



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:31 AM UTC

PDB ID : 9IWR / pdb_00009iwr
EMDB ID : EMD-60960
Title : 26S proteasome trimer
Authors : Qu, L.; Tang, X.; Baumeister, W.
Deposited on : 2024-07-25
Resolution : 9.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

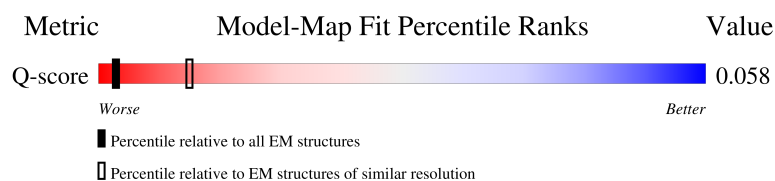
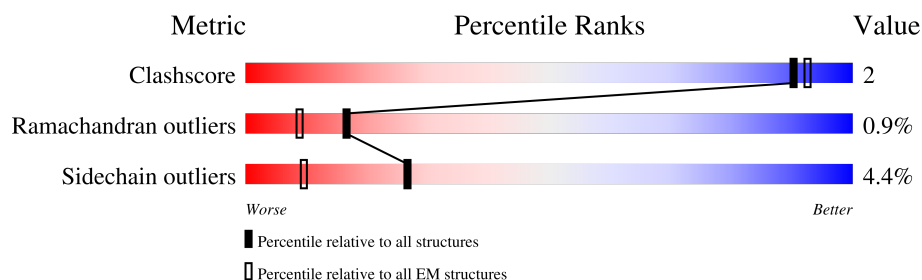
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 9.10 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.



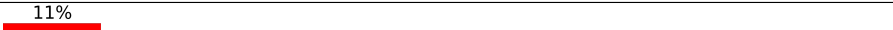
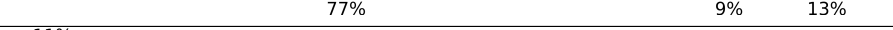
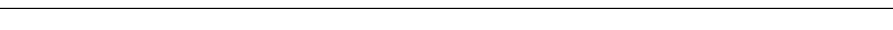
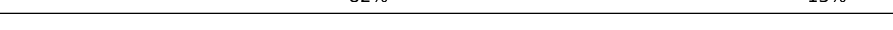
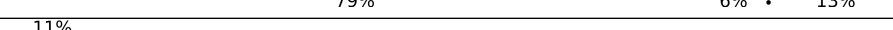
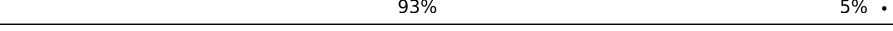
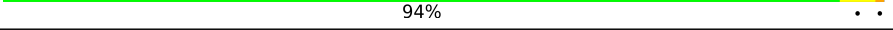
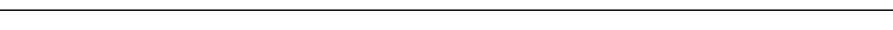
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	244 (8.60 - 9.60)

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	1-1	215	9% 85% 5% • 9%
1	1-h	215	7% 84% 7% 9%
1	2-1	215	85% 5% • 9%
1	2-h	215	85% 6% 9%

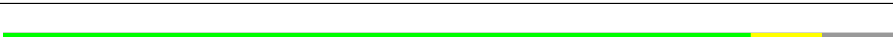
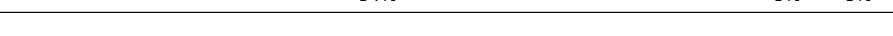
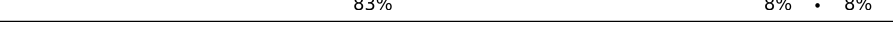
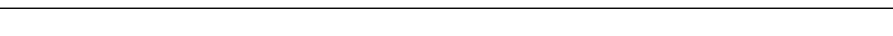
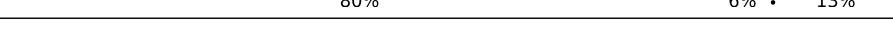
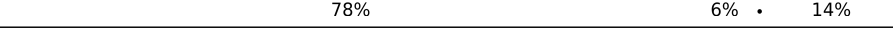
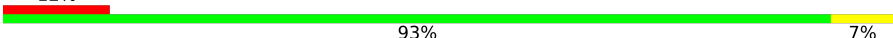
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Mol	Chain	Length	Quality of chain
1	3-1	215	 83% 6% • 9%
1	3-h	215	 81% 8% • 9%
2	1-2	261	 11% 77% 9% 13%
2	1-i	261	 11% 82% • • 13%
2	2-2	261	 77% 9% 13%
2	2-i	261	 82% • • 13%
2	3-2	261	 77% 8% • 13%
2	3-i	261	 79% 6% • 13%
3	1-3	205	 11% 89% 9% •
3	1-j	205	 6% 93% 5% •
3	2-3	205	 89% 9% •
3	2-j	205	 94% • •
3	3-3	205	 87% 11% •
3	3-j	205	 92% • •
4	1-4	198	 19% 90% 8% • •
4	1-k	198	 17% 90% 7% • • •
4	2-4	198	 90% 8% • •
4	2-k	198	 90% 7% • • •
4	3-4	198	 87% 11% • •
4	3-k	198	 87% 10% • • •
5	1-5	287	 7% 69% • • 26%
5	1-l	287	 9% 71% • • 26%
5	2-5	287	 69% • • 26%
5	2-l	287	 71% • • 26%
5	3-5	287	 69% • • 26%

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Mol	Chain	Length	Quality of chain
5	3-1	287	
6	1-6	241	
6	1-m	241	
6	2-6	241	
6	2-m	241	
6	3-6	241	
6	3-m	241	
7	1-7	266	
7	1-n	266	
7	2-7	266	
7	2-n	266	
7	3-7	266	
7	3-n	266	
8	1-A	252	
8	1-a	252	
8	2-A	252	
8	2-a	252	
8	3-A	252	
8	3-a	252	
9	1-B	250	
9	1-b	250	
9	2-B	250	
9	2-b	250	
9	3-B	250	
9	3-b	250	

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Mol	Chain	Length	Quality of chain
10	1-C	258	
10	1-c	258	
10	2-C	258	
10	2-c	258	
10	3-C	258	
10	3-c	258	
11	1-D	254	
11	1-d	254	
11	2-D	254	
11	2-d	254	
11	3-D	254	
11	3-d	254	
12	1-E	260	
12	1-e	260	
12	2-E	260	
12	2-e	260	
12	3-E	260	
12	3-e	260	
13	1-F	234	
13	1-f	234	
13	2-F	234	
13	2-f	234	
13	3-F	234	
13	3-f	234	
14	1-G	288	

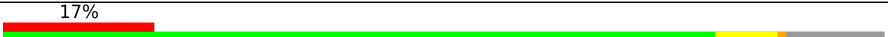
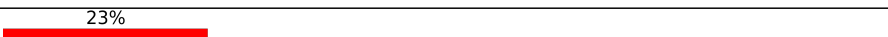
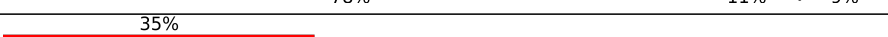
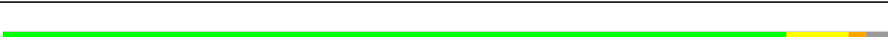
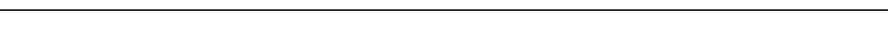
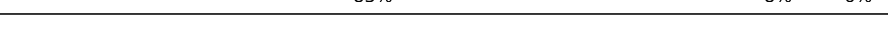
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Mol	Chain	Length	Quality of chain
14	1-g	288	 10% 78% 5% • 16%
14	2-G	288	 77% 6% • 16%
14	2-g	288	 78% 5% • 16%
14	3-G	288	 76% 7% • 16%
14	3-g	288	 76% 7% • 16%
15	1-H	467	 18% 75% 8% • 16%
15	2-H	467	 75% 8% • 16%
15	3-H	467	 72% 11% • 16%
16	1-I	437	 22% 81% 6% • 12%
16	2-I	437	 81% 5% • 12%
16	3-I	437	 79% 7% • 12%
17	1-J	405	 25% 87% 7% • 5%
17	2-J	405	 87% 7% • 5%
17	3-J	405	 84% 9% • 5%
18	1-K	428	 16% 79% 11% 9%
18	2-K	428	 79% 11% 9%
18	3-K	428	 78% 11% • 9%
19	1-L	437	 21% 81% 7% • 11%
19	2-L	437	 80% 7% • 11%
19	3-L	437	 77% 9% • 11%
20	1-M	434	 22% 81% 5% • 12%
20	2-M	434	 82% 5% • 12%
20	3-M	434	 79% 7% • 12%
21	1-N	945	 25% 85% 8% • 6%
21	2-N	945	 86% 8% • 6%

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Mol	Chain	Length	Quality of chain
21	3-N	945	
22	1-O	393	
22	2-O	393	
22	3-O	393	
23	1-P	445	
23	2-P	445	
23	3-P	445	
24	1-Q	434	
24	2-Q	434	
24	3-Q	434	
25	1-R	429	
25	2-R	429	
25	3-R	429	
26	1-S	523	
26	2-S	523	
26	3-S	523	
27	1-T	274	
27	2-T	274	
27	3-T	274	
28	1-U	338	
28	2-U	338	
28	3-U	338	
29	1-V	306	
29	2-V	306	
29	3-V	306	

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Mol	Chain	Length	Quality of chain
30	1-W	268	
30	2-W	268	
30	3-W	268	
31	1-X	156	
31	2-X	156	
31	3-X	156	
32	1-Y	89	
32	2-Y	89	
32	3-Y	89	
33	1-Z	993	
33	2-Z	993	
33	3-Z	993	

2 Entry composition [i](#)

There are 33 unique types of molecules in this entry. The entry contains 653142 atoms, of which 327135 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	1-1	196	Total	C	H	N	O	S	0	0
			2991	955	1479	250	300	7		
1	2-1	196	Total	C	H	N	O	S	0	0
			2991	955	1479	250	300	7		
1	3-1	196	Total	C	H	N	O	S	0	0
			2991	955	1479	250	300	7		
1	1-h	196	Total	C	H	N	O	S	0	0
			2991	955	1479	250	300	7		
1	2-h	196	Total	C	H	N	O	S	0	0
			2991	955	1479	250	300	7		
1	3-h	196	Total	C	H	N	O	S	0	0
			2991	955	1479	250	300	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	1-2	226	Total	C	H	N	O	S	0	0
			3436	1082	1717	298	332	7		
2	2-2	226	Total	C	H	N	O	S	0	0
			3436	1082	1717	298	332	7		
2	3-2	226	Total	C	H	N	O	S	0	0
			3436	1082	1717	298	332	7		
2	1-i	226	Total	C	H	N	O	S	0	0
			3436	1082	1717	298	332	7		
2	2-i	226	Total	C	H	N	O	S	0	0
			3436	1082	1717	298	332	7		
2	3-i	226	Total	C	H	N	O	S	0	0
			3436	1082	1717	298	332	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
3	1-3	204	Total	C	H	N	O	S	0	0
			3153	1010	1572	258	305	8		

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Mol	Chain	Residues	Atoms						AltConf	Trace
3	2-3	204	Total	C	H	N	O	S	0	0
			3153	1010	1572	258	305	8		
3	3-3	204	Total	C	H	N	O	S	0	0
			3153	1010	1572	258	305	8		
3	1-j	204	Total	C	H	N	O	S	0	0
			3153	1010	1572	258	305	8		
3	2-j	204	Total	C	H	N	O	S	0	0
			3153	1010	1572	258	305	8		
3	3-j	204	Total	C	H	N	O	S	0	0
			3153	1010	1572	258	305	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
4	1-4	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		
4	2-4	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		
4	3-4	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		
4	1-k	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		
4	2-k	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		
4	3-k	195	Total	C	H	N	O	S	0	0
			3130	992	1569	264	299	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	1-5	212	Total	C	H	N	O	S	0	0
			3237	1045	1593	280	312	7		
5	2-5	212	Total	C	H	N	O	S	0	0
			3237	1045	1593	280	312	7		
5	3-5	212	Total	C	H	N	O	S	0	0
			3237	1045	1593	280	312	7		
5	1-1	212	Total	C	H	N	O	S	0	0
			3237	1045	1593	280	312	7		
5	2-1	212	Total	C	H	N	O	S	0	0
			3237	1045	1593	280	312	7		
5	3-1	212	Total	C	H	N	O	S	0	0
			3237	1045	1593	280	312	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	1-6	222	Total	C	H	N	O	S	0	0
			3466	1115	1709	303	335	4		
6	2-6	222	Total	C	H	N	O	S	0	0
			3466	1115	1709	303	335	4		
6	3-6	222	Total	C	H	N	O	S	0	0
			3466	1115	1709	303	335	4		
6	1-m	222	Total	C	H	N	O	S	0	0
			3466	1115	1709	303	335	4		
6	2-m	222	Total	C	H	N	O	S	0	0
			3466	1115	1709	303	335	4		
6	3-m	222	Total	C	H	N	O	S	0	0
			3466	1115	1709	303	335	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
7	1-7	229	Total	C	H	N	O	S	0	0
			3581	1133	1791	306	344	7		
7	2-7	229	Total	C	H	N	O	S	0	0
			3581	1133	1791	306	344	7		
7	3-7	229	Total	C	H	N	O	S	0	0
			3581	1133	1791	306	344	7		
7	1-n	232	Total	C	H	N	O	S	0	0
			3634	1148	1819	311	349	7		
7	2-n	232	Total	C	H	N	O	S	0	0
			3634	1148	1819	311	349	7		
7	3-n	232	Total	C	H	N	O	S	0	0
			3634	1148	1819	311	349	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
8	1-A	241	Total	C	H	N	O	S	0	0
			3809	1214	1902	320	365	8		
8	2-A	241	Total	C	H	N	O	S	0	0
			3809	1214	1902	320	365	8		
8	3-A	241	Total	C	H	N	O	S	0	0
			3809	1214	1902	320	365	8		
8	1-a	241	Total	C	H	N	O	S	0	0
			3809	1214	1902	320	365	8		
8	2-a	241	Total	C	H	N	O	S	0	0
			3809	1214	1902	320	365	8		

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Mol	Chain	Residues	Atoms						AltConf	Trace
8	3-a	241	Total	C	H	N	O	S	0	0
			3809	1214	1902	320	365	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
9	1-B	250	Total 3844	C 1219	H 1929	N 315	O 377	S 4	0	0
9	2-B	250	Total 3844	C 1219	H 1929	N 315	O 377	S 4	0	0
9	3-B	250	Total 3844	C 1219	H 1929	N 315	O 377	S 4	0	0
9	1-b	250	Total 3844	C 1219	H 1929	N 315	O 377	S 4	0	0
9	2-b	250	Total 3844	C 1219	H 1929	N 315	O 377	S 4	0	0
9	3-b	250	Total 3844	C 1219	H 1929	N 315	O 377	S 4	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
10	1-C	244	Total 3806	C 1201	H 1902	N 321	O 379	S 3	0	0
10	2-C	244	Total 3806	C 1201	H 1902	N 321	O 379	S 3	0	0
10	3-C	244	Total 3806	C 1201	H 1902	N 321	O 379	S 3	0	0
10	1-c	244	Total 3806	C 1201	H 1902	N 321	O 379	S 3	0	0
10	2-c	244	Total 3806	C 1201	H 1902	N 321	O 379	S 3	0	0
10	3-c	244	Total 3806	C 1201	H 1902	N 321	O 379	S 3	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
11	1-D	240	Total	C	H	N	O	S	0	0
			3774	1176	1893	329	372	4		
11	2-D	240	Total	C	H	N	O	S	0	0
			3774	1176	1893	329	372	4		

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Mol	Chain	Residues	Atoms						AltConf	Trace
11	3-D	240	Total	C	H	N	O	S	0	0
			3774	1176	1893	329	372	4		
11	1-d	240	Total	C	H	N	O	S	0	0
			3774	1176	1893	329	372	4		
11	2-d	240	Total	C	H	N	O	S	0	0
			3774	1176	1893	329	372	4		
11	3-d	240	Total	C	H	N	O	S	0	0
			3774	1176	1893	329	372	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
12	1-E	242	Total 3698	C 1162	H 1837	N 314	O 378	S 7	0	0
12	2-E	242	Total 3698	C 1162	H 1837	N 314	O 378	S 7	0	0
12	3-E	242	Total 3698	C 1162	H 1837	N 314	O 378	S 7	0	0
12	1-e	242	Total 3698	C 1162	H 1837	N 314	O 378	S 7	0	0
12	2-e	242	Total 3698	C 1162	H 1837	N 314	O 378	S 7	0	0
12	3-e	242	Total 3698	C 1162	H 1837	N 314	O 378	S 7	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
13	1-F	233	Total	C	H	N	O	S	0	0
			3595	1129	1800	312	350	4		
13	2-F	233	Total	C	H	N	O	S	0	0
			3595	1129	1800	312	350	4		
13	3-F	233	Total	C	H	N	O	S	0	0
			3595	1129	1800	312	350	4		
13	1-f	231	Total	C	H	N	O	S	0	0
			3551	1114	1778	307	348	4		
13	2-f	231	Total	C	H	N	O	S	0	0
			3551	1114	1778	307	348	4		
13	3-f	231	Total	C	H	N	O	S	0	0
			3551	1114	1778	307	348	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
14	1-G	243	Total	C	H	N	O	S	0	0
			3777	1203	1885	329	356	4		
14	2-G	243	Total	C	H	N	O	S	0	0
			3777	1203	1885	329	356	4		
14	3-G	243	Total	C	H	N	O	S	0	0
			3777	1203	1885	329	356	4		
14	1-g	243	Total	C	H	N	O	S	0	0
			3776	1203	1884	329	356	4		
14	2-g	243	Total	C	H	N	O	S	0	0
			3776	1203	1884	329	356	4		
14	3-g	243	Total	C	H	N	O	S	0	0
			3776	1203	1884	329	356	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
15	1-H	390	Total	C	H	N	O	S	0	0
			6183	1920	3130	546	570	17		
15	2-H	390	Total	C	H	N	O	S	0	0
			6183	1920	3130	546	570	17		
15	3-H	390	Total	C	H	N	O	S	0	0
			6183	1920	3130	546	570	17		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
16	1-I	385	Total	C	H	N	O	S	0	0
			6115	1899	3093	508	598	17		
16	2-I	385	Total	C	H	N	O	S	0	0
			6115	1899	3093	508	598	17		
16	3-I	385	Total	C	H	N	O	S	0	0
			6115	1899	3093	508	598	17		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
17	1-J	386	Total	C	H	N	O	S	0	0
			6190	1906	3157	543	567	17		
17	2-J	386	Total	C	H	N	O	S	0	0
			6190	1906	3157	543	567	17		
17	3-J	386	Total	C	H	N	O	S	0	0
			6190	1906	3157	543	567	17		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
18	1-K	389	Total	C	H	N	O	S	0	0
			6220	1933	3142	540	595	10		
18	2-K	389	Total	C	H	N	O	S	0	0
			6220	1933	3142	540	595	10		
18	3-K	389	Total	C	H	N	O	S	0	0
			6220	1933	3142	540	595	10		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
19	1-L	388	Total	C	H	N	O	S	0	0
			6240	1942	3158	548	580	12		
19	2-L	388	Total	C	H	N	O	S	0	0
			6240	1942	3158	548	580	12		
19	3-L	388	Total	C	H	N	O	S	0	0
			6240	1942	3158	548	580	12		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
20	1-M	381	Total	C	H	N	O	S	0	0
			6043	1870	3057	524	580	12		
20	2-M	381	Total	C	H	N	O	S	0	0
			6043	1870	3057	524	580	12		
20	3-M	381	Total	C	H	N	O	S	0	0
			6043	1870	3057	524	580	12		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
21	1-N	890	Total	C	H	N	O	S	0	0
			13843	4373	6961	1156	1325	28		
21	2-N	890	Total	C	H	N	O	S	0	0
			13843	4373	6961	1156	1325	28		
21	3-N	890	Total	C	H	N	O	S	0	0
			13843	4373	6961	1156	1325	28		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
22	1-O	388	Total	C	H	N	O	S	0	0
			6400	2051	3214	519	608	8		
22	2-O	388	Total	C	H	N	O	S	0	0
			6400	2051	3214	519	608	8		
22	3-O	388	Total	C	H	N	O	S	0	0
			6400	2051	3214	519	608	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
23	1-P	440	Total	C	H	N	O	S	0	0
			7302	2297	3694	604	697	10		
23	2-P	440	Total	C	H	N	O	S	0	0
			7302	2297	3694	604	697	10		
23	3-P	440	Total	C	H	N	O	S	0	0
			7302	2297	3694	604	697	10		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
24	1-Q	434	Total	C	H	N	O	S	0	0
			7023	2225	3524	577	681	16		
24	2-Q	434	Total	C	H	N	O	S	0	0
			7023	2225	3524	577	681	16		
24	3-Q	434	Total	C	H	N	O	S	0	0
			7023	2225	3524	577	681	16		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
25	1-R	381	Total	C	H	N	O	S	0	0
			6145	1955	3085	502	593	10		
25	2-R	381	Total	C	H	N	O	S	0	0
			6145	1955	3085	502	593	10		
25	3-R	381	Total	C	H	N	O	S	0	0
			6145	1955	3085	502	593	10		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
26	1-S	475	Total	C	H	N	O	S	0	0
			7833	2488	3939	653	738	15		

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Mol	Chain	Residues	Atoms						AltConf	Trace
26	2-S	475	Total	C	H	N	O	S	0	0
			7833	2488	3939	653	738	15		
26	3-S	475	Total	C	H	N	O	S	0	0
			7833	2488	3939	653	738	15		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
27	1-T	266	Total	C	H	N	O	S	0	0
			4354	1405	2162	349	432	6		
27	2-T	266	Total	C	H	N	O	S	0	0
			4354	1405	2162	349	432	6		
27	3-T	266	Total	C	H	N	O	S	0	0
			4354	1405	2162	349	432	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
28	1-U	298	Total	C	H	N	O	S	0	0
			4776	1496	2403	404	466	7		
28	2-U	298	Total	C	H	N	O	S	0	0
			4776	1496	2403	404	466	7		
28	3-U	298	Total	C	H	N	O	S	0	0
			4776	1496	2403	404	466	7		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
29	1-V	289	Total	C	H	N	O	S	0	0
			4549	1425	2275	389	446	14		
29	2-V	289	Total	C	H	N	O	S	0	0
			4549	1425	2275	389	446	14		
29	3-V	289	Total	C	H	N	O	S	0	0
			4549	1425	2275	389	446	14		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
30	1-W	197	Total	C	H	N	O	S	0	0
			3076	962	1542	269	300	3		
30	2-W	197	Total	C	H	N	O	S	0	0
			3076	962	1542	269	300	3		

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Mol	Chain	Residues	Atoms						AltConf	Trace
30	3-W	197	Total	C	H	N	O	S	0	0
			3076	962	1542	269	300	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
31	1-X	127	Total	C	H	N	O	S	0	0
			2050	664	1018	169	195	4		
31	2-X	127	Total	C	H	N	O	S	0	0
			2050	664	1018	169	195	4		
31	3-X	127	Total	C	H	N	O	S	0	0
			2050	664	1018	169	195	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1-Y	51	Total	C	H	N	O	0	0
			831	264	396	69	102		
32	2-Y	51	Total	C	H	N	O	0	0
			831	264	396	69	102		
32	3-Y	51	Total	C	H	N	O	0	0
			831	264	396	69	102		

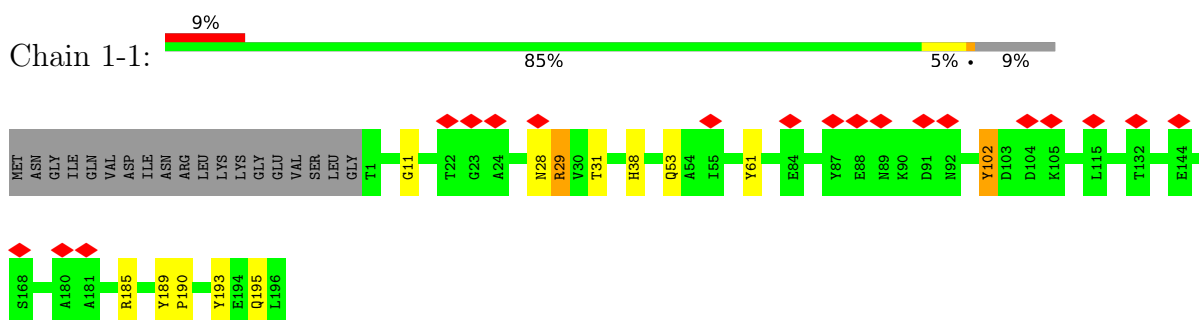
- Molecule 33 is a protein called 26S proteasome regulatory subunit RPN1.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	1-Z	906	Total	C	H	N	O	S	0	0
			13939	4416	6934	1150	1409	30		
33	2-Z	906	Total	C	H	N	O	S	0	0
			13939	4416	6934	1150	1409	30		
33	3-Z	906	Total	C	H	N	O	S	0	0
			13939	4416	6934	1150	1409	30		

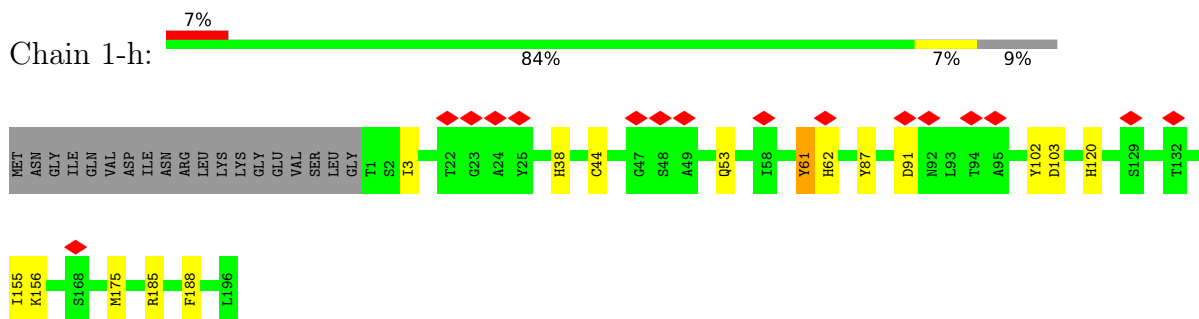
3 Residue-property plots [i](#)

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

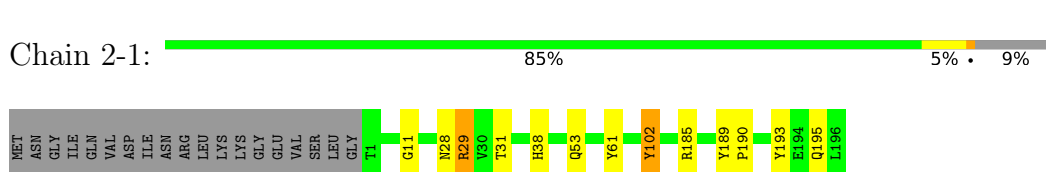
- Molecule 1: Proteasome subunit beta type-1



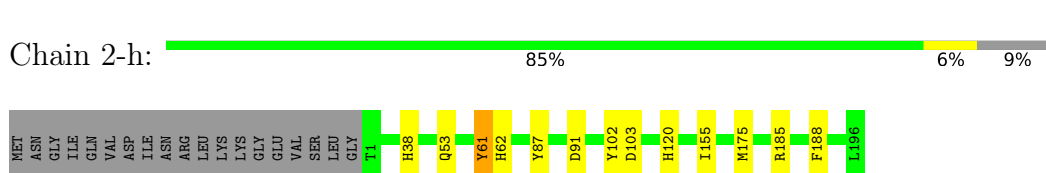
- Molecule 1: Proteasome subunit beta type-1



- Molecule 1: Proteasome subunit beta type-1

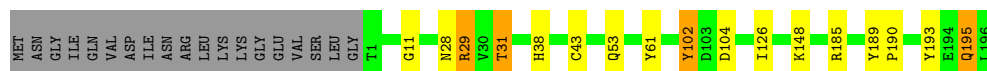


- Molecule 1: Proteasome subunit beta type-1



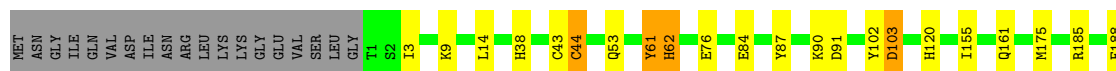
- Molecule 1: Proteasome subunit beta type-1

Chain 3-1:  83% 6% 9%



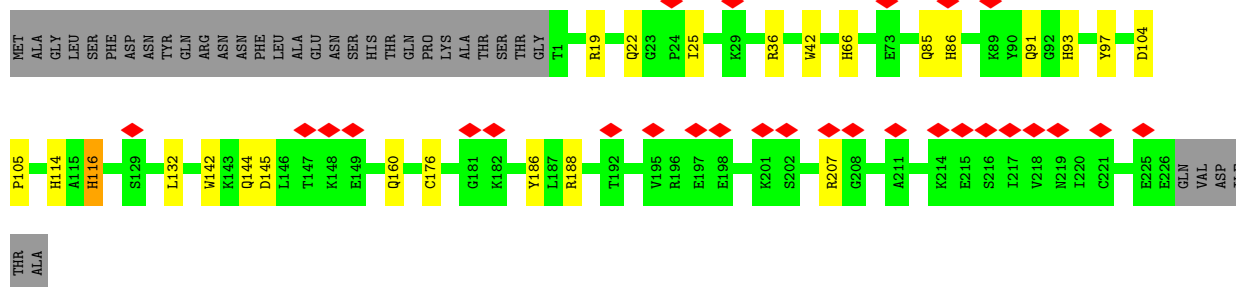
- Molecule 1: Proteasome subunit beta type-1

Chain 3-h:  81% 8% 9%



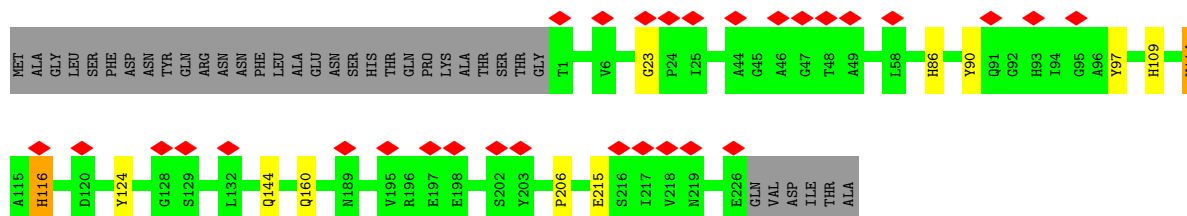
- Molecule 2: Proteasome subunit beta type-2

Chain 1-2:  11% 77% 9% 13%



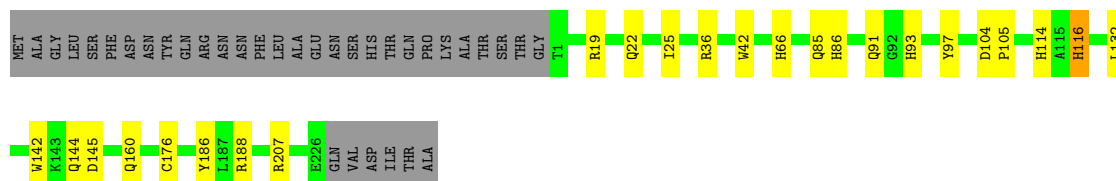
- Molecule 2: Proteasome subunit beta type-2

Chain 1-i:  11% 82% 9% 13%



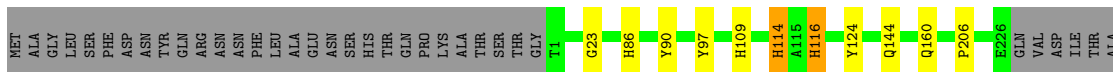
- Molecule 2: Proteasome subunit beta type-2

Chain 2-2:  77% 9% 13%



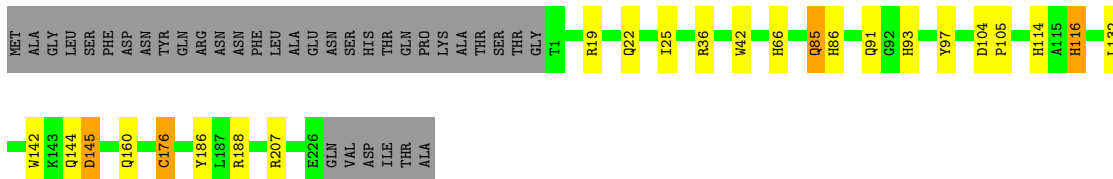
- Molecule 2: Proteasome subunit beta type-2

Chain 2-i:  82% 13%



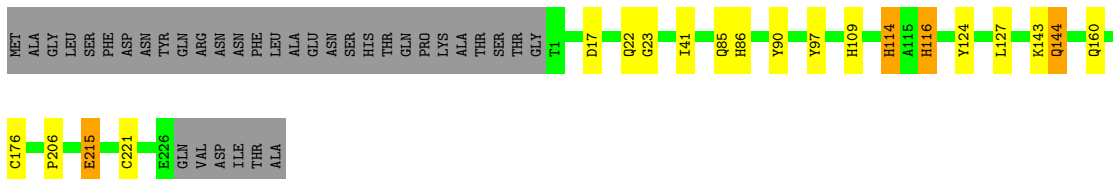
- Molecule 2: Proteasome subunit beta type-2

Chain 3-2:  77% 8% 13%

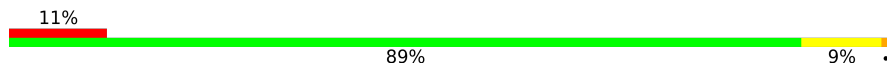


- Molecule 2: Proteasome subunit beta type-2

Chain 3-i:  79% 6% 13%

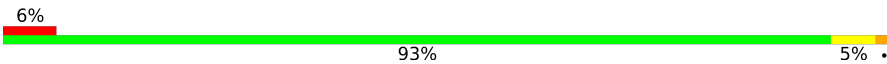


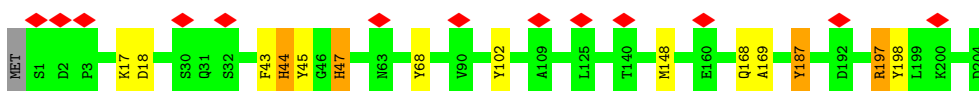
- Molecule 3: Proteasome subunit beta type-3

Chain 1-3:  11% 89% 9%



- Molecule 3: Proteasome subunit beta type-3

Chain 1-j:  6% 93% 5%



- Molecule 3: Proteasome subunit beta type-3

Chain 2-3:  89% 9%



- Molecule 3: Proteasome subunit beta type-3



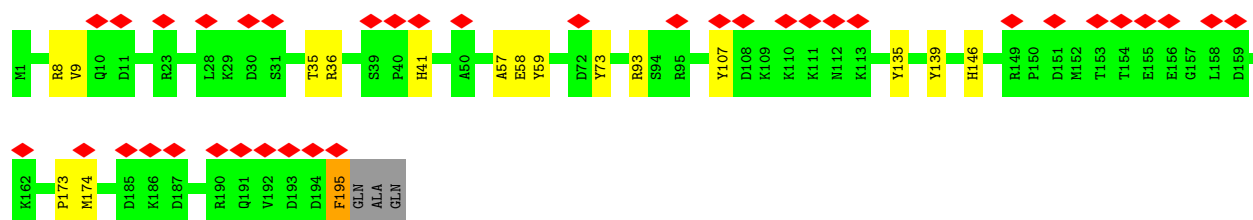
- Molecule 3: Proteasome subunit beta type-3



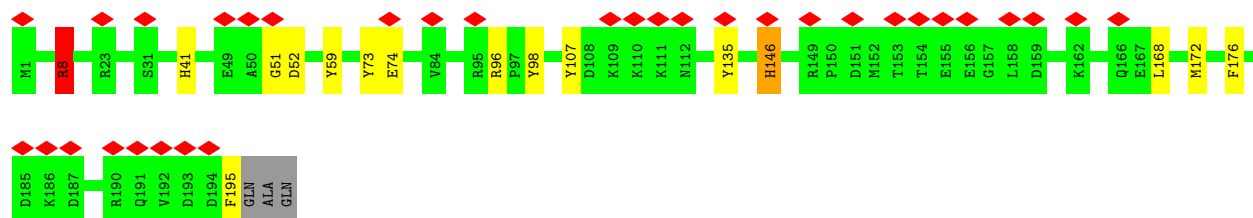
- Molecule 3: Proteasome subunit beta type-3



- Molecule 4: Proteasome subunit beta type-4



- Molecule 4: Proteasome subunit beta type-4



- Molecule 4: Proteasome subunit beta type-4





- Molecule 4: Proteasome subunit beta type-4

Chain 2-k: 90% 7% ..



- Molecule 4: Proteasome subunit beta type-4

Chain 3-4: 87% 11% ..



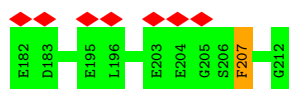
- Molecule 4: Proteasome subunit beta type-4

Chain 3-k: 87% 10% ..



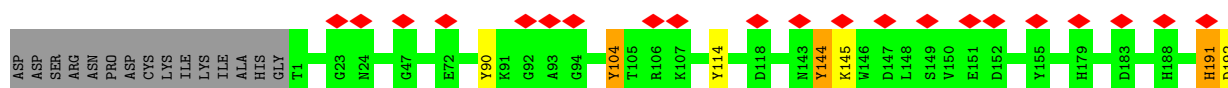
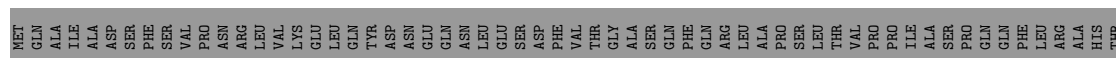
- Molecule 5: Proteasome subunit beta type-5

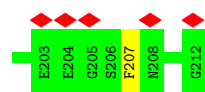
Chain 1-5: 7% 69% 26%



- Molecule 5: Proteasome subunit beta type-5

Chain 1-1: 9% 71% 26%





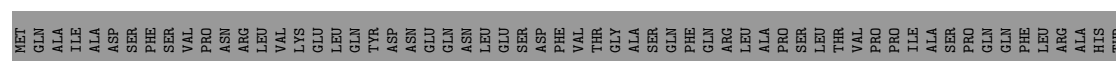
- Molecule 5: Proteasome subunit beta type-5

Chain 2-5: 69% 26%



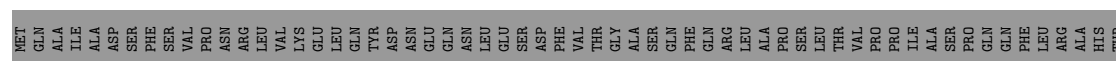
- Molecule 5: Proteasome subunit beta type-5

Chain 2-1: 71% 26%



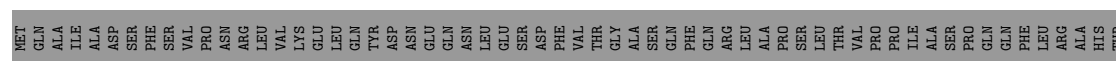
- Molecule 5: Proteasome subunit beta type-5

Chain 3-5: 69% 26%



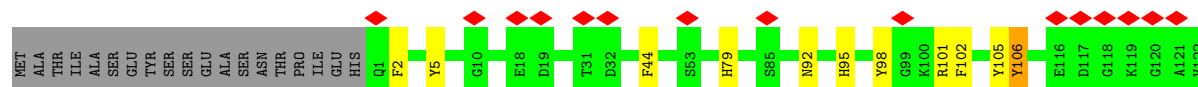
- Molecule 5: Proteasome subunit beta type-5

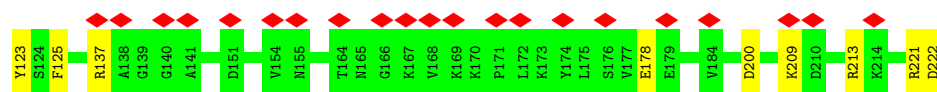
Chain 3-1: 68% 5% 26%



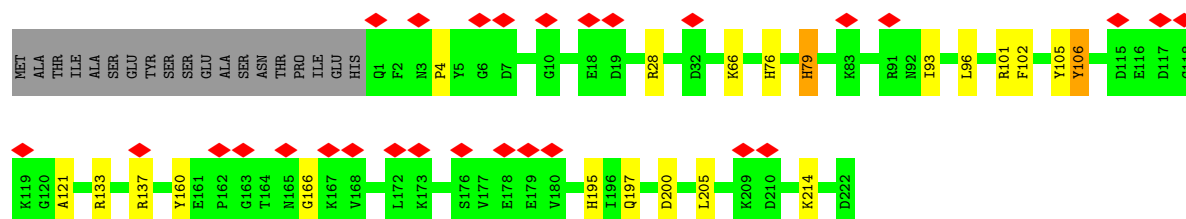
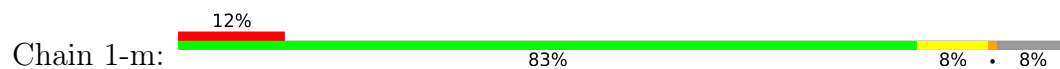
- Molecule 6: Proteasome subunit beta type-6

Chain 1-6: 15% 84% 8% 8%

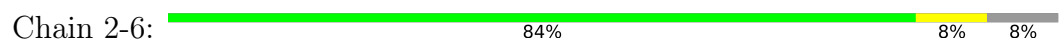




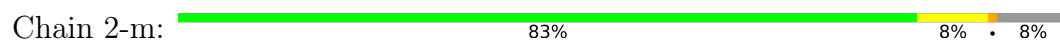
• Molecule 6: Proteasome subunit beta type-6



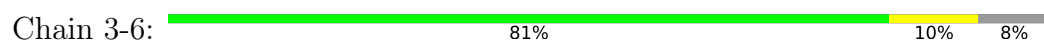
• Molecule 6: Proteasome subunit beta type-6



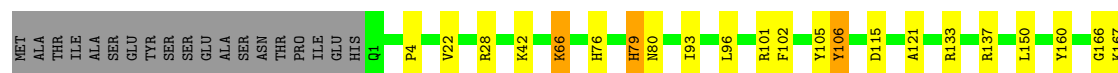
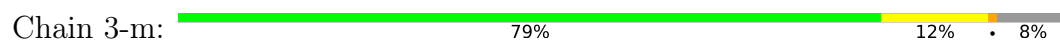
• Molecule 6: Proteasome subunit beta type-6



• Molecule 6: Proteasome subunit beta type-6

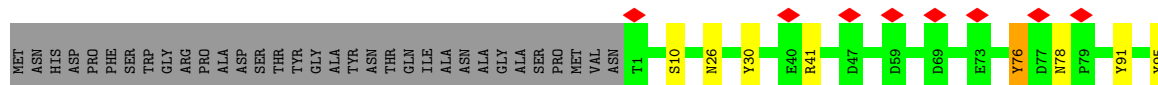
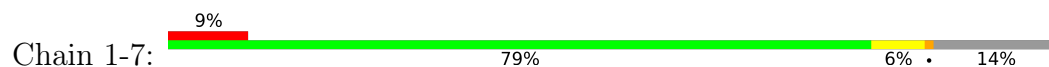


• Molecule 6: Proteasome subunit beta type-6

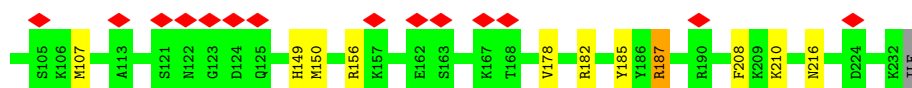
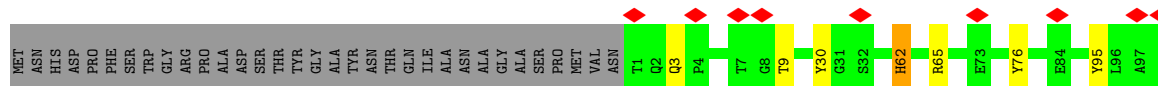
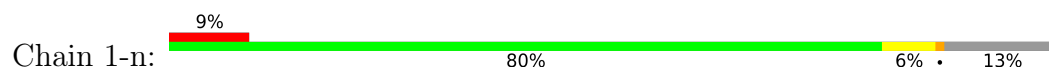




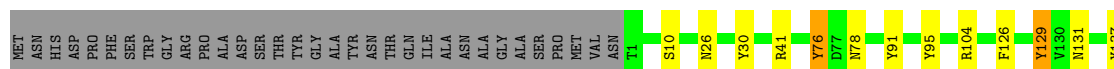
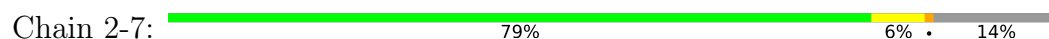
- Molecule 7: Proteasome subunit beta type-7



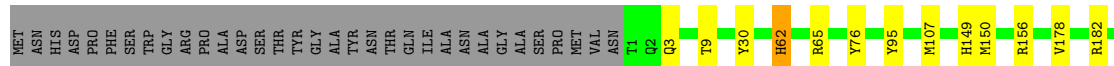
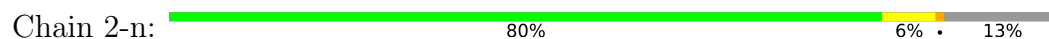
- Molecule 7: Proteasome subunit beta type-7



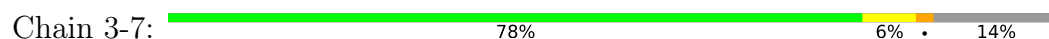
- Molecule 7: Proteasome subunit beta type-7

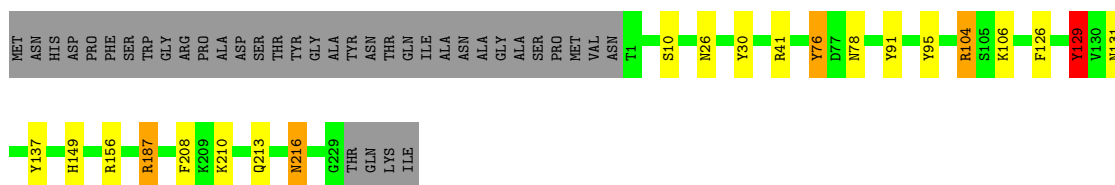


- Molecule 7: Proteasome subunit beta type-7



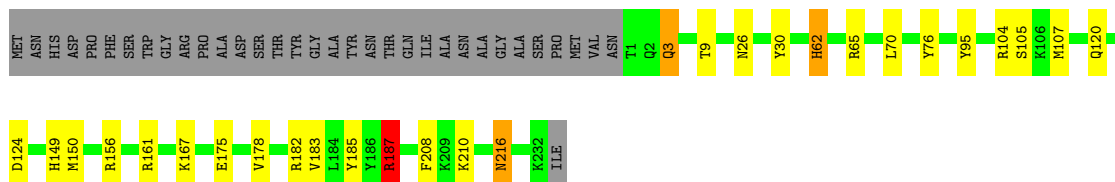
- Molecule 7: Proteasome subunit beta type-7





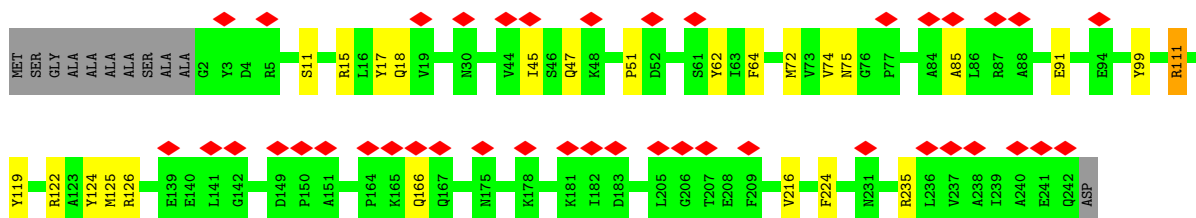
- Molecule 7: Proteasome subunit beta type-7

Chain 3-n: 77% 9% 13%



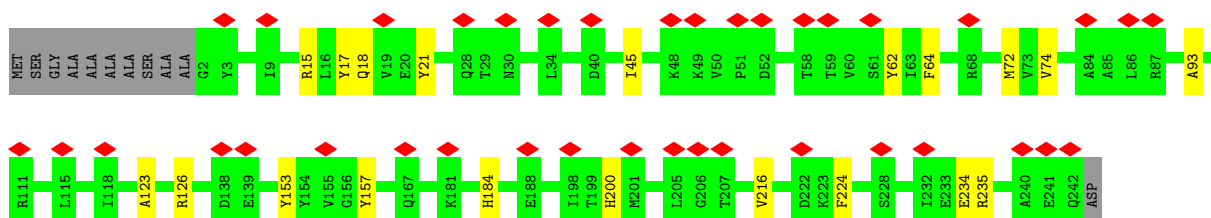
- Molecule 8: Proteasome subunit alpha type-1

Chain 1-A: 16% 86% 10%



- Molecule 8: Proteasome subunit alpha type-1

Chain 1-a: 15% 88% 8%



- Molecule 8: Proteasome subunit alpha type-1

Chain 2-A: 86% 10%



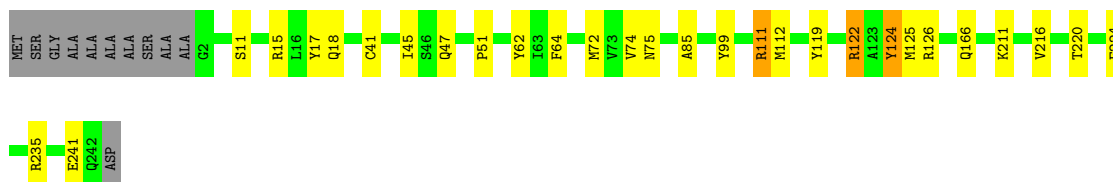
- Molecule 8: Proteasome subunit alpha type-1

Chain 2-a: 88% 8%



- Molecule 8: Proteasome subunit alpha type-1

Chain 3-A: 84% 10% . .



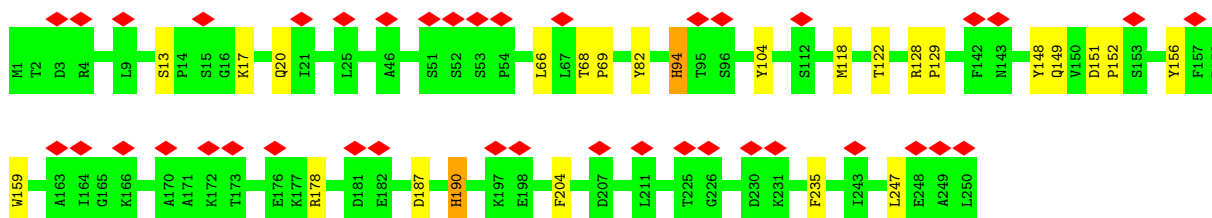
- Molecule 8: Proteasome subunit alpha type-1

Chain 3-a: 83% 12% .



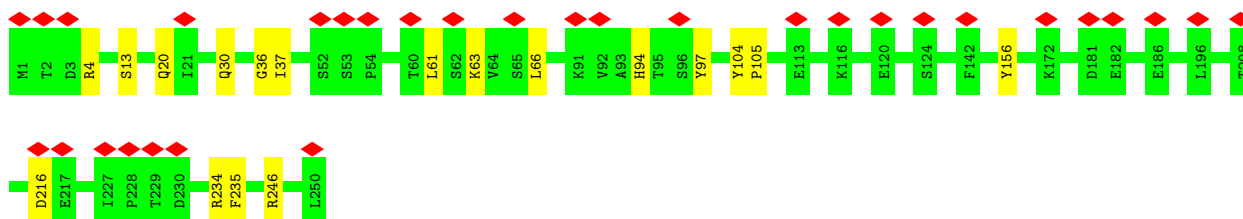
- Molecule 9: Proteasome subunit alpha type-2

Chain 1-B: 16% 90% 9% .



- Molecule 9: Proteasome subunit alpha type-2

Chain 1-b: 12% 93% 7%



- Molecule 9: Proteasome subunit alpha type-2

Chain 2-B: 91% 8% .



- Molecule 9: Proteasome subunit alpha type-2



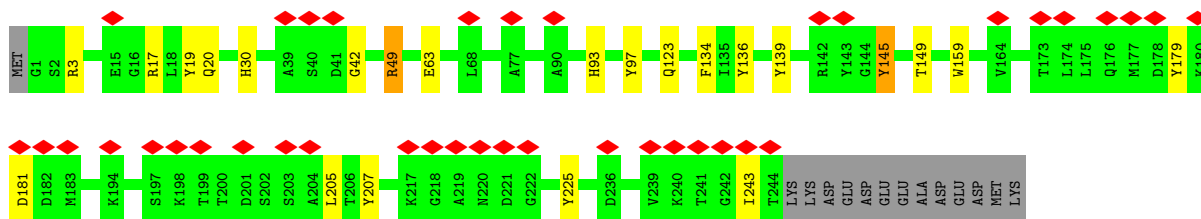
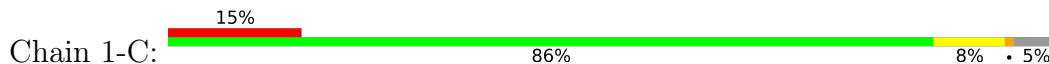
- Molecule 9: Proteasome subunit alpha type-2



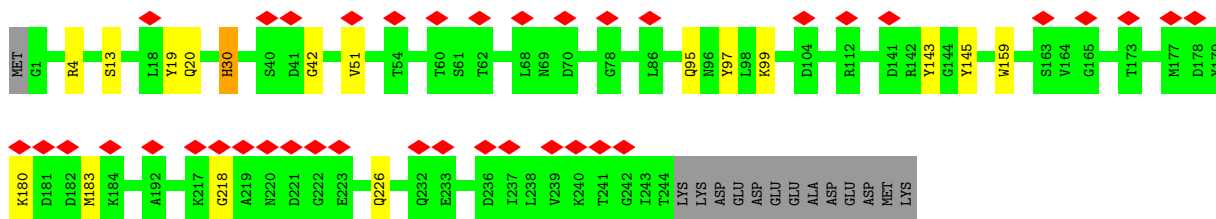
- Molecule 9: Proteasome subunit alpha type-2



- Molecule 10: Proteasome subunit alpha type-3

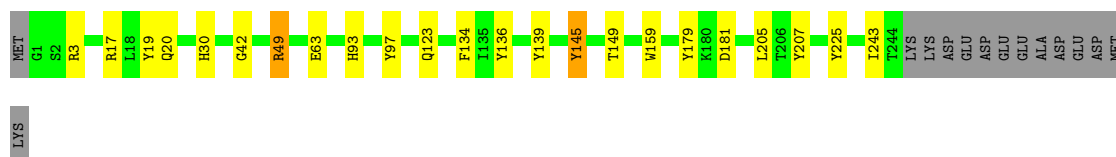


- Molecule 10: Proteasome subunit alpha type-3



- Molecule 10: Proteasome subunit alpha type-3





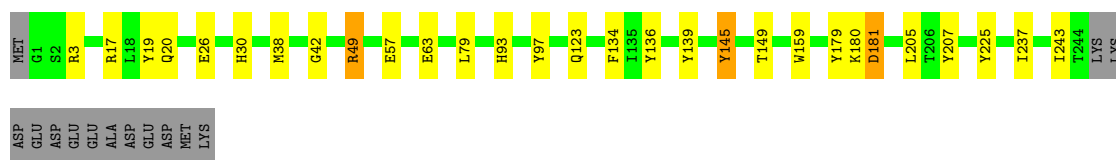
- Molecule 10: Proteasome subunit alpha type-3

Chain 2-c: 88% 6% 5%



- Molecule 10: Proteasome subunit alpha type-3

Chain 3-C: 83% 10% 5%



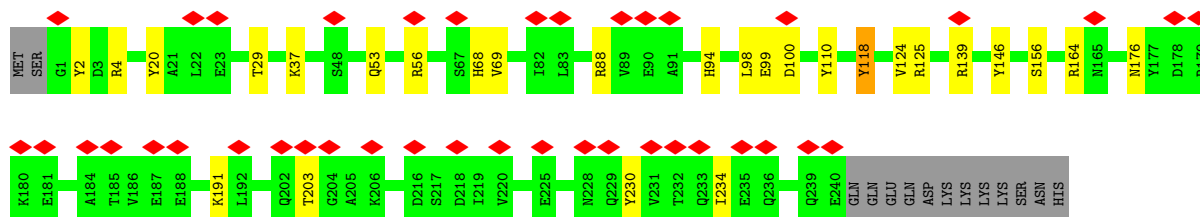
- Molecule 10: Proteasome subunit alpha type-3

Chain 3-c: 86% 7% 5%



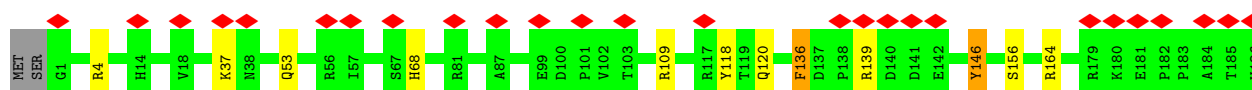
- Molecule 11: Proteasome subunit alpha type-4

Chain 1-D: 16% 84% 10% 6%



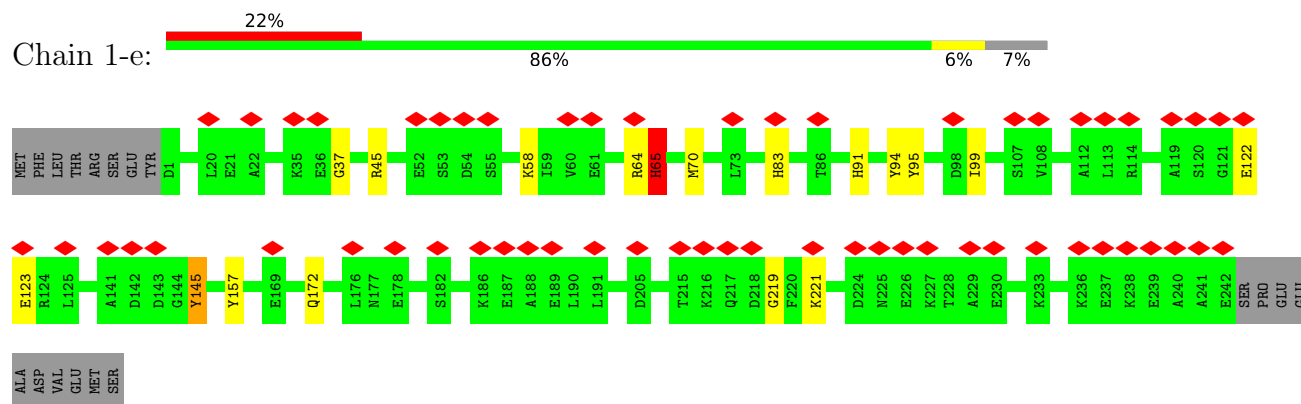
- Molecule 11: Proteasome subunit alpha type-4

Chain 1-d: 18% 87% 6% 6%

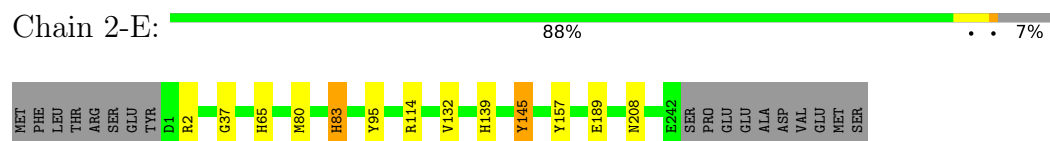




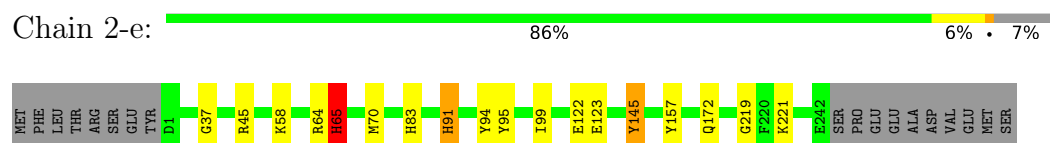
• Molecule 12: Proteasome subunit alpha type-5



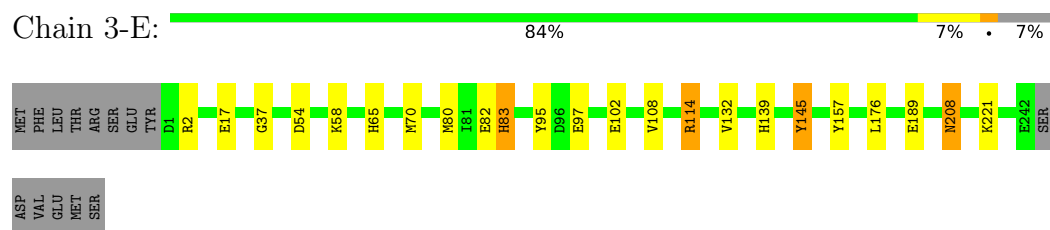
• Molecule 12: Proteasome subunit alpha type-5



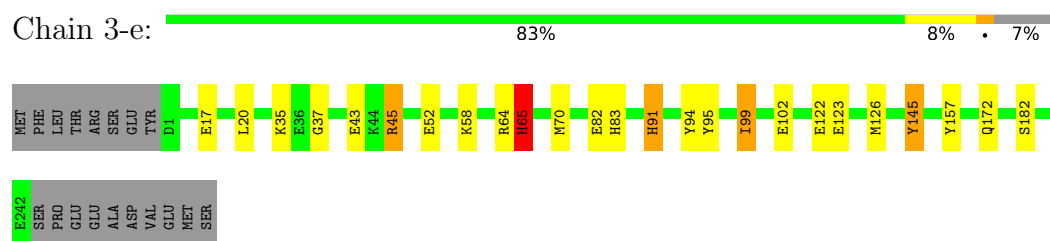
• Molecule 12: Proteasome subunit alpha type-5



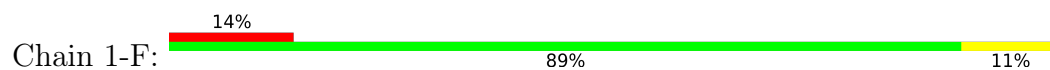
• Molecule 12: Proteasome subunit alpha type-5

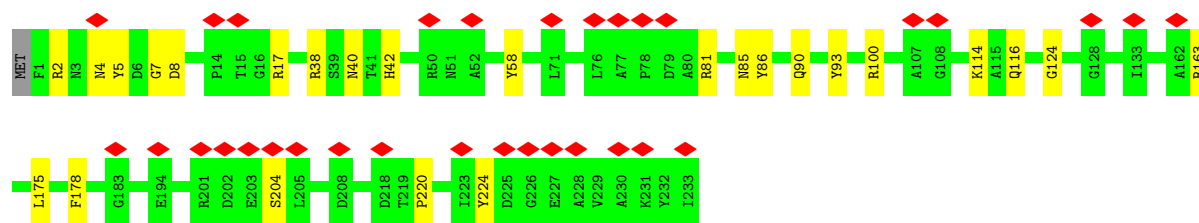


• Molecule 12: Proteasome subunit alpha type-5

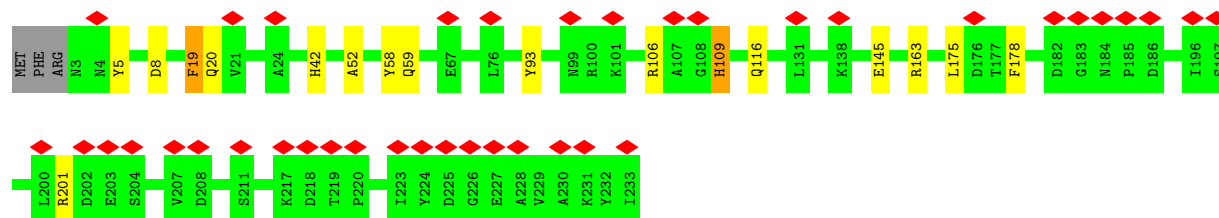


• Molecule 13: Proteasome subunit alpha type-6

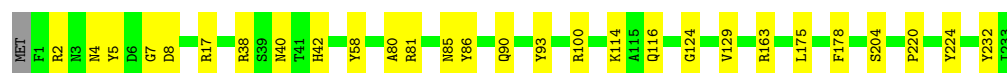




• Molecule 13: Proteasome subunit alpha type-6



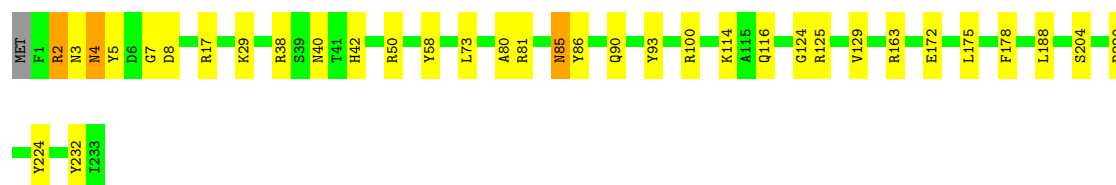
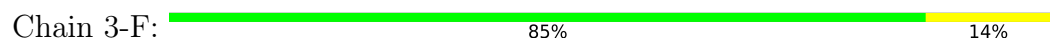
• Molecule 13: Proteasome subunit alpha type-6



• Molecule 13: Proteasome subunit alpha type-6



• Molecule 13: Proteasome subunit alpha type-6



• Molecule 13: Proteasome subunit alpha type-6



ASP
ASP
SER
SER
ASP
ASN
VAL
MET
SER
SER
ASP
ASP
GLU
ASN
ALA
PRO
VAL
ALA
THR
THR
ASN
ALA
ASN
THR
THR
ASP
GLN
GLY
GLY
ASP
ILE
HIS
LEU
GLU

- Molecule 14: Probable proteasome subunit alpha type-7

Chain 3-g:  76% 7% 16%

MET THR SER ILE GLY T2 G3 Y4 F11 S12 P13 R16 K48 T51 Y74 H83 R87 E91 R111 Y115 Y122 N140 M146 S150 L172 L175 H179 I195 E205 C215 E219 H224 Y244 GLY ASP ASP ASP

GLU ASP GLU ASP ASP SER ASP ASN VAL MET SER SER ASP ASP GLU ASP PRO ALA THR THR ASN ASN THR THR ASN ALA THR

- Molecule 15: 26S protease regulatory subunit 7 homolog

Chain 1-H:  18% 75% 8% 16%

MET PRO PRO LYS GLU ASP TRP GLU LYS TYR LYS ALA PRO LEU GLU ASP ASP LYS LYS PRO ASP ASP LYS ILE VAL PRO LEU LYS THR GLY ASP ILE GLN VAL LYS SER TYR GLY A42 A43 P44 Y45 A46 A47 K48 L49 K50 Q51 T52 E53 N54 D55 L56 K57 D58 A61

R62 R66 V69 K70 E71 S72 D73 A77 P78 S79 H80 L81 W82 D83 R83 K107 GLY ASN GLY GLU SER LEU THR THR THR ASP ASN ASN LYS SER GLY ASN SER A42 A43 P44 Y45 A46 A47 K48 L49 K50 Q51 T52 E53 N54 D55 L56 K57 D58 A61

L149 K150 Q151 I152 A153 K154 F155 L159 G160 E161 R162 V163 T166 D167 I168 S179 K180 Y181 E184 L185 P186 D192 P193 S194 E201 E202 D205 V206 T207 D210 C214 E223 V224 L227 L230 S231 P232 E233 R234 T237 L238 Q239 I240 D241 P242 P243

I246 L247 F271 V274 E278 L279 V280 R289 M290 P297 K301 K302 A303 I305 E310 I311 D312 A313 V314 G315 G316 A317 D320 D321 G322 A323 G324 E335 L336 P345 K350 V351 M352 F353 N356 R357 T360 R373 F389 H392 R400

R420 R434 K441 L444 K445 Y454 Y466 W467

- Molecule 15: 26S protease regulatory subunit 7 homolog

Chain 2-H:  75% 8% 16%

MET PRO PRO LYS GLU ASP TRP GLU LYS TYR LYS ALA PRO LEU GLU ASP ASP LYS ILE VAL PRO LEU LYS THR GLY ASP ILE GLN VAL LYS SER TYR GLY A42 A43 P44 Y45 A46 A47 K48 L49 K50 Q51 T52 E53 N54 D55 L56 K57 D58 A61

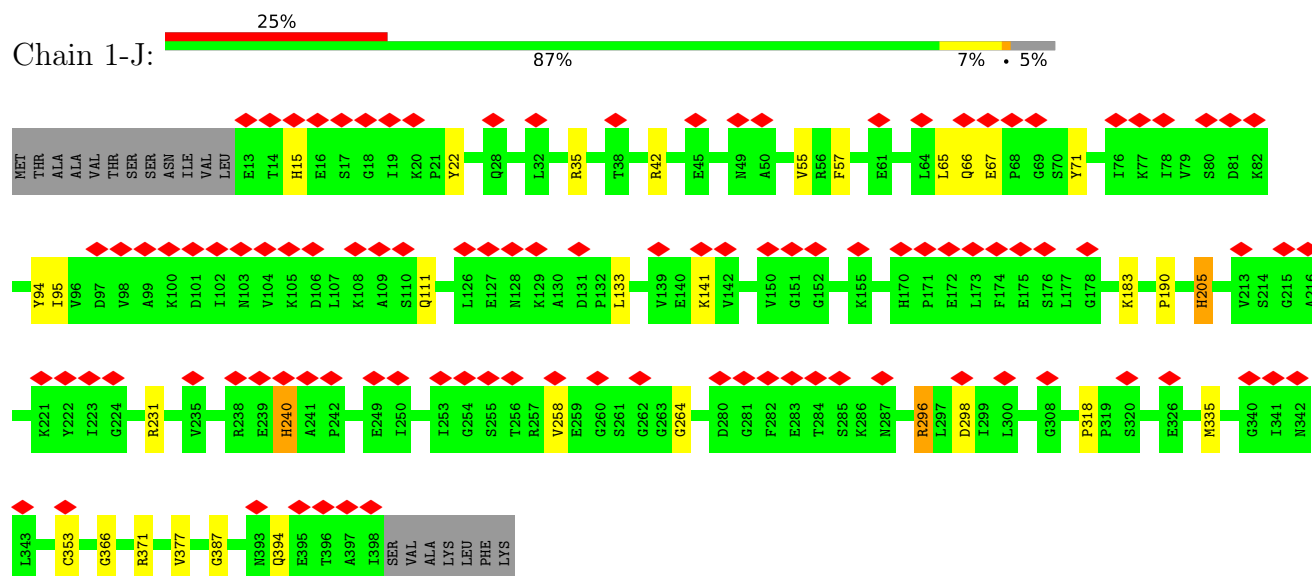
ASP GLU THR THR ASP ASN ASN ASN GLY SER ASN SER ASN SER ASN GLN GLN SER THR ASP ALA ASP ASP GLU ASP F155 S179 K180 Y181 P186 D192 P193 E223 V224 L227 E233 R234 P242 I246 F271 V274

L279 V280 R289 M290 A303 E310 I311 G315 G324 N352 F353 N356 R357 R373 F389 H392 R420 R434 Y454 Y466 W467

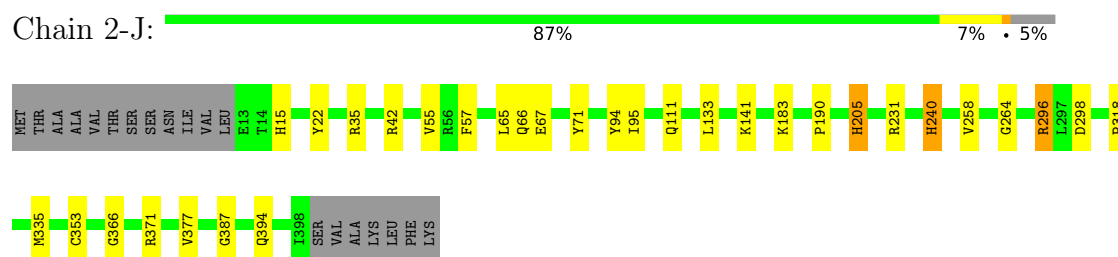
- Molecule 15: 26S protease regulatory subunit 7 homolog

Y436
L437

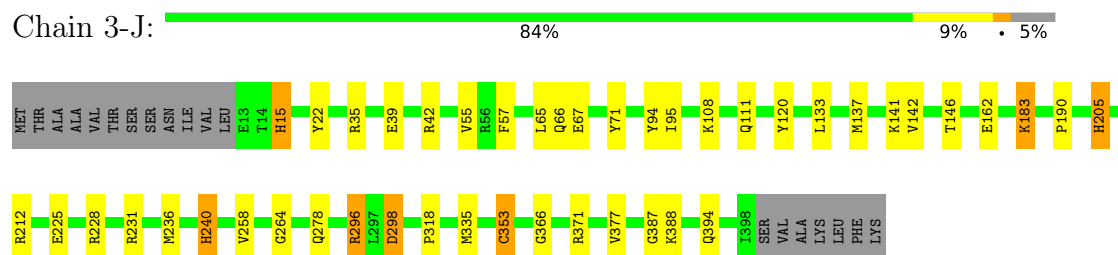
- Molecule 17: 26S protease regulatory subunit 8 homolog



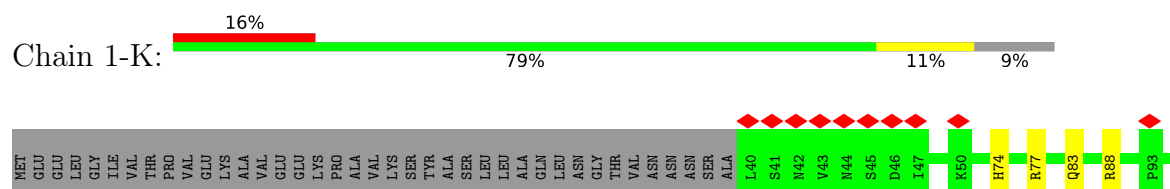
- Molecule 17: 26S protease regulatory subunit 8 homolog

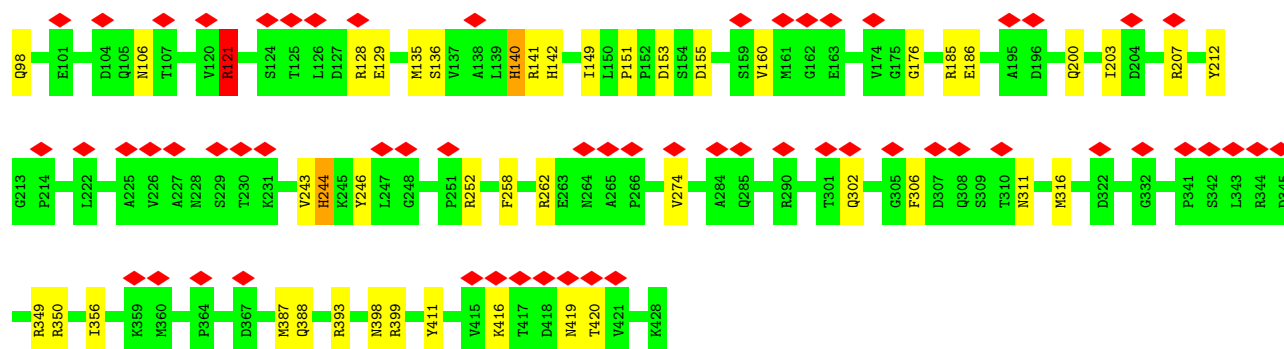


- Molecule 17: 26S protease regulatory subunit 8 homolog



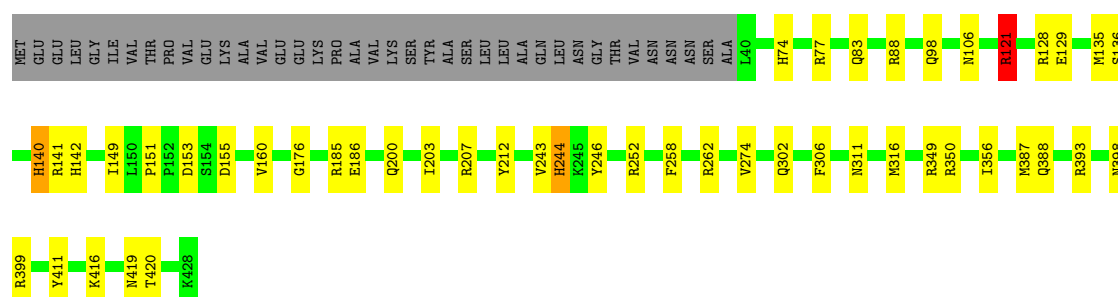
- Molecule 18: 26S protease regulatory subunit 6B homolog





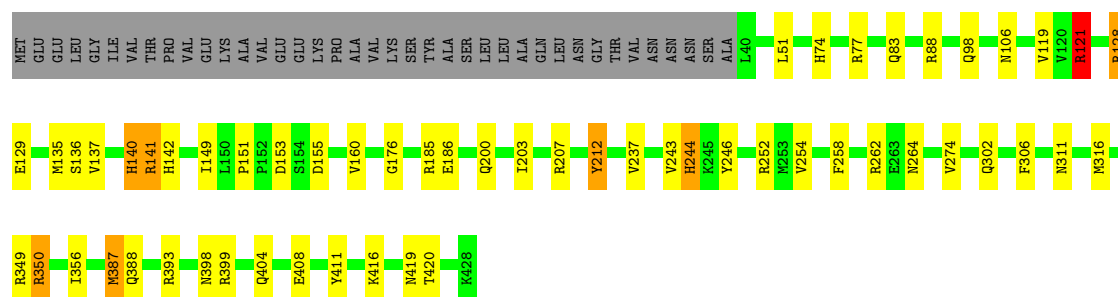
- Molecule 18: 26S protease regulatory subunit 6B homolog

Chain 2-K: 79% 11% 9%



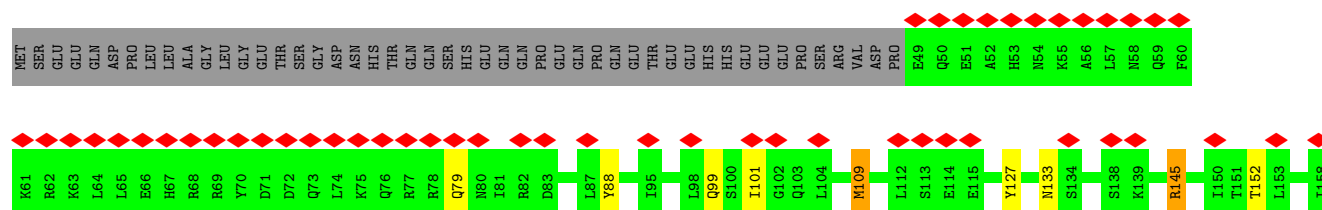
- Molecule 18: 26S protease regulatory subunit 6B homolog

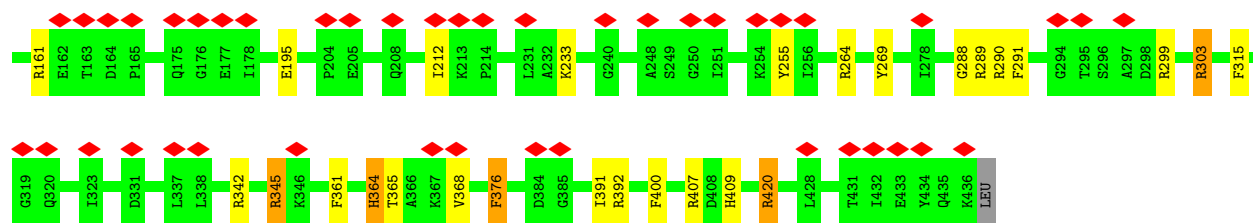
Chain 3-K: 78% 11% 9%



- Molecule 19: 26S protease subunit RPT4

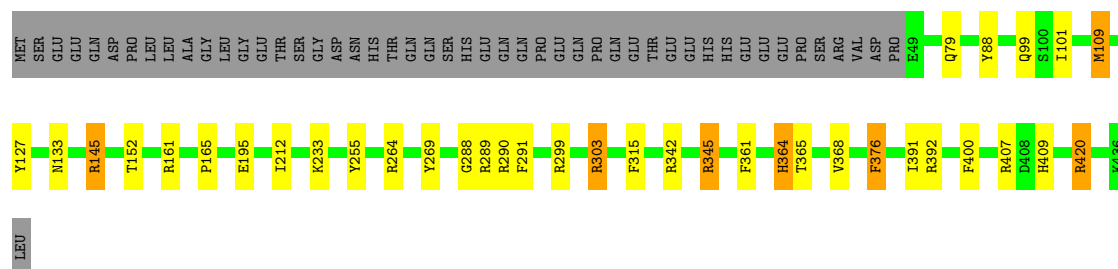
Chain 1-L: 21% 81% 7% 11%





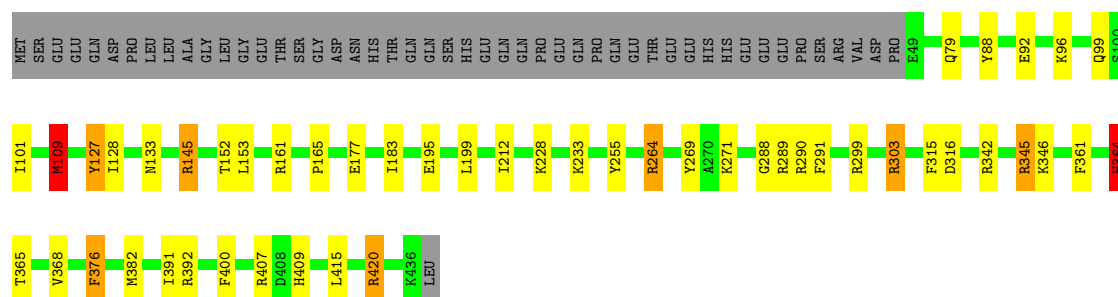
• Molecule 19: 26S protease subunit RPT4

Chain 2-L: 80% 7% 11%



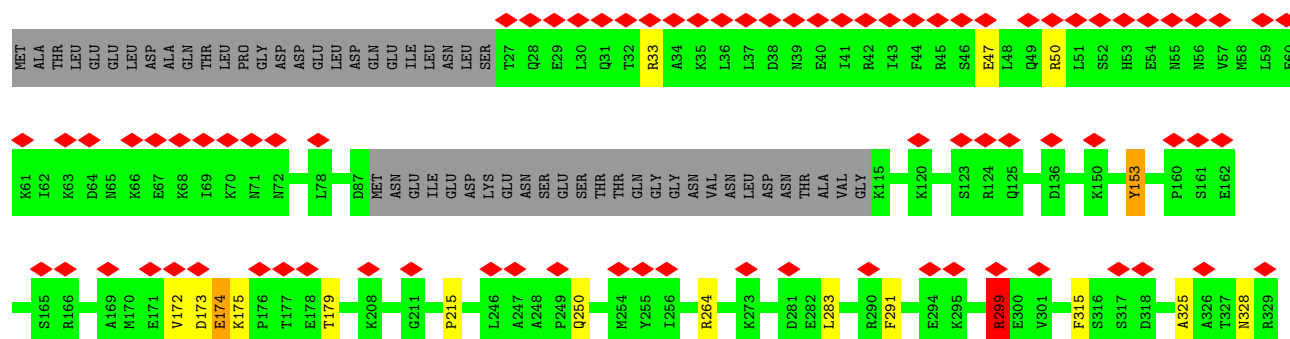
• Molecule 19: 26S protease subunit RPT4

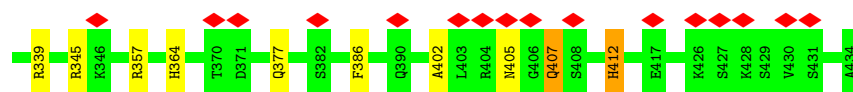
Chain 3-L: 77% 9% 11%



• Molecule 20: 26S protease regulatory subunit 6A

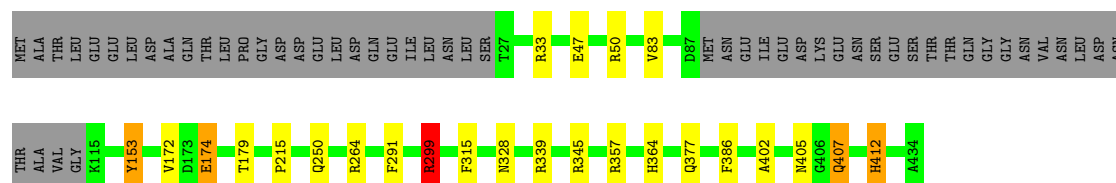
Chain 1-M: 22% 81% 5% 12%





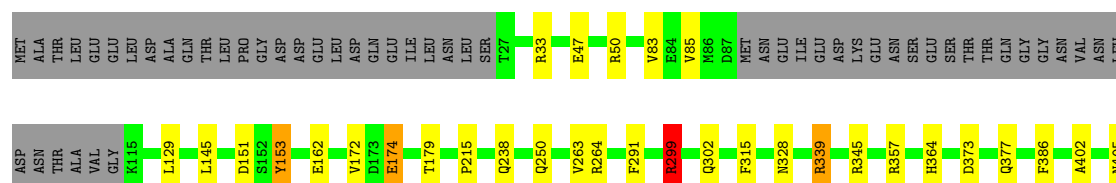
- Molecule 20: 26S protease regulatory subunit 6A

Chain 2-M: 82% 5% • 12%



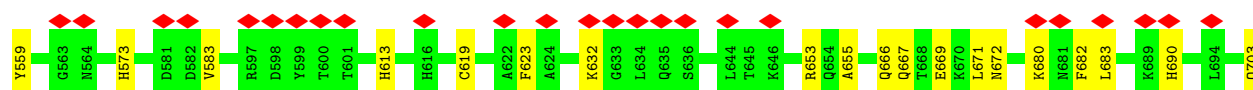
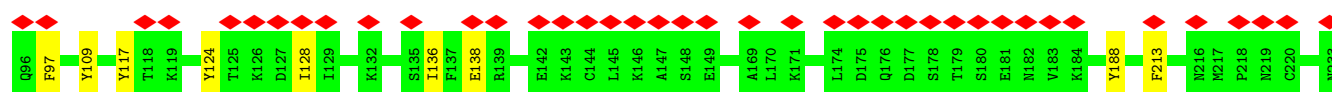
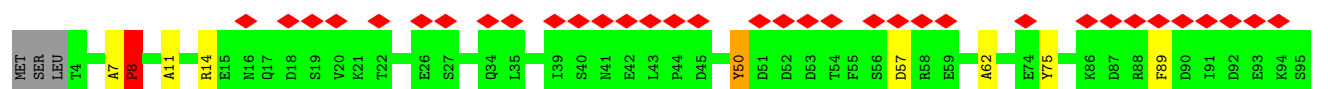
- Molecule 20: 26S protease regulatory subunit 6A

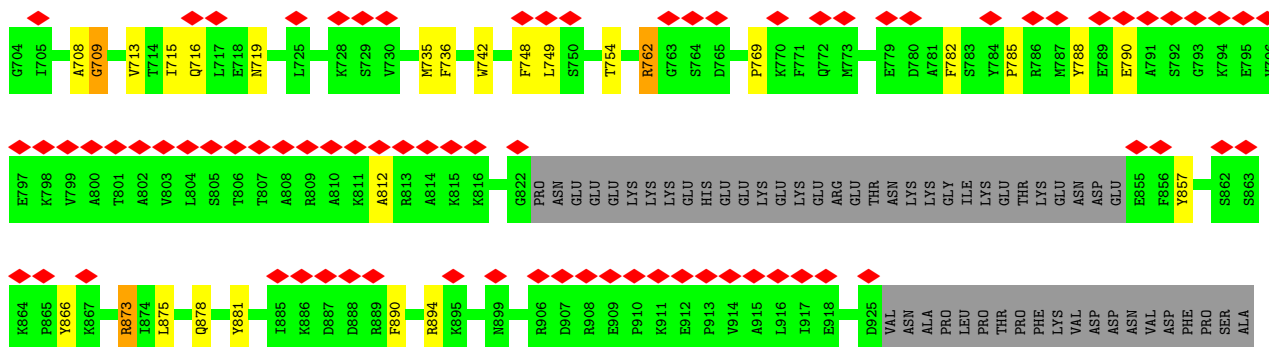
Chain 3-M: 79% 7% • 12%

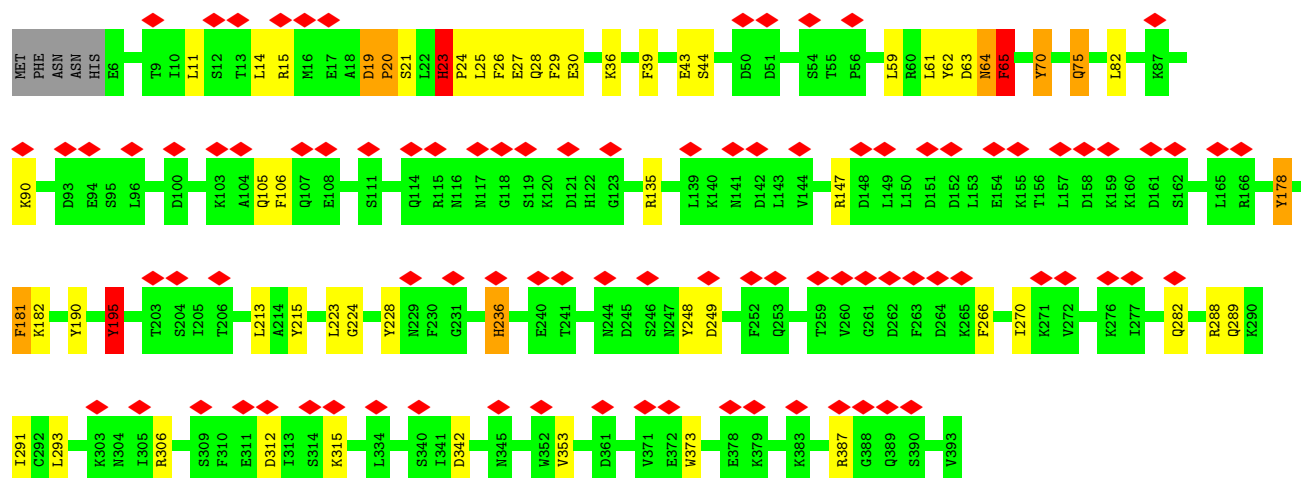


- Molecule 21: 26S proteasome regulatory subunit RPN2

Chain 1-N: 25% 85% 8% • 6%

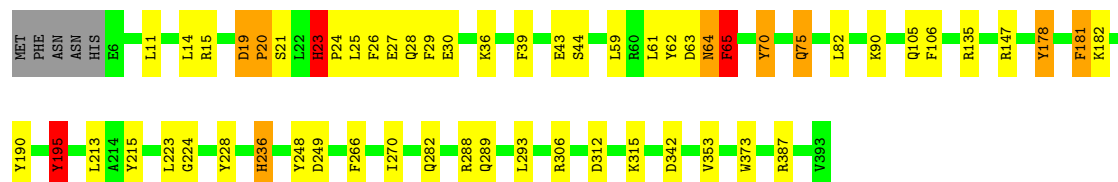






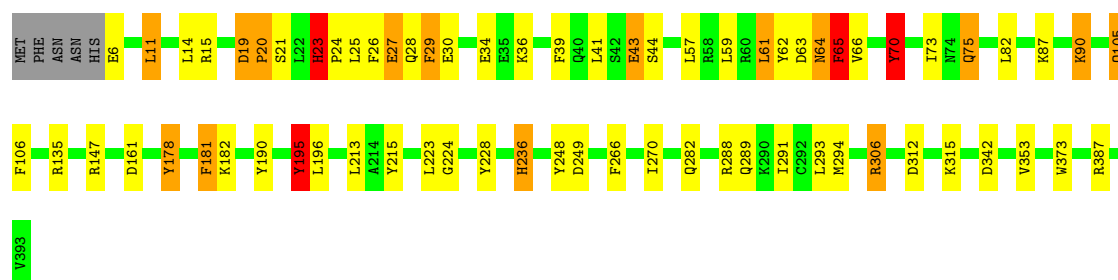
- Molecule 22: 26S proteasome regulatory subunit RPN9

Chain 2-O: 84% 12% ...



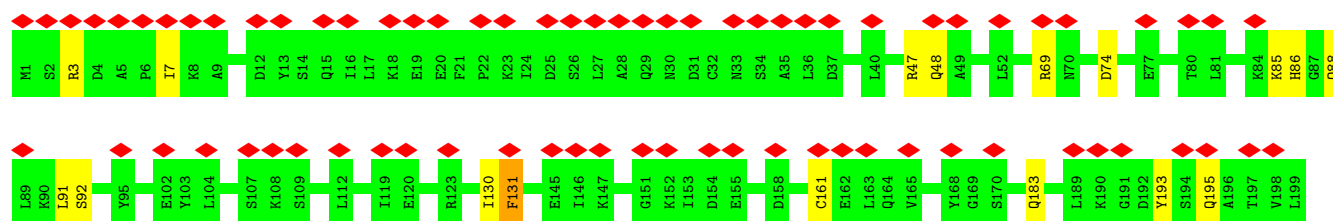
- Molecule 22: 26S proteasome regulatory subunit RPN9

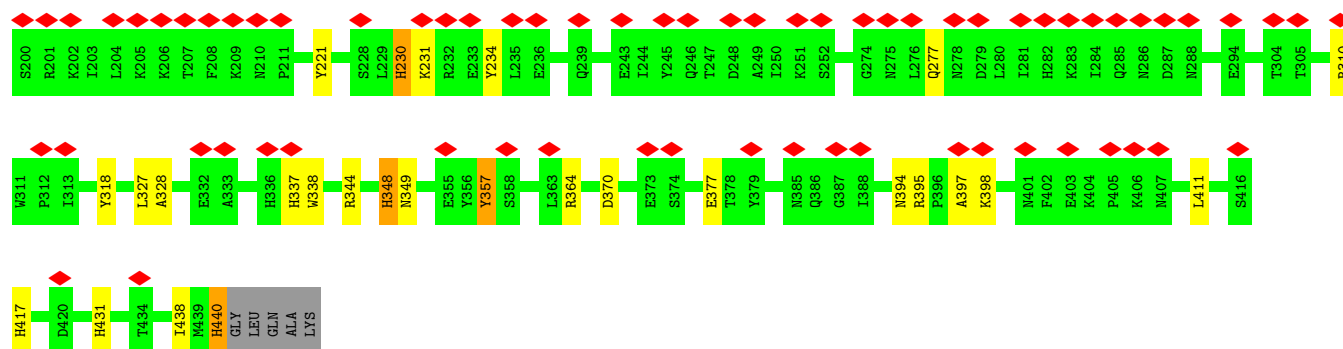
Chain 3-O: 81% 13% ...



- Molecule 23: 26S proteasome regulatory subunit RPN5

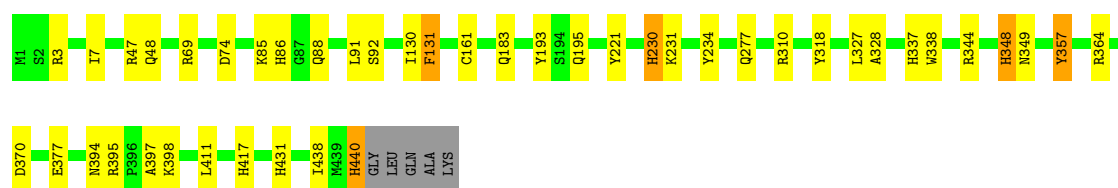
Chain 1-P: 31% 89% 9% ..





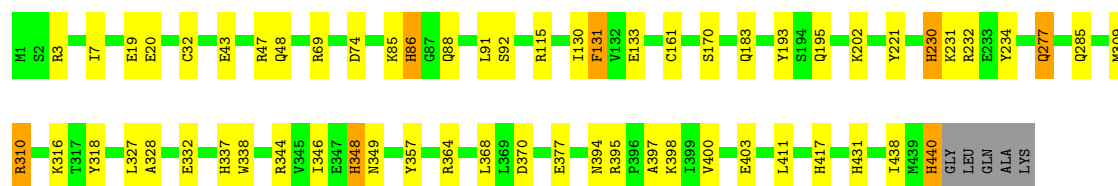
• Molecule 23: 26S proteasome regulatory subunit RPN5

Chain 2-P: 89% 9% ..



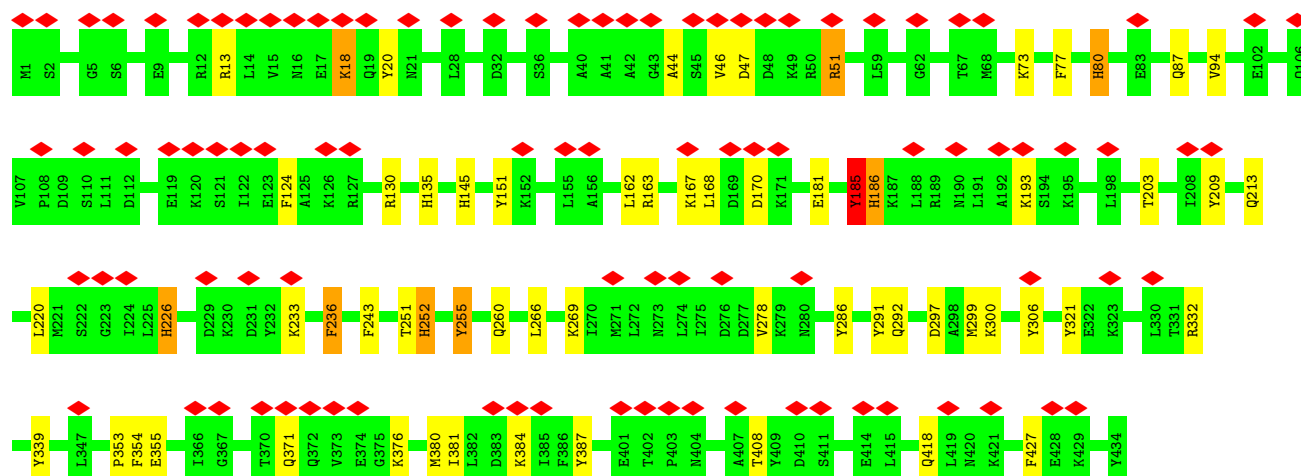
• Molecule 23: 26S proteasome regulatory subunit RPN5

Chain 3-P: 85% 12% ..

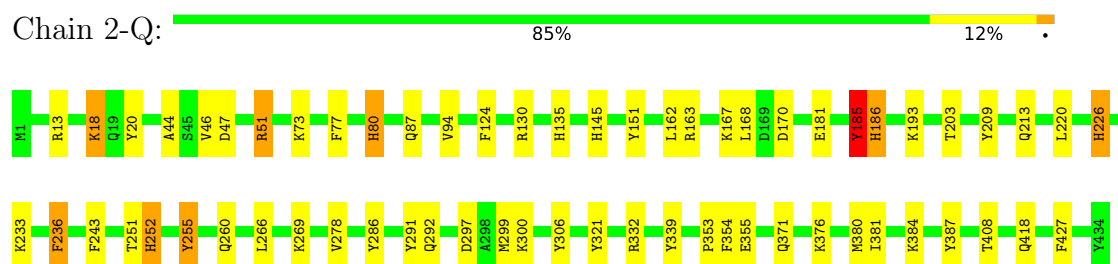


• Molecule 24: 26S proteasome regulatory subunit RPN6

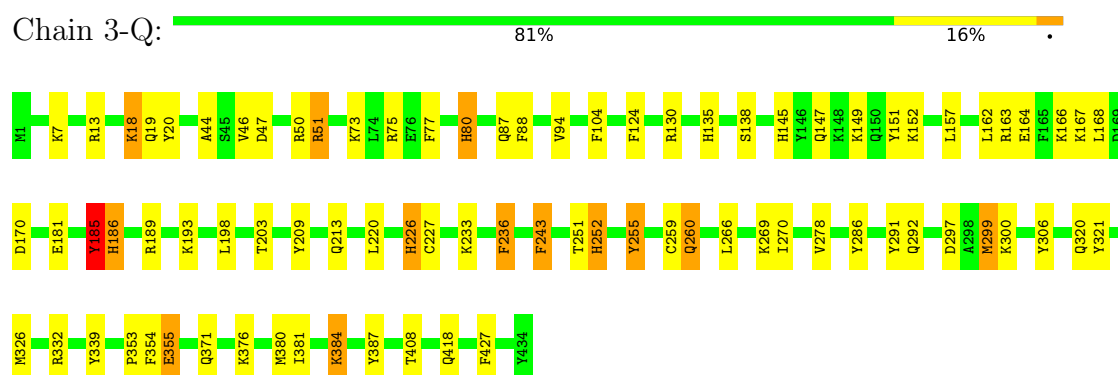
Chain 1-Q: 22% 85% 12% .



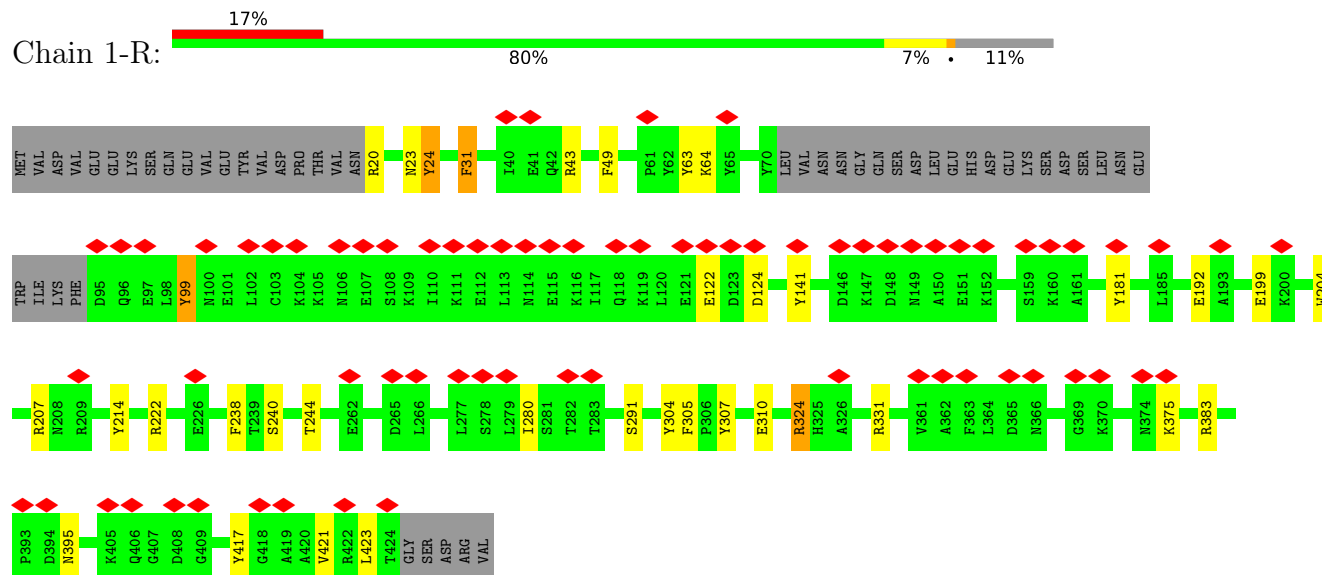
- Molecule 24: 26S proteasome regulatory subunit RPN6



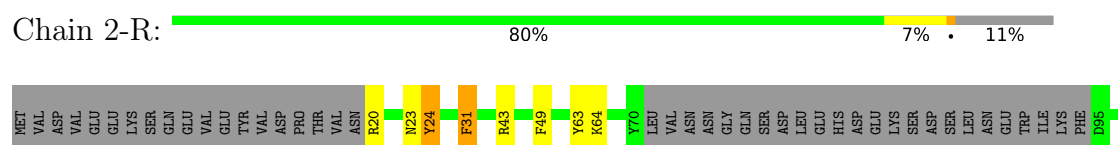
- Molecule 24: 26S proteasome regulatory subunit RPN6



- Molecule 25: 26S proteasome regulatory subunit RPN7

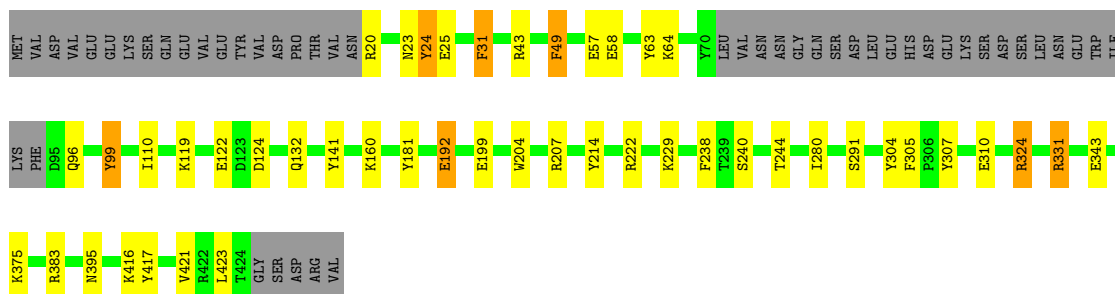


- Molecule 25: 26S proteasome regulatory subunit RPN7



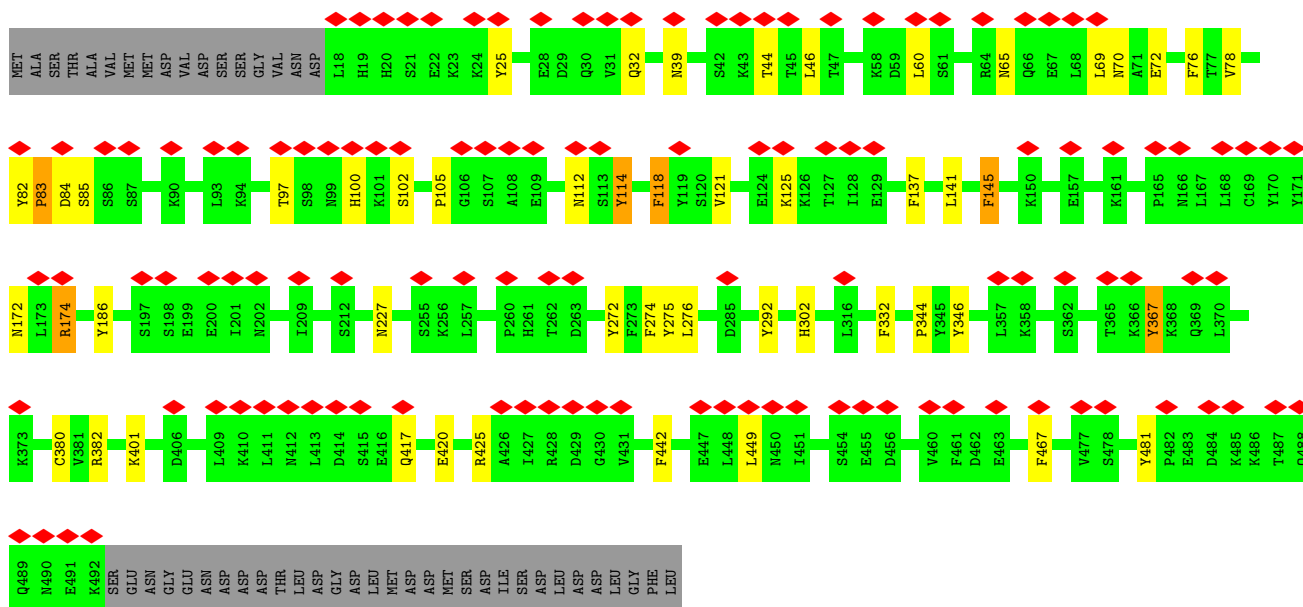
- Molecule 25: 26S proteasome regulatory subunit RPN7

Chain 3-R: 78% 9% • 11%



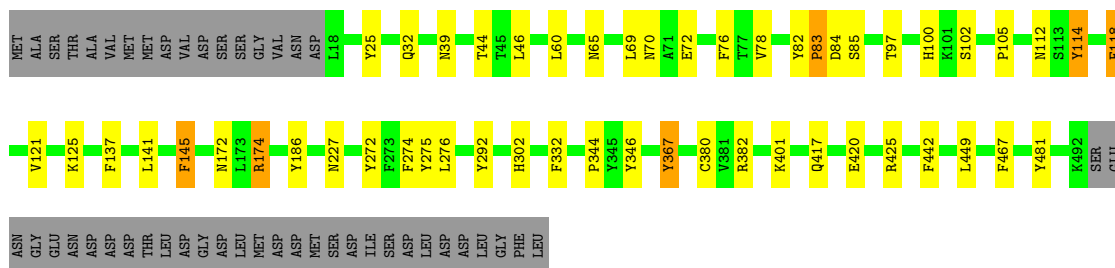
- Molecule 26: 26S proteasome regulatory subunit RPN3

Chain 1-S: 



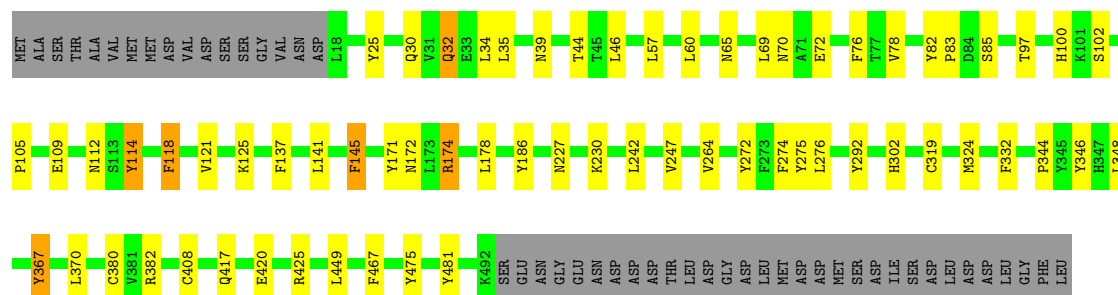
- Molecule 26: 26S proteasome regulatory subunit RPN3

Chain 2-S: 81% 9% 1% 9%

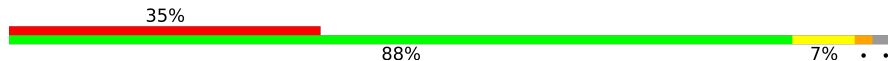


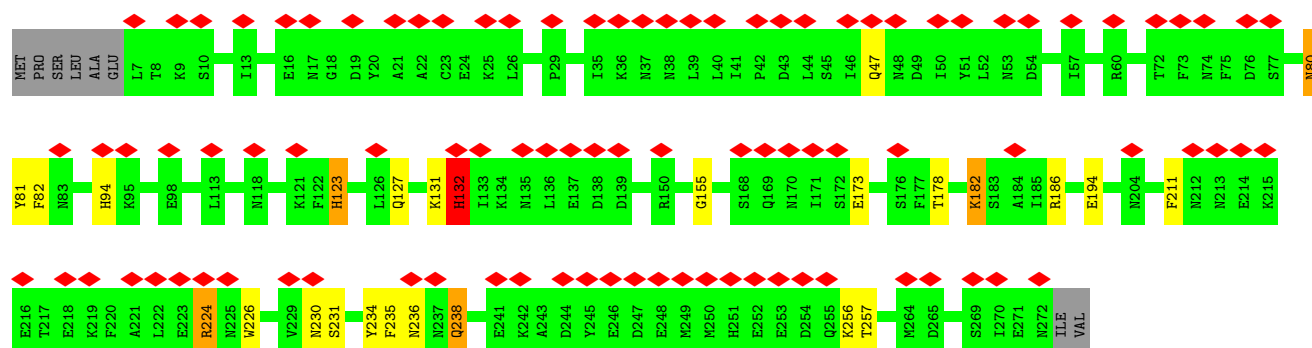
- Molecule 26: 26S proteasome regulatory subunit RPN3

Chain 3-S:  78% 11% 9%



- Molecule 27: 26S proteasome regulatory subunit RPN12

Chain 1-T:  35% 88% 7% ..



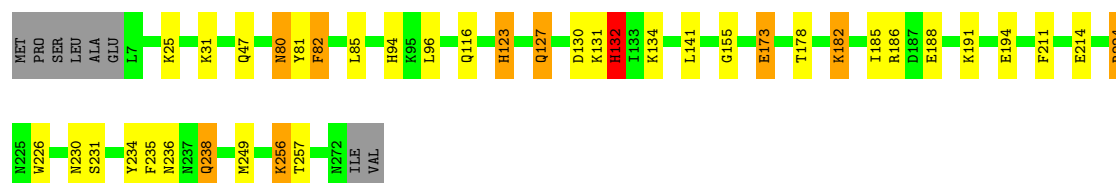
- Molecule 27: 26S proteasome regulatory subunit RPN12

Chain 2-T:  88% 7% ..



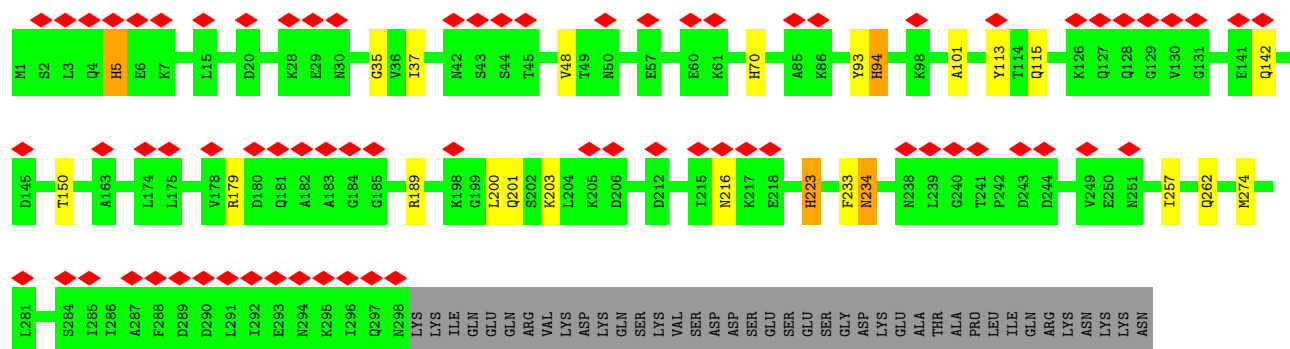
- Molecule 27: 26S proteasome regulatory subunit RPN12

Chain 3-T:  83% 11% ..



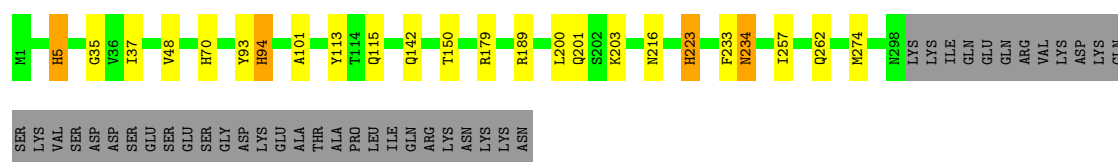
- Molecule 28: 26S proteasome regulatory subunit RPN8

Chain 1-U:  22% 81% 6% 12%



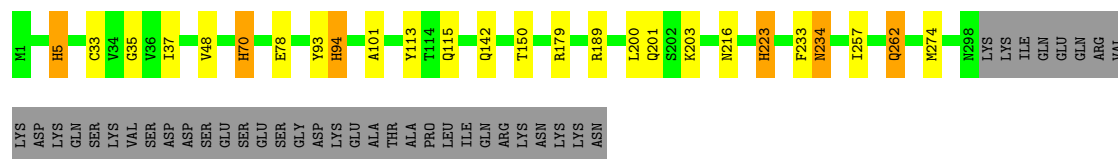
- Molecule 28: 26S proteasome regulatory subunit RPN8

Chain 2-U: 81% 6% • 12%



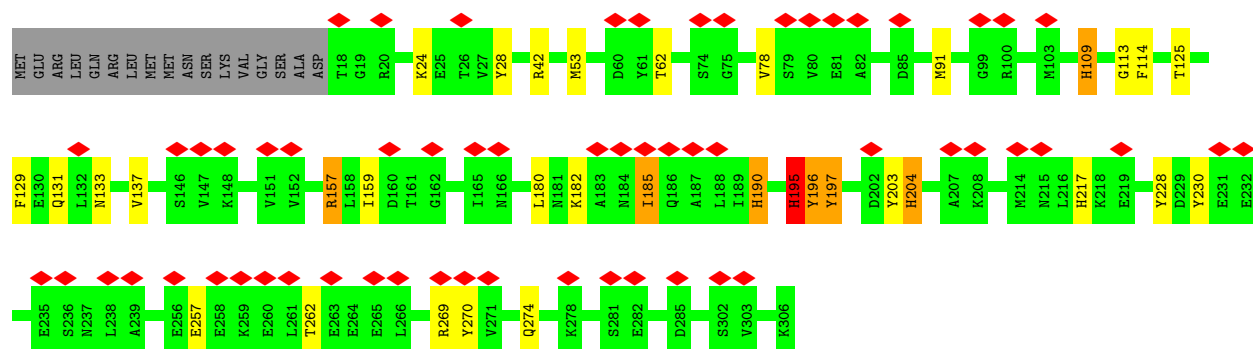
- Molecule 28: 26S proteasome regulatory subunit RPN8

Chain 3-U: 80% 6% • 12%



- Molecule 29: Ubiquitin carboxyl-terminal hydrolase RPN11

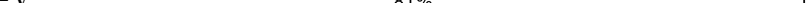
Chain 1-V: 20% 83% 8% • 6%

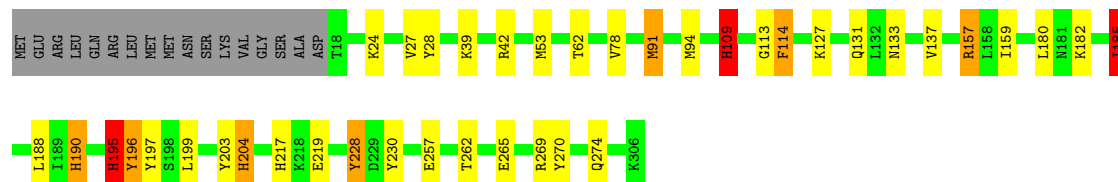


- Molecule 29: Ubiquitin carboxyl-terminal hydrolase RPN11

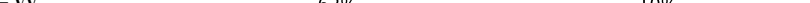
Chain 2-V: 84% 8% • 6%

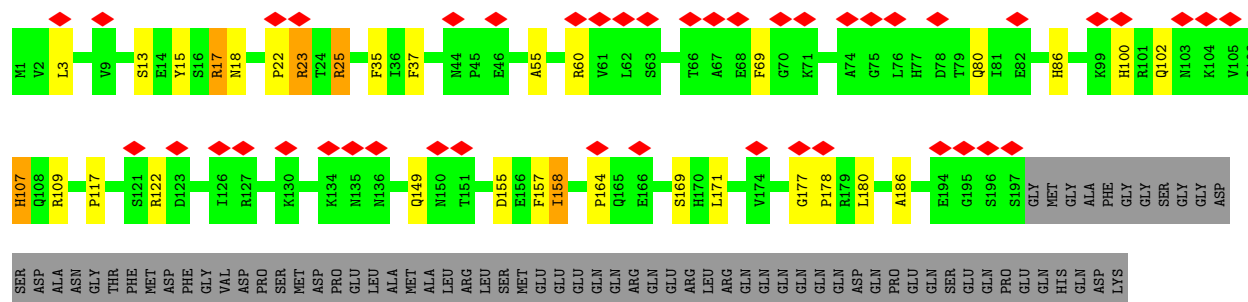
- Molecule 29: Ubiquitin carboxyl-terminal hydrolase RPN11

Chain 3-V:  81% 10% .. 6%

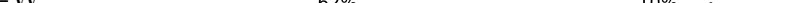


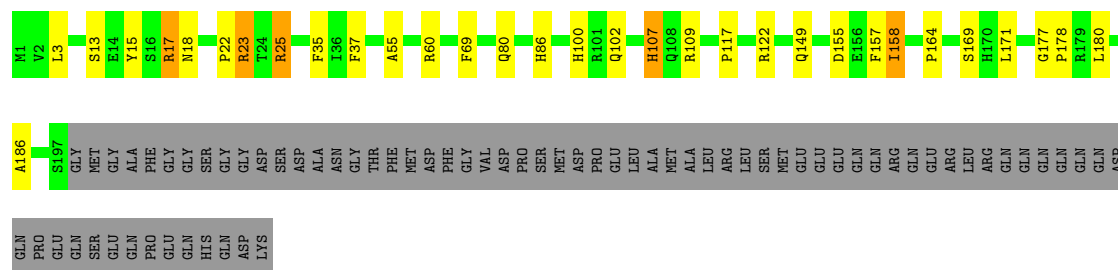
- Molecule 30: 26S proteasome regulatory subunit RPN10

Chain 1-W: 

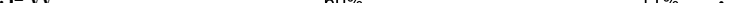


- Molecule 30: 26S proteasome regulatory subunit RPN10

Chain 2-W:  62% 10% 2% 26%

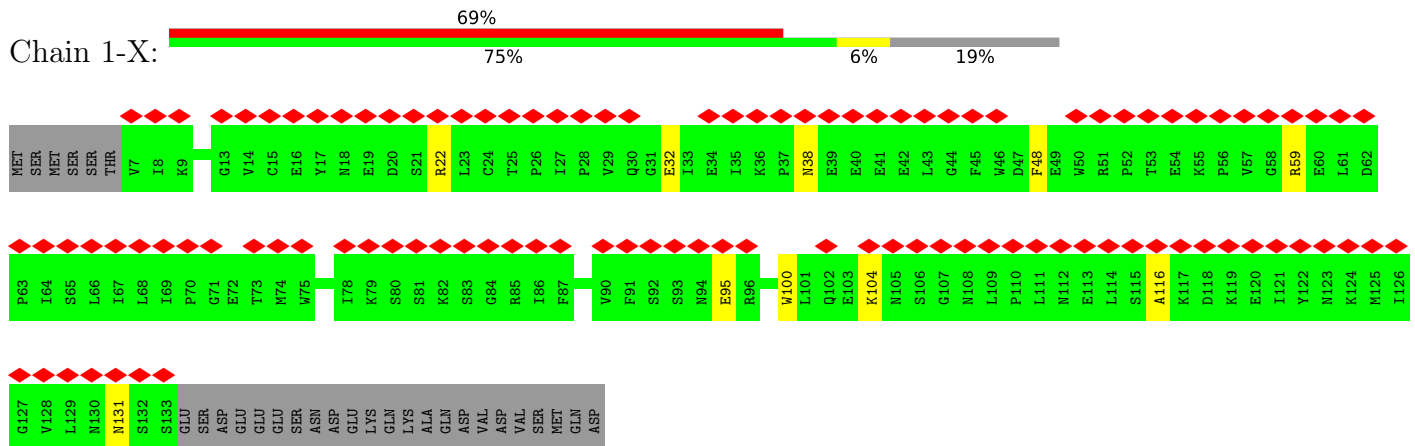


- Molecule 30: 26S proteasome regulatory subunit RPN10

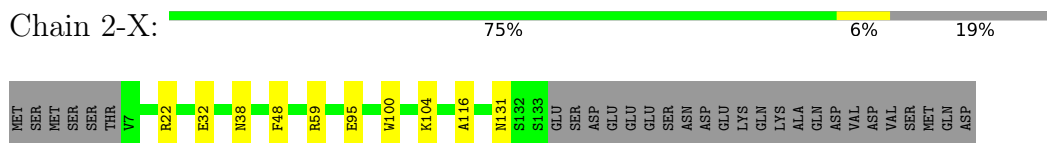
Chain 3-W:  60% 11% . 26%



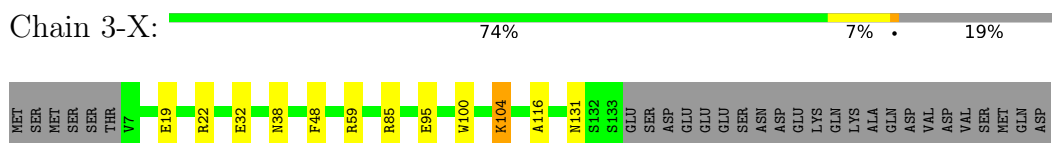
- Molecule 31: 26S proteasome regulatory subunit RPN13



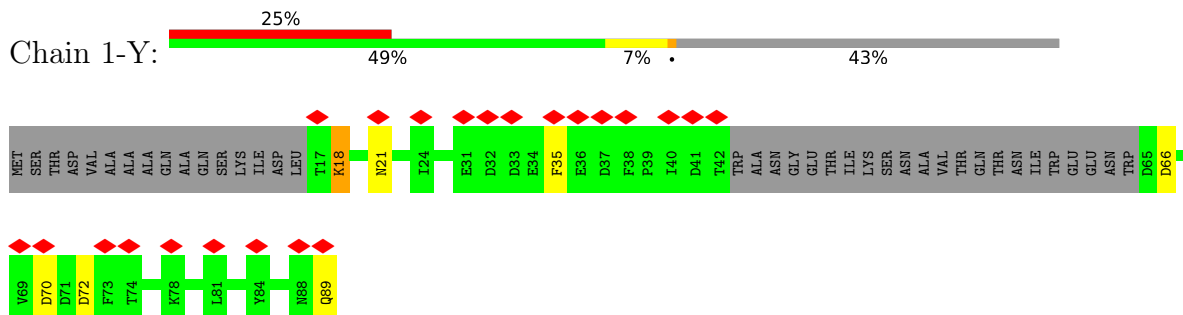
- Molecule 31: 26S proteasome regulatory subunit RPN13



- Molecule 31: 26S proteasome regulatory subunit RPN13



- Molecule 32: 26S proteasome complex subunit SEM1



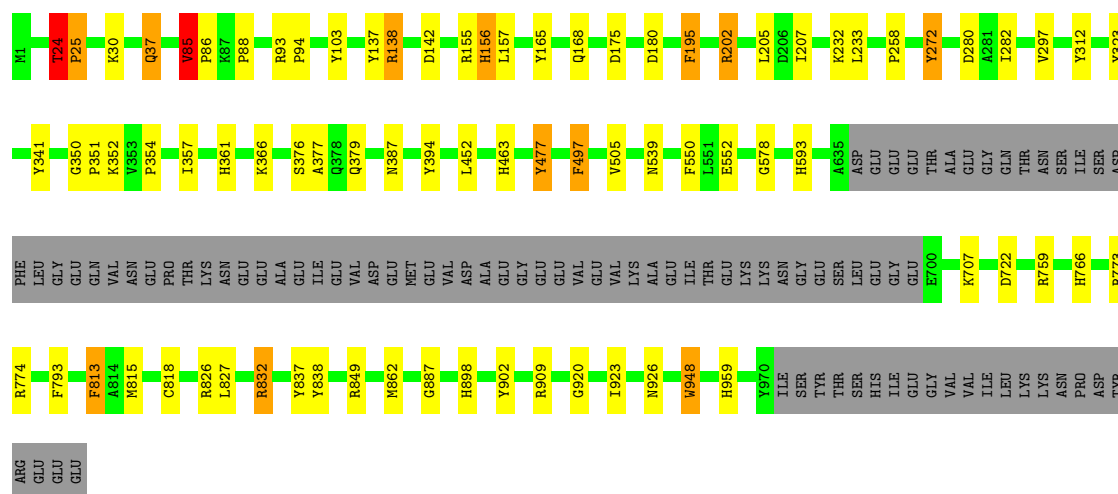
- Molecule 32: 26S proteasome complex subunit SEM1



LEU
LYS
LYS
ASN
PRO
ASP
TYR
ARG
GLU
GLU

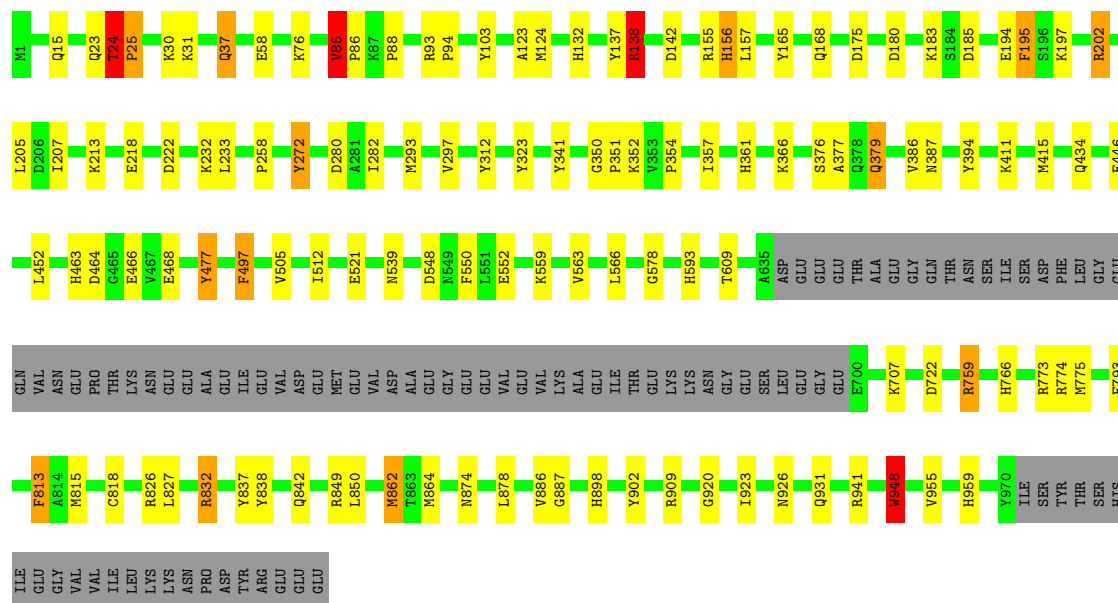
• Molecule 33: 26S proteasome regulatory subunit RPN1

Chain 2-Z:  83% 7% 9%



• Molecule 33: 26S proteasome regulatory subunit RPN1

Chain 3-Z:  79% 11% 9%



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of subtomograms used	1700	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 ($e^-/\text{\AA}^2$)	100	Depositor
Minimum defocus (nm)	3000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.894	Depositor
Minimum map value	-0.848	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.091	Depositor
Recommended contour level	0.27	Depositor
Map size (Å)	890.88, 890.88, 890.88	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.32, 2.32, 2.32	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	1-1	0.74	0/1541	1.29	5/2087 (0.2%)
1	1-h	0.72	0/1541	1.27	6/2087 (0.3%)
1	2-1	0.74	0/1541	1.29	5/2087 (0.2%)
1	2-h	0.72	0/1541	1.27	6/2087 (0.3%)
1	3-1	0.74	0/1541	1.29	5/2087 (0.2%)
1	3-h	0.72	0/1541	1.27	6/2087 (0.3%)
2	1-2	0.74	0/1750	1.37	13/2373 (0.5%)
2	1-i	0.75	0/1750	1.34	9/2373 (0.4%)
2	2-2	0.74	0/1750	1.37	13/2373 (0.5%)
2	2-i	0.75	0/1750	1.34	9/2373 (0.4%)
2	3-2	0.74	0/1750	1.37	13/2373 (0.5%)
2	3-i	0.75	0/1750	1.34	9/2373 (0.4%)
3	1-3	0.74	0/1611	1.29	6/2174 (0.3%)
3	1-j	0.72	0/1611	1.27	5/2174 (0.2%)
3	2-3	0.74	0/1611	1.29	6/2174 (0.3%)
3	2-j	0.72	0/1611	1.27	5/2174 (0.2%)
3	3-3	0.74	0/1611	1.29	6/2174 (0.3%)
3	3-j	0.72	0/1611	1.27	5/2174 (0.2%)
4	1-4	0.74	0/1589	1.33	4/2142 (0.2%)
4	1-k	0.74	0/1589	1.34	10/2142 (0.5%)
4	2-4	0.74	0/1589	1.33	4/2142 (0.2%)
4	2-k	0.74	0/1589	1.34	10/2142 (0.5%)
4	3-4	0.74	0/1589	1.33	4/2142 (0.2%)
4	3-k	0.74	0/1589	1.34	10/2142 (0.5%)
5	1-5	0.77	0/1681	1.28	4/2274 (0.2%)
5	1-l	0.75	0/1681	1.28	3/2274 (0.1%)
5	2-5	0.77	0/1681	1.28	4/2274 (0.2%)
5	2-l	0.75	0/1681	1.28	3/2274 (0.1%)
5	3-5	0.77	0/1681	1.28	4/2274 (0.2%)
5	3-l	0.75	0/1681	1.28	3/2274 (0.1%)
6	1-6	0.74	0/1795	1.34	10/2420 (0.4%)
6	1-m	0.74	0/1795	1.33	9/2420 (0.4%)
6	2-6	0.74	0/1795	1.34	10/2420 (0.4%)
6	2-m	0.74	0/1795	1.33	9/2420 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	3-6	0.74	0/1795	1.34	10/2420 (0.4%)
6	3-m	0.74	0/1795	1.33	9/2420 (0.4%)
7	1-7	0.74	0/1821	1.31	7/2470 (0.3%)
7	1-n	0.73	0/1846	1.34	4/2503 (0.2%)
7	2-7	0.74	0/1821	1.31	7/2470 (0.3%)
7	2-n	0.73	0/1846	1.34	4/2503 (0.2%)
7	3-7	0.74	0/1821	1.31	7/2470 (0.3%)
7	3-n	0.73	0/1846	1.34	4/2503 (0.2%)
8	1-A	0.76	0/1945	1.34	6/2634 (0.2%)
8	1-a	0.75	0/1945	1.33	2/2634 (0.1%)
8	2-A	0.76	0/1945	1.34	6/2634 (0.2%)
8	2-a	0.75	0/1945	1.33	2/2634 (0.1%)
8	3-A	0.76	0/1945	1.34	6/2634 (0.2%)
8	3-a	0.75	0/1945	1.33	2/2634 (0.1%)
9	1-B	0.75	0/1952	1.30	7/2642 (0.3%)
9	1-b	0.76	0/1952	1.29	7/2642 (0.3%)
9	2-B	0.75	0/1952	1.30	7/2642 (0.3%)
9	2-b	0.76	0/1952	1.29	7/2642 (0.3%)
9	3-B	0.75	0/1952	1.30	7/2642 (0.3%)
9	3-b	0.76	0/1952	1.29	7/2642 (0.3%)
10	1-C	0.75	0/1934	1.31	7/2618 (0.3%)
10	1-c	0.76	0/1934	1.30	8/2618 (0.3%)
10	2-C	0.75	0/1934	1.31	7/2618 (0.3%)
10	2-c	0.76	0/1934	1.30	8/2618 (0.3%)
10	3-C	0.75	0/1934	1.31	7/2618 (0.3%)
10	3-c	0.76	0/1934	1.30	8/2618 (0.3%)
11	1-D	0.77	0/1910	1.34	7/2586 (0.3%)
11	1-d	0.77	0/1910	1.32	6/2586 (0.2%)
11	2-D	0.77	0/1910	1.34	7/2586 (0.3%)
11	2-d	0.77	0/1910	1.32	6/2586 (0.2%)
11	3-D	0.77	0/1910	1.34	7/2586 (0.3%)
11	3-d	0.77	0/1910	1.32	6/2586 (0.2%)
12	1-E	0.74	0/1886	1.36	6/2541 (0.2%)
12	1-e	0.73	0/1886	1.33	4/2541 (0.2%)
12	2-E	0.74	0/1886	1.36	6/2541 (0.2%)
12	2-e	0.73	0/1886	1.33	4/2541 (0.2%)
12	3-E	0.74	0/1886	1.36	6/2541 (0.2%)
12	3-e	0.73	0/1886	1.33	4/2541 (0.2%)
13	1-F	0.75	0/1823	1.34	10/2463 (0.4%)
13	1-f	0.74	0/1800	1.31	8/2433 (0.3%)
13	2-F	0.75	0/1823	1.34	10/2463 (0.4%)
13	2-f	0.74	0/1800	1.31	8/2433 (0.3%)
13	3-F	0.75	0/1823	1.34	10/2463 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
13	3-f	0.74	0/1800	1.31	8/2433 (0.3%)
14	1-G	0.74	0/1932	1.36	6/2609 (0.2%)
14	1-g	0.74	0/1932	1.34	4/2609 (0.2%)
14	2-G	0.74	0/1932	1.36	6/2609 (0.2%)
14	2-g	0.74	0/1932	1.34	4/2609 (0.2%)
14	3-G	0.74	0/1932	1.36	6/2609 (0.2%)
14	3-g	0.74	0/1932	1.34	4/2609 (0.2%)
15	1-H	0.81	0/3102	1.37	6/4175 (0.1%)
15	2-H	0.81	0/3102	1.37	6/4175 (0.1%)
15	3-H	0.81	0/3102	1.37	6/4175 (0.1%)
16	1-I	0.77	0/3061	1.37	17/4121 (0.4%)
16	2-I	0.77	0/3061	1.37	17/4121 (0.4%)
16	3-I	0.77	0/3061	1.37	17/4121 (0.4%)
17	1-J	0.81	2/3073 (0.1%)	1.37	13/4129 (0.3%)
17	2-J	0.81	2/3073 (0.1%)	1.37	13/4129 (0.3%)
17	3-J	0.81	2/3073 (0.1%)	1.37	13/4129 (0.3%)
18	1-K	0.80	0/3121	1.39	23/4213 (0.5%)
18	2-K	0.80	0/3121	1.39	23/4213 (0.5%)
18	3-K	0.80	0/3121	1.39	23/4213 (0.5%)
19	1-L	0.79	0/3128	1.37	14/4204 (0.3%)
19	2-L	0.79	0/3128	1.37	14/4204 (0.3%)
19	3-L	0.79	0/3128	1.37	14/4204 (0.3%)
20	1-M	0.75	0/3023	1.38	10/4070 (0.2%)
20	2-M	0.75	0/3023	1.38	10/4070 (0.2%)
20	3-M	0.75	0/3023	1.38	10/4070 (0.2%)
21	1-N	0.78	1/6994 (0.0%)	1.44	34/9455 (0.4%)
21	2-N	0.78	1/6994 (0.0%)	1.44	34/9455 (0.4%)
21	3-N	0.78	1/6994 (0.0%)	1.44	34/9455 (0.4%)
22	1-O	0.78	0/3247	1.53	28/4380 (0.6%)
22	2-O	0.78	0/3247	1.53	28/4380 (0.6%)
22	3-O	0.78	0/3247	1.53	28/4380 (0.6%)
23	1-P	0.78	0/3663	1.45	25/4940 (0.5%)
23	2-P	0.78	0/3663	1.45	25/4940 (0.5%)
23	3-P	0.78	0/3663	1.45	25/4940 (0.5%)
24	1-Q	0.79	0/3556	1.49	22/4787 (0.5%)
24	2-Q	0.79	0/3556	1.49	22/4787 (0.5%)
24	3-Q	0.79	0/3556	1.49	22/4787 (0.5%)
25	1-R	0.77	0/3110	1.44	11/4193 (0.3%)
25	2-R	0.77	0/3110	1.44	11/4193 (0.3%)
25	3-R	0.77	0/3110	1.44	11/4193 (0.3%)
26	1-S	0.81	0/3966	1.49	20/5355 (0.4%)
26	2-S	0.81	0/3966	1.49	20/5355 (0.4%)
26	3-S	0.81	0/3966	1.49	20/5355 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	1-T	0.77	0/2235	1.53	20/3017 (0.7%)
27	2-T	0.77	0/2235	1.53	20/3017 (0.7%)
27	3-T	0.77	0/2235	1.53	20/3017 (0.7%)
28	1-U	0.77	0/2407	1.43	13/3258 (0.4%)
28	2-U	0.77	0/2407	1.43	13/3258 (0.4%)
28	3-U	0.77	0/2407	1.43	13/3258 (0.4%)
29	1-V	0.82	1/2309 (0.0%)	1.51	15/3115 (0.5%)
29	2-V	0.82	1/2309 (0.0%)	1.51	15/3115 (0.5%)
29	3-V	0.82	1/2309 (0.0%)	1.51	15/3115 (0.5%)
30	1-W	0.80	0/1557	1.50	14/2111 (0.7%)
30	2-W	0.80	0/1557	1.50	14/2111 (0.7%)
30	3-W	0.80	0/1557	1.50	14/2111 (0.7%)
31	1-X	0.81	0/1058	1.45	6/1432 (0.4%)
31	2-X	0.81	0/1058	1.45	6/1432 (0.4%)
31	3-X	0.81	0/1058	1.45	6/1432 (0.4%)
32	1-Y	0.79	0/438	1.54	5/583 (0.9%)
32	2-Y	0.79	0/438	1.54	5/583 (0.9%)
32	3-Y	0.79	0/438	1.54	5/583 (0.9%)
33	1-Z	0.79	0/7122	1.47	42/9645 (0.4%)
33	2-Z	0.79	0/7122	1.47	42/9645 (0.4%)
33	3-Z	0.79	0/7122	1.47	42/9645 (0.4%)
All	All	0.77	12/331536 (0.0%)	1.39	1563/447756 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1-1	0	4
1	1-h	0	5
1	2-1	0	4
1	2-h	0	5
1	3-1	0	4
1	3-h	0	5
2	1-2	0	5
2	1-i	0	5
2	2-2	0	5
2	2-i	0	5
2	3-2	0	5
2	3-i	0	5
3	1-3	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	1-j	0	7
3	2-3	0	7
3	2-j	0	7
3	3-3	0	7
3	3-j	0	7
4	1-4	0	8
4	1-k	0	7
4	2-4	0	8
4	2-k	0	7
4	3-4	0	8
4	3-k	0	7
5	1-5	0	7
5	1-l	0	6
5	2-5	0	7
5	2-l	0	6
5	3-5	0	7
5	3-l	0	6
6	1-6	0	9
6	1-m	0	4
6	2-6	0	9
6	2-m	0	4
6	3-6	0	9
6	3-m	0	4
7	1-7	0	4
7	1-n	0	7
7	2-7	0	4
7	2-n	0	7
7	3-7	0	4
7	3-n	0	7
8	1-A	0	7
8	1-a	0	10
8	2-A	0	7
8	2-a	0	9
8	3-A	0	7
8	3-a	0	10
9	1-B	0	7
9	1-b	0	4
9	2-B	0	7
9	2-b	0	4
9	3-B	0	7
9	3-b	0	4
10	1-C	0	11

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	1-c	0	5
10	2-C	0	11
10	2-c	0	5
10	3-C	0	11
10	3-c	0	5
11	1-D	0	5
11	1-d	0	6
11	2-D	0	5
11	2-d	0	6
11	3-D	0	5
11	3-d	0	6
12	1-E	0	5
12	1-e	0	5
12	2-E	0	5
12	2-e	0	5
12	3-E	0	5
12	3-e	0	5
13	1-F	0	7
13	1-f	0	6
13	2-F	0	8
13	2-f	0	6
13	3-F	0	8
13	3-f	0	6
14	1-G	0	7
14	1-g	0	7
14	2-G	0	7
14	2-g	0	7
14	3-G	0	7
14	3-g	0	7
15	1-H	0	12
15	2-H	0	12
15	3-H	0	12
16	1-I	0	10
16	2-I	0	10
16	3-I	0	10
17	1-J	0	6
17	2-J	0	6
17	3-J	0	6
18	1-K	0	10
18	2-K	0	10
18	3-K	0	10
19	1-L	0	14

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Mol	Chain	#Chirality outliers	#Planarity outliers
19	2-L	0	14
19	3-L	0	14
20	1-M	0	7
20	2-M	0	7
20	3-M	0	7
21	1-N	0	22
21	2-N	0	22
21	3-N	0	22
22	1-O	0	12
22	2-O	0	12
22	3-O	0	12
23	1-P	0	12
23	2-P	0	12
23	3-P	0	12
24	1-Q	0	19
24	2-Q	0	19
24	3-Q	0	19
25	1-R	0	11
25	2-R	0	11
25	3-R	0	11
26	1-S	0	14
26	2-S	0	14
26	3-S	0	14
27	1-T	0	3
27	2-T	0	3
27	3-T	0	3
28	1-U	0	5
28	2-U	0	5
28	3-U	0	5
29	1-V	0	10
29	2-V	0	10
29	3-V	0	10
30	1-W	0	8
30	2-W	0	8
30	3-W	0	8
31	1-X	0	1
31	2-X	0	1
31	3-X	0	1
32	1-Y	0	1
32	2-Y	0	1
32	3-Y	0	1
33	1-Z	0	20

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Mol	Chain	#Chirality outliers	#Planarity outliers
33	2-Z	0	20
33	3-Z	0	20
All	All	0	1123

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	1-J	190	PRO	CA-C	6.07	1.55	1.51
17	2-J	190	PRO	CA-C	6.07	1.55	1.51
17	3-J	190	PRO	CA-C	6.07	1.55	1.51
29	1-V	196	TYR	CA-C	5.88	1.55	1.52
29	2-V	196	TYR	CA-C	5.88	1.55	1.52

The worst 5 of 1563 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	1-T	82	PHE	CA-CB-CG	11.04	124.84	113.80
27	2-T	82	PHE	CA-CB-CG	11.04	124.84	113.80
27	3-T	82	PHE	CA-CB-CG	11.04	124.84	113.80
33	1-Z	195	PHE	CA-CB-CG	10.31	124.11	113.80
33	2-Z	195	PHE	CA-CB-CG	10.31	124.11	113.80

There are no chirality outliers.

5 of 1123 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-1	102	TYR	Sidechain
1	1-1	189	TYR	Sidechain
1	1-1	29	ARG	Sidechain
1	1-1	61	TYR	Sidechain
2	1-2	36	ARG	Sidechain

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	1-1	1512	1479	1481	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1-h	1512	1479	1481	5	0
1	2-1	1512	1479	1481	3	0
1	2-h	1512	1479	1481	3	0
1	3-1	1512	1479	1481	3	0
1	3-h	1512	1479	1481	4	0
2	1-2	1719	1717	1719	7	0
2	1-i	1719	1717	1719	1	0
2	2-2	1719	1717	1719	7	0
2	2-i	1719	1717	1719	0	0
2	3-2	1719	1717	1719	7	0
2	3-i	1719	1717	1719	1	0
3	1-3	1581	1572	1574	5	0
3	1-j	1581	1572	1574	5	0
3	2-3	1581	1572	1574	5	0
3	2-j	1581	1572	1574	4	0
3	3-3	1581	1572	1574	5	0
3	3-j	1581	1572	1574	6	0
4	1-4	1561	1569	1569	3	0
4	1-k	1561	1569	1569	3	0
4	2-4	1561	1569	1569	3	0
4	2-k	1561	1569	1569	3	0
4	3-4	1561	1569	1569	2	0
4	3-k	1561	1569	1569	3	0
5	1-5	1644	1593	1595	3	0
5	1-l	1644	1593	1595	2	0
5	2-5	1644	1593	1595	2	0
5	2-l	1644	1593	1595	1	0
5	3-5	1644	1593	1595	2	0
5	3-l	1644	1593	1595	2	0
6	1-6	1757	1709	1711	1	0
6	1-m	1757	1709	1711	7	0
6	2-6	1757	1709	1711	1	0
6	2-m	1757	1709	1711	7	0
6	3-6	1757	1709	1711	1	0
6	3-m	1757	1709	1711	7	0
7	1-7	1790	1791	1793	5	0
7	1-n	1815	1819	1821	8	0
7	2-7	1790	1791	1793	5	0
7	2-n	1815	1819	1821	8	0
7	3-7	1790	1791	1793	5	0
7	3-n	1815	1819	1821	9	0
8	1-A	1907	1902	1901	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	1-a	1907	1902	1901	4	0
8	2-A	1907	1902	1901	6	0
8	2-a	1907	1902	1901	4	0
8	3-A	1907	1902	1901	6	0
8	3-a	1907	1902	1901	4	0
9	1-B	1915	1929	1929	9	0
9	1-b	1915	1929	1929	4	0
9	2-B	1915	1929	1929	8	0
9	2-b	1915	1929	1929	4	0
9	3-B	1915	1929	1929	9	0
9	3-b	1915	1929	1929	4	0
10	1-C	1904	1902	1904	5	0
10	1-c	1904	1902	1904	4	0
10	2-C	1904	1902	1904	5	0
10	2-c	1904	1902	1904	5	0
10	3-C	1904	1902	1904	4	0
10	3-c	1904	1902	1904	5	0
11	1-D	1881	1893	1895	7	0
11	1-d	1881	1893	1895	4	0
11	2-D	1881	1893	1895	7	0
11	2-d	1881	1893	1895	4	0
11	3-D	1881	1893	1895	7	0
11	3-d	1881	1893	1895	4	0
12	1-E	1861	1837	1839	3	0
12	1-e	1861	1837	1839	7	0
12	2-E	1861	1837	1839	3	0
12	2-e	1861	1837	1839	8	0
12	3-E	1861	1837	1839	3	0
12	3-e	1861	1837	1839	8	0
13	1-F	1795	1800	1800	4	0
13	1-f	1773	1778	1775	2	0
13	2-F	1795	1800	1800	5	0
13	2-f	1773	1778	1775	2	0
13	3-F	1795	1800	1800	4	0
13	3-f	1773	1778	1775	1	0
14	1-G	1892	1885	1883	6	0
14	1-g	1892	1884	1883	5	0
14	2-G	1892	1885	1883	6	0
14	2-g	1892	1884	1883	5	0
14	3-G	1892	1885	1883	6	0
14	3-g	1892	1884	1883	6	0
15	1-H	3053	3130	3127	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	2-H	3053	3130	3127	17	0
15	3-H	3053	3130	3127	16	0
16	1-I	3022	3093	3092	9	0
16	2-I	3022	3093	3092	9	0
16	3-I	3022	3093	3092	10	0
17	1-J	3033	3157	3156	9	0
17	2-J	3033	3157	3156	9	0
17	3-J	3033	3157	3156	9	0
18	1-K	3078	3142	3141	13	0
18	2-K	3078	3142	3141	13	0
18	3-K	3078	3142	3141	13	0
19	1-L	3082	3158	3157	12	0
19	2-L	3082	3158	3157	13	0
19	3-L	3082	3158	3157	14	0
20	1-M	2986	3057	3055	8	0
20	2-M	2986	3057	3055	7	0
20	3-M	2986	3057	3055	7	0
21	1-N	6882	6961	6959	34	0
21	2-N	6882	6961	6959	35	0
21	3-N	6882	6961	6959	34	0
22	1-O	3186	3214	3213	39	0
22	2-O	3186	3214	3213	37	0
22	3-O	3186	3214	3213	39	0
23	1-P	3608	3694	3694	8	0
23	2-P	3608	3694	3694	8	0
23	3-P	3608	3694	3694	7	0
24	1-Q	3499	3524	3524	22	0
24	2-Q	3499	3524	3524	22	0
24	3-Q	3499	3524	3524	24	0
25	1-R	3060	3085	3083	10	0
25	2-R	3060	3085	3083	10	0
25	3-R	3060	3085	3083	10	0
26	1-S	3894	3939	3938	14	0
26	2-S	3894	3939	3938	14	0
26	3-S	3894	3939	3938	14	0
27	1-T	2192	2162	2161	10	0
27	2-T	2192	2162	2161	10	0
27	3-T	2192	2162	2161	10	0
28	1-U	2373	2403	2403	12	0
28	2-U	2373	2403	2403	12	0
28	3-U	2373	2403	2403	12	0
29	1-V	2274	2275	2273	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	2-V	2274	2275	2273	23	0
29	3-V	2274	2275	2273	22	0
30	1-W	1534	1542	1542	7	0
30	2-W	1534	1542	1542	7	0
30	3-W	1534	1542	1542	7	0
31	1-X	1032	1018	1017	1	0
31	2-X	1032	1018	1017	1	0
31	3-X	1032	1018	1017	1	0
32	1-Y	435	396	394	1	0
32	2-Y	435	396	394	1	0
32	3-Y	435	396	394	1	0
33	1-Z	7005	6934	6932	37	0
33	2-Z	7005	6934	6932	36	0
33	3-Z	7005	6934	6932	37	0
All	All	326007	327135	327150	1091	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 2.

The worst 5 of 1091 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)
21:N:339:MET:HA	21:N:709:GLY:N	1.73	1.04
21:N:339:MET:HA	21:N:709:GLY:N	1.73	1.04
33:Z:30:LYS:CG	33:Z:37:GLN:HB3	1.89	1.02
21:N:339:MET:HA	21:N:709:GLY:N	1.73	1.02
33:Z:30:LYS:CG	33:Z:37:GLN:HB3	1.89	1.01

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	1-1	194/215 (90%)	190 (98%)	4 (2%)	0	100	100
1	1-h	194/215 (90%)	186 (96%)	8 (4%)	0	100	100
1	2-1	194/215 (90%)	190 (98%)	4 (2%)	0	100	100
1	2-h	194/215 (90%)	186 (96%)	8 (4%)	0	100	100
1	3-1	194/215 (90%)	190 (98%)	4 (2%)	0	100	100
1	3-h	194/215 (90%)	186 (96%)	8 (4%)	0	100	100
2	1-2	224/261 (86%)	210 (94%)	13 (6%)	1 (0%)	30	67
2	1-i	224/261 (86%)	215 (96%)	9 (4%)	0	100	100
2	2-2	224/261 (86%)	210 (94%)	13 (6%)	1 (0%)	30	67
2	2-i	224/261 (86%)	215 (96%)	9 (4%)	0	100	100
2	3-2	224/261 (86%)	210 (94%)	13 (6%)	1 (0%)	30	67
2	3-i	224/261 (86%)	215 (96%)	9 (4%)	0	100	100
3	1-3	202/205 (98%)	189 (94%)	10 (5%)	3 (2%)	8	40
3	1-j	202/205 (98%)	191 (95%)	11 (5%)	0	100	100
3	2-3	202/205 (98%)	189 (94%)	10 (5%)	3 (2%)	8	40
3	2-j	202/205 (98%)	191 (95%)	11 (5%)	0	100	100
3	3-3	202/205 (98%)	189 (94%)	10 (5%)	3 (2%)	8	40
3	3-j	202/205 (98%)	191 (95%)	11 (5%)	0	100	100
4	1-4	193/198 (98%)	191 (99%)	1 (0%)	1 (0%)	24	63
4	1-k	193/198 (98%)	185 (96%)	8 (4%)	0	100	100
4	2-4	193/198 (98%)	191 (99%)	1 (0%)	1 (0%)	24	63
4	2-k	193/198 (98%)	185 (96%)	8 (4%)	0	100	100
4	3-4	193/198 (98%)	191 (99%)	1 (0%)	1 (0%)	24	63
4	3-k	193/198 (98%)	185 (96%)	8 (4%)	0	100	100
5	1-5	210/287 (73%)	196 (93%)	13 (6%)	1 (0%)	24	63
5	1-l	210/287 (73%)	199 (95%)	11 (5%)	0	100	100
5	2-5	210/287 (73%)	196 (93%)	13 (6%)	1 (0%)	24	63
5	2-l	210/287 (73%)	199 (95%)	11 (5%)	0	100	100
5	3-5	210/287 (73%)	196 (93%)	13 (6%)	1 (0%)	24	63
5	3-l	210/287 (73%)	199 (95%)	11 (5%)	0	100	100
6	1-6	220/241 (91%)	212 (96%)	7 (3%)	1 (0%)	24	63
6	1-m	220/241 (91%)	212 (96%)	7 (3%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	2-6	220/241 (91%)	212 (96%)	7 (3%)	1 (0%)	24	63
6	2-m	220/241 (91%)	212 (96%)	7 (3%)	1 (0%)	24	63
6	3-6	220/241 (91%)	212 (96%)	7 (3%)	1 (0%)	24	63
6	3-m	220/241 (91%)	212 (96%)	7 (3%)	1 (0%)	24	63
7	1-7	227/266 (85%)	211 (93%)	13 (6%)	3 (1%)	9	42
7	1-n	230/266 (86%)	223 (97%)	6 (3%)	1 (0%)	30	67
7	2-7	227/266 (85%)	211 (93%)	13 (6%)	3 (1%)	9	42
7	2-n	230/266 (86%)	223 (97%)	6 (3%)	1 (0%)	30	67
7	3-7	227/266 (85%)	211 (93%)	13 (6%)	3 (1%)	9	42
7	3-n	230/266 (86%)	223 (97%)	6 (3%)	1 (0%)	30	67
8	1-A	239/252 (95%)	232 (97%)	6 (2%)	1 (0%)	30	67
8	1-a	239/252 (95%)	232 (97%)	6 (2%)	1 (0%)	30	67
8	2-A	239/252 (95%)	232 (97%)	6 (2%)	1 (0%)	30	67
8	2-a	239/252 (95%)	232 (97%)	6 (2%)	1 (0%)	30	67
8	3-A	239/252 (95%)	232 (97%)	6 (2%)	1 (0%)	30	67
8	3-a	239/252 (95%)	232 (97%)	6 (2%)	1 (0%)	30	67
9	1-B	248/250 (99%)	244 (98%)	3 (1%)	1 (0%)	30	67
9	1-b	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
9	2-B	248/250 (99%)	244 (98%)	3 (1%)	1 (0%)	30	67
9	2-b	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
9	3-B	248/250 (99%)	244 (98%)	3 (1%)	1 (0%)	30	67
9	3-b	248/250 (99%)	241 (97%)	7 (3%)	0	100	100
10	1-C	242/258 (94%)	236 (98%)	6 (2%)	0	100	100
10	1-c	242/258 (94%)	234 (97%)	7 (3%)	1 (0%)	30	67
10	2-C	242/258 (94%)	236 (98%)	6 (2%)	0	100	100
10	2-c	242/258 (94%)	234 (97%)	7 (3%)	1 (0%)	30	67
10	3-C	242/258 (94%)	236 (98%)	6 (2%)	0	100	100
10	3-c	242/258 (94%)	234 (97%)	7 (3%)	1 (0%)	30	67
11	1-D	238/254 (94%)	227 (95%)	7 (3%)	4 (2%)	7	36
11	1-d	238/254 (94%)	228 (96%)	7 (3%)	3 (1%)	9	42
11	2-D	238/254 (94%)	227 (95%)	7 (3%)	4 (2%)	7	36

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	2-d	238/254 (94%)	228 (96%)	7 (3%)	3 (1%)	9	42
11	3-D	238/254 (94%)	227 (95%)	7 (3%)	4 (2%)	7	36
11	3-d	238/254 (94%)	228 (96%)	7 (3%)	3 (1%)	9	42
12	1-E	240/260 (92%)	234 (98%)	6 (2%)	0	100	100
12	1-e	240/260 (92%)	233 (97%)	4 (2%)	3 (1%)	9	42
12	2-E	240/260 (92%)	234 (98%)	6 (2%)	0	100	100
12	2-e	240/260 (92%)	233 (97%)	4 (2%)	3 (1%)	9	42
12	3-E	240/260 (92%)	234 (98%)	6 (2%)	0	100	100
12	3-e	240/260 (92%)	233 (97%)	4 (2%)	3 (1%)	9	42
13	1-F	231/234 (99%)	218 (94%)	9 (4%)	4 (2%)	7	36
13	1-f	229/234 (98%)	218 (95%)	10 (4%)	1 (0%)	30	67
13	2-F	231/234 (99%)	218 (94%)	9 (4%)	4 (2%)	7	36
13	2-f	229/234 (98%)	218 (95%)	10 (4%)	1 (0%)	30	67
13	3-F	231/234 (99%)	218 (94%)	9 (4%)	4 (2%)	7	36
13	3-f	229/234 (98%)	218 (95%)	10 (4%)	1 (0%)	30	67
14	1-G	241/288 (84%)	232 (96%)	8 (3%)	1 (0%)	30	67
14	1-g	241/288 (84%)	228 (95%)	12 (5%)	1 (0%)	30	67
14	2-G	241/288 (84%)	232 (96%)	8 (3%)	1 (0%)	30	67
14	2-g	241/288 (84%)	228 (95%)	12 (5%)	1 (0%)	30	67
14	3-G	241/288 (84%)	232 (96%)	8 (3%)	1 (0%)	30	67
14	3-g	241/288 (84%)	228 (95%)	12 (5%)	1 (0%)	30	67
15	1-H	386/467 (83%)	351 (91%)	28 (7%)	7 (2%)	6	34
15	2-H	386/467 (83%)	351 (91%)	28 (7%)	7 (2%)	6	34
15	3-H	386/467 (83%)	351 (91%)	28 (7%)	7 (2%)	6	34
16	1-I	383/437 (88%)	355 (93%)	25 (6%)	3 (1%)	16	54
16	2-I	383/437 (88%)	355 (93%)	25 (6%)	3 (1%)	16	54
16	3-I	383/437 (88%)	355 (93%)	25 (6%)	3 (1%)	16	54
17	1-J	384/405 (95%)	364 (95%)	17 (4%)	3 (1%)	16	54
17	2-J	384/405 (95%)	364 (95%)	17 (4%)	3 (1%)	16	54
17	3-J	384/405 (95%)	364 (95%)	17 (4%)	3 (1%)	16	54
18	1-K	387/428 (90%)	366 (95%)	16 (4%)	5 (1%)	9	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	2-K	387/428 (90%)	366 (95%)	16 (4%)	5 (1%)	9	42
18	3-K	387/428 (90%)	366 (95%)	16 (4%)	5 (1%)	9	42
19	1-L	386/437 (88%)	362 (94%)	22 (6%)	2 (0%)	24	63
19	2-L	386/437 (88%)	362 (94%)	22 (6%)	2 (0%)	24	63
19	3-L	386/437 (88%)	362 (94%)	22 (6%)	2 (0%)	24	63
20	1-M	377/434 (87%)	346 (92%)	27 (7%)	4 (1%)	11	46
20	2-M	377/434 (87%)	346 (92%)	27 (7%)	4 (1%)	11	46
20	3-M	377/434 (87%)	346 (92%)	27 (7%)	4 (1%)	11	46
21	1-N	886/945 (94%)	833 (94%)	49 (6%)	4 (0%)	24	63
21	2-N	886/945 (94%)	833 (94%)	49 (6%)	4 (0%)	24	63
21	3-N	886/945 (94%)	833 (94%)	48 (5%)	5 (1%)	21	59
22	1-O	386/393 (98%)	360 (93%)	19 (5%)	7 (2%)	6	34
22	2-O	386/393 (98%)	360 (93%)	19 (5%)	7 (2%)	6	34
22	3-O	386/393 (98%)	359 (93%)	20 (5%)	7 (2%)	6	34
23	1-P	438/445 (98%)	412 (94%)	20 (5%)	6 (1%)	9	40
23	2-P	438/445 (98%)	412 (94%)	20 (5%)	6 (1%)	9	40
23	3-P	438/445 (98%)	412 (94%)	20 (5%)	6 (1%)	9	40
24	1-Q	432/434 (100%)	400 (93%)	26 (6%)	6 (1%)	9	40
24	2-Q	432/434 (100%)	400 (93%)	26 (6%)	6 (1%)	9	40
24	3-Q	432/434 (100%)	400 (93%)	26 (6%)	6 (1%)	9	40
25	1-R	377/429 (88%)	361 (96%)	14 (4%)	2 (0%)	24	63
25	2-R	377/429 (88%)	361 (96%)	14 (4%)	2 (0%)	24	63
25	3-R	377/429 (88%)	361 (96%)	14 (4%)	2 (0%)	24	63
26	1-S	473/523 (90%)	447 (94%)	19 (4%)	7 (2%)	8	40
26	2-S	473/523 (90%)	447 (94%)	19 (4%)	7 (2%)	8	40
26	3-S	473/523 (90%)	447 (94%)	19 (4%)	7 (2%)	8	40
27	1-T	264/274 (96%)	245 (93%)	17 (6%)	2 (1%)	16	54
27	2-T	264/274 (96%)	245 (93%)	17 (6%)	2 (1%)	16	54
27	3-T	264/274 (96%)	245 (93%)	17 (6%)	2 (1%)	16	54
28	1-U	296/338 (88%)	283 (96%)	12 (4%)	1 (0%)	36	72
28	2-U	296/338 (88%)	283 (96%)	12 (4%)	1 (0%)	36	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	3-U	296/338 (88%)	283 (96%)	12 (4%)	1 (0%)	36	72
29	1-V	287/306 (94%)	263 (92%)	19 (7%)	5 (2%)	7	36
29	2-V	287/306 (94%)	263 (92%)	19 (7%)	5 (2%)	7	36
29	3-V	287/306 (94%)	263 (92%)	19 (7%)	5 (2%)	7	36
30	1-W	195/268 (73%)	176 (90%)	11 (6%)	8 (4%)	2	18
30	2-W	195/268 (73%)	176 (90%)	11 (6%)	8 (4%)	2	18
30	3-W	195/268 (73%)	176 (90%)	11 (6%)	8 (4%)	2	18
31	1-X	125/156 (80%)	111 (89%)	11 (9%)	3 (2%)	4	27
31	2-X	125/156 (80%)	111 (89%)	11 (9%)	3 (2%)	4	27
31	3-X	125/156 (80%)	111 (89%)	11 (9%)	3 (2%)	4	27
32	1-Y	47/89 (53%)	41 (87%)	4 (8%)	2 (4%)	2	17
32	2-Y	47/89 (53%)	41 (87%)	4 (8%)	2 (4%)	2	17
32	3-Y	47/89 (53%)	41 (87%)	4 (8%)	2 (4%)	2	17
33	1-Z	902/993 (91%)	827 (92%)	64 (7%)	11 (1%)	10	44
33	2-Z	902/993 (91%)	827 (92%)	64 (7%)	11 (1%)	10	44
33	3-Z	902/993 (91%)	827 (92%)	64 (7%)	11 (1%)	10	44
All	All	41130/45417 (91%)	38849 (94%)	1917 (5%)	364 (1%)	16	51

5 of 364 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	1-F	8	ASP
16	1-I	84	PRO
16	1-I	125	MET
22	1-O	19	ASP
22	1-O	20	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	3-1	162/178 (91%)	156 (96%)	6 (4%)	30	51
1	3-h	162/178 (91%)	152 (94%)	10 (6%)	16	38
2	3-2	185/214 (86%)	182 (98%)	3 (2%)	55	70
2	3-i	185/214 (86%)	175 (95%)	10 (5%)	20	41
3	3-3	172/173 (99%)	168 (98%)	4 (2%)	44	64
3	3-j	172/173 (99%)	167 (97%)	5 (3%)	37	58
4	3-4	173/175 (99%)	167 (96%)	6 (4%)	32	53
4	3-k	173/175 (99%)	165 (95%)	8 (5%)	24	45
5	3-5	169/235 (72%)	166 (98%)	3 (2%)	51	68
5	3-l	169/235 (72%)	158 (94%)	11 (6%)	15	37
6	3-6	185/201 (92%)	179 (97%)	6 (3%)	34	56
6	3-m	185/201 (92%)	174 (94%)	11 (6%)	18	39
7	3-7	195/224 (87%)	189 (97%)	6 (3%)	35	56
7	3-n	198/224 (88%)	186 (94%)	12 (6%)	17	38
8	3-A	206/210 (98%)	198 (96%)	8 (4%)	28	49
8	3-a	206/210 (98%)	194 (94%)	12 (6%)	18	40
9	3-B	209/209 (100%)	205 (98%)	4 (2%)	50	67
9	3-b	209/209 (100%)	193 (92%)	16 (8%)	12	32
10	3-C	203/216 (94%)	195 (96%)	8 (4%)	28	49
10	3-c	203/216 (94%)	196 (97%)	7 (3%)	32	54
11	3-D	212/226 (94%)	200 (94%)	12 (6%)	18	40
11	3-d	212/226 (94%)	202 (95%)	10 (5%)	23	45
12	3-E	198/215 (92%)	186 (94%)	12 (6%)	17	38
12	3-e	198/215 (92%)	187 (94%)	11 (6%)	19	40
13	3-F	192/193 (100%)	182 (95%)	10 (5%)	21	42
13	3-f	190/193 (98%)	182 (96%)	8 (4%)	26	48
14	3-G	201/239 (84%)	195 (97%)	6 (3%)	36	57
14	3-g	201/239 (84%)	194 (96%)	7 (4%)	32	53
15	3-H	330/399 (83%)	315 (96%)	15 (4%)	24	46
16	3-I	342/385 (89%)	331 (97%)	11 (3%)	34	56
17	3-J	336/352 (96%)	319 (95%)	17 (5%)	21	42
18	3-K	342/374 (91%)	329 (96%)	13 (4%)	29	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	3-L	332/377 (88%)	317 (96%)	15 (4%)	24	46
20	3-M	329/375 (88%)	317 (96%)	12 (4%)	31	52
21	3-N	745/797 (94%)	718 (96%)	27 (4%)	31	52
22	3-O	363/368 (99%)	342 (94%)	21 (6%)	18	40
23	3-P	412/415 (99%)	392 (95%)	20 (5%)	22	43
24	3-Q	391/391 (100%)	367 (94%)	24 (6%)	17	38
25	3-R	333/379 (88%)	319 (96%)	14 (4%)	26	48
26	3-S	447/489 (91%)	431 (96%)	16 (4%)	31	52
27	3-T	249/256 (97%)	232 (93%)	17 (7%)	14	36
28	3-U	271/308 (88%)	267 (98%)	4 (2%)	57	72
29	3-V	253/268 (94%)	240 (95%)	13 (5%)	21	42
30	3-W	171/230 (74%)	162 (95%)	9 (5%)	20	41
31	3-X	116/144 (81%)	113 (97%)	3 (3%)	40	62
32	3-Y	50/81 (62%)	49 (98%)	1 (2%)	48	66
33	3-Z	773/850 (91%)	730 (94%)	43 (6%)	19	40
All	All	11910/13054 (91%)	11383 (96%)	527 (4%)	27	47

5 of 527 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	3-h	44	CYS
2	3-i	144	GLN
1	3-h	43	CYS
7	3-n	120	GLN
21	3-N	546	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 199 such sidechains are listed below:

Mol	Chain	Res	Type
26	3-S	135	ASN
30	3-W	44	ASN
26	3-S	177	ASN
28	3-U	50	ASN
33	3-Z	129	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

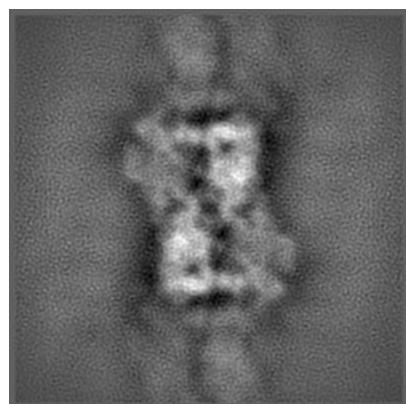
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60960. These allow visual inspection of the internal detail of the map and identification of artifacts.

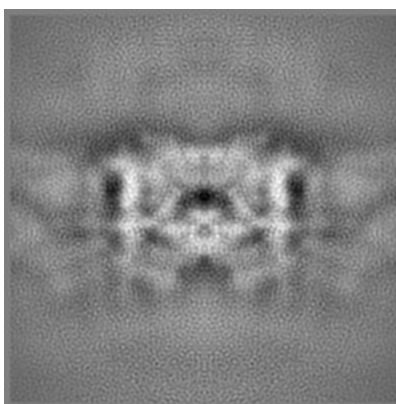
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

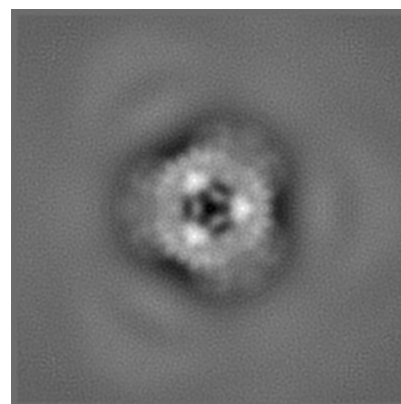
6.1.1 Primary map



X

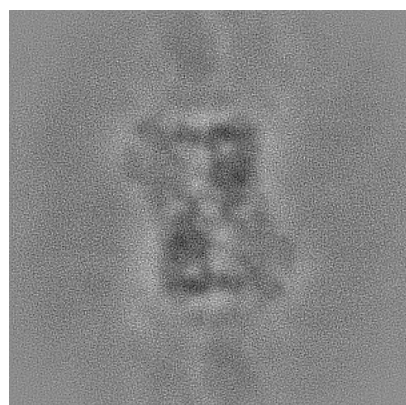


Y

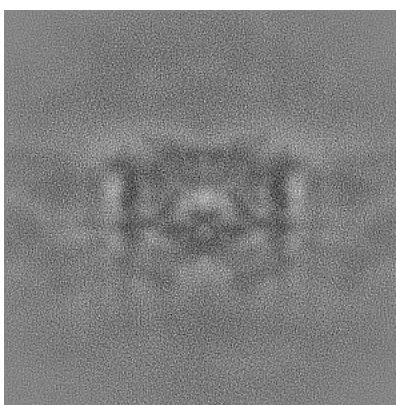


Z

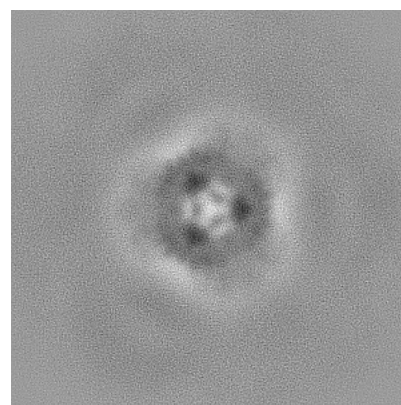
6.1.2 Raw map



X



Y

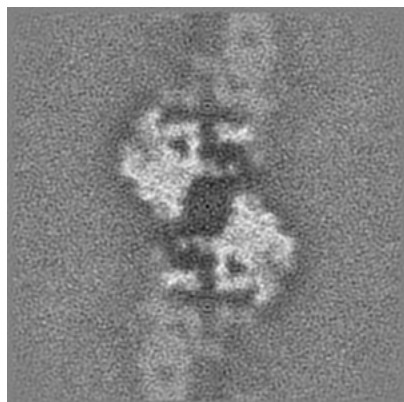


Z

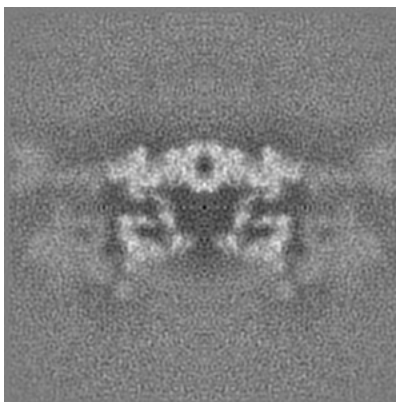
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

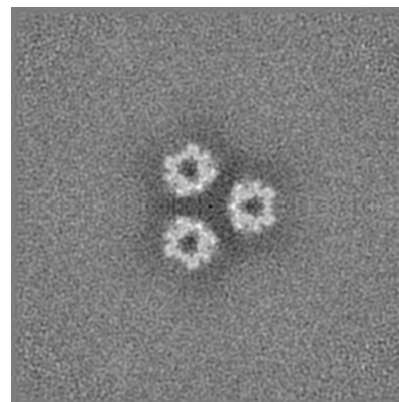
6.2.1 Primary map



X Index: 192

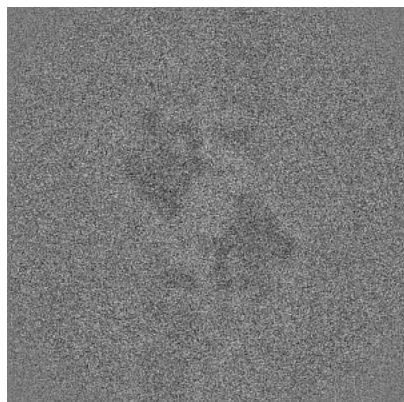


Y Index: 192

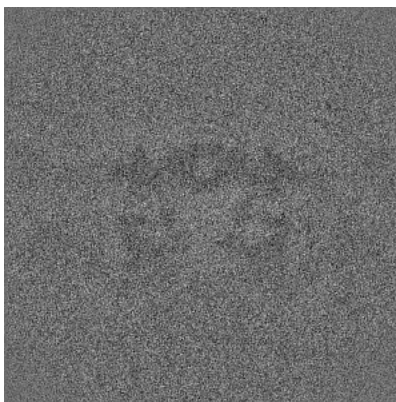


Z Index: 192

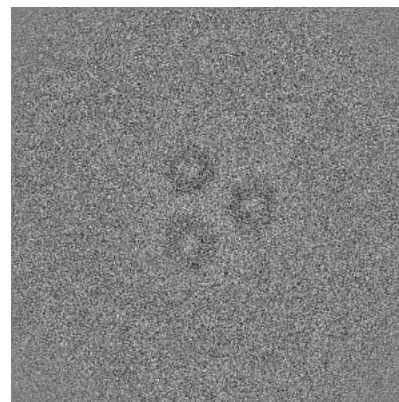
6.2.2 Raw map



X Index: 192



Y Index: 192

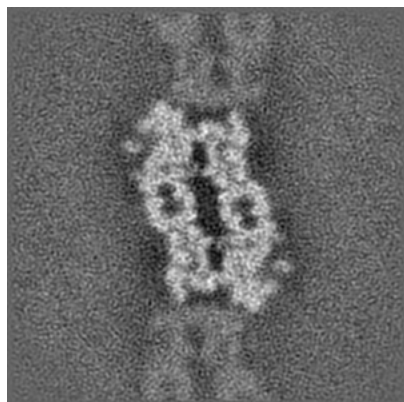


Z Index: 192

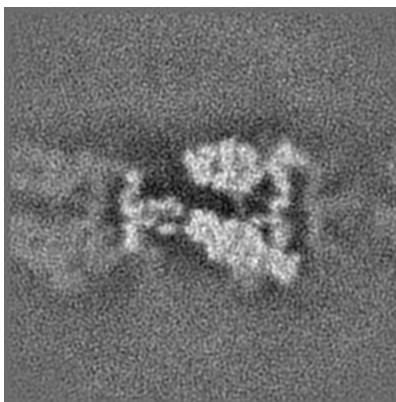
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

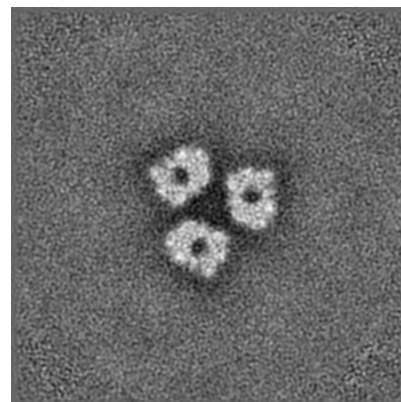
6.3.1 Primary map



X Index: 176

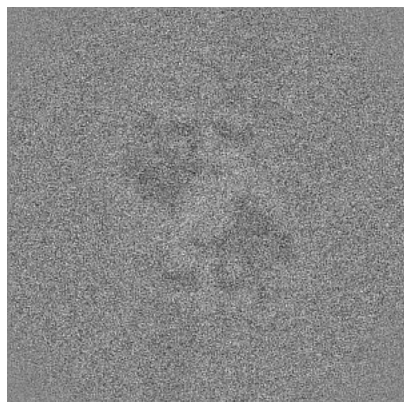


Y Index: 209

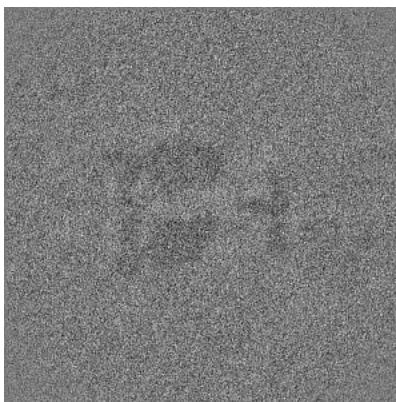


Z Index: 205

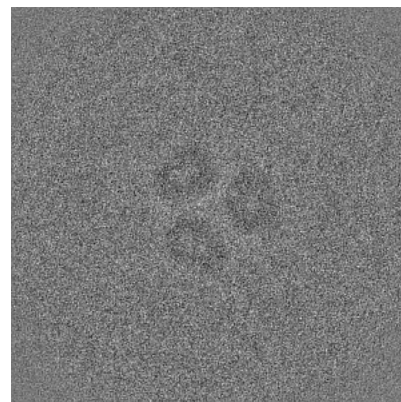
6.3.2 Raw map



X Index: 194



Y Index: 178

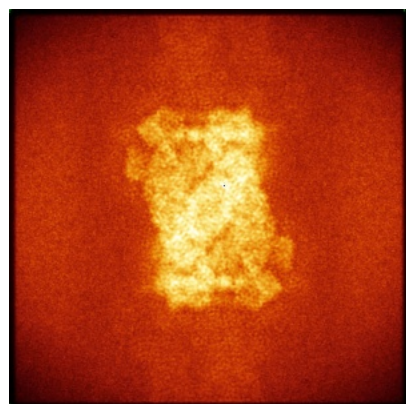


Z Index: 199

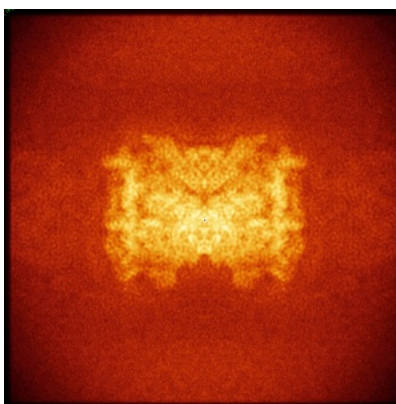
The images above show the largest variance slices of the map in three orthogonal directions.

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

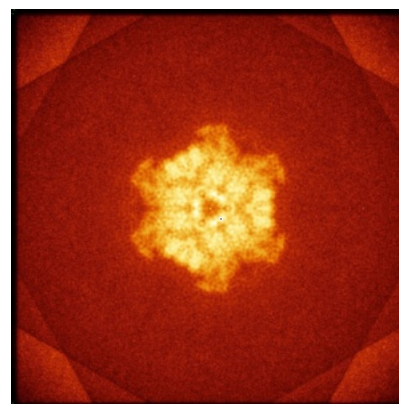
6.4.1 Primary map



X

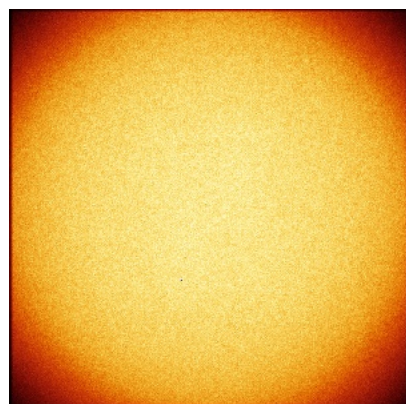


Y

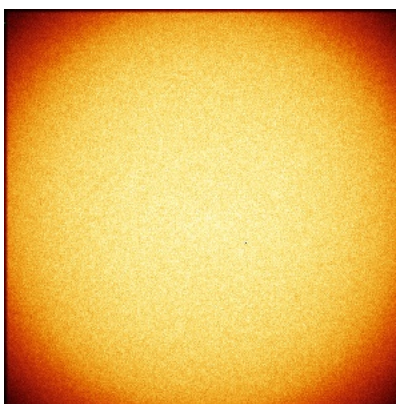


Z

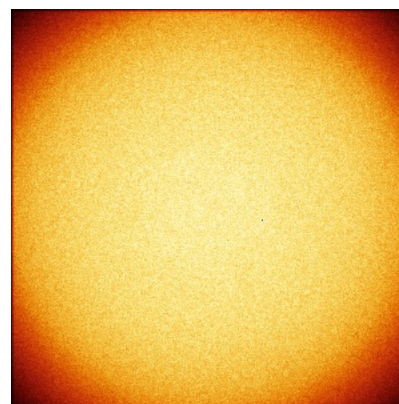
6.4.2 Raw map



X



Y

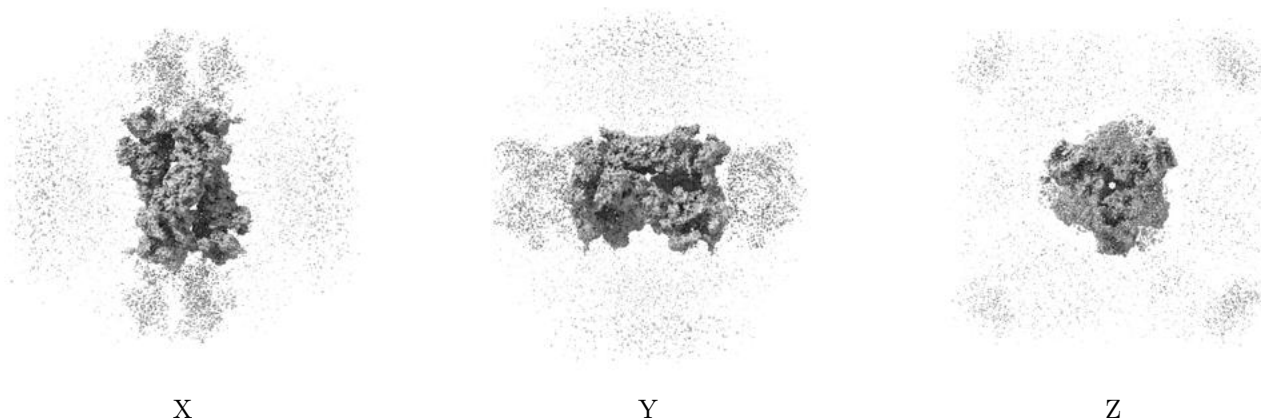


Z

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.

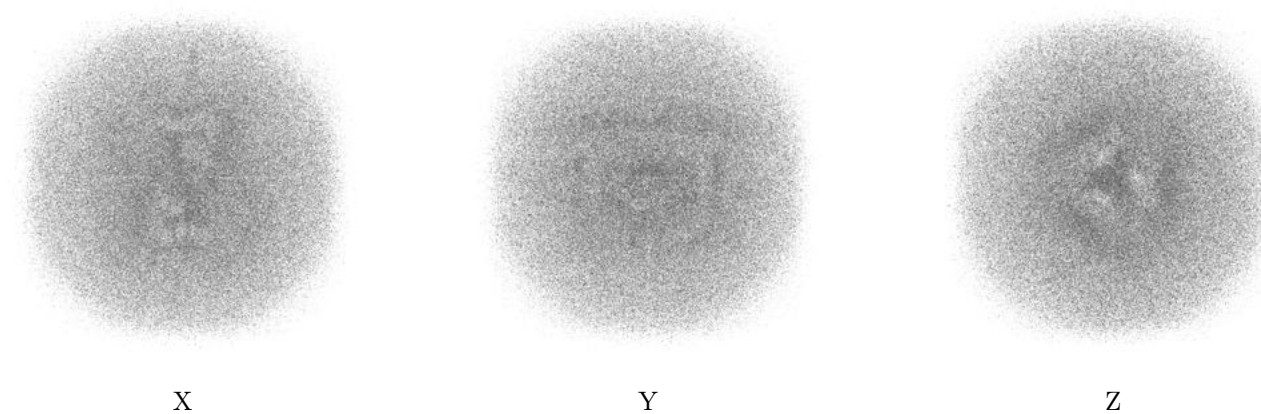
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.27. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

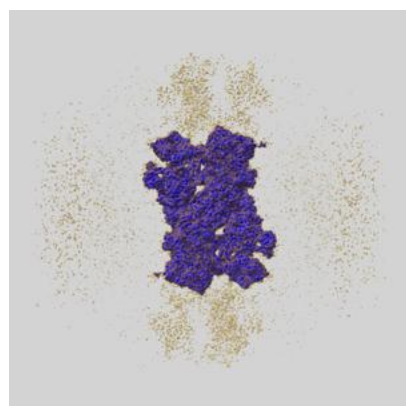
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

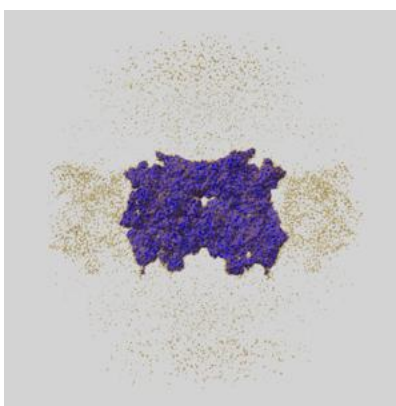
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

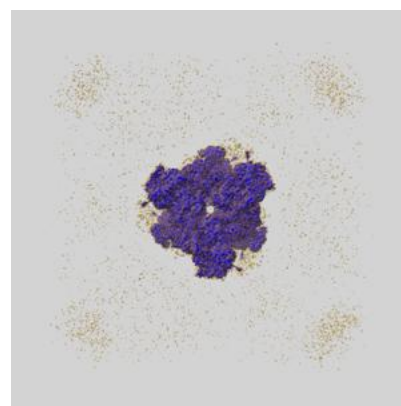
6.6.1 emd_60960_msk_1.map [i](#)



X



Y

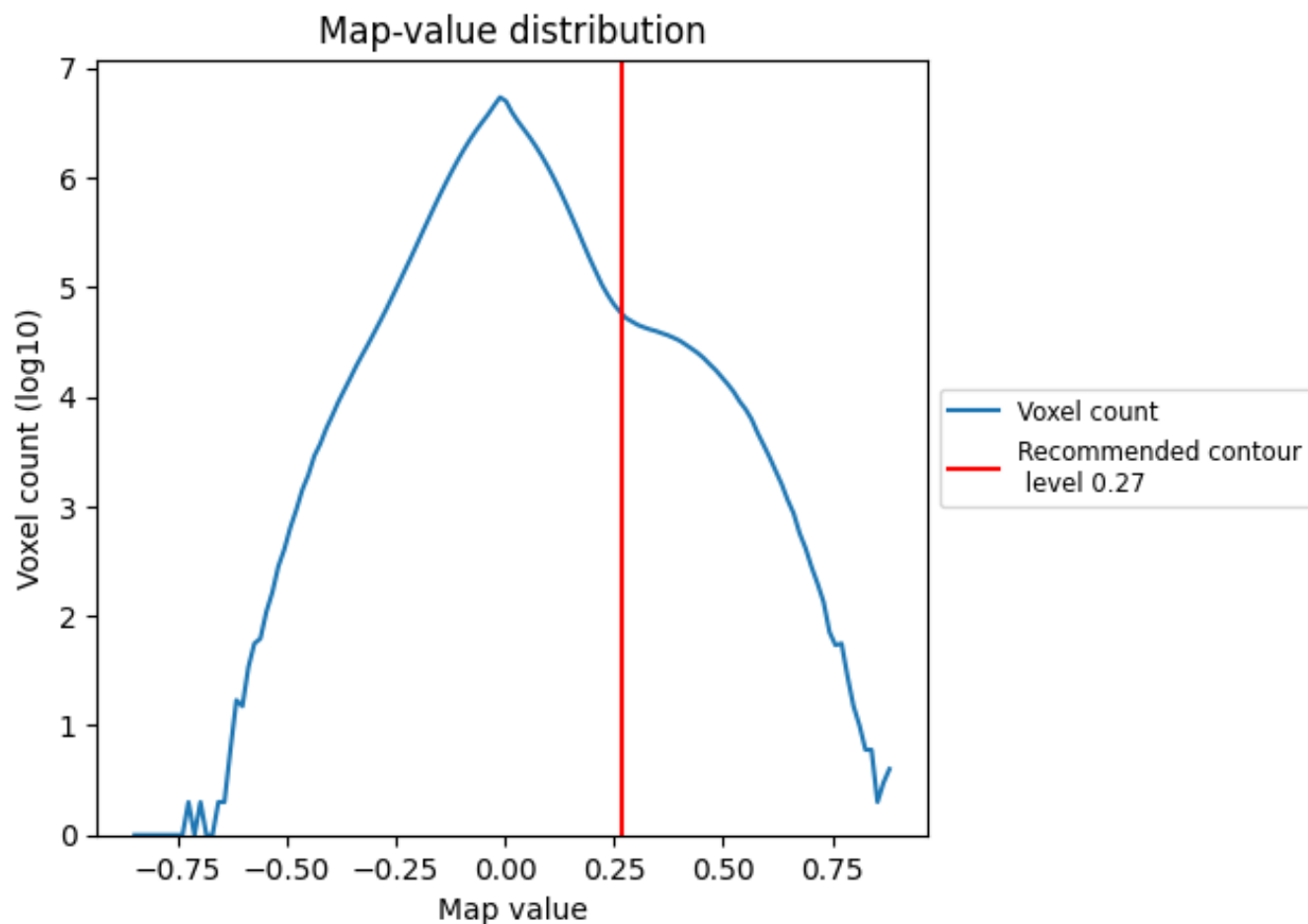


Z

7 Map analysis [i](#)

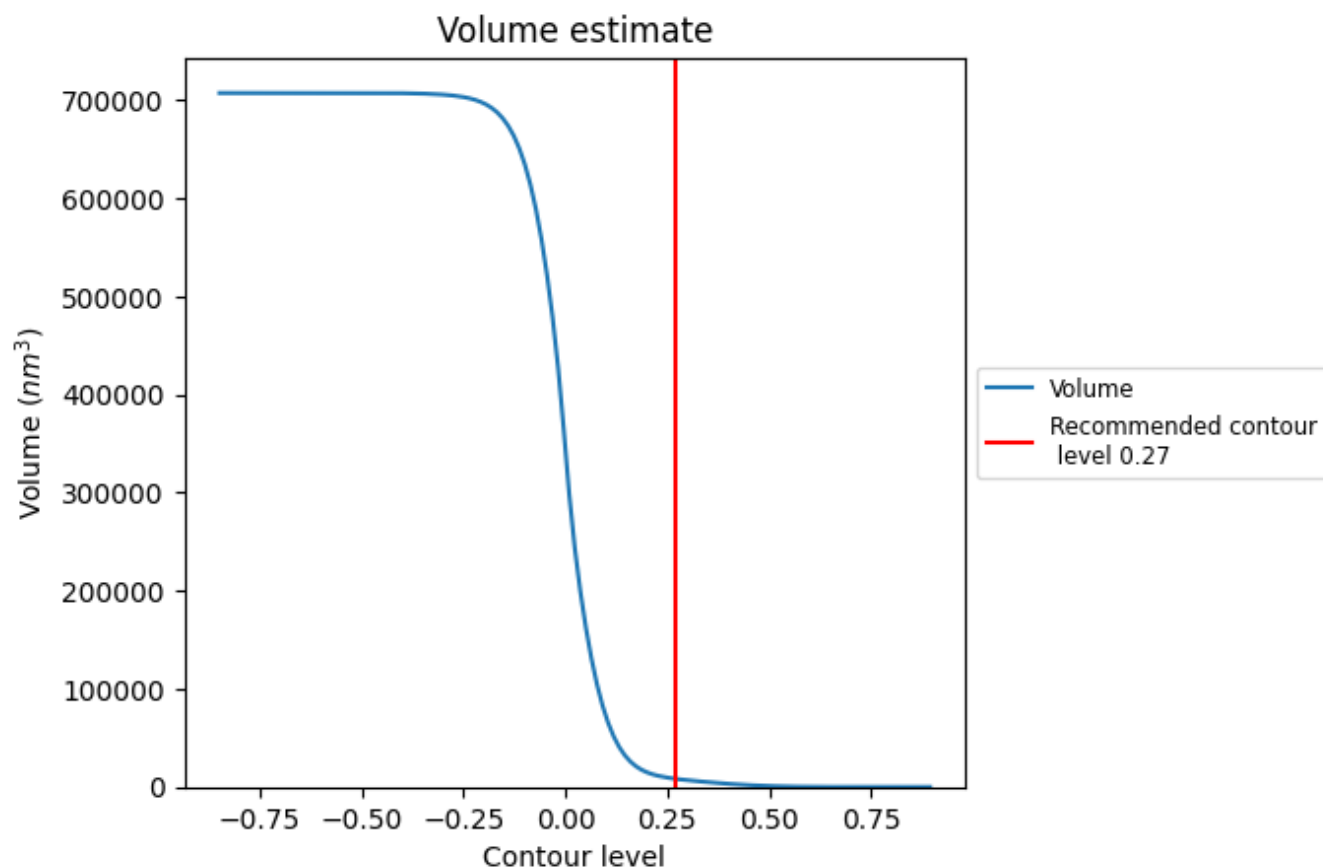
This section contains the results of statistical analysis of the map.

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.

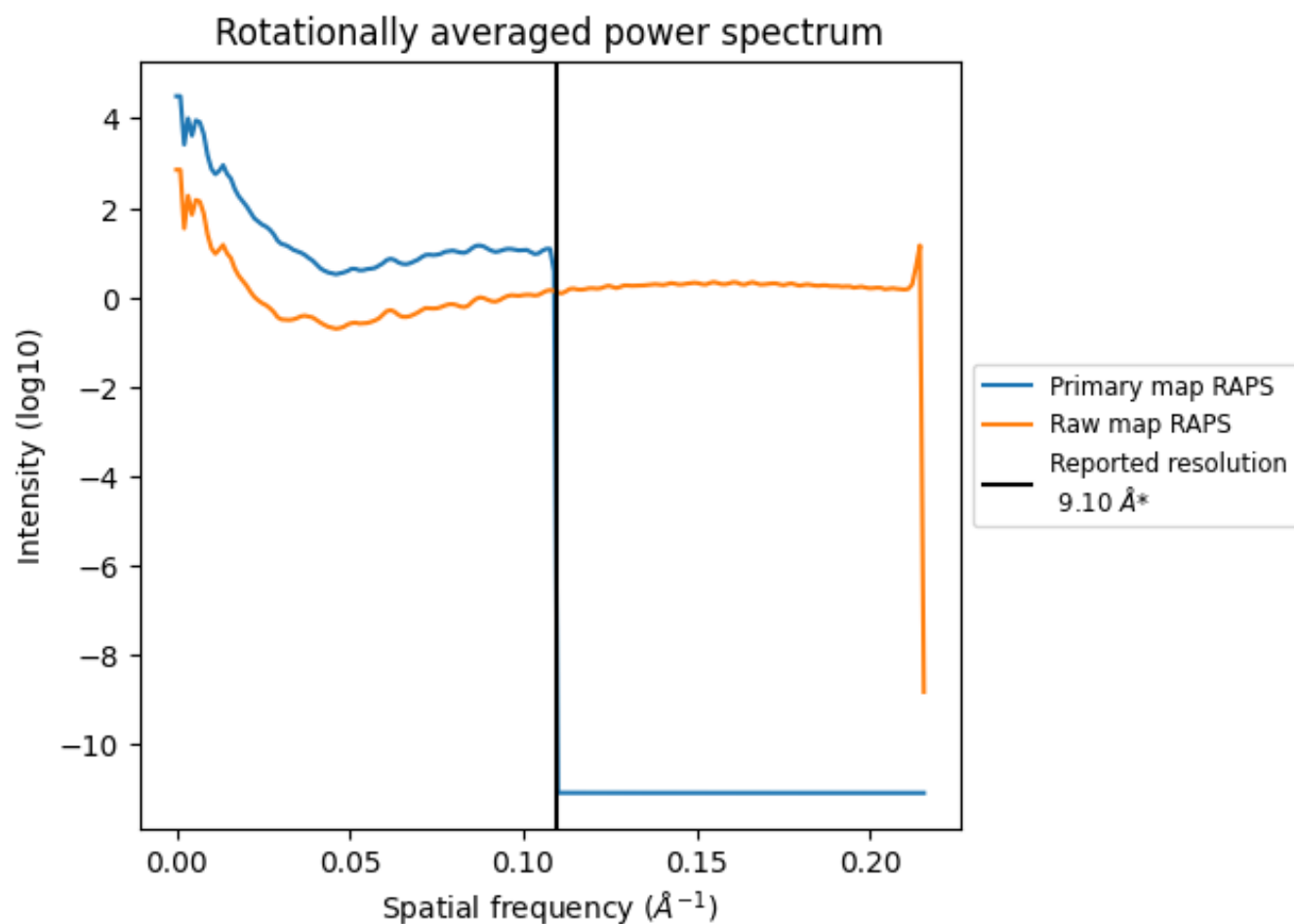
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 8289 nm^3 ; this corresponds to an approximate mass of 7488 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

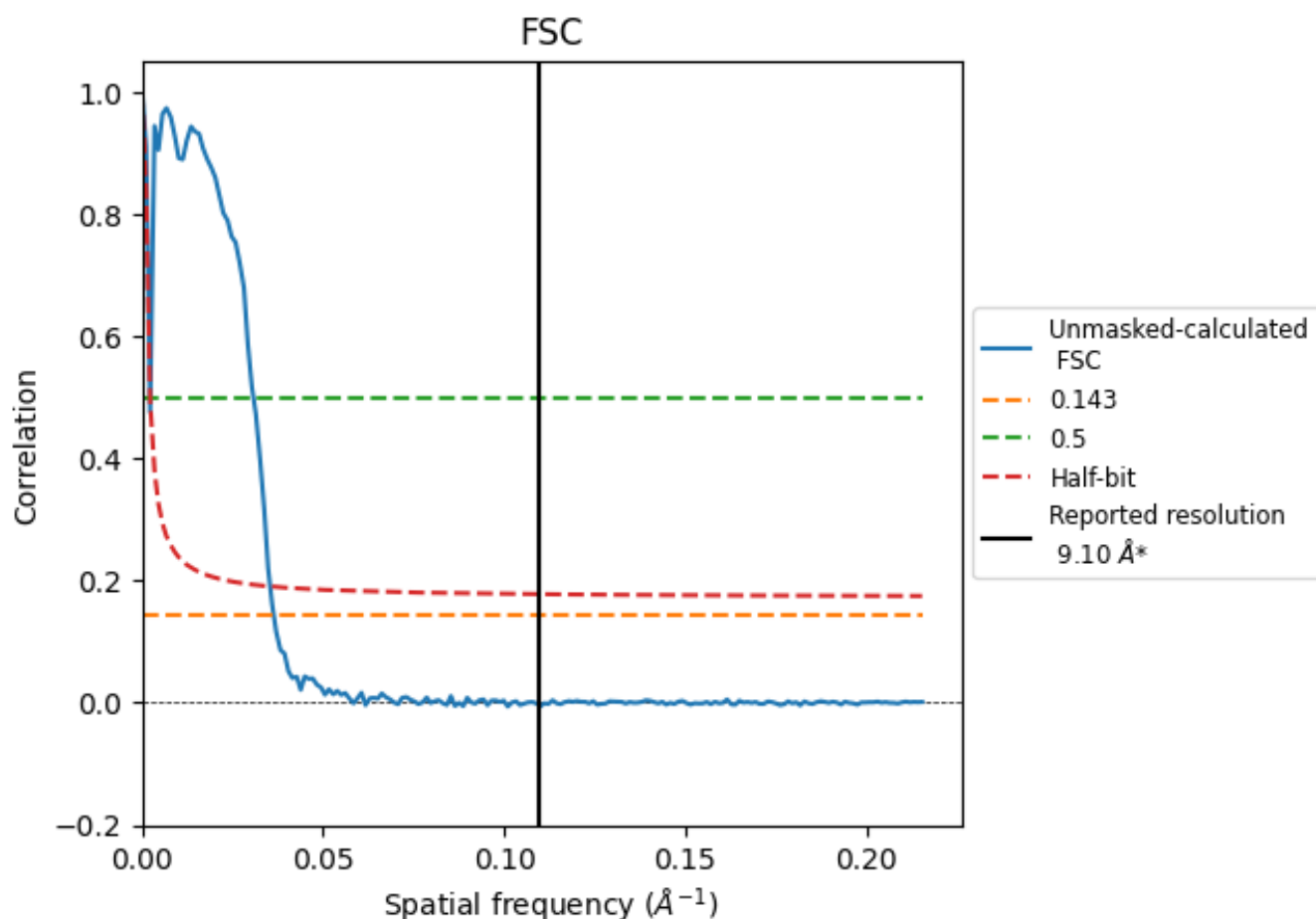


*Reported resolution corresponds to spatial frequency of 0.110 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.110 Å⁻¹

8.2 Resolution estimates [i](#)

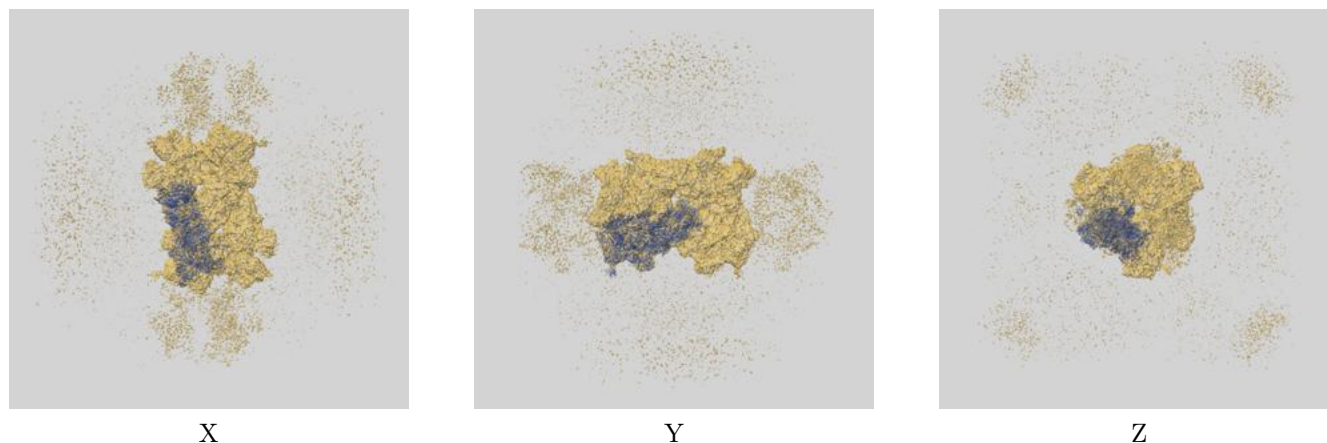
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	27.47	454.55	500.00

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 27.47 differs from the reported value 9.1 by more than 10 %

9 Map-model fit [i](#)

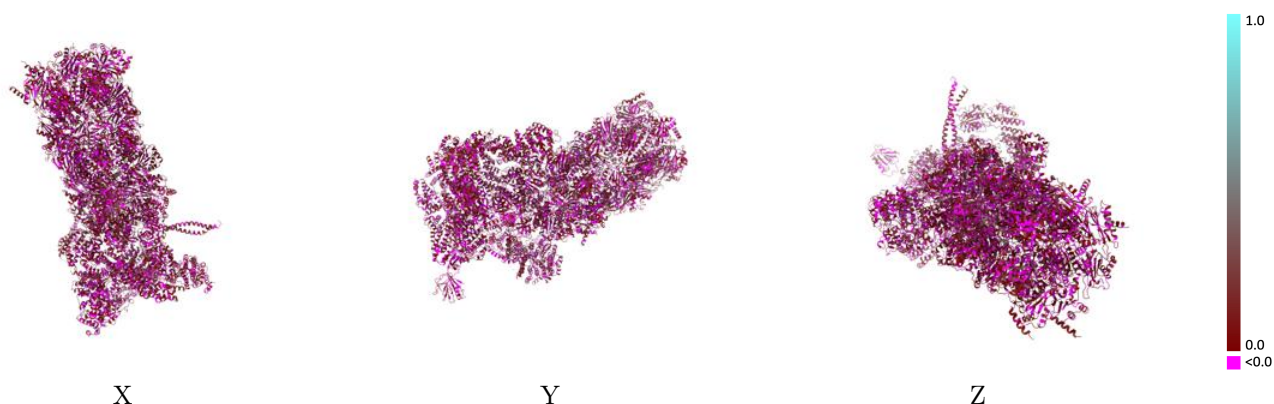
This section contains information regarding the fit between EMDB map EMD-60960 and PDB model 9IWR. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.27 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](#)

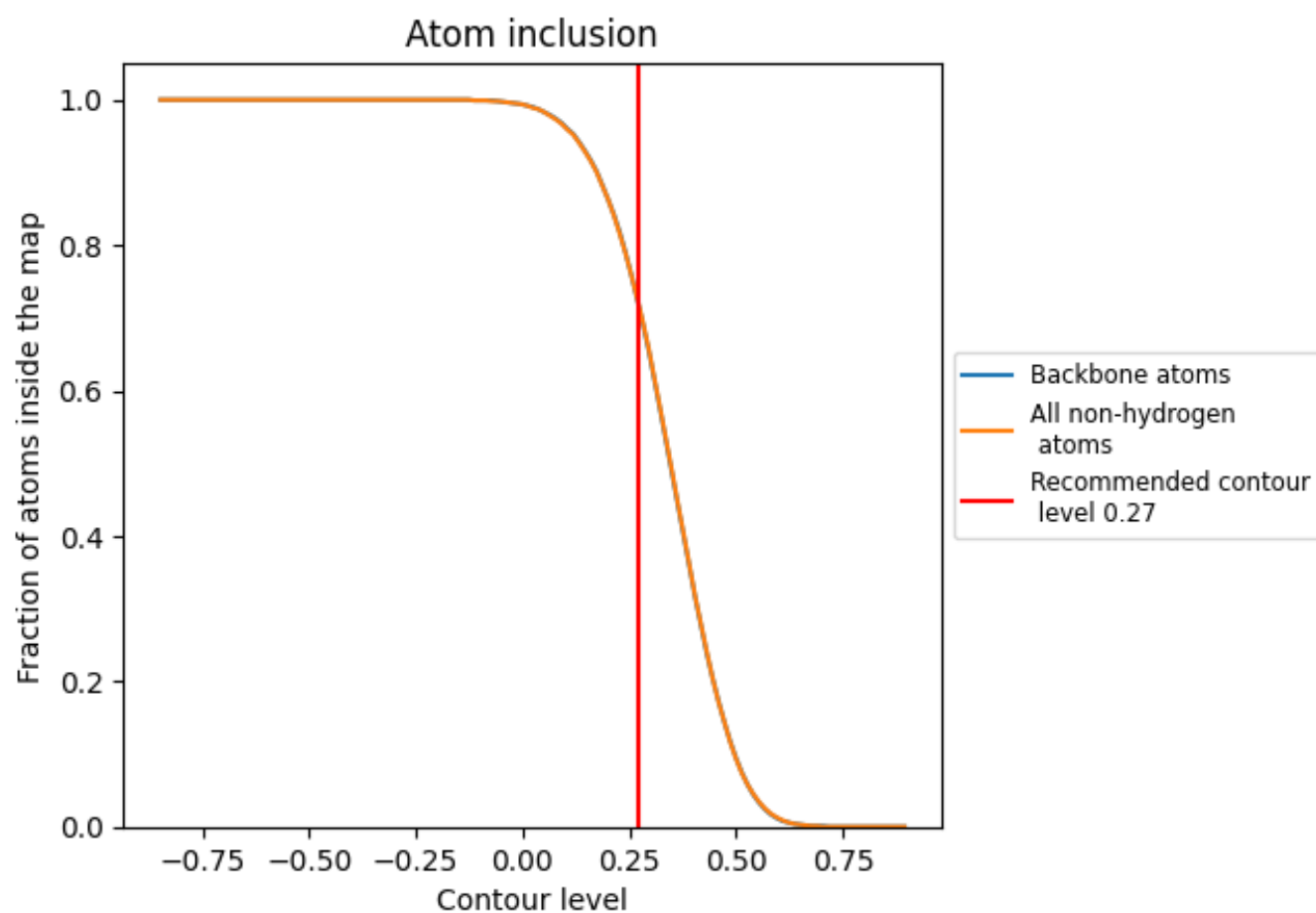


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 72% 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 (0.27) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7230	 0.0580
1	 0.8610	 0.0680
2	 0.8010	 0.0650
3	 0.8250	 0.0630
4	 0.7490	 0.0650
5	 0.8380	 0.0770
6	 0.7980	 0.0650
7	 0.8440	 0.0620
A	 0.7610	 0.0410
B	 0.7770	 0.0590
C	 0.7800	 0.0600
D	 0.7560	 0.0630
E	 0.7430	 0.0430
F	 0.7910	 0.0610
G	 0.8410	 0.0770
H	 0.7070	 0.0540
I	 0.6900	 0.0640
J	 0.6660	 0.0690
K	 0.7390	 0.0690
L	 0.6910	 0.0520
M	 0.6990	 0.0630
N	 0.6680	 0.0490
O	 0.6970	 0.0740
P	 0.6330	 0.0660
Q	 0.7220	 0.0770
R	 0.7430	 0.0680
S	 0.6860	 0.0390
T	 0.6100	 0.0430
U	 0.6920	 0.0570
V	 0.7200	 0.0430
W	 0.7280	 0.0570
X	 0.1580	 0.0210
Y	 0.4880	 0.0490
Z	 0.5700	 0.0430
a	 0.7650	 0.0460



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Chain	Atom inclusion	Q-score
b	 0.8070	 0.0570
c	 0.7890	 0.0560
d	 0.7420	 0.0660
e	 0.7150	 0.0470
f	 0.7750	 0.0540
g	 0.7960	 0.0580
h	 0.8740	 0.0720
i	 0.8330	 0.0630
j	 0.8630	 0.0600
k	 0.7740	 0.0500
l	 0.8280	 0.0600
m	 0.8290	 0.0600
n	 0.8450	 0.0520