



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:30 PM UTC

PDB ID : 9YF5 / pdb_00009yf5
EMDB ID : EMD-72877
Title : N4 Empty Particle C6 Tail
Authors : Bellis, N.F.; Cingolani, G.
Deposited on : 2025-09-25
Resolution : 3.65 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:

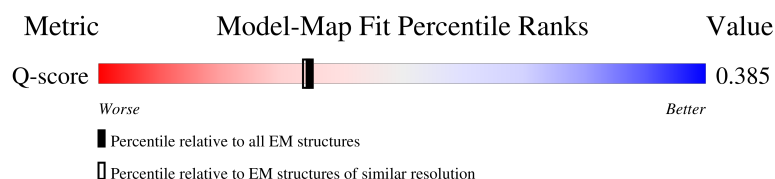
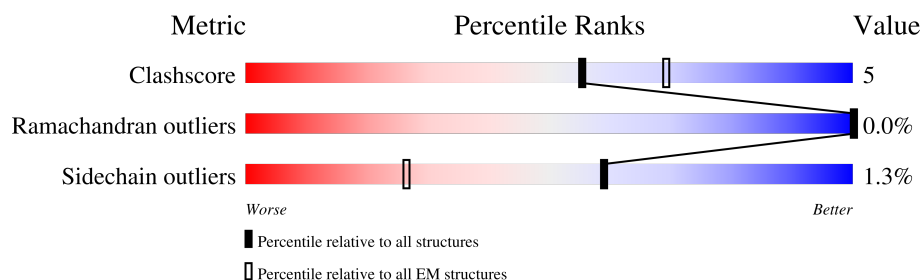
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.65 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	11564 (3.15 - 4.15)

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	AA	236	17% 91% 8%
1	AB	236	20% 88% 12%
1	AC	236	16% 90% 9%
1	AD	236	19% 90% 10%

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Mol	Chain	Length	Quality of chain
1	AE	236	16% 92% 8%
1	AF	236	18% 88% 11%
1	AG	236	17% 91% 9%
1	AH	236	20% 88% 11%
1	AI	236	16% 91% 8%
1	AJ	236	19% 89% 11%
1	AK	236	16% 90% 9%
1	AL	236	18% 89% 11%
2	LA	1382	70% 70% 15% 15%
2	LB	1382	70% 69% 16% 15%
2	LC	1382	70% 69% 16% 15%
2	LD	1382	70% 69% 16% 15%
2	LE	1382	70% 70% 15% 15%
2	LF	1382	70% 70% 15% 15%
3	SA	417	78% 83% 15% .
3	SB	417	79% 84% 15% .
3	SC	417	79% 86% 13% .
3	SD	417	78% 84% 15% .
3	SE	417	79% 85% 14% .
3	SF	417	79% 85% 14% .
4	TA	299	25% 87% 13%
4	TB	299	25% 87% 13%
4	TC	299	23% 88% 12%
4	TD	299	26% 87% 13%
4	TE	299	25% 88% 11%

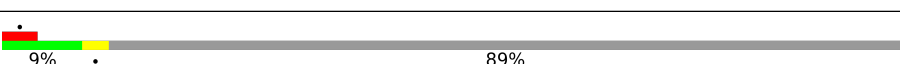
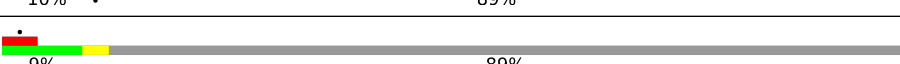
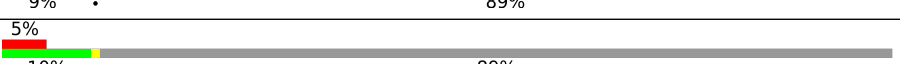
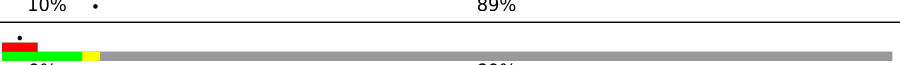
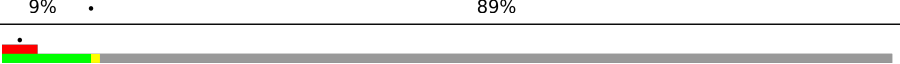
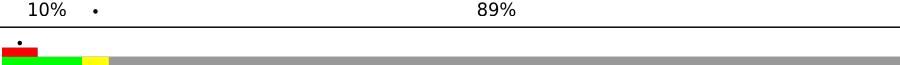
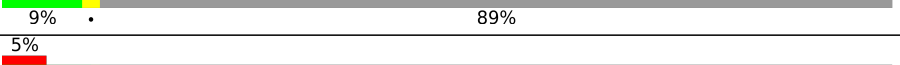
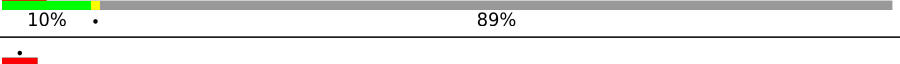
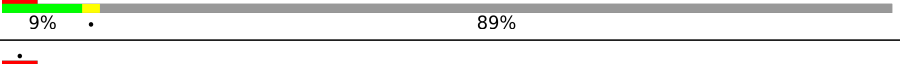
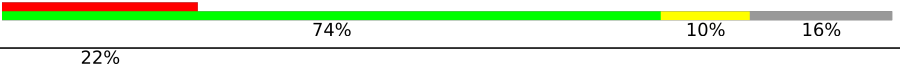
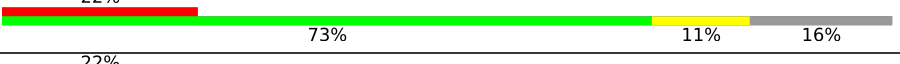
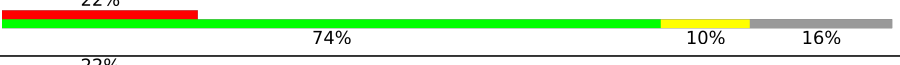
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Mol	Chain	Length	Quality of chain
4	TF	299	24% 87% 13%
4	TG	299	25% 88% 12%
4	TH	299	25% 87% 13%
4	TI	299	23% 87% 12%
4	TJ	299	26% 86% 14%
4	TK	299	25% 87% 12%
4	TL	299	24% 85% 14%
5	XA	556	6% 10% 87%
5	XB	556	5% 11% 87%
5	XC	556	6% 10% 87%
5	XD	556	11% 87%
5	XE	556	6% 9% 87%
5	XF	556	11% 87%
5	XG	556	5% 10% 87%
5	XH	556	5% 11% 87%
5	XI	556	5% 10% 87%
5	XJ	556	11% 87%
5	XK	556	6% 10% 87%
5	XL	556	12% 87%
5	YA	556	5% 10% 88%
5	YB	556	5% 10% 88%
5	YC	556	5% 10% 88%
5	YD	556	5% 10% 88%
5	YE	556	10% 88%
5	YF	556	6% 10% 88%

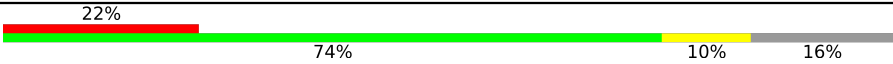
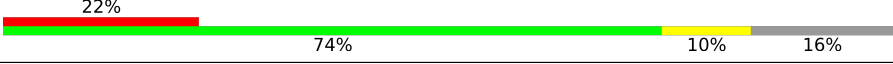
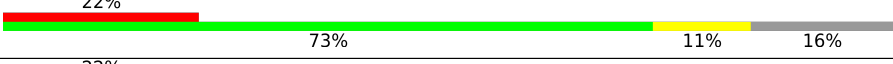
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Mol	Chain	Length	Quality of chain
5	YG	556	
5	YH	556	
5	YI	556	
5	YJ	556	
5	YK	556	
5	YL	556	
5	ZA	556	
5	ZB	556	
5	ZC	556	
5	ZD	556	
5	ZE	556	
5	ZF	556	
5	ZG	556	
5	ZH	556	
5	ZI	556	
5	ZJ	556	
5	ZK	556	
5	ZL	556	
6	PA	763	
6	PB	763	
6	PC	763	
6	PD	763	
6	PE	763	
6	PF	763	
6	PG	763	

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Mol	Chain	Length	Quality of chain
6	PH	763	
6	PI	763	
6	PJ	763	
6	PK	763	
6	PL	763	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 207084 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 30 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AB	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AC	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AD	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AE	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AF	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AG	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AH	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AI	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AJ	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AK	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		
1	AL	236	Total	C	N	O	S	0	0
			1912	1201	327	375	9		

- Molecule 2 is a protein called Non-contractile tail sheath.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LA	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		
2	LB	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		
2	LC	1181	Total	C	N	O	S	0	0
			9341	5952	1572	1776	41		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	LD	1181	Total 9341	C 5952	N 1572	O 1776	S 41	0	0
2	LE	1181	Total 9341	C 5952	N 1572	O 1776	S 41	0	0
2	LF	1181	Total 9341	C 5952	N 1572	O 1776	S 41	0	0

- Molecule 3 is a protein called Gp64.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	415	Total 3383	C 2212	N 537	O 616	S 18	0	0
3	SB	415	Total 3383	C 2212	N 537	O 616	S 18	0	0
3	SC	415	Total 3383	C 2212	N 537	O 616	S 18	0	0
3	SD	415	Total 3383	C 2212	N 537	O 616	S 18	0	0
3	SE	415	Total 3383	C 2212	N 537	O 616	S 18	0	0
3	SF	415	Total 3383	C 2212	N 537	O 616	S 18	0	0

- Molecule 4 is a protein called Gp54.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	TA	298	Total 2263	C 1408	N 381	O 464	S 10	0	0
4	TB	298	Total 2263	C 1408	N 381	O 464	S 10	0	0
4	TC	298	Total 2263	C 1408	N 381	O 464	S 10	0	0
4	TD	298	Total 2263	C 1408	N 381	O 464	S 10	0	0
4	TE	298	Total 2263	C 1408	N 381	O 464	S 10	0	0
4	TF	298	Total 2263	C 1408	N 381	O 464	S 10	0	0
4	TG	298	Total 2263	C 1408	N 381	O 464	S 10	0	0
4	TH	298	Total 2263	C 1408	N 381	O 464	S 10	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	TI	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TJ	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TK	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		
4	TL	298	Total	C	N	O	S	0	0
			2263	1408	381	464	10		

- Molecule 5 is a protein called 60 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	XA	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XB	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YA	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	YB	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZA	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZB	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	XC	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XD	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YC	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	YD	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZC	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZD	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	XE	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XF	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YE	68	Total	C	N	O	S	0	0
			543	355	89	96	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	YF	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZE	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZF	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	XG	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XH	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YG	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	YH	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZG	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZH	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	XI	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XJ	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YI	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	YJ	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZI	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZJ	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	XK	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	XL	72	Total	C	N	O	S	0	0
			575	371	92	107	5		
5	YK	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	YL	68	Total	C	N	O	S	0	0
			543	355	89	96	3		
5	ZK	63	Total	C	N	O	S	0	0
			508	330	82	93	3		
5	ZL	63	Total	C	N	O	S	0	0
			508	330	82	93	3		

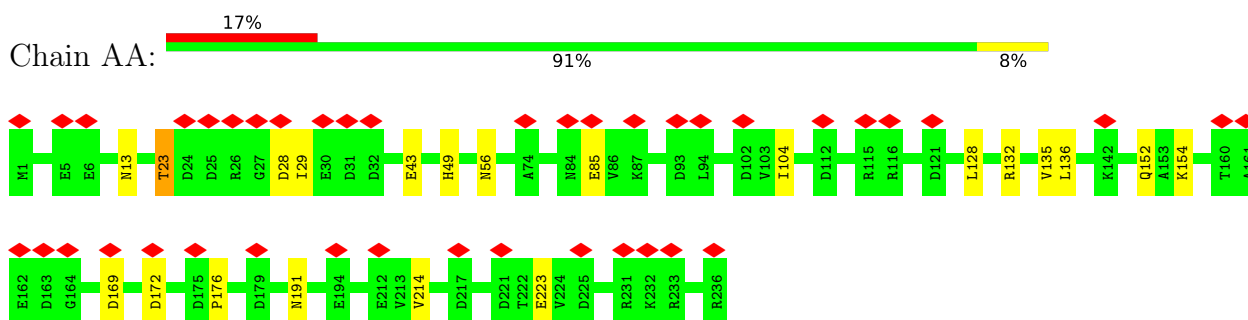
- Molecule 6 is a protein called Probable portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	PA	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PB	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PC	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PD	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PE	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PF	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PG	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PH	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PI	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PJ	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PK	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		
6	PL	642	Total	C	N	O	S	0	0
			5094	3200	895	977	22		

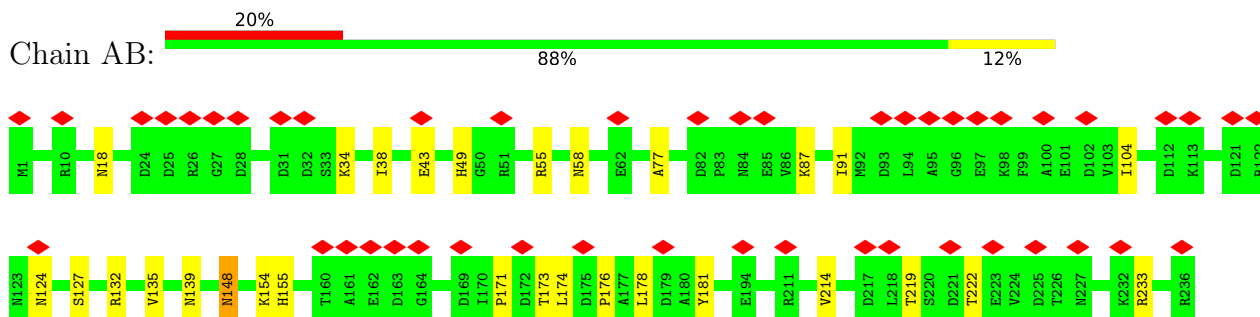
3 Residue-property plots

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

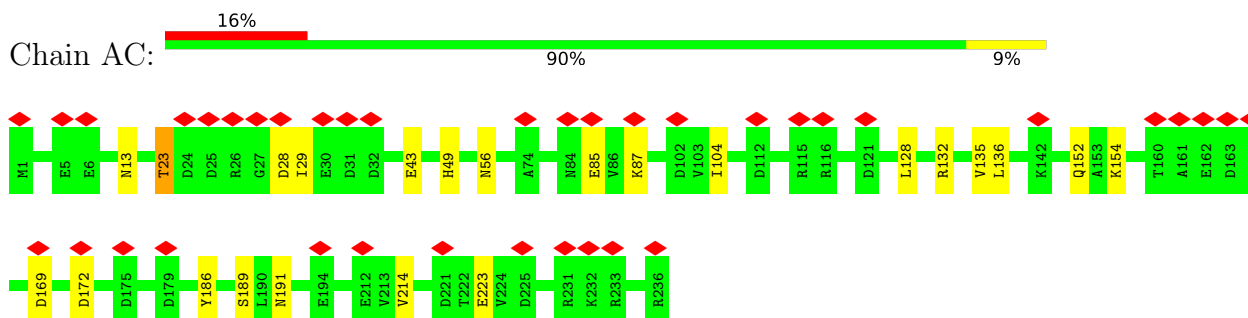
- Molecule 1: 30 kDa protein



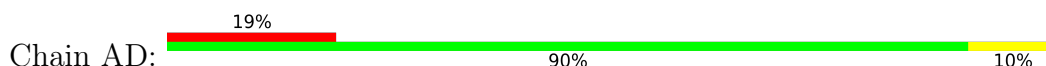
- Molecule 1: 30 kDa protein

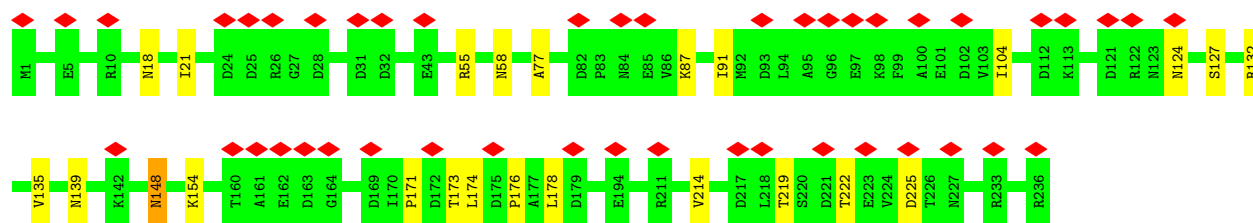


- Molecule 1: 30 kDa protein

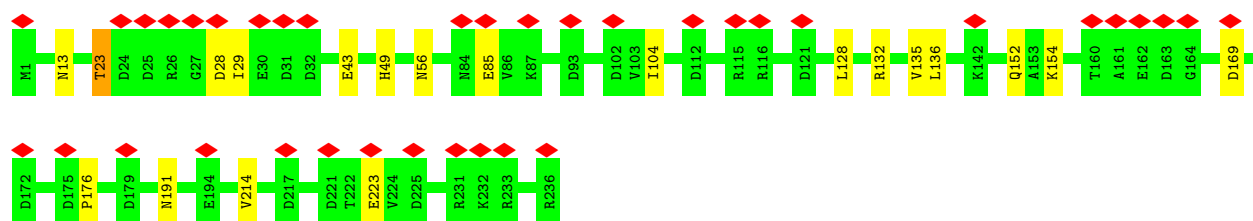


- Molecule 1: 30 kDa protein

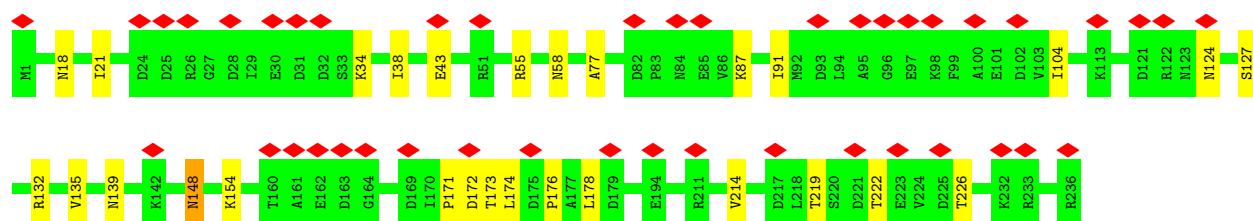
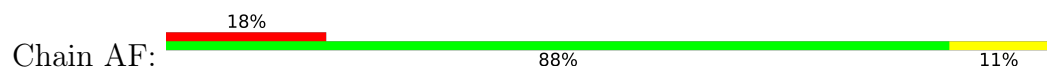




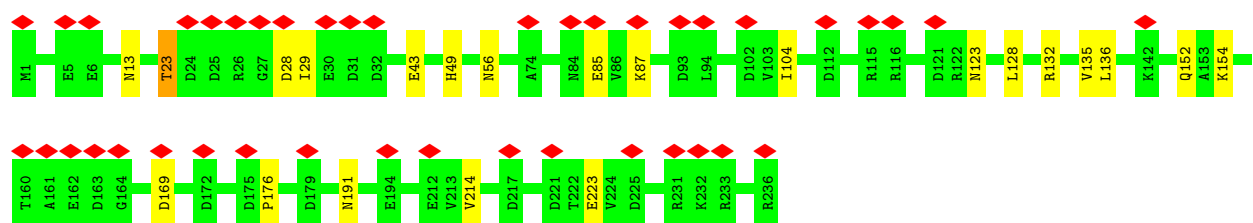
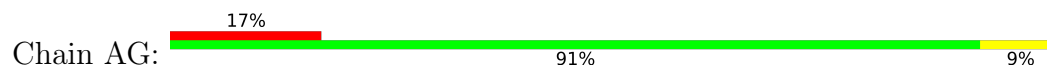
- Molecule 1: 30 kDa protein



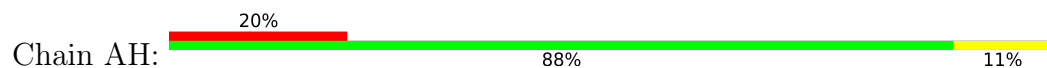
- Molecule 1: 30 kDa protein

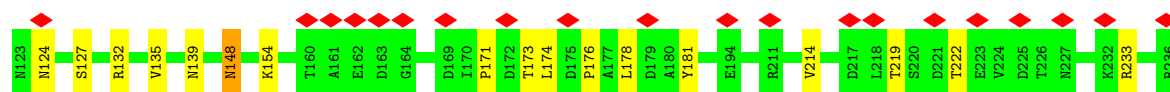


- Molecule 1: 30 kDa protein

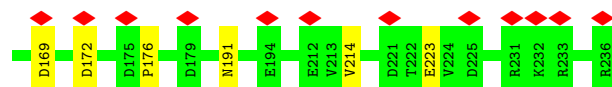
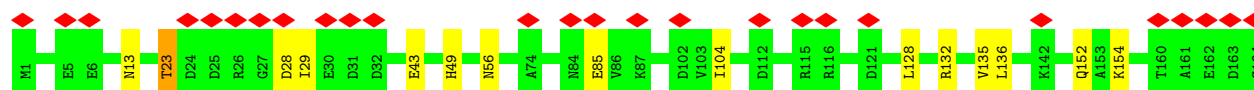


- Molecule 1: 30 kDa protein

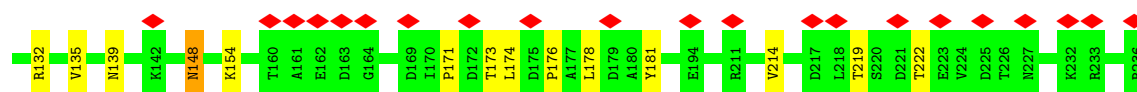
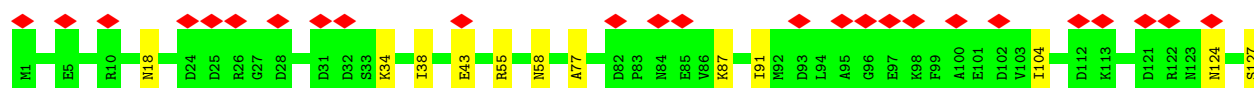
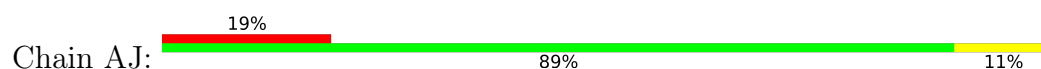




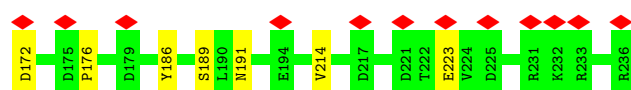
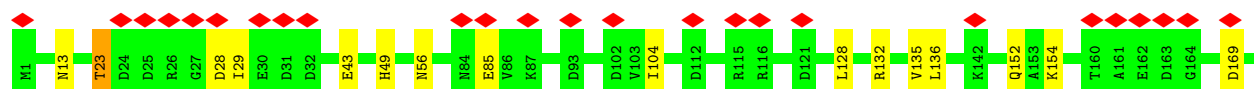
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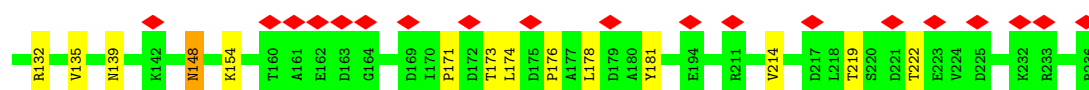
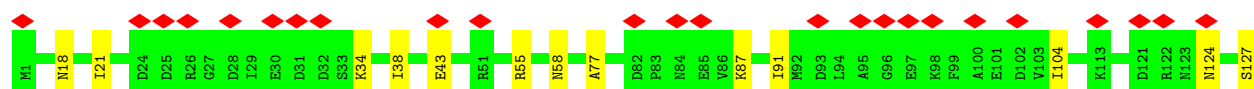
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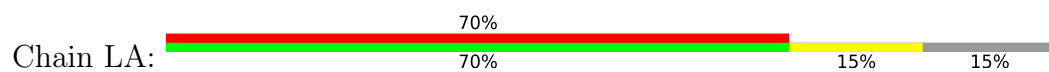
- Molecule 1: 30 kDa protein



- Molecule 1: 30 kDa protein



- Molecule 2: Non-contractile tail sheath



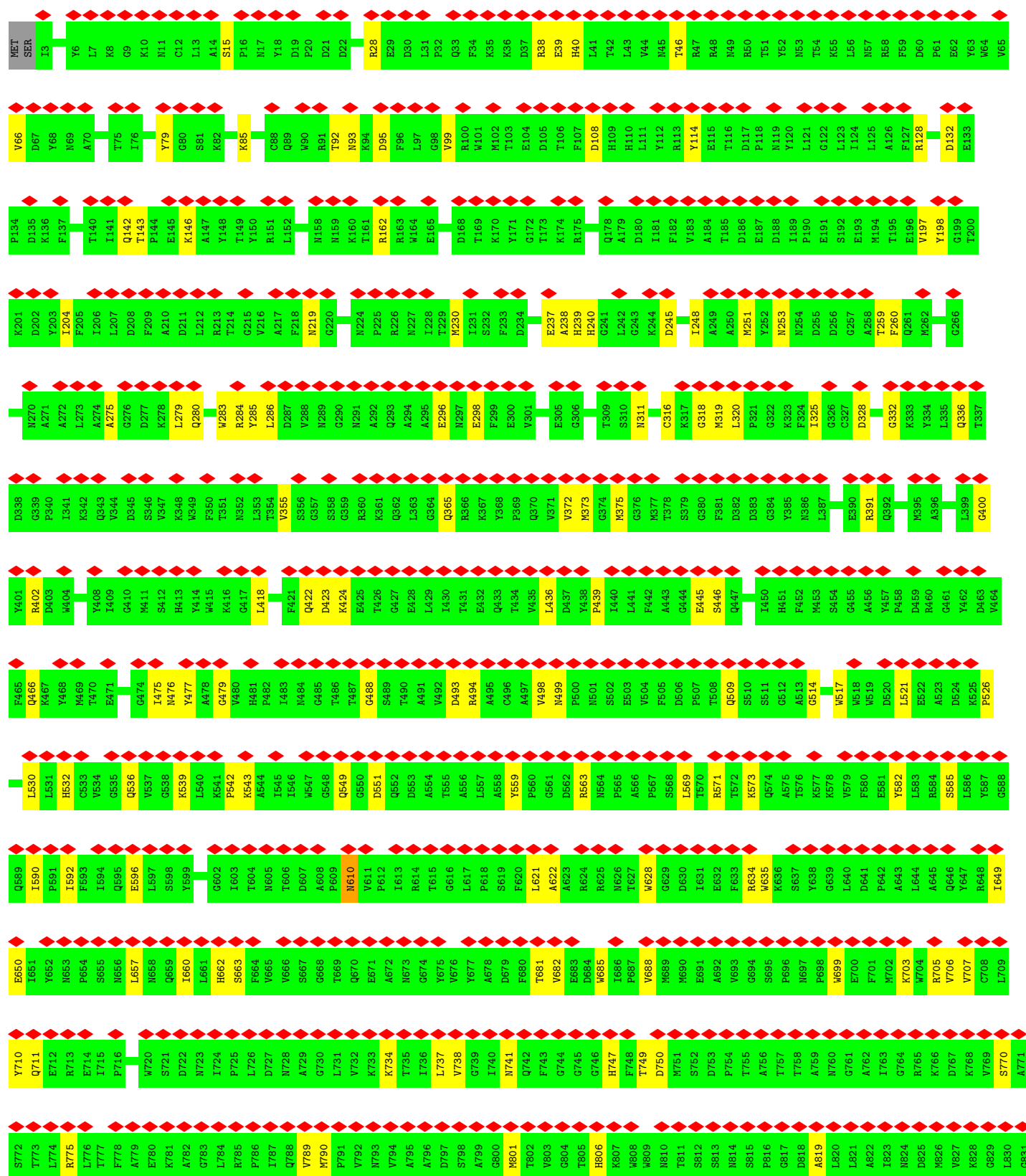
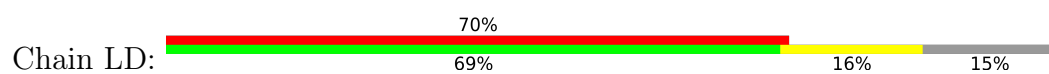
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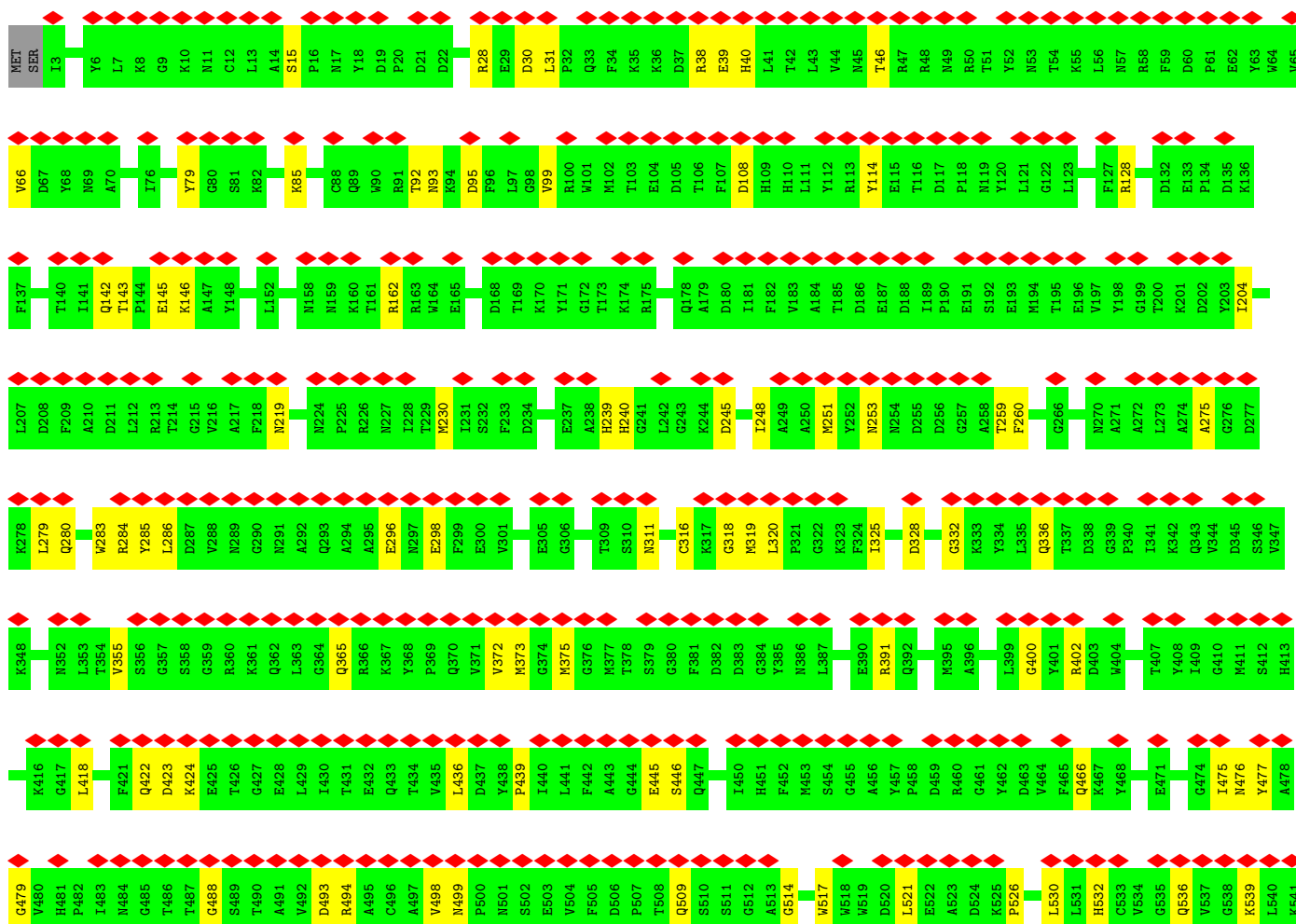
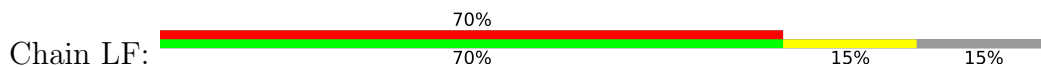


- Molecule 2: Non-contractile tail sheath



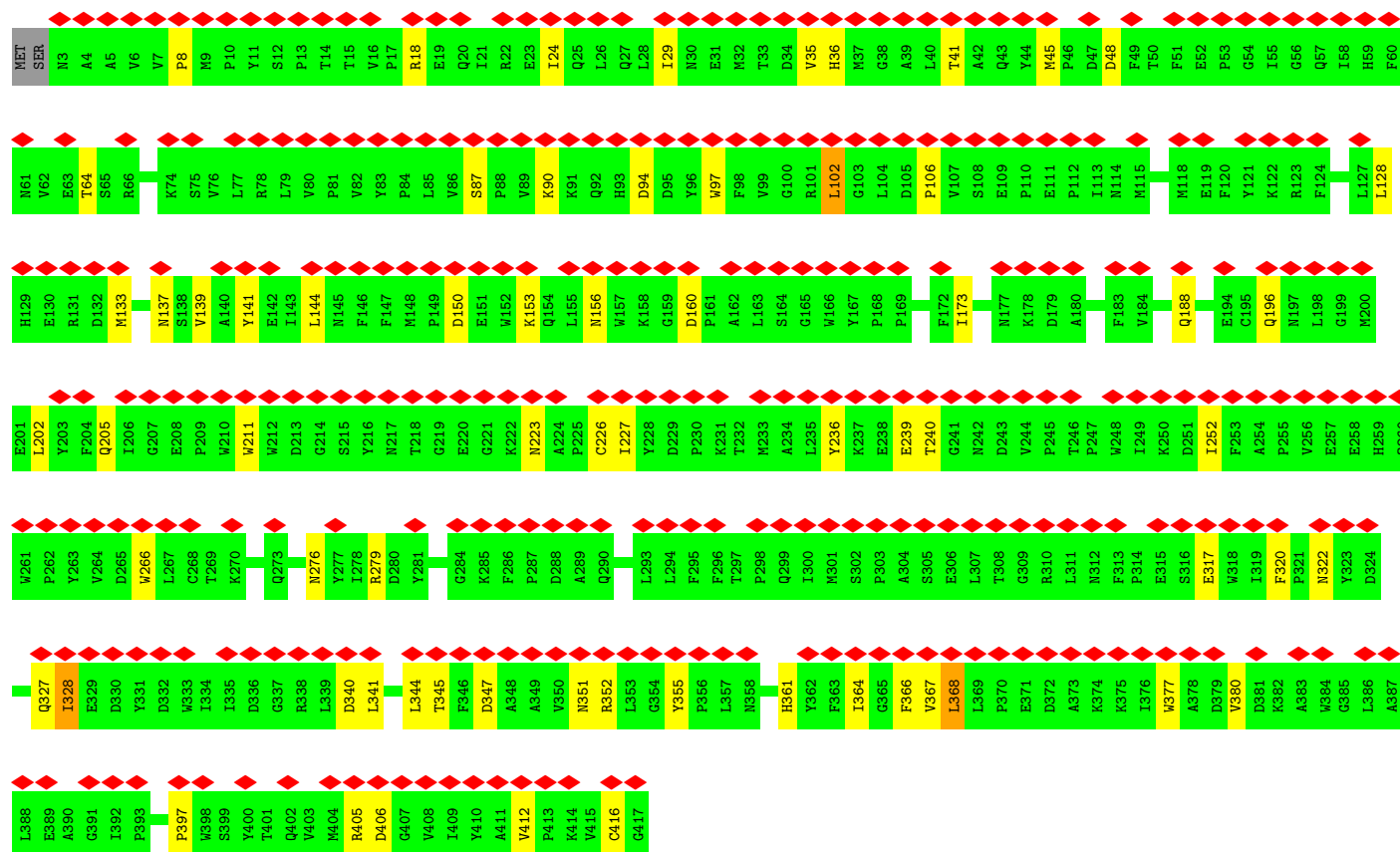
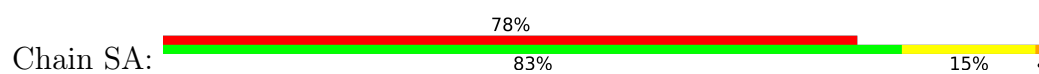
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G1021	N901	K781	N841	K781	S721	L661	G602	L540	A478	N413	D345	A274
A1022	D902	A782	P842	A782	D722	H662	I603	P542	G479	K416	S346	A275
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- Molecule 2: Non-contractile tail sheath

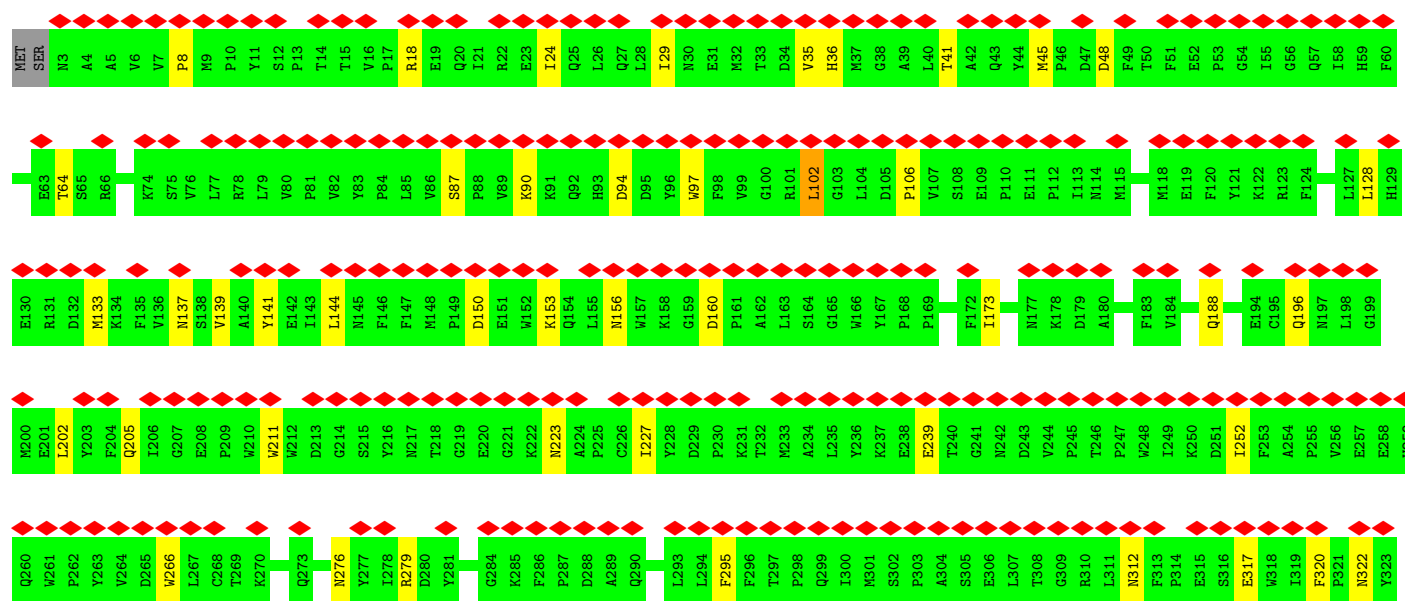
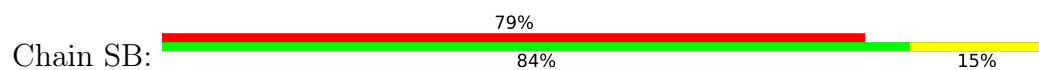


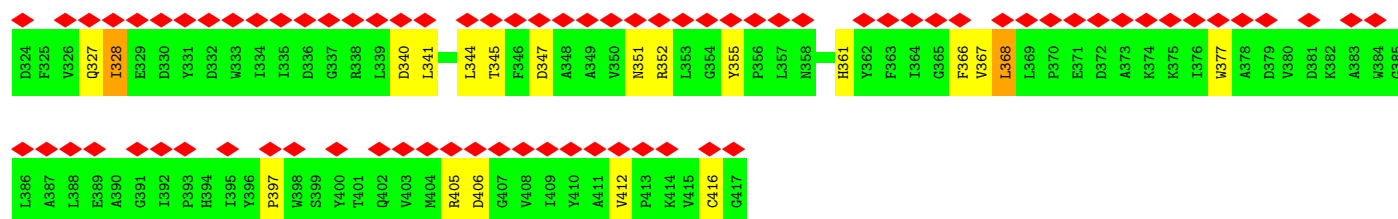
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LYS	GLU	LYS	Q1087	G1027	A967	A907	Y947	F787	D727	V665	T605	A544
TRP	ASP	MET	L1088	T1028	L968	T908	M948	F788	N728	V666	T606	I545
LYS	ASP	ASP	K1089	I1029	N969	T909	K949	F789	N729	S667	D607	I546
LYS	ASP	ASP	A1090	T1030	N970	T910	D950	F790	A730	G668	A608	W547
PRO	GLY	PRO	A1091	S1031	N971	V911	V851	F791	L731	T669	P609	G548
VAL	GLY	VAL	K1092	E1032	R972	R912	N952	F792	V732	Q670	N610	Q549
VAL	GLY	VAL	P1093	E1033	A973	D913	S953	F793	K733	E671	V611	G550
GLY	GLY	GLY	L1094	V1034	T974	K914	S954	F794	K734	A672	P612	D551
ARG	GLY	ARG	N1095	V1035	N975	Q915	T955	F795	T735	N673	I613	Q552
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VAL	VAL	VAL	D1097	T1037	P977	Q917	P857	F797	L737	G675	T615	A554
ARG	THR	ARG	I1098	L1038	D978	N918	A858	F798	V738	V676	G616	T555
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ALA	ALA	ALA	F1100	D1040	W980	T920	M860	G800	I740	A678	P618	L557
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THR	THR	THR	W1102	Q1042	L981	N922	T862	T802	T742	F680	F620	Y559
VAL	THR	VAL	V1103	M1043	R983	T923	F963	V903	F743	T681	L621	P560
THR	GLY	THR	G1104	A1044	P984	G924	E964	G804	G744	A622	A622	G561
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ALA	ALA	ALA	P1106	N1046	A986	K926	S966	H806	G746	D684	R624	R563
THR	GLY	THR	G1047	G1047	N987	L927	N967	K907	H747	W685	R625	N564
ILE	ILE	ILE	W1108	D1048	L988	G928	K968	W908	F748	I686	N626	P565
SER	GLN	SER	Q1109	T1049	Q989	S929	A969	W909	T749	P687	T627	P566
ASP	GLN	ASP	L1110	L1050	L990	F930	M870	N810	D750	W688	W628	A566
GLN	ALA	GLN	W1111	M1051	G991	V931	L871	T811	M751	M689	G629	P567
PHE	LYS	PHE	F1112	M1052	R992	P932	A872	S812	S752	M690	D630	S568
VAL	LYS	VAL	W1113	S1053	K993	G933	W873	N813	D753	E691	I631	L569
ASN	ASN	ASN	V1114	F1054	L994	S934	M874	N814	P754	A692	E632	T571
LEU	LEU	LEU	N1115	S1055	A994	N935	R875	S815	T755	G694	F633	K572
VAL	VAL	VAL	T1116	V1056	T995	L936	T876	P816	A756	S695	R634	K573
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THR	THR	THR	W1118	E1058	D997	T938	W878	D818	T758	S637	K636	A575
ARG	ARG	ARG	N1119	Y1059	I998	T939	N879	N819	A759	Y638	Y638	T576
GLU	GLU	GLU	D1120	A1060	K999	Y940	G879	A819	A759	P698	G639	K577
GLY	GLY	GLY	S1121	A1061	M1000	R941	N880	L820	N760	W699	L640	V579
VAL	VAL	VAL	K1122	S1062	T1001	N942	P881	L821	G761	E700	D641	F580
ALA	ALA	ALA	T1123	G1063	W1002	V943	N882	A822	A762	P642	P642	E581
ALA	ALA	ALA	W1124	G1064	D1003	E944	L883	I823	I763	M702	A643	Y582
TYR	TYR	TYR	I1125	A1065	N1004	S945	E884	N824	G764	K703	L644	L583
GLY	GLY	GLY	F1126	V1066	R1005	S946	I885	D825	T765	W704	A645	R584
ASN	ASN	ASN	F1127	G1067	A1006	W947	W886	M826	K766	R705	A645	R584
THR	THR	THR	K1128	A1068	G1007	W948	F887	V827	D767	V706	Q646	L586
VAL	VAL	VAL	E1129	S1069	I1008	Y949	Q888	K828	K768	V707	Y687	S585
ALA	ALA	ALA	W1130	S1070	T1009	Y950	G889	G829	V769	C708	G648	G588
LEU	LEU	LEU	S1131	S1071	H1010	T951	A890	L830	S770	L709	I649	Q589
TYR	TYR	TYR	S1132	F1072	W1011	V952	T891	G831	A771	Y710	E650	I590
ALA	ALA	ALA	E1133	G1073	K1012	E963	N993	V832	T772	Q711	I651	F591
PHE	PHE	PHE	L1135	V1075	A1014	F965	W894	P834	L774	E712	Y652	I592
GLY	GLY	GLY	T1136	V1076	N1015	H956	F995	D835	R775	E714	P654	I594
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GLY	GLY	GLY	W1137	N1078	H1017	T858	V897	F837	T777	P716	N656	E596
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SER	SER	SER	A1140	S1080	T1019	P960	P899	E839	A779	S721	N658	S598
			E1141	Y1081	T1020	E961	N901	A840	F780	D722	Q659	Y599
			Q1142	G1083	G1021	L962	D902	N841	K781	D723	I660	G602
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• Molecule 3: Gp64

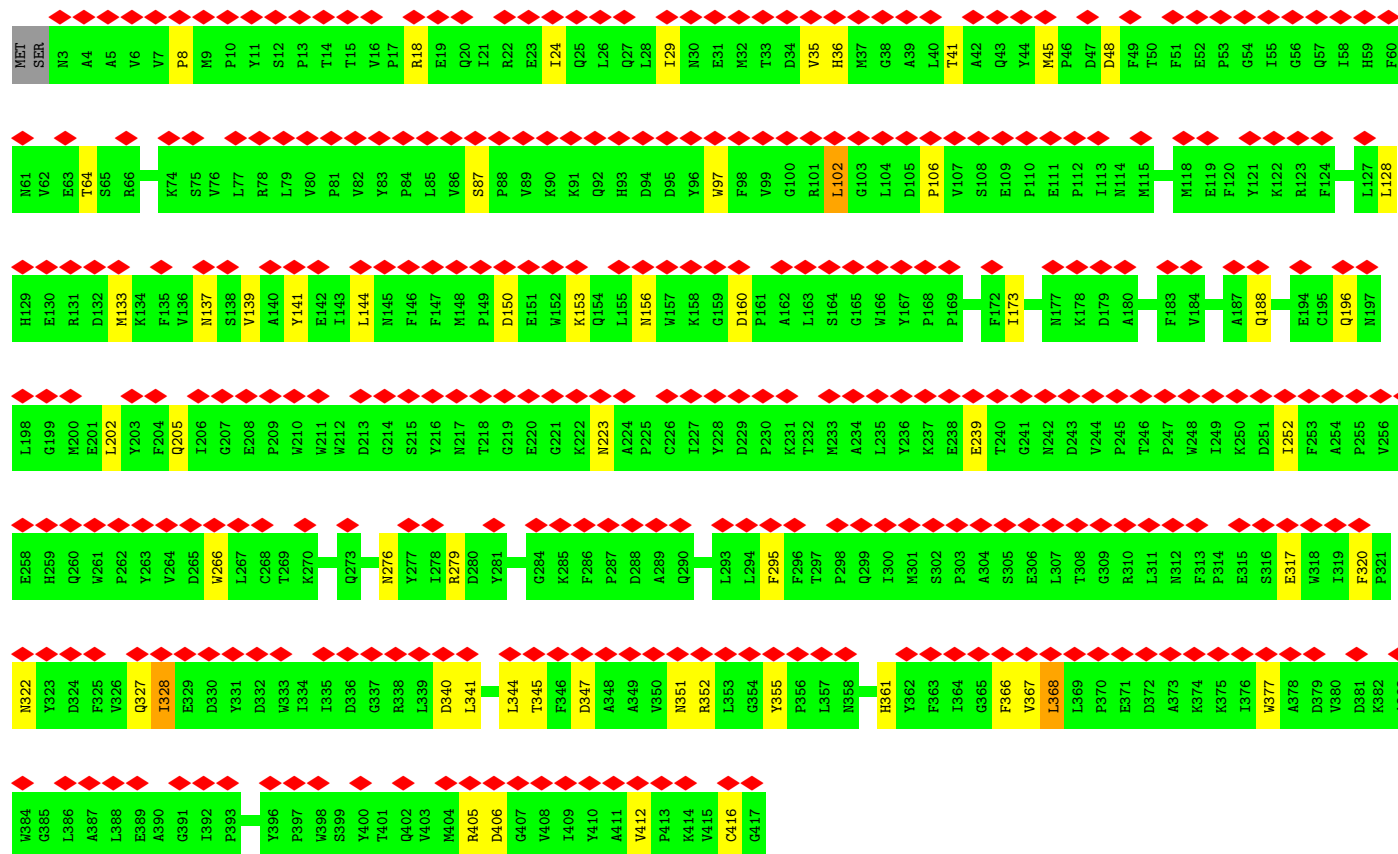
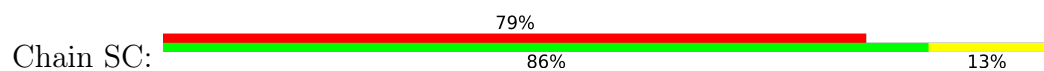


• Molecule 3: Gp64

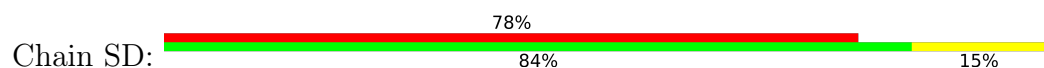


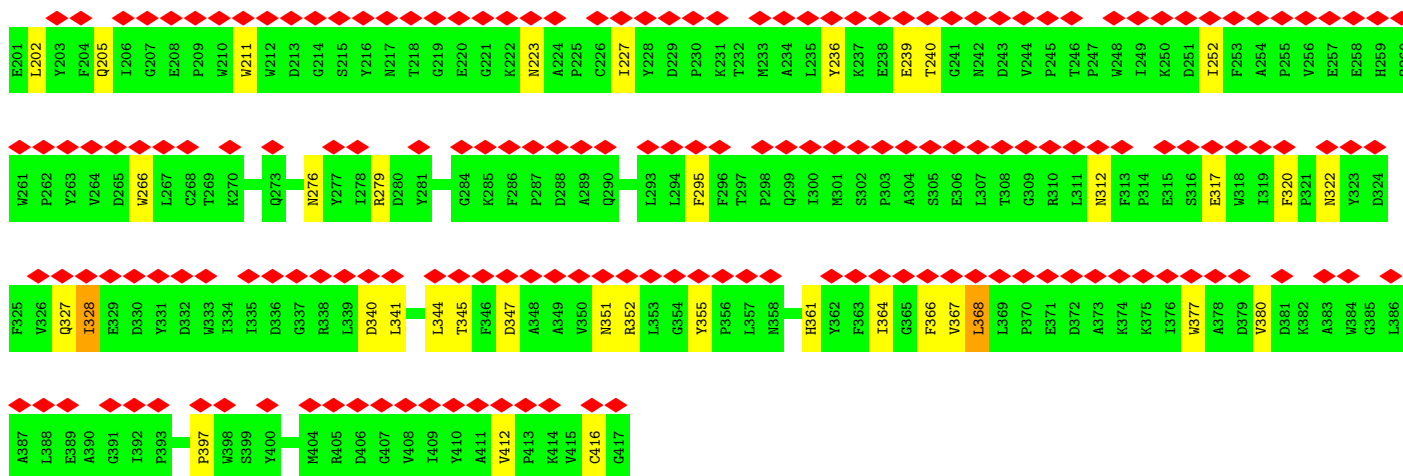


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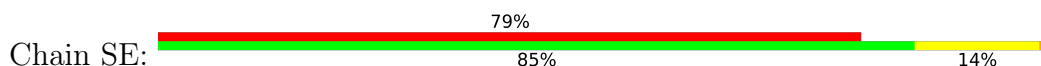


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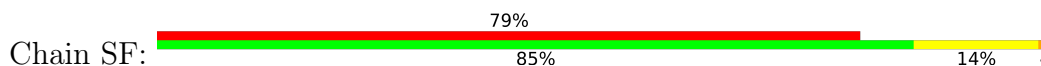


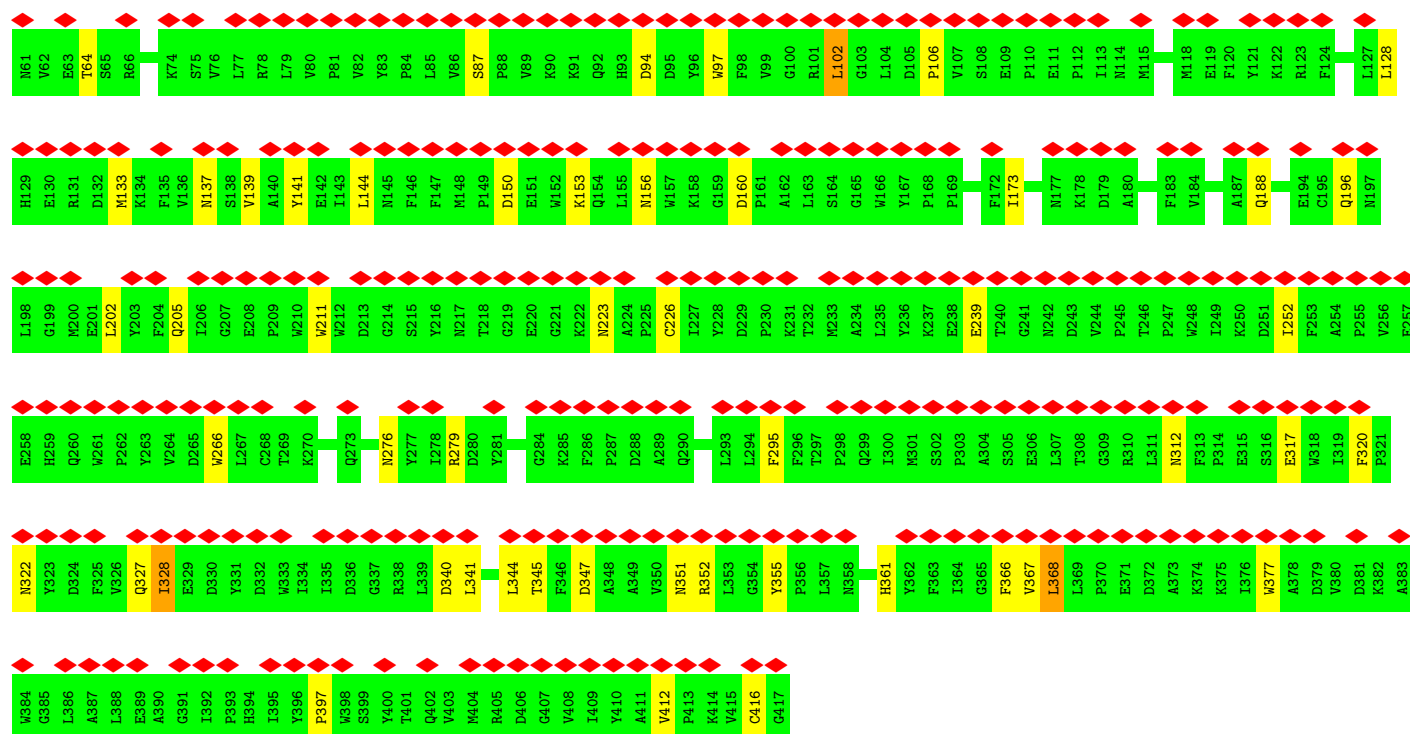


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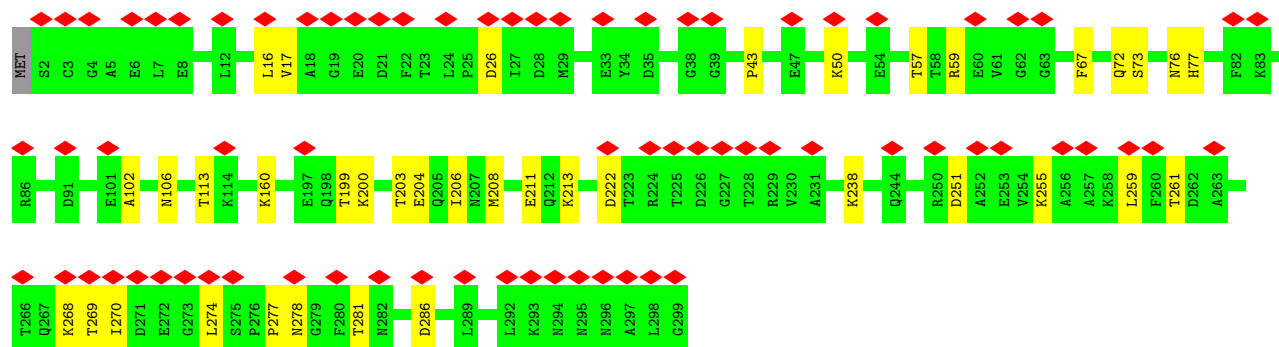
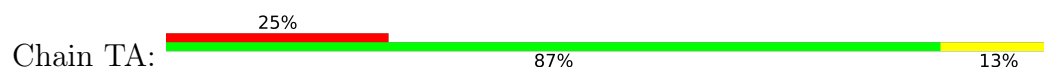


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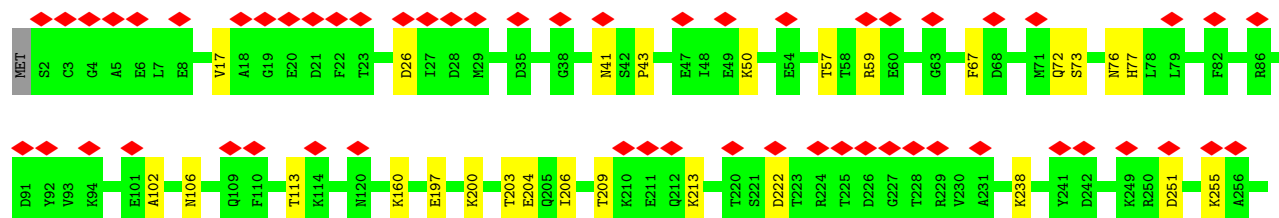
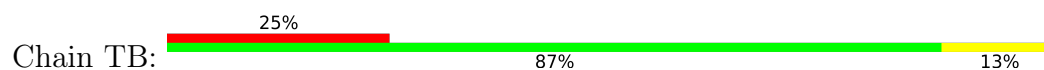


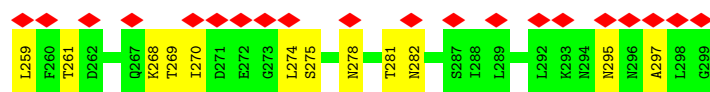


• Molecule 4: Gp54

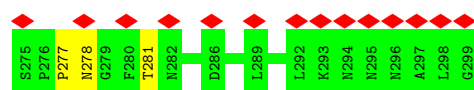
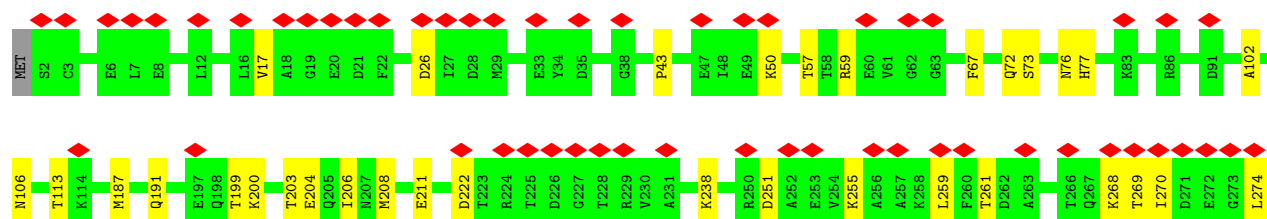
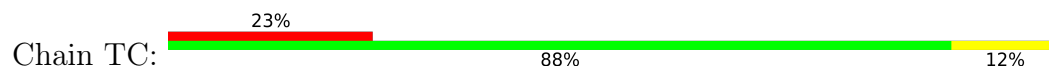


• Molecule 4: Gp54

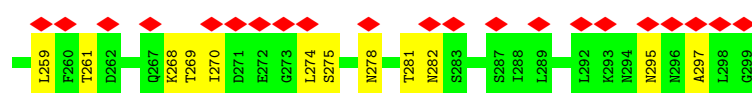
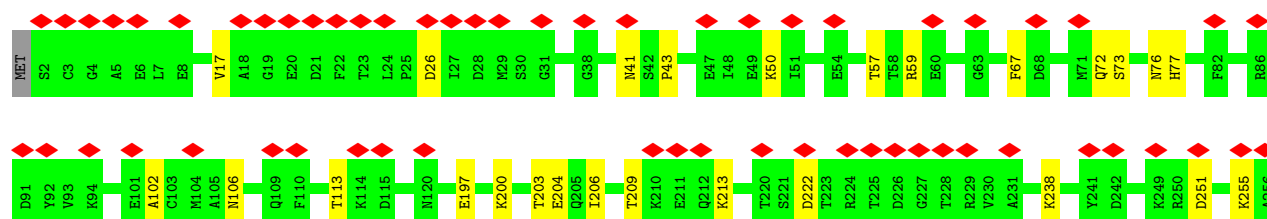
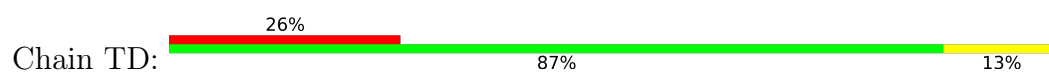




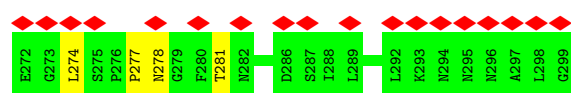
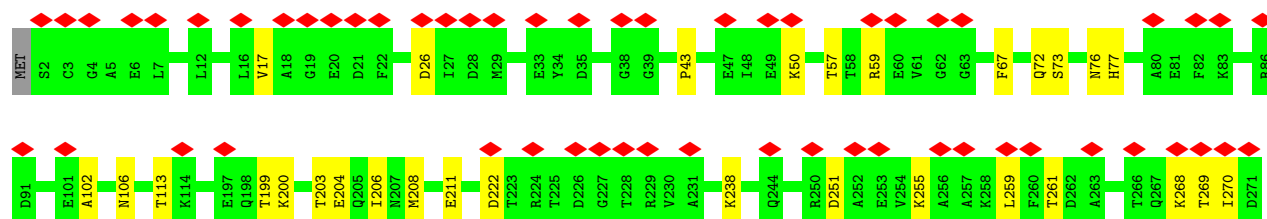
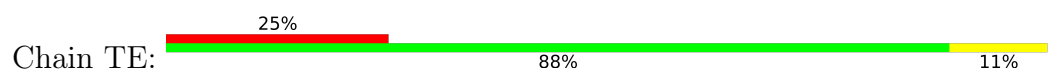
- Molecule 4: Gp54



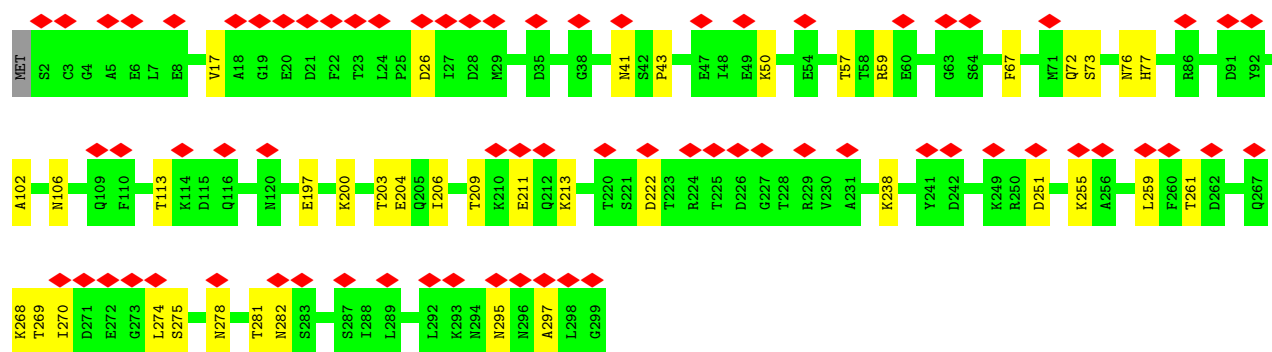
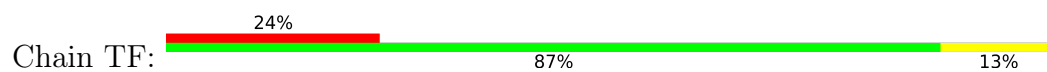
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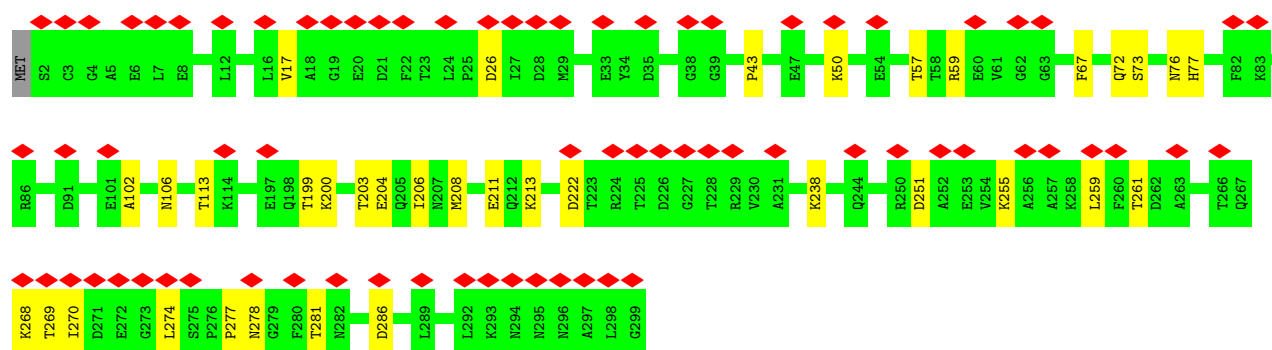
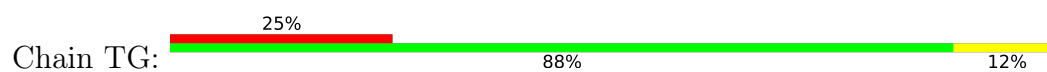
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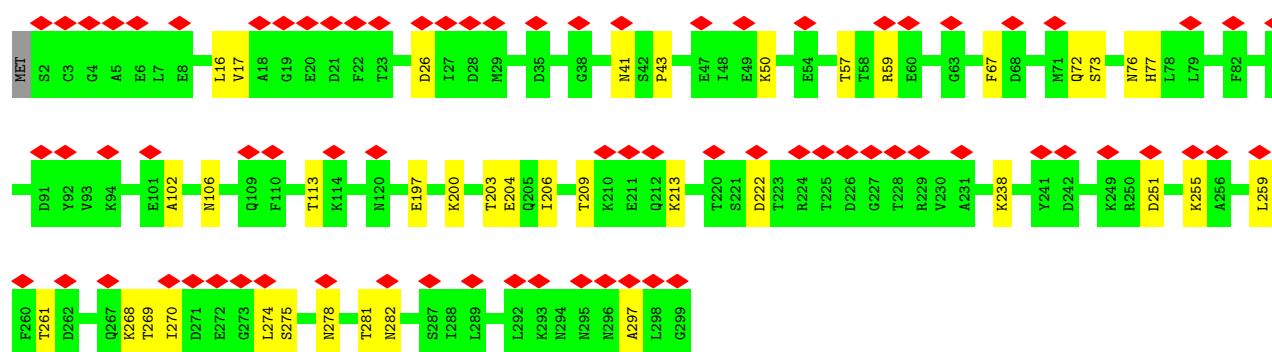
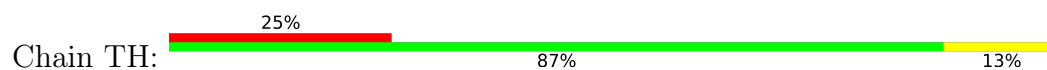
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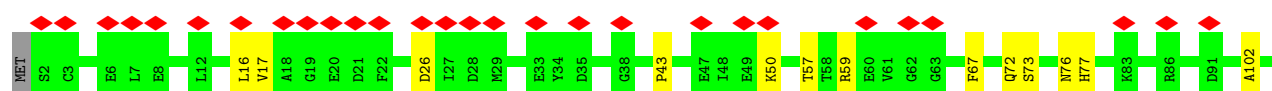
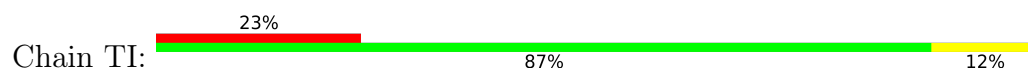
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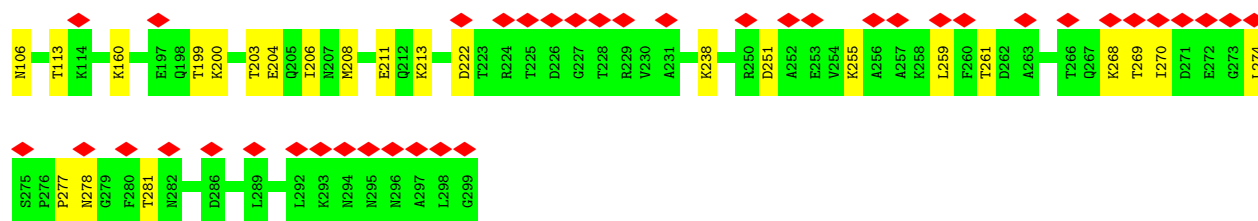


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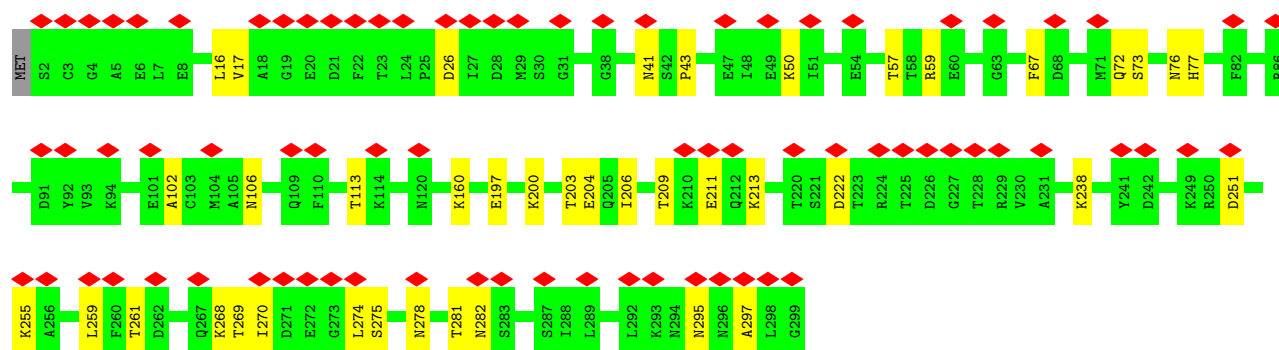
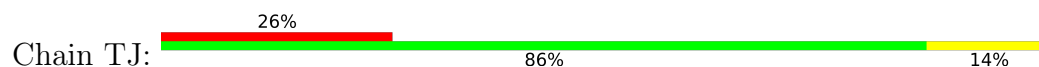


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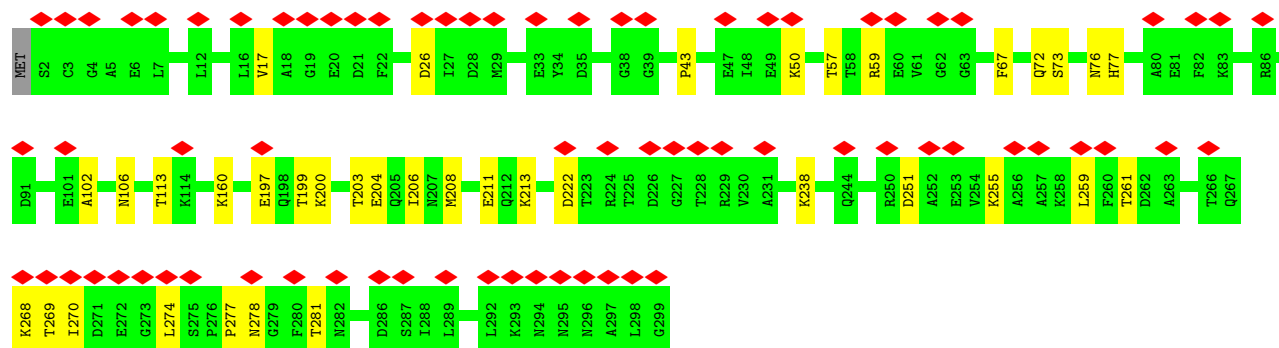




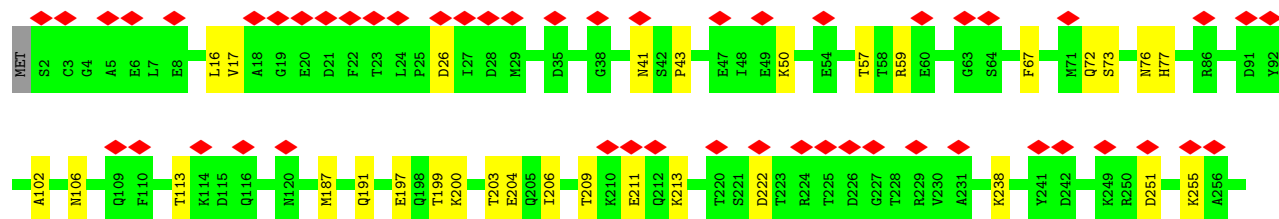
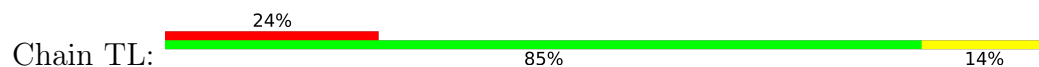
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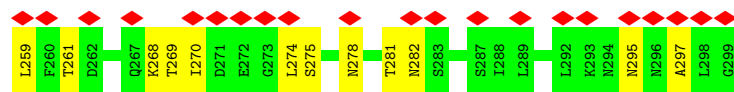


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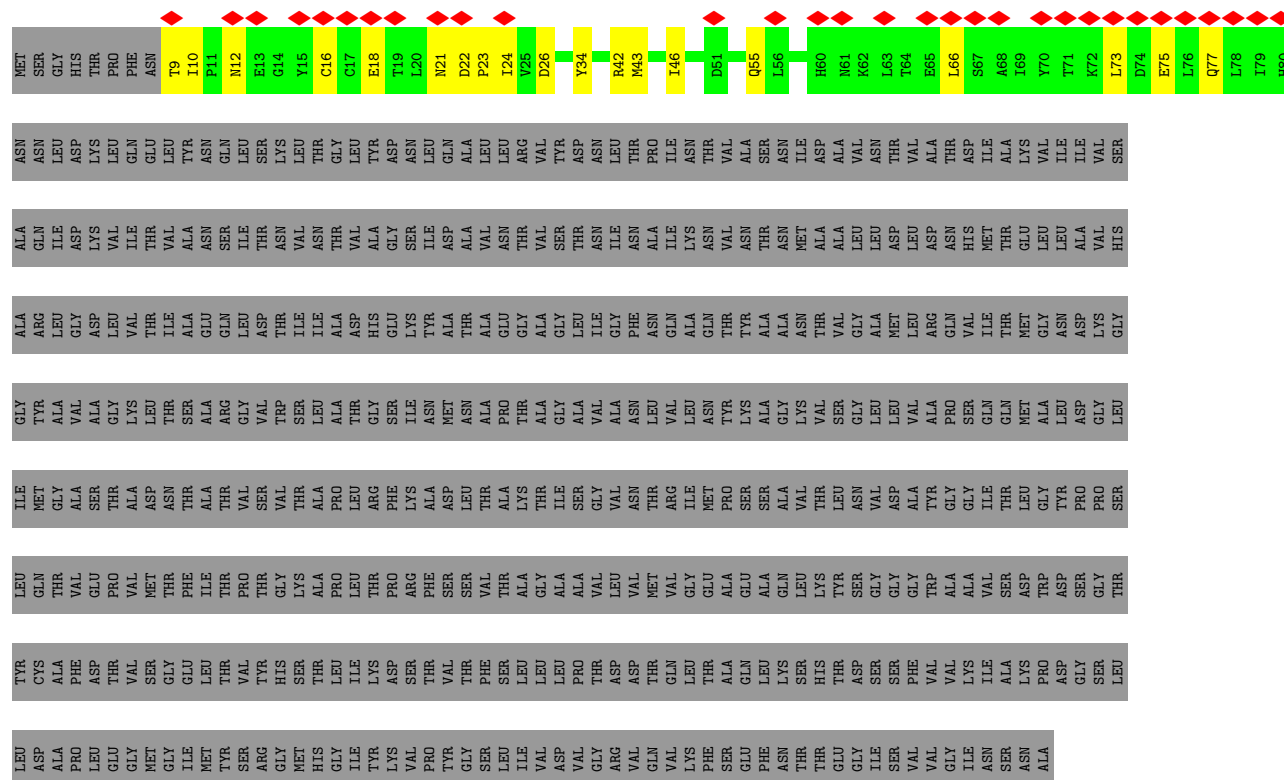


• Molecule 4: Gp54

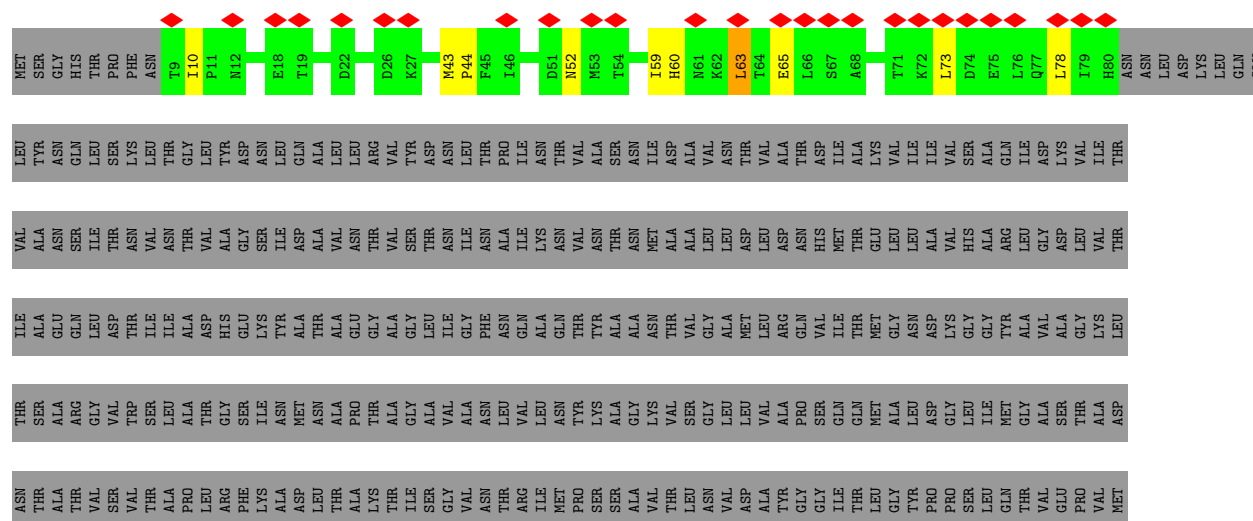


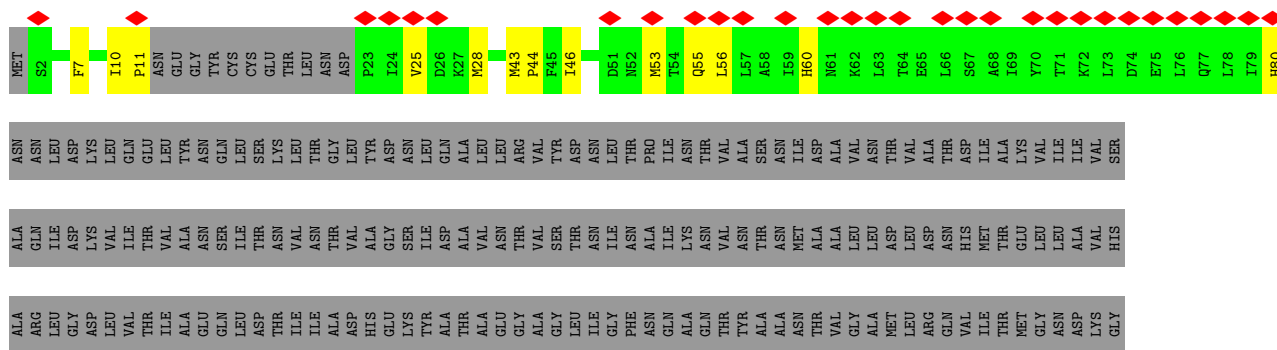


• Molecule 5: 60 kDa protein



• Molecule 5: 60 kDa protein





[illegible]

- Molecule 5: 60 kDa protein

Chain ZA: 9% 89%

[illegible]

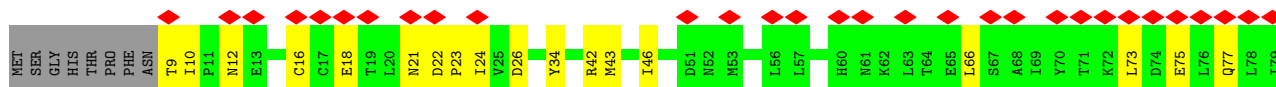
- Molecule 5: 60 kDa protein

Chain ZB: 5% 10% 89%

[illegible]

[illegible]

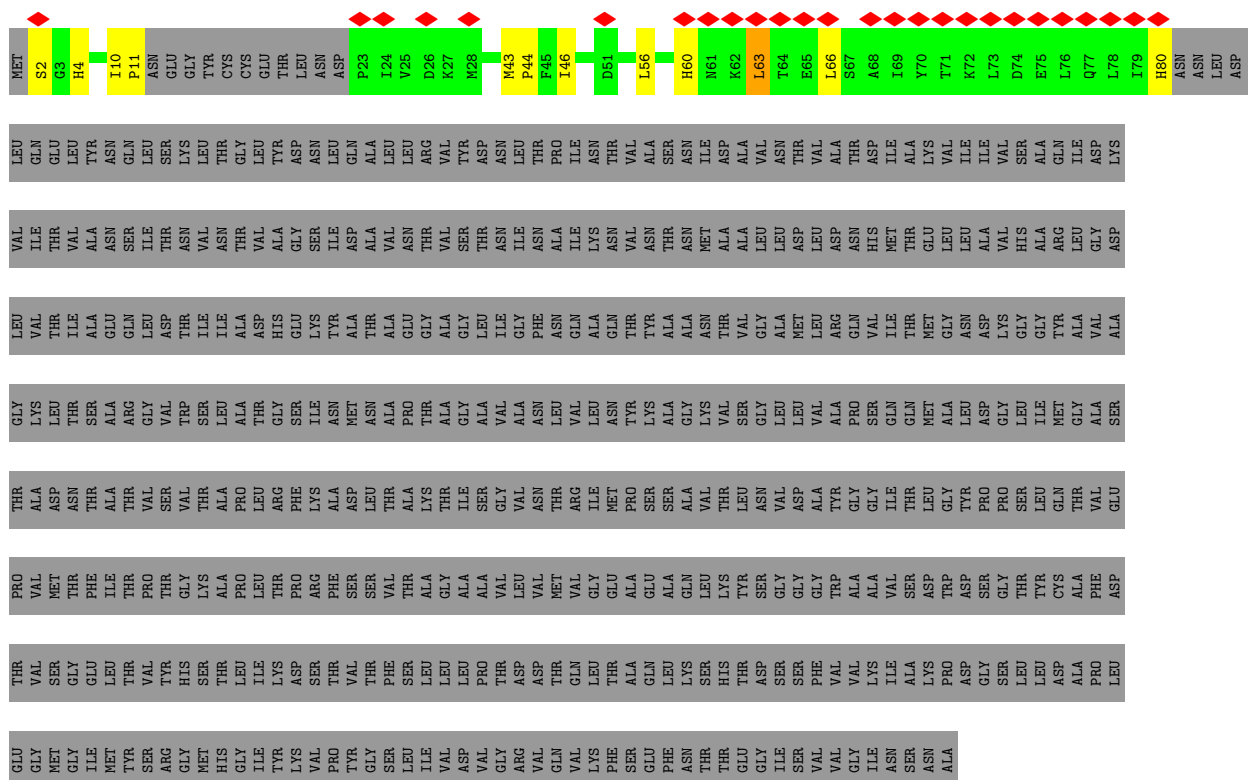
- Molecule 5: 60 kDa protein

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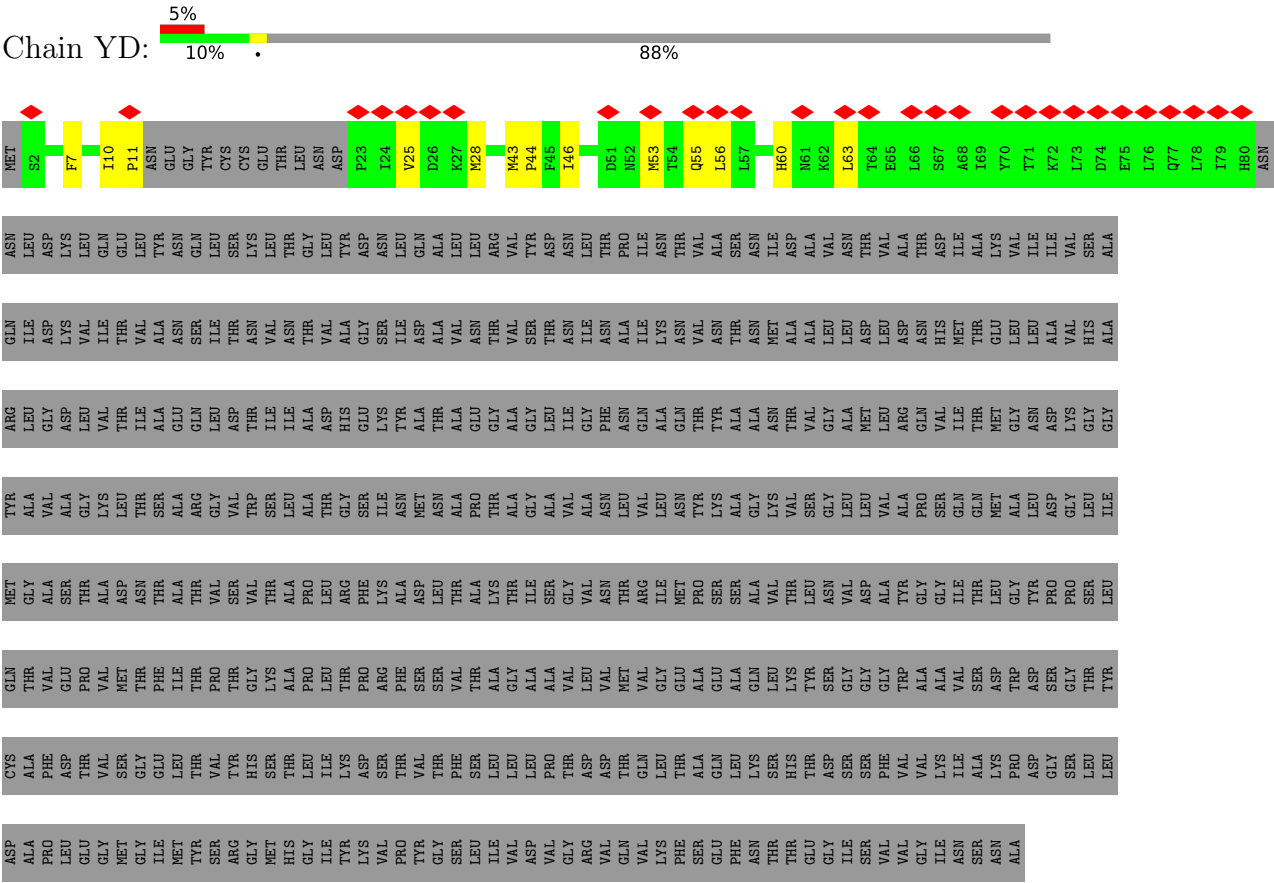
- Molecule 5: 60 kDa protein



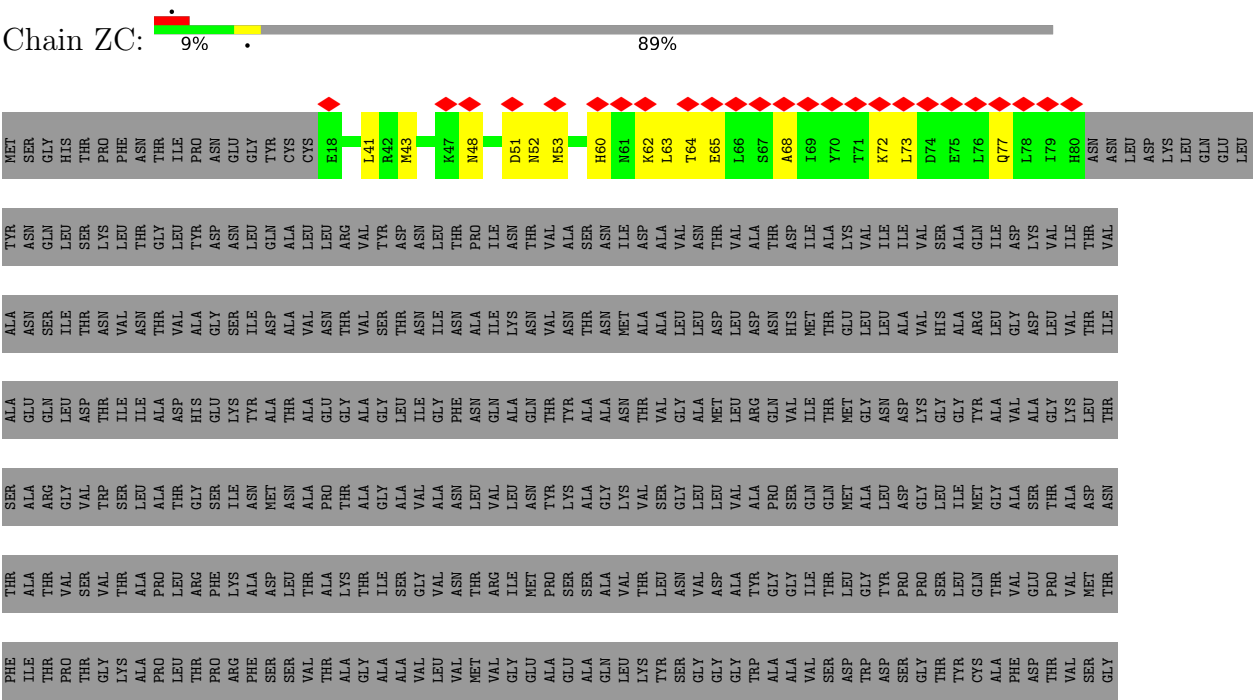
- Molecule 5: 60 kDa protein



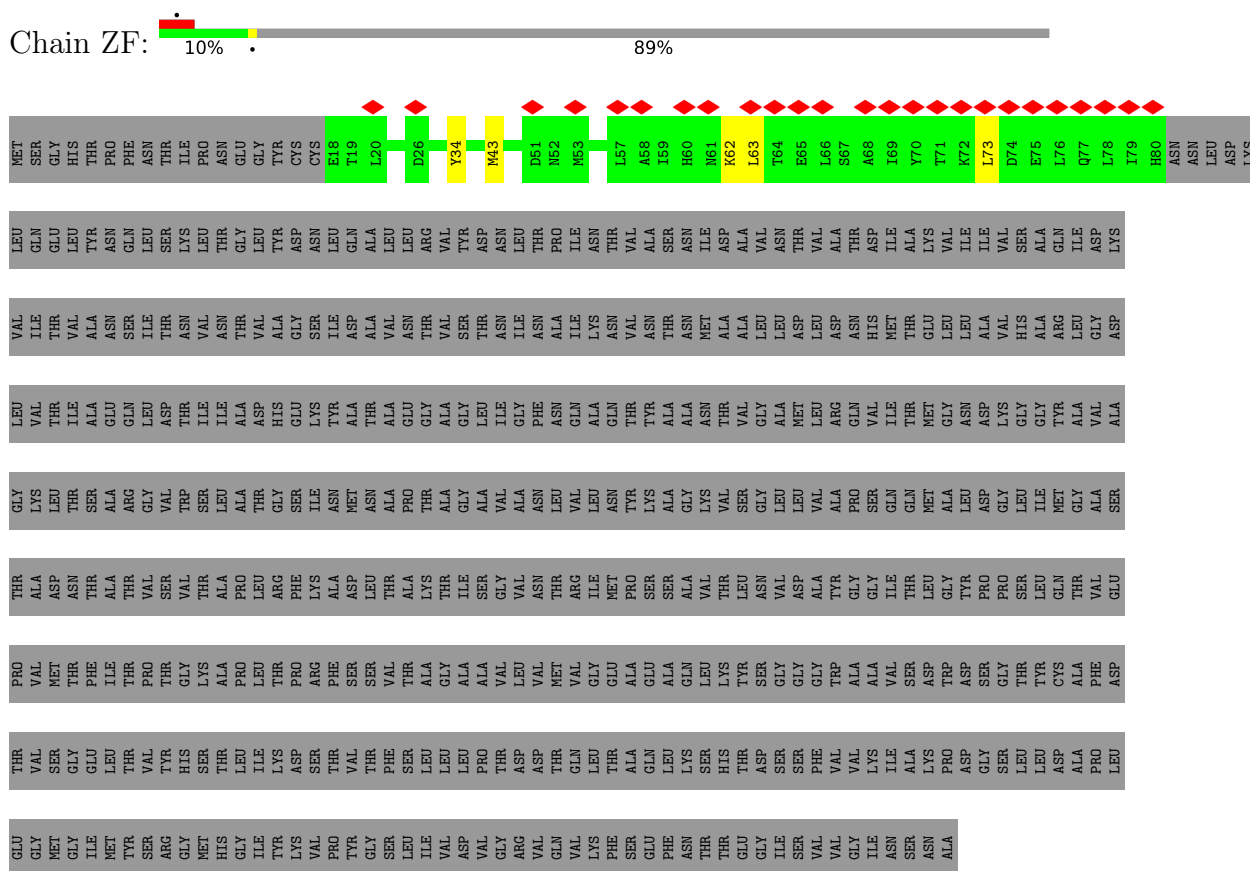
● Molecule 5: 60 kDa protein



● Molecule 5: 60 kDa protein



- Molecule 5: 60 kDa protein



- Molecule 5: 60 kDa protein



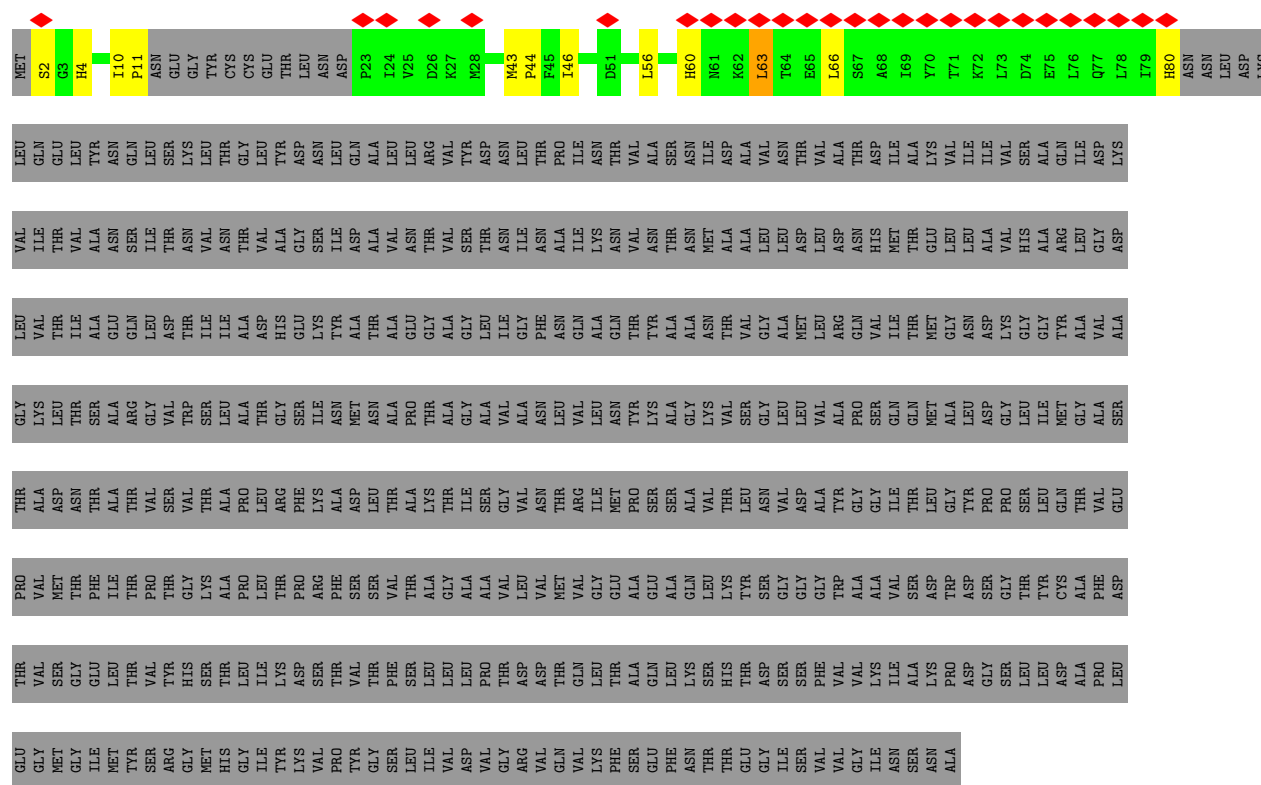
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ASN	ASN	LEU	ASP	LYS	THR	LEU	GLN	GLU	ASN	LEU	TYR	GLN	ASN	GLN	SER	GLN	SER	LYS	LEU	THR	GLY	LEU	TYR	ASP	ASN	GLN	ALA	LEU	LEU	ARG	TYR	ASP	ASN	ASN	THR	ALA	ILE	ASN	THR	VAL	SER	ASN	ALA	ASN	ASN	ILE	ASP	ALA	VAL	LEU	ASN	THR	ALA	GLY	ASP	LEU	ILE	ILE	VAL	SER																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
ALA	GLN	ILE	ASP	LYS	VAL	ILE	THR	THR	VAL	ASN	ASN	THR	VAL	ASN	SER	ILE	THR	ASN	VAL	ASN	THR	VAL	ALA	GLY	ILE	ALA	VAL	VAL	THR	GLY	SER	ILE	THR	GLY	ILE	ASN	THR	VAL	ASN	ALA	THR	ASN	ASN	MET	ALA	ALA	LEU	VAL	ASP	LEU	LEU	THR	THR	THR	GLY	LEU	VAL	ILE	ALA	VAL	HIS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
ALA	ARG	LEU	GLY	ASP	LEU	VAL	THR	THR	THR	THR	ILE	VAL	ALA	GLN	ASP	THR	HIS	GLY	THR	ILE	ALA	ASP	GLY	LYS	TYR	ASN	ALA	THR	ALA	GLY	THR	ALA	PHE	ASN	ASN	GLN	ALA	THR	VAL	ASN	THR	VAL	GLY	ARG	VAL	GLN	THR	THR	THR	GLY	ASN	ASP	LYS	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
GLY	TYR	ALA	VAL	ALA	GLY	LYS	LEU	THR	THR	ALA	ALA	LEU	SER	ALA	ALA	ARG	GLY	VAL	THR	THR	THR	GLY	VAL	ASN	MET	ASN	ALA	PRO	THR	ALA	GLY	VAL	ALA	ASN	LEU	ALA	GLY	LYS	ALA	GLY	THR	VAL	ASN	THR	VAL	SER	GLY	VAL	PRO	ALA	ALA	GLY	VAL	ASP	LEU	LEU																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
ILE	MET	GLY	ALA	SER	THR	ALA	THR	THR	THR	THR	ALA	THR	THR	THR	THR	THR	ARG	PHE	LYS	THR	LEU	THR	GLY	ILE	ASP	LEU	THR	ALA	THR	ALA	ILE	GLY	VAL	VAL	ASN	THR	THR	THR	THR	VAL	SER	ALA	SER	ALA	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
LEU	GLN	THR	VAL	THR	PRO	VAL	THR	THR	THR	THR	ILE	THR	THR	THR	THR	THR	PRO	ARG	GLY	ALA	LEU	THR	THR	ALA	THR	SER	VAL	THR	ALA	GLY	VAL	VAL	VAL	VAL	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
TYR	CYS	ALA	PHE	THR	THR	VAL	SER	GLY	GLY	THR	THR	THR	THR	THR	THR	THR	THR	HIS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
LEU	ASP	ALA	PRO	THR	GLU	GLY	MET	GLY	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	HIS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

● Molecule 5: 60 kDa protein

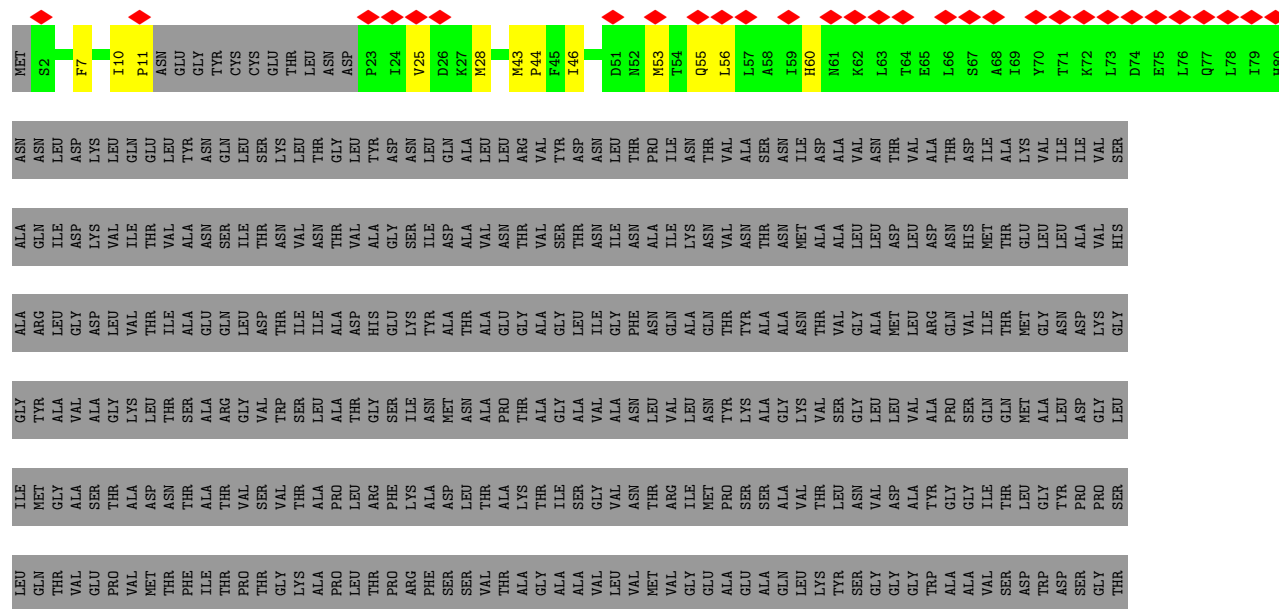


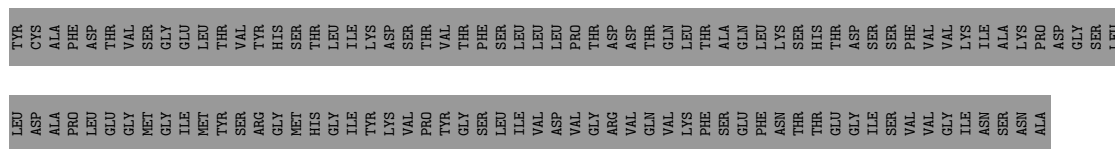
MET	SER	GLY	HIS	THR	PRO	PHE	ASN	T9	I10	P11	N12	E18	T19	D22	D26	K27	M43	P44	F45	I46	D51	N52	M53	T54	Q55	I59	H60	N61	K62	L63	T64	E65	L66	S67	A68	T71	K72	L73	D74	E75	L76	Q77	L78	I79	H80	ASN	ASN	LEU	ASP	LYS	GLN	
GLU	TYR	ASN	GLN	SER	LEU	SER	LYS	LEU	THR	GLY	TYR	ASN	LEU	GLN	LEU	VAL	TYR	ASP	ASN	THR	PRO	ILE	ASN	THR	VAL	SER	ILE	ASP	ALA	ALA	VAL	ASP	HIS	THR	ILE	ALA	LYS	VAL	ILE	GLN	ASP	GLY	LYS	VAL	ILE	ASN	ASN	LEU	ASP	LYS	GLN	
THR	VAL	ALA	ASN	SER	THR	THR	THR	VAL	ASN	THR	VAL	GLY	ILE	ASP	ASN	SER	THR	THR	ILE	ASN	ALA	ILE	LYS	VAL	VAL	THR	VAL	ALA	ALA	VAL	ASP	ASN	HIS	THR	MET	THR	GLU	LEU	VAL	ARG	LEU	GLY	ASP	LEU	VAL	LYS	VAL	ASN	ASN	LEU	ASP	GLN
THR	ILE	ALA	GLU	GLN	THR	THR	THR	ILE	ALA	ASP	HIS	GLU	TYR	THR	ALA	GLY	LEU	GLY	PHE	ASN	ASN	GLN	THR	TYR	THR	ALA	ASN	MET	VAL	VAL	ARG	GLN	VAL	ILE	THR	MET	GLY	ASN	ASP	TYR	ALA	VAL	GLY	ALA	THR	GLY	LYS	VAL	ASN	ASN	LEU	GLN
LEU	THR	SER	ARG	ALA	GLY	THR	THR	LEU	THR	GLY	LYS	ILE	ASN	MET	PRO	ALA	GLY	VAL	VAL	THR	LEU	LEU	TYR	LYS	ALA	GLY	LYS	VAL	PRO	GLY	THR	PRO	GLN	ILE	GLM	MET	LEU	ALA	MET	GLY	GLY	GLY	GLY	THR	SER	THR	ALA	ASN	ASN	LEU	GLN	
ASP	ASN	THR	THR	THR	VAL	THR	THR	VAL	ALA	THR	ARG	LYS	ALA	ASP	ALA	LYS	THR	SER	ASN	THR	ARG	ILE	MET	PRO	SER	ALA	VAL	THR	THR	GLY	GLY	ALA	GLY	THR	ILE	THR	LEU	LEU	THR	GLN	THR	VAL	VAL	GLU	PRO	THR	VAL	ASN	THR	THR	THR	
MET	THR	PHE	ILE	THR	PRO	THR	THR	ALA	PRO	LEU	THR	ARG	PHE	SER	THR	ALA	SER	VAL	LEU	THR	GLY	GLY	ALA	ALA	GLN	LEU	LYS	TYR	THR	SER	GLY	ASP	ALA	ALA	THR	TRP	ASP	ASP	THR	CYS	ALA	PHE	ASP	THR	VAL	ASN	ASN	LEU	GLN			
SER	GLY	GLU	LEU	THR	VAL	THR	THR	SER	THR	ILE	LYS	SER	THR	VAL	LEU	LEU	PRO	THR	ASP	THR	GLN	LEU	ALA	GLM	LYS	SER	HIS	THR	ASP	SER	GLY	PHE	VAL	ALA	ALA	THR	THR	GLY	THR	ASP	ALA	PRO	LEU	GLU	GLY	THR	THR	THR	THR	THR		

● Molecule 5: 60 kDa protein

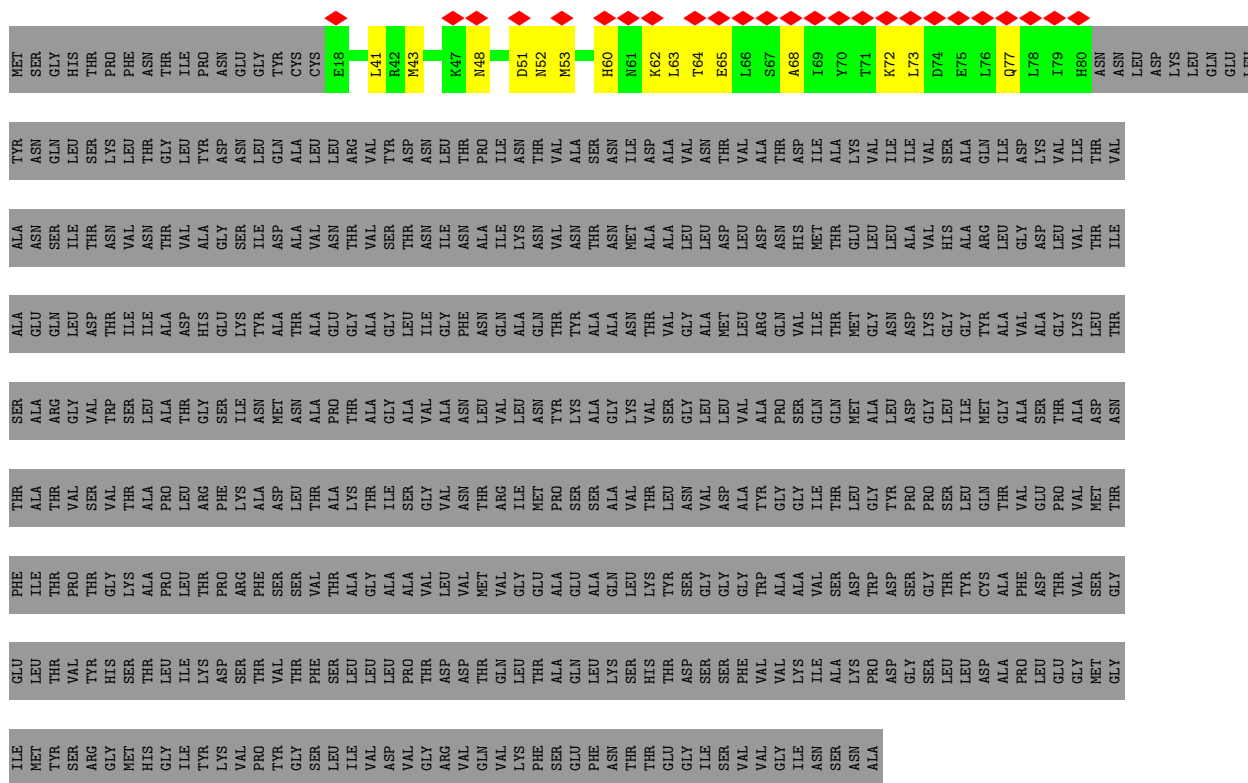
Chain YG:  5%
10% 88%

● Molecule 5: 60 kDa protein

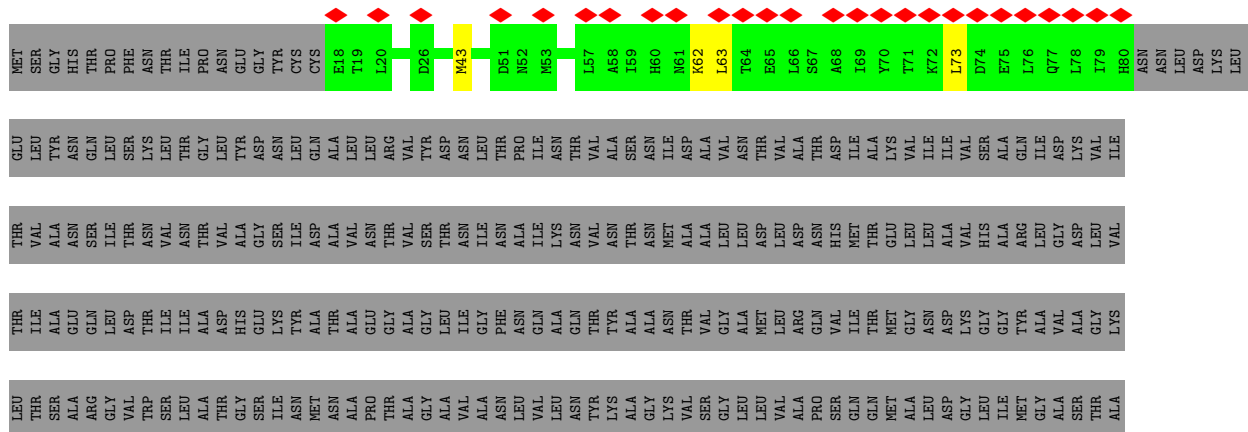
Chain YH:  5%
10% 88%

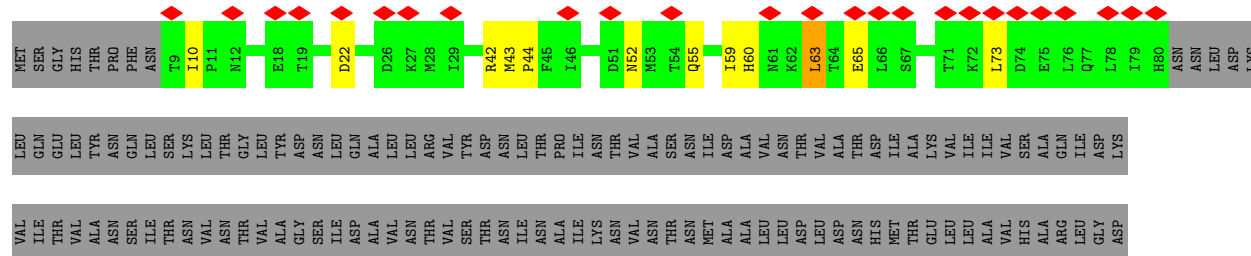


- Molecule 5: 60 kDa protein

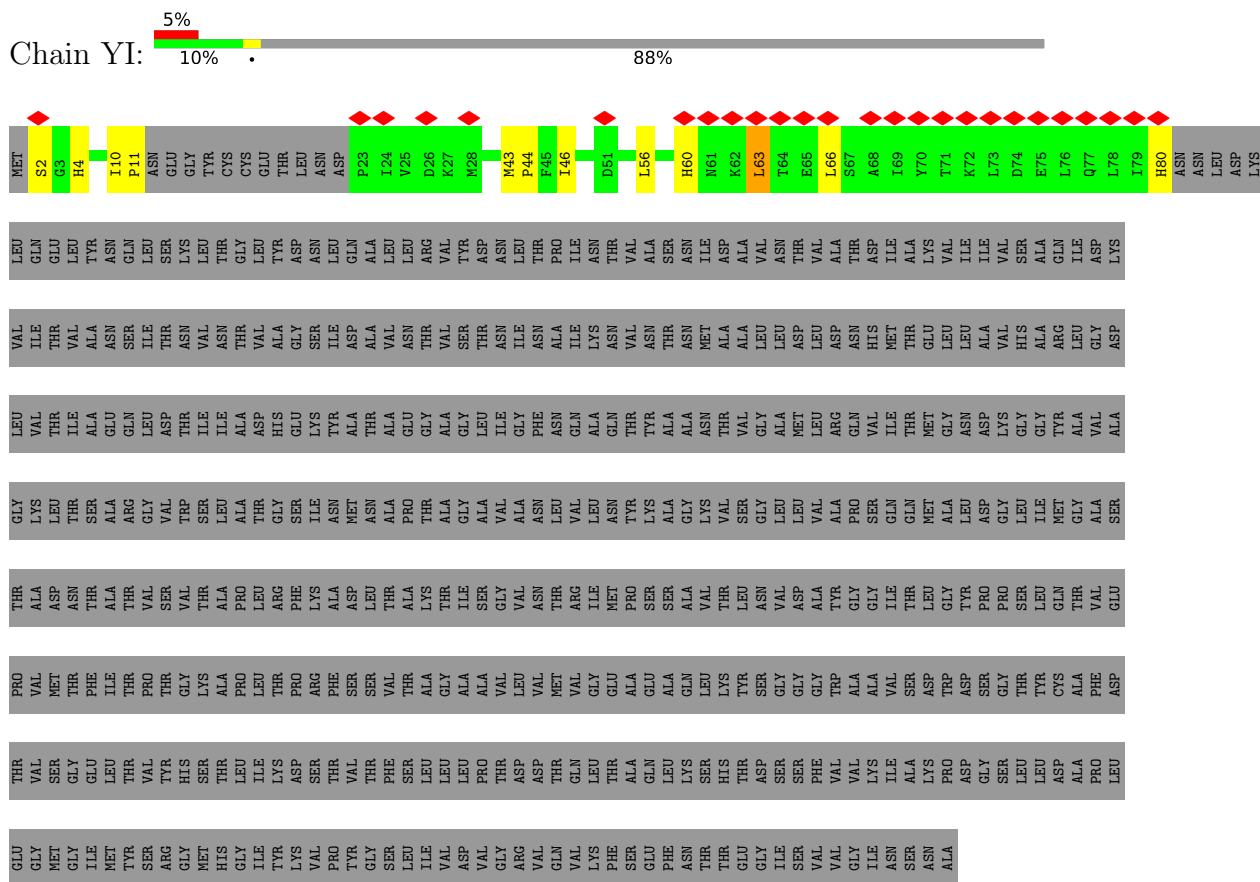


- Molecule 5: 60 kDa protein

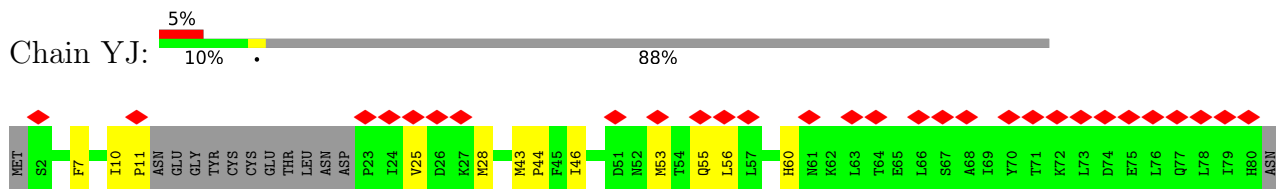




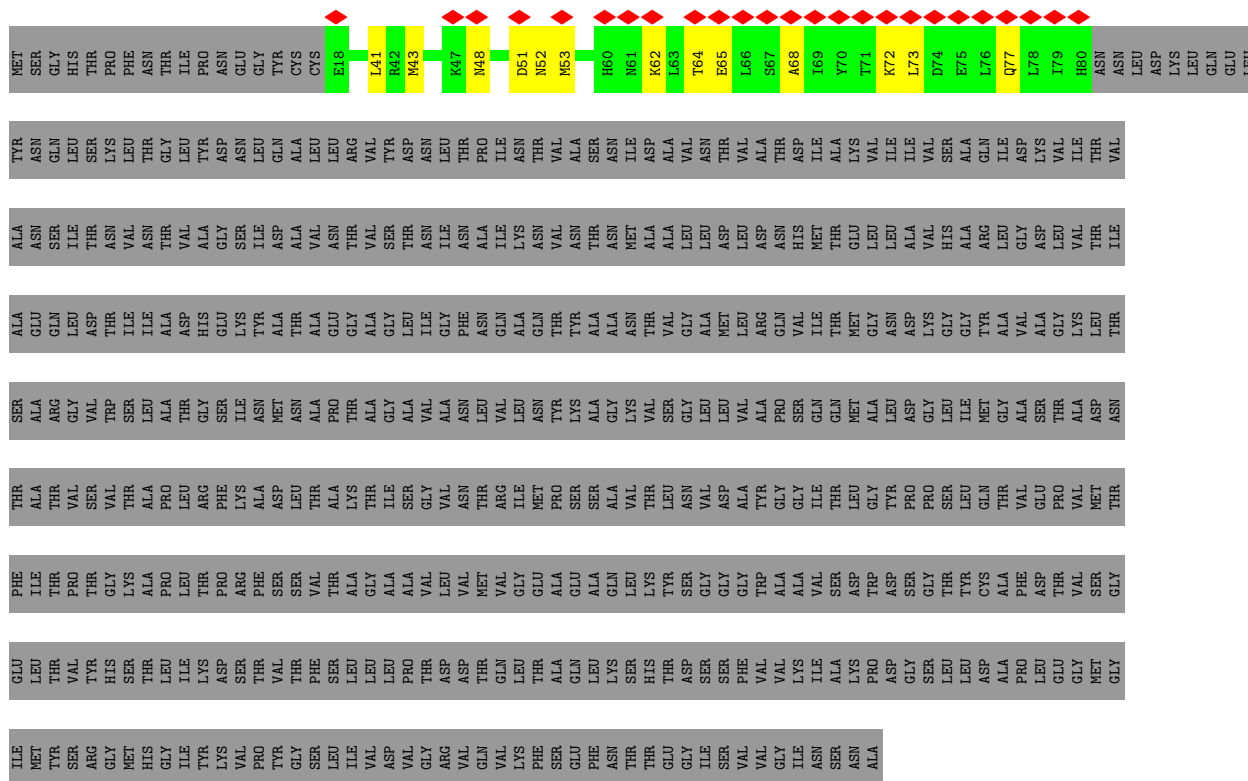
- Molecule 5: 60 kDa protein



- Molecule 5: 60 kDa protein



- Molecule 5: 60 kDa protein

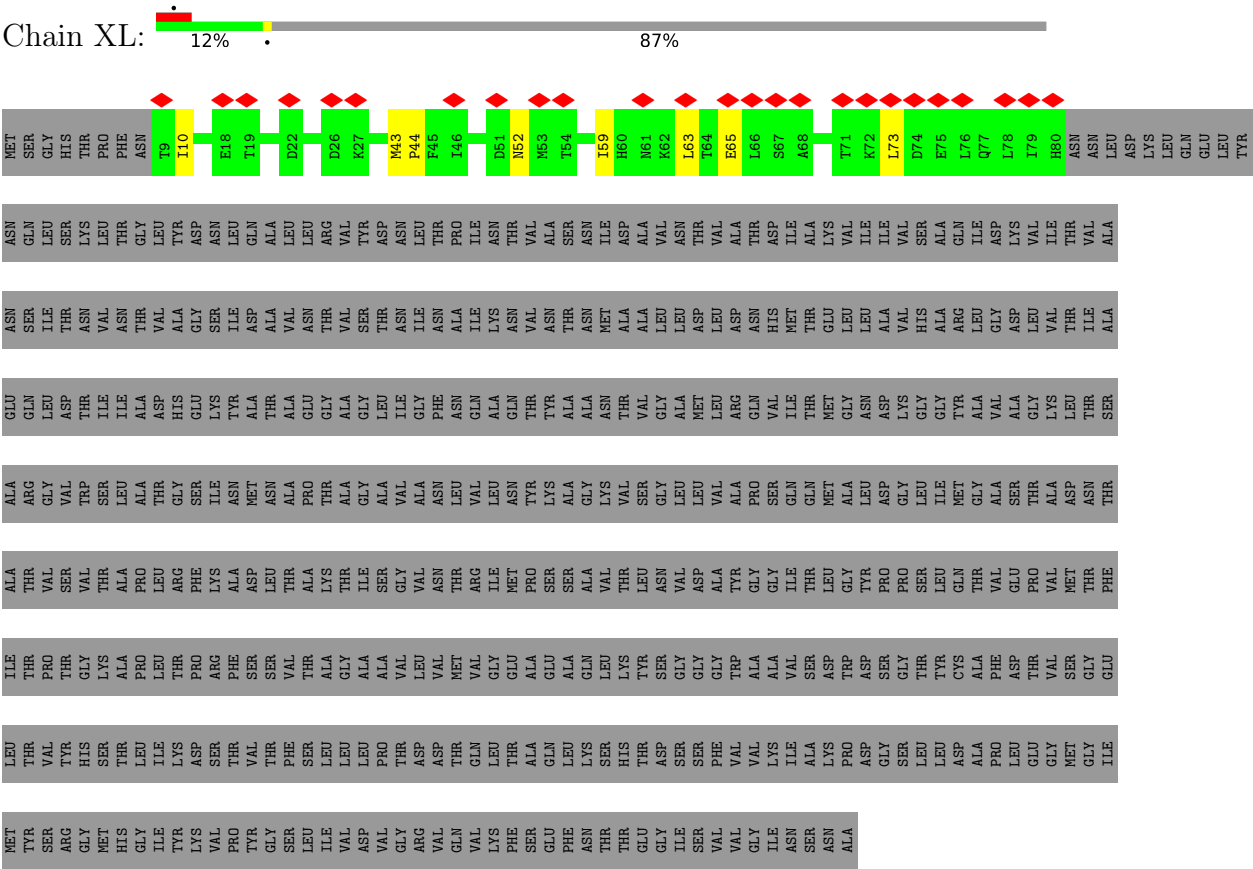


- Molecule 5: 60 kDa protein

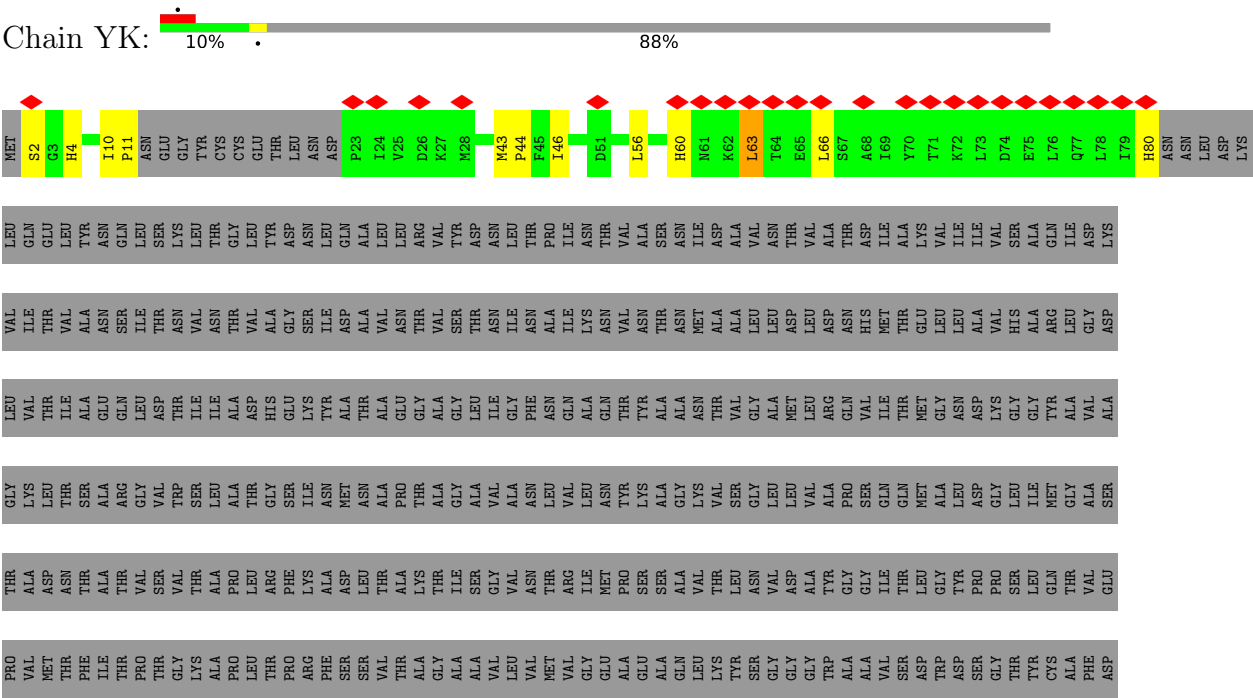




● Molecule 5: 60 kDa protein



● Molecule 5: 60 kDa protein



[illegible]

- Molecule 5: 60 kDa protein



MET	S2	F7	I10	P11	ASN	GLU	GLY	TYR	CYS	CYS	GLU	THR	LEU	ASN	ASP	P23	I24	V25	D26	K27	M28	M43	P44	F45	I46	D51	M52	M53	T54	Q55	L56	L57	A58	I59	H60	N61	K62	L63	L64	T65	E66	L66	S67	A68	I69	Y70	T71	K72	L73	D74	E75	L76	Q77	L78	I79	H80
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ASN	ASN	LEU	GLN	LYS	LEU	ASN	GLN	LEU	SER	LYS	LEU	THR	GLY	LEU	TYR	ASP	ASN	ASN	LEU	GLN	ALA	LEU	LEU	ARG	VAL	TYR	ASP	ASN	THR	THR	PRO	ILE	ASN	THR	VAL	VAL	SER	ASN	ILE	ASP	ALA	VAL	VAL	ASN	THR	VAL	ALA	THR	ASP	ILE	ALA	LYS	VAL	ILE	ILE	VAL	FED
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ALA GLN ILE ILE ASP LYS VAL ILE THR VAL ALA ALA ASN SER ILE THR ASN VAL VAL THR THR SER THR ILE ALA ILE LYS ASN VAL VAL ASN THR THR SER THR ASN ALA ALA ASP ASP ASN HIS MET THR GLU LEU LEU VAL HIS

ALA ARG LEU GLY ASP LEU VAL THR THR ILE ALA ALA GLN GLN LEU ASP THR ILE ILE ALA HIS LYS GLU TYR TYR ALA THR ALA ALA GLY LEU ILE ILE GLY PHE ASN ASN GLN ALA ALA GLN THR TYR THR THR ALA ALA VAL GLY VAL THR THR THR THR MET LEU ARG GLN VAL ILE THR MET GLY ASN ASN ASP LYS TYR

GLY	TYR	ALA	ALA	VAL	ALA	GLY	LYS	LEU	THR	SER	SER	ARG	ALA	GLY	VAL	TRP	SER	LEU	ALA	THR	GLY	SER	ILE	ASN	ASN	ALA	ALA	PRO	THR	ALA	GLY	ALA	VAL	ALA	ASN	ASN	VAL	LEU	LEU	LEU	VAL	ASN	TYR	LYS	GLY	GLY	VAL	LYS	SER	GLY	LEU	LEU	VAL	ALA	ALA	PRO	SER	SER	GLN	GLN	GLN	MET	ALA	ALA	LEU	ASP	GLY	LEU
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[illegible]

LEU GLN THR VAL GLU PRO VAL MET THR PHE ILE THR PRO THR GLY LYS ALA ALA PRO LEU THR PRO ARG PHE SER SER VAL THR VAL GLU GLY ALA ALA VAL LEU VAL MET VAL GLY GLU ALA ALA GLN LEU LYS TYR SER SER GLY GLY GLY TRP TRP ASP ASP SER GLY THR

TYR	CYS	ALA	ALA	PHE	ASP	THR	VAL	SER	GLY	LEU	THR	VAL	TYR	HIS	SER	THR	SER	LEU	LEU	LYS	ASP	SER	THR	THR	THR	SER	SER	LEU	LEU	LEU	PRO	THR	THR	THR	GLN	LEU	ALA	ALA	LEU	LYS	SER	HIS	THR	THR	ASP	SER	SER	SER	PHE	VAL	VAL	VAL	ILE	LYS	ALA	ALA	LYS	PRO	ASP	GLY	ASP	SER	LEU
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LEU ASP ALA ALA PRO LEU LEU MET MET MET MET TYR ARG ARG MET MET HIS HIS LEU LEU TYR TYR LYS VAL VAL PRO TYR TYR GLY GLY SER SER SER SER LEU LEU VAL VAL ASP ASP VAL GLY GLY GLY ARG ARG VAL VAL GLN VAL VAL LYS PHE SER SER SER GLU GLU PHE ASN ASN THR THR GLU GLU GLY GLY LEU LEU SER SER VAL VAL VAL GLY GLY LEU LEU ASN ASN ALA

- Molecule 5: 60 kDa protein



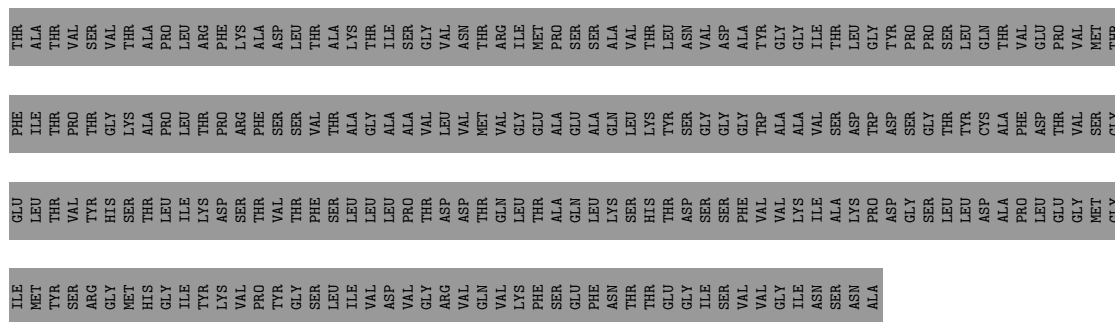
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Tyr	Asn	Gln	Ser	Leu	Lys	Leu	Thr	Gly	Leu	Tyr	Asp	Asn	Gln	Ala	Leu	Arg	Val	Tyr	Asp	Asn	Leu	Thr	Ile	Asn	Val	Val	Ala	Ser	Asn	Ile	Ala	Val	Val	Asn	Thr	Thr	Thr	Val	Val	Ala	Ala	Ala	Thr	Asp	Ile	Ala	Lys	Val	Val	Ile	Ile	Ile	Val	Ser	Val	Gln	Ile	Asp	Lys	Val	Ile	Thr	Val
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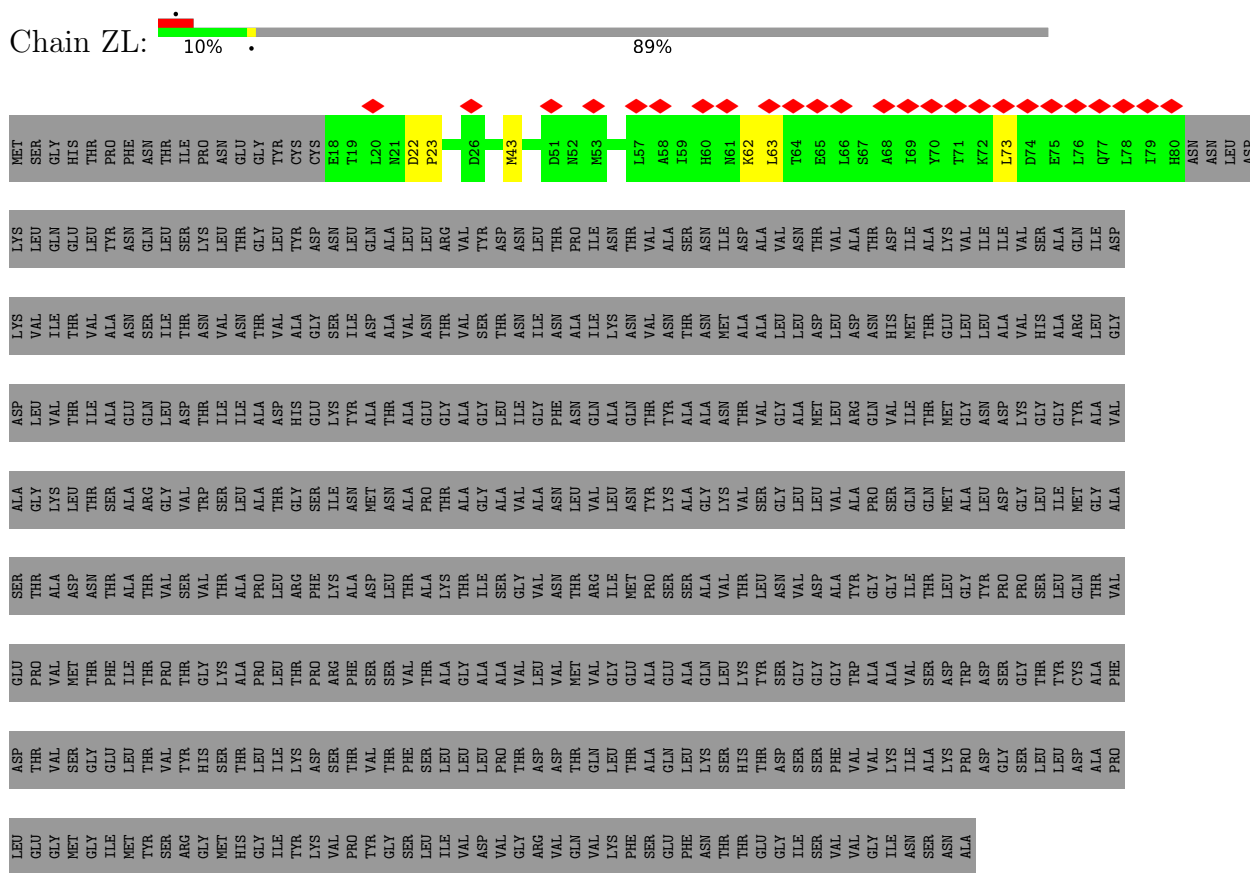
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ALA GLU GLN LEU LEU THR THR ILE ILE ALA ALA ASP ASP HIS HIS GLU GLU LYS TYR TYR ALA ALA ALA ALA GLU GLY GLY PHE ASN ASN GLN GLN ALA ALA THR THR TYR TYR ALA ALA ALA ALA THR THR THR THR VAL VAL GLY GLY MET MET MET MET LEU LEU ARG ARG GLN GLN VAL VAL ILE ILE THR THR MET MET MET MET GLY GLY TYR TYR TYR TYR ALA ALA VAL VAL ALA ALA GLY GLY LYS LYS LEU LEU

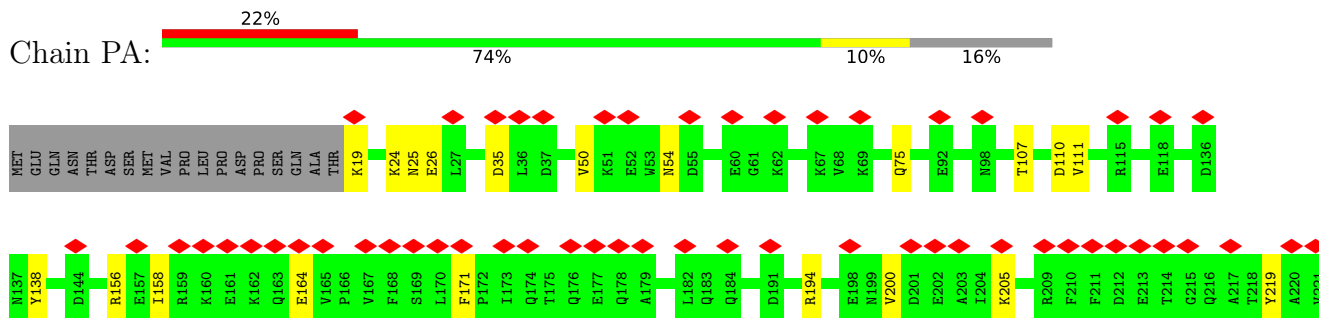
SER	ALA	ARG	GLY	VAL	TRP	SER	LEU	ALA	ALA	THR	GLY	SER	ILE	ASN	MET	ASN	ALA	ALA	PRO	THR	ALA	ALA	ALA	ALA	ALA	ASN	VAL	LEU	LEU	ASN	TYR	LYS	ALA	ALA	GLY	LYS	VAL	SER	GLY	LEU	LEU	VAL	VAL	ALA	ALA	PRO	SER	GLN	GLN	MET	MET	ALA	LEU	ALA	LEU	ASP	GLY	GLY	ILE	ILE	MET	MET	GLY	ALA	SER	THR	ALA	ALA	ASP	ASN
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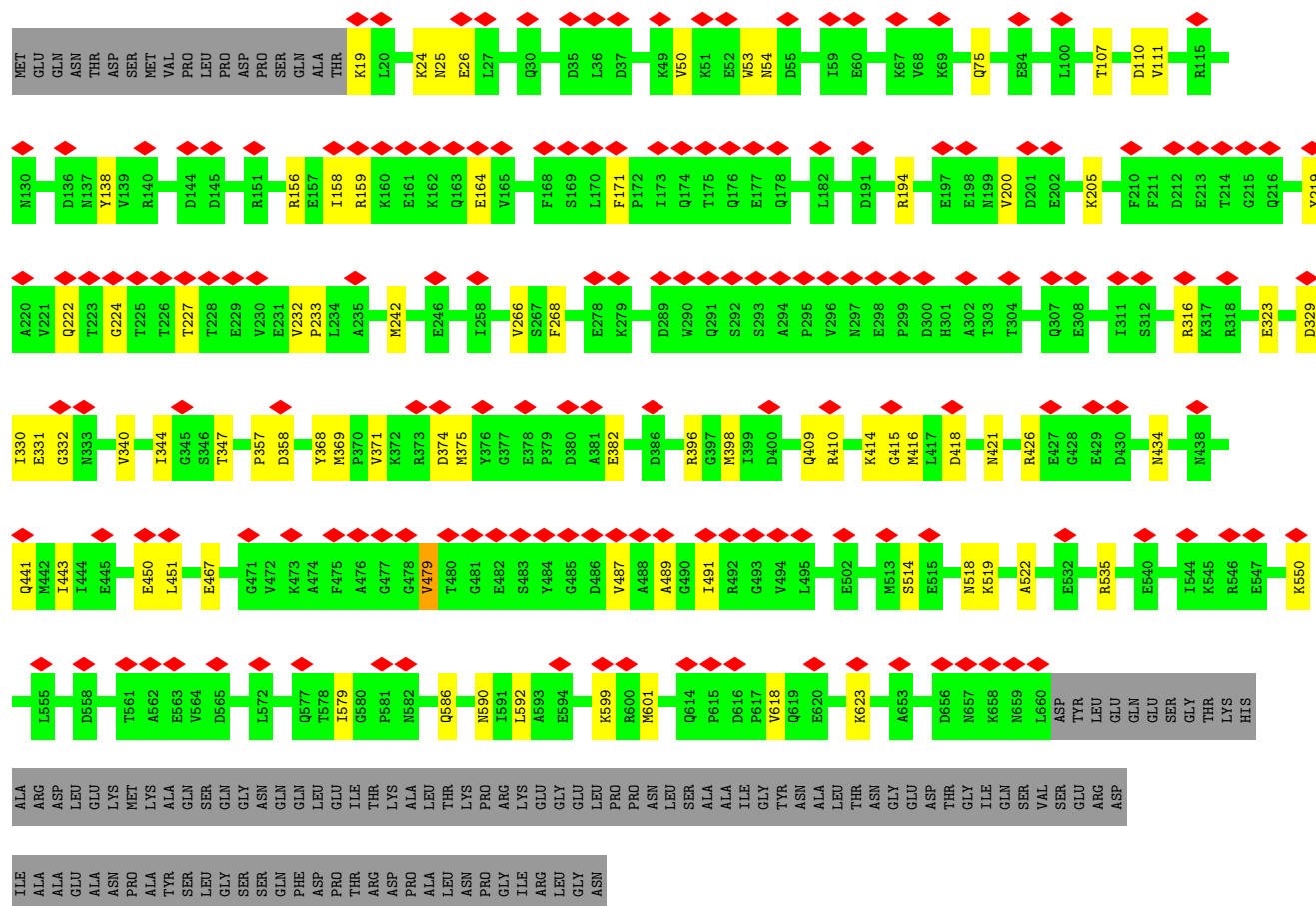
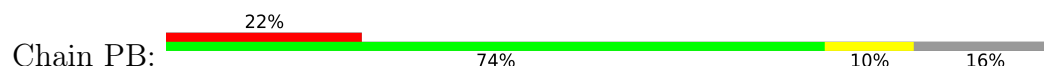
- Molecule 5: 60 kDa protein



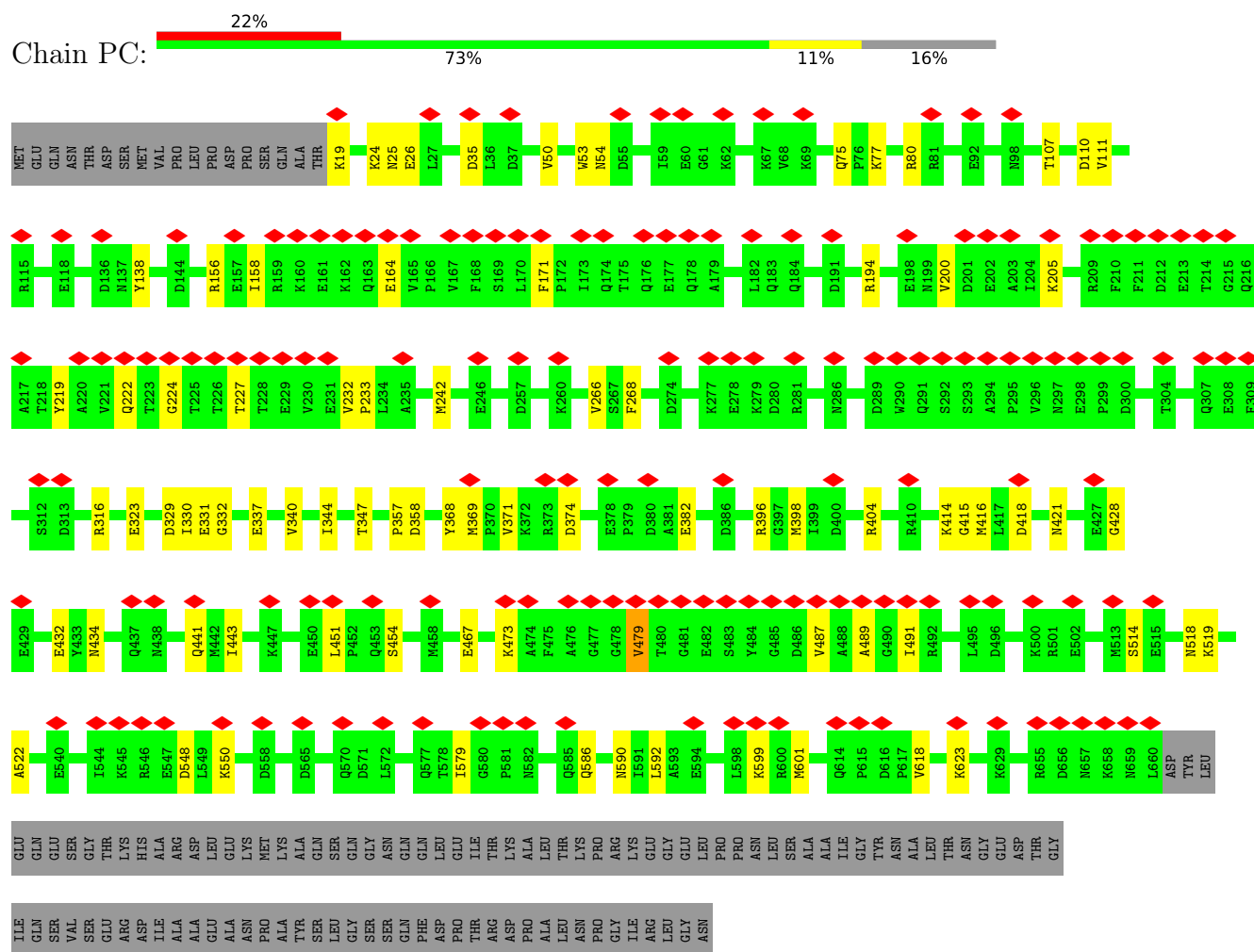
- Molecule 6: Probable portal protein



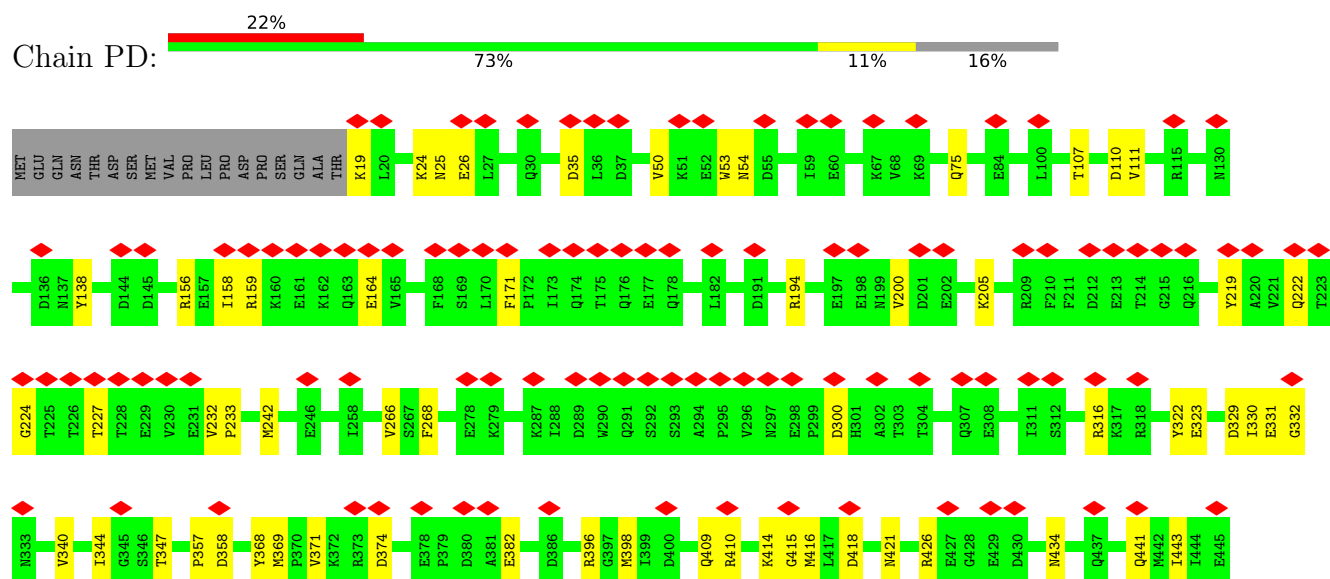
- Molecule 6: Probable portal protein

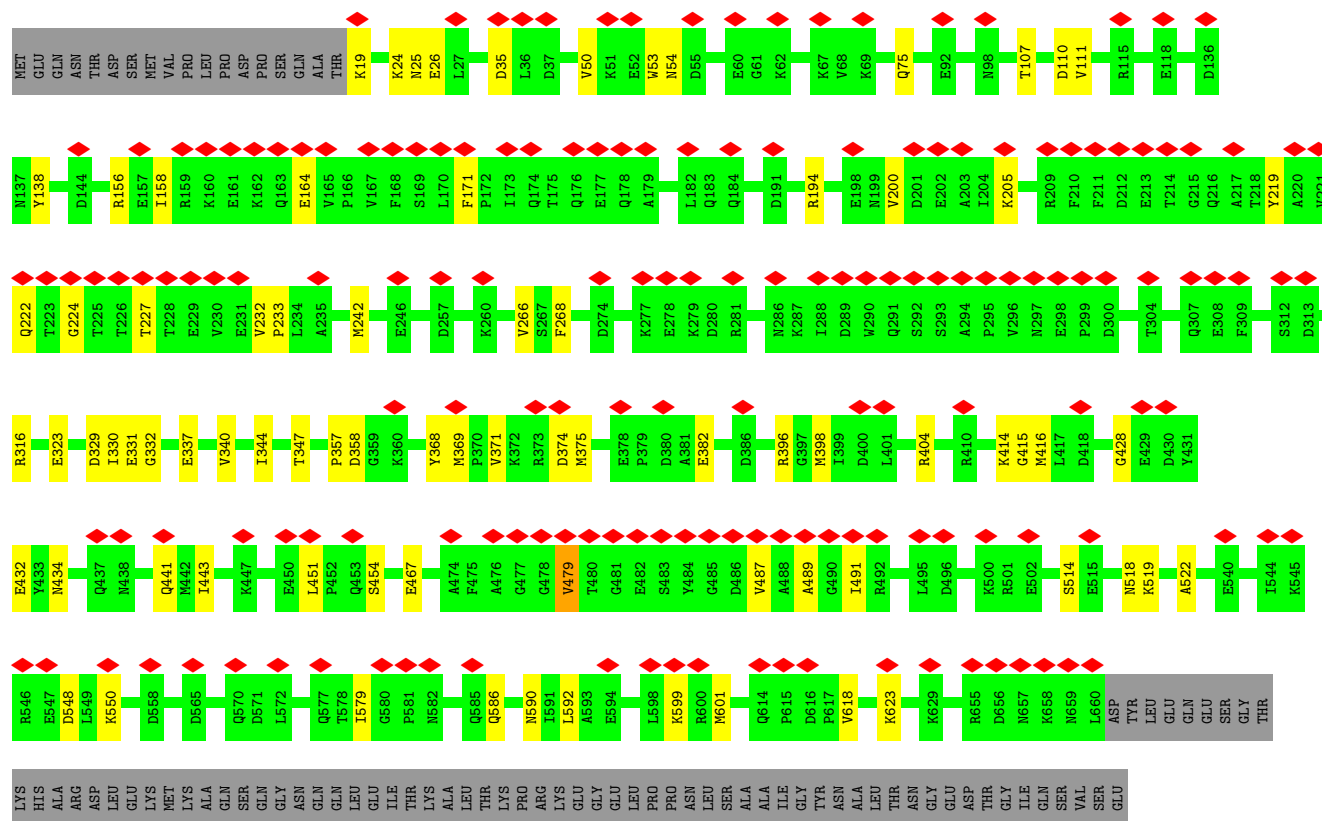


- Molecule 6: Probable portal protein

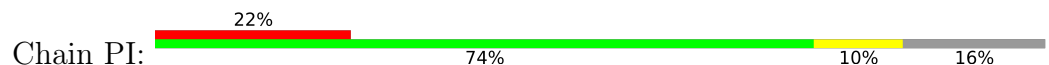


- Molecule 6: Probable portal protein

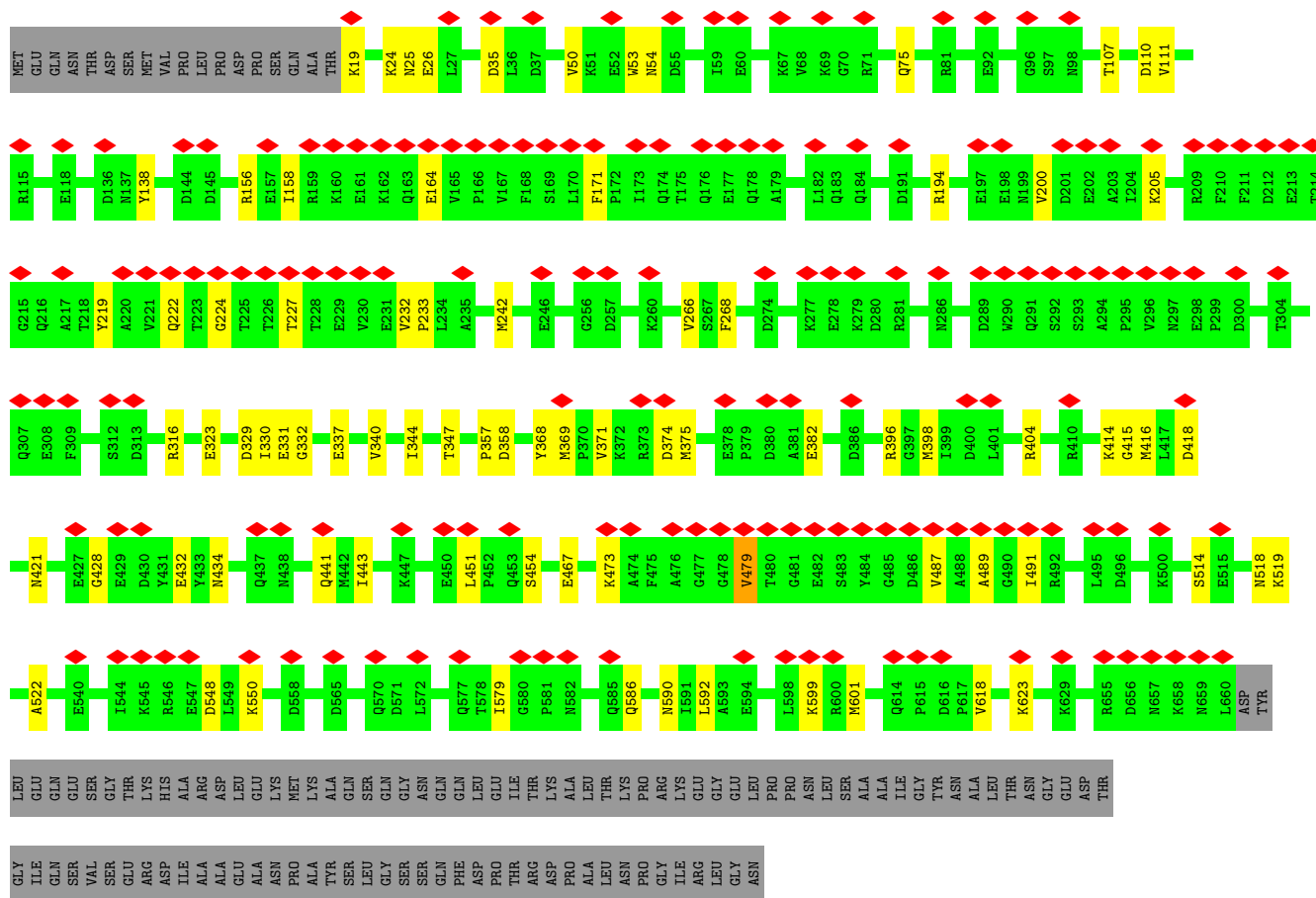




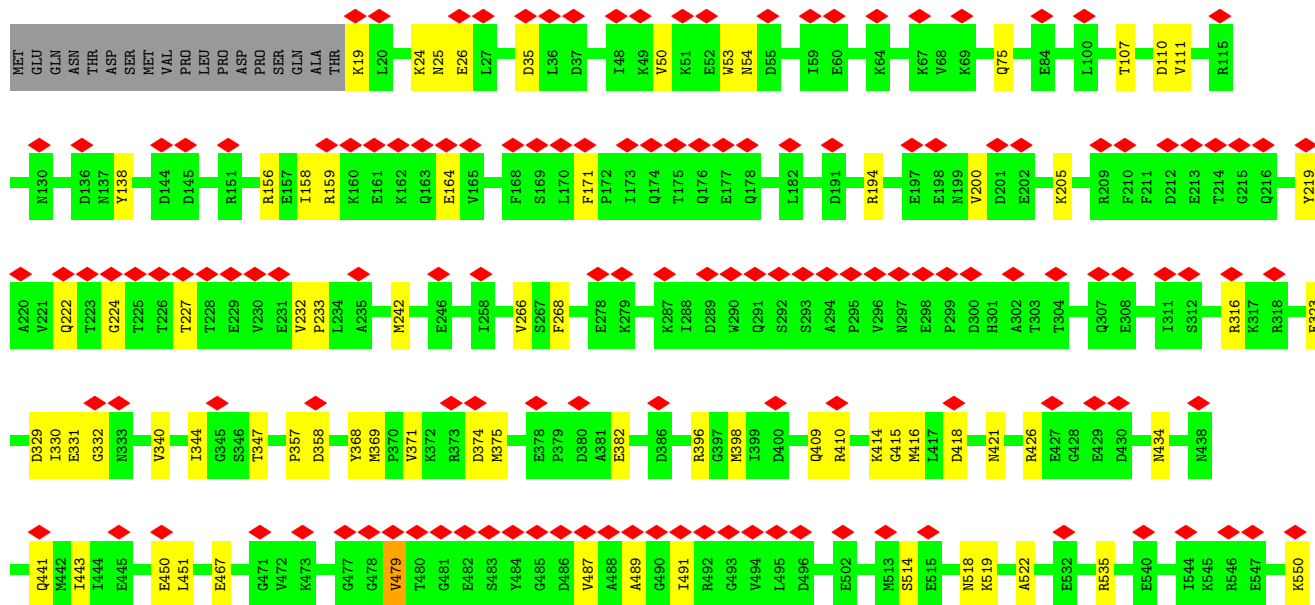
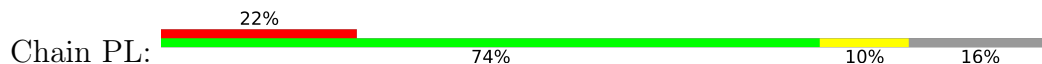
Chain PH:

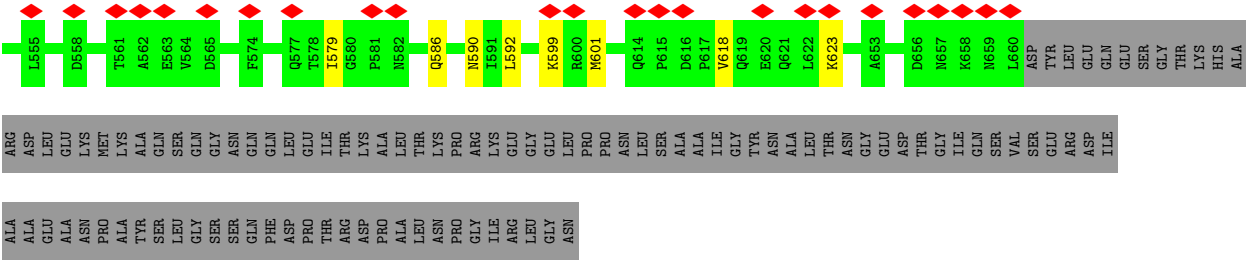






• Molecule 6: Probable portal protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	10265	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.443	Depositor
Minimum map value	-0.141	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.056	Depositor
Recommended contour level	0.17	Depositor
Map size (Å)	266.262, 268.65, 456.108	wwPDB
Map dimensions	382, 225, 223	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.194, 1.194, 1.194	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	AA	0.07	0/1953	0.19	0/2654
1	AB	0.07	0/1953	0.19	0/2654
1	AC	0.07	0/1953	0.18	0/2654
1	AD	0.07	0/1953	0.19	0/2654
1	AE	0.07	0/1953	0.19	0/2654
1	AF	0.07	0/1953	0.19	0/2654
1	AG	0.07	0/1953	0.19	0/2654
1	AH	0.07	0/1953	0.19	0/2654
1	AI	0.07	0/1953	0.19	0/2654
1	AJ	0.07	0/1953	0.19	0/2654
1	AK	0.07	0/1953	0.19	0/2654
1	AL	0.07	0/1953	0.19	0/2654
2	LA	0.07	0/9606	0.22	0/13093
2	LB	0.07	0/9606	0.22	0/13093
2	LC	0.07	0/9606	0.22	0/13093
2	LD	0.07	0/9606	0.22	0/13093
2	LE	0.07	0/9606	0.22	0/13093
2	LF	0.07	0/9606	0.22	0/13093
3	SA	0.07	0/3498	0.22	0/4781
3	SB	0.07	0/3498	0.22	0/4781
3	SC	0.07	0/3498	0.22	0/4781
3	SD	0.07	0/3498	0.22	0/4781
3	SE	0.07	0/3498	0.22	0/4781
3	SF	0.07	0/3498	0.22	0/4781
4	TA	0.06	0/2290	0.17	0/3103
4	TB	0.06	0/2290	0.17	0/3103
4	TC	0.06	0/2290	0.17	0/3103
4	TD	0.06	0/2290	0.17	0/3103
4	TE	0.06	0/2290	0.17	0/3103
4	TF	0.06	0/2290	0.17	0/3103
4	TG	0.06	0/2290	0.17	0/3103
4	TH	0.06	0/2290	0.17	0/3103
4	TI	0.06	0/2290	0.17	0/3103
4	TJ	0.06	0/2290	0.17	0/3103

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	TK	0.06	0/2290	0.17	0/3103
4	TL	0.06	0/2290	0.17	0/3103
5	XA	0.08	0/585	0.21	0/794
5	XB	0.07	0/585	0.19	0/794
5	XC	0.08	0/585	0.21	0/794
5	XD	0.07	0/585	0.19	0/794
5	XE	0.08	0/585	0.21	0/794
5	XF	0.07	0/585	0.19	0/794
5	XG	0.08	0/585	0.21	0/794
5	XH	0.07	0/585	0.19	0/794
5	XI	0.08	0/585	0.21	0/794
5	XJ	0.07	0/585	0.19	0/794
5	XK	0.08	0/585	0.21	0/794
5	XL	0.07	0/585	0.19	0/794
5	YA	0.08	0/554	0.24	0/750
5	YB	0.07	0/554	0.21	0/750
5	YC	0.07	0/554	0.24	0/750
5	YD	0.07	0/554	0.21	0/750
5	YE	0.08	0/554	0.24	0/750
5	YF	0.07	0/554	0.21	0/750
5	YG	0.08	0/554	0.24	0/750
5	YH	0.07	0/554	0.21	0/750
5	YI	0.08	0/554	0.24	0/750
5	YJ	0.07	0/554	0.21	0/750
5	YK	0.08	0/554	0.24	0/750
5	YL	0.07	0/554	0.21	0/750
5	ZA	0.07	0/516	0.21	0/699
5	ZB	0.07	0/516	0.21	0/699
5	ZC	0.08	0/516	0.20	0/699
5	ZD	0.07	0/516	0.21	0/699
5	ZE	0.08	0/516	0.20	0/699
5	ZF	0.07	0/516	0.21	0/699
5	ZG	0.07	0/516	0.21	0/699
5	ZH	0.07	0/516	0.21	0/699
5	ZI	0.07	0/516	0.20	0/699
5	ZJ	0.07	0/516	0.21	0/699
5	ZK	0.07	0/516	0.21	0/699
5	ZL	0.07	0/516	0.21	0/699
6	PA	0.07	0/5188	0.18	0/7024
6	PB	0.07	0/5188	0.18	0/7024
6	PC	0.07	0/5188	0.18	0/7024
6	PD	0.07	0/5188	0.18	0/7024
6	PE	0.07	0/5188	0.18	0/7024

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	PF	0.07	0/5188	0.18	0/7024
6	PG	0.07	0/5188	0.18	0/7024
6	PH	0.07	0/5188	0.18	0/7024
6	PI	0.07	0/5188	0.18	0/7024
6	PJ	0.07	0/5188	0.18	0/7024
6	PK	0.07	0/5188	0.18	0/7024
6	PL	0.07	0/5188	0.18	0/7024
All	All	0.07	0/211656	0.20	0/287532

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1912	0	1842	17	0
1	AB	1912	0	1843	21	0
1	AC	1912	0	1842	18	0
1	AD	1912	0	1843	18	0
1	AE	1912	0	1842	16	0
1	AF	1912	0	1843	21	0
1	AG	1912	0	1842	18	0
1	AH	1912	0	1843	21	0
1	AI	1912	0	1842	17	0
1	AJ	1912	0	1843	19	0
1	AK	1912	0	1842	18	0
1	AL	1912	0	1843	20	0
2	LA	9341	0	8931	124	0
2	LB	9341	0	8931	132	0
2	LC	9341	0	8931	128	0
2	LD	9341	0	8931	128	0
2	LE	9341	0	8931	125	0
2	LF	9341	0	8931	125	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	SA	3383	0	3269	41	0
3	SB	3383	0	3269	43	0
3	SC	3383	0	3269	37	0
3	SD	3383	0	3269	43	0
3	SE	3383	0	3269	39	0
3	SF	3383	0	3269	38	0
4	TA	2263	0	2258	28	0
4	TB	2263	0	2258	29	0
4	TC	2263	0	2258	25	0
4	TD	2263	0	2258	28	0
4	TE	2263	0	2258	24	0
4	TF	2263	0	2258	29	0
4	TG	2263	0	2258	26	0
4	TH	2263	0	2258	29	0
4	TI	2263	0	2258	27	0
4	TJ	2263	0	2258	32	0
4	TK	2263	0	2258	28	0
4	TL	2263	0	2258	32	0
5	XA	575	0	586	13	0
5	XB	575	0	586	10	0
5	XC	575	0	586	12	0
5	XD	575	0	586	10	0
5	XE	575	0	586	14	0
5	XF	575	0	586	10	0
5	XG	575	0	586	11	0
5	XH	575	0	586	9	0
5	XI	575	0	586	13	0
5	XJ	575	0	586	11	0
5	XK	575	0	586	13	0
5	XL	575	0	586	7	0
5	YA	543	0	563	9	0
5	YB	543	0	563	10	0
5	YC	543	0	563	9	0
5	YD	543	0	563	10	0
5	YE	543	0	563	9	0
5	YF	543	0	563	9	0
5	YG	543	0	563	10	0
5	YH	543	0	563	9	0
5	YI	543	0	563	10	0
5	YJ	543	0	563	9	0
5	YK	543	0	563	10	0
5	YL	543	0	563	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	ZA	508	0	528	11	0
5	ZB	508	0	528	5	0
5	ZC	508	0	528	12	0
5	ZD	508	0	528	5	0
5	ZE	508	0	528	10	0
5	ZF	508	0	528	4	0
5	ZG	508	0	528	11	0
5	ZH	508	0	528	3	0
5	ZI	508	0	528	11	0
5	ZJ	508	0	528	4	0
5	ZK	508	0	528	11	0
5	ZL	508	0	528	4	0
6	PA	5094	0	5082	51	0
6	PB	5094	0	5082	54	0
6	PC	5094	0	5082	53	0
6	PD	5094	0	5082	55	0
6	PE	5094	0	5082	50	0
6	PF	5094	0	5082	53	0
6	PG	5094	0	5082	51	0
6	PH	5094	0	5082	53	0
6	PI	5094	0	5082	52	0
6	PJ	5094	0	5082	52	0
6	PK	5094	0	5082	53	0
6	PL	5094	0	5082	55	0
All	All	207084	0	203514	2067	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 5.

The worst 5 of 2067 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)
2:LA:840:ALA:HA	2:LA:888:GLN:HB3	1.64	0.80
2:LD:840:ALA:HA	2:LD:888:GLN:HB3	1.64	0.80
2:LE:840:ALA:HA	2:LE:888:GLN:HB3	1.64	0.80
6:PA:24:LYS:HE2	6:PA:332:GLY:H	1.48	0.79
2:LB:840:ALA:HA	2:LB:888:GLN:HB3	1.64	0.79

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	234/236 (99%)	234 (100%)	0	0	100	100
1	AB	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AC	234/236 (99%)	234 (100%)	0	0	100	100
1	AD	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AE	234/236 (99%)	234 (100%)	0	0	100	100
1	AF	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AG	234/236 (99%)	234 (100%)	0	0	100	100
1	AH	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AI	234/236 (99%)	234 (100%)	0	0	100	100
1	AJ	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
1	AK	234/236 (99%)	234 (100%)	0	0	100	100
1	AL	234/236 (99%)	233 (100%)	1 (0%)	0	100	100
2	LA	1179/1382 (85%)	1155 (98%)	24 (2%)	0	100	100
2	LB	1179/1382 (85%)	1154 (98%)	25 (2%)	0	100	100
2	LC	1179/1382 (85%)	1155 (98%)	24 (2%)	0	100	100
2	LD	1179/1382 (85%)	1155 (98%)	24 (2%)	0	100	100
2	LE	1179/1382 (85%)	1153 (98%)	26 (2%)	0	100	100
2	LF	1179/1382 (85%)	1153 (98%)	26 (2%)	0	100	100
3	SA	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
3	SB	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
3	SC	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
3	SD	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
3	SE	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
3	SF	413/417 (99%)	405 (98%)	7 (2%)	1 (0%)	43	70
4	TA	296/299 (99%)	291 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	TB	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TC	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TD	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TE	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TF	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TG	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TH	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TI	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TJ	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TK	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
4	TL	296/299 (99%)	291 (98%)	5 (2%)	0	100	100
5	XA	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XB	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	XC	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XD	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	XE	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XF	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	XG	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XH	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	XI	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XJ	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	XK	70/556 (13%)	67 (96%)	3 (4%)	0	100	100
5	XL	70/556 (13%)	69 (99%)	1 (1%)	0	100	100
5	YA	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YB	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YC	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YD	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YE	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YF	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YG	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YH	64/556 (12%)	63 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	YI	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YJ	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YK	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	YL	64/556 (12%)	63 (98%)	1 (2%)	0	100	100
5	ZA	61/556 (11%)	61 (100%)	0	0	100	100
5	ZB	61/556 (11%)	61 (100%)	0	0	100	100
5	ZC	61/556 (11%)	61 (100%)	0	0	100	100
5	ZD	61/556 (11%)	61 (100%)	0	0	100	100
5	ZE	61/556 (11%)	61 (100%)	0	0	100	100
5	ZF	61/556 (11%)	61 (100%)	0	0	100	100
5	ZG	61/556 (11%)	61 (100%)	0	0	100	100
5	ZH	61/556 (11%)	61 (100%)	0	0	100	100
5	ZI	61/556 (11%)	61 (100%)	0	0	100	100
5	ZJ	61/556 (11%)	61 (100%)	0	0	100	100
5	ZK	61/556 (11%)	61 (100%)	0	0	100	100
5	ZL	61/556 (11%)	61 (100%)	0	0	100	100
6	PA	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PB	640/763 (84%)	633 (99%)	7 (1%)	0	100	100
6	PC	640/763 (84%)	631 (99%)	9 (1%)	0	100	100
6	PD	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PE	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PF	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PG	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PH	640/763 (84%)	633 (99%)	7 (1%)	0	100	100
6	PI	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PJ	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
6	PK	640/763 (84%)	633 (99%)	7 (1%)	0	100	100
6	PL	640/763 (84%)	632 (99%)	8 (1%)	0	100	100
All	All	25932/46386 (56%)	25539 (98%)	387 (2%)	6 (0%)	100	100

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	SA	368	LEU
3	SB	368	LEU
3	SC	368	LEU
3	SD	368	LEU
3	SE	368	LEU

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	AA	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AB	209/209 (100%)	206 (99%)	3 (1%)	59	68
1	AC	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AD	209/209 (100%)	206 (99%)	3 (1%)	59	68
1	AE	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AF	209/209 (100%)	206 (99%)	3 (1%)	59	68
1	AG	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AH	209/209 (100%)	206 (99%)	3 (1%)	59	68
1	AI	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AJ	209/209 (100%)	206 (99%)	3 (1%)	59	68
1	AK	209/209 (100%)	208 (100%)	1 (0%)	81	79
1	AL	209/209 (100%)	206 (99%)	3 (1%)	59	68
2	LA	989/1155 (86%)	971 (98%)	18 (2%)	51	65
2	LB	989/1155 (86%)	971 (98%)	18 (2%)	51	65
2	LC	989/1155 (86%)	971 (98%)	18 (2%)	51	65
2	LD	989/1155 (86%)	971 (98%)	18 (2%)	51	65
2	LE	989/1155 (86%)	971 (98%)	18 (2%)	51	65
2	LF	989/1155 (86%)	971 (98%)	18 (2%)	51	65
3	SA	369/371 (100%)	365 (99%)	4 (1%)	65	71
3	SB	369/371 (100%)	365 (99%)	4 (1%)	65	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	SC	369/371 (100%)	365 (99%)	4 (1%)	65	71
3	SD	369/371 (100%)	365 (99%)	4 (1%)	65	71
3	SE	369/371 (100%)	365 (99%)	4 (1%)	65	71
3	SF	369/371 (100%)	365 (99%)	4 (1%)	65	71
4	TA	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TB	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TC	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TD	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TE	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TF	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TG	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TH	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TI	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TJ	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TK	243/244 (100%)	241 (99%)	2 (1%)	73	74
4	TL	243/244 (100%)	241 (99%)	2 (1%)	73	74
5	XA	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XB	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	XC	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XD	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	XE	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XF	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	XG	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XH	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	XI	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XJ	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	XK	66/455 (14%)	64 (97%)	2 (3%)	36	56
5	XL	66/455 (14%)	65 (98%)	1 (2%)	57	67
5	YA	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YB	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YC	62/455 (14%)	61 (98%)	1 (2%)	55	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	YD	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YE	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YF	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YG	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YH	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YI	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YJ	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YK	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	YL	62/455 (14%)	61 (98%)	1 (2%)	55	66
5	ZA	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZB	58/455 (13%)	56 (97%)	2 (3%)	32	53
5	ZC	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZD	58/455 (13%)	56 (97%)	2 (3%)	32	53
5	ZE	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZF	58/455 (13%)	56 (97%)	2 (3%)	32	53
5	ZG	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZH	58/455 (13%)	56 (97%)	2 (3%)	32	53
5	ZI	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZJ	58/455 (13%)	56 (97%)	2 (3%)	32	53
5	ZK	58/455 (13%)	57 (98%)	1 (2%)	53	65
5	ZL	58/455 (13%)	56 (97%)	2 (3%)	32	53
6	PA	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PB	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PC	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PD	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PE	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PF	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PG	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PH	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PI	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PJ	551/652 (84%)	545 (99%)	6 (1%)	65	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	PK	551/652 (84%)	545 (99%)	6 (1%)	65	71
6	PL	551/652 (84%)	545 (99%)	6 (1%)	65	71
All	All	22416/38796 (58%)	22116 (99%)	300 (1%)	59	69

5 of 300 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	ZK	64	THR
6	PJ	441	GLN
6	PB	441	GLN
6	PF	266	VAL
2	LC	1038	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 340 such sidechains are listed below:

Mol	Chain	Res	Type
5	ZL	61	ASN
6	PG	570	GLN
6	PB	524	ASN
6	PE	82	GLN
6	PI	291	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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.

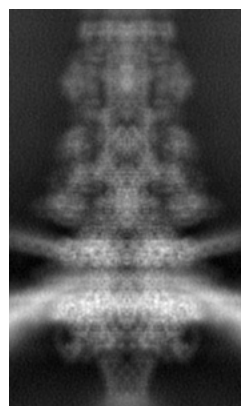
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72877. These allow visual inspection of the internal detail of the map and identification of artifacts.

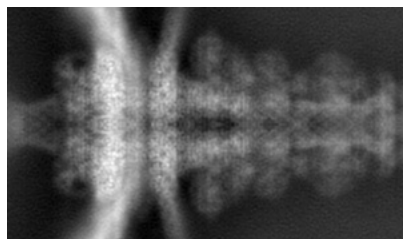
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

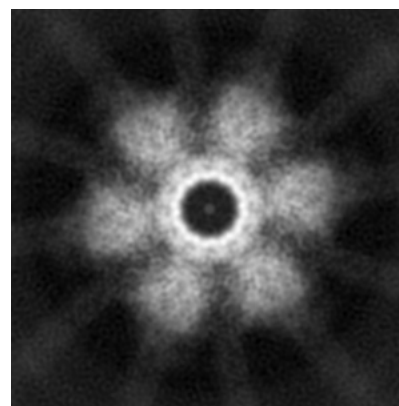
6.1.1 Primary map



X

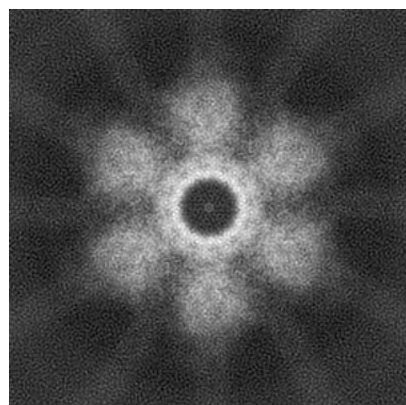


Y

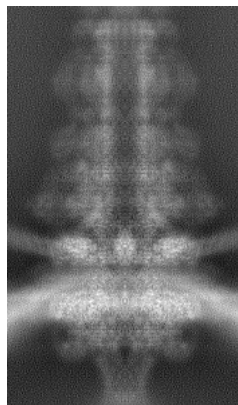


Z

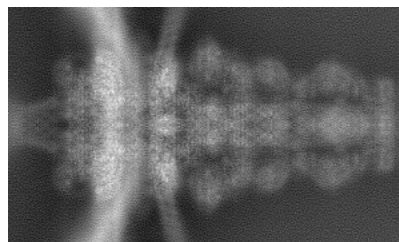
6.1.2 Raw map



X



Y

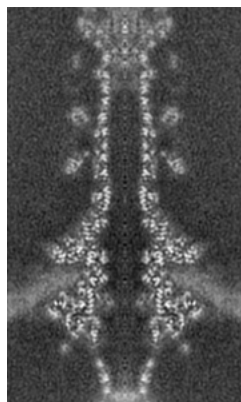


Z

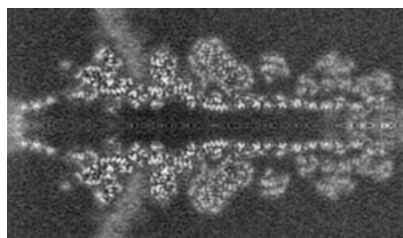
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

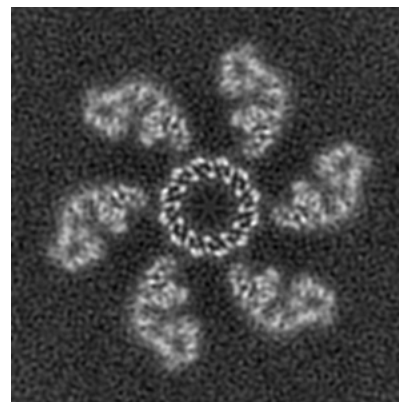
6.2.1 Primary map



X Index: 111

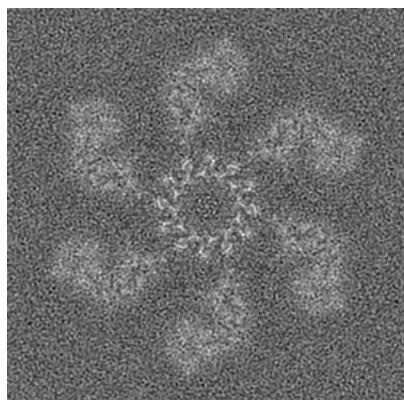


Y Index: 112

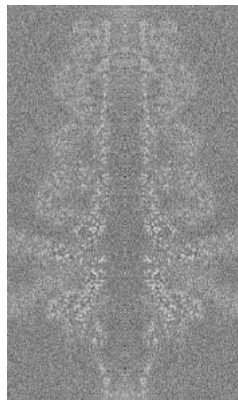


Z Index: 191

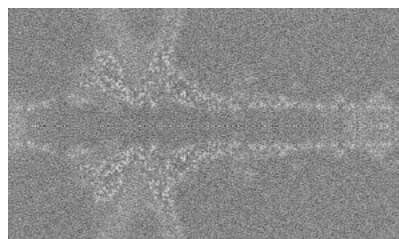
6.2.2 Raw map



X Index: 191



Y Index: 112



Z Index: 111

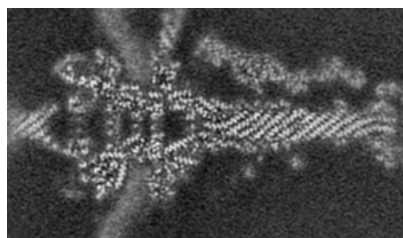
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

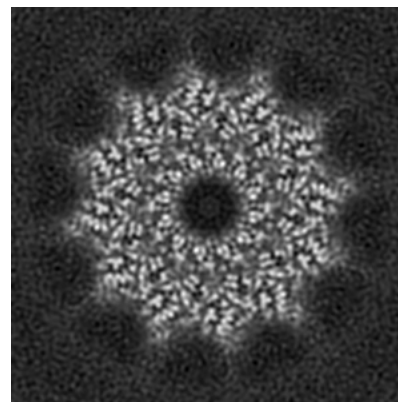
6.3.1 Primary map



X Index: 93

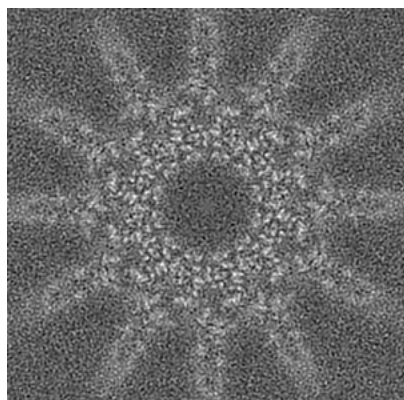


Y Index: 130

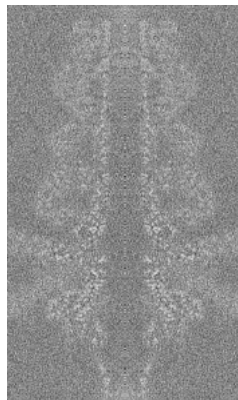


Z Index: 143

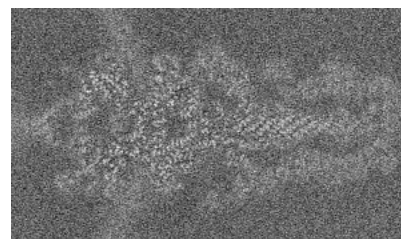
6.3.2 Raw map



X Index: 151



Y Index: 112

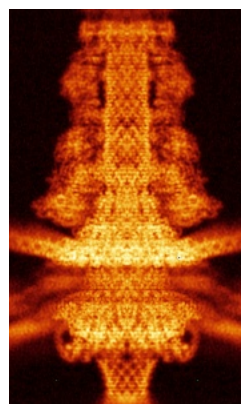


Z Index: 91

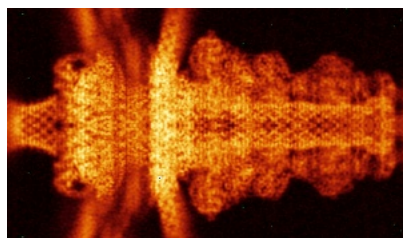
The images above show the largest variance slices of the map in three orthogonal directions.

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

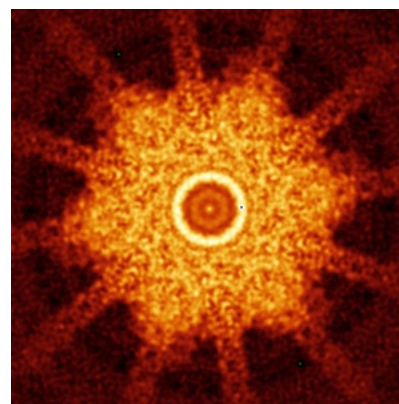
6.4.1 Primary map



X

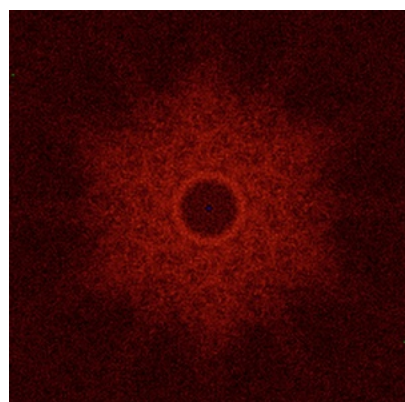


Y

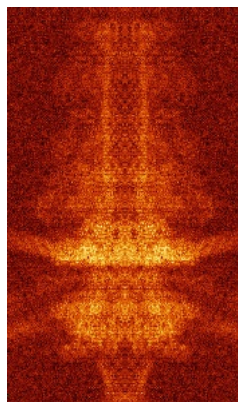


Z

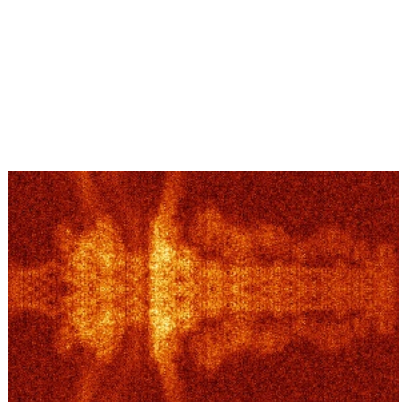
6.4.2 Raw map



X



Y

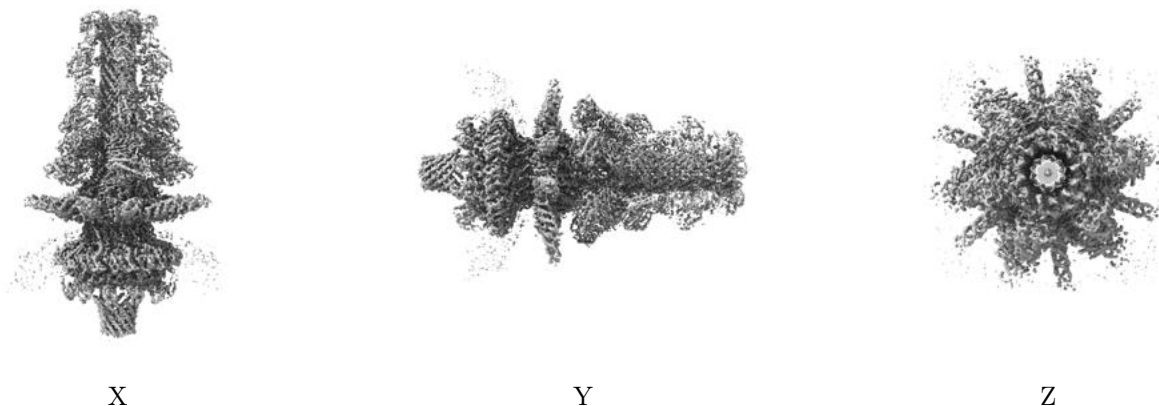


Z

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.

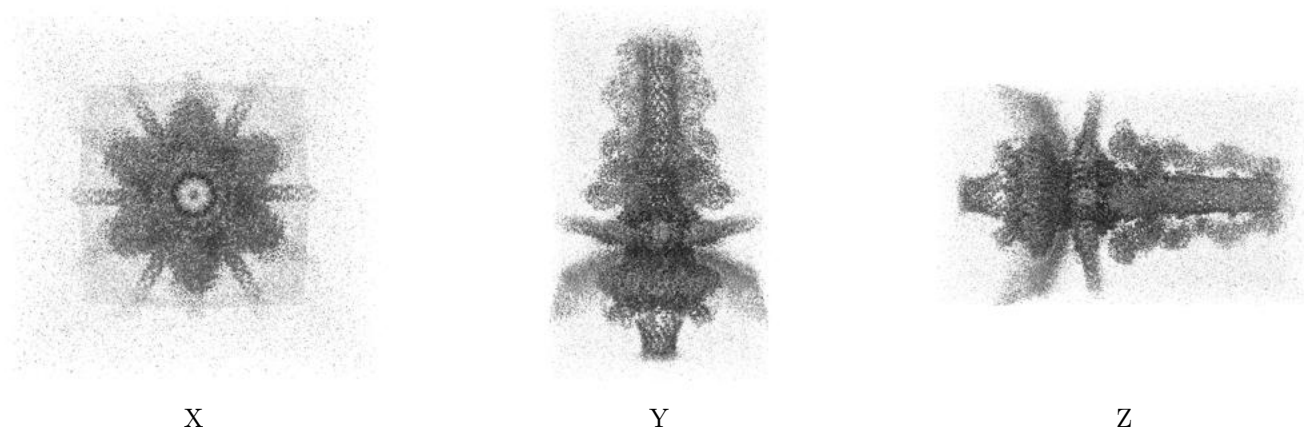
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.17. 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.

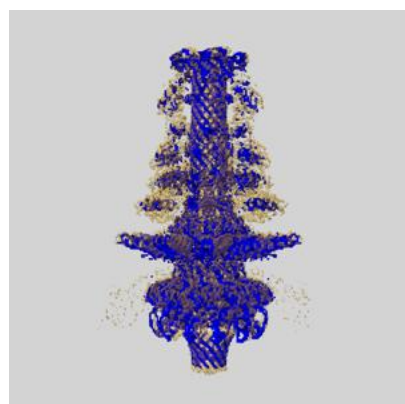
6.6 Mask visualisation [i](#)

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

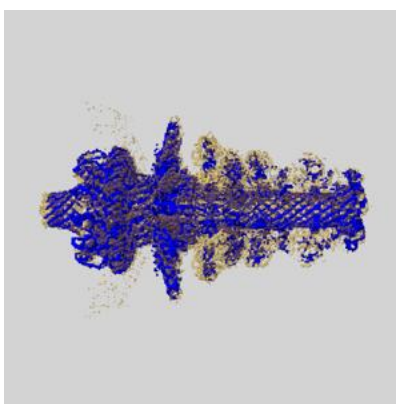
A mask typically either:

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

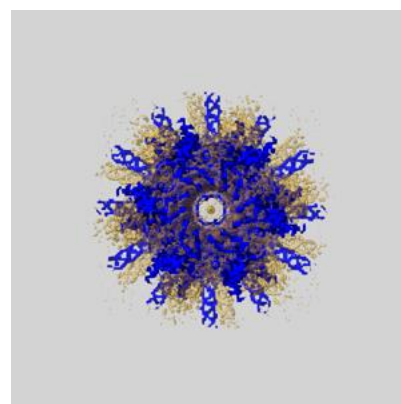
6.6.1 emd_72877_msk_1.map [i](#)



X



Y

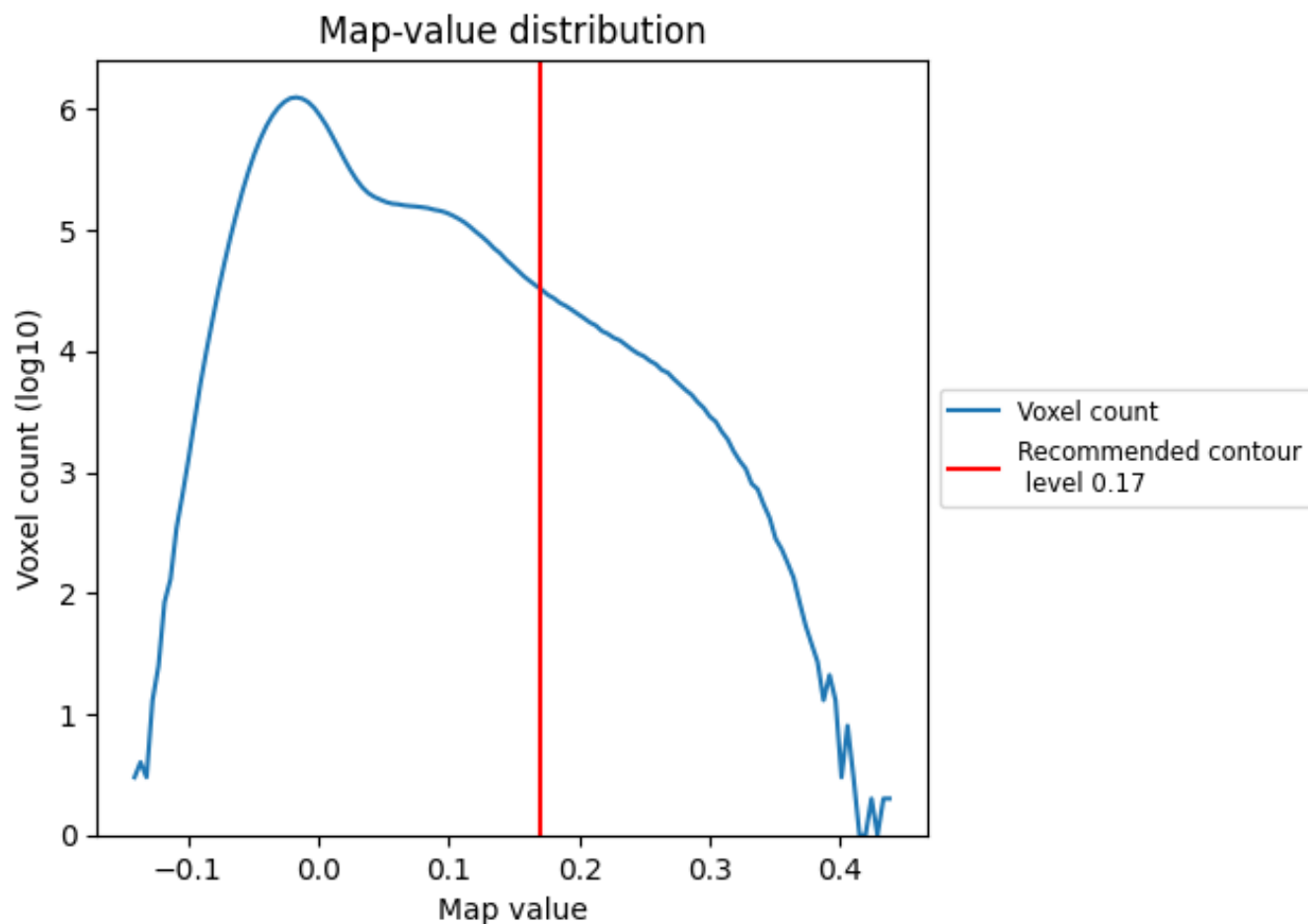


Z

7 Map analysis [i](#)

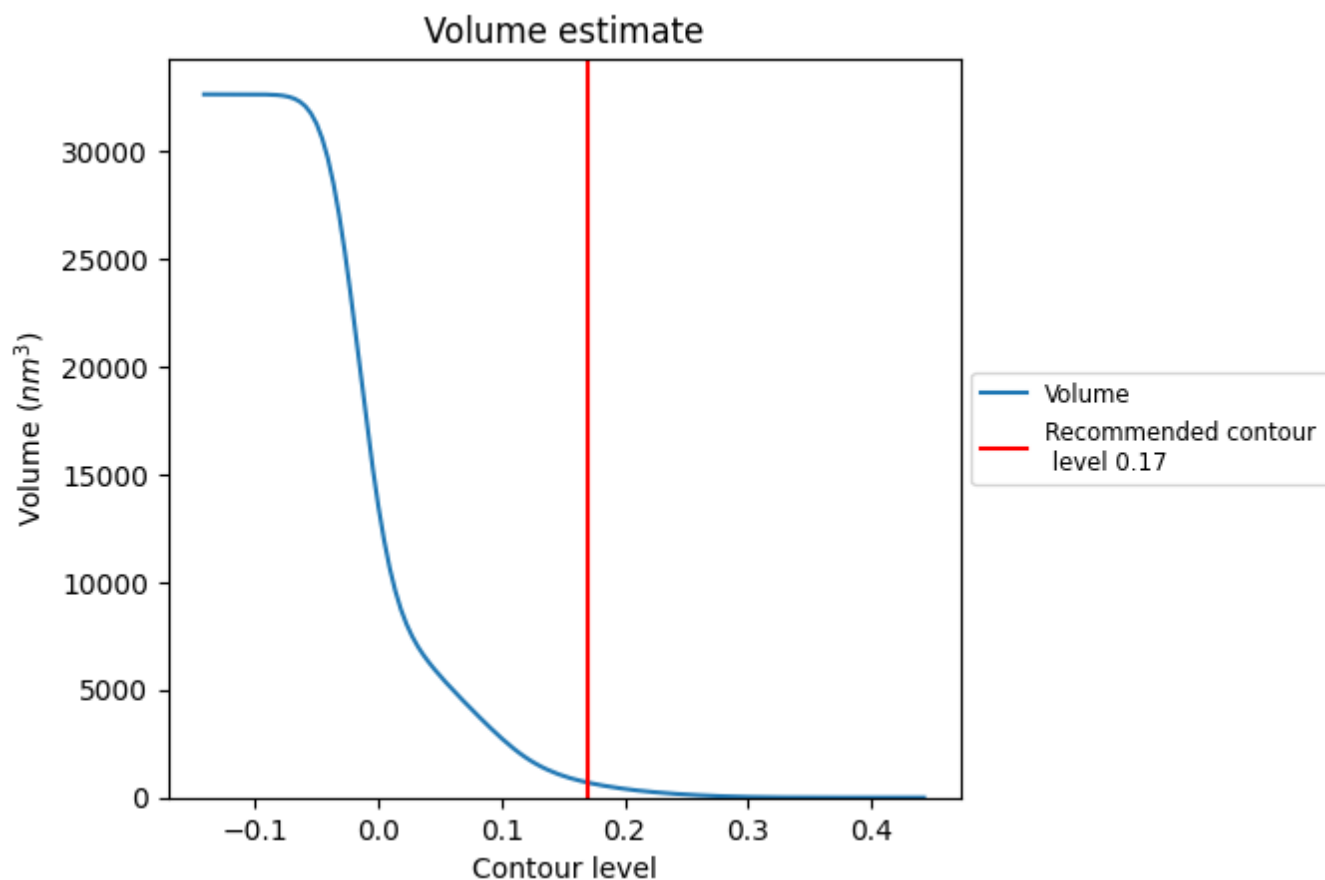
This section contains the results of statistical analysis of the map.

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 698 nm³; this corresponds to an approximate mass of 631 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](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

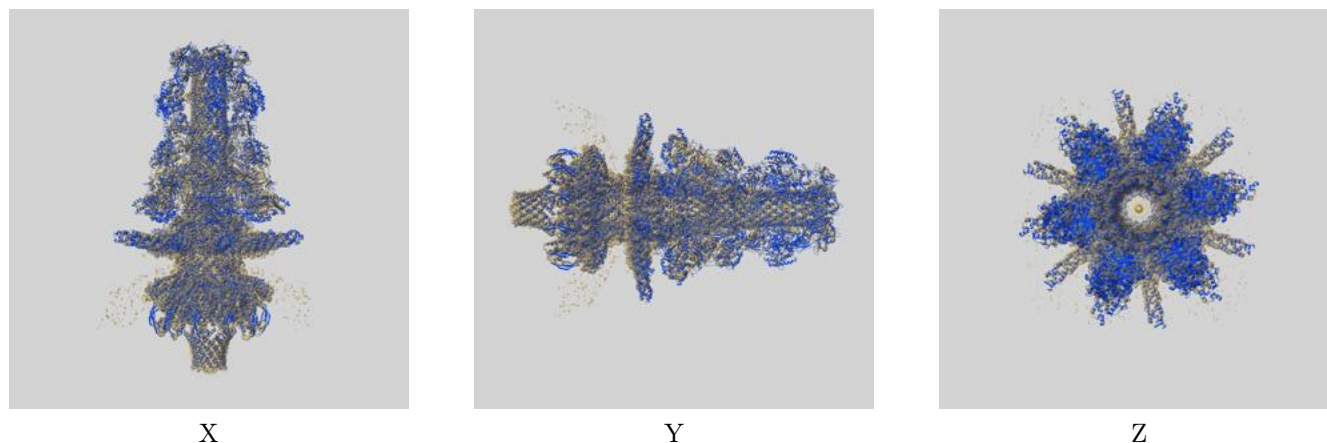
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

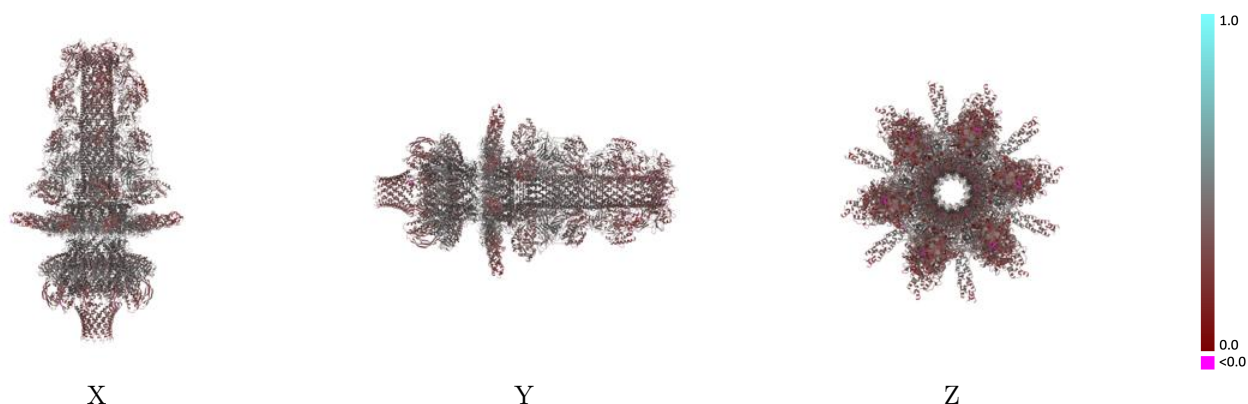
This section contains information regarding the fit between EMDB map EMD-72877 and PDB model 9YF5. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



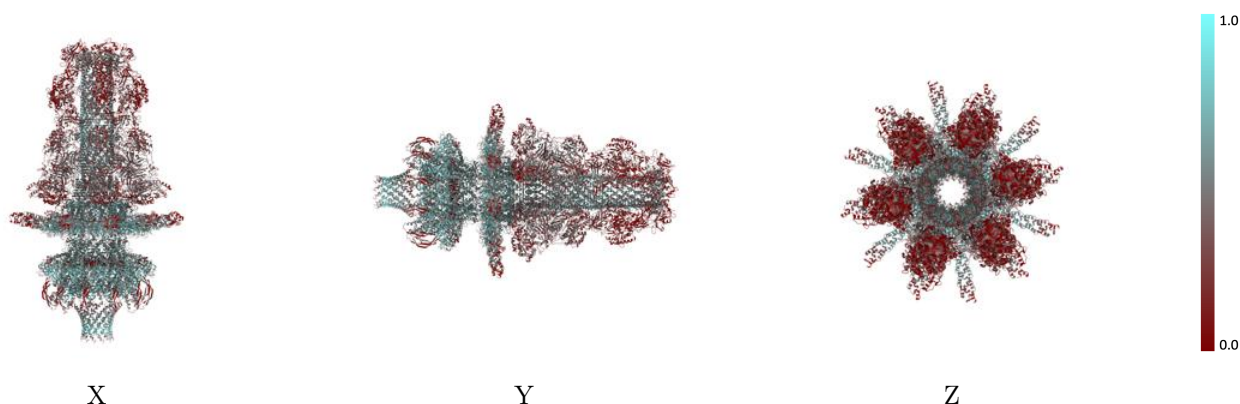
The images above show the 3D surface view of the map at the recommended contour level 0.17 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



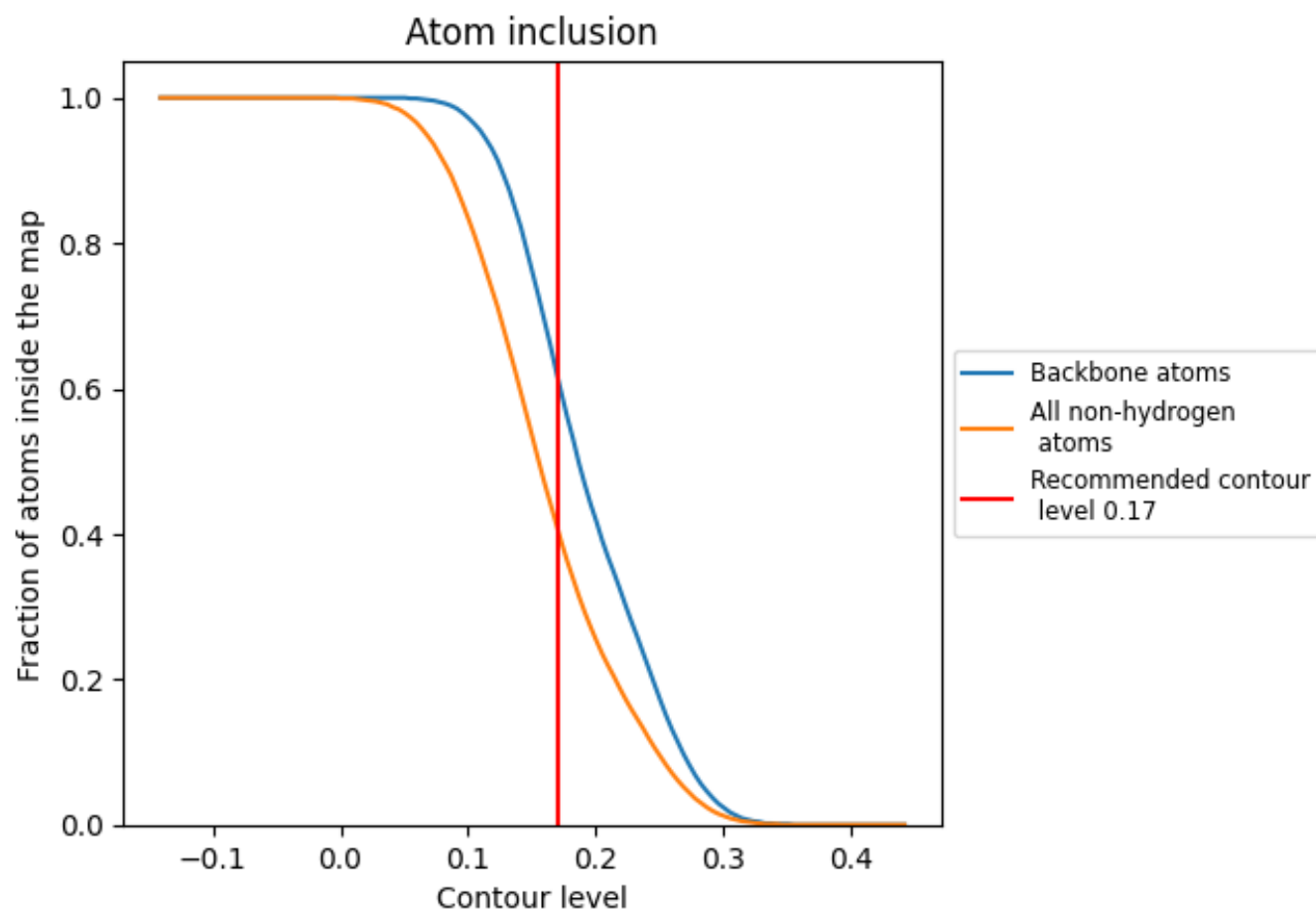
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.17).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 41% 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 (0.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4100	 0.3850
AA	 0.5740	 0.4470
AB	 0.5760	 0.4450
AC	 0.5740	 0.4440
AD	 0.5800	 0.4460
AE	 0.5800	 0.4450
AF	 0.5830	 0.4460
AG	 0.5740	 0.4470
AH	 0.5760	 0.4460
AI	 0.5740	 0.4460
AJ	 0.5810	 0.4470
AK	 0.5800	 0.4460
AL	 0.5830	 0.4460
LA	 0.2220	 0.3590
LB	 0.2220	 0.3590
LC	 0.2220	 0.3600
LD	 0.2220	 0.3600
LE	 0.2220	 0.3600
LF	 0.2220	 0.3610
PA	 0.5280	 0.3990
PB	 0.5190	 0.3980
PC	 0.5260	 0.3990
PD	 0.5210	 0.3990
PE	 0.5250	 0.3990
PF	 0.5230	 0.3960
PG	 0.5280	 0.3990
PH	 0.5200	 0.3960
PI	 0.5270	 0.3990
PJ	 0.5200	 0.3970
PK	 0.5250	 0.3990
PL	 0.5230	 0.3980
SA	 0.2420	 0.3550
SB	 0.2390	 0.3540
SC	 0.2350	 0.3560
SD	 0.2420	 0.3560



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Chain	Atom inclusion	Q-score
SE	 0.2390	 0.3560
SF	 0.2350	 0.3550
TA	 0.4960	 0.3910
TB	 0.5020	 0.3920
TC	 0.5020	 0.3900
TD	 0.4970	 0.3910
TE	 0.5000	 0.3880
TF	 0.5030	 0.3890
TG	 0.4960	 0.3900
TH	 0.5020	 0.3900
TI	 0.5020	 0.3900
TJ	 0.4970	 0.3910
TK	 0.5010	 0.3900
TL	 0.5030	 0.3920
XA	 0.4530	 0.3640
XB	 0.4550	 0.3620
XC	 0.4500	 0.3670
XD	 0.4550	 0.3670
XE	 0.4430	 0.3640
XF	 0.4570	 0.3670
XG	 0.4550	 0.3680
XH	 0.4620	 0.3670
XI	 0.4520	 0.3650
XJ	 0.4530	 0.3620
XK	 0.4460	 0.3640
XL	 0.4570	 0.3610
YA	 0.4850	 0.3690
YB	 0.4460	 0.3700
YC	 0.4780	 0.3740
YD	 0.4480	 0.3740
YE	 0.4870	 0.3720
YF	 0.4500	 0.3750
YG	 0.4830	 0.3720
YH	 0.4500	 0.3770
YI	 0.4780	 0.3720
YJ	 0.4460	 0.3710
YK	 0.4870	 0.3710
YL	 0.4500	 0.3710
ZA	 0.4290	 0.3600
ZB	 0.4020	 0.3510
ZC	 0.4190	 0.3570
ZD	 0.4040	 0.3520

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Chain	Atom inclusion	Q-score
ZE	 0.4230	 0.3600
ZF	 0.4080	 0.3520
ZG	 0.4270	 0.3600
ZH	 0.4020	 0.3540
ZI	 0.4190	 0.3590
ZJ	 0.4040	 0.3560
ZK	 0.4230	 0.3590
ZL	 0.4080	 0.3520