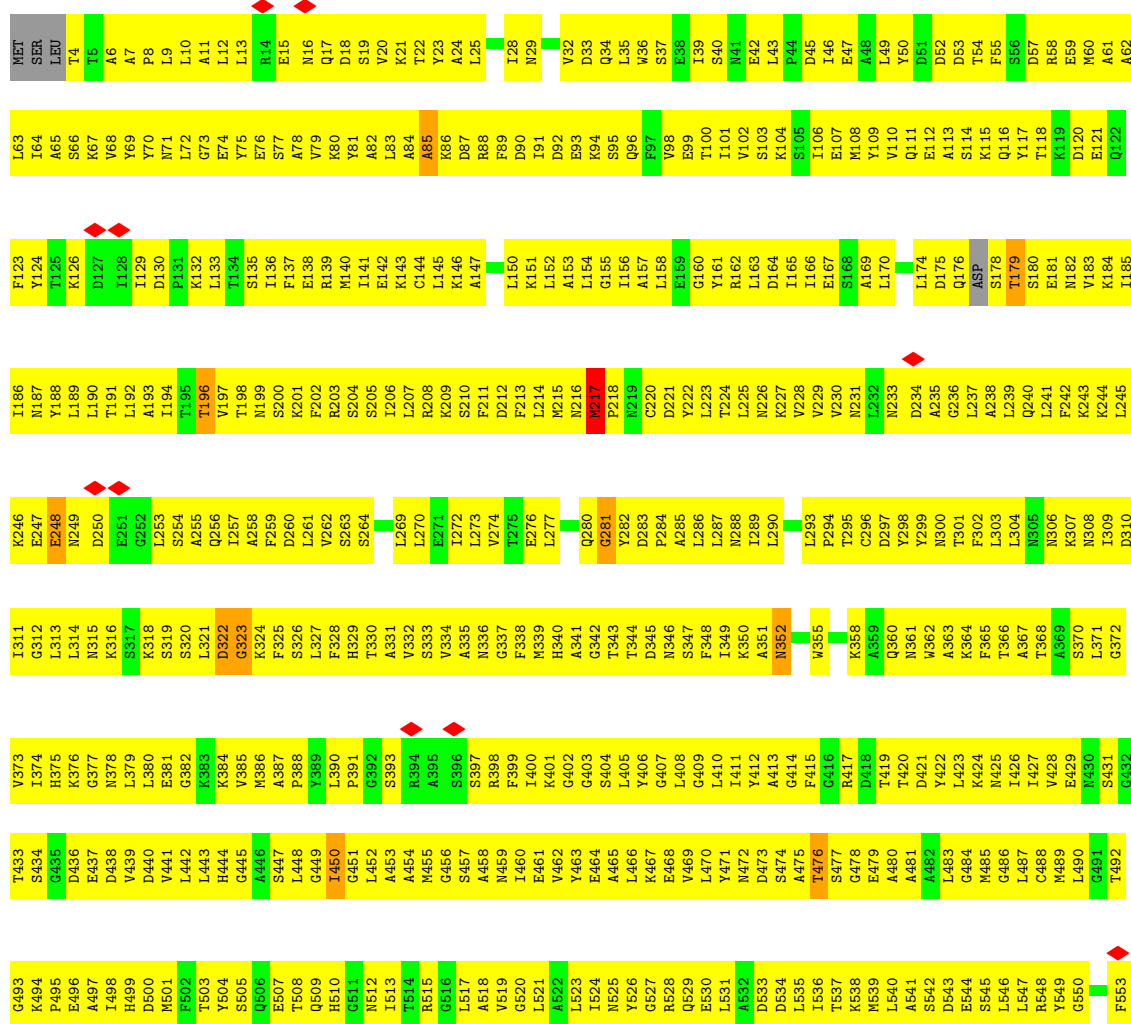
• Molecule 20: 26S protease regulatory subunit 6A

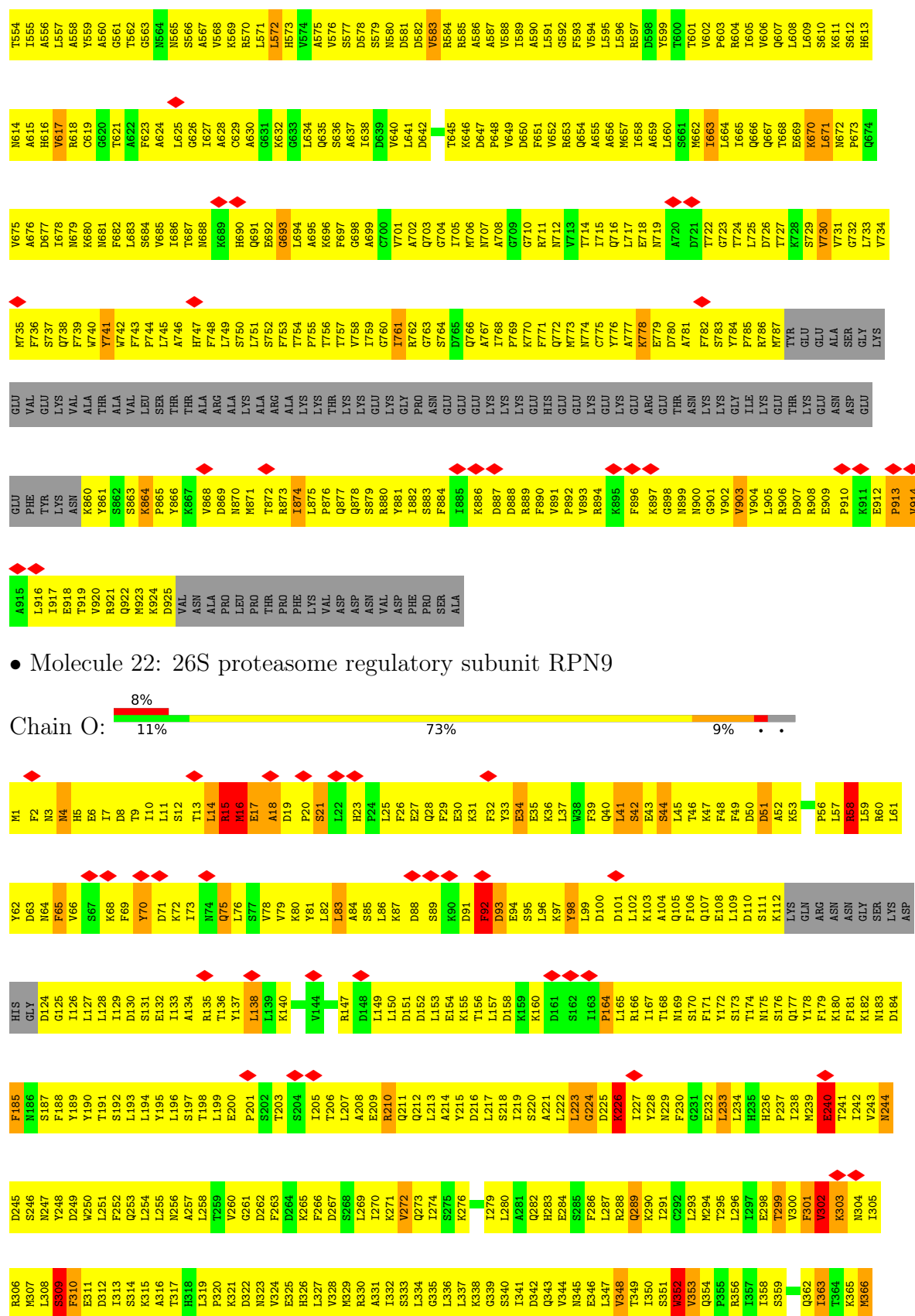


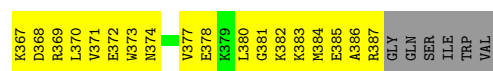


• Molecule 21: 26S proteasome regulatory subunit RPN2

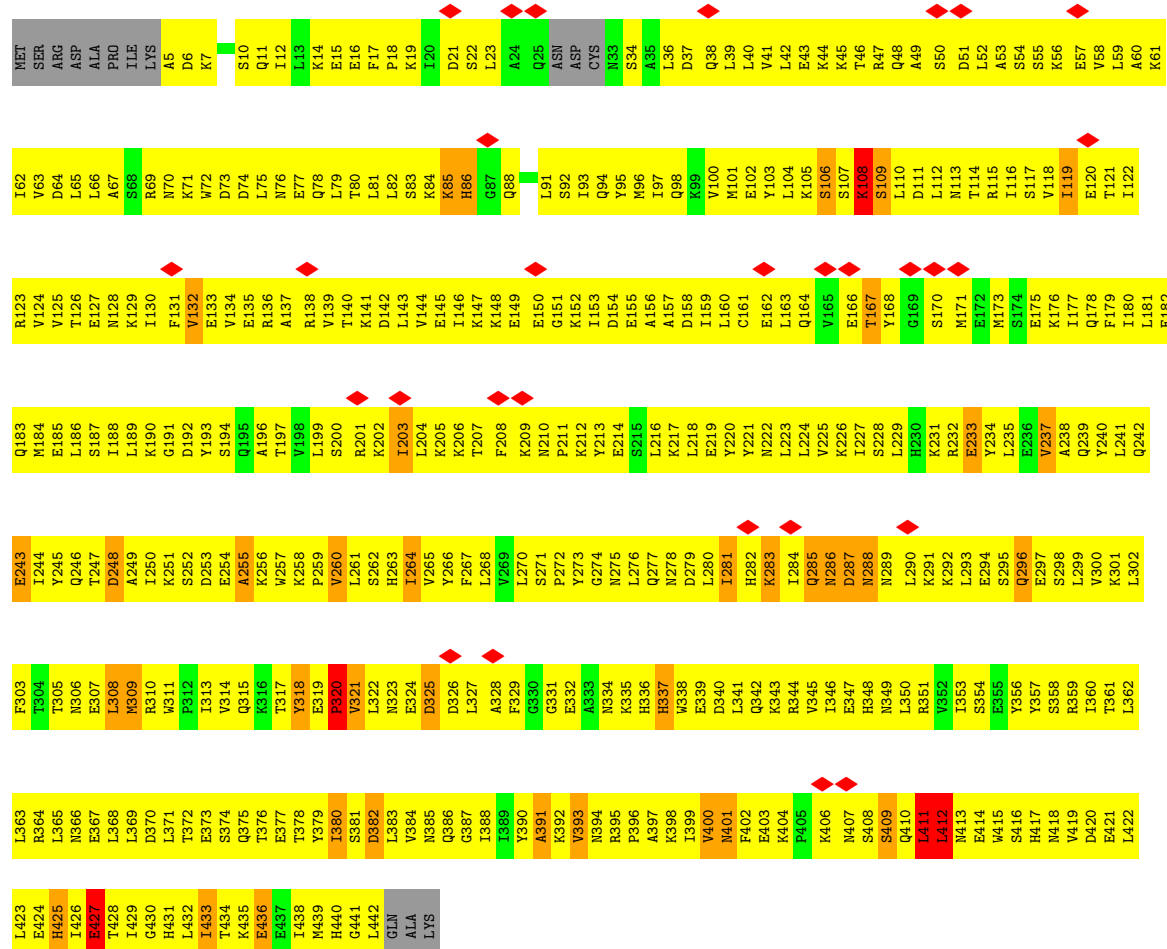
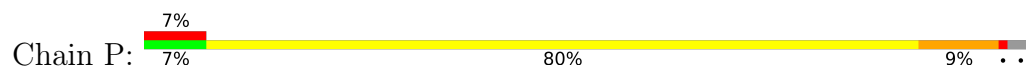
Chain N: 11% 76% 10%



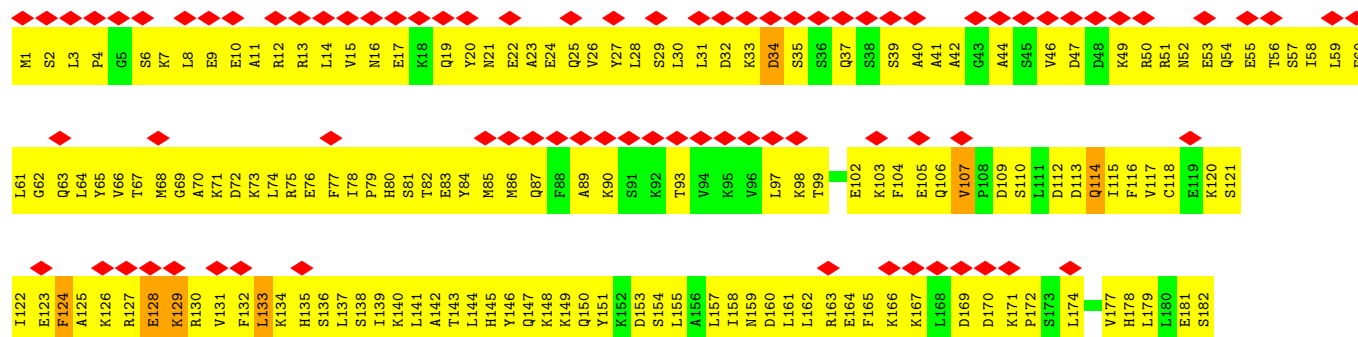




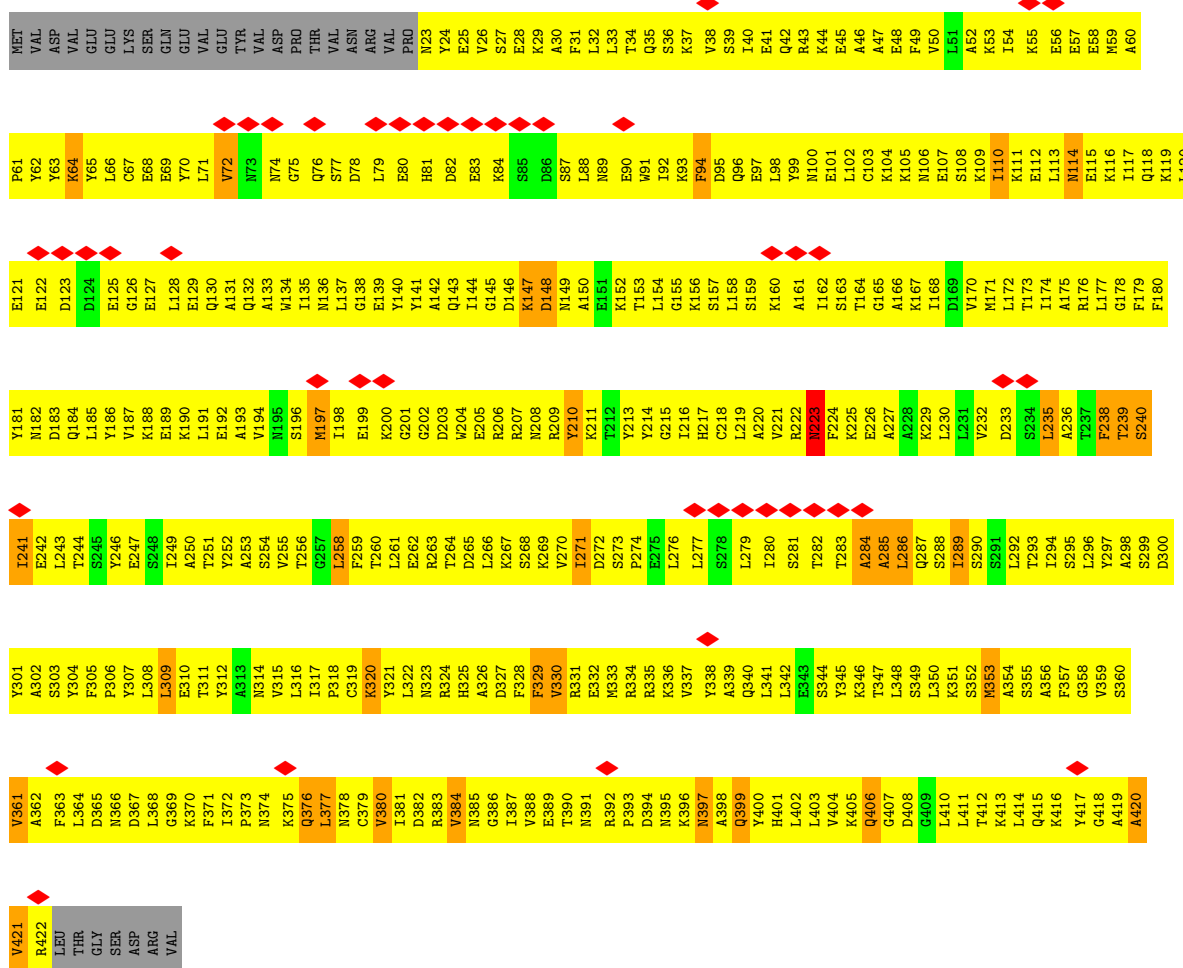
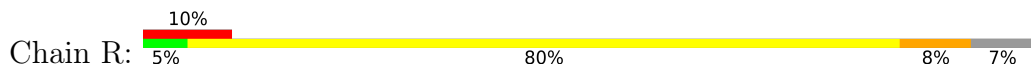
• Molecule 23: 26S proteasome regulatory subunit RPN5



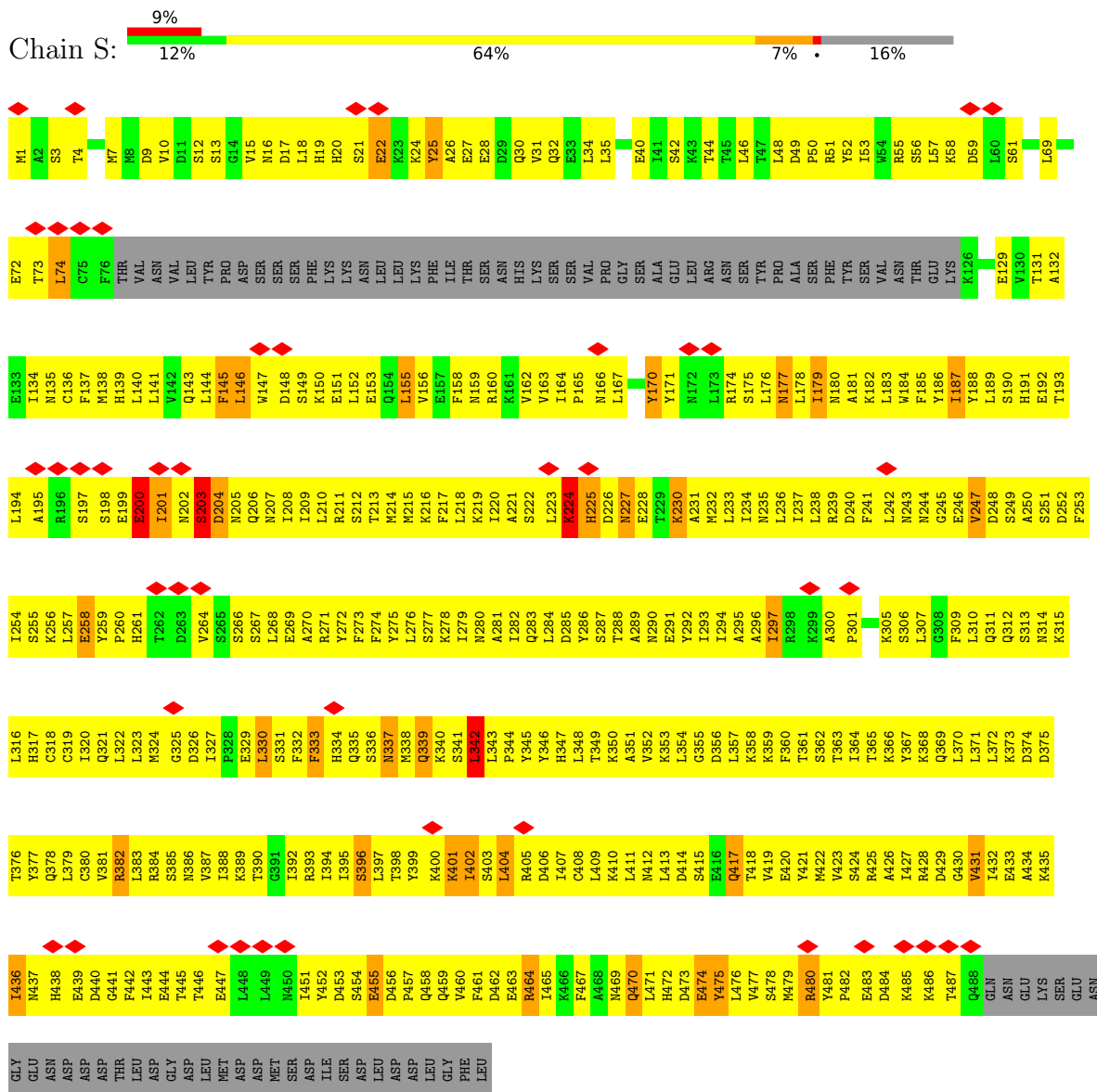
• Molecule 24: 26S proteasome regulatory subunit RPN6



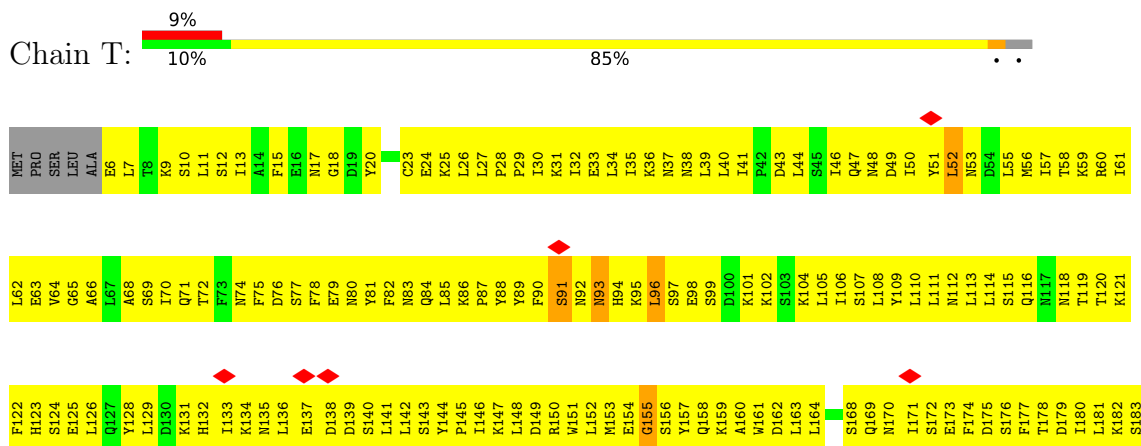
- Molecule 25: 26S proteasome regulatory subunit RPN7

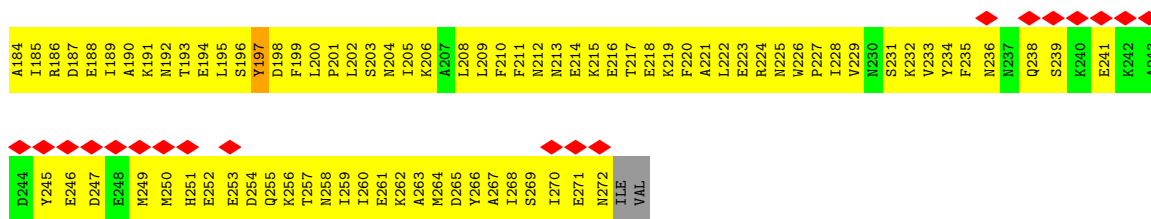


- Molecule 26: 26S proteasome regulatory subunit RPN3

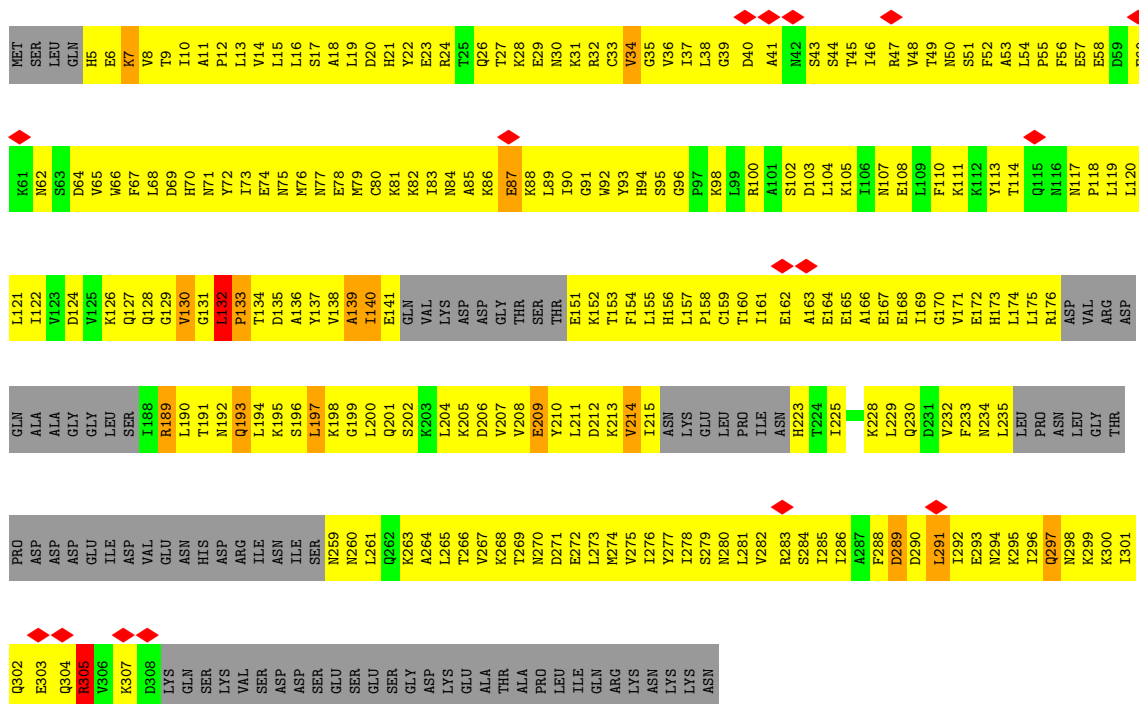
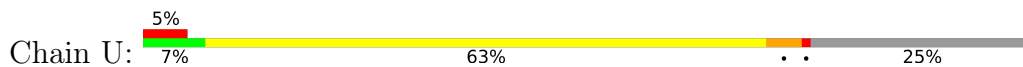


- Molecule 27: 26S proteasome regulatory subunit RPN12

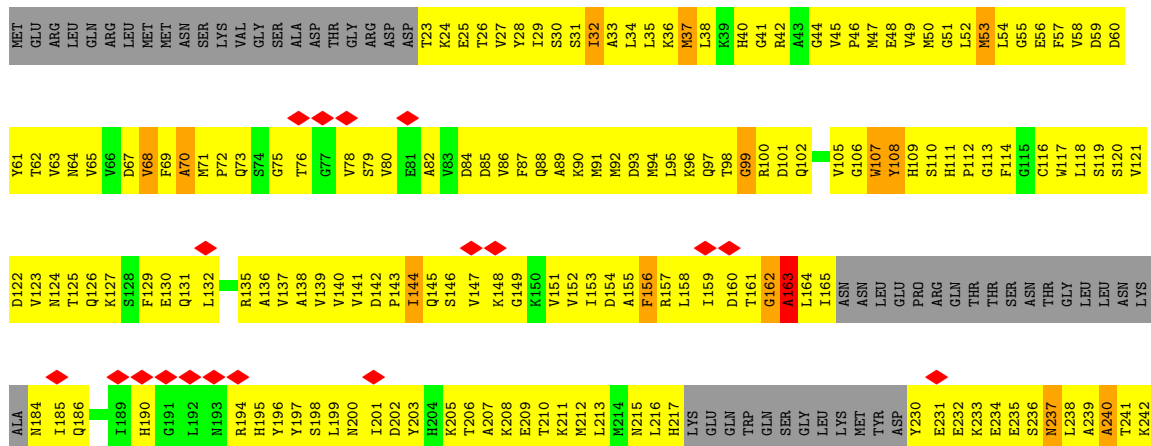
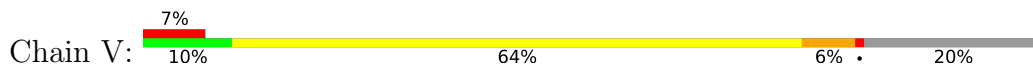


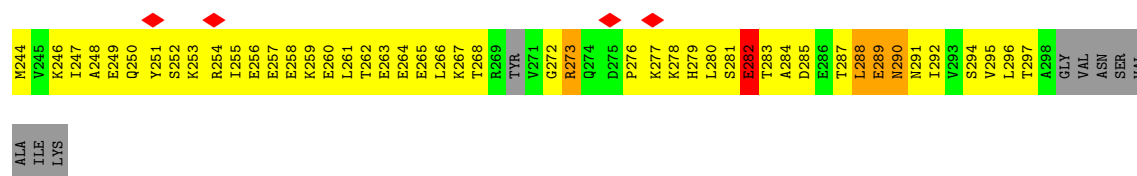


• Molecule 28: 26S proteasome regulatory subunit RPN8

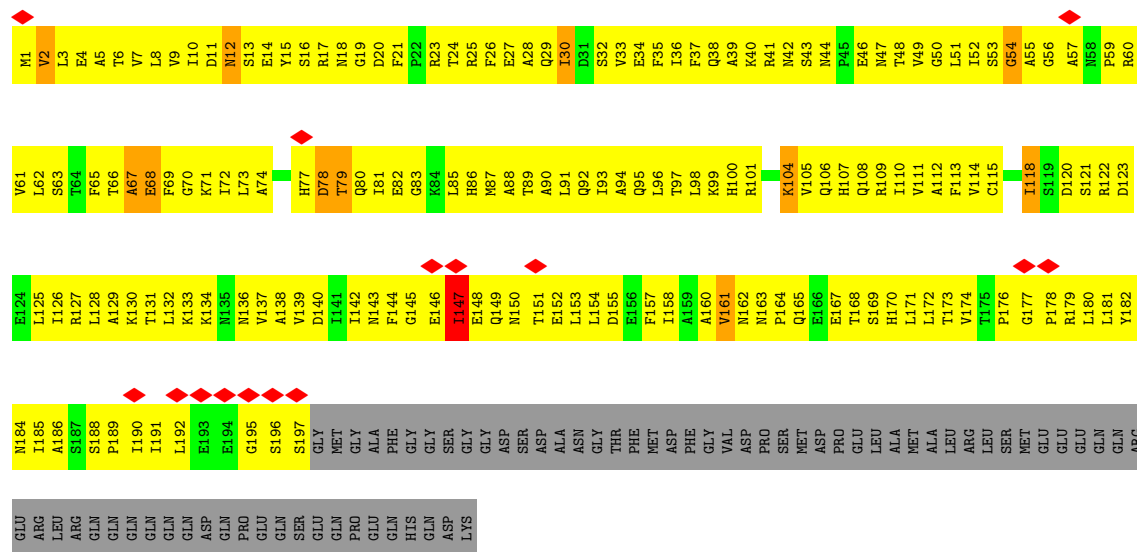
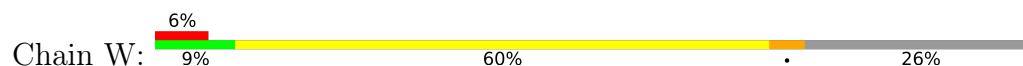


• Molecule 29: Ubiquitin carboxyl-terminal hydrolase RPN11

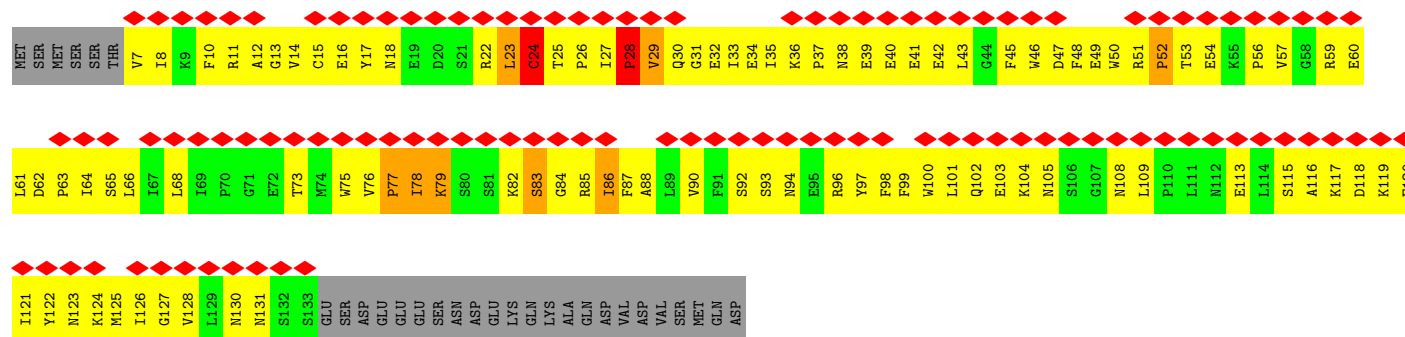




• Molecule 30: 26S proteasome regulatory subunit RPN10



• Molecule 31: 26S proteasome regulatory subunit RPN13

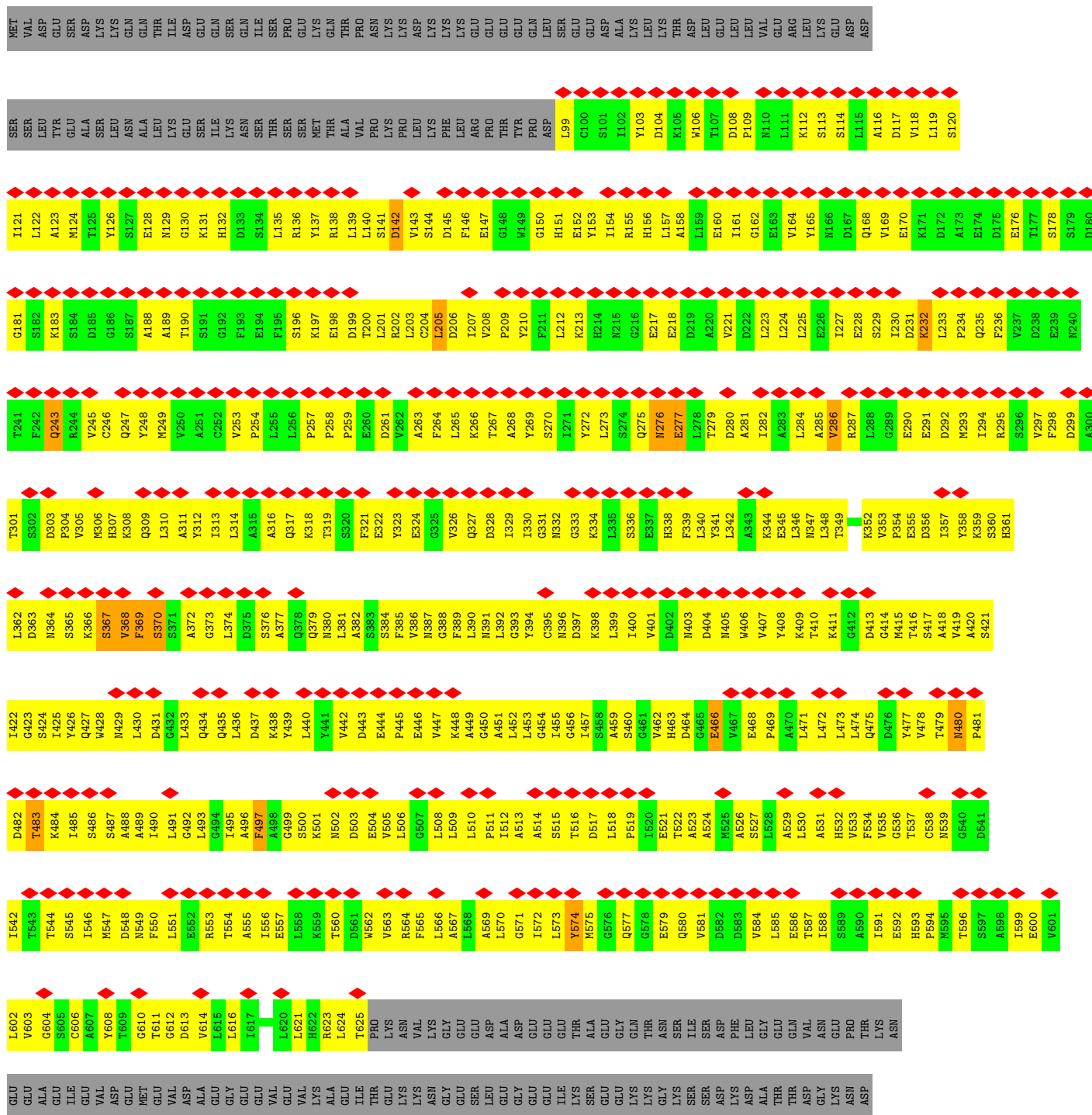
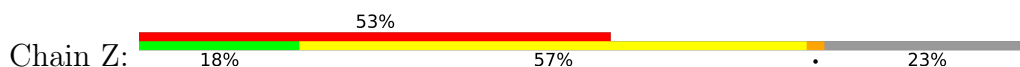


• Molecule 32: 26S proteasome complex subunit SEM1





• Molecule 33: 26S proteasome regulatory subunit RPN1



A963	E964	L965	E966	T967	D968	E969	Y970	I971	S972	Y973	T974	S975	H976	I977	E978	G979	V980	V981	I982	L983	K984	K985	N986	P987	D988	Y989	R990	E991	E992	E993																												
M903	L904	N905	A906	G907	I908	R909	P910	K911	F912	I913	L914	A915	L916	N917	D918	E919	G920	E921	P922	I923	K924	V925	N926	V927	R928	V929	G930	Q931	ALA	VAL	GLU	THR	VAL	GLY	GLN	ALA	GLY	ARG	PRO	LYS	LYS	ILE	THR	THR	GLN	SER	THR	P954	V955	L956	L957	N958	H959	G960	E961	R962		
D843	A844	L845	F846	I847	T848	R849	L850	A851	Q852	G853	L854	L855	H856	L857	G858	K859	G860	T861	M862	M864	D865	V866	F867	N868	D869	A870	H871	V872	L873	N874	K875	V876	T877	L878	A879	S880	I881	L882	T883	T884	A885	V886	G887	L888	V889	S890	P891	S892	F893	M894	L895	K896	H897	H898	Q899	L900	F901	Y902
V783	S784	V785	S786	D787	P788	Q789	M790	K791	V792	F793	D794	T795	L796	T797	R798	F799	S800	H801	D802	A803	D804	L805	E806	V807	S808	M809	N810	S811	I812	F813	A814	M815	G816	L817	C818	G819	A820	G821	T822	N823	N824	A825	R826	L827	A828	Q829	L830	L831	R832	Q833	L834	A835	S836	Y837	Y838	R840	E841	Q842
ASP	GLU	GLU	GLU	LYS	GLU	ALA	GLY	ILE	VAL	ASP	GLU	L736	A737	Y738	A739	V740	L741	G742	I743	A744	L745	I746	A747	L748	G749	E750	D751	I752	G753	K754	E755	M756	S757	L758	R759	H760	F761	G762	H763	L764	M765	H766	Y767	G768	N769	E770	H771	I772	R773	R774	M775	V776	P777	L778	A779	M780	G781	I782

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	81782	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	each micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1.5	Depositor
Maximum defocus (nm)	2.5	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.230	Depositor
Minimum map value	-0.079	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.0796	Depositor
Map size ($\text{\AA}$)	537.6, 537.6, 537.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.1, 2.1, 2.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.61	0/1795	0.80	2/2420 (0.1%)
1	8	0.60	0/1795	0.78	2/2420 (0.1%)
2	2	0.63	1/1855 (0.1%)	0.77	2/2514 (0.1%)
2	9	0.63	1/1855 (0.1%)	0.77	2/2514 (0.1%)
3	3	0.60	0/1603	0.77	1/2168 (0.0%)
3	h	0.60	0/1603	0.77	2/2168 (0.1%)
4	4	0.59	0/1715	0.73	0/2326
4	i	0.59	0/1715	0.73	0/2326
5	5	0.57	0/1611	0.69	0/2174
5	j	0.58	0/1611	0.69	0/2174
6	6	0.61	0/1613	0.76	0/2173
6	k	0.61	0/1613	0.76	0/2173
7	7	0.58	0/1681	0.75	0/2274
7	l	0.58	0/1681	0.76	0/2274
8	A	0.60	0/1959	0.76	0/2652
8	a	0.60	0/1959	0.77	0/2652
9	B	0.54	0/1952	0.70	0/2642
9	b	0.54	0/1952	0.70	0/2642
10	C	0.55	0/1934	0.73	1/2618 (0.0%)
10	c	0.55	0/1934	0.73	1/2618 (0.0%)
11	D	0.56	0/1919	0.76	0/2598
11	d	0.56	0/1919	0.76	0/2598
12	E	0.57	0/1886	0.75	0/2541
12	e	0.58	0/1886	0.76	0/2541
13	F	0.58	0/1823	0.79	0/2463
13	f	0.58	0/1823	0.79	0/2463
14	G	0.60	0/1936	0.80	4/2614 (0.2%)
14	g	0.60	1/1936 (0.1%)	0.80	4/2614 (0.2%)
15	H	0.49	1/2810 (0.0%)	0.81	4/3780 (0.1%)
16	I	0.38	0/2543	0.67	2/3429 (0.1%)
17	J	0.51	3/2964 (0.1%)	0.79	6/3981 (0.2%)
18	K	0.49	1/2887 (0.0%)	0.80	3/3894 (0.1%)
19	L	0.45	0/2870	0.72	2/3858 (0.1%)
20	M	0.43	0/2785	0.76	4/3763 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
21	N	0.56	1/6670 (0.0%)	0.80	7/9023 (0.1%)
22	O	0.62	0/3142	1.06	10/4241 (0.2%)
23	P	0.65	1/3520 (0.0%)	0.95	10/4752 (0.2%)
24	Q	0.55	0/3527	0.76	2/4748 (0.0%)
25	R	0.59	0/3272	0.88	3/4412 (0.1%)
26	S	0.58	0/3410	0.96	12/4621 (0.3%)
27	T	0.57	1/2244 (0.0%)	0.85	1/3029 (0.0%)
28	U	0.57	0/2059	0.92	7/2774 (0.3%)
29	V	0.58	0/1939	1.01	8/2613 (0.3%)
30	W	0.52	0/1557	0.84	2/2111 (0.1%)
31	X	0.43	0/1058	0.82	4/1432 (0.3%)
32	Y	0.63	0/244	1.08	2/328 (0.6%)
33	Z	0.31	0/6001	0.66	1/8141 (0.0%)
All	All	0.55	11/106066 (0.0%)	0.80	111/143284 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	6	0	1
6	k	0	1
8	A	0	1
8	a	0	1
10	C	0	1
10	c	0	1
13	F	0	1
13	f	0	1
15	H	0	10
16	I	0	2
17	J	0	3
18	K	0	4
19	L	0	4
20	M	0	4
21	N	0	11
22	O	0	22
23	P	0	17
24	Q	0	8
25	R	0	8
26	S	0	16
27	T	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	U	0	8
29	V	0	6
30	W	0	8
31	X	0	6
32	Y	0	2
33	Z	0	5
All	All	0	156

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	N	217	MET	CA-C	-6.61	1.49	1.53
17	J	316	PHE	C-N	6.34	1.40	1.33
18	K	362	LEU	C-N	-6.13	1.20	1.33
23	P	287	ASP	CA-C	-5.71	1.48	1.53
27	T	93	ASN	CA-C	-5.59	1.45	1.52

The worst 5 of 111 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	V	70	ALA	CA-C-N	-11.82	102.71	120.68
29	V	70	ALA	C-N-CA	-11.82	102.71	120.68
23	P	287	ASP	N-CA-C	-11.36	97.62	110.91
22	O	240	GLU	N-CA-C	10.20	126.04	112.88
28	U	289	ASP	N-CA-C	10.05	125.70	113.23

There are no chirality outliers.

5 of 156 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	6	196	GLN	Peptide
8	A	64	LEU	Peptide
10	C	221	ASN	Peptide
13	F	175	THR	Peptide
15	H	97	LEU	Peptide

5.2 Too-close contacts

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1757	0	1708	353	0
1	8	1757	0	1708	355	0
2	2	1824	0	1829	354	0
2	9	1824	0	1829	372	0
3	3	1574	0	1547	344	0
3	h	1574	0	1547	345	0
4	4	1684	0	1685	345	0
4	i	1684	0	1685	337	0
5	5	1581	0	1571	340	0
5	j	1581	0	1571	322	0
6	6	1585	0	1590	359	0
6	k	1585	0	1590	364	0
7	7	1644	0	1592	350	0
7	l	1644	0	1592	369	0
8	A	1921	0	1910	395	0
8	a	1921	0	1910	315	0
9	B	1915	0	1929	344	0
9	b	1915	0	1929	299	0
10	C	1904	0	1901	367	0
10	c	1904	0	1901	336	0
11	D	1890	0	1900	365	0
11	d	1890	0	1900	329	0
12	E	1861	0	1836	370	0
12	e	1861	0	1836	319	0
13	F	1795	0	1797	395	0
13	f	1795	0	1797	350	0
14	G	1896	0	1886	497	0
14	g	1896	0	1886	408	0
15	H	2771	0	2866	589	0
16	I	2513	0	2564	489	0
17	J	2928	0	3057	561	0
18	K	2849	0	2928	580	0
19	L	2829	0	2902	578	0
20	M	2754	0	2799	572	0
21	N	6562	0	6625	1361	0
22	O	3083	0	3099	870	0
23	P	3470	0	3500	956	0
24	Q	3471	0	3495	811	0
25	R	3218	0	3211	854	0
26	S	3357	0	3180	879	0
27	T	2201	0	2167	490	0
28	U	2034	0	2072	587	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	V	1912	0	1906	564	0
30	W	1534	0	1542	372	0
31	X	1032	0	1017	170	0
32	Y	243	0	182	50	0
33	Z	5894	0	5828	887	0
All	All	104317	0	104302	20016	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 96.

The worst 5 of 20016 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)
22:O:11:LEU:CD2	22:O:14:LEU:HD12	1.22	1.64
22:O:11:LEU:CD2	22:O:14:LEU:CD1	1.80	1.58
16:I:249:GLY:CA	16:I:252:LEU:HD11	1.08	1.55
24:Q:413:LEU:CD1	25:R:406:GLN:HG3	1.33	1.53
16:I:249:GLY:C	16:I:252:LEU:HD11	1.22	1.52

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	220/241 (91%)	202 (92%)	17 (8%)	1 (0%)	24	63
1	8	220/241 (91%)	202 (92%)	17 (8%)	1 (0%)	24	63
2	2	231/266 (87%)	210 (91%)	21 (9%)	0	100	100
2	9	231/266 (87%)	210 (91%)	21 (9%)	0	100	100
3	3	203/215 (94%)	180 (89%)	22 (11%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	h	203/215 (94%)	179 (88%)	23 (11%)	1 (0%)	24	63
4	4	220/261 (84%)	206 (94%)	14 (6%)	0	100	100
4	i	220/261 (84%)	206 (94%)	14 (6%)	0	100	100
5	5	202/205 (98%)	185 (92%)	16 (8%)	1 (0%)	24	63
5	j	202/205 (98%)	185 (92%)	16 (8%)	1 (0%)	24	63
6	6	196/198 (99%)	175 (89%)	19 (10%)	2 (1%)	12	47
6	k	196/198 (99%)	174 (89%)	19 (10%)	3 (2%)	8	38
7	7	210/287 (73%)	188 (90%)	20 (10%)	2 (1%)	12	47
7	l	210/287 (73%)	190 (90%)	19 (9%)	1 (0%)	24	63
8	A	241/252 (96%)	220 (91%)	21 (9%)	0	100	100
8	a	241/252 (96%)	220 (91%)	21 (9%)	0	100	100
9	B	248/250 (99%)	225 (91%)	23 (9%)	0	100	100
9	b	248/250 (99%)	225 (91%)	23 (9%)	0	100	100
10	C	242/258 (94%)	220 (91%)	19 (8%)	3 (1%)	10	42
10	c	242/258 (94%)	220 (91%)	19 (8%)	3 (1%)	10	42
11	D	239/254 (94%)	215 (90%)	24 (10%)	0	100	100
11	d	239/254 (94%)	215 (90%)	24 (10%)	0	100	100
12	E	240/260 (92%)	215 (90%)	23 (10%)	2 (1%)	16	52
12	e	240/260 (92%)	215 (90%)	23 (10%)	2 (1%)	16	52
13	F	231/234 (99%)	210 (91%)	19 (8%)	2 (1%)	14	49
13	f	231/234 (99%)	210 (91%)	19 (8%)	2 (1%)	14	49
14	G	242/288 (84%)	216 (89%)	25 (10%)	1 (0%)	30	67
14	g	242/288 (84%)	216 (89%)	24 (10%)	2 (1%)	16	52
15	H	350/467 (75%)	286 (82%)	56 (16%)	8 (2%)	5	28
16	I	321/437 (74%)	286 (89%)	33 (10%)	2 (1%)	21	58
17	J	371/405 (92%)	332 (90%)	31 (8%)	8 (2%)	5	28
18	K	357/428 (83%)	306 (86%)	45 (13%)	6 (2%)	7	35
19	L	354/437 (81%)	302 (85%)	51 (14%)	1 (0%)	36	71
20	M	349/434 (80%)	306 (88%)	40 (12%)	3 (1%)	14	49
21	N	843/945 (89%)	656 (78%)	174 (21%)	13 (2%)	8	38
22	O	372/393 (95%)	250 (67%)	103 (28%)	19 (5%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	P	427/445 (96%)	305 (71%)	99 (23%)	23 (5%)	1	15
24	Q	429/434 (99%)	350 (82%)	76 (18%)	3 (1%)	18	55
25	R	398/429 (93%)	281 (71%)	94 (24%)	23 (6%)	1	14
26	S	435/523 (83%)	313 (72%)	103 (24%)	19 (4%)	2	17
27	T	265/274 (97%)	190 (72%)	74 (28%)	1 (0%)	30	67
28	U	244/338 (72%)	198 (81%)	39 (16%)	7 (3%)	3	23
29	V	237/306 (78%)	176 (74%)	53 (22%)	8 (3%)	3	20
30	W	195/268 (73%)	157 (80%)	30 (15%)	8 (4%)	2	17
31	X	125/156 (80%)	94 (75%)	26 (21%)	5 (4%)	2	18
32	Y	32/89 (36%)	21 (66%)	9 (28%)	2 (6%)	1	13
33	Z	757/993 (76%)	665 (88%)	80 (11%)	12 (2%)	7	37
All	All	13191/15139 (87%)	11208 (85%)	1781 (14%)	202 (2%)	11	38

5 of 202 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	I	253	ILE
17	J	321	VAL
18	K	342	SER
18	K	344	ARG
25	R	239	THR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	185/201 (92%)	185 (100%)	0	100	100
1	8	185/201 (92%)	185 (100%)	0	100	100
2	2	199/224 (89%)	198 (100%)	1 (0%)	81	82
2	9	199/224 (89%)	198 (100%)	1 (0%)	81	82
3	3	168/178 (94%)	167 (99%)	1 (1%)	78	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	h	168/178 (94%)	168 (100%)	0	100	100
4	4	181/214 (85%)	181 (100%)	0	100	100
4	i	181/214 (85%)	181 (100%)	0	100	100
5	5	172/173 (99%)	172 (100%)	0	100	100
5	j	172/173 (99%)	172 (100%)	0	100	100
6	6	175/175 (100%)	174 (99%)	1 (1%)	78	81
6	k	175/175 (100%)	174 (99%)	1 (1%)	78	81
7	7	169/235 (72%)	168 (99%)	1 (1%)	78	81
7	l	169/235 (72%)	168 (99%)	1 (1%)	78	81
8	A	207/210 (99%)	207 (100%)	0	100	100
8	a	207/210 (99%)	207 (100%)	0	100	100
9	B	209/209 (100%)	209 (100%)	0	100	100
9	b	209/209 (100%)	209 (100%)	0	100	100
10	C	203/216 (94%)	203 (100%)	0	100	100
10	c	203/216 (94%)	203 (100%)	0	100	100
11	D	213/226 (94%)	213 (100%)	0	100	100
11	d	213/226 (94%)	213 (100%)	0	100	100
12	E	198/215 (92%)	197 (100%)	1 (0%)	81	82
12	e	198/215 (92%)	198 (100%)	0	100	100
13	F	192/193 (100%)	192 (100%)	0	100	100
13	f	192/193 (100%)	192 (100%)	0	100	100
14	G	201/239 (84%)	201 (100%)	0	100	100
14	g	201/239 (84%)	201 (100%)	0	100	100
15	H	301/399 (75%)	300 (100%)	1 (0%)	86	84
16	I	284/385 (74%)	282 (99%)	2 (1%)	76	79
17	J	325/352 (92%)	324 (100%)	1 (0%)	86	84
18	K	316/374 (84%)	315 (100%)	1 (0%)	86	84
19	L	306/377 (81%)	306 (100%)	0	100	100
20	M	303/375 (81%)	303 (100%)	0	100	100
21	N	713/797 (90%)	713 (100%)	0	100	100
22	O	350/368 (95%)	345 (99%)	5 (1%)	59	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	P	384/415 (92%)	380 (99%)	4 (1%)	68	76
24	Q	388/391 (99%)	387 (100%)	1 (0%)	86	84
25	R	351/379 (93%)	346 (99%)	5 (1%)	59	71
26	S	342/489 (70%)	334 (98%)	8 (2%)	44	64
27	T	250/256 (98%)	250 (100%)	0	100	100
28	U	228/308 (74%)	225 (99%)	3 (1%)	61	72
29	V	211/268 (79%)	205 (97%)	6 (3%)	38	59
30	W	171/230 (74%)	171 (100%)	0	100	100
31	X	116/144 (81%)	116 (100%)	0	100	100
32	Y	18/81 (22%)	18 (100%)	0	100	100
33	Z	645/850 (76%)	643 (100%)	2 (0%)	86	84
All	All	11346/13054 (87%)	11299 (100%)	47 (0%)	81	83

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	S	297	ILE
28	U	291	LEU
26	S	396	SER
26	S	474	GLU
29	V	37	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 284 such sidechains are listed below:

Mol	Chain	Res	Type
8	a	175	GLN
10	c	96	GLN
3	h	160	ASN
18	K	404	GLN
18	K	285	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

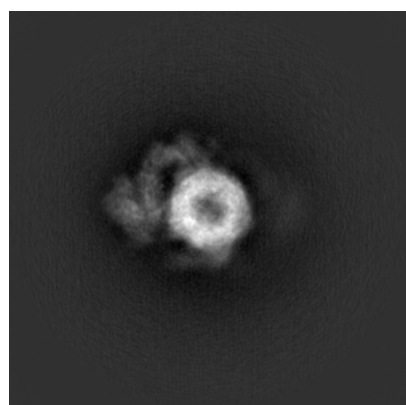
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6574. These allow visual inspection of the internal detail of the map and identification of artifacts.

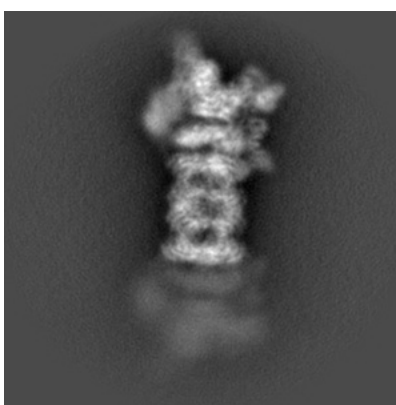
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

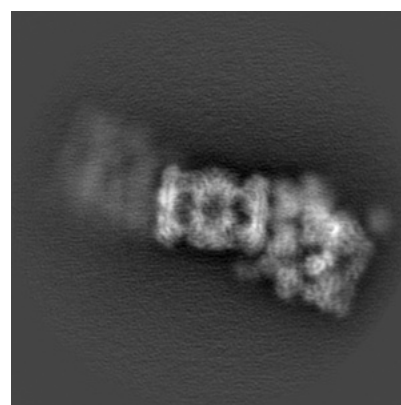
6.1.1 Primary map



X



Y

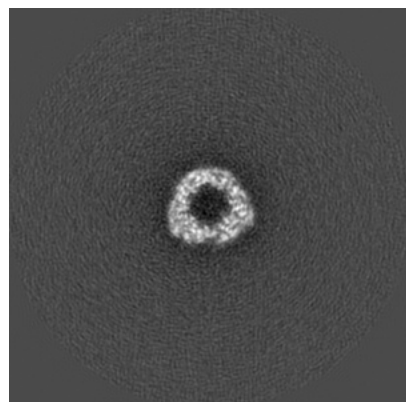


Z

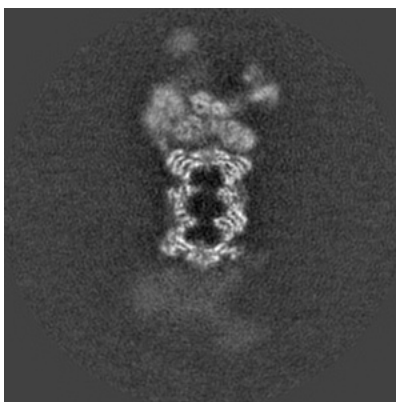
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

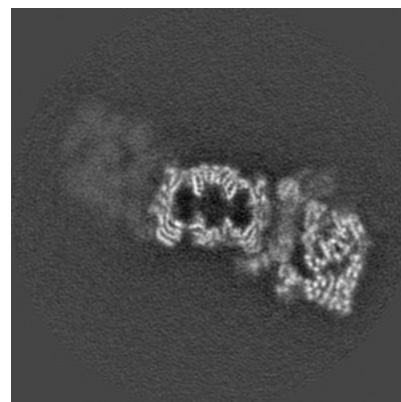
6.2.1 Primary map



X Index: 128



Y Index: 128

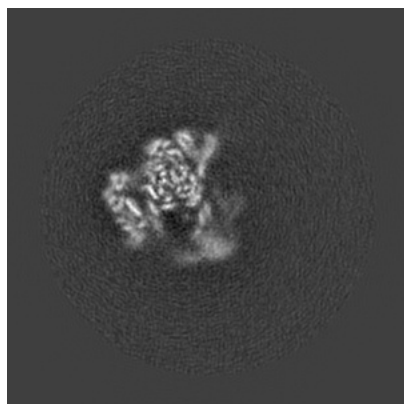


Z Index: 128

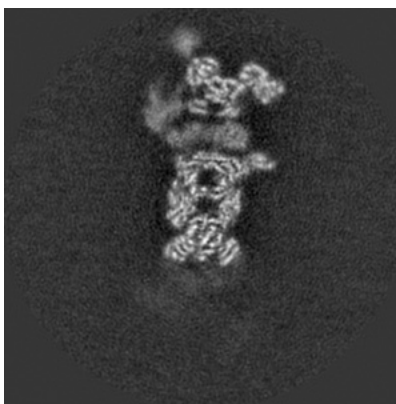
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

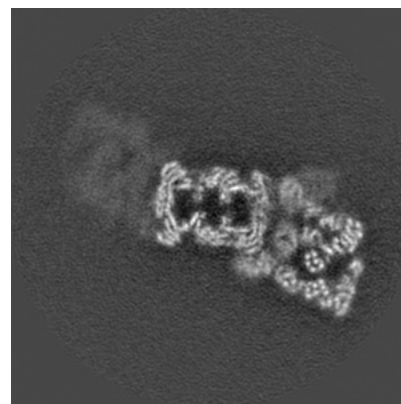
6.3.1 Primary map



X Index: 200



Y Index: 117

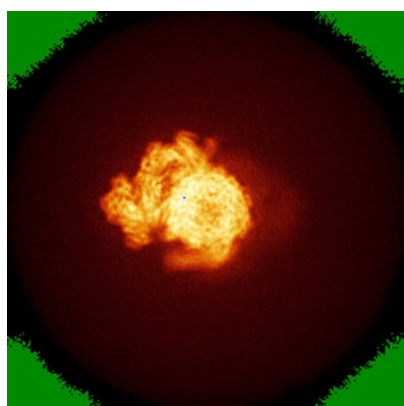


Z Index: 132

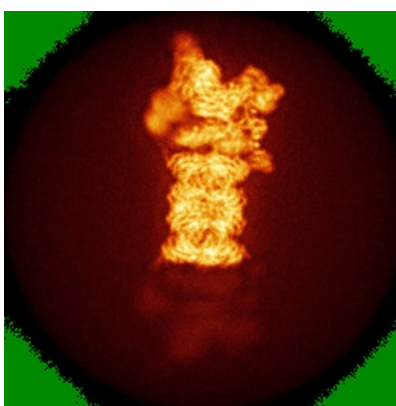
The images above show the largest variance slices of the map in three orthogonal directions.

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

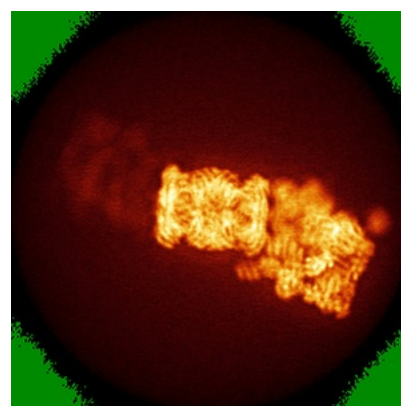
6.4.1 Primary map



X



Y

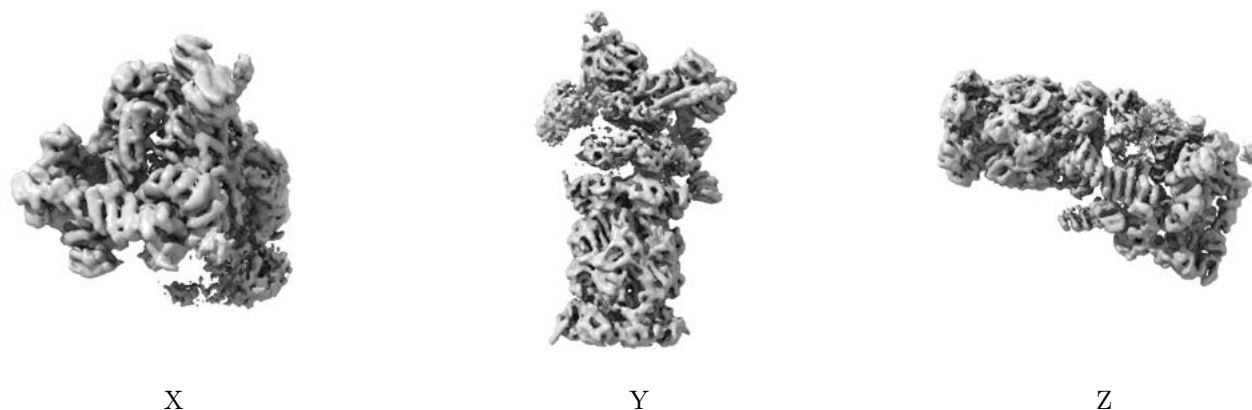


Z

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 0.0796. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

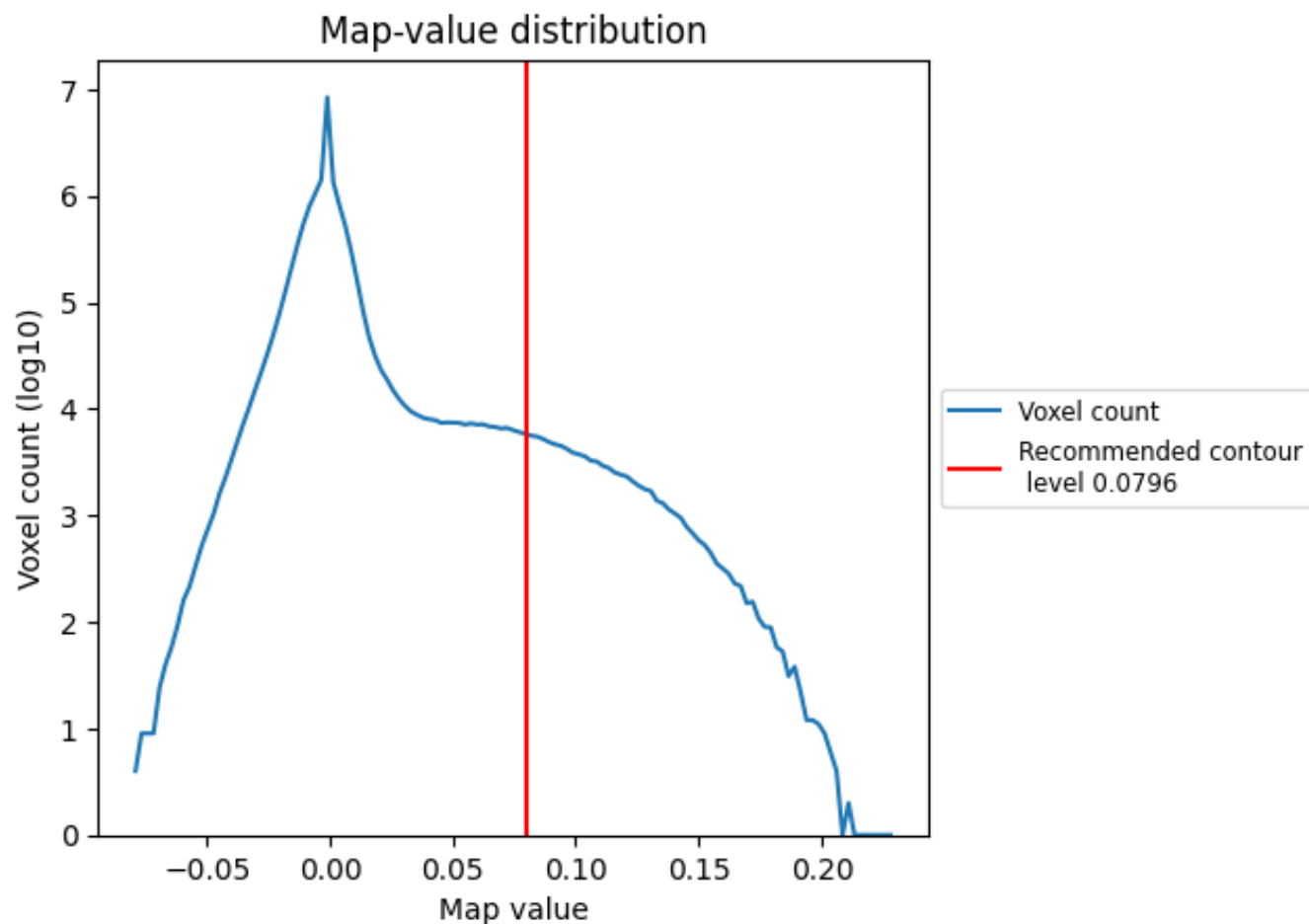
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

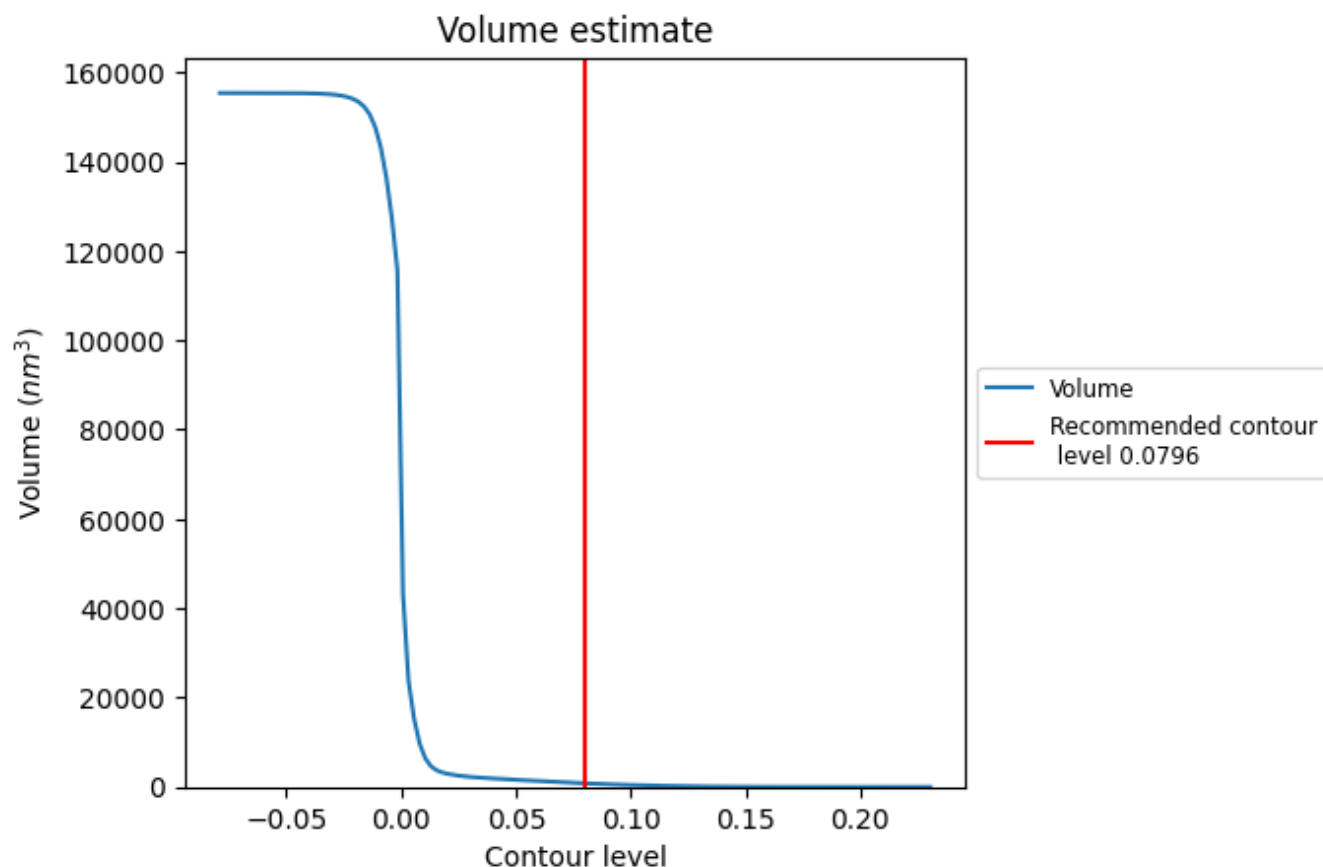
This section contains the results of statistical analysis of the map.

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.

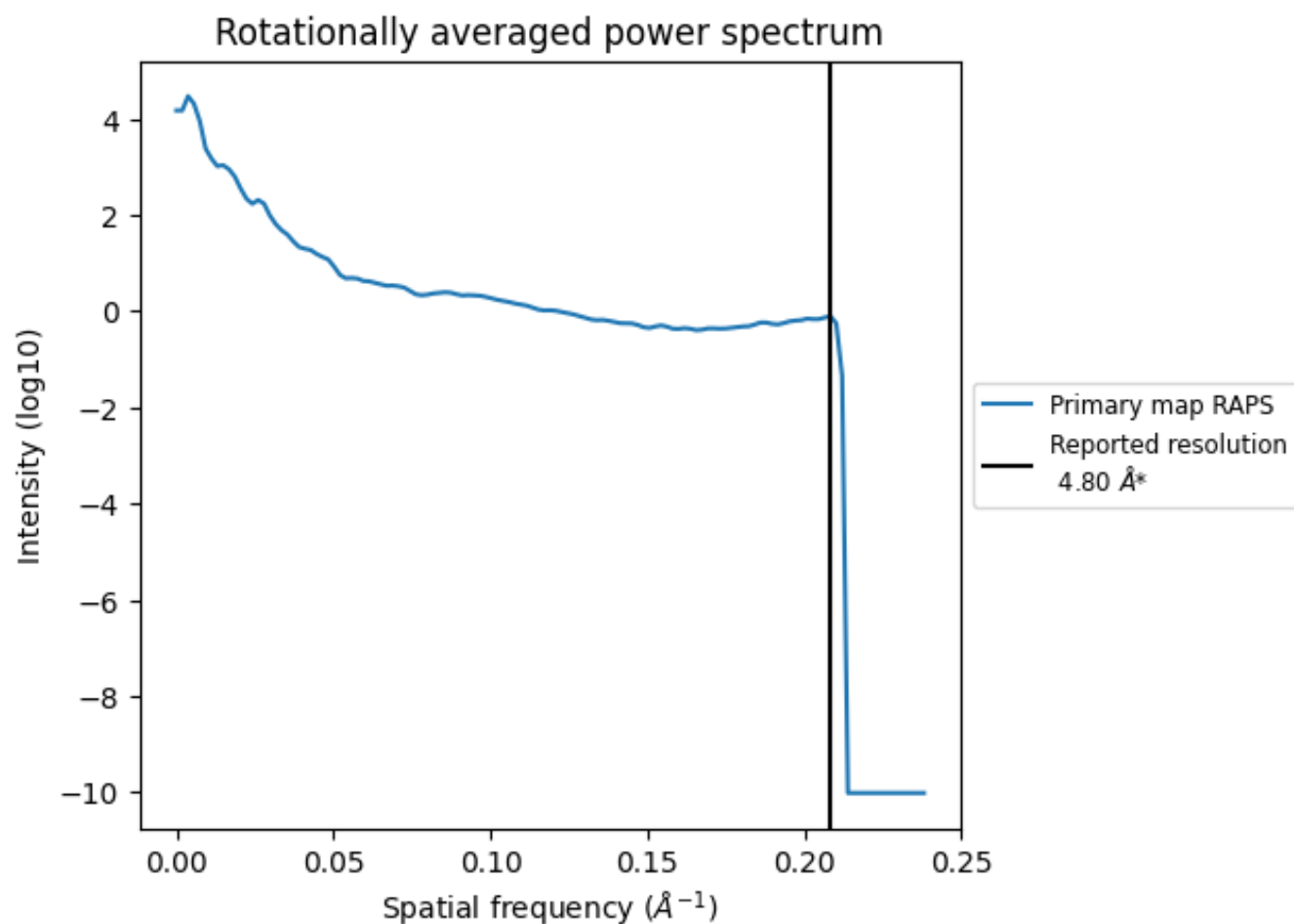
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 826 nm³; this corresponds to an approximate mass of 746 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

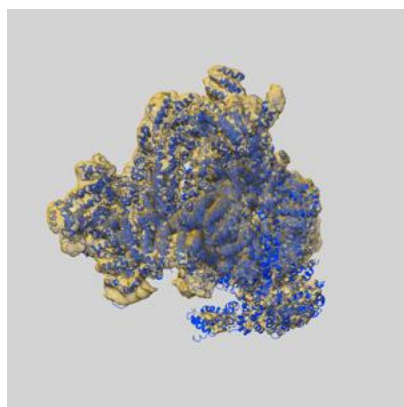
8 Fourier-Shell correlation

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

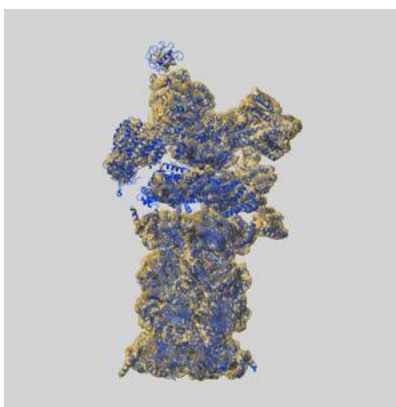
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6574 and PDB model 3JCO. Per-residue inclusion information can be found in section [3](#) on page [11](#).

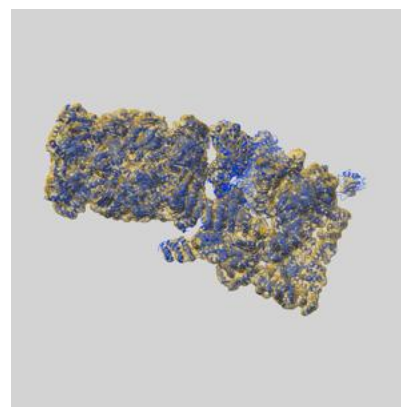
9.1 Map-model overlay [i](#)



X



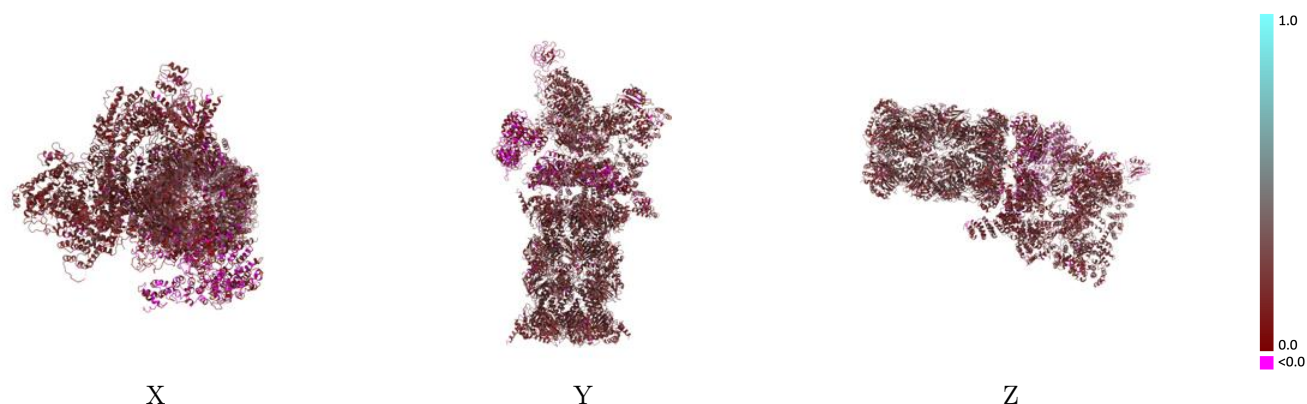
Y



Z

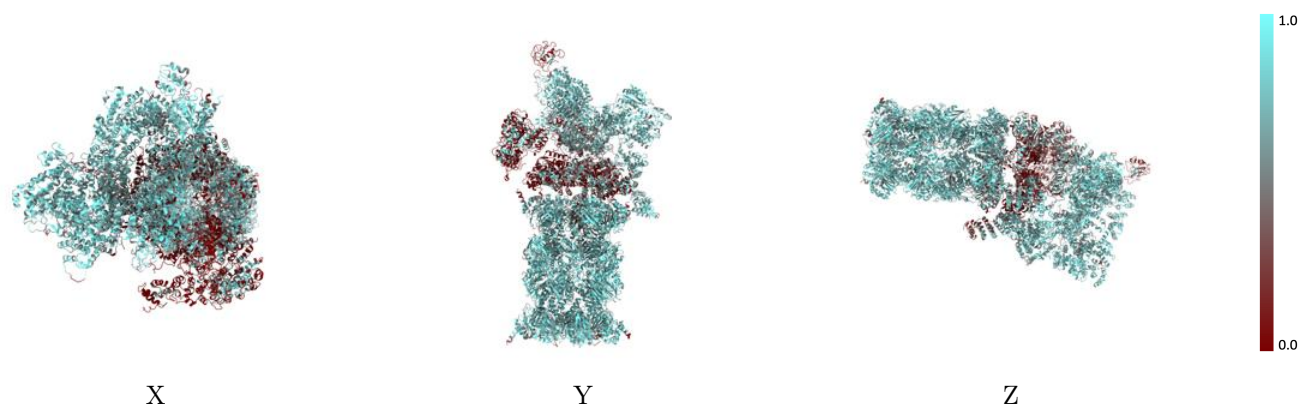
The images above show the 3D surface view of the map at the recommended contour level 0.0796 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



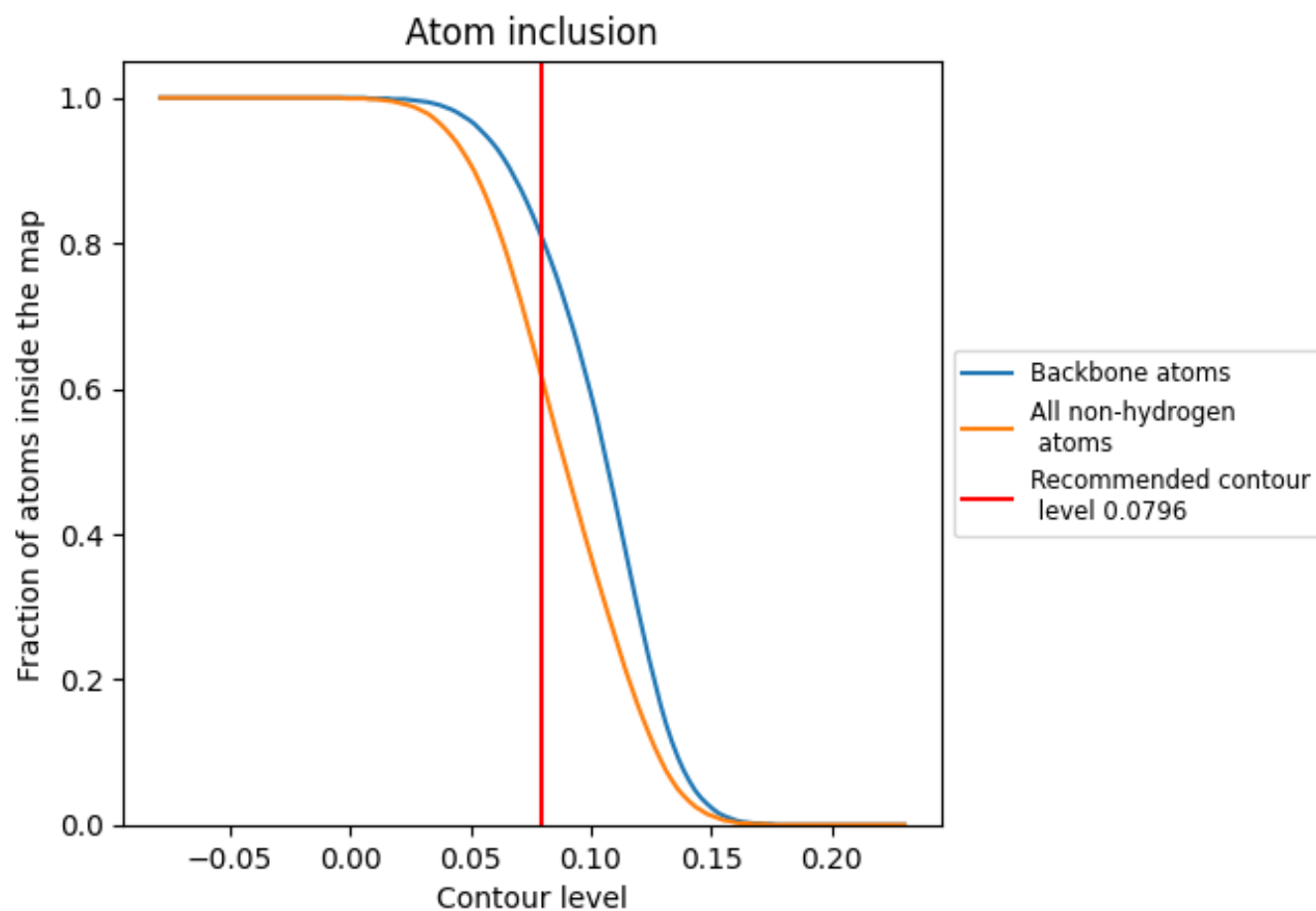
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0796).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 62% 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 (0.0796) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6150	 0.1970
1	 0.7600	 0.2350
2	 0.7590	 0.2410
3	 0.7480	 0.2260
4	 0.7700	 0.2470
5	 0.7450	 0.2370
6	 0.7400	 0.2460
7	 0.7870	 0.2420
8	 0.7450	 0.2370
9	 0.7690	 0.2520
A	 0.7390	 0.2260
B	 0.7170	 0.2290
C	 0.7310	 0.2230
D	 0.7380	 0.2270
E	 0.7170	 0.2180
F	 0.7710	 0.2260
G	 0.7640	 0.2280
H	 0.4060	 0.1470
I	 0.1910	 0.1290
J	 0.1750	 0.1340
K	 0.2910	 0.1550
L	 0.3850	 0.1530
M	 0.3830	 0.1410
N	 0.7290	 0.2100
O	 0.7200	 0.1850
P	 0.7060	 0.1950
Q	 0.5650	 0.1860
R	 0.6670	 0.1940
S	 0.7030	 0.1980
T	 0.6840	 0.1910
U	 0.6970	 0.2230
V	 0.6860	 0.2170
W	 0.7470	 0.1710
X	 0.1390	 0.0830
Y	 0.6850	 0.2300



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Chain	Atom inclusion	Q-score
Z	 0.2790	 0.0830
a	 0.6550	 0.2270
b	 0.5630	 0.2210
c	 0.5780	 0.2030
d	 0.6210	 0.2070
e	 0.6690	 0.2200
f	 0.7220	 0.2280
g	 0.6890	 0.2260
h	 0.7570	 0.2380
i	 0.7460	 0.2500
j	 0.7390	 0.2330
k	 0.7170	 0.2370
l	 0.7920	 0.2390