



wwPDB EM Validation Summary Report ⓘ

Nov 7, 2022 – 02:14 PM JST

PDB ID : 5WVK
EMDB ID : EMD-6694
Title : Yeast proteasome-ADP-AlFx
Authors : Ding, Z.; Cong, Y.
Deposited on : 2016-12-25
Resolution : 4.20 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

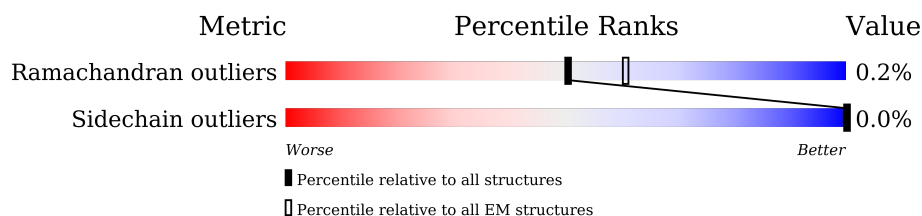
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	215	<div> <div>7%</div> <div>91%</div> <div>9%</div> </div>
1	b	215	<div> <div>7%</div> <div>91%</div> <div>9%</div> </div>
2	2	261	<div> <div>11%</div> <div>85%</div> <div>15%</div> </div>
2	i	261	<div> <div>13%</div> <div>85%</div> <div>15%</div> </div>
3	3	205	<div> <div>11%</div> <div>99%</div> </div>
3	h	205	<div> <div>10%</div> <div>99%</div> </div>
4	4	198	<div> <div>14%</div> <div>100%</div> </div>
4	g	198	<div> <div>11%</div> <div>100%</div> </div>
5	5	287	<div> <div>6%</div> <div>74%</div> <div>26%</div> </div>

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Mol	Chain	Length	Quality of chain
5	f	287	
6	6	241	
6	e	241	
7	7	266	
7	a	266	
8	A	252	
8	c	252	
9	B	250	
9	j	250	
10	C	258	
10	d	258	
11	D	254	
11	n	254	
12	E	260	
12	m	260	
13	F	234	
13	l	234	
14	G	288	
14	k	288	
15	H	467	
16	I	437	
17	J	405	
18	K	428	
19	L	437	
20	M	434	

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Mol	Chain	Length	Quality of chain
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 105261 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-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	196	Total	C	N	O	S	0	0
			1512	955	250	300	7		
1	b	196	Total	C	N	O	S	0	0
			1512	955	250	300	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	223	Total	C	N	O	S	0	0
			1692	1067	294	324	7		
2	i	223	Total	C	N	O	S	0	0
			1692	1067	294	324	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	204	Total	C	N	O	S	0	0
			1581	1010	258	305	8		
3	h	204	Total	C	N	O	S	0	0
			1581	1010	258	305	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	198	Total	C	N	O	S	0	0
			1585	1005	269	305	6		
4	g	198	Total	C	N	O	S	0	0
			1585	1005	269	305	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	212	Total	C	N	O	S	0	0
			1644	1045	280	312	7		
5	f	212	Total	C	N	O	S	0	0
			1644	1045	280	312	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	222	Total	C	N	O	S	0	0
			1757	1115	303	335	4		
6	e	222	Total	C	N	O	S	0	0
			1757	1115	303	335	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	233	Total	C	N	O	S	0	0
			1824	1154	312	351	7		
7	a	233	Total	C	N	O	S	0	0
			1824	1154	312	351	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	c	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	j	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	d	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	n	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	m	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	l	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	k	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	359	Total	C	N	O	S	0	0
			2792	1755	499	523	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	362	Total	C	N	O	S	0	0
			2822	1773	471	563	15		

- 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	381	Total	C	N	O	S	0	0
			3019	1898	530	581	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	361	Total	C	N	O	S	0	0
			2853	1798	507	536	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	367	Total	C	N	O	S	0	0
			2866	1799	503	553	11		

- 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	387	Total	C	N	O	S	0	0
			3182	2047	520	606	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	432	Total	C	N	O	S	0	0
			3545	2260	592	684	9		

- 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	353	Total	C	N	O	S	0	0
			2893	1857	482	541	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	272	Total	C	N	O	S	0	0
			2235	1432	355	441	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	255	Total	C	N	O	S	0	0
			2061	1312	352	391	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	V	284	Total	C	N	O	S	0	0
			2236	1405	381	436	14		

- 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	19	Total	C	N	O	0	0
			168	101	30	37		

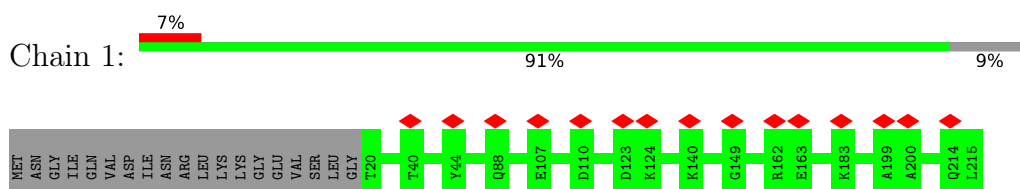
- Molecule 33 is a protein called 26S proteasome regulatory subunit RPN1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	813	Total	C	N	O	S	0	0
			6290	3995	1029	1237	29		

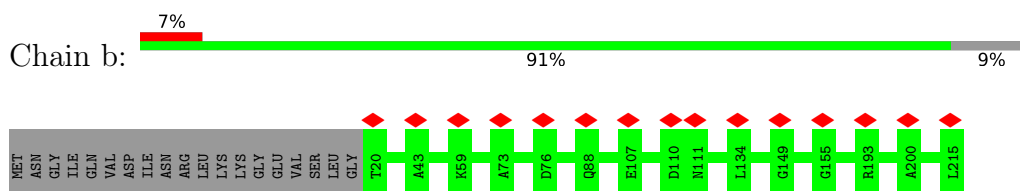
3 Residue-property plots

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.

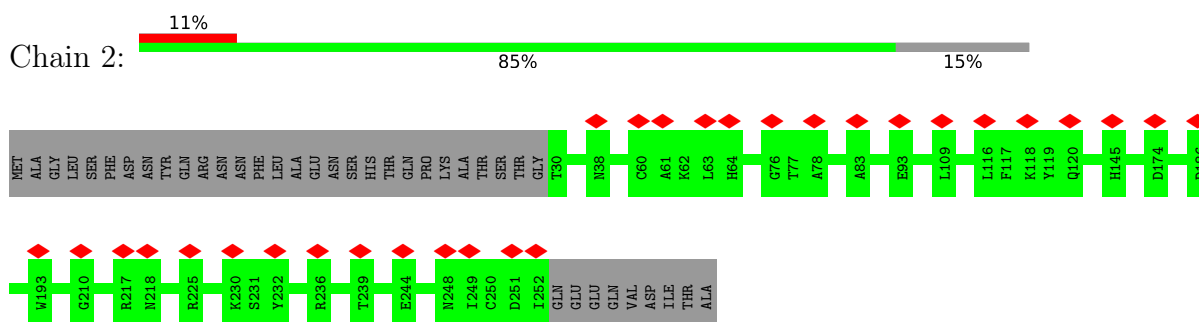
- Molecule 1: Proteasome subunit beta type-1



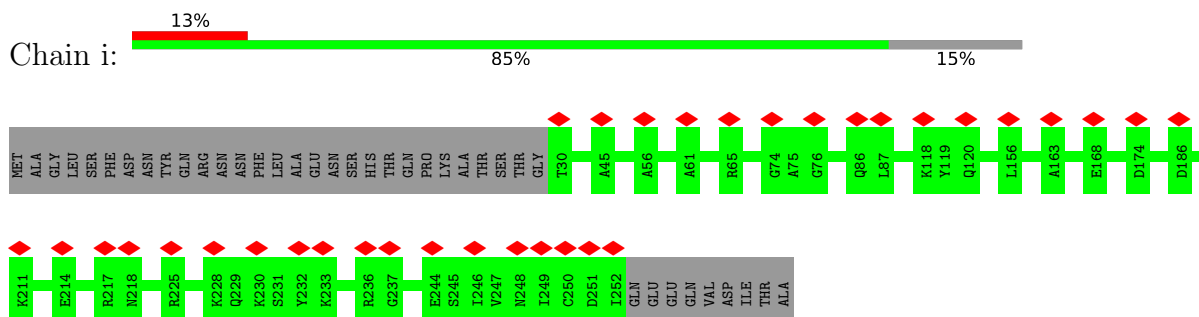
- Molecule 1: Proteasome subunit beta type-1



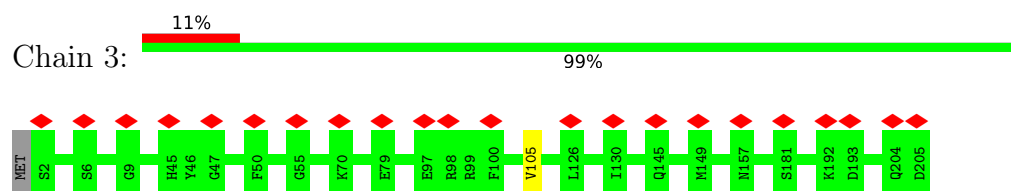
- Molecule 2: Proteasome subunit beta type-2



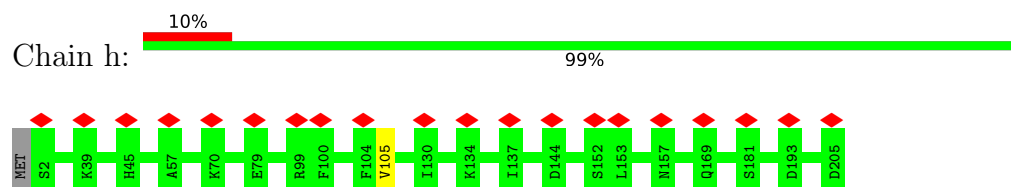
- Molecule 2: Proteasome subunit beta type-2



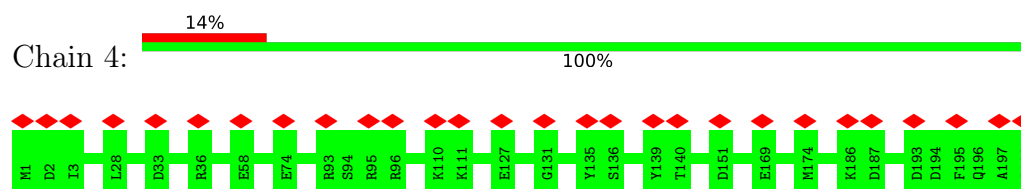
- Molecule 3: Proteasome subunit beta type-3



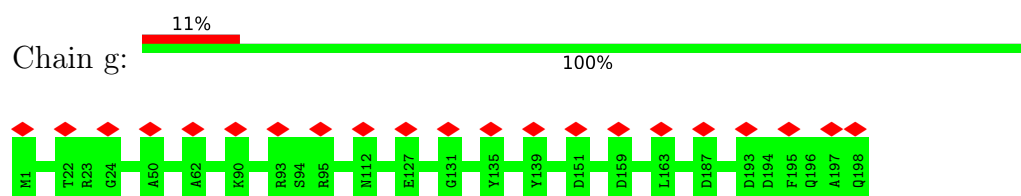
- Molecule 3: Proteasome subunit beta type-3



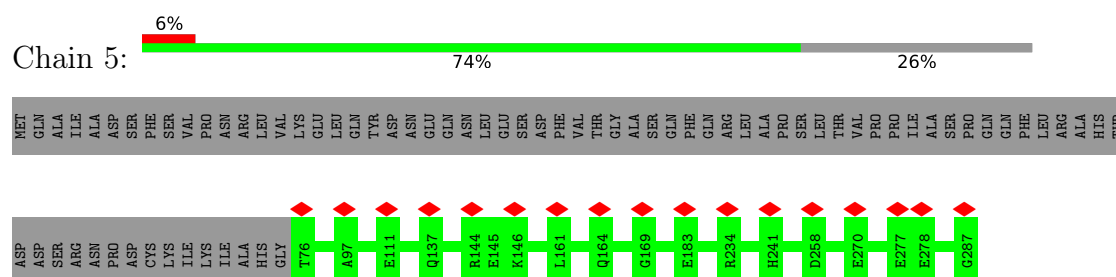
- Molecule 4: Proteasome subunit beta type-4



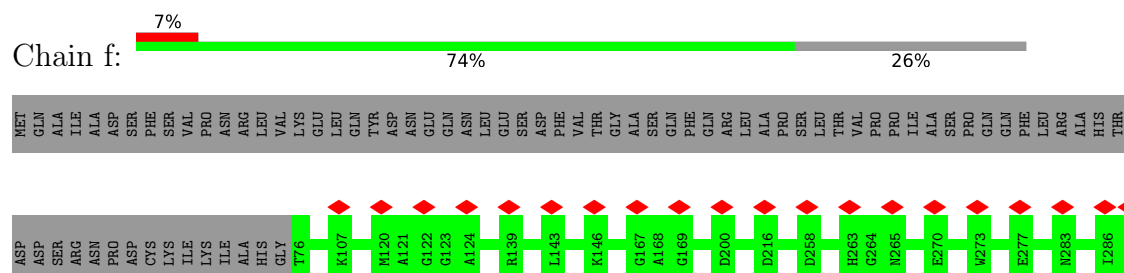
- Molecule 4: Proteasome subunit beta type-4



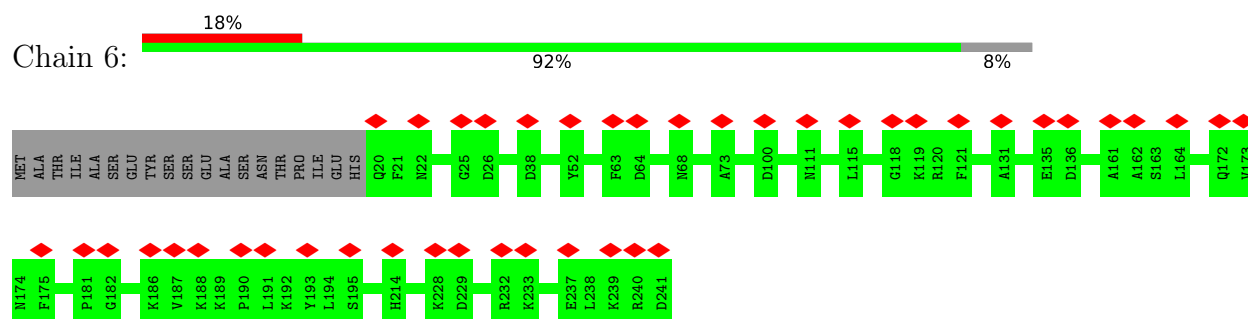
- Molecule 5: Proteasome subunit beta type-5



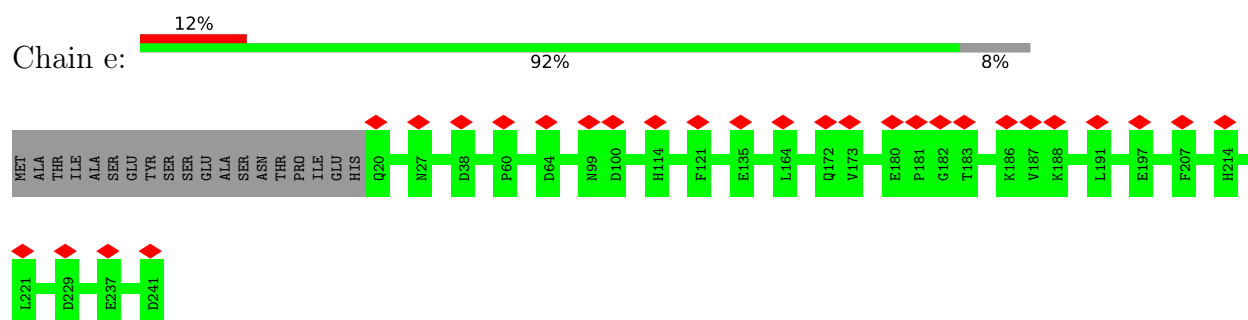
- Molecule 5: Proteasome subunit beta type-5



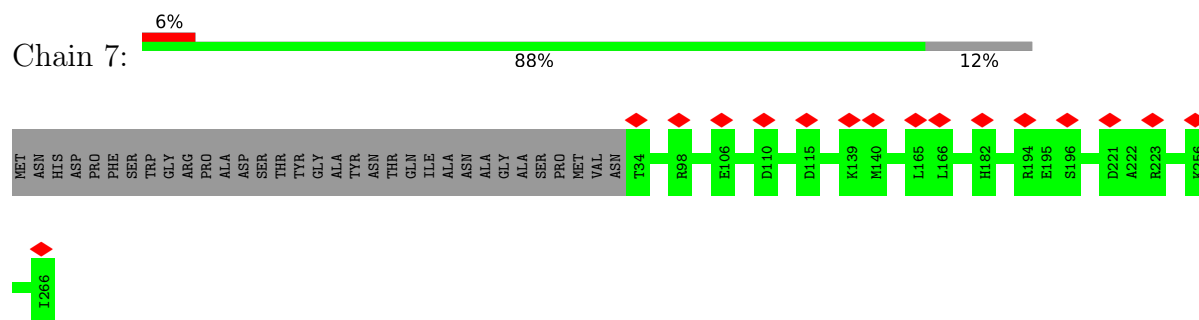
- Molecule 6: Proteasome subunit beta type-6



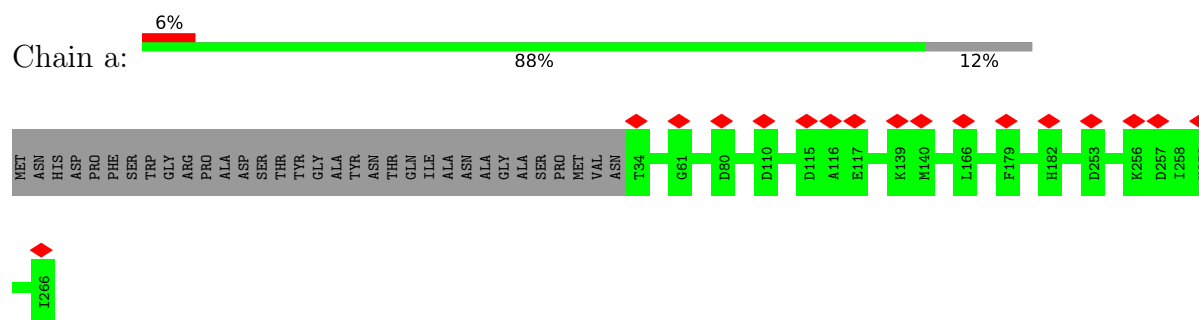
- Molecule 6: Proteasome subunit beta type-6



- Molecule 7: Proteasome subunit beta type-7

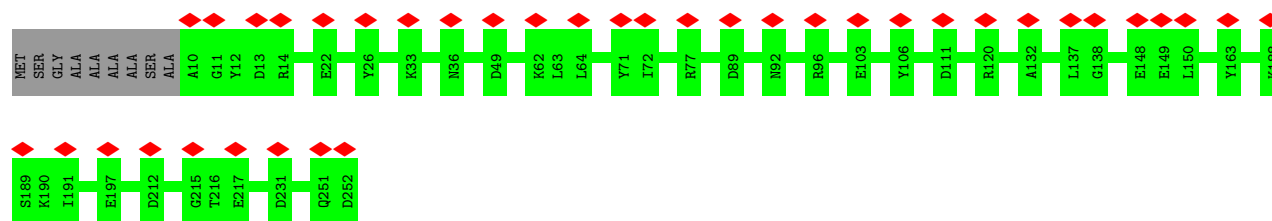


- Molecule 7: Proteasome subunit beta type-7

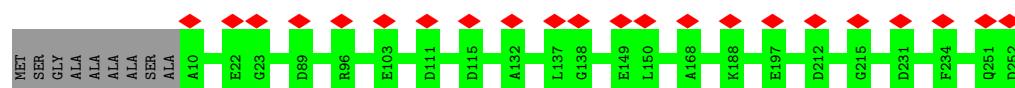


- Molecule 8: Proteasome subunit alpha type-1

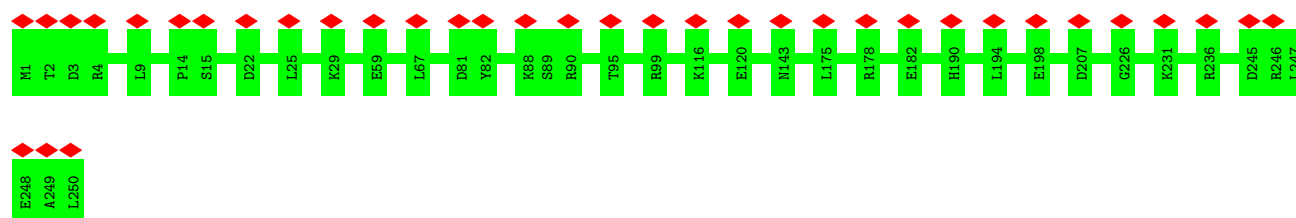




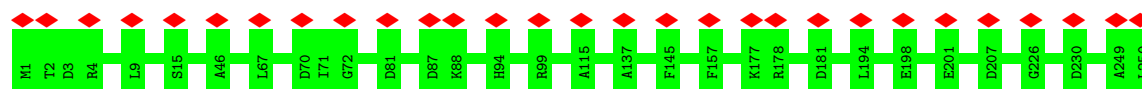
- Molecule 8: Proteasome subunit alpha type-1



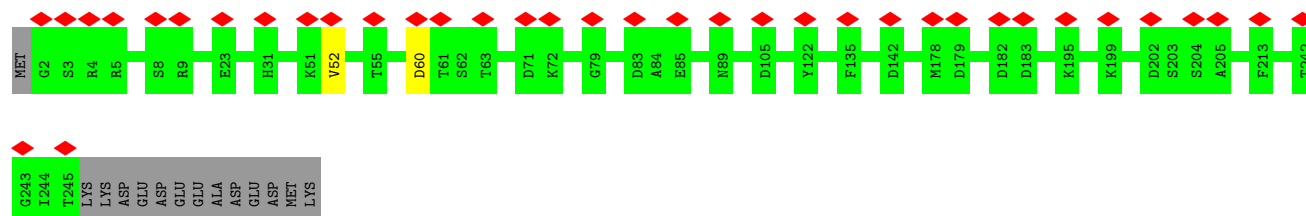
- Molecule 9: Proteasome subunit alpha type-2



- Molecule 9: Proteasome subunit alpha type-2

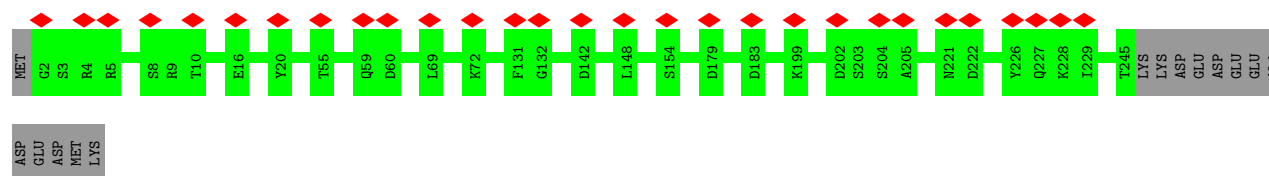


- Molecule 10: Proteasome subunit alpha type-3



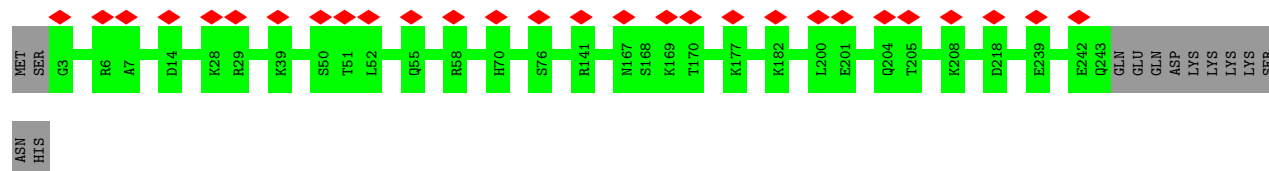
- Molecule 10: Proteasome subunit alpha type-3





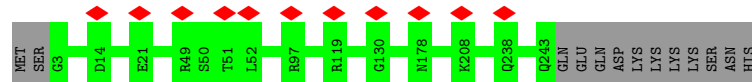
- Molecule 11: Proteasome subunit alpha type-4

Chain D:



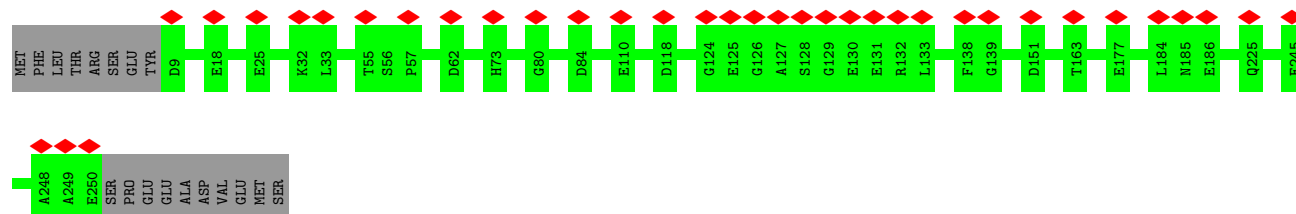
- Molecule 11: Proteasome subunit alpha type-4

Chain n:



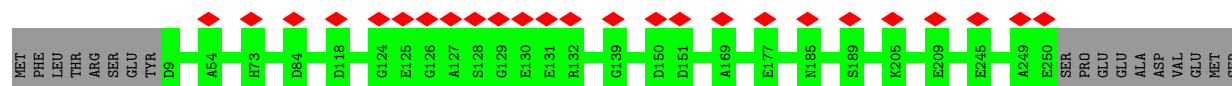
- Molecule 12: Proteasome subunit alpha type-5

Chain E:



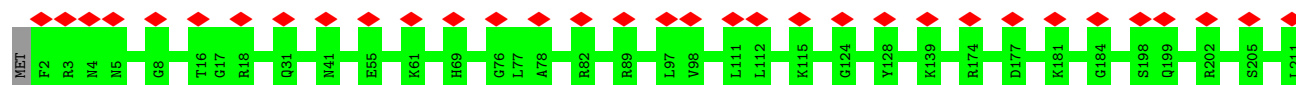
- Molecule 12: Proteasome subunit alpha type-5

Chain m:

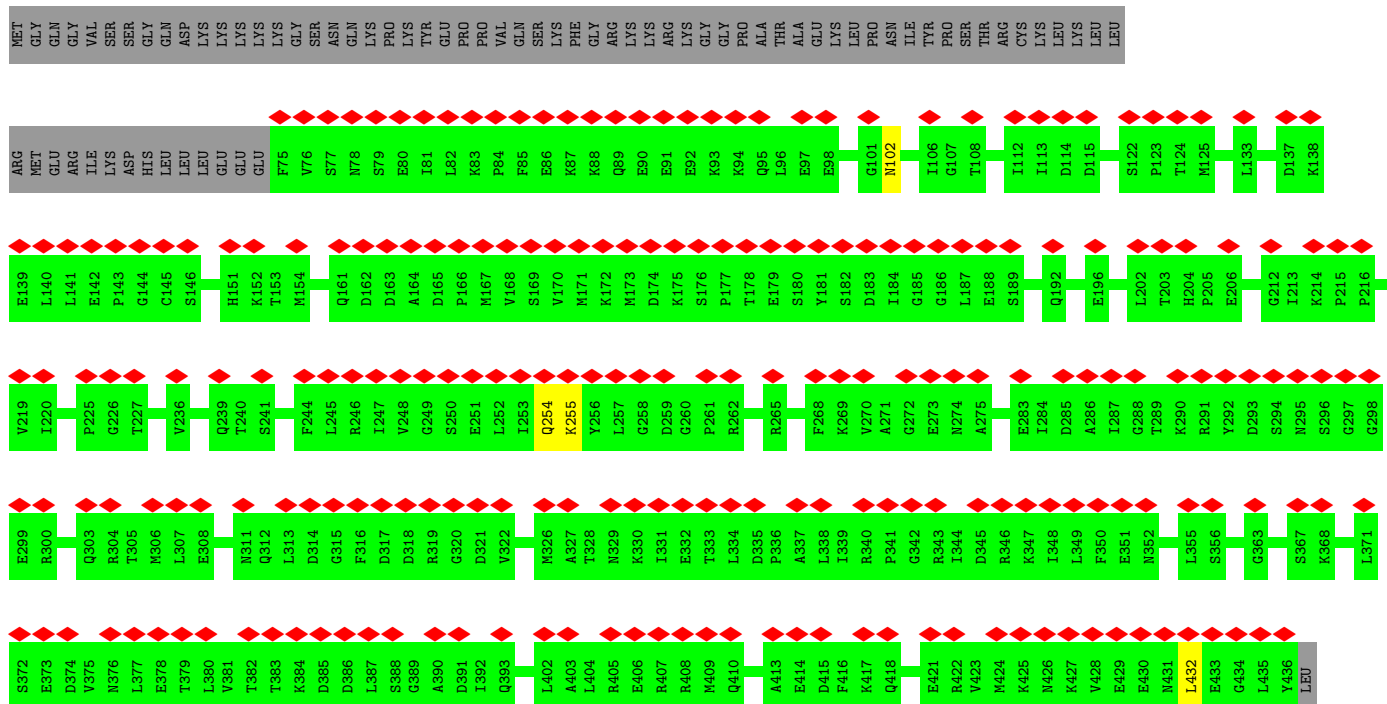
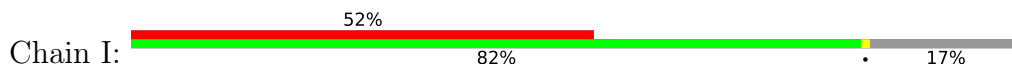


- Molecule 13: Proteasome subunit alpha type-6

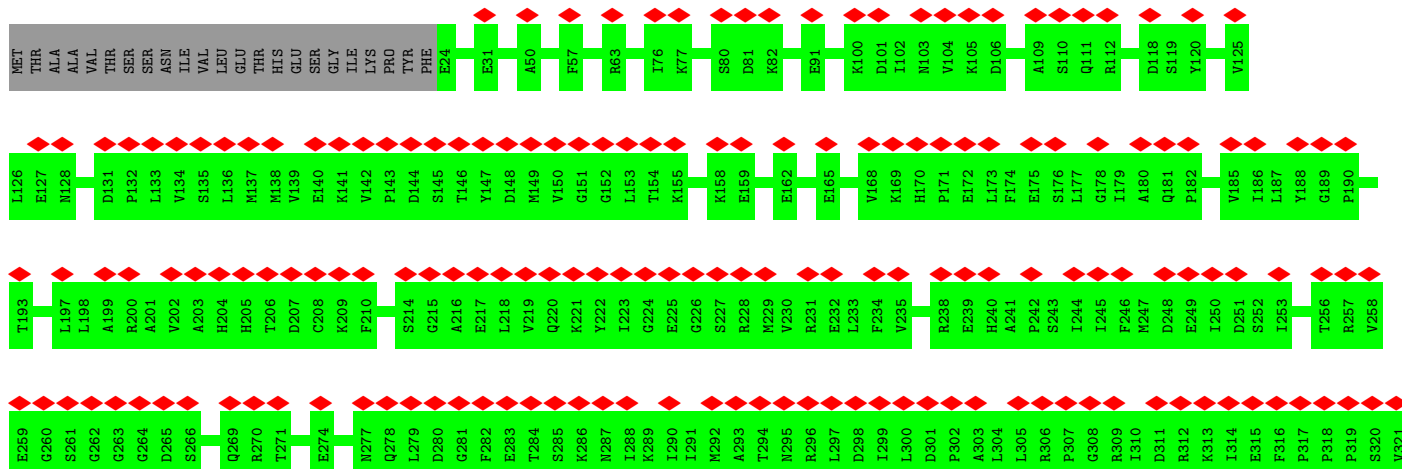
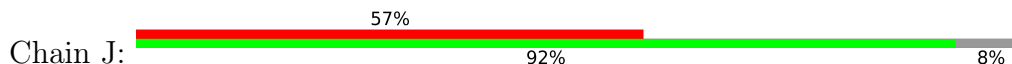
Chain F:

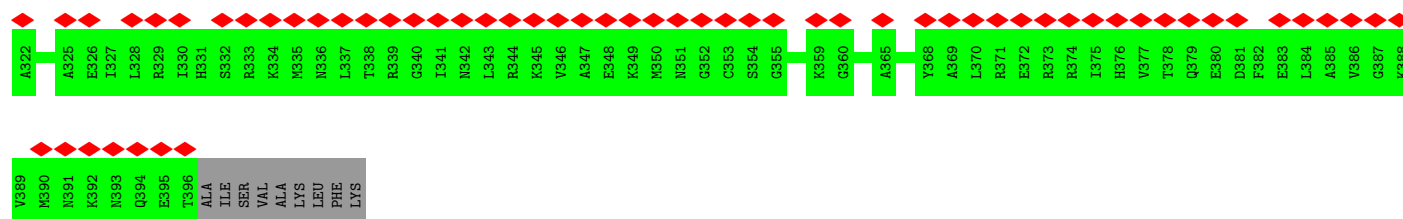


- Molecule 16: 26S protease regulatory subunit 4 homolog



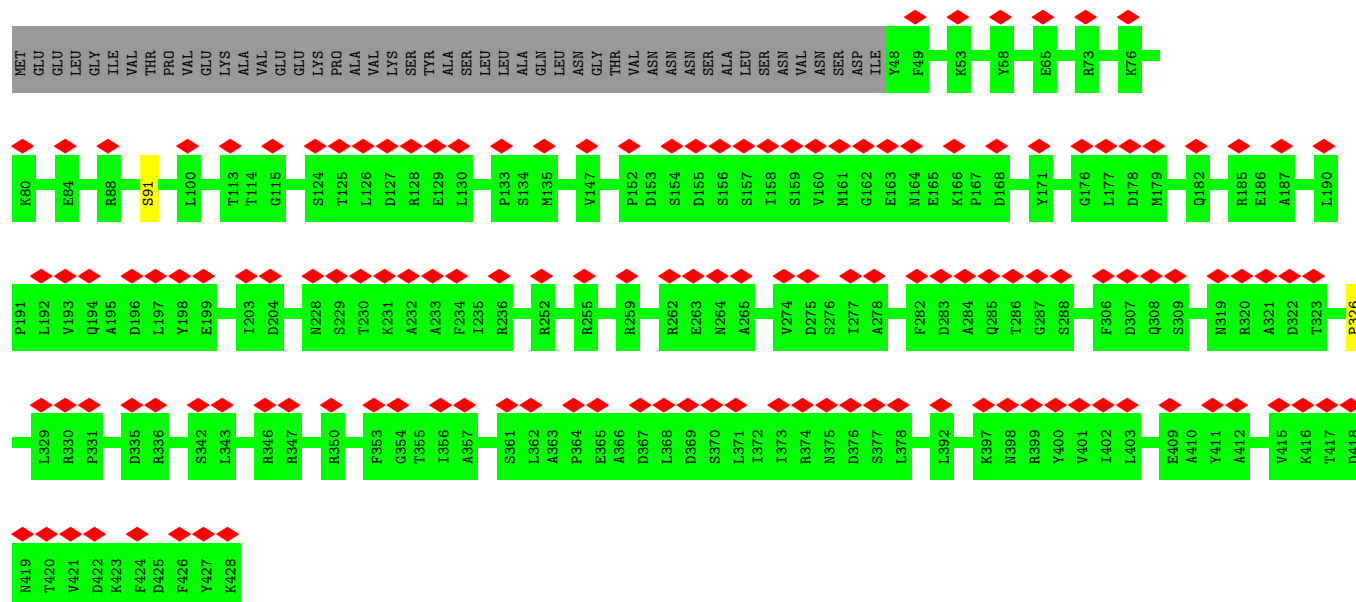
- Molecule 17: 26S protease regulatory subunit 8 homolog





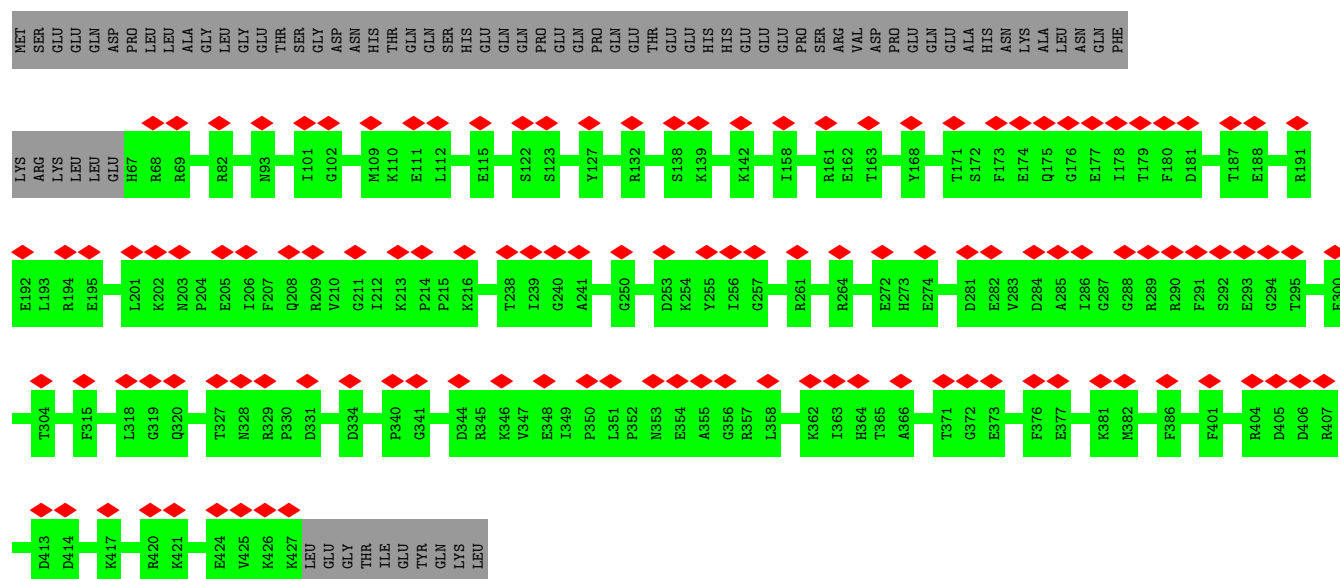
- Molecule 18: 26S protease regulatory subunit 6B homolog

Chain K: 33% 89% 11%

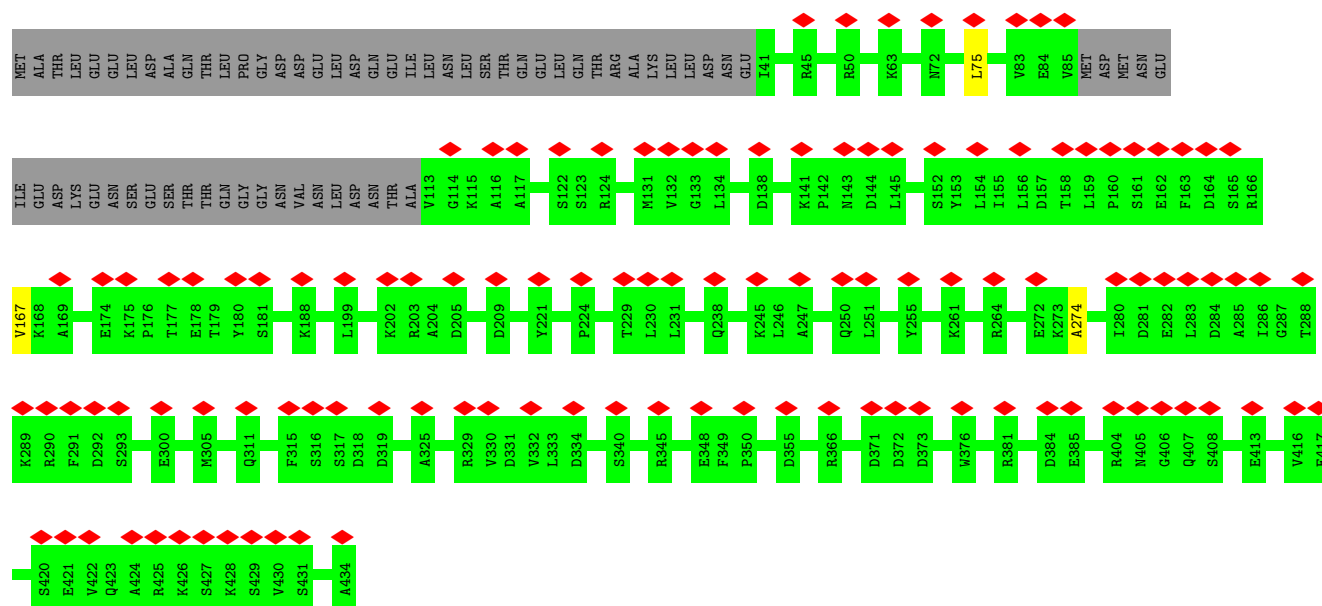
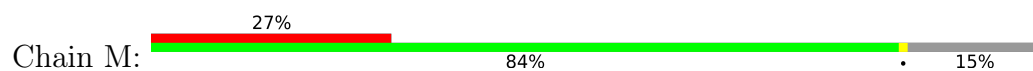


- Molecule 19: 26S protease subunit RPT4

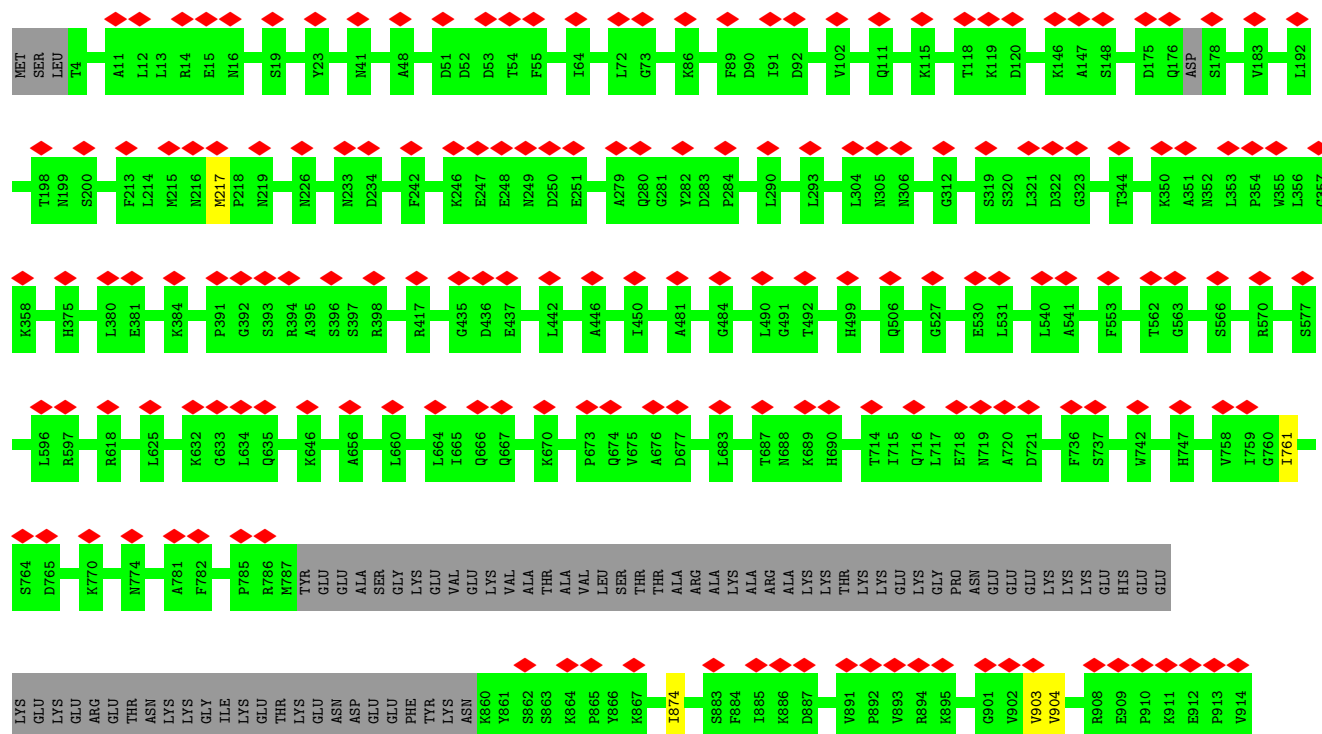
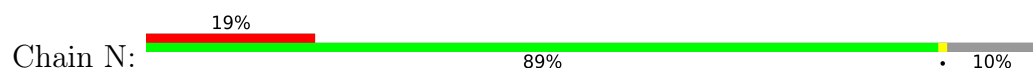
Chain L: 28% 83% 17%

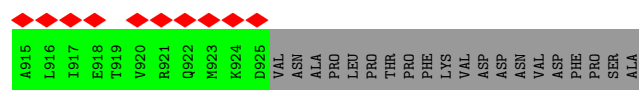


• Molecule 20: 26S protease regulatory subunit 6A

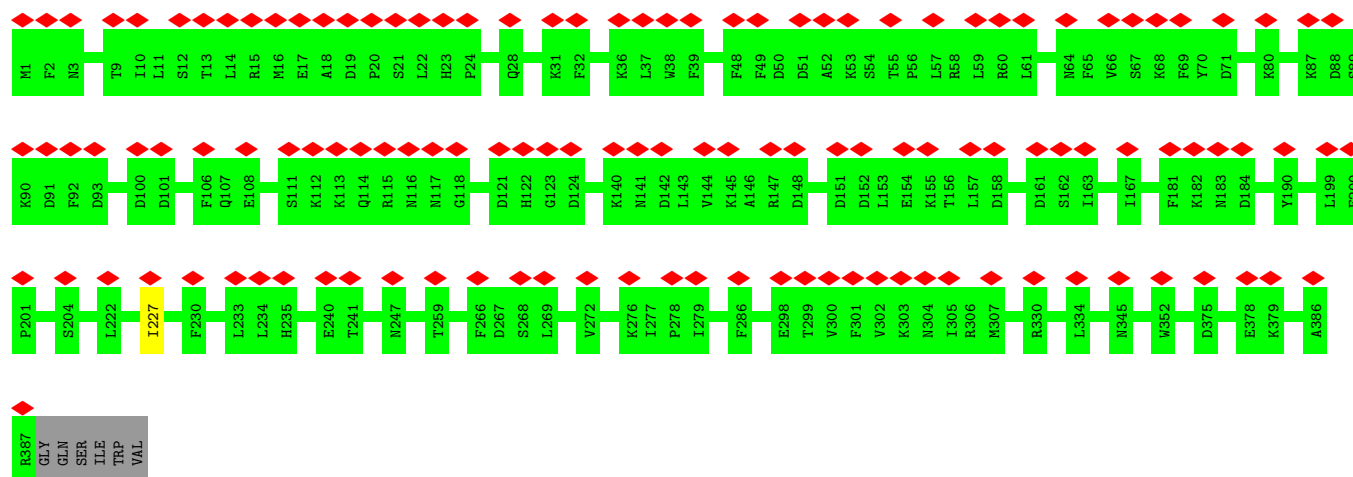


• Molecule 21: 26S proteasome regulatory subunit RPN2

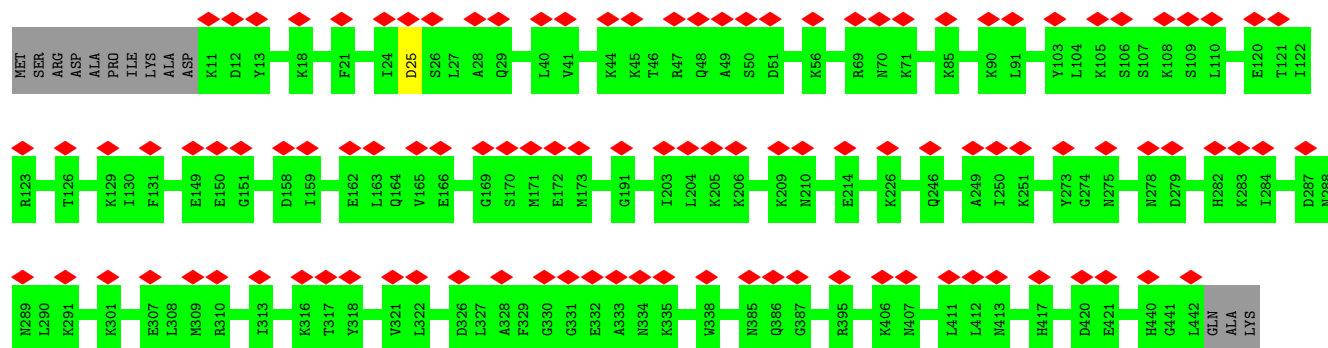




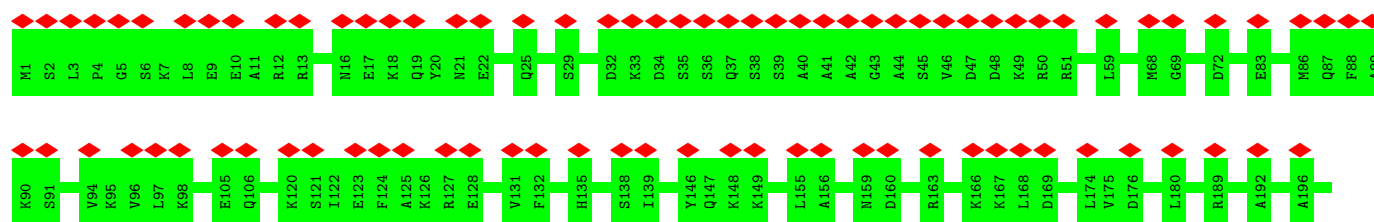
• Molecule 22: 26S proteasome regulatory subunit RPN9

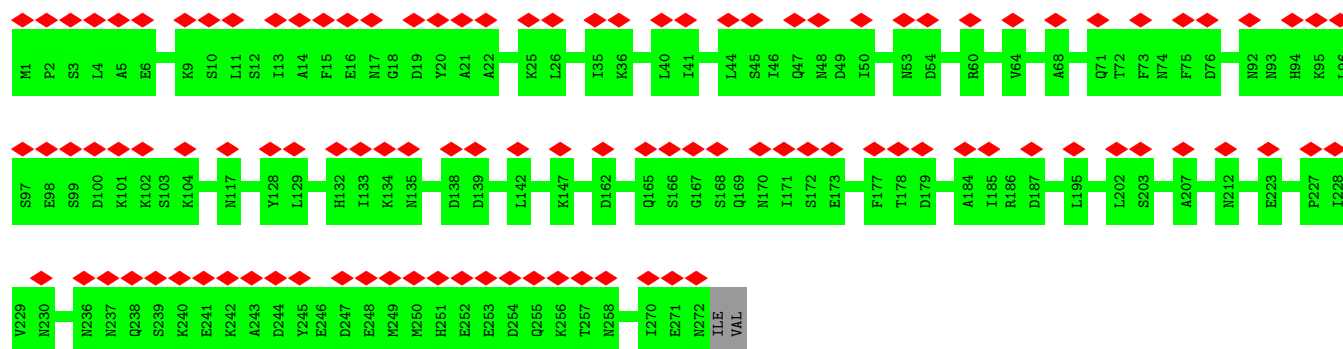


• Molecule 23: 26S proteasome regulatory subunit RPN5



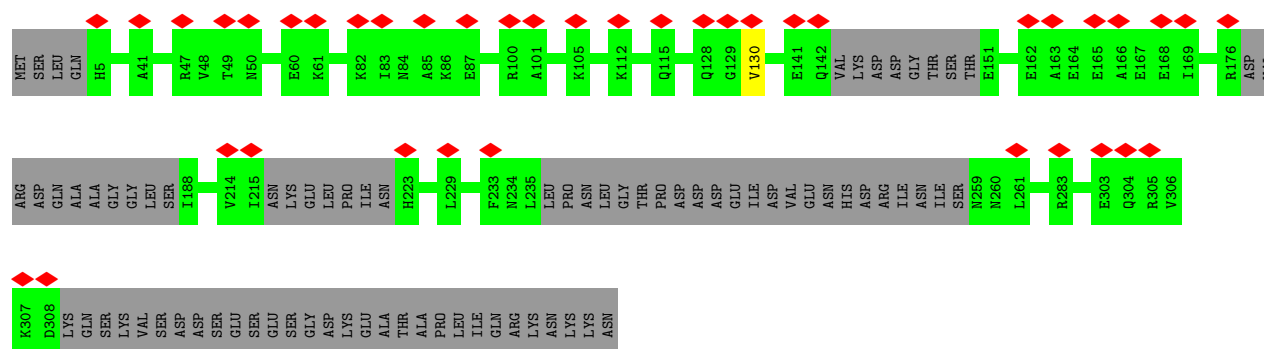
• Molecule 24: 26S proteasome regulatory subunit RPN6





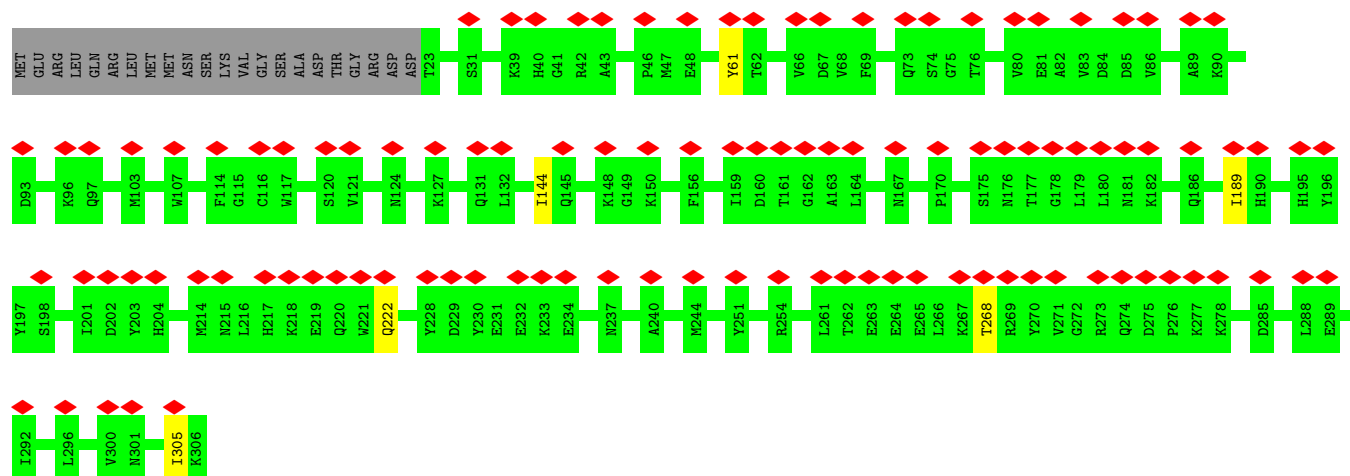
- Molecule 28: 26S proteasome regulatory subunit RPN8

Chain U: 12% 75% 25%



- Molecule 29: Ubiquitin carboxyl-terminal hydrolase RPN11

Chain V: 36% 91% 7%



- Molecule 30: 26S proteasome regulatory subunit RPN10

Chain W: 23% 72% 26%

I971	S972	Y973	T974	S975	H976	I977	E978	G979	V980	V981	I982	L983	K984	K985	N986	P987	D988	Y989	G990	E991	E992	E993																																					
K911	F912	I913	L914	A915	L916	N917	D918	E919	G920	E921	P922	I923	K924	V925	N926	V927	R928	V929	G930	G931	ALA	VAL	GLU	THR	VAL	GLY	GLN	ALA	GLY	ARG	PRO	LYS	ILE	THR	GLY	TRP	ILE	THR	GLN	SER	THR	P954	V955	L956	L957	N958	H959	G960	G961	R962	A963	E964	L965	E966	T967	D968	E969	Y970	
A851	Q852	G853	L854	L855	H856	L857	G858	K859	G860	T861	M862	T863	M864	D865	V866	F867	S868	D869	A870	H871	H872	L873	N874	K875	V876	T877	L878	G879	S880	I881	L882	T883	G884	A885	V886	G887	L888	V889	S890	P891	S892	F893	M894	L895	K896	H897	H898	Q899	L900	F901	Y902	M903	D968	E969	Y970				
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	L823	N824	A825	R826	L827	A828	Q829	L830	L831	R832	Q833	L834	A835	S836	Y837	Y838	S839	R840	E841	Q842	D843	A844	L845	F846	I847	T848	Q849	L850
GLY	ILE	VAL	ASP	GLU	L736	A737	Y738	V739	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	V769	E770	H771	I772	R773	R774	M775	V776	P777	L778	A779	M780	G781	I782	S783	S784	V785	S786	P788	Q789	M790		
GLU	MET	GLU	VAL	ASP	ALA	GLU	GLY	VAL	GLU	VAL	LYS	ALA	ILE	THR	GLU	LYS	ASN	GLY	LEU	GLU	ASP	GLY	GLU	ILE	SER	GLU	THR	LYS	GLY	GLN	THR	ASN	SER	ILE	SER	ASP	PHE	LEU	GLY	GLU	GLN	VAL	ASN	ASP	PRO	GLU	THR	LYS	ASN	GLU	LYS	GLU	ALA	VAL	ASP				
T611	G612	D613	V614	L615	L616	L617	Q618	D619	L620	L621	H622	GLU	R623	L624	T625	PRO	LYS	ASN	VAL	LYS	GLY	GLU	ASP	ALA	ILE	LYS	SER	GLU	THR	LYS	GLY	THR	ASN	SER	ILE	SER	ASP	ALA	THR	LEU	GLY	GLU	GLN	VAL	ASN	ASP	PRO	THR	LYS	ASN	GLU	GLY	ALA	VAL	ASP				
L551	E552	R553	T554	A555	L556	E557	L558	K559	T560	D561	V562	V563	R564	F565	L566	A567	L568	A569	L570	G571	L572	L573	Y574	M575	G576	Q577	G578	E579	Q580	V581	D582	S583	V584	L585	E586	T587	L588	S589	A590	L591	E592	H593	P594	M595	T596	S597	A598	L599	E600	V601	L602	V603	G604	S605	C606	A607	Y608	T609	G610
I485	S486	S487	A488	L491	G492	L493	G494	L495	G499	S500	K501	M502	D503	E504	V505	L506	G507	L508	L509	L510	P511	I512	A513	A514	S515	T516	D517	L518	P519	S520	E521	A526	S527	L528	A529	L530	A531	H532	V533	F534	V535	G536	T537	C538	N539	G540	D541	T542	T543	T544	S545	I546	M547	D548	N549	F550			
G423	S424	I425	Y426	Q427	W428	N429	L430	D431	G432	L433	Q434	Q435	L436	D437	K438	Y439	L440	Y441	V442	D443	E444	P445	E446	V447	A449	L453	G454	I455	G456	I457	G458	A459	S460	G461	V462	H463	G465	E466	V467	E468	P469	A470	L471	L472	L473	L474	Q475	D476	Y477	V478	T479	N480	P481	D482	T483	K484			
H361	L362	D363	N364	S365	K366	S367	V368	F369	S370	S371	A372	G373	L374	D375	S376	A377	Q378	Q379	N380	L381	A382	S383	S384	F385	V386	N387	G388	F389	L390	N391	L392	G393	Y394	C395	N396	D397	L398	L399	I400	V401	D402	N403	D404	N405	W406	V407	Y408	T410	K411	G412	D413	G414	M415	T416	A420	S421	I422		
T301	S302	D303	P304	V305	M306	H307	K308	Q309	L310	A311	Y312	I313	L314	A315	A316	K317	Q318	T319	S320	F321	A322	Y323	E324	G325	V326	Q327	D328	I329	I330	G331	N332	G333	K334	L335	S336	E337	H338	F339	L340	Y341	L342	A343	K344	E345	L346	N347	L348	T349	G350	P351	K352	V353	P354	E355	D356	I357	Y358	K359	S360
T241	F242	Q243	R244	V245	C246	Q247	Y248	M249	V250	A251	C252	V253	P254	L255	L256	P257	P258	P259	E260	D261	V262	A263	F264	L265	K266	T267	A268	Y269	S270	I271	Y272	L273	S274	Q275	N276	E277	L278	T279	D280	A281	I282	A283	L284	A285	V286	R287	L288	G289	E290	E291	D292	M293	I294	R295	S296	V297	F298	D299	A300
G181	S182	K183	S184	D185	H186	S187	A188	T189	T190	S191	G192	F193	E194	F195	S196	K197	E198	D199	T200	L201	R202	L203	C204	L205	D206	T207	V208	P209	Y210	F211	L212	K213	H214	N215	G216	E217	E218	D219	A220	V221	D222	L223	L224	L225	E226	I227	E228	S229	I230	D231	K232	L233	P234	Q235	F236	V237	D238	E239	N240

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	178576	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 ($e^-/\text{\AA}^2$)	38	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.666	Depositor
Minimum map value	-0.738	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.082	Depositor
Recommended contour level	0.543	Depositor
Map size (Å)	474.47998, 474.47998, 474.47998	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.318, 1.318, 1.318	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	0.23	0/1541	0.41	0/2087
1	b	0.23	0/1541	0.42	0/2087
2	2	0.23	0/1723	0.41	0/2337
2	i	0.23	0/1723	0.41	0/2337
3	3	0.24	0/1611	0.40	0/2174
3	h	0.24	0/1611	0.41	0/2174
4	4	0.23	0/1613	0.39	0/2173
4	g	0.23	0/1613	0.40	0/2173
5	5	0.23	0/1681	0.40	0/2274
5	f	0.23	0/1681	0.41	0/2274
6	6	0.24	0/1795	0.40	0/2420
6	e	0.24	0/1795	0.39	0/2420
7	7	0.23	0/1855	0.41	0/2514
7	a	0.23	0/1855	0.42	0/2514
8	A	0.24	0/1959	0.40	0/2652
8	c	0.23	0/1959	0.39	0/2652
9	B	0.24	0/1952	0.40	0/2642
9	j	0.25	0/1952	0.40	0/2642
10	C	0.23	0/1934	0.43	0/2618
10	d	0.23	0/1934	0.41	0/2618
11	D	0.23	0/1919	0.39	0/2598
11	n	0.23	0/1919	0.40	0/2598
12	E	0.23	0/1886	0.41	0/2541
12	m	0.23	0/1886	0.39	0/2541
13	F	0.24	0/1823	0.42	0/2463
13	l	0.24	0/1823	0.42	0/2463
14	G	0.23	0/1936	0.39	0/2614
14	k	0.24	0/1936	0.39	0/2614
15	H	0.23	0/2831	0.41	0/3808
16	I	0.34	1/2860 (0.0%)	0.43	1/3856 (0.0%)
17	J	0.23	0/2964	0.40	0/3981
18	K	0.25	0/3062	0.42	0/4132
19	L	0.24	0/2896	0.39	0/3895
20	M	0.35	2/2903 (0.1%)	0.41	0/3909

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
21	N	0.25	1/6670 (0.0%)	0.39	0/9023
22	O	0.23	0/3243	0.41	0/4374
23	P	0.23	0/3599	0.37	0/4854
24	Q	0.23	0/3527	0.38	0/4748
25	R	0.23	0/3272	0.38	0/4412
26	S	0.23	0/2945	0.39	0/3976
27	T	0.23	0/2279	0.40	0/3077
28	U	0.23	0/2087	0.37	0/2811
29	V	0.24	0/2271	0.49	0/3064
30	W	0.25	0/1557	0.43	0/2111
31	X	0.26	0/1058	0.43	0/1432
32	Y	0.22	0/169	0.30	0/223
33	Z	0.25	1/6404 (0.0%)	0.41	1/8686 (0.0%)
All	All	0.24	5/107053 (0.0%)	0.40	2/144586 (0.0%)

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
15	H	0	1
16	I	0	1
29	V	0	3
30	W	0	1
33	Z	0	1
All	All	0	7

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	I	102	ASN	C-N	13.06	1.59	1.34
20	M	274	ALA	C-N	10.62	1.54	1.34
20	M	75	LEU	C-N	9.21	1.51	1.34
21	N	217	MET	C-N	7.33	1.48	1.34
33	Z	468	GLU	C-N	6.91	1.47	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	I	432	LEU	CA-CB-CG	5.89	128.84	115.30
33	Z	558	LEU	CA-CB-CG	5.03	126.87	115.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	H	185	LEU	Peptide
16	I	254	GLN	Peptide
29	V	222	GLN	Peptide
29	V	268	THR	Peptide
29	V	61	TYR	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	194/215 (90%)	186 (96%)	8 (4%)	0	100	100
1	b	194/215 (90%)	185 (95%)	9 (5%)	0	100	100
2	2	221/261 (85%)	208 (94%)	13 (6%)	0	100	100
2	i	221/261 (85%)	209 (95%)	12 (5%)	0	100	100
3	3	202/205 (98%)	192 (95%)	9 (4%)	1 (0%)	29	68
3	h	202/205 (98%)	192 (95%)	9 (4%)	1 (0%)	29	68
4	4	196/198 (99%)	183 (93%)	13 (7%)	0	100	100
4	g	196/198 (99%)	186 (95%)	10 (5%)	0	100	100
5	5	210/287 (73%)	198 (94%)	12 (6%)	0	100	100
5	f	210/287 (73%)	198 (94%)	12 (6%)	0	100	100
6	6	220/241 (91%)	211 (96%)	9 (4%)	0	100	100
6	e	220/241 (91%)	206 (94%)	14 (6%)	0	100	100
7	7	231/266 (87%)	220 (95%)	11 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	a	231/266 (87%)	218 (94%)	13 (6%)	0	100	100
8	A	241/252 (96%)	230 (95%)	11 (5%)	0	100	100
8	c	241/252 (96%)	229 (95%)	12 (5%)	0	100	100
9	B	248/250 (99%)	237 (96%)	11 (4%)	0	100	100
9	j	248/250 (99%)	235 (95%)	13 (5%)	0	100	100
10	C	242/258 (94%)	224 (93%)	16 (7%)	2 (1%)	19	60
10	d	242/258 (94%)	228 (94%)	14 (6%)	0	100	100
11	D	239/254 (94%)	230 (96%)	9 (4%)	0	100	100
11	n	239/254 (94%)	224 (94%)	15 (6%)	0	100	100
12	E	240/260 (92%)	230 (96%)	10 (4%)	0	100	100
12	m	240/260 (92%)	231 (96%)	9 (4%)	0	100	100
13	F	231/234 (99%)	220 (95%)	11 (5%)	0	100	100
13	l	231/234 (99%)	221 (96%)	10 (4%)	0	100	100
14	G	242/288 (84%)	235 (97%)	7 (3%)	0	100	100
14	k	242/288 (84%)	232 (96%)	10 (4%)	0	100	100
15	H	353/467 (76%)	321 (91%)	32 (9%)	0	100	100
16	I	360/437 (82%)	334 (93%)	25 (7%)	1 (0%)	41	76
17	J	371/405 (92%)	351 (95%)	20 (5%)	0	100	100
18	K	379/428 (89%)	345 (91%)	33 (9%)	1 (0%)	41	76
19	L	359/437 (82%)	334 (93%)	25 (7%)	0	100	100
20	M	363/434 (84%)	343 (94%)	19 (5%)	1 (0%)	41	76
21	N	843/945 (89%)	796 (94%)	43 (5%)	4 (0%)	29	68
22	O	385/393 (98%)	339 (88%)	45 (12%)	1 (0%)	41	76
23	P	430/445 (97%)	387 (90%)	42 (10%)	1 (0%)	47	80
24	Q	429/434 (99%)	400 (93%)	29 (7%)	0	100	100
25	R	398/429 (93%)	366 (92%)	29 (7%)	3 (1%)	19	60
26	S	351/523 (67%)	320 (91%)	30 (8%)	1 (0%)	41	76
27	T	270/274 (98%)	244 (90%)	26 (10%)	0	100	100
28	U	245/338 (72%)	237 (97%)	7 (3%)	1 (0%)	34	72
29	V	282/306 (92%)	242 (86%)	37 (13%)	3 (1%)	14	52
30	W	195/268 (73%)	170 (87%)	22 (11%)	3 (2%)	10	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	X	125/156 (80%)	100 (80%)	25 (20%)	0	100	100
32	Y	17/89 (19%)	17 (100%)	0	0	100	100
33	Z	807/993 (81%)	736 (91%)	71 (9%)	0	100	100
All	All	13276/15139 (88%)	12380 (93%)	872 (7%)	24 (0%)	50	80

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	C	52	VAL
16	I	255	LYS
21	N	874	ILE
28	U	130	VAL
3	3	105	VAL

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	162/178 (91%)	162 (100%)	0	100	100
1	b	162/178 (91%)	162 (100%)	0	100	100
2	2	182/214 (85%)	182 (100%)	0	100	100
2	i	182/214 (85%)	182 (100%)	0	100	100
3	3	172/173 (99%)	172 (100%)	0	100	100
3	h	172/173 (99%)	172 (100%)	0	100	100
4	4	175/175 (100%)	175 (100%)	0	100	100
4	g	175/175 (100%)	175 (100%)	0	100	100
5	5	169/235 (72%)	169 (100%)	0	100	100
5	f	169/235 (72%)	169 (100%)	0	100	100
6	6	185/201 (92%)	185 (100%)	0	100	100
6	e	185/201 (92%)	185 (100%)	0	100	100
7	7	199/224 (89%)	199 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	a	199/224 (89%)	199 (100%)	0	100	100
8	A	207/210 (99%)	207 (100%)	0	100	100
8	c	207/210 (99%)	207 (100%)	0	100	100
9	B	209/209 (100%)	209 (100%)	0	100	100
9	j	209/209 (100%)	209 (100%)	0	100	100
10	C	203/216 (94%)	203 (100%)	0	100	100
10	d	203/216 (94%)	203 (100%)	0	100	100
11	D	213/226 (94%)	213 (100%)	0	100	100
11	n	213/226 (94%)	213 (100%)	0	100	100
12	E	198/215 (92%)	198 (100%)	0	100	100
12	m	198/215 (92%)	198 (100%)	0	100	100
13	F	192/193 (100%)	192 (100%)	0	100	100
13	l	192/193 (100%)	192 (100%)	0	100	100
14	G	201/239 (84%)	201 (100%)	0	100	100
14	k	201/239 (84%)	201 (100%)	0	100	100
15	H	303/399 (76%)	303 (100%)	0	100	100
16	I	319/385 (83%)	319 (100%)	0	100	100
17	J	325/352 (92%)	325 (100%)	0	100	100
18	K	334/374 (89%)	333 (100%)	1 (0%)	92	95
19	L	308/377 (82%)	308 (100%)	0	100	100
20	M	315/375 (84%)	315 (100%)	0	100	100
21	N	713/797 (90%)	713 (100%)	0	100	100
22	O	363/368 (99%)	363 (100%)	0	100	100
23	P	405/415 (98%)	405 (100%)	0	100	100
24	Q	388/391 (99%)	388 (100%)	0	100	100
25	R	351/379 (93%)	351 (100%)	0	100	100
26	S	330/489 (68%)	330 (100%)	0	100	100
27	T	254/256 (99%)	254 (100%)	0	100	100
28	U	234/308 (76%)	234 (100%)	0	100	100
29	V	249/268 (93%)	249 (100%)	0	100	100
30	W	171/230 (74%)	171 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	X	116/144 (81%)	116 (100%)	0	100	100
32	Y	18/81 (22%)	18 (100%)	0	100	100
33	Z	692/850 (81%)	692 (100%)	0	100	100
All	All	11522/13054 (88%)	11521 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	K	91	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
21	N	240	GLN
23	P	440	HIS
21	N	329	HIS
21	N	922	GLN
25	R	184	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

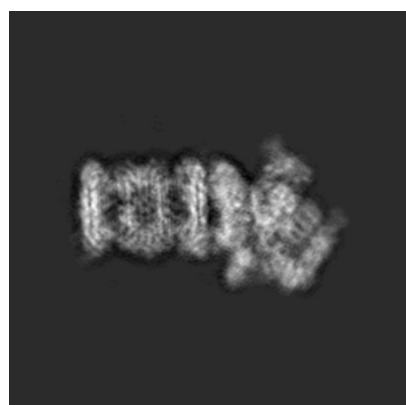
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6694. These allow visual inspection of the internal detail of the map and identification of artifacts.

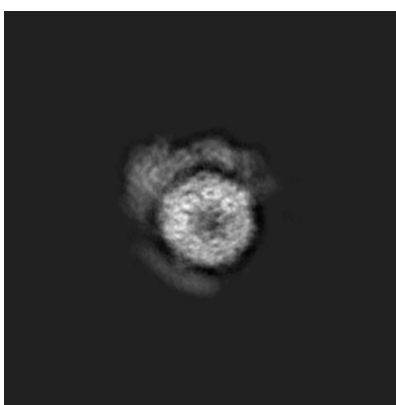
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

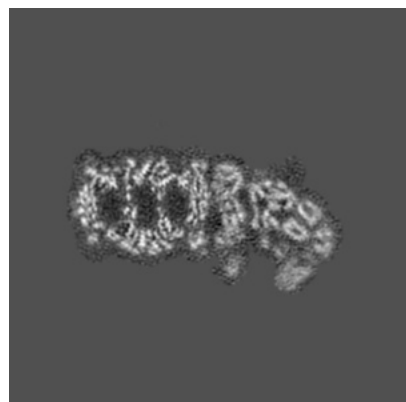


Z

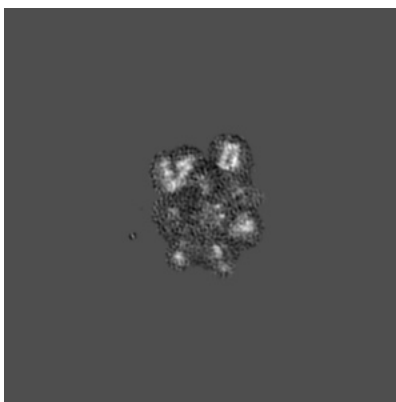
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

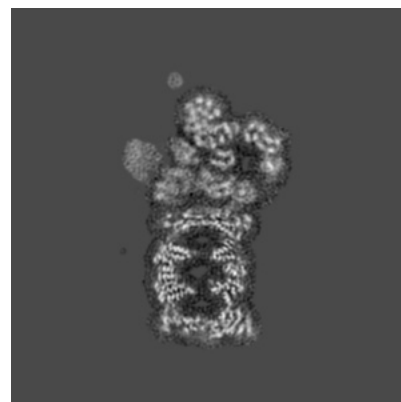
6.2.1 Primary map



X Index: 180



Y Index: 180

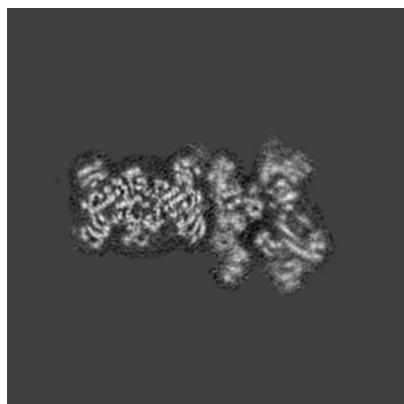


Z Index: 180

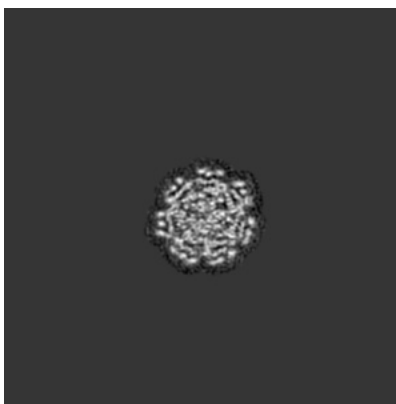
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

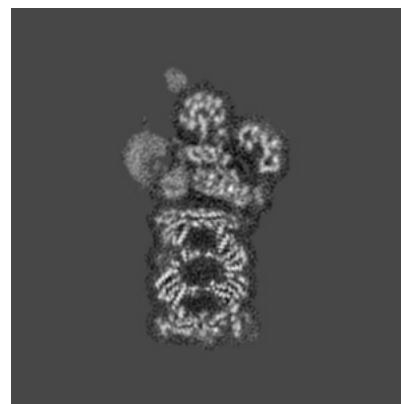
6.3.1 Primary map



X Index: 192



Y Index: 77

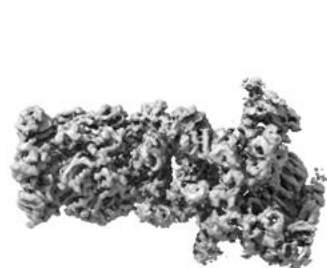


Z Index: 173

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.543. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

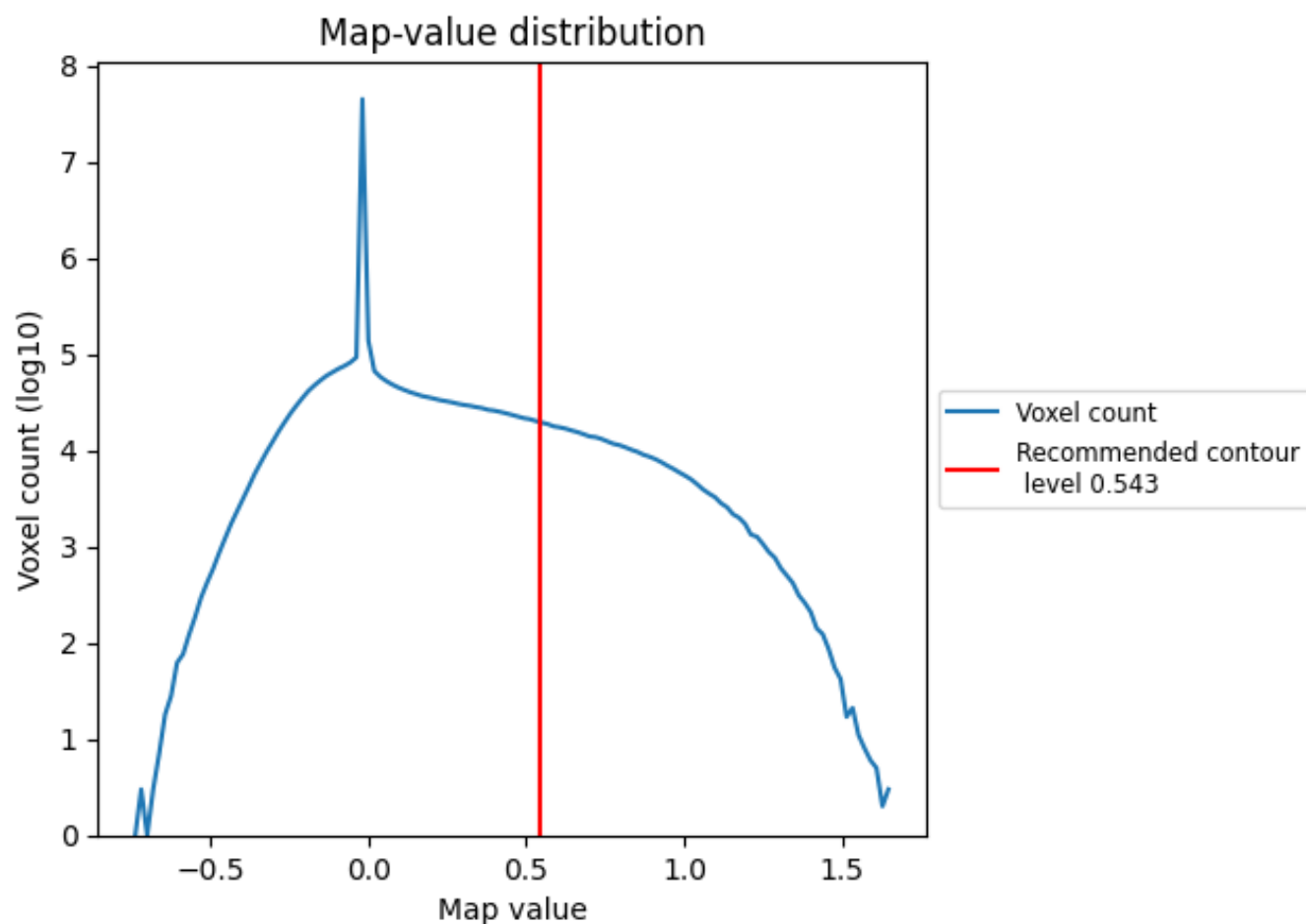
6.5 Mask visualisation

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

7 Map analysis [i](#)

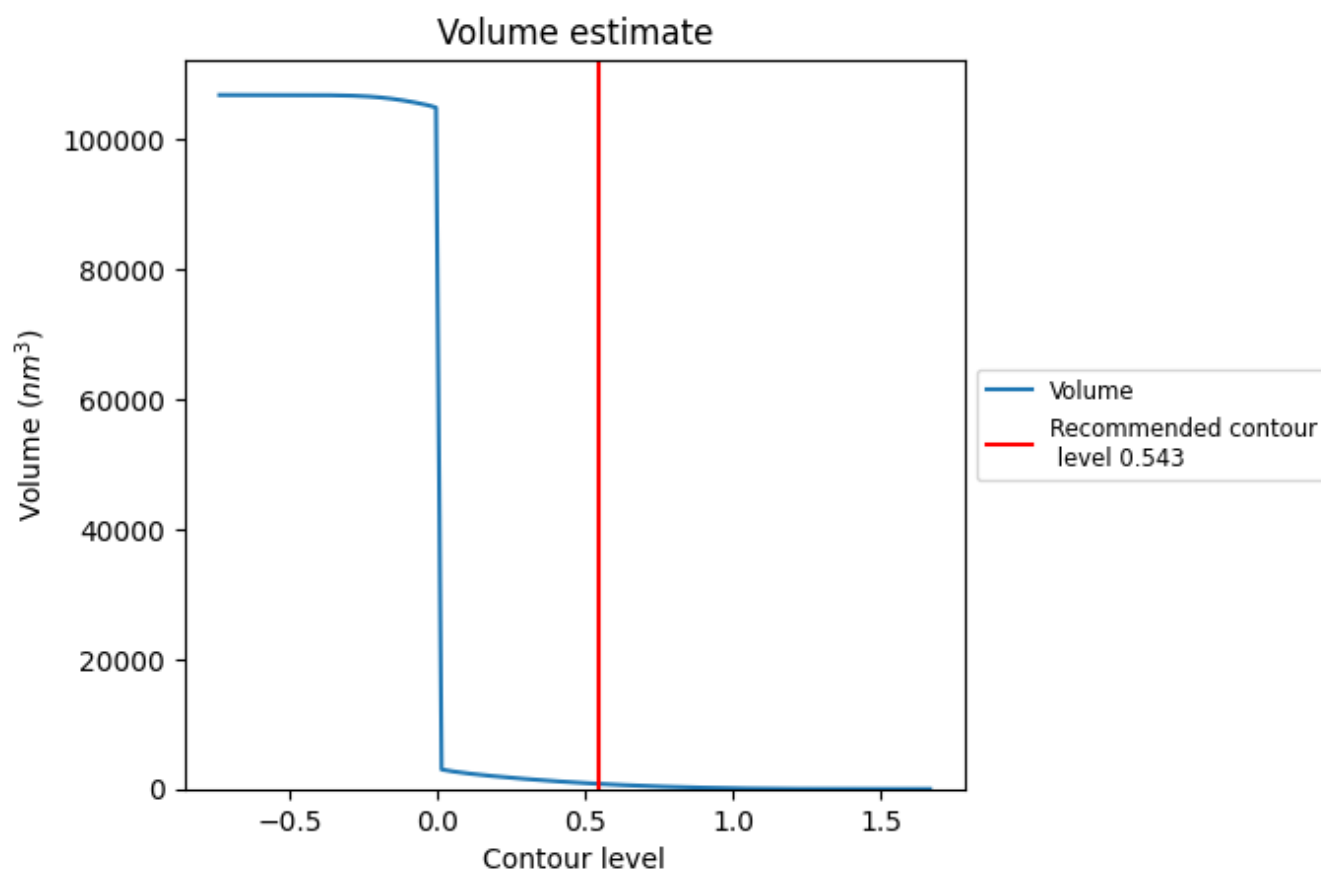
This section contains the results of statistical analysis of the map.

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.

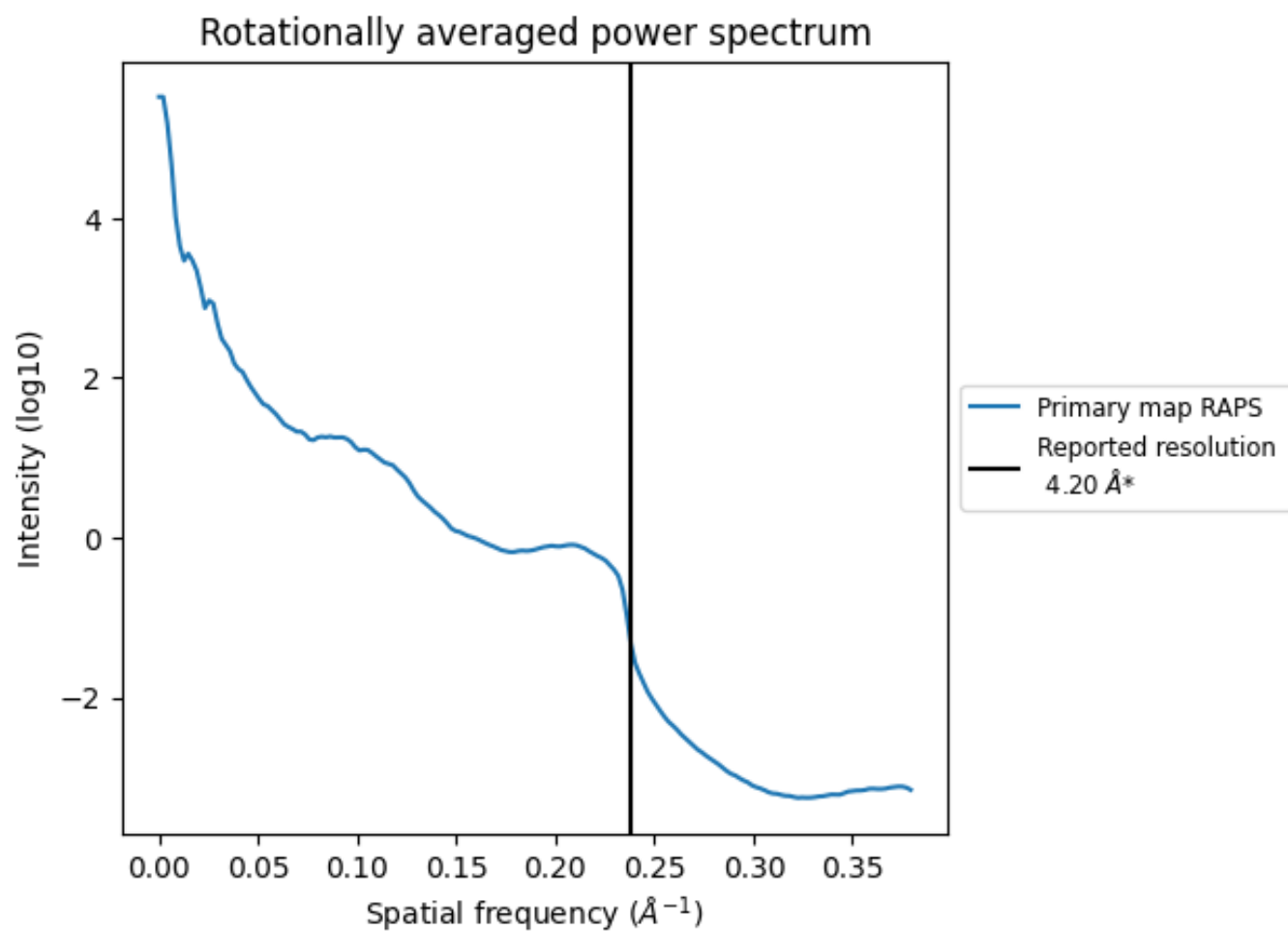
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 792 nm³; this corresponds to an approximate mass of 715 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 0.238 Å⁻¹

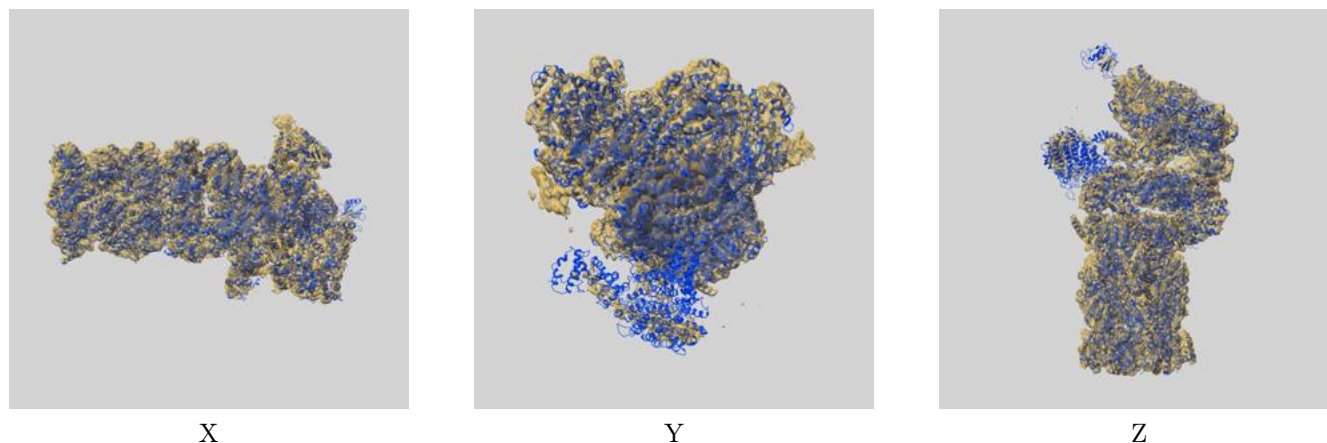
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

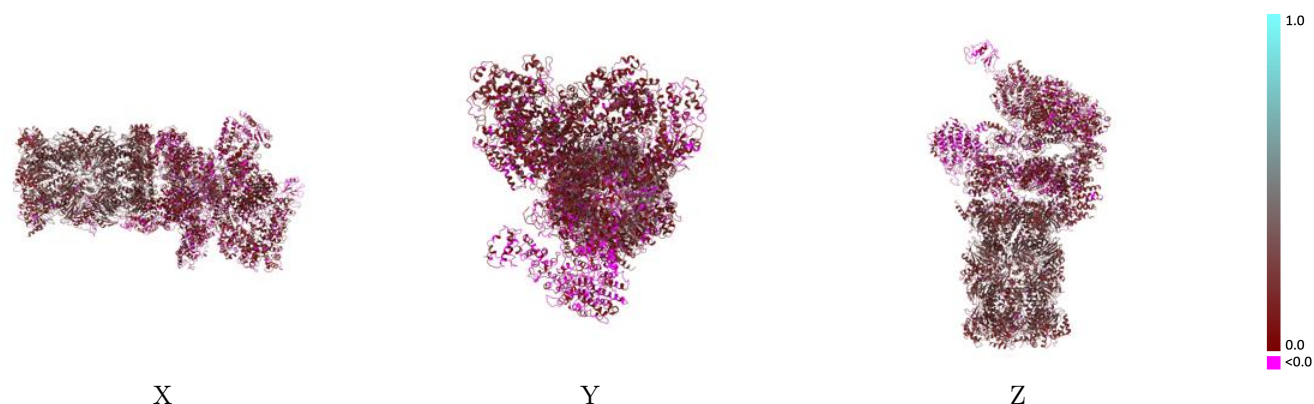
This section contains information regarding the fit between EMDB map EMD-6694 and PDB model 5WVK. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



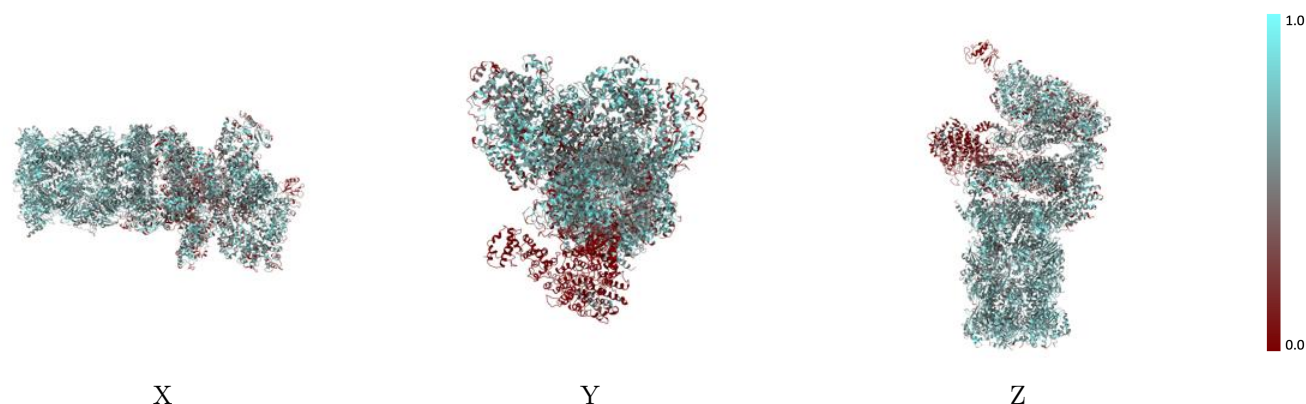
The images above show the 3D surface view of the map at the recommended contour level 0.543 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



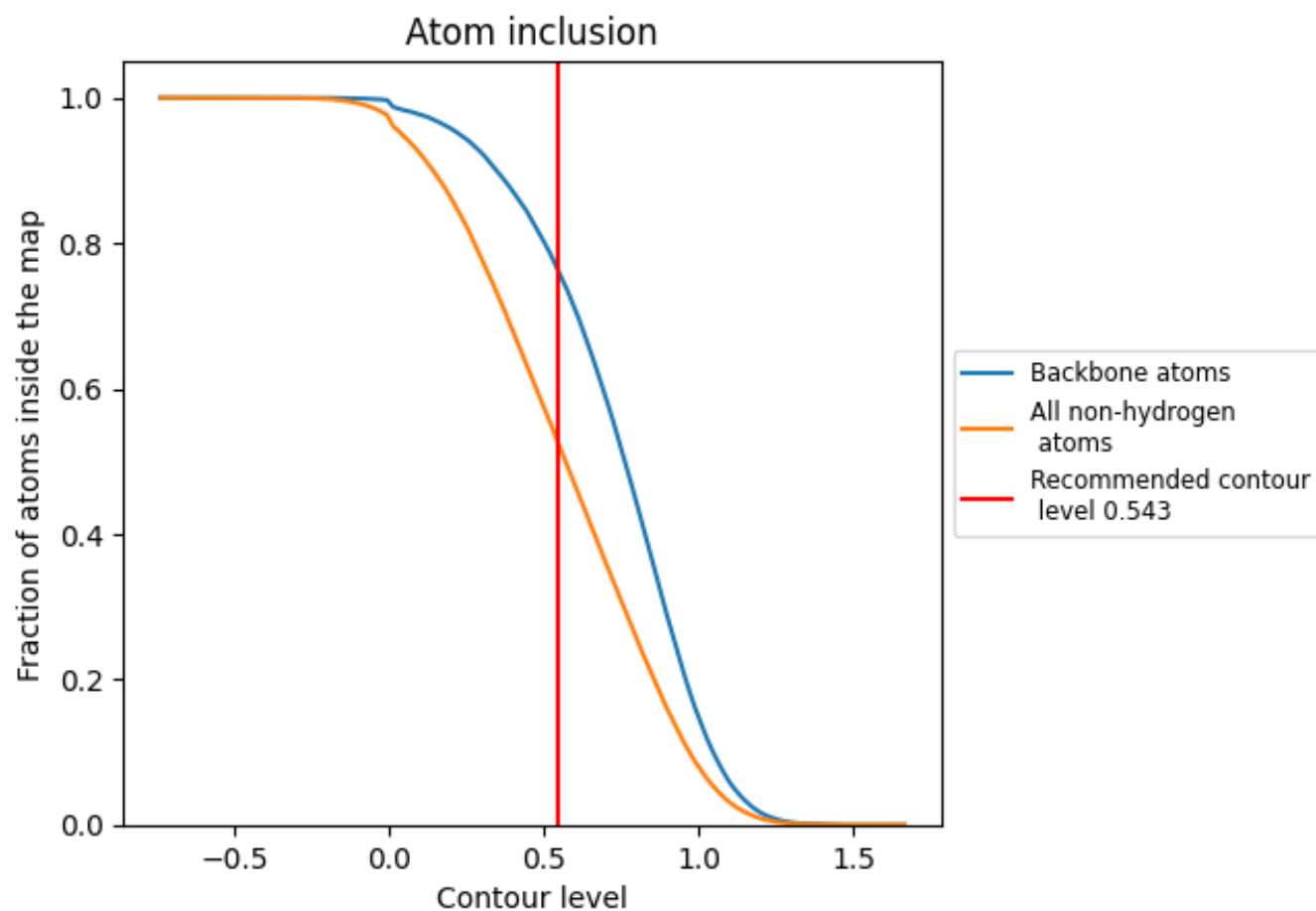
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.543).

9.4 Atom inclusion ⓘ



At the recommended contour level, 77% of all backbone atoms, 53% 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 (0.543) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5293	0.1690
1	0.6543	0.2880
2	0.6191	0.2380
3	0.6189	0.2580
4	0.6089	0.2530
5	0.6321	0.2570
6	0.5801	0.2350
7	0.6323	0.2730
A	0.5995	0.2470
B	0.5947	0.2350
C	0.5963	0.2100
D	0.6142	0.2250
E	0.6077	0.2210
F	0.6077	0.2210
G	0.6190	0.2380
H	0.4705	0.1010
I	0.2985	0.1050
J	0.3153	0.1100
K	0.4834	0.1280
L	0.4955	0.1090
M	0.5343	0.1160
N	0.5853	0.1410
O	0.5112	0.1140
P	0.5455	0.1280
Q	0.5453	0.1160
R	0.5784	0.1210
S	0.5383	0.1170
T	0.4645	0.1310
U	0.5923	0.1770
V	0.4649	0.1180
W	0.5476	0.1080
X	0.0207	-0.0290
Y	0.5521	0.1430
Z	0.0496	0.0070
a	0.6475	0.2620



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Chain	Atom inclusion	Q-score
b	 0.6489	 0.2850
c	 0.6430	 0.2330
d	 0.6409	 0.2160
e	 0.6138	 0.2250
f	 0.6364	 0.2320
g	 0.6276	 0.2620
h	 0.6073	 0.2550
i	 0.5975	 0.2350
j	 0.6403	 0.2250
k	 0.6608	 0.2330
l	 0.6600	 0.2140
m	 0.6318	 0.2110
n	 0.6596	 0.2240