



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:21 PM UTC

PDB ID : 9YA0 / pdb_00009ya0
EMDB ID : EMD-72716
Title : Cryo-EM structure of pre-conoid ring 2 (PCR P2 ring)from Toxoplasma gondii
Authors : Zeng, J.; Zhang, R.
Deposited on : 2025-09-15
Resolution : 3.54 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:

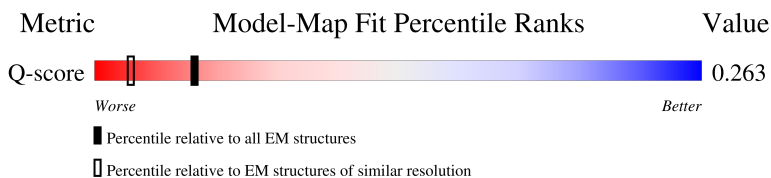
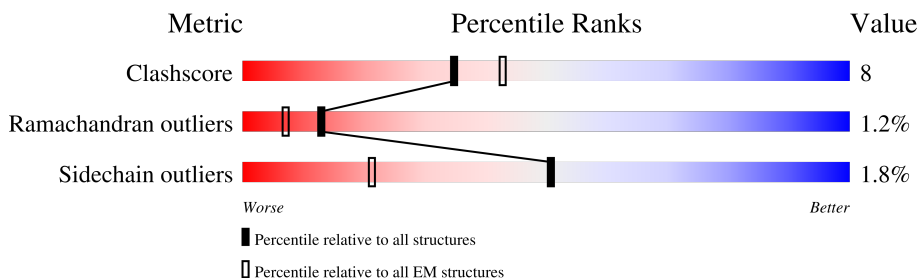
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.54 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.



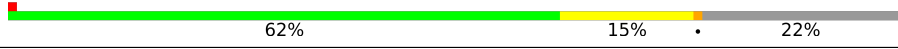
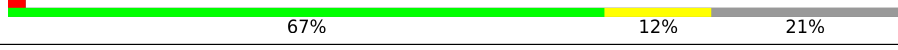
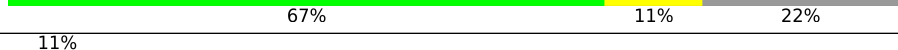
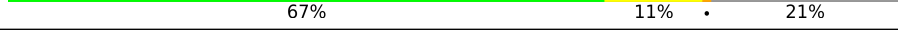
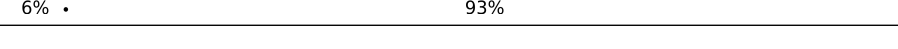
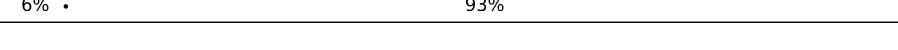
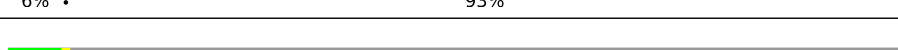
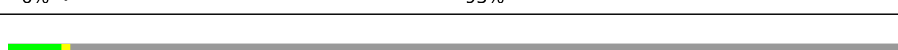
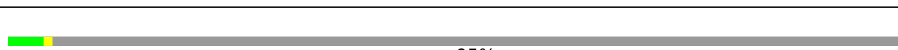
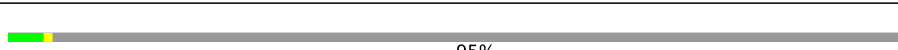
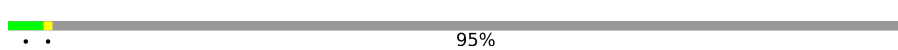
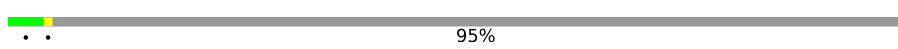
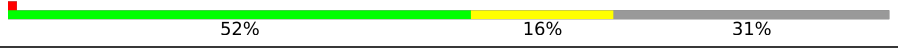
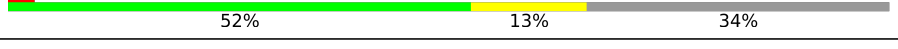
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12891 (3.04 - 4.04)

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	1073	
1	AD	1073	
1	AE	1073	
1	AH	1073	

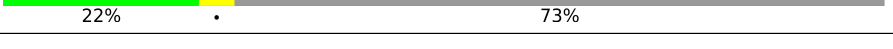
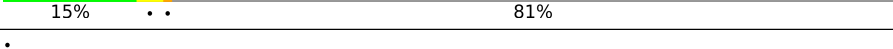
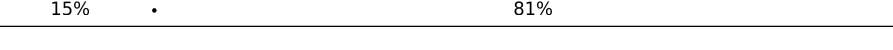
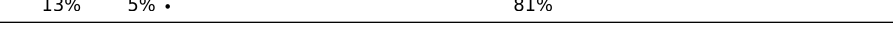
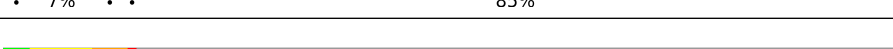
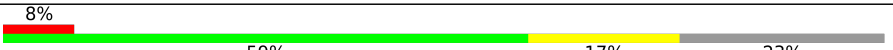
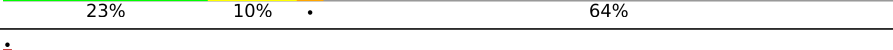
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Mol	Chain	Length	Quality of chain
1	AI	1073	
1	AL	1073	
2	AB	603	
2	AC	603	
2	AF	603	
2	AG	603	
2	AJ	603	
2	AK	603	
3	BA	5051	
3	BB	5051	
3	BC	5051	
3	CA	5051	
3	CB	5051	
3	CC	5051	
3	CE	5051	
3	CF	5051	
3	CG	5051	
3	CI	5051	
3	CJ	5051	
3	CL	5051	
4	DA	505	
4	DB	505	
4	DC	505	
4	DD	505	
4	DE	505	

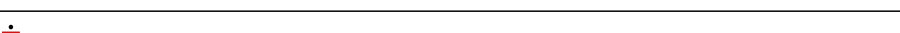
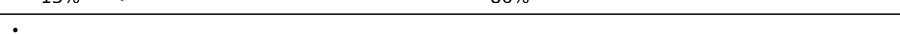
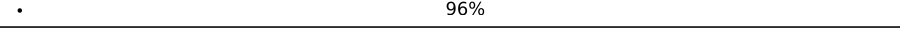
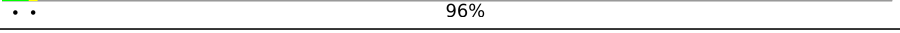
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Mol	Chain	Length	Quality of chain
4	DF	505	
5	EA	4956	
5	EB	4956	
5	EC	4956	
6	FA	2777	
6	FB	2777	
6	FC	2777	
6	FD	2777	
6	FE	2777	
6	FF	2777	
7	GA	1019	
7	GC	1019	
7	GE	1019	
7	GG	1019	
7	GI	1019	
7	GK	1019	
8	GB	791	
8	GD	791	
8	GF	791	
8	GH	791	
8	GJ	791	
8	GL	791	
9	HA	1192	
9	HB	1192	
9	HC	1192	

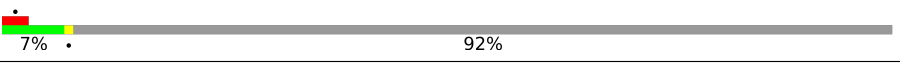
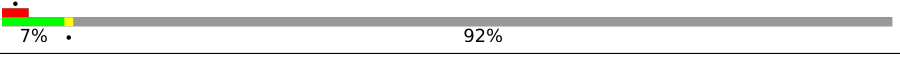
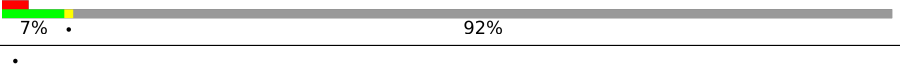
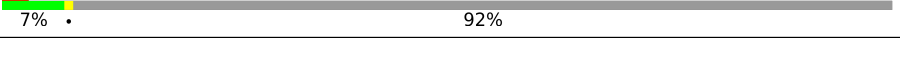
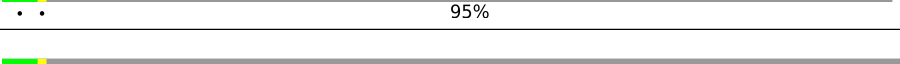
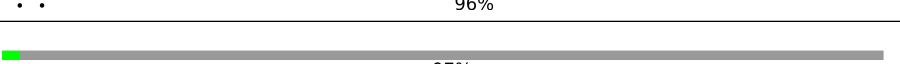
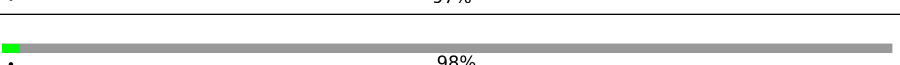
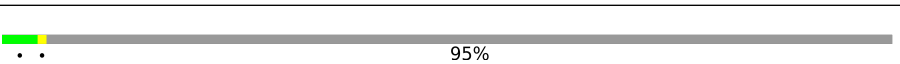
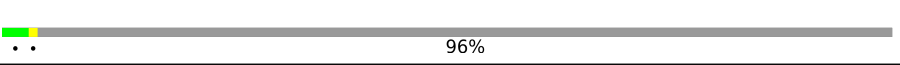
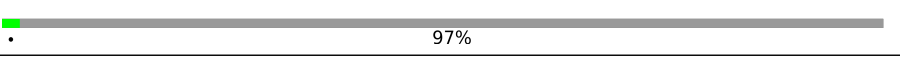
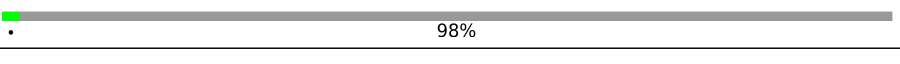
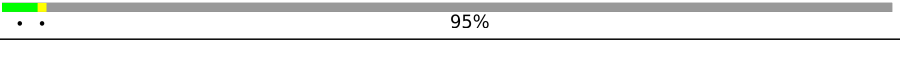
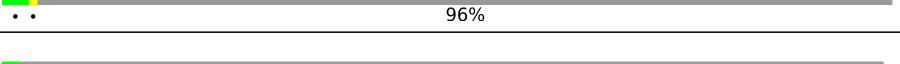
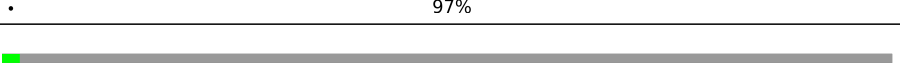
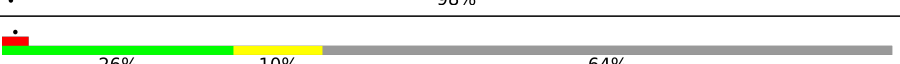
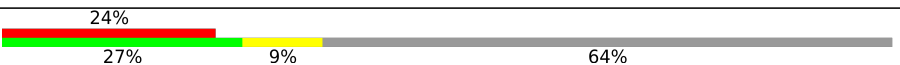
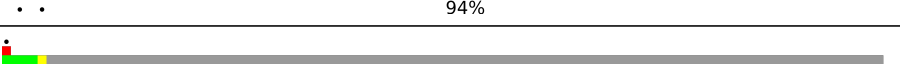
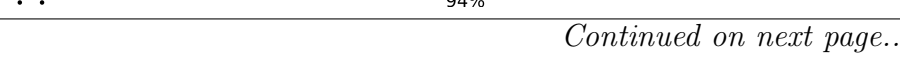
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Mol	Chain	Length	Quality of chain
9	HD	1192	 5% 5% 89%
10	IA	1599	 61% 11% 28%
10	IB	1599	 59% 13% 28%
10	IC	1599	 60% 12% 28%
11	JA	2316	 55% 14% 31%
11	JB	2316	 6% 56% 12% 31%
11	JC	2316	 54% 14% 31%
12	KA	728	 45% 18% 36%
12	KB	728	 49% 14% 36%
12	KC	728	 8% 44% 17% 36%
12	KE	728	 19% 48% 13% 39%
12	KF	728	 15% 49% 13% 39%
12	KG	728	 16% 51% 11% 39%
13	LA	1322	 12% 86%
13	LB	1322	 13% 86%
13	LC	1322	 12% 88%
13	LD	1322	 11% 88%
13	LE	1322	 9% 89%
13	LF	1322	 10% 89%
13	LG	1322	 96%
13	LH	1322	 96%
13	LI	1322	 11% 86%
13	LJ	1322	 11% 86%
13	LK	1322	 11% 88%
13	LL	1322	 11% 88%

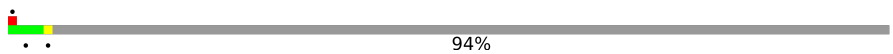
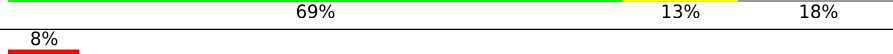
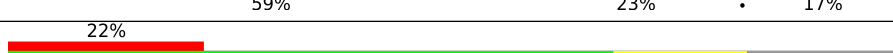
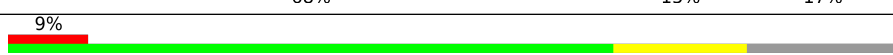
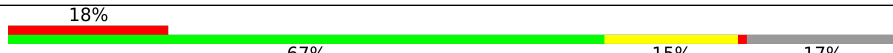
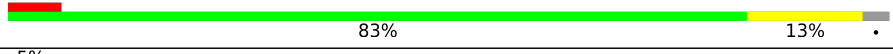
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Mol	Chain	Length	Quality of chain
13	LM	1322	 7% 92%
13	LN	1322	 7% 92%
13	LO	1322	 7% 92%
13	LP	1322	 7% 92%
14	MA	2736	 95%
14	MB	2736	 96%
14	MC	2736	 97%
14	MD	2736	 98%
14	ME	2736	 95%
14	MF	2736	 96%
14	MG	2736	 97%
14	MH	2736	 98%
14	MI	2736	 95%
14	MJ	2736	 96%
14	MK	2736	 97%
14	ML	2736	 98%
15	NA	2484	 26% 10% 64%
15	NB	2484	 24% 27% 9% 64%
15	NC	2484	 25% 10% 64%
15	ND	2484	 20% 28% 8% 64%
16	OA	2333	 16% 81%
16	OB	2333	 16% 81%
16	OC	2333	 16% 81%
17	PA	1822	 94%
17	PB	1822	 94%

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Mol	Chain	Length	Quality of chain
17	PC	1822	 94%
18	QA	172	 72% 10% 18%
18	QB	172	 33% 70% 12% 18%
18	QC	172	 72% 10% 18%
18	QD	172	 69% 13% 18%
19	RA	179	 8% 59% 23% 17%
19	RB	179	 22% 68% 15% 17%
19	RC	179	 9% 68% 15% 17%
19	RD	179	 18% 67% 15% 17%
20	SA	149	 85% 11%
20	SB	149	 44% 83% 12%
20	SC	149	 6% 83% 13%
20	SD	149	 5% 85% 11%

2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 415078 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 PCR5, TGME49_242320.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	829	Total	C	N	O	S	0	0
			6540	4168	1127	1203	42		
1	AD	865	Total	C	N	O	S	0	0
			6810	4327	1180	1262	41		
1	AE	829	Total	C	N	O	S	0	0
			6540	4168	1127	1203	42		
1	AH	865	Total	C	N	O	S	0	0
			6810	4327	1180	1262	41		
1	AI	829	Total	C	N	O	S	0	0
			6540	4168	1127	1203	42		
1	AL	865	Total	C	N	O	S	0	0
			6810	4327	1180	1262	41		

- Molecule 2 is a protein called PCR4, TGME49_201220.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	473	Total	C	N	O	S	0	0
			3821	2396	699	696	30		
2	AC	479	Total	C	N	O	S	0	0
			3847	2418	699	700	30		
2	AF	473	Total	C	N	O	S	0	0
			3821	2396	699	696	30		
2	AG	479	Total	C	N	O	S	0	0
			3847	2418	699	700	30		
2	AJ	473	Total	C	N	O	S	0	0
			3815	2393	696	696	30		
2	AK	479	Total	C	N	O	S	0	0
			3847	2418	699	700	30		

- Molecule 3 is a protein called Formin 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BA	346	Total	C	N	O	S	0	0
			2727	1731	482	500	14		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	BB	346	Total	C	N	O	S	0	0
			2727	1731	482	500	14		
3	BC	346	Total	C	N	O	S	0	0
			2727	1731	482	500	14		
3	CA	344	Total	C	N	O	S	0	0
			2712	1720	480	498	14		
3	CB	344	Total	C	N	O	S	0	0
			2712	1720	480	498	14		
3	CC	344	Total	C	N	O	S	0	0
			2712	1720	480	498	14		
3	CE	242	Total	C	N	O	S	0	0
			1874	1207	318	342	7		
3	CF	242	Total	C	N	O	S	0	0
			1874	1207	318	342	7		
3	CG	242	Total	C	N	O	S	0	0
			1874	1207	318	342	7		
3	CI	259	Total	C	N	O	S	0	0
			2012	1293	346	365	8		
3	CJ	259	Total	C	N	O	S	0	0
			2012	1293	346	365	8		
3	CL	259	Total	C	N	O	S	0	0
			2012	1293	346	365	8		

- Molecule 4 is a protein called PCR11, TGME49_209490.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	DA	347	Total	C	N	O	S	0	0
			2753	1754	487	496	16		
4	DB	347	Total	C	N	O	S	0	0
			2753	1754	487	496	16		
4	DC	347	Total	C	N	O	S	0	0
			2753	1754	487	496	16		
4	DD	332	Total	C	N	O	S	0	0
			2631	1674	474	468	15		
4	DE	332	Total	C	N	O	S	0	0
			2631	1674	474	468	15		
4	DF	332	Total	C	N	O	S	0	0
			2631	1674	474	468	15		

- Molecule 5 is a protein called CGP, TGME49_240380.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	EA	1349	Total	C	N	O	S	0	0
			10670	6808	1899	1905	58		
5	EB	1349	Total	C	N	O	S	0	0
			10670	6808	1899	1905	58		
5	EC	1349	Total	C	N	O	S	0	0
			10666	6805	1898	1905	58		

- Molecule 6 is a protein called FLM1, TGME49_271780.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	FA	531	Total	C	N	O	S	0	0
			4210	2640	742	802	26		
6	FB	531	Total	C	N	O	S	0	0
			4210	2640	742	802	26		
6	FC	531	Total	C	N	O	S	0	0
			4210	2640	742	802	26		
6	FD	423	Total	C	N	O	S	0	0
			3255	2086	573	580	16		
6	FE	423	Total	C	N	O	S	0	0
			3261	2089	576	580	16		
6	FF	413	Total	C	N	O	S	0	0
			3182	2038	561	567	16		

- Molecule 7 is a protein called Transport protein Sec24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	GA	837	Total	C	N	O	S	0	0
			6320	3979	1124	1183	34		
7	GC	781	Total	C	N	O	S	0	0
			5960	3767	1055	1105	33		
7	GE	781	Total	C	N	O	S	0	0
			5960	3767	1055	1105	33		
7	GG	837	Total	C	N	O	S	0	0
			6320	3979	1124	1183	34		
7	GI	781	Total	C	N	O	S	0	0
			5960	3767	1055	1105	33		
7	GK	837	Total	C	N	O	S	0	0
			6320	3979	1124	1183	34		

- Molecule 8 is a protein called Protein transport protein SEC23.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	GB	758	Total	C	N	O	S	0	0
			5949	3791	1016	1101	41		
8	GD	758	Total	C	N	O	S	0	0
			5949	3791	1016	1101	41		
8	GF	791	Total	C	N	O	S	0	0
			6155	3916	1054	1142	43		
8	GH	738	Total	C	N	O	S	0	0
			5781	3687	984	1070	40		
8	GJ	791	Total	C	N	O	S	0	0
			6155	3916	1054	1142	43		
8	GL	791	Total	C	N	O	S	0	0
			6155	3916	1054	1142	43		

- Molecule 9 is a protein called FLM2, TGME49_285990.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	HA	432	Total	C	N	O	S	0	0
			3361	2105	589	657	10		
9	HB	432	Total	C	N	O	S	0	0
			3361	2105	589	657	10		
9	HC	296	Total	C	N	O	S	0	0
			2288	1435	403	444	6		
9	HD	136	Total	C	N	O	S	0	0
			1073	670	186	213	4		

- Molecule 10 is a protein called PCR12, TGME49_292170.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	IA	1156	Total	C	N	O	S	0	0
			9113	5757	1663	1633	60		
10	IB	1156	Total	C	N	O	S	0	0
			9113	5757	1663	1633	60		
10	IC	1156	Total	C	N	O	S	0	0
			9113	5757	1663	1633	60		

- Molecule 11 is a protein called PCR10, TGME49_298010.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	JA	1593	Total	C	N	O	S	0	0
			12718	8089	2293	2271	65		
11	JB	1593	Total	C	N	O	S	0	0
			12718	8089	2293	2271	65		

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	JC	1593	Total	C	N	O	S	0	0
			12718	8089	2293	2271	65		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JA	2314	VAL	-	expression tag	UNP S8FEI7
JA	2315	SER	-	expression tag	UNP S8FEI7
JA	2316	SER	-	expression tag	UNP S8FEI7
JB	2314	VAL	-	expression tag	UNP S8FEI7
JB	2315	SER	-	expression tag	UNP S8FEI7
JB	2316	SER	-	expression tag	UNP S8FEI7
JC	2314	VAL	-	expression tag	UNP S8FEI7
JC	2315	SER	-	expression tag	UNP S8FEI7
JC	2316	SER	-	expression tag	UNP S8FEI7

- Molecule 12 is a protein called PCR14, TGME49_311880.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	KA	464	Total	C	N	O	S	0	0
			3674	2356	645	653	20		
12	KB	464	Total	C	N	O	S	0	0
			3674	2356	645	653	20		
12	KC	464	Total	C	N	O	S	0	0
			3668	2353	642	653	20		
12	KE	447	Total	C	N	O	S	0	0
			3544	2270	626	629	19		
12	KF	447	Total	C	N	O	S	0	0
			3544	2270	626	629	19		
12	KG	447	Total	C	N	O	S	0	0
			3544	2270	626	629	19		

- Molecule 13 is a protein called ICAP16, TGME49_202120.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LA	190	Total	C	N	O	S	0	0
			1516	925	286	299	6		
13	LB	191	Total	C	N	O	S	0	0
			1529	934	289	300	6		
13	LC	162	Total	C	N	O	S	0	0
			1312	802	245	259	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
13	LD	161	Total	C	N	O	S	0	0
			1304	801	240	257	6		
13	LE	149	Total	C	N	O	S	0	0
			1190	727	227	231	5		
13	LF	150	Total	C	N	O	S	0	0
			1198	732	227	233	6		
13	LG	57	Total	C	N	O	S	0	0
			461	287	83	88	3		
13	LH	55	Total	C	N	O	S	0	0
			448	280	80	85	3		
13	LI	190	Total	C	N	O	S	0	0
			1516	925	286	299	6		
13	LJ	191	Total	C	N	O	S	0	0
			1529	934	289	300	6		
13	LK	163	Total	C	N	O	S	0	0
			1320	808	246	260	6		
13	LL	161	Total	C	N	O	S	0	0
			1304	801	240	257	6		
13	LM	106	Total	C	N	O	S	0	0
			859	521	163	172	3		
13	LN	106	Total	C	N	O	S	0	0
			856	521	160	172	3		
13	LO	105	Total	C	N	O	S	0	0
			841	508	159	171	3		
13	LP	110	Total	C	N	O	S	0	0
			882	535	167	177	3		

- Molecule 14 is a protein called PCR12, TGME49_219070.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	MA	142	Total	C	N	O	S	0	0
			1132	694	210	222	6		
14	MB	120	Total	C	N	O	S	0	0
			976	594	185	192	5		
14	MC	75	Total	C	N	O		0	0
			594	365	114	115			
14	MD	65	Total	C	N	O		0	0
			521	319	103	99			
14	ME	142	Total	C	N	O	S	0	0
			1132	694	210	222	6		
14	MF	120	Total	C	N	O	S	0	0
			976	594	185	192	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	MG	75	Total	C	N	O		0	0
			594	365	114	115			
14	MH	65	Total	C	N	O		0	0
			521	319	103	99			
14	MI	142	Total	C	N	O	S	0	0
			1132	694	210	222	6		
14	MJ	120	Total	C	N	O	S	0	0
			976	594	185	192	5		
14	MK	75	Total	C	N	O		0	0
			594	365	114	115			
14	ML	65	Total	C	N	O		0	0
			521	319	103	99			

There are 204 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
MA	999	GLU	-	insertion	UNP S8EN17
MA	1000	LYS	-	insertion	UNP S8EN17
MA	1001	SER	-	insertion	UNP S8EN17
MA	1002	GLY	-	insertion	UNP S8EN17
MA	1003	THR	-	insertion	UNP S8EN17
MA	1004	ALA	-	insertion	UNP S8EN17
MA	1005	ALA	-	insertion	UNP S8EN17
MA	1006	SER	-	insertion	UNP S8EN17
MA	1007	HIS	-	insertion	UNP S8EN17
MA	1008	ILE	-	insertion	UNP S8EN17
MA	1009	ASP	-	insertion	UNP S8EN17
MA	1010	GLU	-	insertion	UNP S8EN17
MA	1011	GLU	-	insertion	UNP S8EN17
MA	1012	ASP	-	insertion	UNP S8EN17
MA	1013	SER	-	insertion	UNP S8EN17
MA	1014	ARG	-	insertion	UNP S8EN17
MA	1015	SER	ALA	conflict	UNP S8EN17
MB	999	GLU	-	insertion	UNP S8EN17
MB	1000	LYS	-	insertion	UNP S8EN17
MB	1001	SER	-	insertion	UNP S8EN17
MB	1002	GLY	-	insertion	UNP S8EN17
MB	1003	THR	-	insertion	UNP S8EN17
MB	1004	ALA	-	insertion	UNP S8EN17
MB	1005	ALA	-	insertion	UNP S8EN17
MB	1006	SER	-	insertion	UNP S8EN17
MB	1007	HIS	-	insertion	UNP S8EN17
MB	1008	ILE	-	insertion	UNP S8EN17

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Chain	Residue	Modelled	Actual	Comment	Reference
MB	1009	ASP	-	insertion	UNP S8EN17
MB	1010	GLU	-	insertion	UNP S8EN17
MB	1011	GLU	-	insertion	UNP S8EN17
MB	1012	ASP	-	insertion	UNP S8EN17
MB	1013	SER	-	insertion	UNP S8EN17
MB	1014	ARG	-	insertion	UNP S8EN17
MB	1015	SER	ALA	conflict	UNP S8EN17
MC	999	GLU	-	insertion	UNP S8EN17
MC	1000	LYS	-	insertion	UNP S8EN17
MC	1001	SER	-	insertion	UNP S8EN17
MC	1002	GLY	-	insertion	UNP S8EN17
MC	1003	THR	-	insertion	UNP S8EN17
MC	1004	ALA	-	insertion	UNP S8EN17
MC	1005	ALA	-	insertion	UNP S8EN17
MC	1006	SER	-	insertion	UNP S8EN17
MC	1007	HIS	-	insertion	UNP S8EN17
MC	1008	ILE	-	insertion	UNP S8EN17
MC	1009	ASP	-	insertion	UNP S8EN17
MC	1010	GLU	-	insertion	UNP S8EN17
MC	1011	GLU	-	insertion	UNP S8EN17
MC	1012	ASP	-	insertion	UNP S8EN17
MC	1013	SER	-	insertion	UNP S8EN17
MC	1014	ARG	-	insertion	UNP S8EN17
MC	1015	SER	ALA	conflict	UNP S8EN17
MD	999	GLU	-	insertion	UNP S8EN17
MD	1000	LYS	-	insertion	UNP S8EN17
MD	1001	SER	-	insertion	UNP S8EN17
MD	1002	GLY	-	insertion	UNP S8EN17
MD	1003	THR	-	insertion	UNP S8EN17
MD	1004	ALA	-	insertion	UNP S8EN17
MD	1005	ALA	-	insertion	UNP S8EN17
MD	1006	SER	-	insertion	UNP S8EN17
MD	1007	HIS	-	insertion	UNP S8EN17
MD	1008	ILE	-	insertion	UNP S8EN17
MD	1009	ASP	-	insertion	UNP S8EN17
MD	1010	GLU	-	insertion	UNP S8EN17
MD	1011	GLU	-	insertion	UNP S8EN17
MD	1012	ASP	-	insertion	UNP S8EN17
MD	1013	SER	-	insertion	UNP S8EN17
MD	1014	ARG	-	insertion	UNP S8EN17
MD	1015	SER	ALA	conflict	UNP S8EN17
ME	999	GLU	-	insertion	UNP S8EN17

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Chain	Residue	Modelled	Actual	Comment	Reference
ME	1000	LYS	-	insertion	UNP S8EN17
ME	1001	SER	-	insertion	UNP S8EN17
ME	1002	GLY	-	insertion	UNP S8EN17
ME	1003	THR	-	insertion	UNP S8EN17
ME	1004	ALA	-	insertion	UNP S8EN17
ME	1005	ALA	-	insertion	UNP S8EN17
ME	1006	SER	-	insertion	UNP S8EN17
ME	1007	HIS	-	insertion	UNP S8EN17
ME	1008	ILE	-	insertion	UNP S8EN17
ME	1009	ASP	-	insertion	UNP S8EN17
ME	1010	GLU	-	insertion	UNP S8EN17
ME	1011	GLU	-	insertion	UNP S8EN17
ME	1012	ASP	-	insertion	UNP S8EN17
ME	1013	SER	-	insertion	UNP S8EN17
ME	1014	ARG	-	insertion	UNP S8EN17
ME	1015	SER	ALA	conflict	UNP S8EN17
MF	999	GLU	-	insertion	UNP S8EN17
MF	1000	LYS	-	insertion	UNP S8EN17
MF	1001	SER	-	insertion	UNP S8EN17
MF	1002	GLY	-	insertion	UNP S8EN17
MF	1003	THR	-	insertion	UNP S8EN17
MF	1004	ALA	-	insertion	UNP S8EN17
MF	1005	ALA	-	insertion	UNP S8EN17
MF	1006	SER	-	insertion	UNP S8EN17
MF	1007	HIS	-	insertion	UNP S8EN17
MF	1008	ILE	-	insertion	UNP S8EN17
MF	1009	ASP	-	insertion	UNP S8EN17
MF	1010	GLU	-	insertion	UNP S8EN17
MF	1011	GLU	-	insertion	UNP S8EN17
MF	1012	ASP	-	insertion	UNP S8EN17
MF	1013	SER	-	insertion	UNP S8EN17
MF	1014	ARG	-	insertion	UNP S8EN17
MF	1015	SER	ALA	conflict	UNP S8EN17
MG	999	GLU	-	insertion	UNP S8EN17
MG	1000	LYS	-	insertion	UNP S8EN17
MG	1001	SER	-	insertion	UNP S8EN17
MG	1002	GLY	-	insertion	UNP S8EN17
MG	1003	THR	-	insertion	UNP S8EN17
MG	1004	ALA	-	insertion	UNP S8EN17
MG	1005	ALA	-	insertion	UNP S8EN17
MG	1006	SER	-	insertion	UNP S8EN17
MG	1007	HIS	-	insertion	UNP S8EN17

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Chain	Residue	Modelled	Actual	Comment	Reference
MG	1008	ILE	-	insertion	UNP S8EN17
MG	1009	ASP	-	insertion	UNP S8EN17
MG	1010	GLU	-	insertion	UNP S8EN17
MG	1011	GLU	-	insertion	UNP S8EN17
MG	1012	ASP	-	insertion	UNP S8EN17
MG	1013	SER	-	insertion	UNP S8EN17
MG	1014	ARG	-	insertion	UNP S8EN17
MG	1015	SER	ALA	conflict	UNP S8EN17
MH	999	GLU	-	insertion	UNP S8EN17
MH	1000	LYS	-	insertion	UNP S8EN17
MH	1001	SER	-	insertion	UNP S8EN17
MH	1002	GLY	-	insertion	UNP S8EN17
MH	1003	THR	-	insertion	UNP S8EN17
MH	1004	ALA	-	insertion	UNP S8EN17
MH	1005	ALA	-	insertion	UNP S8EN17
MH	1006	SER	-	insertion	UNP S8EN17
MH	1007	HIS	-	insertion	UNP S8EN17
MH	1008	ILE	-	insertion	UNP S8EN17
MH	1009	ASP	-	insertion	UNP S8EN17
MH	1010	GLU	-	insertion	UNP S8EN17
MH	1011	GLU	-	insertion	UNP S8EN17
MH	1012	ASP	-	insertion	UNP S8EN17
MH	1013	SER	-	insertion	UNP S8EN17
MH	1014	ARG	-	insertion	UNP S8EN17
MH	1015	SER	ALA	conflict	UNP S8EN17
MI	999	GLU	-	insertion	UNP S8EN17
MI	1000	LYS	-	insertion	UNP S8EN17
MI	1001	SER	-	insertion	UNP S8EN17
MI	1002	GLY	-	insertion	UNP S8EN17
MI	1003	THR	-	insertion	UNP S8EN17
MI	1004	ALA	-	insertion	UNP S8EN17
MI	1005	ALA	-	insertion	UNP S8EN17
MI	1006	SER	-	insertion	UNP S8EN17
MI	1007	HIS	-	insertion	UNP S8EN17
MI	1008	ILE	-	insertion	UNP S8EN17
MI	1009	ASP	-	insertion	UNP S8EN17
MI	1010	GLU	-	insertion	UNP S8EN17
MI	1011	GLU	-	insertion	UNP S8EN17
MI	1012	ASP	-	insertion	UNP S8EN17
MI	1013	SER	-	insertion	UNP S8EN17
MI	1014	ARG	-	insertion	UNP S8EN17
MI	1015	SER	ALA	conflict	UNP S8EN17

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Chain	Residue	Modelled	Actual	Comment	Reference
MJ	999	GLU	-	insertion	UNP S8EN17
MJ	1000	LYS	-	insertion	UNP S8EN17
MJ	1001	SER	-	insertion	UNP S8EN17
MJ	1002	GLY	-	insertion	UNP S8EN17
MJ	1003	THR	-	insertion	UNP S8EN17
MJ	1004	ALA	-	insertion	UNP S8EN17
MJ	1005	ALA	-	insertion	UNP S8EN17
MJ	1006	SER	-	insertion	UNP S8EN17
MJ	1007	HIS	-	insertion	UNP S8EN17
MJ	1008	ILE	-	insertion	UNP S8EN17
MJ	1009	ASP	-	insertion	UNP S8EN17
MJ	1010	GLU	-	insertion	UNP S8EN17
MJ	1011	GLU	-	insertion	UNP S8EN17
MJ	1012	ASP	-	insertion	UNP S8EN17
MJ	1013	SER	-	insertion	UNP S8EN17
MJ	1014	ARG	-	insertion	UNP S8EN17
MJ	1015	SER	ALA	conflict	UNP S8EN17
MK	999	GLU	-	insertion	UNP S8EN17
MK	1000	LYS	-	insertion	UNP S8EN17
MK	1001	SER	-	insertion	UNP S8EN17
MK	1002	GLY	-	insertion	UNP S8EN17
MK	1003	THR	-	insertion	UNP S8EN17
MK	1004	ALA	-	insertion	UNP S8EN17
MK	1005	ALA	-	insertion	UNP S8EN17
MK	1006	SER	-	insertion	UNP S8EN17
MK	1007	HIS	-	insertion	UNP S8EN17
MK	1008	ILE	-	insertion	UNP S8EN17
MK	1009	ASP	-	insertion	UNP S8EN17
MK	1010	GLU	-	insertion	UNP S8EN17
MK	1011	GLU	-	insertion	UNP S8EN17
MK	1012	ASP	-	insertion	UNP S8EN17
MK	1013	SER	-	insertion	UNP S8EN17
MK	1014	ARG	-	insertion	UNP S8EN17
MK	1015	SER	ALA	conflict	UNP S8EN17
ML	999	GLU	-	insertion	UNP S8EN17
ML	1000	LYS	-	insertion	UNP S8EN17
ML	1001	SER	-	insertion	UNP S8EN17
ML	1002	GLY	-	insertion	UNP S8EN17
ML	1003	THR	-	insertion	UNP S8EN17
ML	1004	ALA	-	insertion	UNP S8EN17
ML	1005	ALA	-	insertion	UNP S8EN17
ML	1006	SER	-	insertion	UNP S8EN17

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Chain	Residue	Modelled	Actual	Comment	Reference
ML	1007	HIS	-	insertion	UNP S8EN17
ML	1008	ILE	-	insertion	UNP S8EN17
ML	1009	ASP	-	insertion	UNP S8EN17
ML	1010	GLU	-	insertion	UNP S8EN17
ML	1011	GLU	-	insertion	UNP S8EN17
ML	1012	ASP	-	insertion	UNP S8EN17
ML	1013	SER	-	insertion	UNP S8EN17
ML	1014	ARG	-	insertion	UNP S8EN17
ML	1015	SER	ALA	conflict	UNP S8EN17

- Molecule 15 is a protein called myosin L, TGME49_291020.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	NA	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		
15	NB	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		
15	NC	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		
15	ND	897	Total	C	N	O	S	0	0
			7263	4638	1283	1315	27		

- Molecule 16 is a protein called PCR13, TGME49_284620.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	OA	448	Total	C	N	O	S	0	0
			3510	2191	650	661	8		
16	OB	448	Total	C	N	O	S	0	0
			3510	2191	650	661	8		
16	OC	448	Total	C	N	O	S	0	0
			3510	2191	650	661	8		

- Molecule 17 is a protein called PCR15, TGME49_232560.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	PA	101	Total	C	N	O	S	0	0
			807	507	142	156	2		
17	PB	101	Total	C	N	O	S	0	0
			807	507	142	156	2		
17	PC	101	Total	C	N	O	S	0	0
			807	507	142	156	2		

- Molecule 18 is a protein called MLC4, TGME49_294390.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	QA	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		
18	QB	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		
18	QC	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		
18	QD	141	Total	C	N	O	S	0	0
			1129	720	196	208	5		

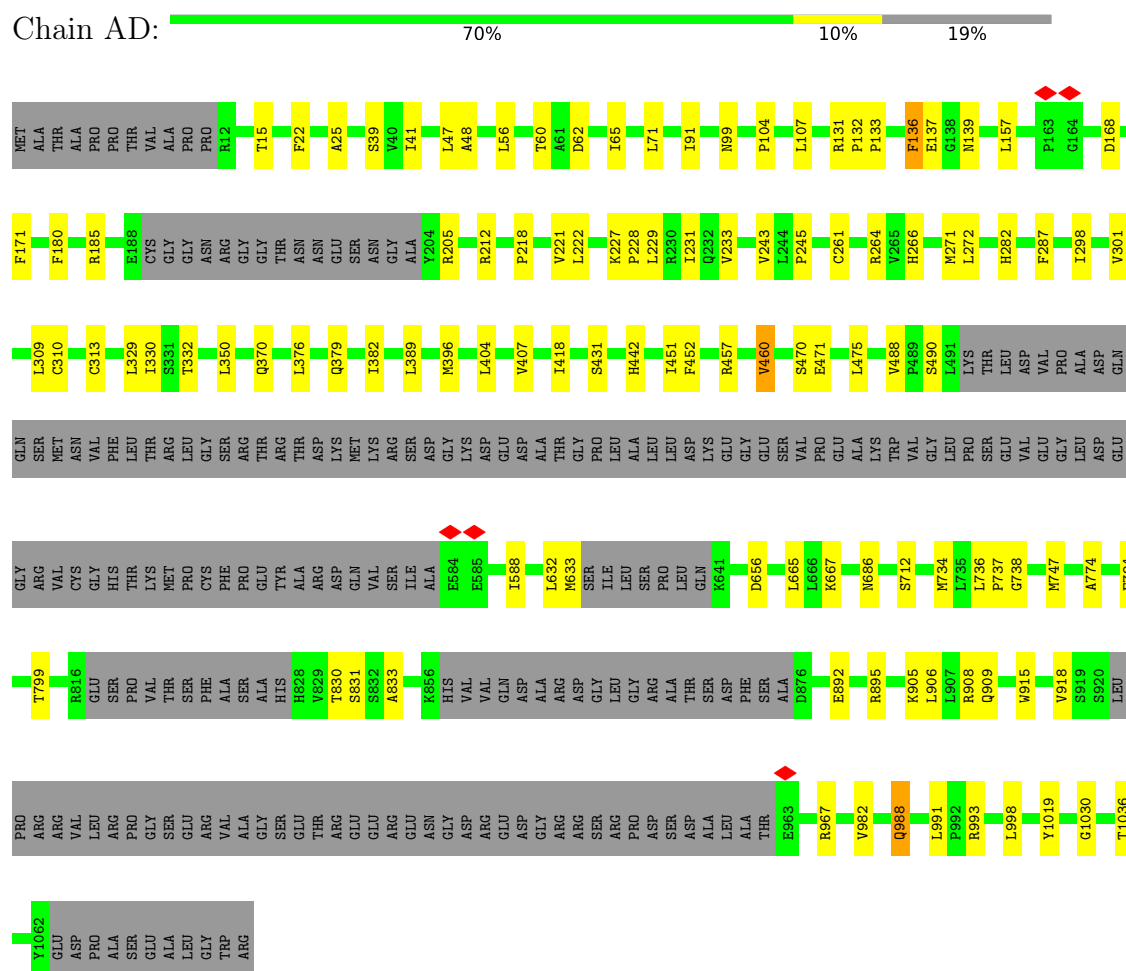
- Molecule 19 is a protein called Calmodulin.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	RA	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		
19	RB	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		
19	RC	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		
19	RD	148	Total	C	N	O	S	0	0
			1143	724	195	218	6		

- Molecule 20 is a protein called Calmodulin.

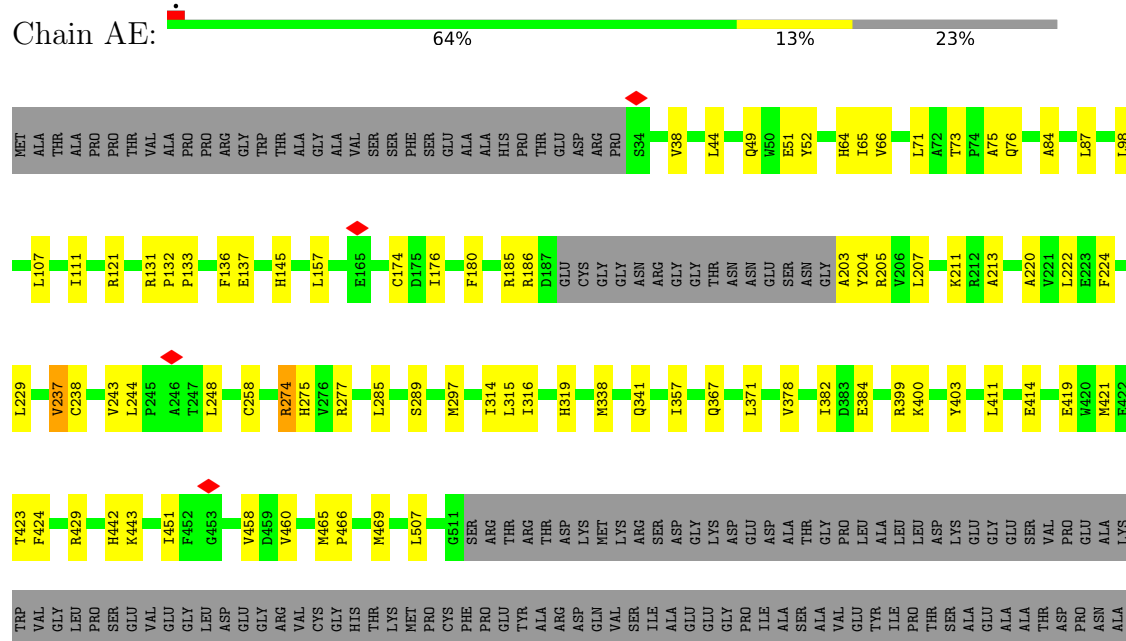
Mol	Chain	Residues	Atoms					AltConf	Trace
20	SA	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		
20	SB	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		
20	SC	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		
20	SD	144	Total	C	N	O	S	0	0
			1134	700	180	245	9		

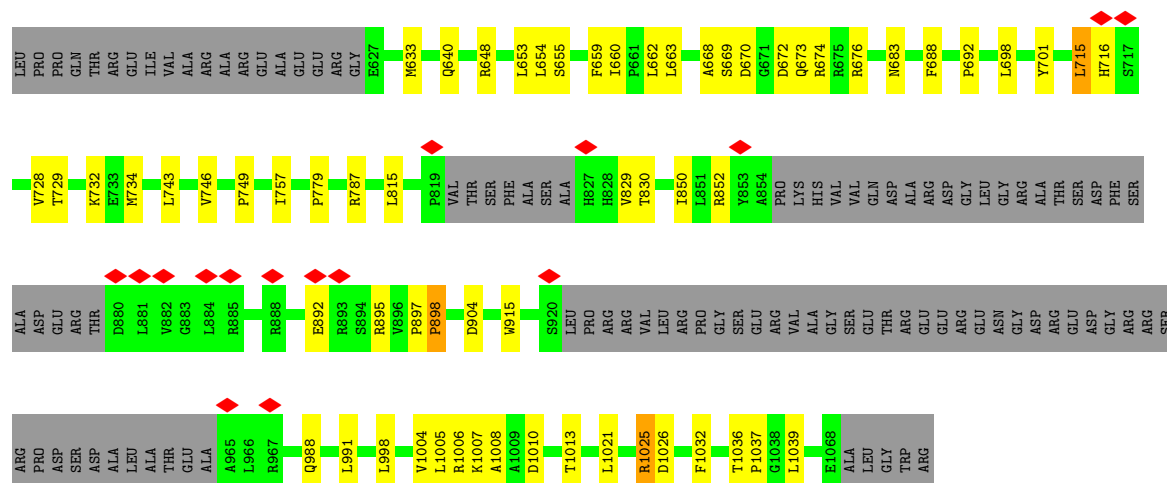
Chain AD:



- Molecule 1: PCR5, TGME49_242320

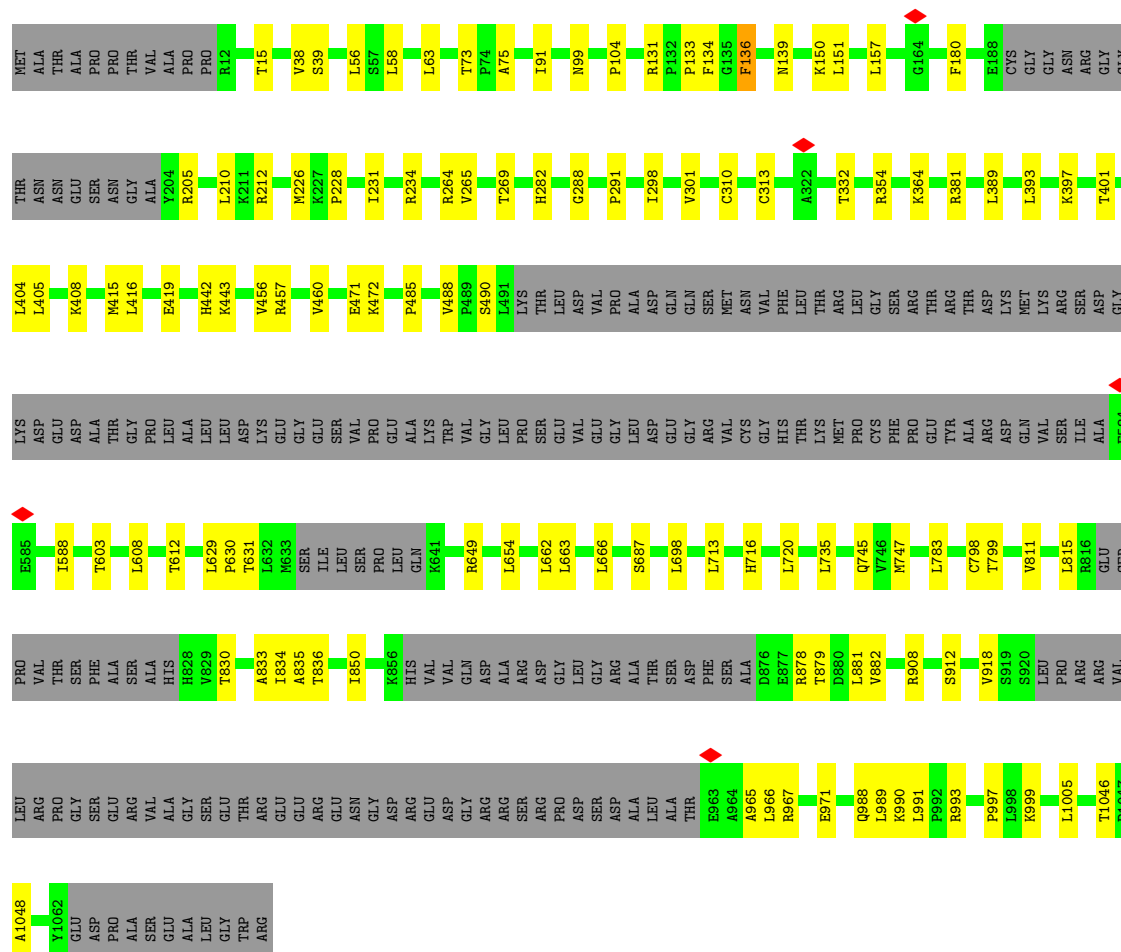
Chain AE:





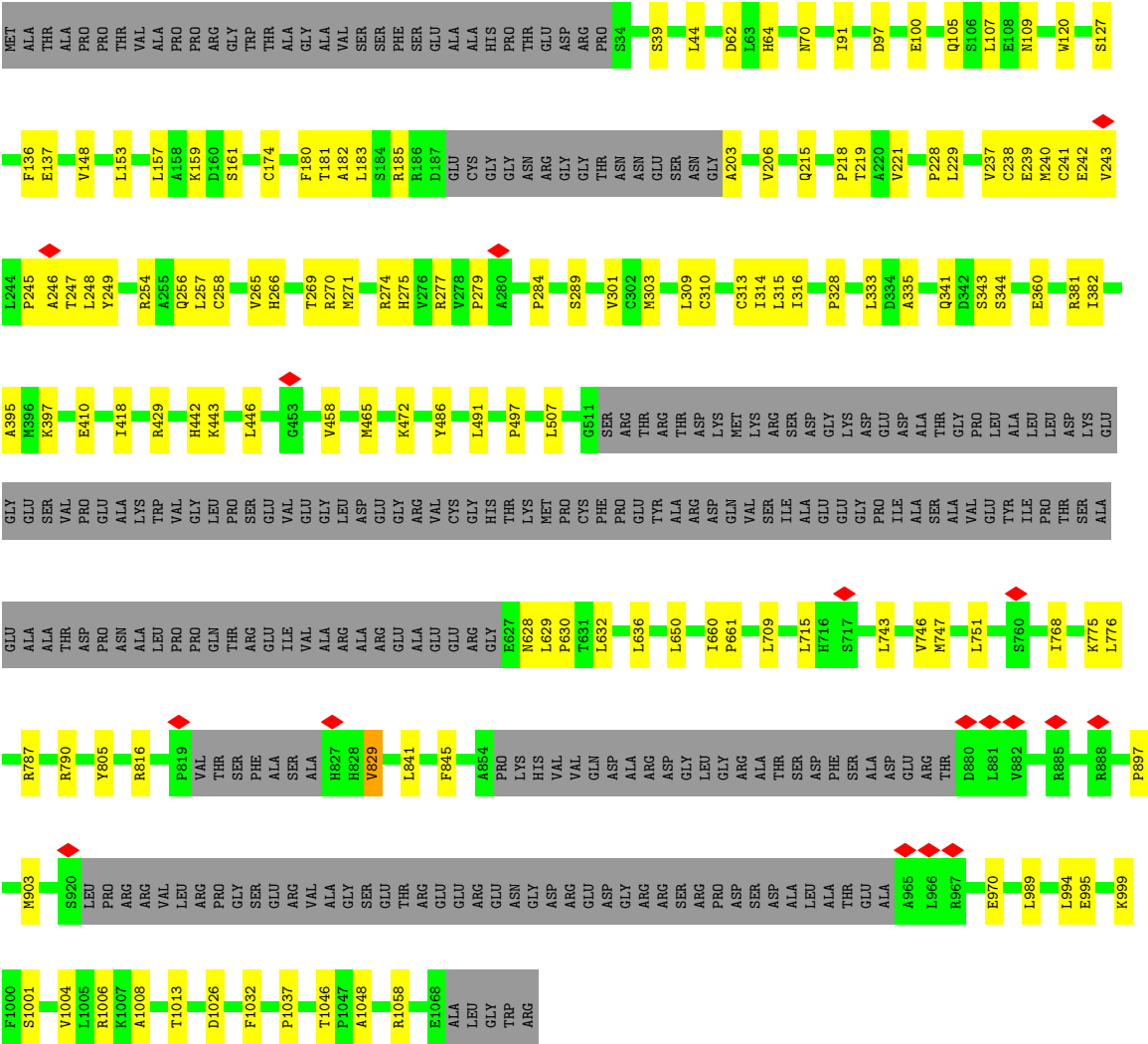
● Molecule 1: PCR5, TGME49_242320

Chain AH: 70% 10% 19%

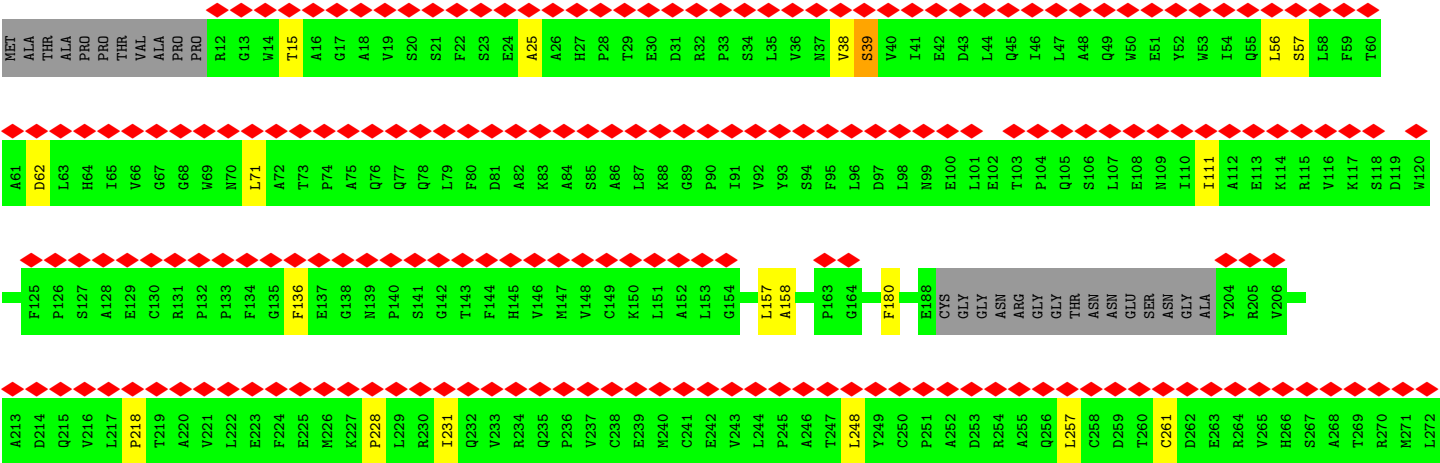


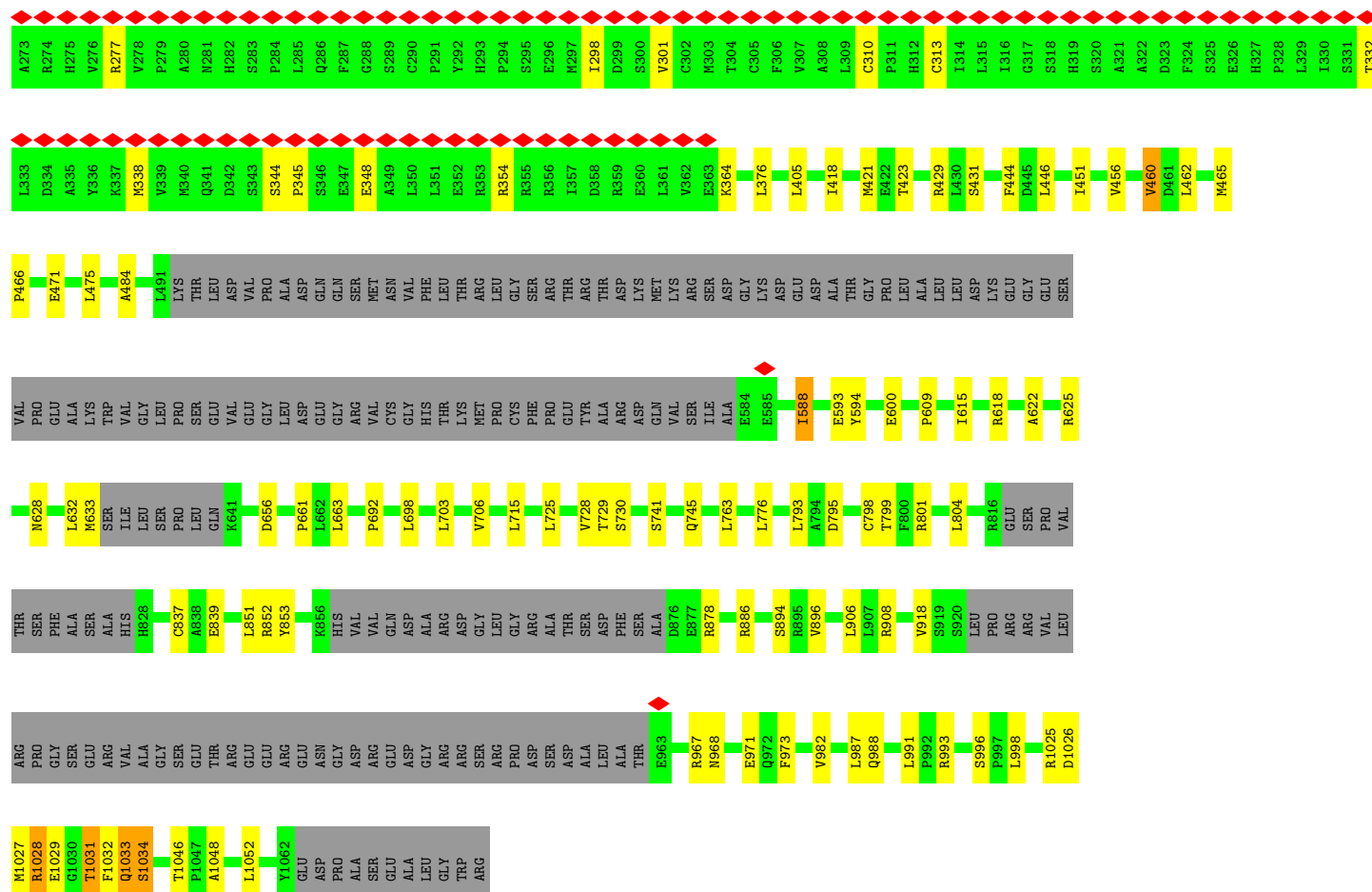
● Molecule 1: PCR5, TGME49_242320

Chain AI: 65% 12% 23%



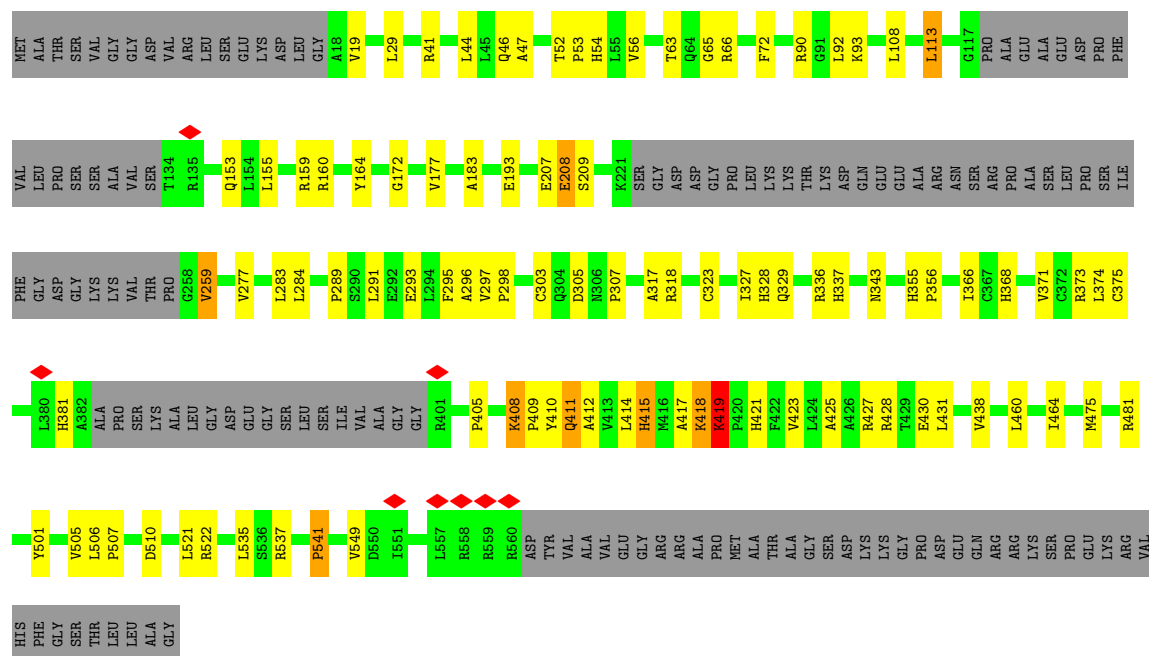
● Molecule 1: PCR5, TGME49_242320



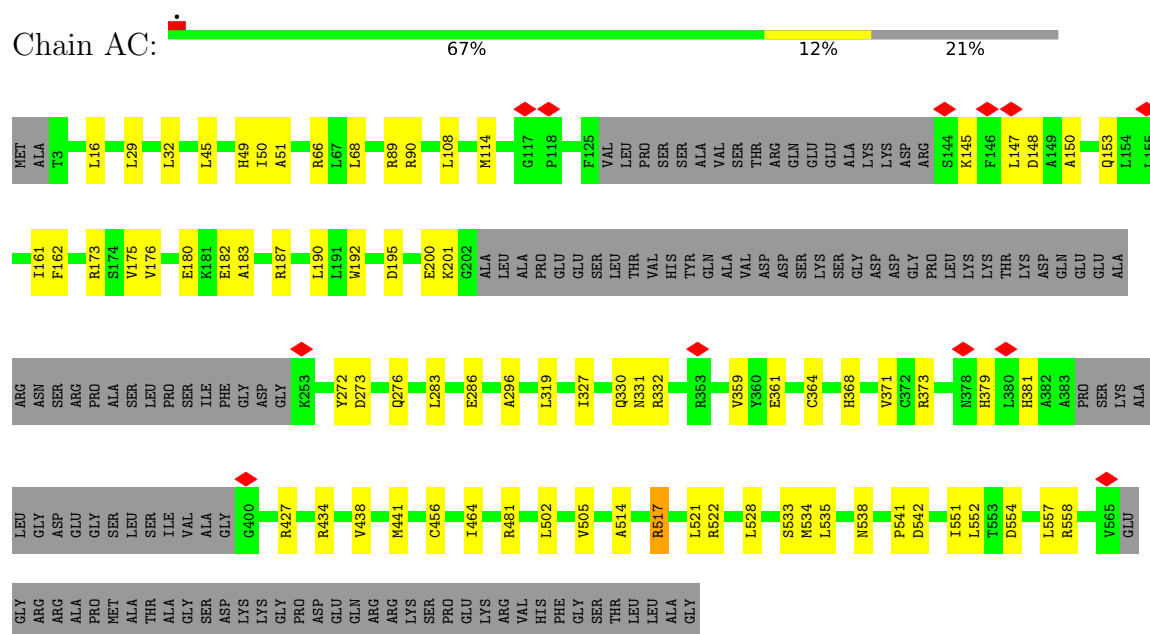


• Molecule 2: PCR4, TGME49_201220

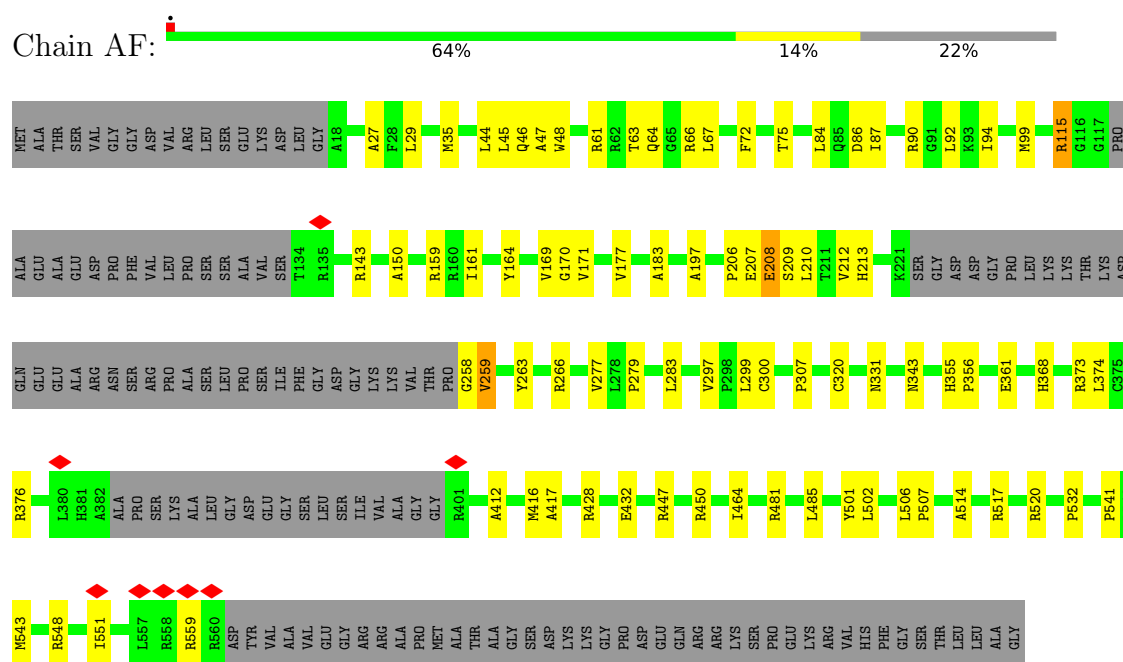
Chain AB: 62% 15% 22%



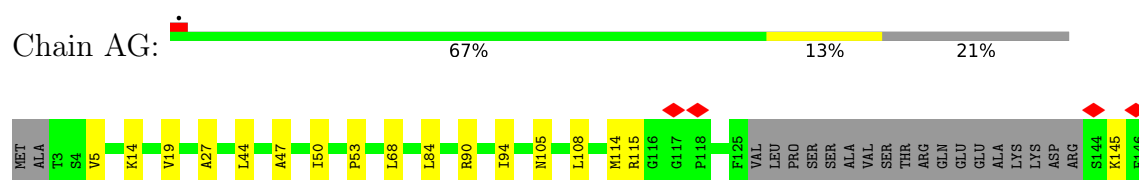
- Molecule 2: PCR4, TGME49_201220



- Molecule 2: PCR4, TGME49_201220



- Molecule 2: PCR4, TGME49_201220



















- Molecule 3: Formin 1

Chain BC: 6% . 93%

[illegible]

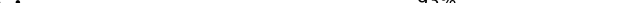






[illegible]

- Molecule 3: Formin 1

Chain CA:  6% . 93%

[illegible]















MET	SER	CYS	PRO	ALA	SER	CYS	PRO	PRO	ARG	ARG	GLY	GLY	ALA	SER	PRO	LEU	PRO	PRO	MET	PRO	PRO	SER	VAL	ASN	ASP	ARG	ASN	ALA	VAL	LEU	ASN	ALA	LEU	PRO	SER	THR	SER	PHE	SER	ALA	ALA	PRO	LEU	CYS	SER	ALA	THR	SER	CYS	LEU	PRO	GLU	ARG	PRO	VAL	PHE	ALA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----













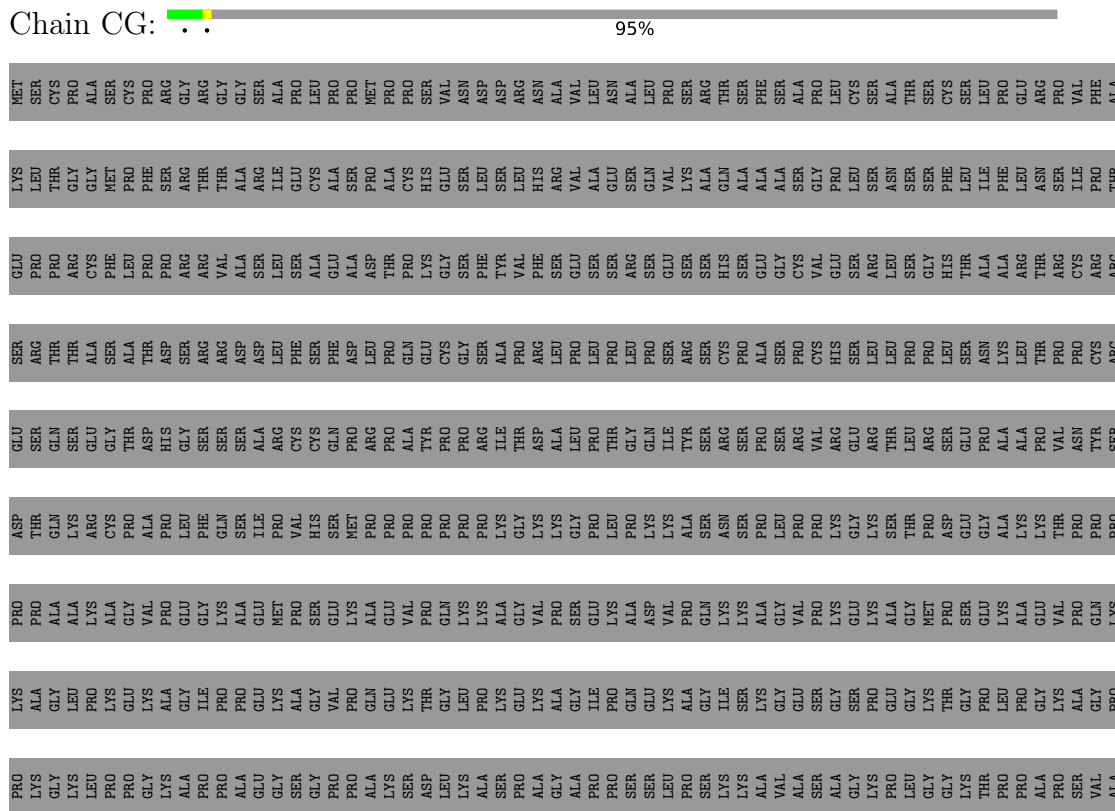








- Molecule 3: Formin 1









- Molecule 3: Formin 1

Chain CI: 95%

[illegible]





- Molecule 3: Formin 1

95%

[illegible]

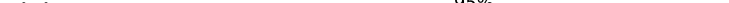






[illegible]

- Molecule 3: Formin 1

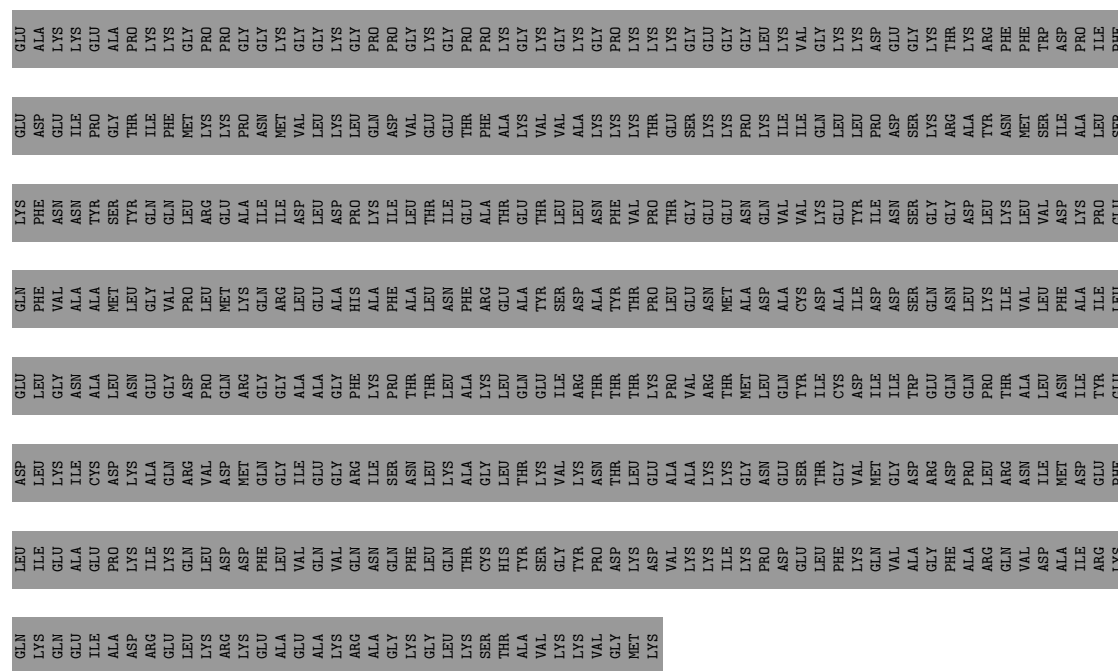
Chain CL:  95%

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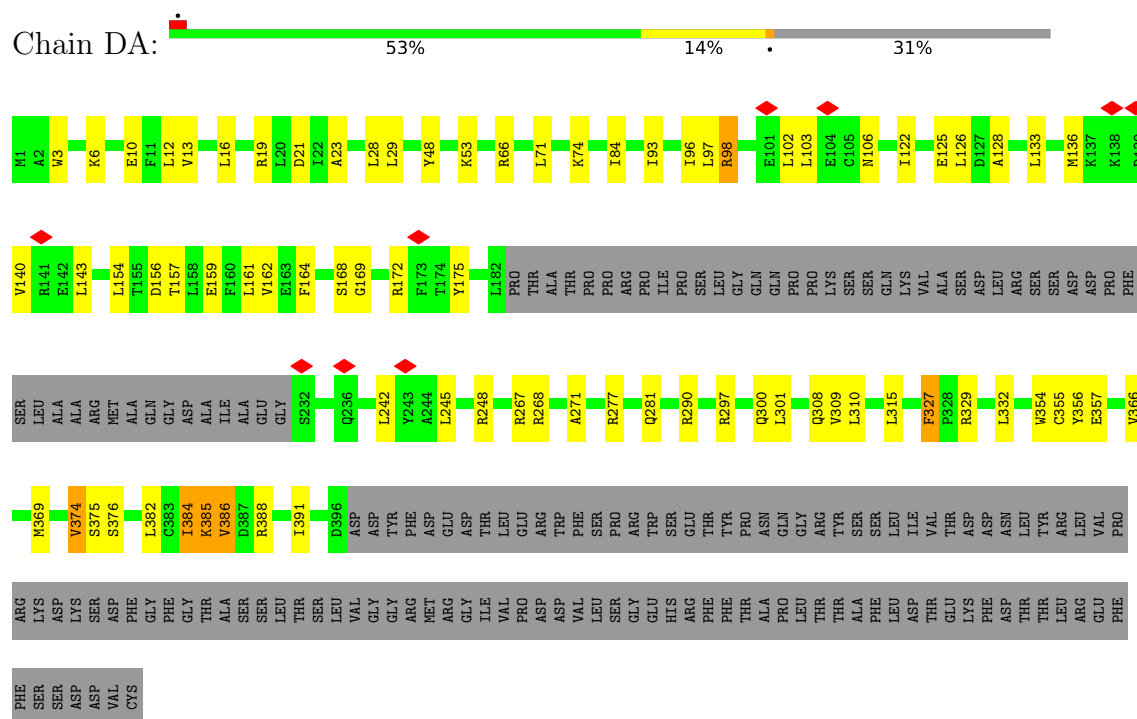




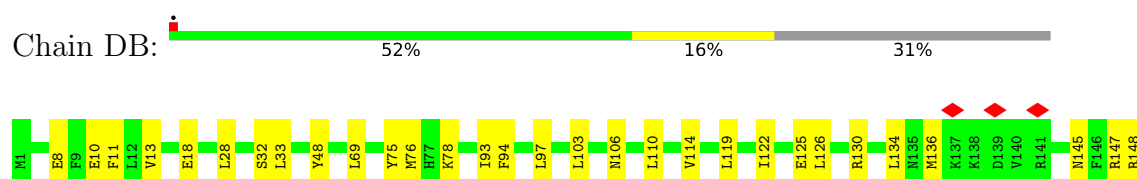


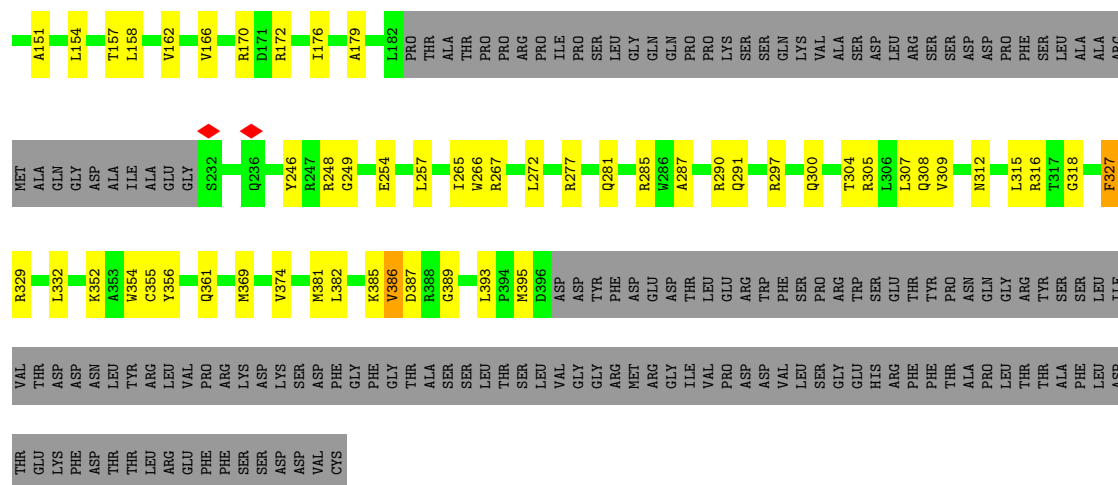


- Molecule 4: PCR11, TGME49 209490

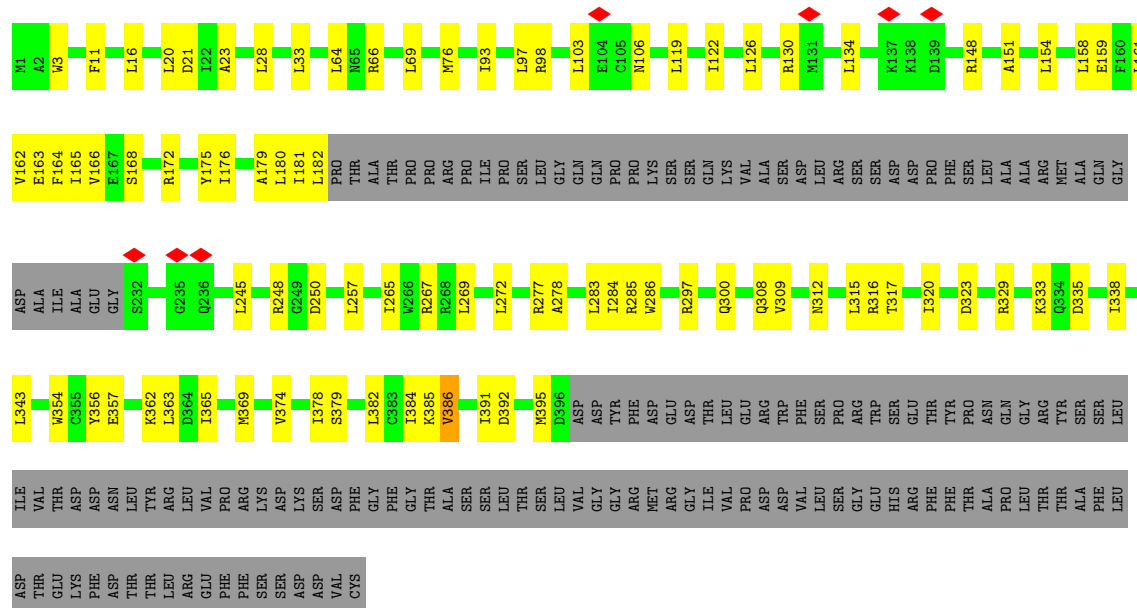


- Molecule 4: PCR11, TGME49_209490

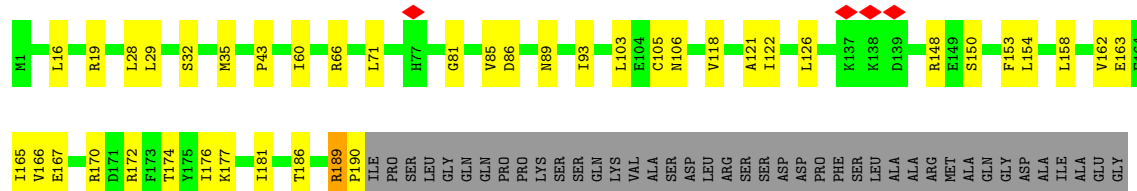




● Molecule 4: PCR11, TGME49_209490



● Molecule 4: PCR11, TGME49_209490









WORLDWIDE
PDB
PROTEIN DATA BANK

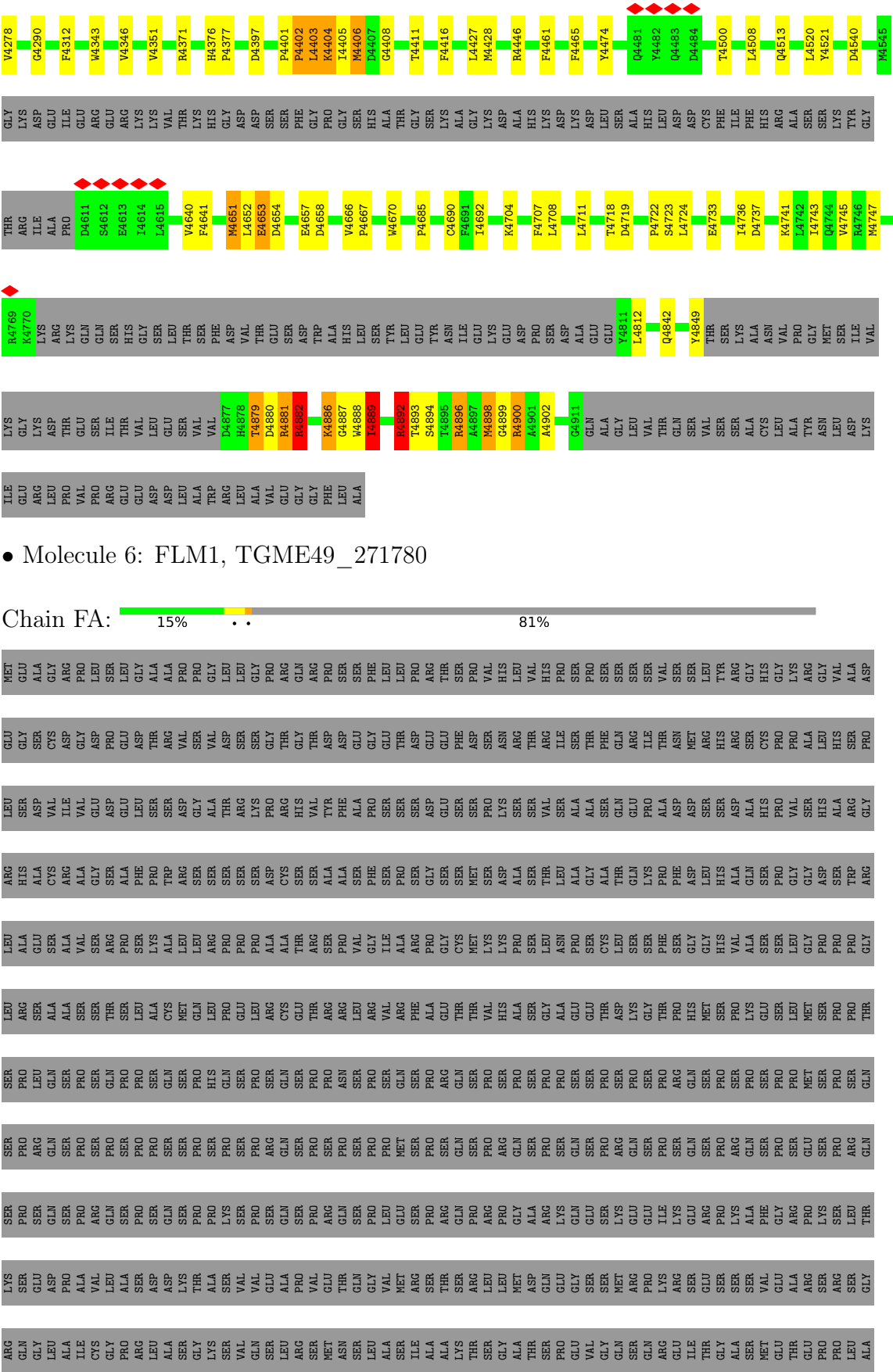






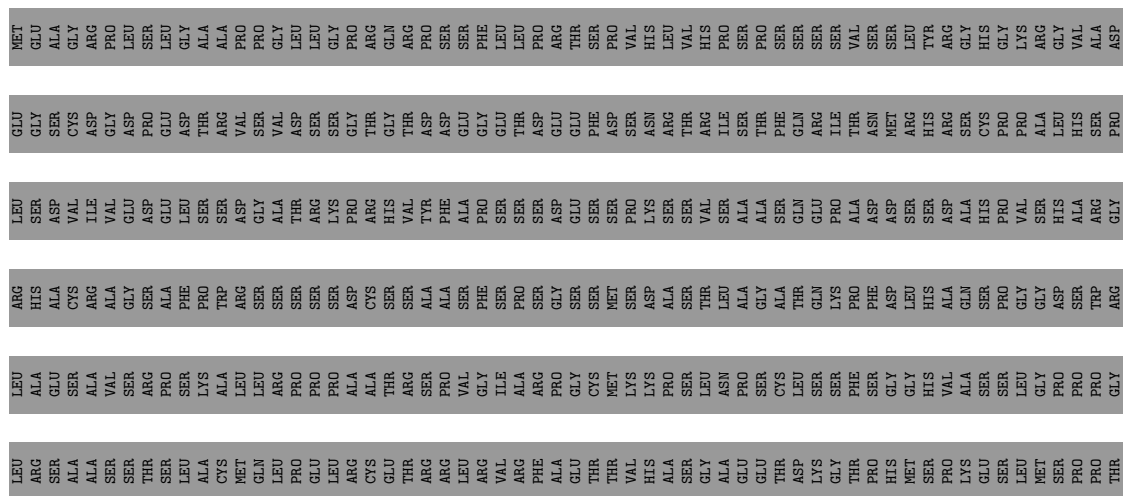




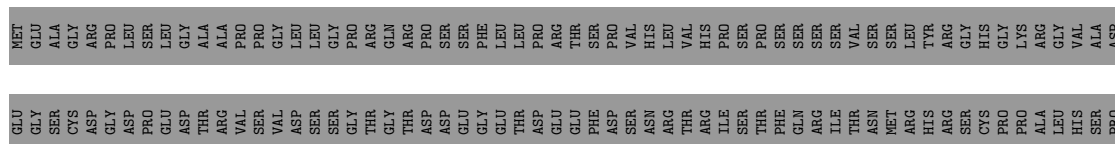


• Molecule 6: FLM1, TGME49_271780















- Molecule 6: FLM1, TGME49_271780





- Molecule 6: FLM1, TGME49_271780

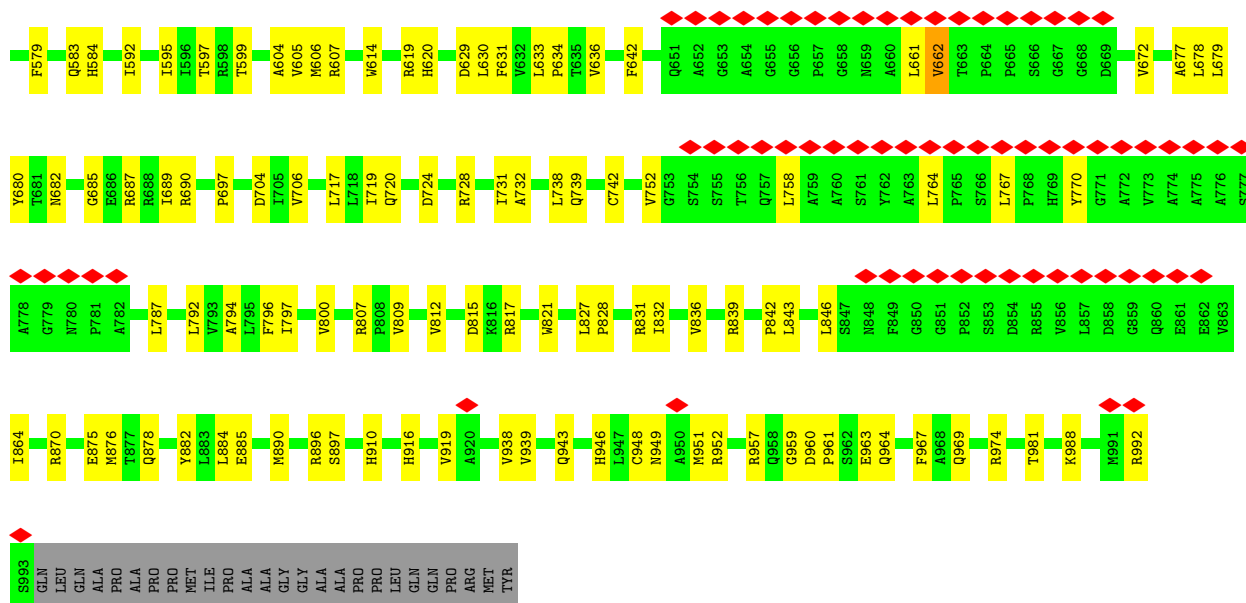
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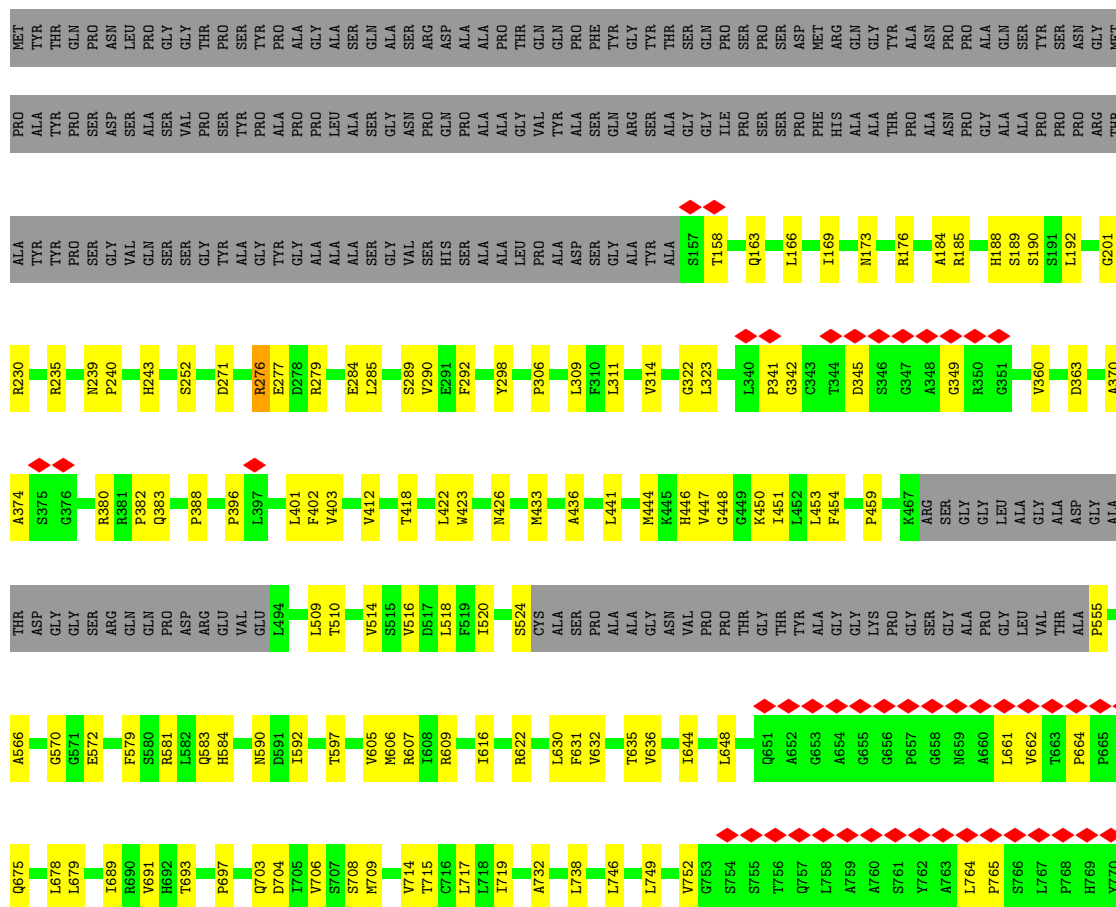
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ASN	GLY	ARG	PRO	GLY	ILE	MET	PRO	ILE	ASP	GLN	GLN	GLN	GLN	ASN	THR	GLY	GLY	GLY
LYS	LEU	ALA	PRO	LEU	VAL	LEU	HIS	VAL	GLN	HIS	ALA	ALA	ALA	LEU	LYS	ASN	LEU	LEU
PHE	ARG	ILE	LYS	TYR	PHE	TYR	PHE	PHE	SER	CYS	LEU	LEU	TYR	ARG	ASP	TYR	PRO	GLY
ARG	ARG	GLY	ALA	ASN	LEU	ASN	LEU	LEU	GLY	ARG	GLU	ARG	ASP	ARG	ASP	GLY	ILE	GLY
LEU	LEU	GLY	GLN	ASN	TRP	TRP	TRP	TRP	GLY	LEU	ALA	ALA	ALA	GLU	GLU	GLU	HIS	CYS
HIS	LEU	ALA	PHE	ASP	PRO	CYS	VAL	VAL	VAL	THR	LYS	LYS	LYS	GLY	VAL	THR	GLY	ALA
LEU	LEU	ALA	THR	GLY	VAL	VAL	THR	THR	VAL	VAL	GLN	GLN	GLN	HIS	ARG	SER	ALA	TYR
PHE	PHE	SER	ARG	ARG	GLY	GLY	VAL	VAL	VAL	VAL	LYS	LYS	GLN	HIS	ARG	MET	GLY	ARG
PRO	PRO	ASN	PHE	ILE	LEU	LEU	ILE	ASP	LEU	LEU	THR	THR	THR	GLN	ILE	ASP	ASN	TYR
ILE	GLU	ASN	ASN	SER	SER	GLU	GLU	GLU	PHE	ARG	PHE	PHE	GLU	GLU	GLU	TRP	GLU	GLU
ALA	ALA	ALA	VAL	THR	ALA	ALA	ALA	ALA	GLN	VAL	HIS	HIS	LEU	ARG	VAL	VAL	LEU	ALA
ASP	GLU	VAL	ALA	SER	SER	SER	VAL	TYR	SER	VAL	LYS	LYS	HIS	GLU	GLU	GLN	ASN	VAL
VAL	VAL	GLY	GLN	THR	ILE	ILE	ILE	LEU	PHE	THR	LYS	ARG	GLN	ILE	ILE	ASP	ASN	TYR
SER	GLY	ARG	SER	MET	ASP	LEU	LEU	LEU	LEU	THR	THR	ALA	ALA	GLU	GLU	GLN	ASN	GLN
ARG	ARG	THR	THR	SER	GLY	GLY	GLY	GLY	GLU	GLU	THR	THR	THR	GLU	GLU	GLU	GLU	GLU
PRO	LEU	ALA	LEU	GLY	LEU	LEU	LEU	LEU	PHE	TRP	GLN	GLN	GLN	SER	GLU	GLU	GLN	PRO
TYR	LEU	TYR	LEU	GLY	LEU	LEU	ALA	VAL	CYS	ILE	VAL	VAL	ILE	VAL	LEU	VAL	VAL	GLY
LEU	LEU	PHE	ALA	ALA	HIS	HIS	VAL	VAL	ASN	ILE	VAL	VAL	ILE	LEU	ARG	VAL	VAL	LYS
LEU	LEU	ARG	ALA	VAL	ALA	THR	ALA	ASP	GLY	THR	ARG	ARG	GLU	GLY	ASN	GLY	GLY	GLY
THR	THR	ASN	THR	GLY	ILE	THR	GLY	GLY	ASN	GLY	THR	THR	GLU	ILE	ASN	VAL	VAL	VAL
ASN	PHE	PRO	ALA	ALA	CYS	ASP	ILE	ILE	ALA	VAL	MET	MET	GLN	PRO	ASP	ASP	GLY	CYS
ARG	VAL	GLY	GLU	VAL	GLU	VAL	GLY	GLY	VAL	ASP	ASP	ASP	GLU	GLN	GLY	GLY	GLY	GLY
VAL	VAL	THR	ARG	VAL	GLY	SER	THR	LEU	VAL	THR	ARG	ARG	ILE	THR	ARG	VAL	VAL	VAL
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GLY	VAL	VAL	ARG	THR	GLY	GLY	GLY	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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GLY	VAL	VAL	ARG	THR	GLY	GLY	GLY	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
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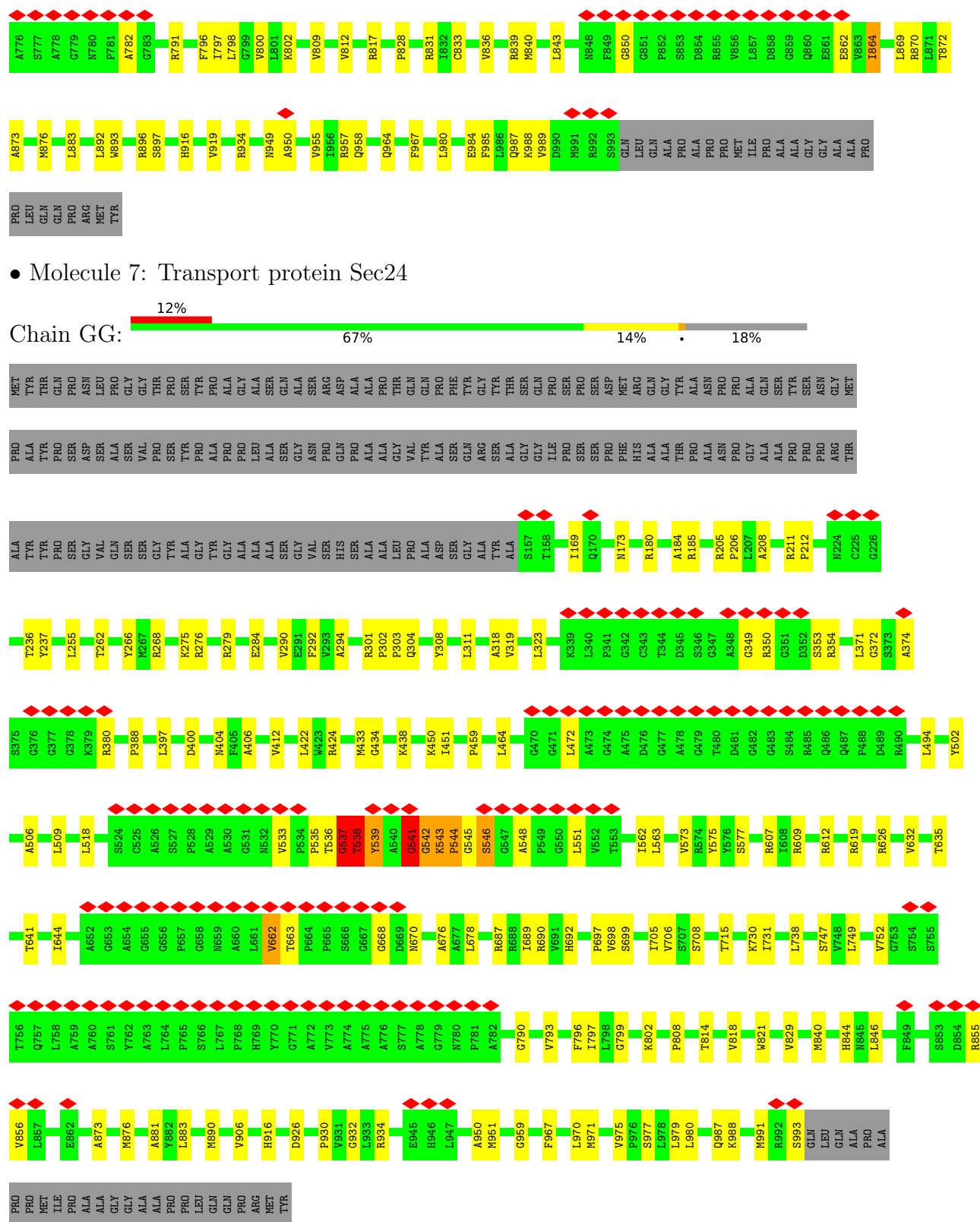
- Molecule 7: Transport protein Sec24

[illegible]



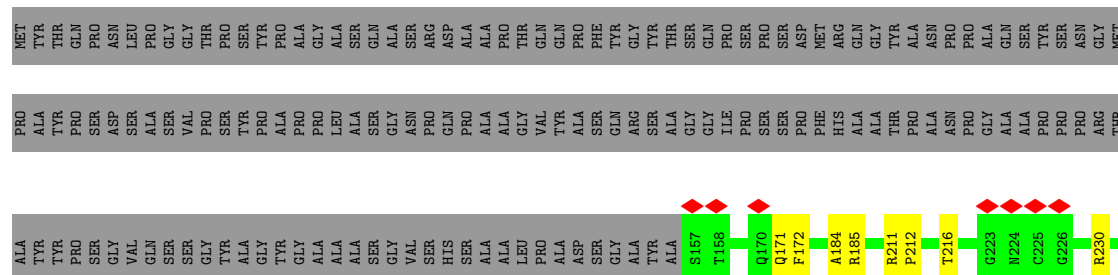
• Molecule 7: Transport protein Sec24

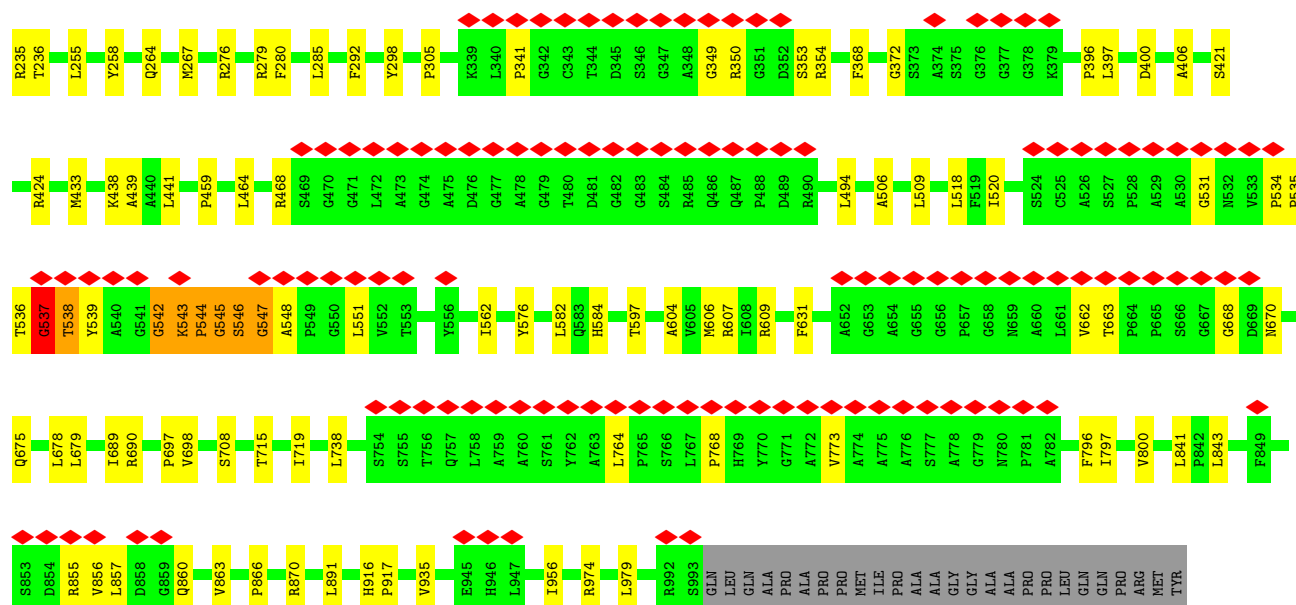




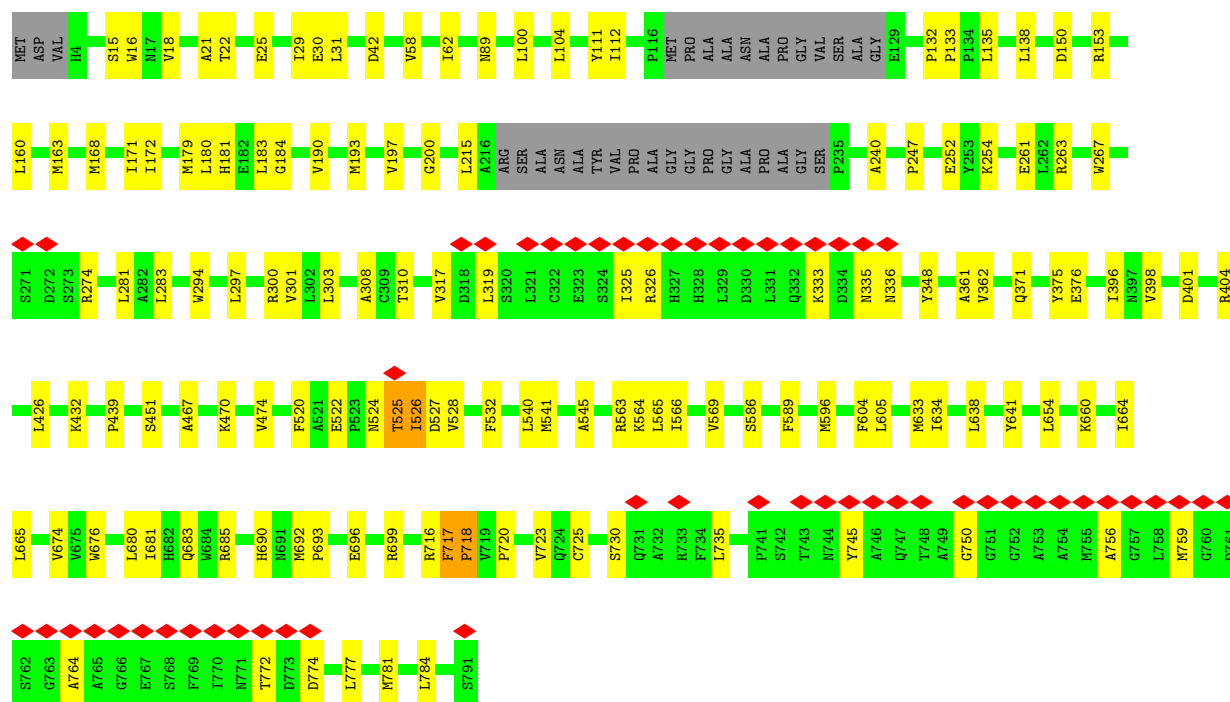
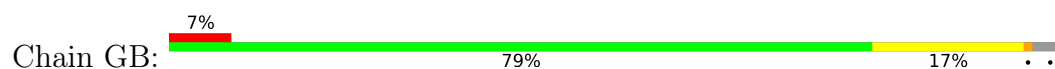
• Molecule 7: Transport protein Sec24



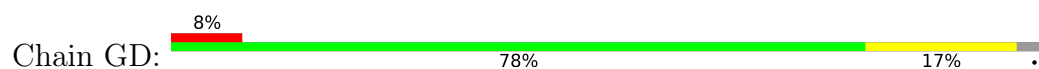


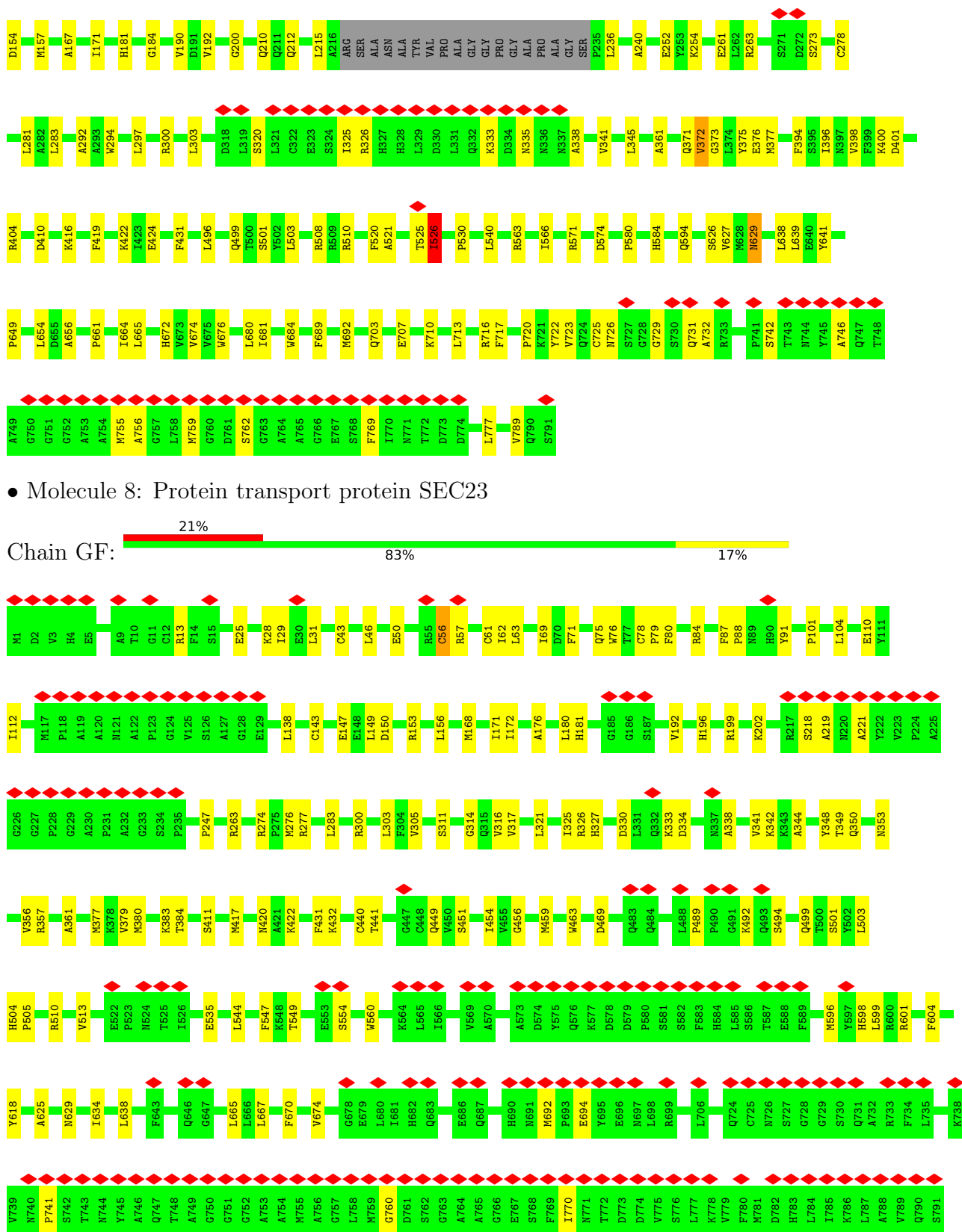


• Molecule 8: Protein transport protein SEC23

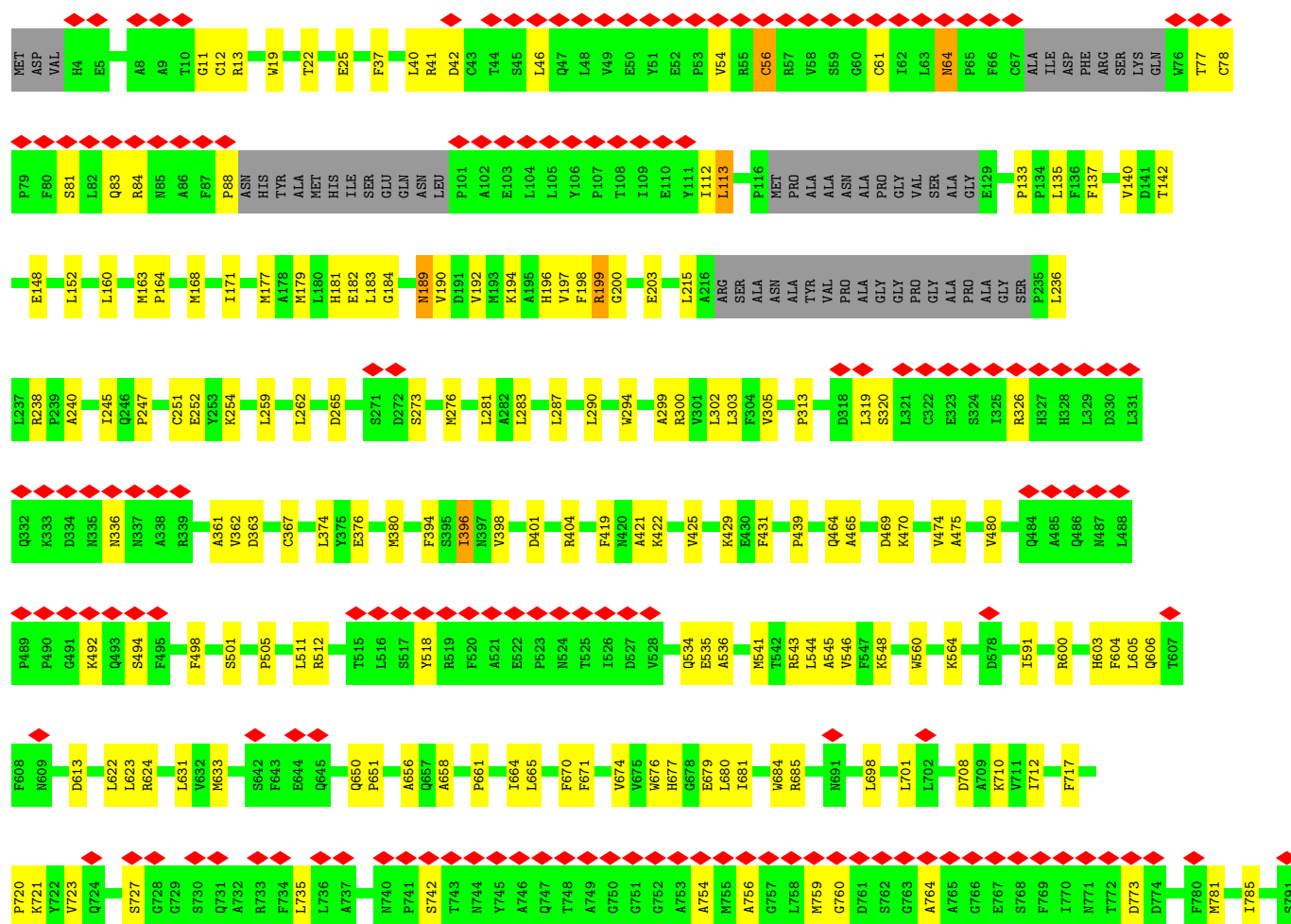
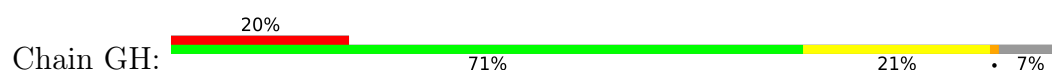


• Molecule 8: Protein transport protein SEC23

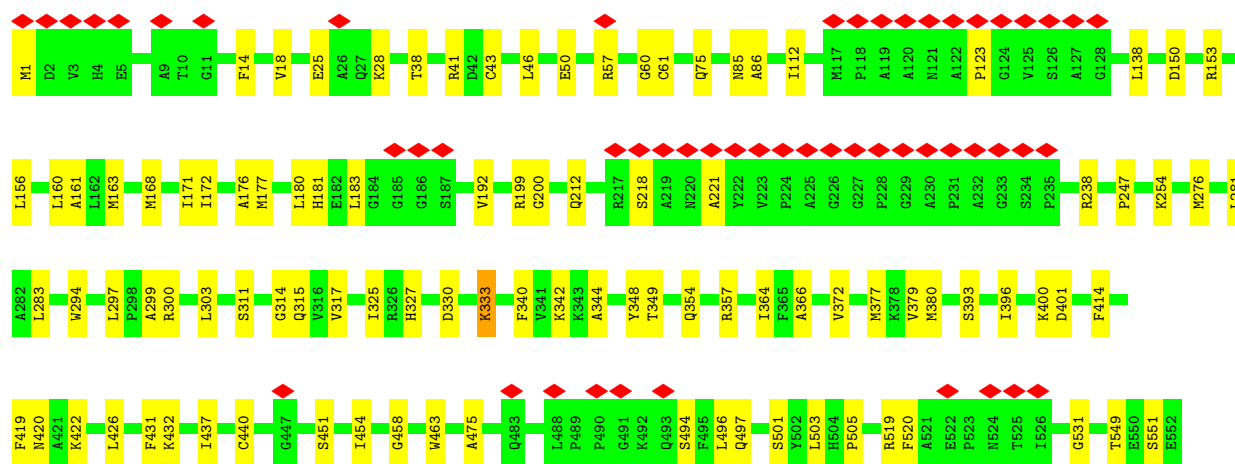
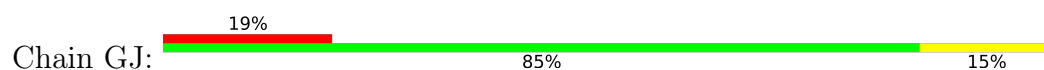


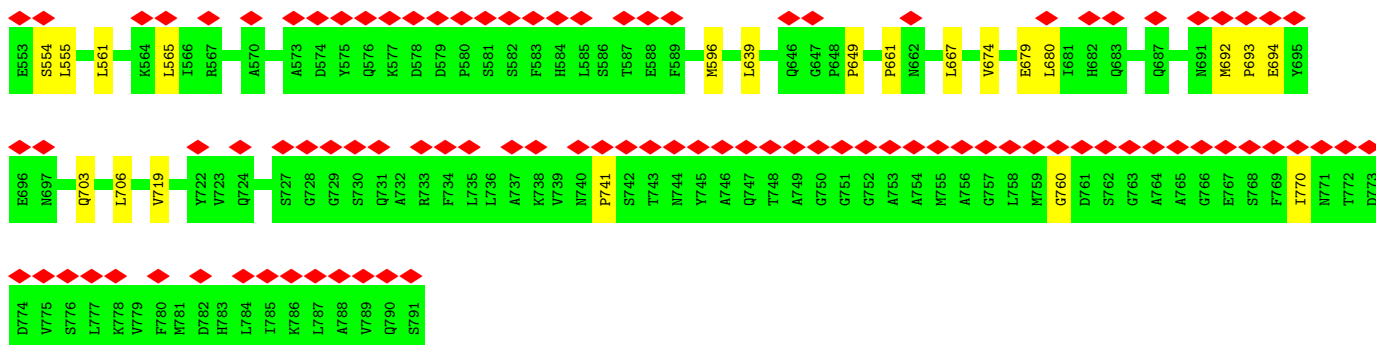


• Molecule 8: Protein transport protein SEC23

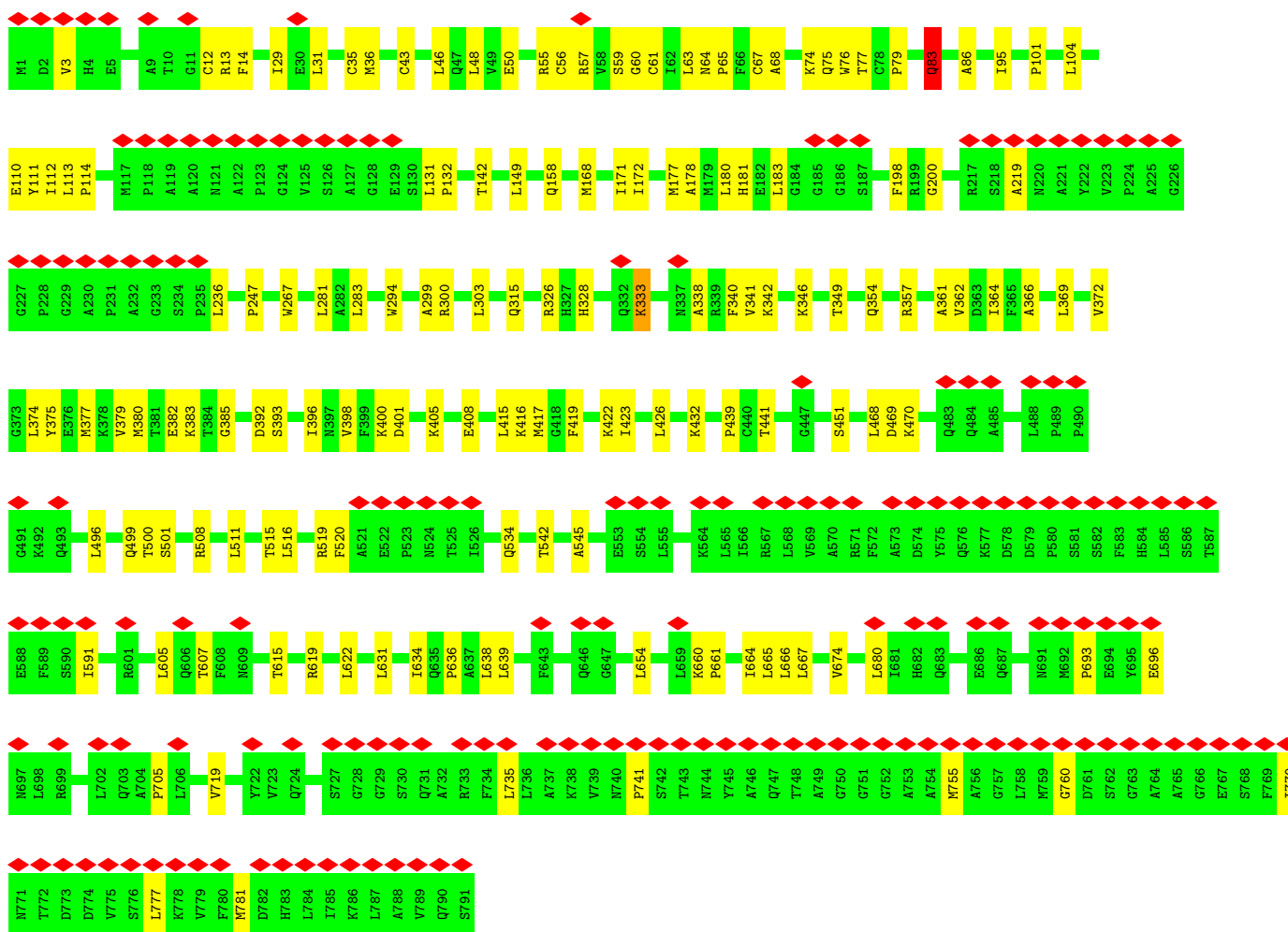
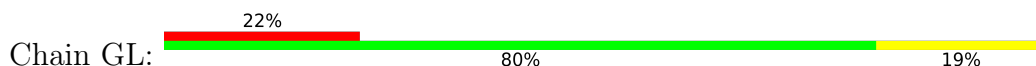


• Molecule 8: Protein transport protein SEC23





• Molecule 8: Protein transport protein SEC23



• Molecule 9: FLM2, TGME49_285990





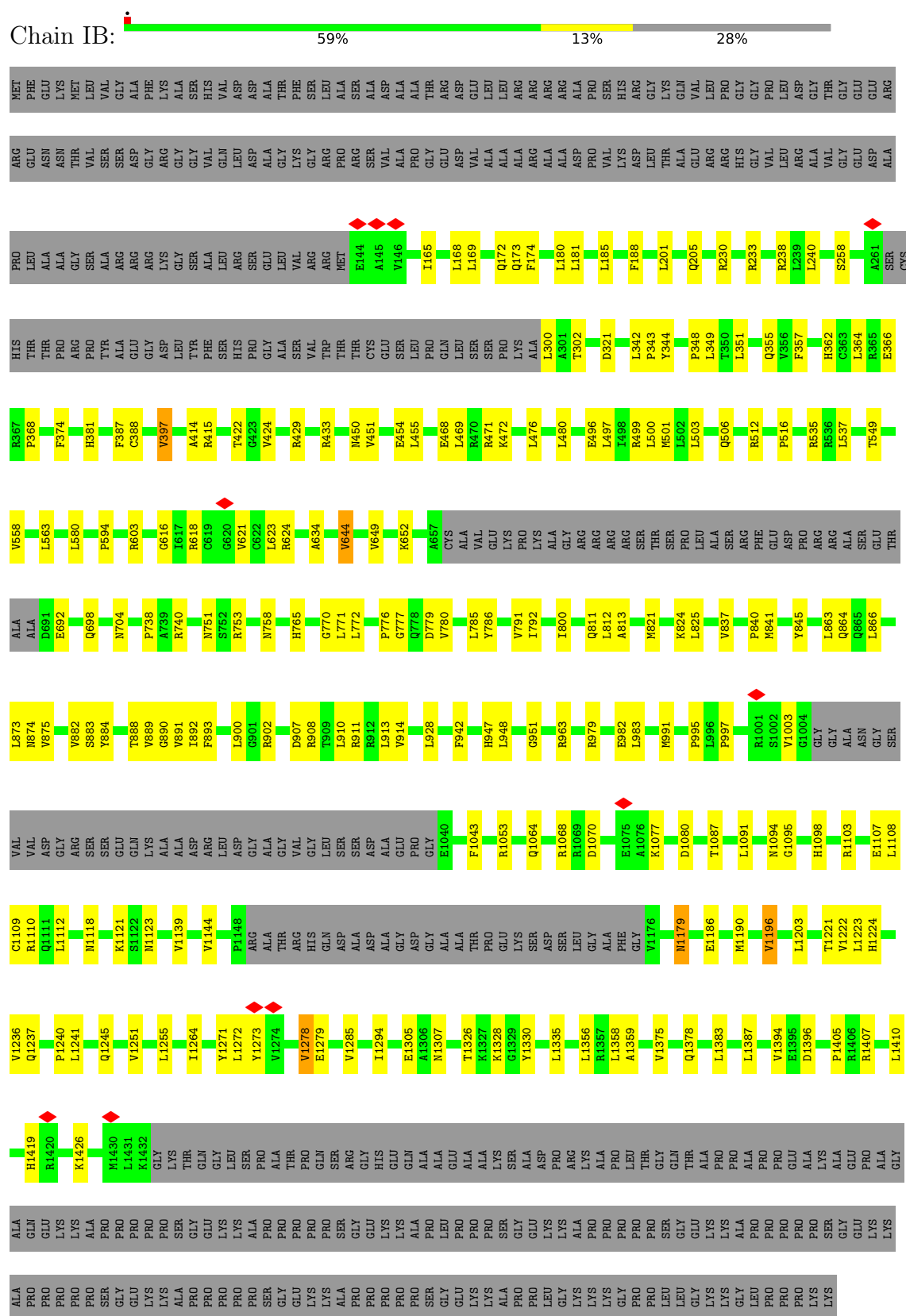




Chain IA:



• Molecule 10: PCR12, TGME49_292170



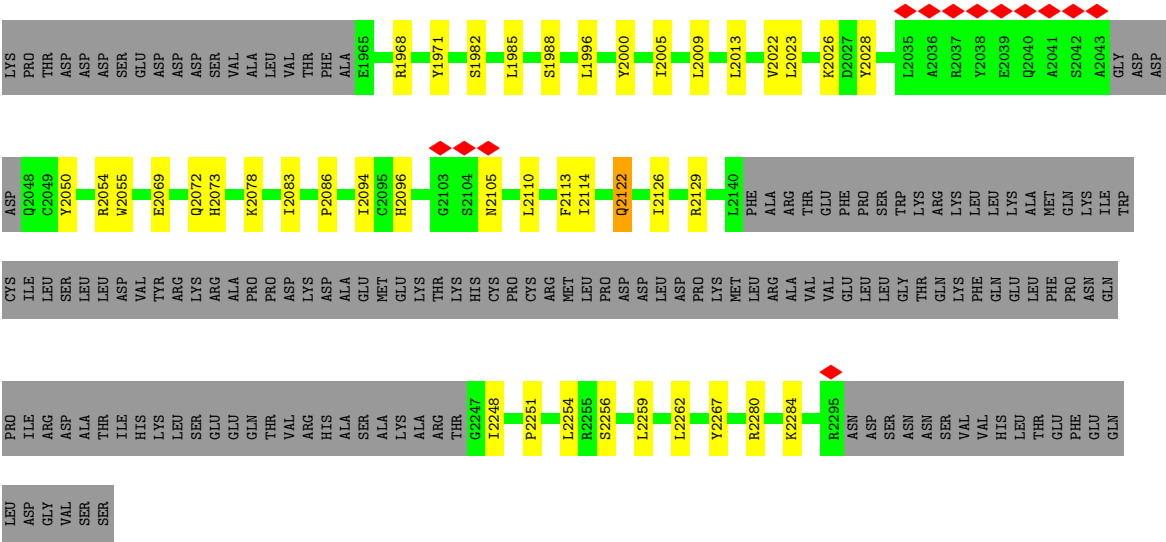
• Molecule 10: PCR12, TGME49_292170

- Molecule 11: PCR10, TGME49 298010

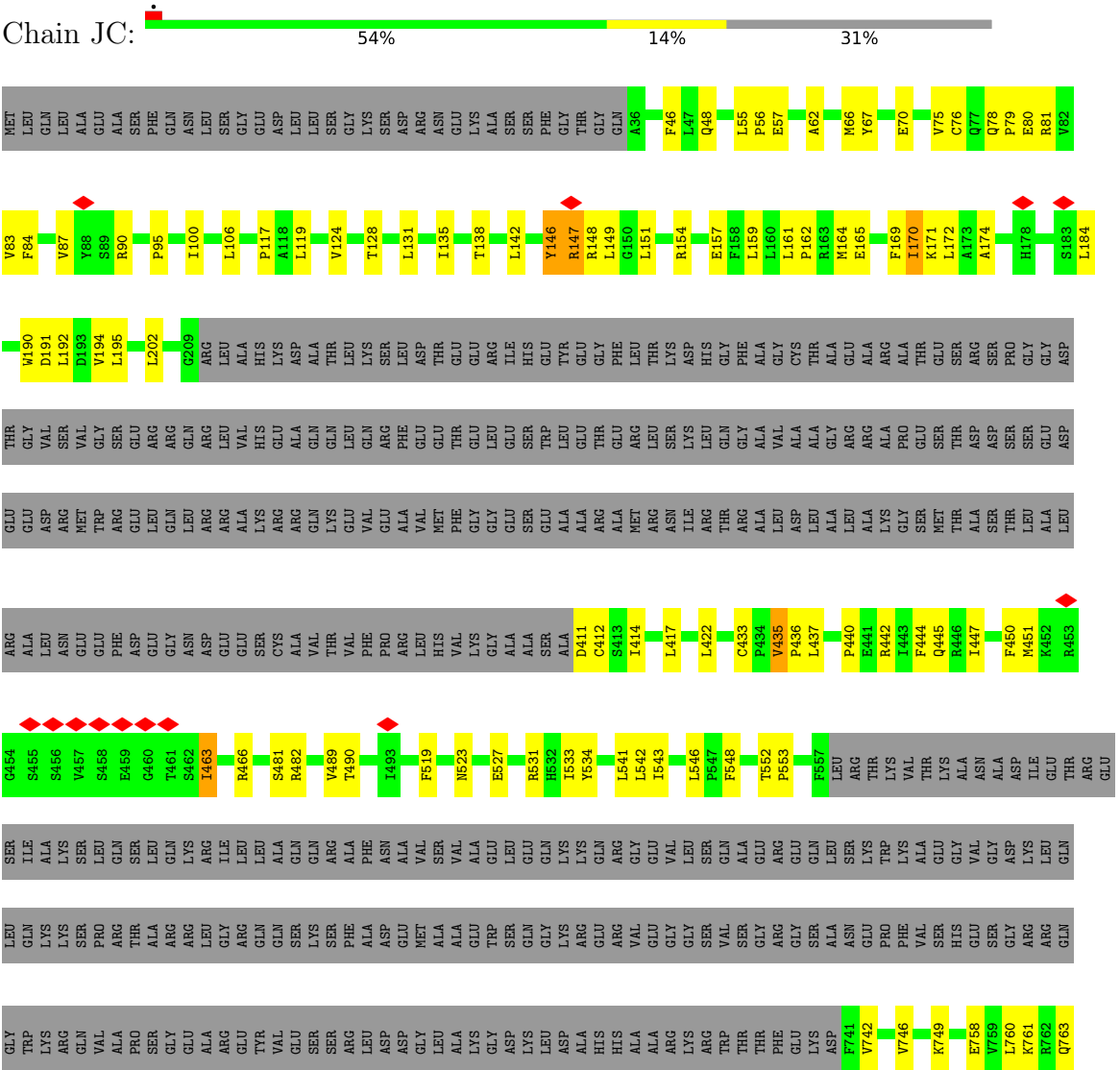


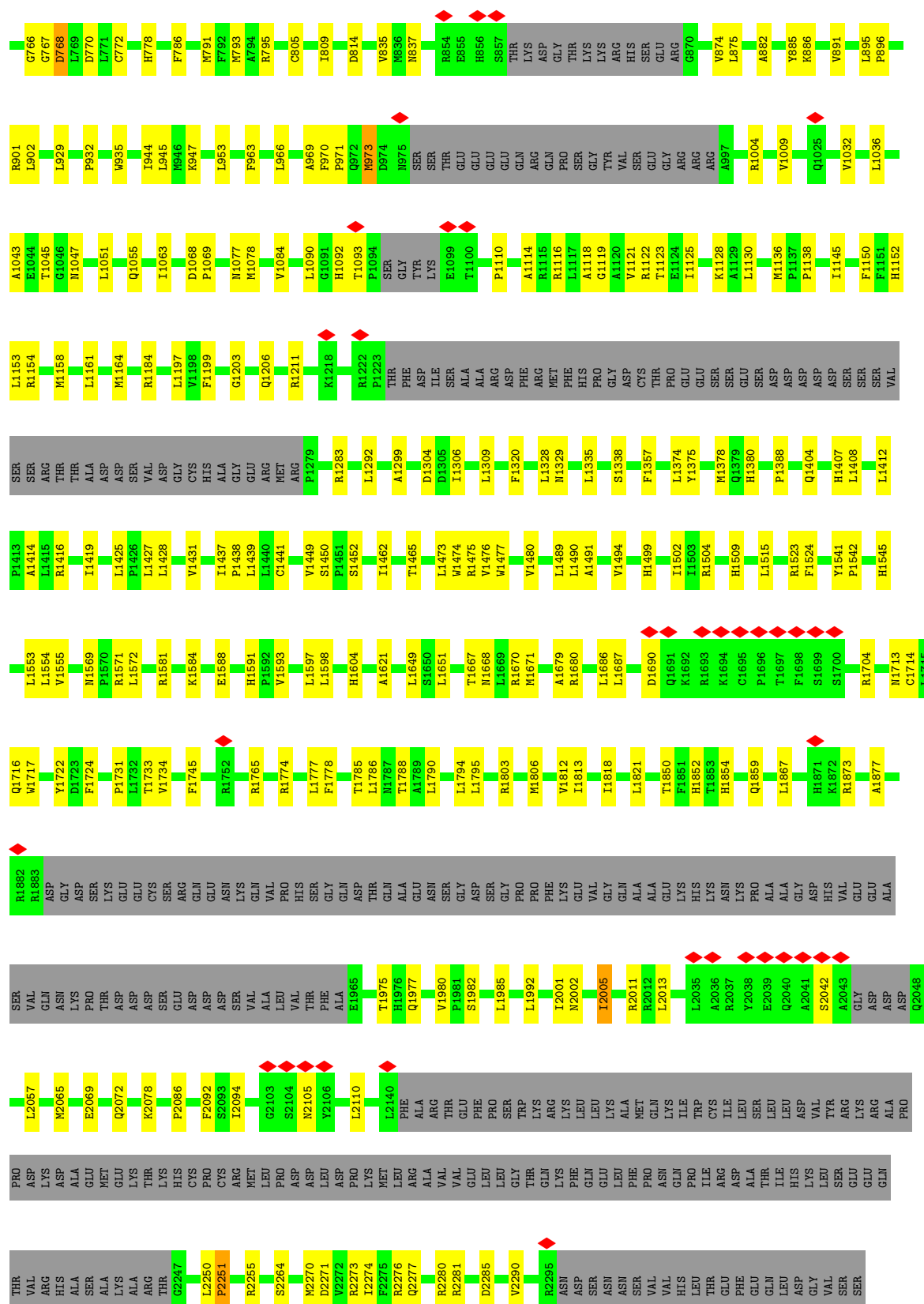






● Molecule 11: PCR10, TGME49_298010



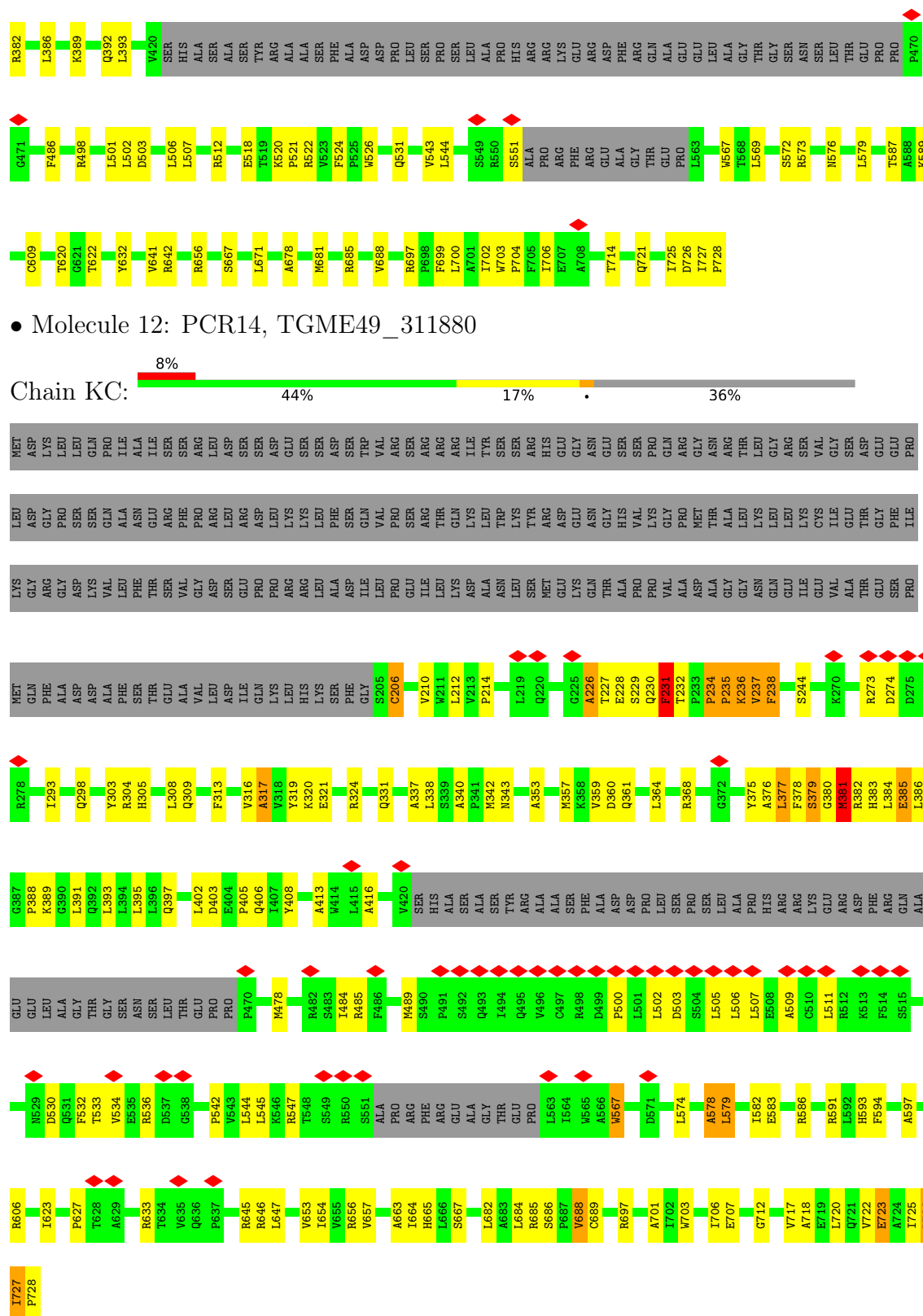


Frequency	Percentage
Daily	45%
Weekly	18%
Monthly	36%
Other	1%



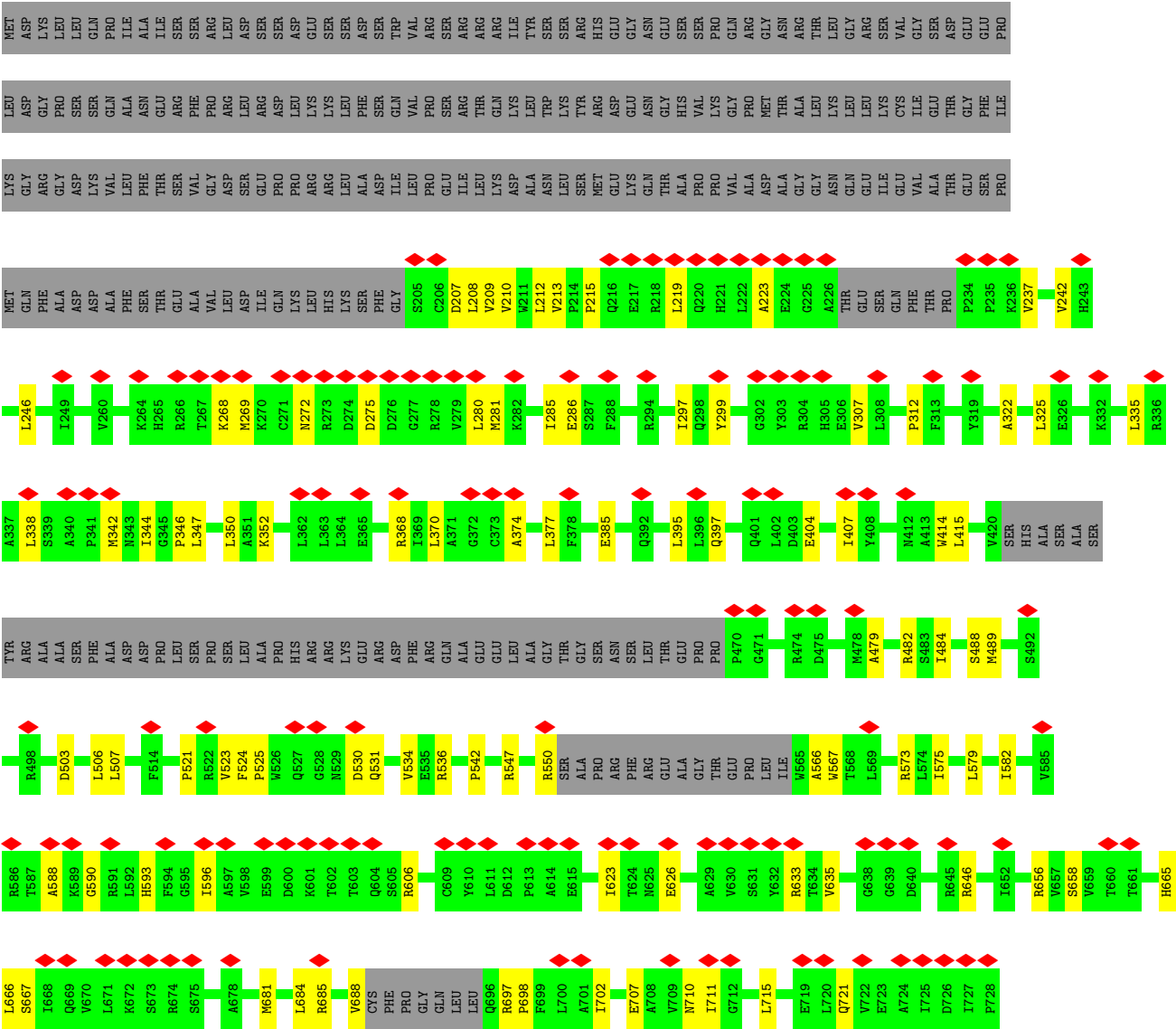
Response Category	Percentage
Not at all	49%
A little	14%
A lot	36%



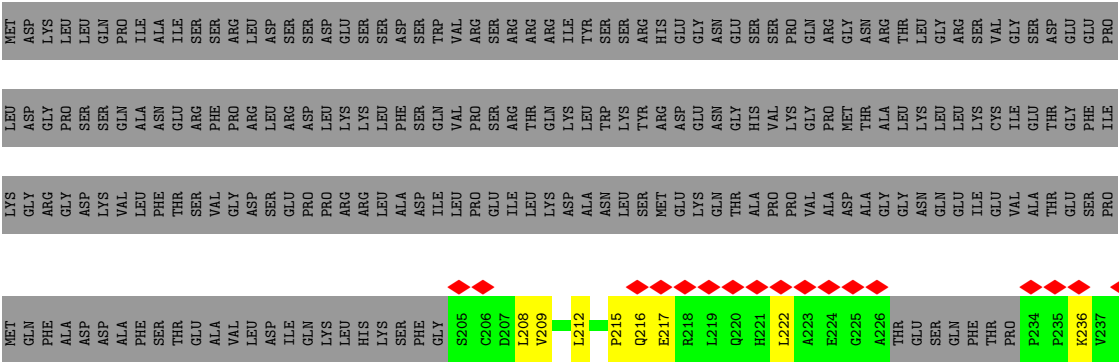


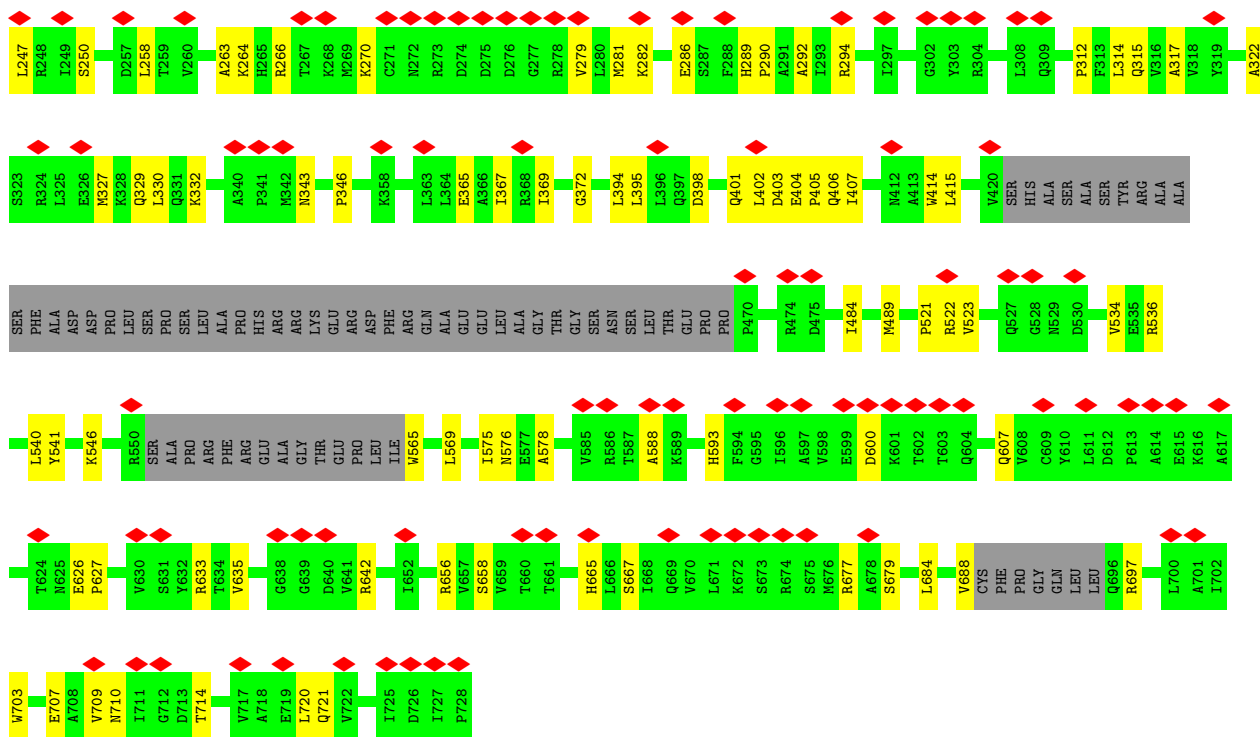
• Molecule 12: PCR14, TGME49_311880



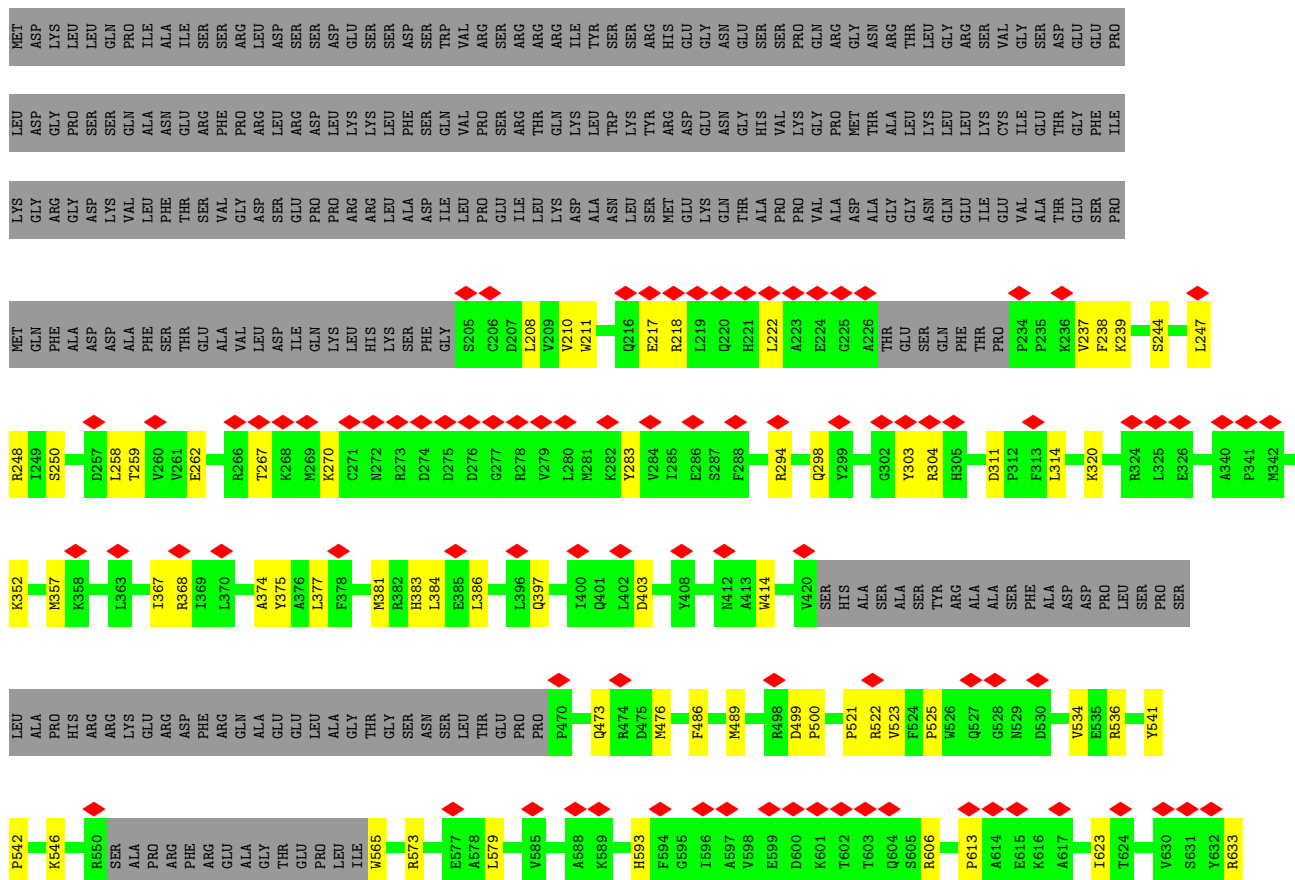


● Molecule 12: PCR14, TGME49_311880

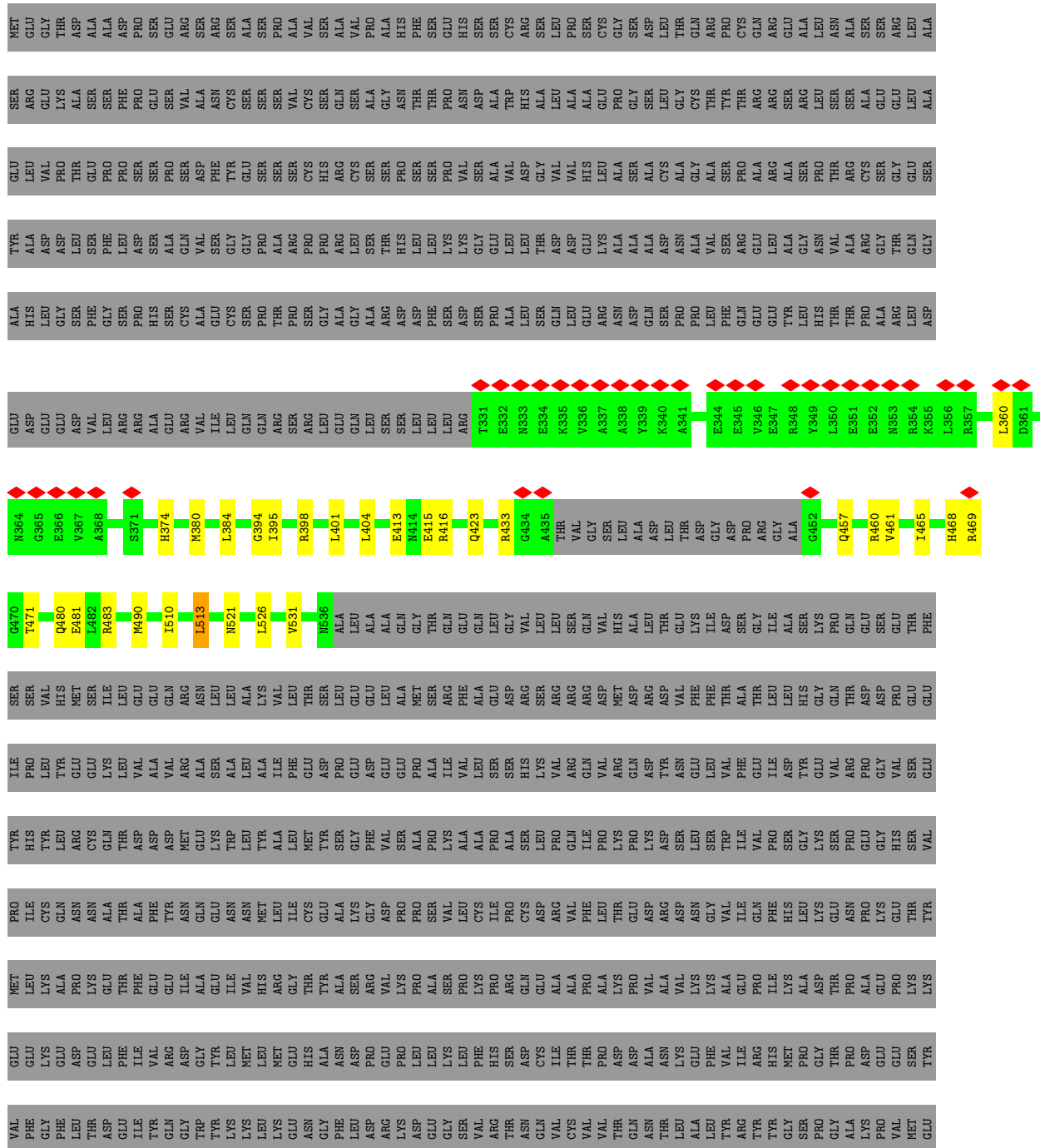




- Molecule 12: PCR14, TGME49_311880



● Molecule 13: ICAP16, TGME49 202120





• Molecule 13: ICAP16, TGME49 202120

Government	Percentage
Current government	89%

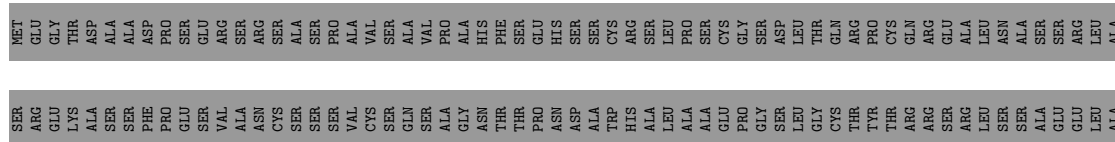
89%

[illegible]



- Molecule 13: ICAP16, TGME49_202120

[illegible]



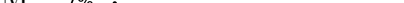


Chain LL: 11% 88%



VAL	SER	ALA	PRO	ALA	ALA	ASP	LEU	ARG	GLY	PRO	GLY	ARG	MET	PHE	GLY	ARG	GLY	LEU	LEU	ASP	THR	PRO	LYS	ASP	ARG	VAL	SER	PHE	ALA	VAL	PRO	GLU	ASP	ASP	ALA	GLN	ASP	LEU	SER	SER	ARG	SER	SER	THR	SER	GLY	SER	GLY
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● Molecule 13: ICAP16, TGME49 202120

Chain LM:  7% 92%

SER	ARG	GLU	LYS	ALA	SER	SER	PHE	PRO	GLU	SER	SER	VAL	ALA	ASN	CYS	SER	SER	SER	VAL	CYS	SER	GLN	ALA	GLY	ASN	THR	PRO	THR	ASN	ASP	ALA	TRP	ALA	ALA	LEU	LEU	ALA	ALA	GLU	GLY	PRO	SER	SER	LEU	GLY	CYS	THR	TYR	THR	THR	ARG	SER	SER	ARG	ARG	LEU	SER	SER	ALA	GLU	GLU	LEU	ALA
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GLU	LEU	VAL	PRO	THR	GLU	PRO	PRO	SER	SER	SER	ASP	PHE	TYR	GLU	SER	SER	SER	CYS	HIS	ARG	CYS	SER	SER	PRO	PRO	VAL	SER	ALA	VAL	ASP	GLY	VAL	VAL	HIS	LEU	ALA	ALA	SER	SER	SER	PRO	THR	ARG	CYS	SER	GLY	GLU	SER
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Tyr	Ala	Asp	Leu	Ser	Phe	Leu	Asp	Ser	Ala	Gln	Val	Ser	Gly	Gly	Pro	Pro	Ala	Arg	Pro	Pro	Arg	Arg	Leu	Lys	Lys	Gly	Gly	Leu	Leu	Leu	Thr	Asp	Asp	Glu	Lys	Lys	Ala	Ala	Ala	Ala	Ala	Asn	Val	Ala	Ala	Arg	Gly	Thr	Gln	Gly
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ALA HIS LEU GLY SER PHE GLY SER PRO HIS SER CYS ALA ALA GLU GLY CYS PRO SER THR PRO SER GLY ALA ALA GLY ALA ARG ASP ASP PHE SER ASP SER PRO PRO ALA LEU LEU LEU PHE GLN GLU GLU TYR LEU LEU HIS THR THR PRO PRO ALA ALA ARG ARG LEU

Category	Item	Value
L	GLU	1328
	ASP	1329
	GLU	R330
	GLU	R331
	ASP	E332
	VAL	
	LEU	
	ARG	
	ALA	
	GLU	
V	VAL	
	ILE	
	LEU	
	GLN	
	GLN	
	ARG	
	SER	
	ARG	
	LEU	
	GLU	
S	GLN	
	LEU	
	SER	
	SER	
	SER	
	LEU	
	L328	
	L329	
	R330	
	T331	
K	E332	
	K335	
	V336	
	A337	
	A338	
	Y339	
	K340	
	N353	
	R354	
	K355	
H	H359	
	Q377	
	E378	
	L388	
	A389	
	E392	
	R398	
	D399	
	R400	
	L404	

[illegible]

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

[illegible]

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

VAL	ARG	ALA	ARG	SER	ALA	LEU	ALA	ILE	PHE	GLU	ASP	PRO	GLU	ASP	GLU	GLU	PRO	ALA	ILE	VAL	VAL	LEU	SER	SER	HIS	LYS	VAL	ARG	GLN	GLN	VAL	ARG	GLN	ASP	TYR	LEU	LEU	VAL	PHE	GLU	ILE	ASP	TYR	GLU	VAL	ARG	PRO	GLY	VAL	SER	GLU	TYR	HIS	TYR	LEU	ARG	CYS	GLN	THR	ASP	ASP
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[illegible]

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

- Molecule 13: ICAP16, TGME49_202120

Chain LN: 7% 92%

[illegible]

LEU	Tyr	Val	Glu	Leu
Tyr	His	His	Ser	Ala
Glu	Met	Ser	Leu	Arg
Glu	Ser	Ile	Asn	Gln
Lys	Ile	Leu	Gly	Arg
Val	Glu	Glu	Lys	Asp
Ala	Glu	Glu	Ser	Ile
Val	Gln	Gln	Leu	Asp
Arg	Arg	Val	Val	Gln
Ala	Asn	Pro	Pro	His
Ser	Leu	Pro	Arg	Arg
Ala	Leu	Val	Gly	Gly
Leu	Ala	Leu	Thr	Thr
Ala	Lys	Lys	Leu	Gly
Ile	Val	Val	Ala	Lys
Phe	Leu	Leu	Pro	Gln
Gly	Thr	Ser	Ala	Leu
Glu	Ser	Ser	Asn	Gly
Asp	Ser	Leu	Ala	Leu
Pro	Pro	Glu	Ala	Leu
Glu	Glu	Glu	Leu	Thr
Glu	Leu	Leu	Ala	Phe
Pro	Met	Ala	Gln	Gln
Pro	Met	Ala	Gly	Glu
Ile	Ser	Arg	Thr	Leu
Val	Phe	Arg	Gln	Val
Val	Arg	Ala	Ser	Arg
Ser	Glu	Glu	Leu	Met
Ser	Asp	Asp	Gly	Ser
His	Arg	Arg	Val	Leu
Lys	Ser	Leu	Val	Leu
Val	Arg	Arg	Leu	Gln
Arg	Arg	Arg	Ser	Ser
Gln	Arg	Arg	Gln	Gln
Val	Asp	Asp	Ser	Ser
Arg	Met	His	Asp	Asp
Gln	Asp	Ala	Ala	Leu
Asp	Arg	Arg	Leu	Leu
Tyr	Asp	Thr	Thr	Glu
Asn	Val	Glu	Glu	Ala
Glu	Phe	Ile	Lys	Gln
Leu	Phe	Thr	Ile	Lys
Val	Thr	Ala	Ser	Val
Phe	Ala	Thr	Gly	Glu
Glu	Leu	Leu	Ile	Glu
Asp	Leu	Leu	Ala	Gln
Tyr	His	Gly	Ser	Arg
Glu	Gly	Gln	Lys	Leu
Val	Gln	Thr	Pro	Glu
Arg	Gln	Glu	Gln	Ile
Pro	Asp	Asp	Glu	Gln
Gly	Asp	Asp	Ser	Arg
Val	Pro	Glu	Glu	Leu
Ser	Glu	Glu	Thr	Tyr
Glu	Glu	Glu	Phe	Lys
Tyr	Ile	Ser	Ser	Thr
Trp	Pro	Pro	Ser	Ile

[illegible]

- Molecule 13: ICAP16, TGME49 202120

[illegible]



Chain MA: 95%





[illegible]

- Molecule 14: PCR12, TGME49_219070

Chain MB: 96%

[illegible]



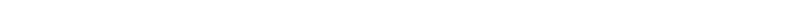
WORLDWIDE
PDB
PROTEIN DATA BANK





[illegible]

- Molecule 14: PCR12, TGME49 219070

Chain ME:  95%

[illegible]



[illegible]

- Molecule 14: PCR12, TGME49 219070

Chain MF: 96%

ALA	GLY	A287	PRO	GLN	ARG	MET
VAL	VAL	R290	VAL	ALA	ARG	THR
PRO	PRO	L291	VAL	ASN	LEU	ARG
GLY	GLY	A292	ARG	ALA	SER	ALA
CYS	CYS	L293	ASP	LEU	GLN	MET
GLU	GLU	A294	ASP	ARG	LEU	LEU
ARG	ARG	L296	ASN	SER	VAL	GLY
GLU	GLU	E295	LYS	ASP	ASN	ALA
SER	SER	G296	HIS	GLU	CYS	PRO
LEU	LEU	V297	LEU	GLU	PRO	THR
ARG	ARG		ARG	LYS	ASP	SER
LEU	LEU	L301	LEU	ARG	ALA	ALA
LEU	LEU	E308	ARG	TYR	ALA	GLU
ARG	ARG	R309	ALA	ALA	GLU	GLY
GLN	GLN	S310	ASP	PHE	THR	GLY
ALA	ALA	R310	ALA	GLY	ARG	GLY
ALA	ALA	L311	ASN	LEU	GLU	ASP
ASP	ASP	S312	GLU	ALA	LEU	GLY
ASP	ASP	R313	HIS	ARG	ALA	VAL
ILE	ILE	S314	ASP	ASP	ARG	ALA
ASP	ASP	W315	LYS	ALA	ASP	ASP
SER	SER	Q316	C203	ALA	TYR	PRO
ASP	ASP			ARG	GLY	ASP
ALA	ALA	R320	L210	GLY	PRO	ARG
LYS	LYS	Q323	L218	SER	GLU	LEU
ARG	ARG	R324		ILE	LEU	TYR
LEU	LEU	R325	Q227	SER	ALA	THR
GLU	GLU	L326		LYS	HIS	ARG
VAL	VAL		V230	VAL	ALA	SER
TYR	TYR	L330		VAL	PHE	LEU
SER	SER		K243	ALA	SER	ARG
ARG	ARG	L333		MET	SER	GLU
ILE	ILE			LEU	LEU	ASP
ALA	ALA	R339	L254	GLU	SER	LEU
GLU	GLU	SER		ALA	ASP	GLU
LEU	LEU	L258	K257	GLY	GLU	GLU
GLU	GLU	MET	W259	CYS	ASN	ALA
ARG	ARG	GLY		LYS	LYS	ARG
GLU	GLU	SER	W260	GLY	TYR	ASP
VAL	VAL	CYS	ASP	SER	LEU	LYS
VAL	VAL	ASP	PRO	SER	LYS	LEU
LYS	LYS	LEU	PHE	ALA	VAL	LEU
ASP	ASP	PHE	LEU	ARG	LYS	LYS
LEU	LEU	ARG	SER	GLY	LEU	LYS
ARG	ARG	GLY	ALA	ASP	GLN	LYS
PHE	PHE	GLY	LYS	VAL	SER	LYS
SER	SER	ILE	TYR	GLY	SER	MET
ASN	ASN	LEU	ALA	ASP	GLN	ASN
THR	THR	GLN	ALA	SER	ALA	GLU
ARG	ARG	ALA	ALA	PRO	ARG	LEU
LEU	LEU	ALA	GLY	VAL	GLU	LEU
ALA	ALA	GLU	THR	PHE	VAL	GLU
GLU	GLU	ALA	PRO	ARG	ARG	GLY
SER	SER	ALA	GLY	GLY	ALA	GLU
THR	THR	ALA	ALA	ASP	GLU	ASN
THR	THR	ALA	VAL	ASP	ILE	GLN
ARG	ARG	ARG	P278	VAL	ARG	ASP
VAL	VAL	LEU		PRO	ALA	LEU
LYS	LYS	LEU	R382	GLY	THR	ARG









[illegible]

- Molecule 14: PCR12, TGME49 219070

Chain MH: 98%

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

WORLDWIDE
PDB
PROTEIN DATA BANK

WORLDWIDE
PDB
PROTEIN DATA BANK







[illegible]

- Molecule 14: PCR12, TGME49 219070

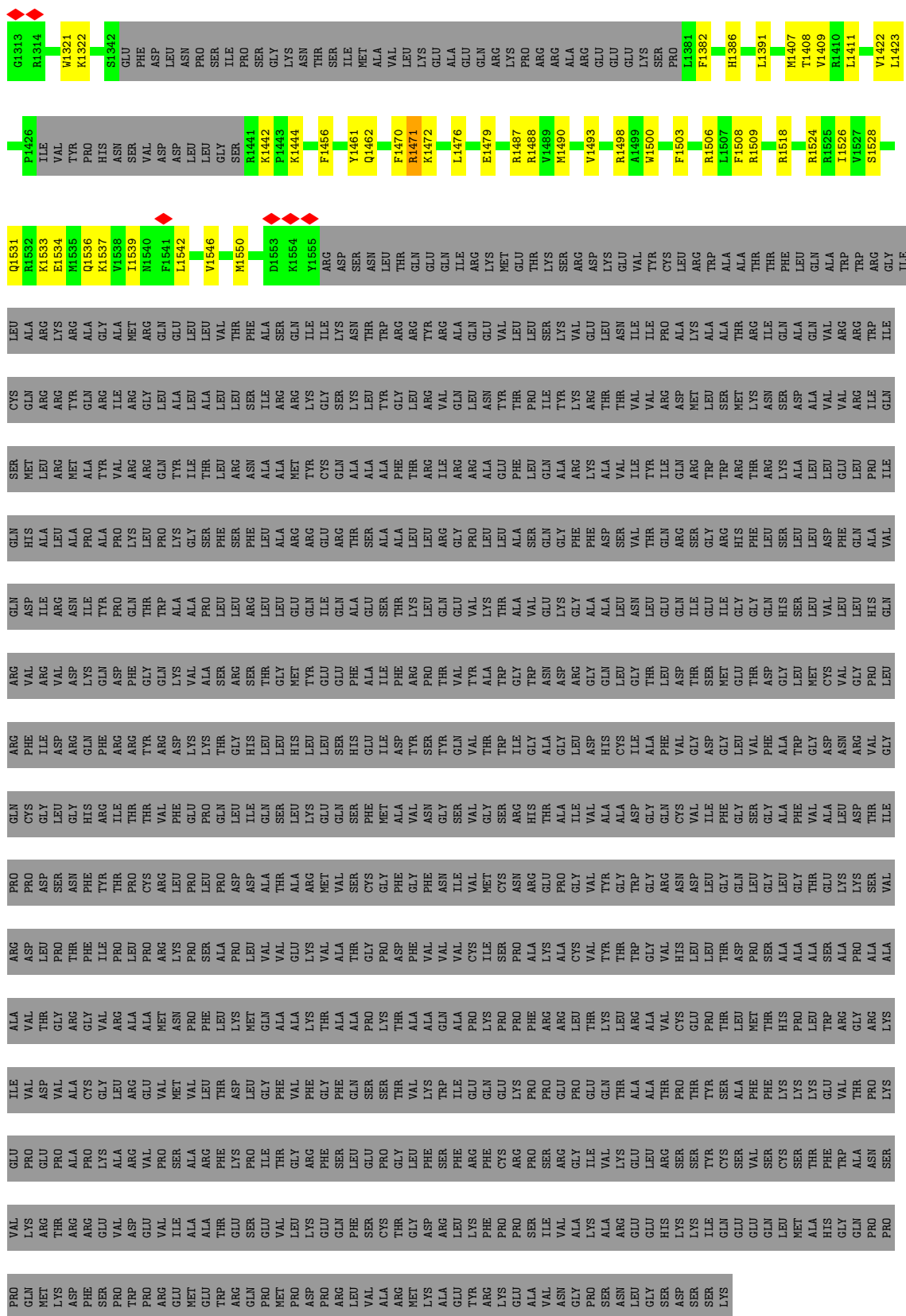
Chain MK: 97%

[illegible]

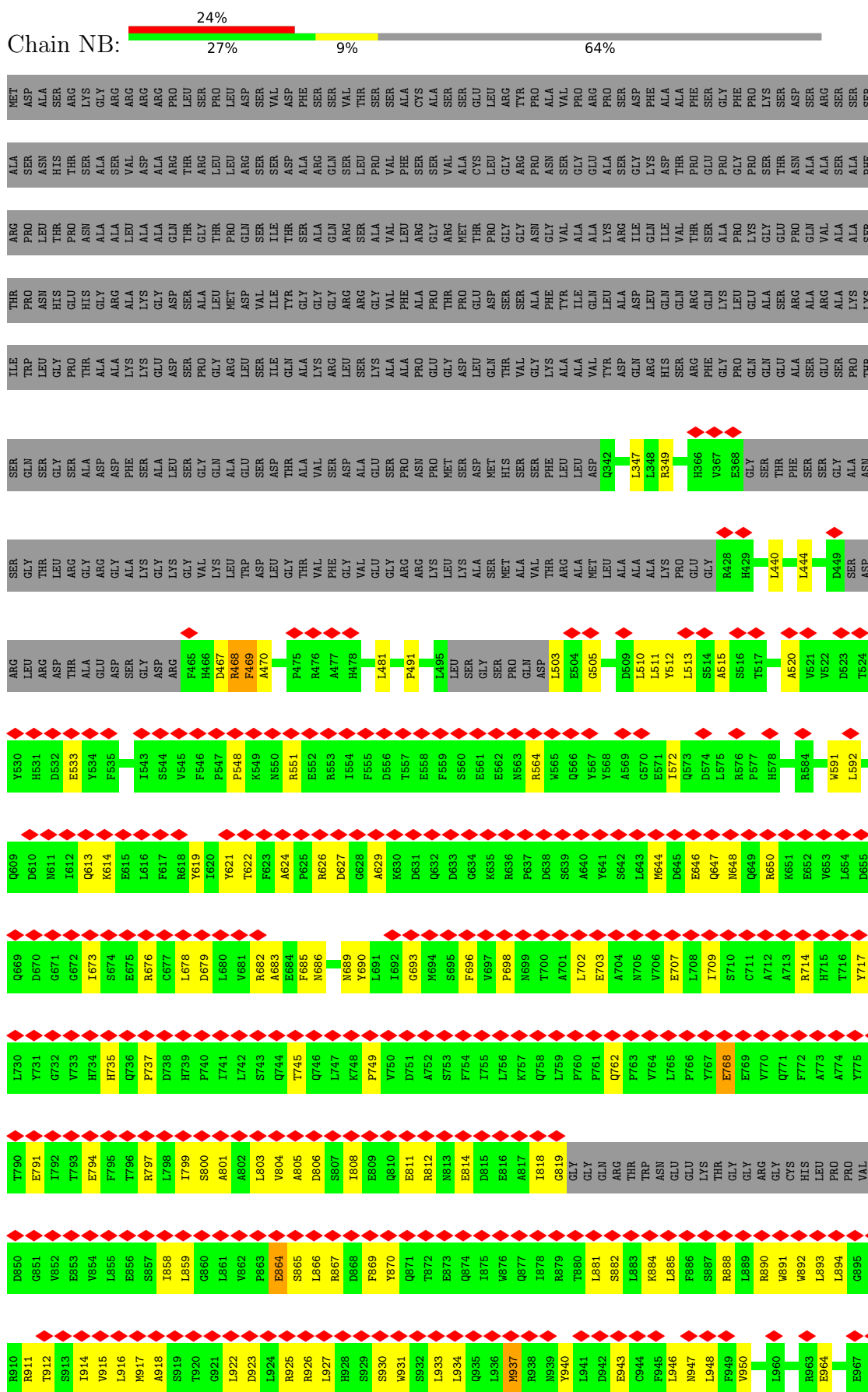
WORLDWIDE
PDB
PROTEIN DATA BANK

WORLDWIDE
PDB
PROTEIN DATA BANK





- Molecule 15: myosin L, TGME49 291020

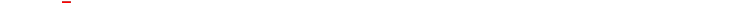










Chain OA:  16% 81%





Chain OB:





Chain OC: 16% 81%



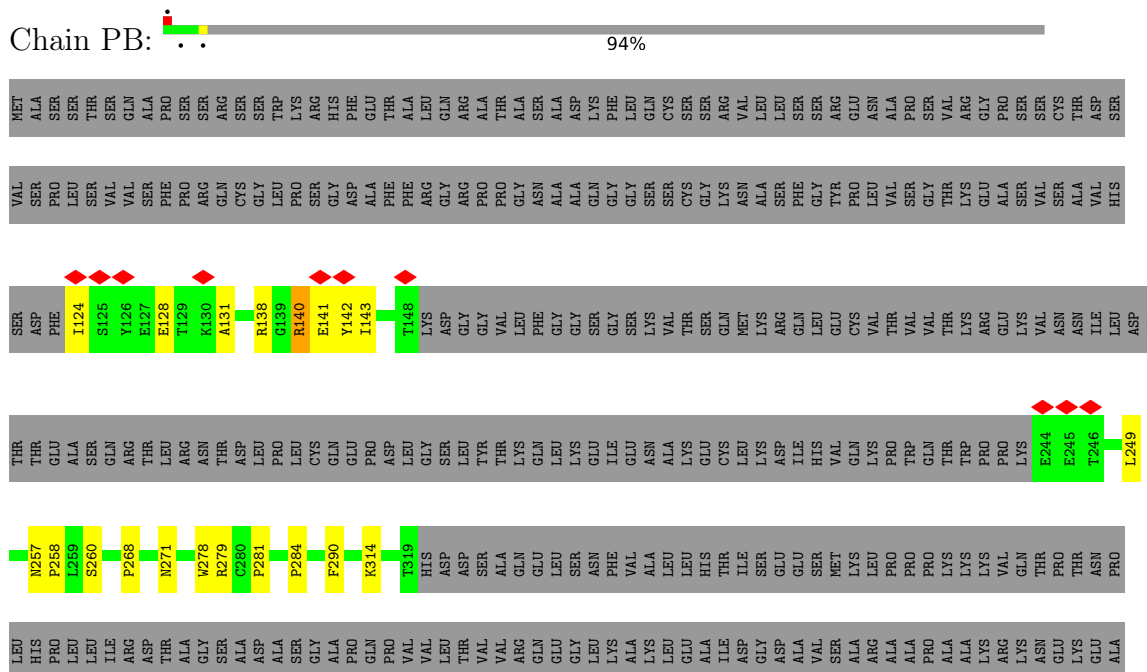
GLU
ARG
SER
GLU
LYS
SER
ASP

- 

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

- Molecule 17: PCR15, TGME49_232560



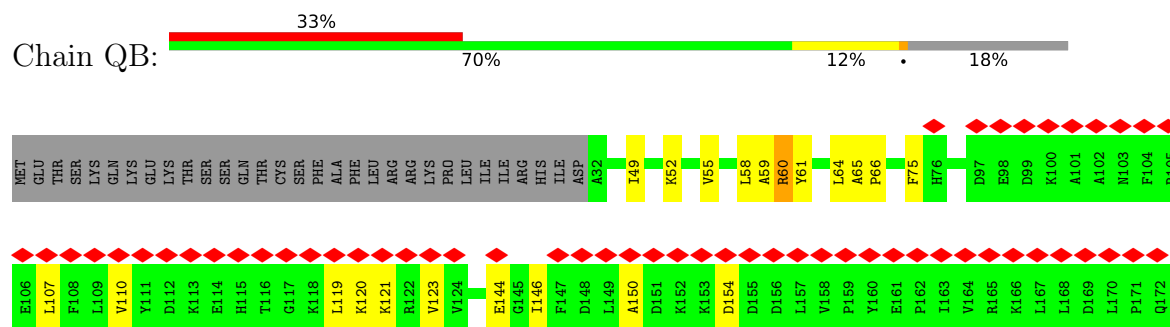


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SER	SER	SER	SER	GLY	GLY	ARG	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	ALA
HIS	SER	SER	SER	GLY	GLY	ARG	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	ASP
PHE	GLN	ARG	GLN	ARG	VAL	VAL	THR	ARG	VAL	VAL	THR	ARG	VAL	VAL	THR	ARG	VAL	CYS
GLN	ARG	GLN	ARG	VAL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

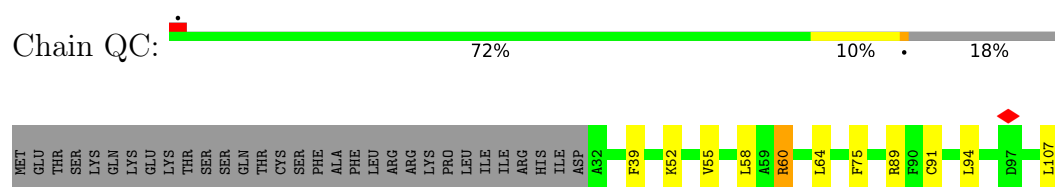
- Molecule 17: PCR15, TGME49 232560

[illegible]

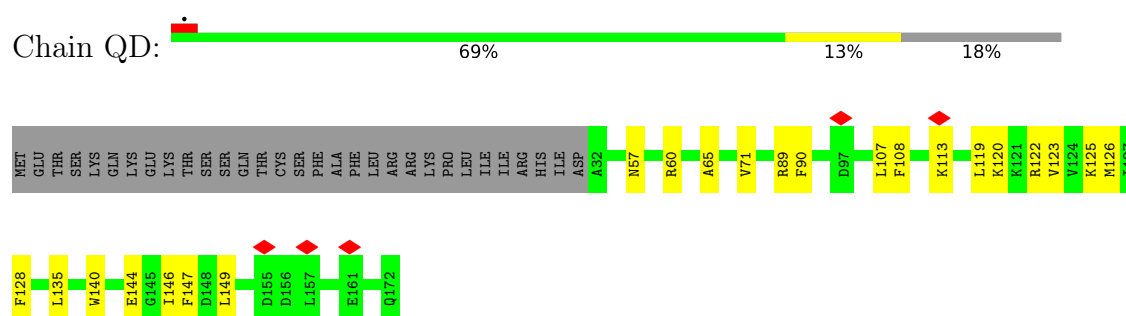
- Molecule 18: MLC4, TGME49_294390



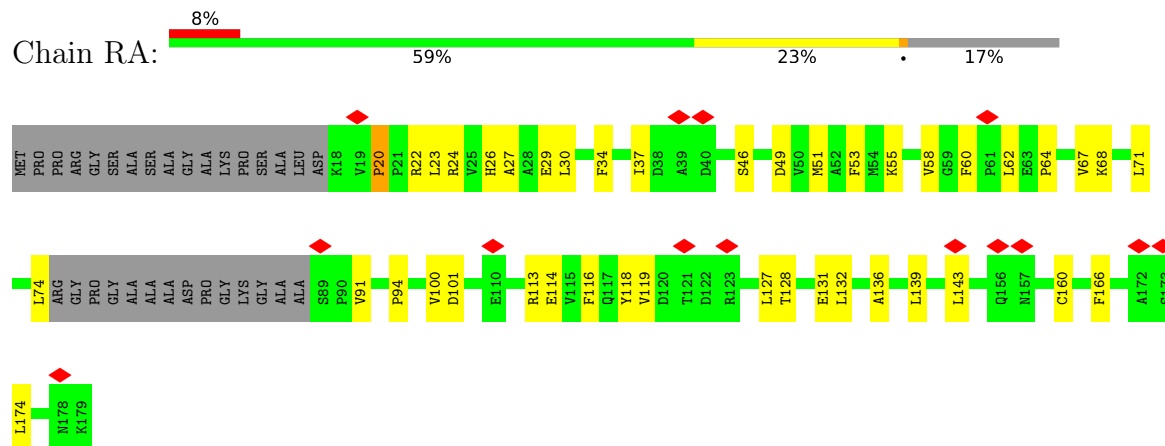
- Molecule 18: MLC4, TGME49_294390



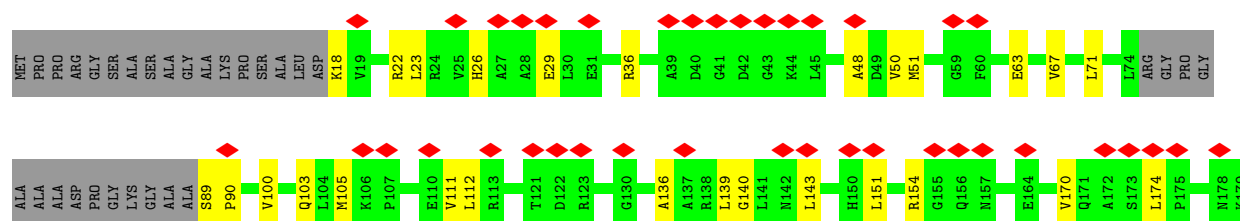
- Molecule 18: MLC4, TGME49_294390



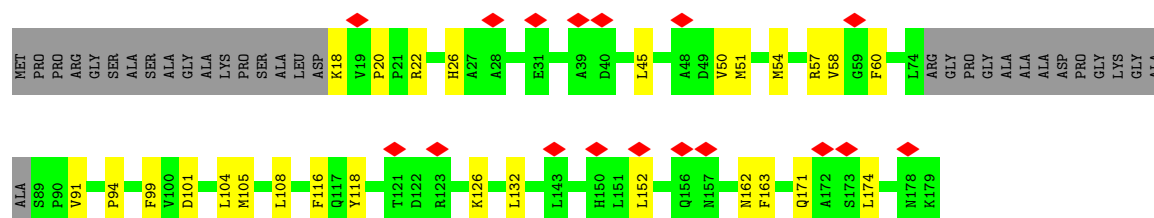
- Molecule 19: Calmodulin



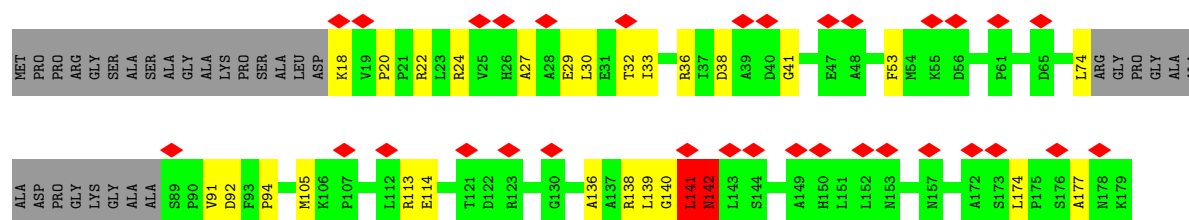
- Molecule 19: Calmodulin



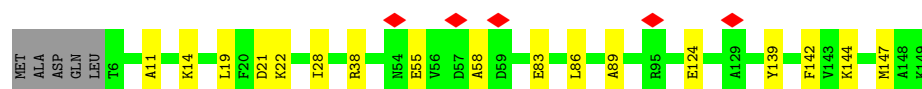
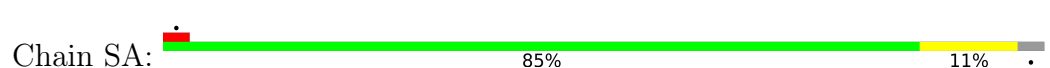
• Molecule 19: Calmodulin



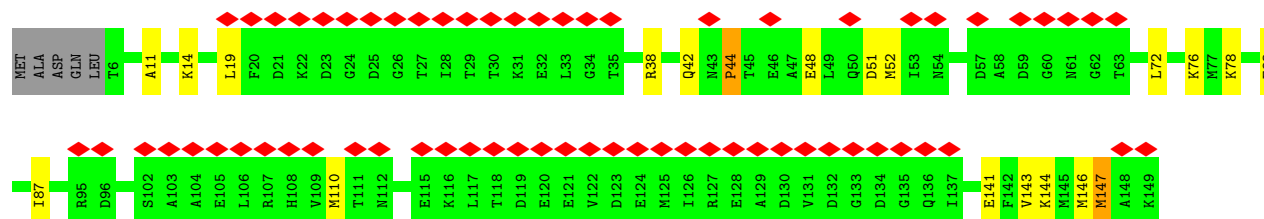
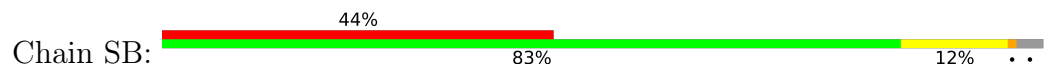
• Molecule 19: Calmodulin



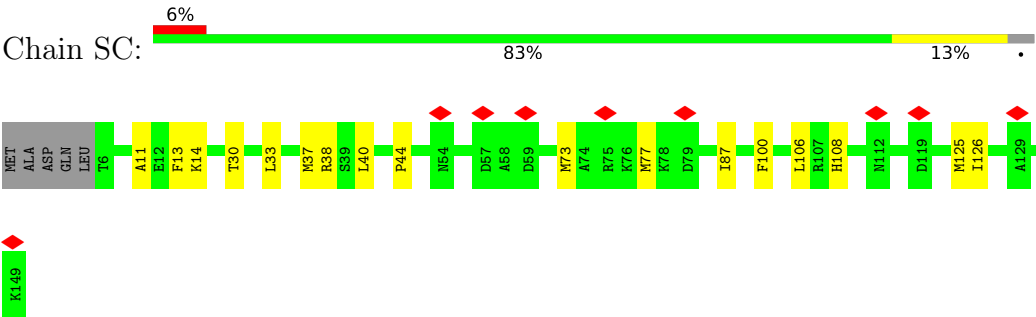
• Molecule 20: Calmodulin



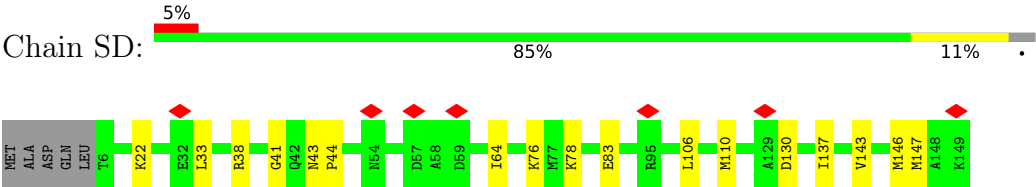
• Molecule 20: Calmodulin



• Molecule 20: Calmodulin



• Molecule 20: Calmodulin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	131707	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	5000	Depositor
Maximum defocus (nm)	25000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.073	Depositor
Minimum map value	0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.039	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	686.08, 686.08, 686.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	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	0.24	1/6682 (0.0%)	0.65	5/9057 (0.1%)
1	AD	0.22	0/6958	0.58	0/9433
1	AE	0.24	0/6682	0.67	4/9057 (0.0%)
1	AH	0.22	0/6958	0.59	3/9433 (0.0%)
1	AI	0.24	0/6682	0.64	3/9057 (0.0%)
1	AL	0.23	0/6958	0.57	0/9433
2	AB	0.34	1/3898 (0.0%)	0.66	4/5265 (0.1%)
2	AC	0.20	0/3926	0.51	0/5305
2	AF	0.25	0/3898	0.65	3/5265 (0.1%)
2	AG	0.21	0/3926	0.54	0/5305
2	AJ	0.23	0/3892	0.60	2/5258 (0.0%)
2	AK	0.22	0/3926	0.57	1/5305 (0.0%)
3	BA	0.22	0/2777	0.60	0/3759
3	BB	0.23	0/2777	0.62	0/3759
3	BC	0.22	0/2777	0.64	0/3759
3	CA	0.23	0/2762	0.60	1/3738 (0.0%)
3	CB	0.23	0/2762	0.62	0/3738
3	CC	0.22	0/2762	0.61	1/3738 (0.0%)
3	CE	0.24	0/1921	0.66	0/2628
3	CF	0.28	0/1921	0.74	0/2628
3	CG	0.32	0/1921	0.74	0/2628
3	CI	0.23	0/2062	0.68	0/2816
3	CJ	0.25	0/2062	0.67	1/2816 (0.0%)
3	CL	0.24	0/2062	0.69	0/2816
4	DA	0.27	0/2795	0.74	6/3763 (0.2%)
4	DB	0.25	0/2795	0.70	2/3763 (0.1%)
4	DC	0.26	0/2795	0.73	2/3763 (0.1%)
4	DD	0.23	0/2672	0.63	3/3600 (0.1%)
4	DE	0.24	0/2672	0.69	3/3600 (0.1%)
4	DF	0.25	0/2672	0.68	0/3600
5	EA	0.24	0/10890	0.64	2/14730 (0.0%)
5	EB	0.28	0/10890	0.66	4/14730 (0.0%)
5	EC	0.28	0/10886	0.67	7/14726 (0.0%)
6	FA	0.39	0/4286	0.77	2/5798 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	FB	0.34	0/4286	0.70	0/5798
6	FC	0.57	0/4286	0.89	1/5798 (0.0%)
6	FD	0.98	0/3323	1.16	4/4521 (0.1%)
6	FE	0.98	0/3329	1.12	3/4528 (0.1%)
6	FF	0.98	0/3245	1.11	2/4410 (0.0%)
7	GA	0.25	0/6456	0.59	10/8779 (0.1%)
7	GC	0.25	1/6087 (0.0%)	0.61	0/8272
7	GE	0.24	0/6087	0.62	0/8272
7	GG	0.24	0/6456	0.61	11/8779 (0.1%)
7	GI	0.24	0/6087	0.64	0/8272
7	GK	0.23	0/6456	0.58	9/8779 (0.1%)
8	GB	0.23	0/6087	0.61	3/8257 (0.0%)
8	GD	0.23	0/6087	0.61	1/8257 (0.0%)
8	GF	0.19	0/6301	0.52	2/8556 (0.0%)
8	GH	0.24	0/5913	0.66	5/8019 (0.1%)
8	GJ	0.21	0/6301	0.55	0/8556
8	GL	0.21	0/6301	0.59	3/8556 (0.0%)
9	HA	0.67	3/3439 (0.1%)	0.95	7/4668 (0.1%)
9	HB	0.66	1/3439 (0.0%)	0.93	9/4668 (0.2%)
9	HC	0.27	0/2345	0.73	7/3182 (0.2%)
9	HD	1.11	1/1094 (0.1%)	1.24	0/1486
10	IA	0.22	0/9289	0.59	6/12571 (0.0%)
10	IB	0.22	0/9289	0.61	6/12571 (0.0%)
10	IC	0.22	1/9289 (0.0%)	0.60	4/12571 (0.0%)
11	JA	0.25	0/12997	0.67	16/17611 (0.1%)
11	JB	0.23	0/12997	0.66	18/17611 (0.1%)
11	JC	0.24	0/12997	0.68	9/17611 (0.1%)
12	KA	0.29	0/3752	0.83	5/5093 (0.1%)
12	KB	0.29	0/3752	0.79	2/5093 (0.0%)
12	KC	0.39	0/3746	0.90	7/5086 (0.1%)
12	KE	0.18	0/3616	0.52	0/4901
12	KF	0.18	0/3616	0.49	0/4901
12	KG	0.20	0/3616	0.55	0/4901
13	LA	0.18	0/1524	0.51	1/2040 (0.0%)
13	LB	0.17	0/1536	0.51	0/2055
13	LC	0.18	0/1318	0.47	0/1763
13	LD	0.16	0/1310	0.51	0/1753
13	LE	0.24	0/1195	0.70	5/1598 (0.3%)
13	LF	0.22	0/1202	0.66	3/1606 (0.2%)
13	LG	0.21	0/464	0.53	0/623
13	LH	0.22	0/451	0.70	0/605
13	LI	0.38	0/1524	0.77	2/2040 (0.1%)
13	LJ	0.26	0/1536	0.74	3/2055 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
13	LK	0.15	0/1326	0.50	0/1774
13	LL	0.21	0/1310	0.58	1/1753 (0.1%)
13	LM	0.16	0/862	0.50	0/1151
13	LN	0.17	0/859	0.55	0/1148
13	LO	0.16	0/844	0.55	0/1127
13	LP	0.18	0/885	0.56	0/1183
14	MA	0.27	0/1144	0.80	2/1541 (0.1%)
14	MB	0.24	0/981	0.72	1/1315 (0.1%)
14	MC	0.17	0/601	0.51	0/807
14	MD	0.16	0/527	0.40	0/703
14	ME	0.30	0/1144	0.85	2/1541 (0.1%)
14	MF	0.27	0/981	0.83	1/1315 (0.1%)
14	MG	0.21	0/601	0.59	0/807
14	MH	0.17	0/527	0.52	0/703
14	MI	0.26	0/1144	0.78	0/1541
14	MJ	0.32	0/981	0.88	3/1315 (0.2%)
14	MK	0.18	0/601	0.51	0/807
14	ML	0.30	0/527	0.61	0/703
15	NA	0.27	0/7422	0.71	9/10053 (0.1%)
15	NB	0.24	0/7422	0.64	4/10053 (0.0%)
15	NC	0.28	0/7422	0.74	6/10053 (0.1%)
15	ND	0.27	0/7422	0.72	17/10053 (0.2%)
16	OA	0.24	0/3570	0.69	4/4821 (0.1%)
16	OB	0.24	0/3570	0.70	3/4821 (0.1%)
16	OC	0.25	0/3570	0.72	4/4821 (0.1%)
17	PA	0.26	0/831	0.74	2/1127 (0.2%)
17	PB	0.28	0/831	0.77	2/1127 (0.2%)
17	PC	0.25	0/831	0.69	0/1127
18	QA	0.22	0/1151	0.59	0/1548
18	QB	0.20	0/1151	0.52	0/1548
18	QC	0.21	0/1151	0.58	0/1548
18	QD	0.25	0/1151	0.59	0/1548
19	RA	0.28	0/1163	0.71	0/1573
19	RB	0.22	0/1163	0.63	0/1573
19	RC	0.24	0/1163	0.65	0/1573
19	RD	0.27	0/1163	0.86	7/1573 (0.4%)
20	SA	0.25	0/1146	0.65	0/1536
20	SB	0.19	0/1146	0.56	1/1536 (0.1%)
20	SC	0.23	0/1146	0.65	0/1536
20	SD	0.23	0/1146	0.64	0/1536
All	All	0.31	9/423302 (0.0%)	0.67	292/573059 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	3
1	AE	0	5
1	AI	0	3
1	AL	0	2
2	AB	0	3
2	AC	0	1
2	AK	0	1
3	BC	0	1
3	CB	0	1
3	CC	0	1
3	CF	0	2
3	CG	0	1
3	CL	0	1
4	DC	0	1
4	DD	0	1
5	EA	0	5
5	EB	0	6
5	EC	0	7
6	FA	0	8
6	FB	0	3
6	FC	0	13
6	FD	0	26
6	FE	0	22
6	FF	0	26
7	GA	0	6
7	GC	0	1
7	GE	0	1
7	GG	0	8
7	GI	0	1
7	GK	0	7
8	GB	0	4
8	GD	0	4
8	GF	0	1
8	GH	0	6
8	GJ	0	4
8	GL	0	4
9	HA	0	8
9	HB	0	7
9	HC	0	2
9	HD	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	IA	0	2
10	IB	0	1
10	IC	0	1
11	JA	0	10
11	JB	0	7
11	JC	0	10
12	KA	0	5
12	KB	0	4
12	KC	0	5
12	KE	0	1
12	KF	0	1
12	KG	0	2
13	LE	0	4
13	LF	0	1
13	LI	0	3
13	LJ	0	2
13	LO	0	1
14	MC	0	1
14	ME	0	3
14	MG	0	1
14	MI	0	2
14	MJ	0	2
14	MK	0	1
15	NA	0	5
15	NB	0	5
15	NC	0	10
15	ND	0	7
16	OA	0	3
16	OB	0	2
16	OC	0	1
17	PB	0	1
18	QB	0	1
18	QC	0	1
19	RA	0	1
19	RB	0	1
19	RD	0	4
20	SB	0	1
All	All	0	325

The worst 5 of 9 bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	415	HIS	C-O	8.28	1.33	1.24
9	HA	749	ASN	C-O	6.18	1.31	1.24
9	HB	749	ASN	C-O	6.12	1.31	1.24
9	HD	749	ASN	C-O	5.95	1.31	1.24
1	AA	714	PHE	CA-C	5.84	1.60	1.52

The worst 5 of 292 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	RD	141	LEU	CA-CB-CG	10.66	153.62	116.30
19	RD	141	LEU	CB-CA-C	9.90	130.13	110.42
7	GK	546	SER	N-CA-C	9.12	121.58	110.91
7	GA	543	LYS	N-CA-C	8.84	129.34	109.81
7	GG	543	LYS	N-CA-C	8.81	129.28	109.81

There are no chirality outliers.

5 of 325 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	136	PHE	Peptide
1	AA	715	LEU	Peptide
1	AA	897	PRO	Peptide
2	AB	207	GLU	Peptide
2	AB	295	PHE	Peptide

5.2 Too-close contacts [i](#)

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	6540	0	6548	95	0
1	AD	6810	0	6785	85	0
1	AE	6540	0	6548	107	0
1	AH	6810	0	6785	81	0
1	AI	6540	0	6548	91	0
1	AL	6810	0	6785	84	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AB	3821	0	3771	71	0
2	AC	3847	0	3808	65	0
2	AF	3821	0	3771	61	0
2	AG	3847	0	3808	61	0
2	AJ	3815	0	3760	43	0
2	AK	3847	0	3808	56	0
3	BA	2727	0	2744	42	0
3	BB	2727	0	2744	37	0
3	BC	2727	0	2744	33	0
3	CA	2712	0	2724	24	0
3	CB	2712	0	2724	29	0
3	CC	2712	0	2724	30	0
3	CE	1874	0	1903	32	0
3	CF	1874	0	1903	29	0
3	CG	1874	0	1903	33	0
3	CI	2012	0	2046	31	0
3	CJ	2012	0	2046	40	0
3	CL	2012	0	2046	32	0
4	DA	2753	0	2847	60	0
4	DB	2753	0	2847	57	0
4	DC	2753	0	2847	58	0
4	DD	2631	0	2743	40	0
4	DE	2631	0	2743	45	0
4	DF	2631	0	2743	39	0
5	EA	10670	0	10838	157	0
5	EB	10670	0	10838	169	0
5	EC	10666	0	10827	146	0
6	FA	4210	0	4162	97	0
6	FB	4210	0	4162	72	0
6	FC	4210	0	4162	136	0
6	FD	3255	0	3343	295	0
6	FE	3261	0	3354	271	0
6	FF	3182	0	3272	236	0
7	GA	6320	0	6301	101	0
7	GC	5960	0	5962	130	0
7	GE	5960	0	5962	113	0
7	GG	6320	0	6301	102	0
7	GI	5960	0	5962	123	0
7	GK	6320	0	6301	78	0
8	GB	5949	0	5884	85	0
8	GD	5949	0	5884	84	0
8	GF	6155	0	6082	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	GH	5781	0	5723	114	0
8	GJ	6155	0	6081	68	0
8	GL	6155	0	6082	97	0
9	HA	3361	0	3225	143	0
9	HB	3361	0	3225	153	0
9	HC	2288	0	2172	45	0
9	HD	1073	0	1053	59	0
10	IA	9113	0	9248	120	0
10	IB	9113	0	9248	139	0
10	IC	9113	0	9248	134	0
11	JA	12718	0	12853	190	0
11	JB	12718	0	12853	168	0
11	JC	12718	0	12853	201	0
12	KA	3674	0	3771	97	0
12	KB	3674	0	3771	73	0
12	KC	3668	0	3760	101	0
12	KE	3544	0	3640	55	0
12	KF	3544	0	3640	53	0
12	KG	3544	0	3640	41	0
13	LA	1516	0	1551	30	0
13	LB	1529	0	1573	18	0
13	LC	1312	0	1352	6	0
13	LD	1304	0	1350	9	0
13	LE	1190	0	1235	34	0
13	LF	1198	0	1247	19	0
13	LG	461	0	486	2	0
13	LH	448	0	475	8	0
13	LI	1516	0	1551	35	0
13	LJ	1529	0	1573	43	0
13	LK	1320	0	1363	16	0
13	LL	1304	0	1350	18	0
13	LM	859	0	877	10	0
13	LN	856	0	875	10	0
13	LO	841	0	850	11	0
13	LP	882	0	901	10	0
14	MA	1132	0	1134	24	0
14	MB	976	0	982	15	0
14	MC	594	0	593	6	0
14	MD	521	0	517	7	0
14	ME	1132	0	1134	27	0
14	MF	976	0	982	23	0
14	MG	594	0	593	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	MH	521	0	517	4	0
14	MI	1132	0	1135	22	0
14	MJ	976	0	983	28	0
14	MK	594	0	593	5	0
14	ML	521	0	517	7	0
15	NA	7263	0	7230	177	0
15	NB	7263	0	7230	161	0
15	NC	7263	0	7230	190	0
15	ND	7263	0	7230	155	0
16	OA	3510	0	3532	55	0
16	OB	3510	0	3532	59	0
16	OC	3510	0	3532	50	0
17	PA	807	0	769	23	0
17	PB	807	0	769	18	0
17	PC	807	0	769	21	0
18	QA	1129	0	1127	12	0
18	QB	1129	0	1127	18	0
18	QC	1129	0	1127	16	0
18	QD	1129	0	1127	19	0
19	RA	1143	0	1133	33	0
19	RB	1143	0	1133	16	0
19	RC	1143	0	1133	19	0
19	RD	1143	0	1133	27	0
20	SA	1134	0	1074	12	0
20	SB	1134	0	1074	14	0
20	SC	1134	0	1074	12	0
20	SD	1134	0	1074	11	0
All	All	415078	0	416877	6651	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 8.

The worst 5 of 6651 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)
6:FD:1002:ALA:HB3	6:FD:1010:ARG:NH1	1.37	1.36
6:FD:803:ARG:CG	6:FD:1118:GLN:HG3	1.76	1.14
6:FD:1002:ALA:CB	6:FD:1010:ARG:HH11	1.60	1.14
9:HB:776:PRO:HA	13:LE:521:ASN:HD21	1.09	1.13
6:FD:803:ARG:HG2	6:FD:1118:GLN:HE21	1.10	1.11

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	817/1073 (76%)	730 (89%)	81 (10%)	6 (1%)	18	52
1	AD	851/1073 (79%)	782 (92%)	64 (8%)	5 (1%)	21	55
1	AE	817/1073 (76%)	731 (90%)	82 (10%)	4 (0%)	24	58
1	AH	851/1073 (79%)	781 (92%)	65 (8%)	5 (1%)	21	55
1	AI	817/1073 (76%)	725 (89%)	88 (11%)	4 (0%)	24	58
1	AL	851/1073 (79%)	779 (92%)	65 (8%)	7 (1%)	16	50
2	AB	465/603 (77%)	406 (87%)	53 (11%)	6 (1%)	9	40
2	AC	471/603 (78%)	439 (93%)	30 (6%)	2 (0%)	30	61
2	AF	465/603 (77%)	411 (88%)	50 (11%)	4 (1%)	14	47
2	AG	471/603 (78%)	427 (91%)	43 (9%)	1 (0%)	43	73
2	AJ	465/603 (77%)	417 (90%)	46 (10%)	2 (0%)	30	61
2	AK	471/603 (78%)	427 (91%)	42 (9%)	2 (0%)	30	61
3	BA	344/5051 (7%)	313 (91%)	30 (9%)	1 (0%)	36	66
3	BB	344/5051 (7%)	308 (90%)	35 (10%)	1 (0%)	36	66
3	BC	344/5051 (7%)	312 (91%)	31 (9%)	1 (0%)	36	66
3	CA	342/5051 (7%)	313 (92%)	29 (8%)	0	100	100
3	CB	342/5051 (7%)	312 (91%)	29 (8%)	1 (0%)	36	66
3	CC	342/5051 (7%)	306 (90%)	35 (10%)	1 (0%)	36	66
3	CE	238/5051 (5%)	195 (82%)	42 (18%)	1 (0%)	30	61
3	CF	238/5051 (5%)	188 (79%)	48 (20%)	2 (1%)	16	50
3	CG	238/5051 (5%)	190 (80%)	43 (18%)	5 (2%)	5	31
3	CI	255/5051 (5%)	228 (89%)	24 (9%)	3 (1%)	10	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CJ	255/5051 (5%)	224 (88%)	28 (11%)	3 (1%)	10	42
3	CL	255/5051 (5%)	222 (87%)	30 (12%)	3 (1%)	10	42
4	DA	343/505 (68%)	317 (92%)	21 (6%)	5 (2%)	8	37
4	DB	343/505 (68%)	322 (94%)	16 (5%)	5 (2%)	8	37
4	DC	343/505 (68%)	318 (93%)	22 (6%)	3 (1%)	14	47
4	DD	328/505 (65%)	317 (97%)	11 (3%)	0	100	100
4	DE	328/505 (65%)	316 (96%)	12 (4%)	0	100	100
4	DF	328/505 (65%)	316 (96%)	11 (3%)	1 (0%)	36	66
5	EA	1333/4956 (27%)	1186 (89%)	130 (10%)	17 (1%)	9	40
5	EB	1333/4956 (27%)	1175 (88%)	142 (11%)	16 (1%)	10	42
5	EC	1333/4956 (27%)	1168 (88%)	151 (11%)	14 (1%)	11	44
6	FA	529/2777 (19%)	484 (92%)	42 (8%)	3 (1%)	21	55
6	FB	529/2777 (19%)	477 (90%)	50 (10%)	2 (0%)	30	61
6	FC	529/2777 (19%)	472 (89%)	53 (10%)	4 (1%)	16	50
6	FD	409/2777 (15%)	236 (58%)	112 (27%)	61 (15%)	0	2
6	FE	409/2777 (15%)	214 (52%)	133 (32%)	62 (15%)	0	2
6	FF	397/2777 (14%)	215 (54%)	137 (34%)	45 (11%)	0	4
7	GA	835/1019 (82%)	784 (94%)	47 (6%)	4 (0%)	24	58
7	GC	775/1019 (76%)	712 (92%)	59 (8%)	4 (0%)	24	58
7	GE	775/1019 (76%)	702 (91%)	67 (9%)	6 (1%)	16	50
7	GG	835/1019 (82%)	781 (94%)	52 (6%)	2 (0%)	43	73
7	GI	775/1019 (76%)	706 (91%)	65 (8%)	4 (0%)	24	58
7	GK	835/1019 (82%)	781 (94%)	52 (6%)	2 (0%)	43	73
8	GB	752/791 (95%)	667 (89%)	80 (11%)	5 (1%)	18	52
8	GD	752/791 (95%)	661 (88%)	87 (12%)	4 (0%)	24	58
8	GF	789/791 (100%)	746 (95%)	43 (5%)	0	100	100
8	GH	728/791 (92%)	650 (89%)	75 (10%)	3 (0%)	30	61
8	GJ	789/791 (100%)	744 (94%)	45 (6%)	0	100	100
8	GL	789/791 (100%)	743 (94%)	44 (6%)	2 (0%)	36	66
9	HA	424/1192 (36%)	359 (85%)	56 (13%)	9 (2%)	5	31
9	HB	424/1192 (36%)	360 (85%)	54 (13%)	10 (2%)	4	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	HC	290/1192 (24%)	242 (83%)	43 (15%)	5 (2%)	7	35
9	HD	134/1192 (11%)	114 (85%)	15 (11%)	5 (4%)	2	21
10	IA	1146/1599 (72%)	1045 (91%)	94 (8%)	7 (1%)	21	55
10	IB	1146/1599 (72%)	1046 (91%)	93 (8%)	7 (1%)	21	55
10	IC	1146/1599 (72%)	1054 (92%)	84 (7%)	8 (1%)	18	52
11	JA	1573/2316 (68%)	1374 (87%)	182 (12%)	17 (1%)	11	44
11	JB	1573/2316 (68%)	1357 (86%)	199 (13%)	17 (1%)	11	44
11	JC	1573/2316 (68%)	1368 (87%)	191 (12%)	14 (1%)	14	47
12	KA	458/728 (63%)	355 (78%)	92 (20%)	11 (2%)	4	29
12	KB	458/728 (63%)	365 (80%)	84 (18%)	9 (2%)	6	32
12	KC	458/728 (63%)	334 (73%)	101 (22%)	23 (5%)	1	15
12	KE	437/728 (60%)	408 (93%)	27 (6%)	2 (0%)	24	58
12	KF	437/728 (60%)	408 (93%)	28 (6%)	1 (0%)	43	73
12	KG	437/728 (60%)	409 (94%)	27 (6%)	1 (0%)	43	73
13	LA	186/1322 (14%)	184 (99%)	2 (1%)	0	100	100
13	LB	187/1322 (14%)	184 (98%)	2 (1%)	1 (0%)	24	58
13	LC	158/1322 (12%)	158 (100%)	0	0	100	100
13	LD	157/1322 (12%)	155 (99%)	2 (1%)	0	100	100
13	LE	145/1322 (11%)	138 (95%)	5 (3%)	2 (1%)	9	38
13	LF	146/1322 (11%)	137 (94%)	7 (5%)	2 (1%)	9	38
13	LG	55/1322 (4%)	54 (98%)	1 (2%)	0	100	100
13	LH	53/1322 (4%)	52 (98%)	1 (2%)	0	100	100
13	LI	186/1322 (14%)	176 (95%)	7 (4%)	3 (2%)	7	36
13	LJ	187/1322 (14%)	179 (96%)	6 (3%)	2 (1%)	11	44
13	LK	159/1322 (12%)	156 (98%)	3 (2%)	0	100	100
13	LL	157/1322 (12%)	156 (99%)	1 (1%)	0	100	100
13	LM	104/1322 (8%)	104 (100%)	0	0	100	100
13	LN	104/1322 (8%)	104 (100%)	0	0	100	100
13	LO	103/1322 (8%)	102 (99%)	1 (1%)	0	100	100
13	LP	108/1322 (8%)	106 (98%)	2 (2%)	0	100	100
14	MA	140/2736 (5%)	128 (91%)	11 (8%)	1 (1%)	18	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	MB	116/2736 (4%)	109 (94%)	6 (5%)	1 (1%)	14	47
14	MC	71/2736 (3%)	65 (92%)	6 (8%)	0	100	100
14	MD	63/2736 (2%)	63 (100%)	0	0	100	100
14	ME	140/2736 (5%)	125 (89%)	13 (9%)	2 (1%)	9	38
14	MF	116/2736 (4%)	112 (97%)	4 (3%)	0	100	100
14	MG	71/2736 (3%)	65 (92%)	5 (7%)	1 (1%)	9	38
14	MH	63/2736 (2%)	60 (95%)	3 (5%)	0	100	100
14	MI	140/2736 (5%)	126 (90%)	13 (9%)	1 (1%)	18	52
14	MJ	116/2736 (4%)	108 (93%)	6 (5%)	2 (2%)	7	35
14	MK	71/2736 (3%)	66 (93%)	5 (7%)	0	100	100
14	ML	63/2736 (2%)	63 (100%)	0	0	100	100
15	NA	879/2484 (35%)	763 (87%)	107 (12%)	9 (1%)	12	45
15	NB	879/2484 (35%)	757 (86%)	107 (12%)	15 (2%)	7	35
15	NC	879/2484 (35%)	758 (86%)	110 (12%)	11 (1%)	9	40
15	ND	879/2484 (35%)	757 (86%)	111 (13%)	11 (1%)	9	40
16	OA	432/2333 (18%)	369 (85%)	51 (12%)	12 (3%)	4	25
16	OB	432/2333 (18%)	373 (86%)	45 (10%)	14 (3%)	3	24
16	OC	432/2333 (18%)	373 (86%)	46 (11%)	13 (3%)	3	25
17	PA	97/1822 (5%)	77 (79%)	19 (20%)	1 (1%)	12	45
17	PB	97/1822 (5%)	75 (77%)	20 (21%)	2 (2%)	5	31
17	PC	97/1822 (5%)	81 (84%)	15 (16%)	1 (1%)	12	45
18	QA	139/172 (81%)	136 (98%)	3 (2%)	0	100	100
18	QB	139/172 (81%)	137 (99%)	2 (1%)	0	100	100
18	QC	139/172 (81%)	135 (97%)	4 (3%)	0	100	100
18	QD	139/172 (81%)	135 (97%)	4 (3%)	0	100	100
19	RA	144/179 (80%)	135 (94%)	9 (6%)	0	100	100
19	RB	144/179 (80%)	130 (90%)	14 (10%)	0	100	100
19	RC	144/179 (80%)	135 (94%)	9 (6%)	0	100	100
19	RD	144/179 (80%)	136 (94%)	8 (6%)	0	100	100
20	SA	142/149 (95%)	133 (94%)	9 (6%)	0	100	100
20	SB	142/149 (95%)	137 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	SC	142/149 (95%)	138 (97%)	4 (3%)	0	100	100
20	SD	142/149 (95%)	138 (97%)	4 (3%)	0	100	100
All	All	51874/215354 (24%)	46217 (89%)	5060 (10%)	597 (1%)	13	42

5 of 597 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AA	174	CYS
1	AD	136	PHE
1	AD	460	VAL
1	AD	588	ILE
1	AE	137	GLU

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	718/908 (79%)	718 (100%)	0	100	100
1	AD	740/908 (82%)	739 (100%)	1 (0%)	88	87
1	AE	718/908 (79%)	718 (100%)	0	100	100
1	AH	740/908 (82%)	740 (100%)	0	100	100
1	AI	718/908 (79%)	717 (100%)	1 (0%)	88	87
1	AL	740/908 (82%)	736 (100%)	4 (0%)	81	81
2	AB	415/516 (80%)	410 (99%)	5 (1%)	63	73
2	AC	418/516 (81%)	418 (100%)	0	100	100
2	AF	415/516 (80%)	415 (100%)	0	100	100
2	AG	418/516 (81%)	418 (100%)	0	100	100
2	AJ	414/516 (80%)	414 (100%)	0	100	100
2	AK	418/516 (81%)	415 (99%)	3 (1%)	76	78
3	BA	286/4189 (7%)	286 (100%)	0	100	100
3	BB	286/4189 (7%)	286 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	BC	286/4189 (7%)	286 (100%)	0	100	100
3	CA	284/4189 (7%)	284 (100%)	0	100	100
3	CB	284/4189 (7%)	283 (100%)	1 (0%)	84	81
3	CC	284/4189 (7%)	283 (100%)	1 (0%)	84	81
3	CE	206/4189 (5%)	206 (100%)	0	100	100
3	CF	206/4189 (5%)	206 (100%)	0	100	100
3	CG	206/4189 (5%)	206 (100%)	0	100	100
3	CI	221/4189 (5%)	221 (100%)	0	100	100
3	CJ	221/4189 (5%)	221 (100%)	0	100	100
3	CL	221/4189 (5%)	221 (100%)	0	100	100
4	DA	297/435 (68%)	297 (100%)	0	100	100
4	DB	297/435 (68%)	297 (100%)	0	100	100
4	DC	297/435 (68%)	297 (100%)	0	100	100
4	DD	285/435 (66%)	285 (100%)	0	100	100
4	DE	285/435 (66%)	285 (100%)	0	100	100
4	DF	285/435 (66%)	285 (100%)	0	100	100
5	EA	1150/4160 (28%)	1147 (100%)	3 (0%)	86	83
5	EB	1150/4160 (28%)	1135 (99%)	15 (1%)	61	72
5	EC	1149/4160 (28%)	1135 (99%)	14 (1%)	63	73
6	FA	453/2343 (19%)	435 (96%)	18 (4%)	28	53
6	FB	453/2343 (19%)	436 (96%)	17 (4%)	29	56
6	FC	453/2343 (19%)	391 (86%)	62 (14%)	3	20
6	FD	356/2343 (15%)	189 (53%)	167 (47%)	0	0
6	FE	357/2343 (15%)	192 (54%)	165 (46%)	0	0
6	FF	348/2343 (15%)	184 (53%)	164 (47%)	0	0
7	GA	680/807 (84%)	680 (100%)	0	100	100
7	GC	647/807 (80%)	647 (100%)	0	100	100
7	GE	647/807 (80%)	647 (100%)	0	100	100
7	GG	680/807 (84%)	680 (100%)	0	100	100
7	GI	647/807 (80%)	647 (100%)	0	100	100
7	GK	680/807 (84%)	680 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	GB	647/665 (97%)	646 (100%)	1 (0%)	87	85
8	GD	647/665 (97%)	645 (100%)	2 (0%)	86	83
8	GF	665/665 (100%)	665 (100%)	0	100	100
8	GH	629/665 (95%)	628 (100%)	1 (0%)	87	85
8	GJ	665/665 (100%)	665 (100%)	0	100	100
8	GL	665/665 (100%)	664 (100%)	1 (0%)	87	85
9	HA	353/1003 (35%)	306 (87%)	47 (13%)	4	21
9	HB	353/1003 (35%)	309 (88%)	44 (12%)	4	22
9	HC	234/1003 (23%)	234 (100%)	0	100	100
9	HD	119/1003 (12%)	77 (65%)	42 (35%)	0	1
10	IA	978/1309 (75%)	978 (100%)	0	100	100
10	IB	978/1309 (75%)	977 (100%)	1 (0%)	88	87
10	IC	978/1309 (75%)	978 (100%)	0	100	100
11	JA	1388/1993 (70%)	1388 (100%)	0	100	100
11	JB	1388/1993 (70%)	1387 (100%)	1 (0%)	88	87
11	JC	1388/1993 (70%)	1388 (100%)	0	100	100
12	KA	401/626 (64%)	401 (100%)	0	100	100
12	KB	401/626 (64%)	401 (100%)	0	100	100
12	KC	400/626 (64%)	388 (97%)	12 (3%)	36	60
12	KE	385/626 (62%)	385 (100%)	0	100	100
12	KF	385/626 (62%)	385 (100%)	0	100	100
12	KG	385/626 (62%)	385 (100%)	0	100	100
13	LA	165/1137 (14%)	164 (99%)	1 (1%)	78	80
13	LB	167/1137 (15%)	167 (100%)	0	100	100
13	LC	146/1137 (13%)	146 (100%)	0	100	100
13	LD	146/1137 (13%)	146 (100%)	0	100	100
13	LE	132/1137 (12%)	132 (100%)	0	100	100
13	LF	134/1137 (12%)	134 (100%)	0	100	100
13	LG	54/1137 (5%)	54 (100%)	0	100	100
13	LH	53/1137 (5%)	53 (100%)	0	100	100
13	LI	165/1137 (14%)	161 (98%)	4 (2%)	43	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	LJ	167/1137 (15%)	167 (100%)	0	100	100
13	LK	147/1137 (13%)	147 (100%)	0	100	100
13	LL	146/1137 (13%)	146 (100%)	0	100	100
13	LM	93/1137 (8%)	93 (100%)	0	100	100
13	LN	93/1137 (8%)	93 (100%)	0	100	100
13	LO	90/1137 (8%)	90 (100%)	0	100	100
13	LP	95/1137 (8%)	95 (100%)	0	100	100
14	MA	123/2310 (5%)	123 (100%)	0	100	100
14	MB	107/2310 (5%)	107 (100%)	0	100	100
14	MC	63/2310 (3%)	63 (100%)	0	100	100
14	MD	51/2310 (2%)	51 (100%)	0	100	100
14	ME	123/2310 (5%)	123 (100%)	0	100	100
14	MF	107/2310 (5%)	107 (100%)	0	100	100
14	MG	63/2310 (3%)	63 (100%)	0	100	100
14	MH	51/2310 (2%)	51 (100%)	0	100	100
14	MI	123/2310 (5%)	123 (100%)	0	100	100
14	MJ	107/2310 (5%)	107 (100%)	0	100	100
14	MK	63/2310 (3%)	63 (100%)	0	100	100
14	ML	51/2310 (2%)	51 (100%)	0	100	100
15	NA	785/2093 (38%)	785 (100%)	0	100	100
15	NB	785/2093 (38%)	785 (100%)	0	100	100
15	NC	785/2093 (38%)	785 (100%)	0	100	100
15	ND	785/2093 (38%)	785 (100%)	0	100	100
16	OA	370/1912 (19%)	370 (100%)	0	100	100
16	OB	370/1912 (19%)	370 (100%)	0	100	100
16	OC	370/1912 (19%)	370 (100%)	0	100	100
17	PA	88/1558 (6%)	88 (100%)	0	100	100
17	PB	88/1558 (6%)	88 (100%)	0	100	100
17	PC	88/1558 (6%)	88 (100%)	0	100	100
18	QA	120/150 (80%)	120 (100%)	0	100	100
18	QB	120/150 (80%)	120 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	QC	120/150 (80%)	120 (100%)	0	100	100
18	QD	120/150 (80%)	120 (100%)	0	100	100
19	RA	123/139 (88%)	123 (100%)	0	100	100
19	RB	123/139 (88%)	123 (100%)	0	100	100
19	RC	123/139 (88%)	123 (100%)	0	100	100
19	RD	123/139 (88%)	122 (99%)	1 (1%)	73	77
20	SA	123/127 (97%)	123 (100%)	0	100	100
20	SB	123/127 (97%)	123 (100%)	0	100	100
20	SC	123/127 (97%)	123 (100%)	0	100	100
20	SD	123/127 (97%)	123 (100%)	0	100	100
All	All	44894/180824 (25%)	44095 (98%)	799 (2%)	51	69

5 of 799 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	FE	1417	ILE
6	FF	1190	ARG
6	FE	1444	ARG
6	FE	1416	GLN
6	FF	924	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 520 such sidechains are listed below:

Mol	Chain	Res	Type
14	MJ	316	GLN
15	NB	1188	HIS
14	MJ	246	ASN
6	FE	811	ASN
6	FD	907	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

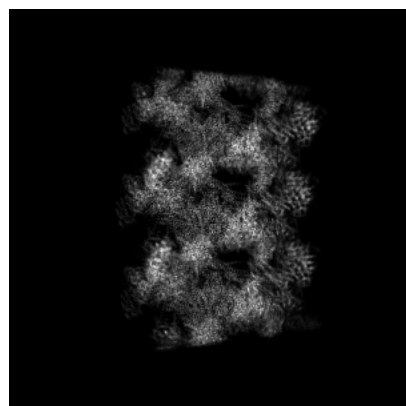
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72716. These allow visual inspection of the internal detail of the map and identification of artifacts.

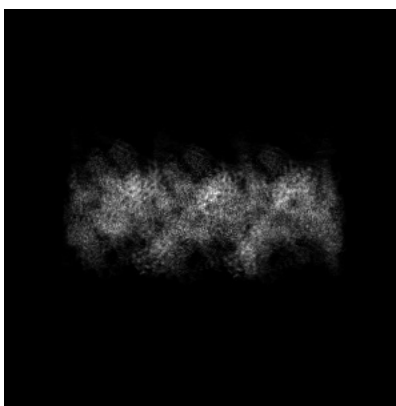
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

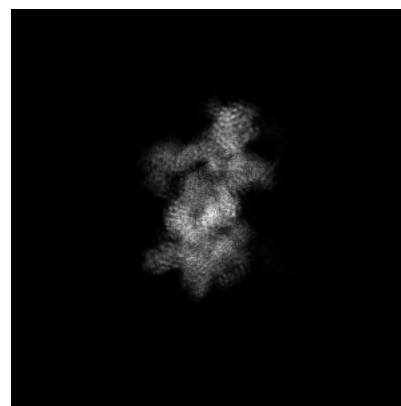
6.1.1 Primary map



X

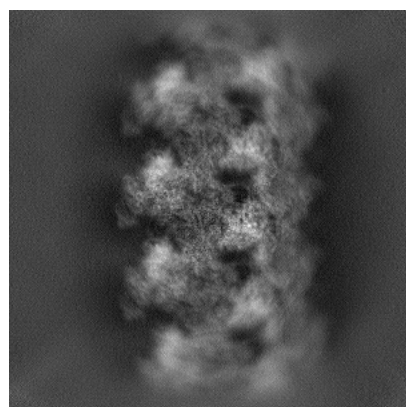


Y

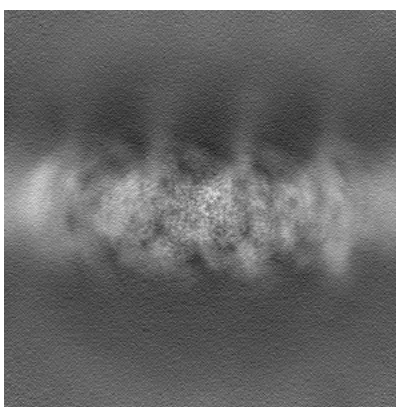


Z

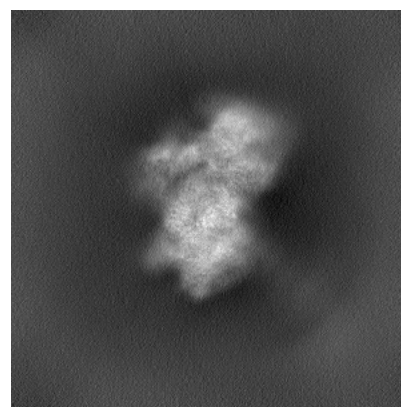
6.1.2 Raw map



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: 256

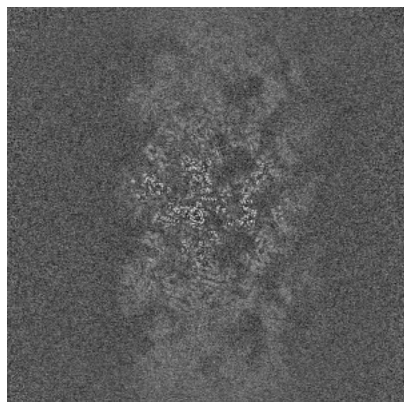


Y Index: 256

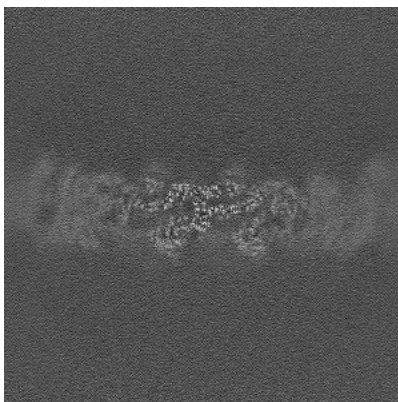


Z Index: 256

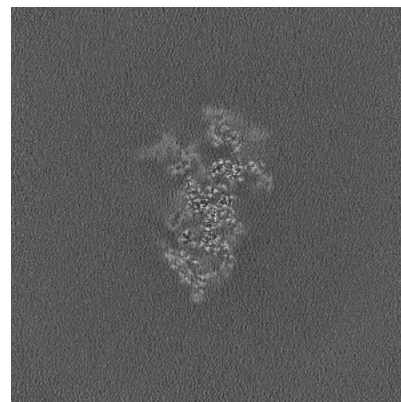
6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

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

6.3 Largest variance slices [i](#)

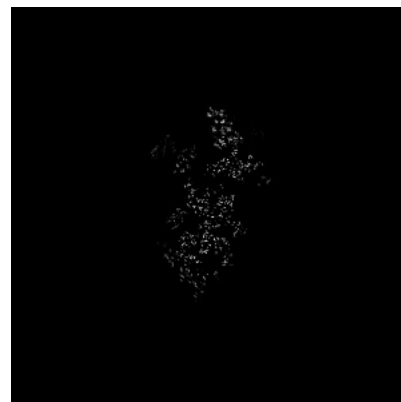
6.3.1 Primary map



X Index: 279

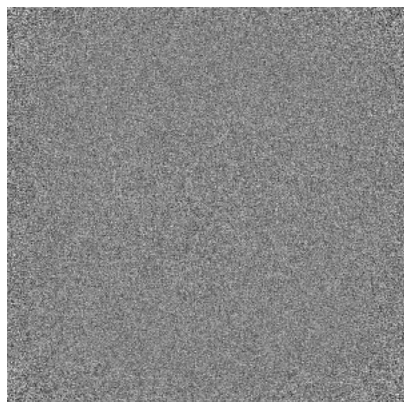


Y Index: 249

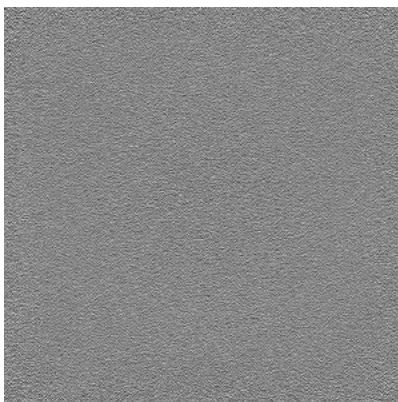


Z Index: 258

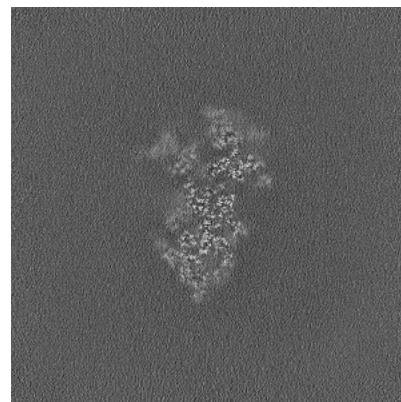
6.3.2 Raw map



X Index: 0



Y Index: 0

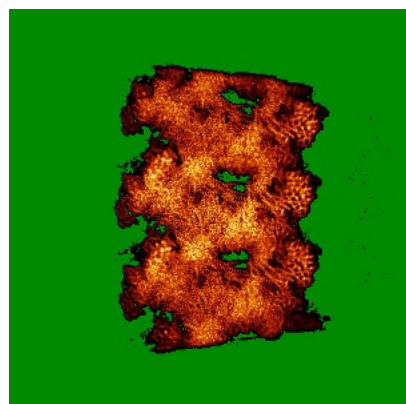


Z Index: 258

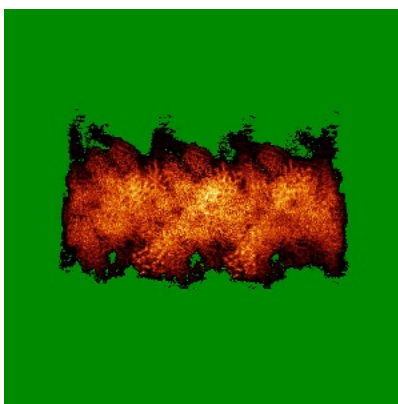
The images above show the largest variance slices of the map in three orthogonal directions.

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

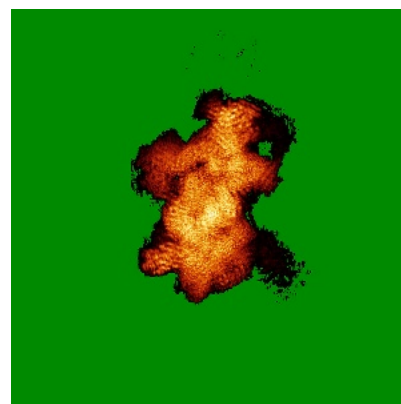
6.4.1 Primary map



X

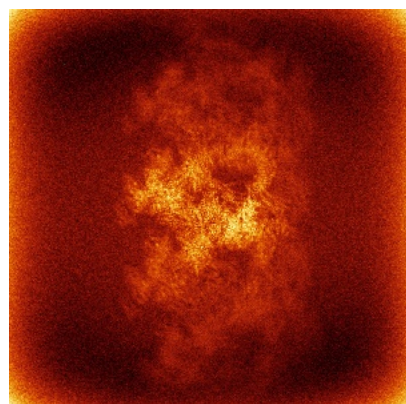


Y

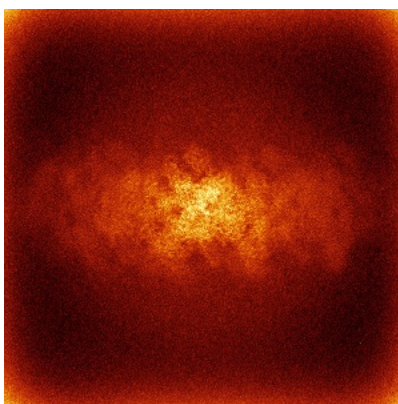


Z

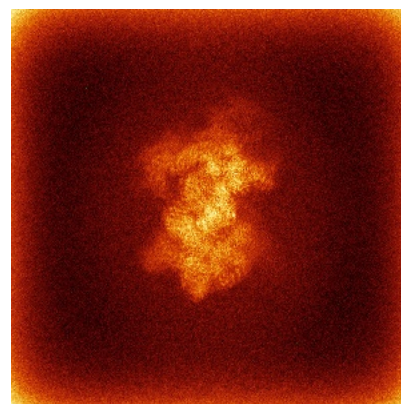
6.4.2 Raw map



X



Y

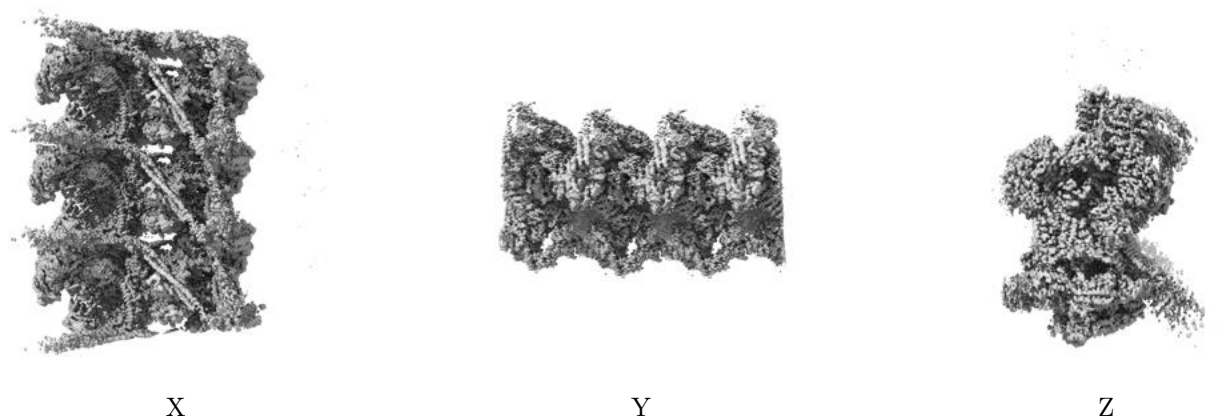


Z

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.

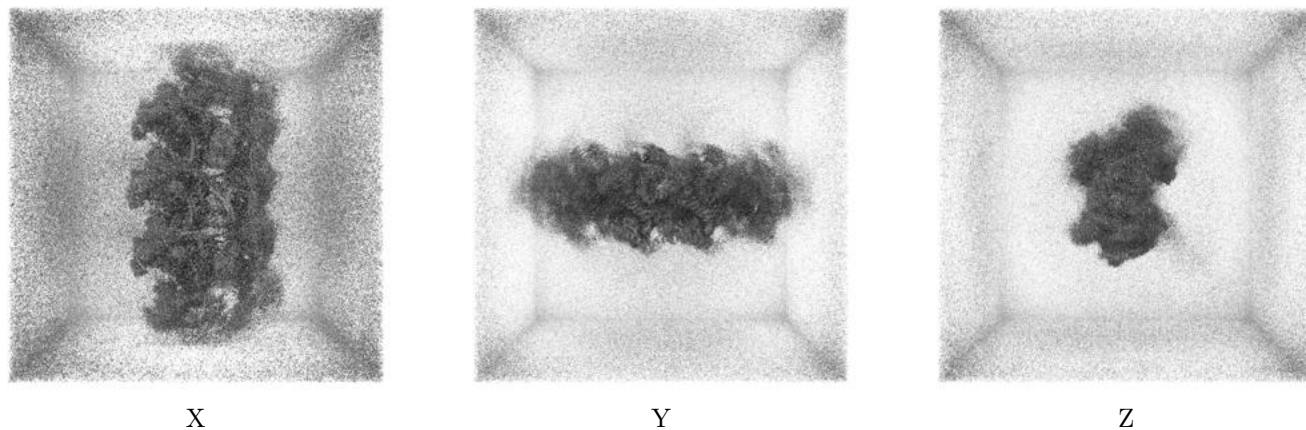
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

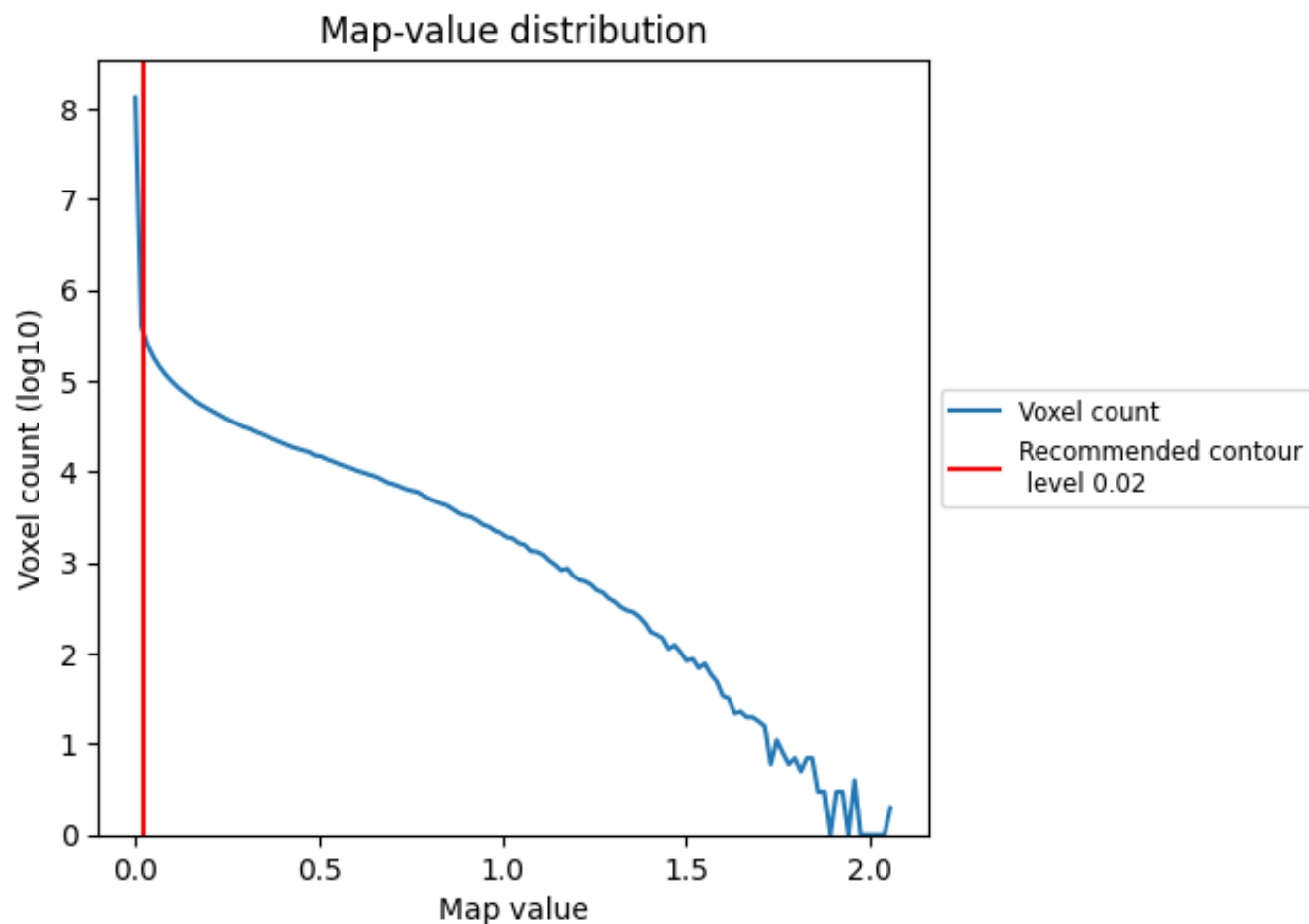
6.6 Mask visualisation [i](#)

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

7 Map analysis ⓘ

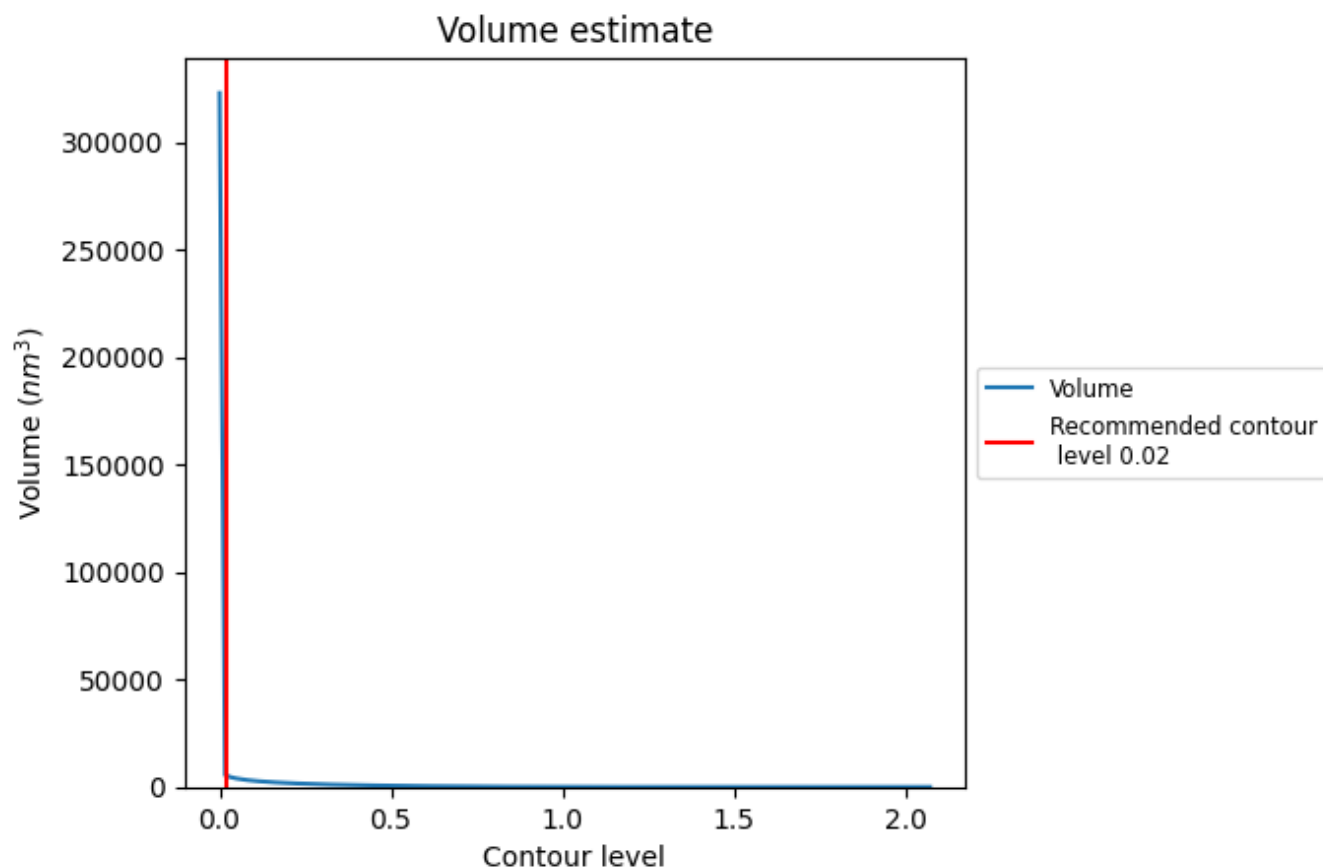
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

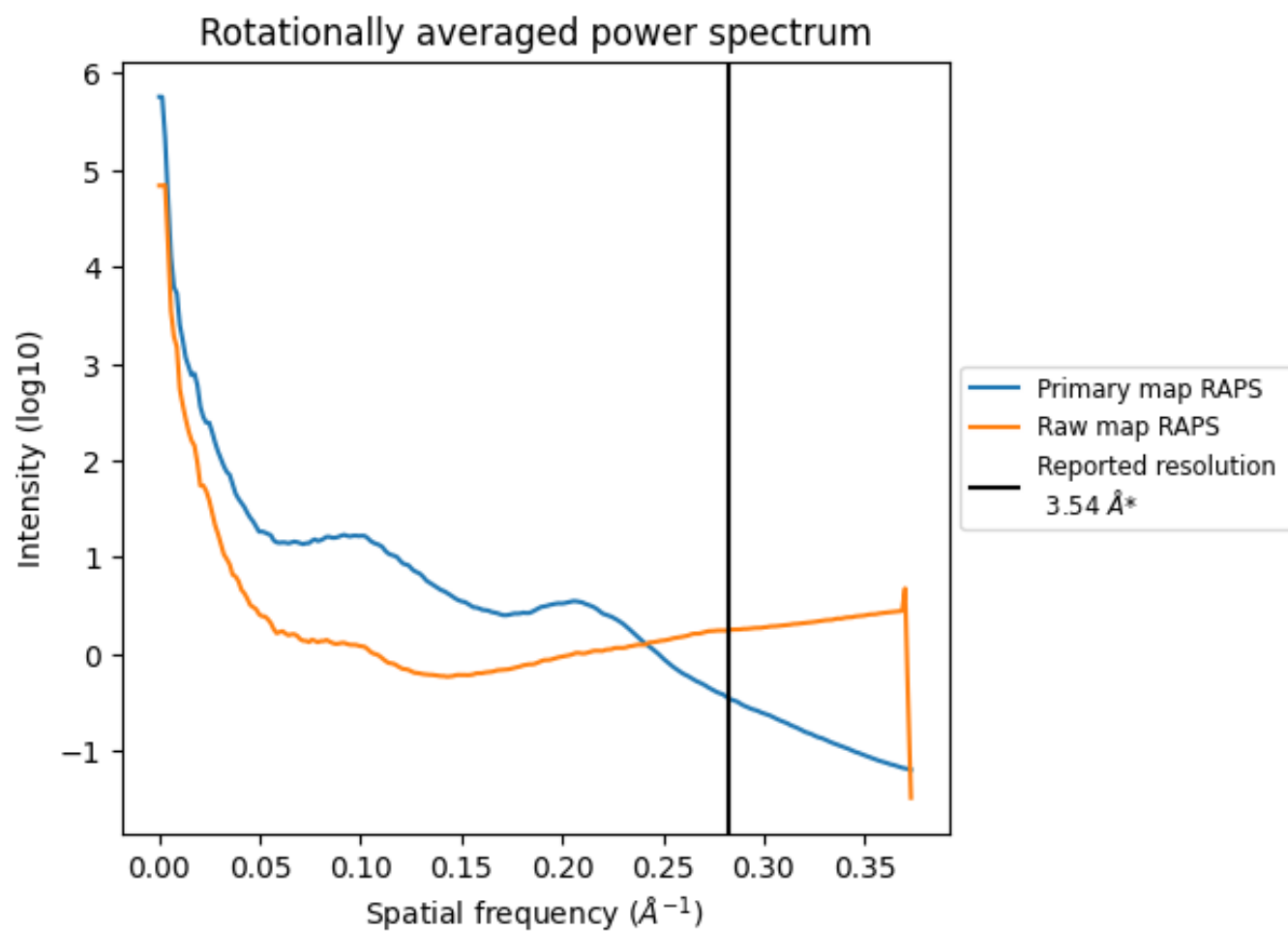
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5300 nm^3 ; this corresponds to an approximate mass of 4787 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

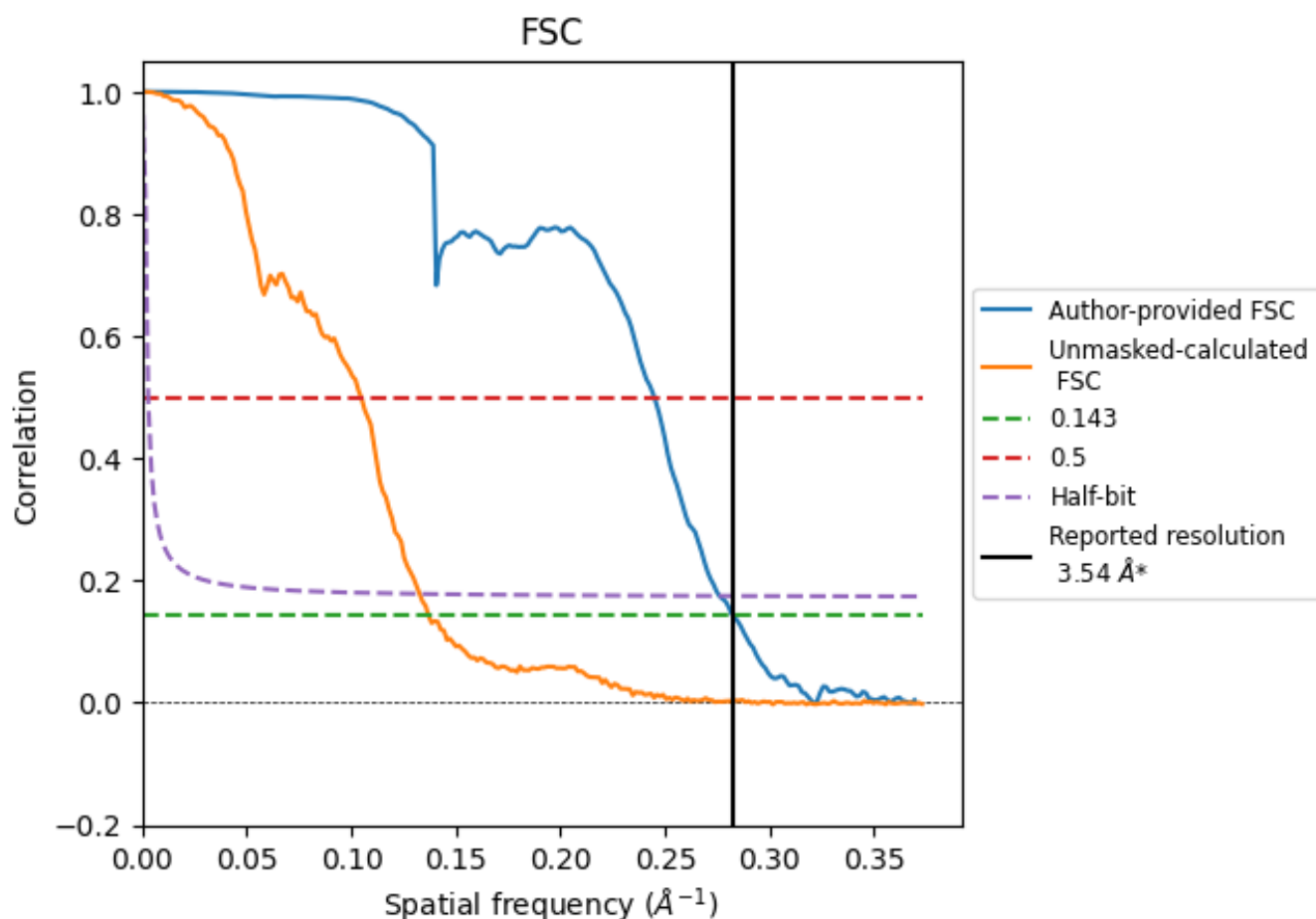


*Reported resolution corresponds to spatial frequency of 0.282 $\text{\AA}^{-1}$

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 0.282 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

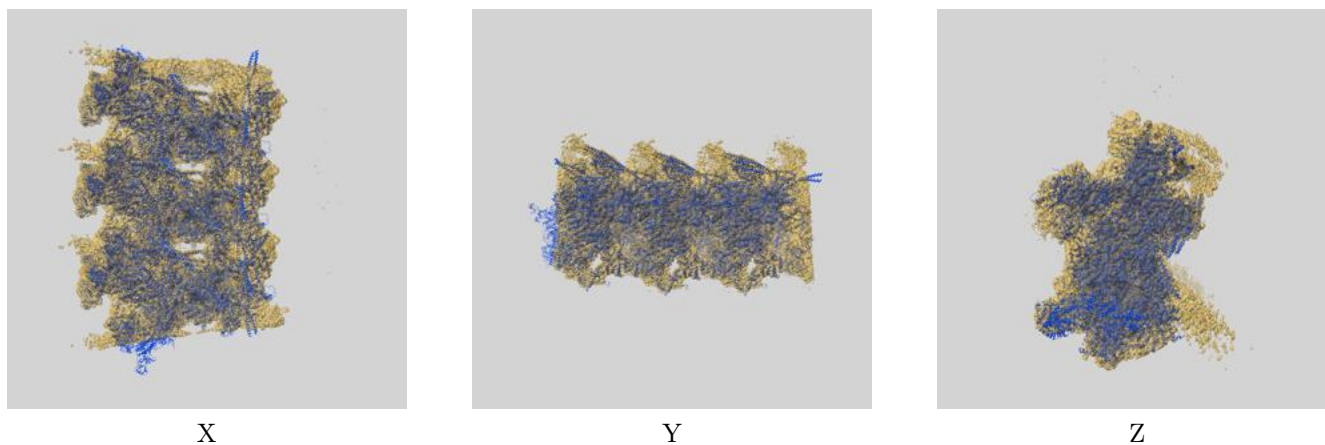
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	3.54	4.08	3.62
Unmasked-calculated*	7.30	9.55	7.53

*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 7.30 differs from the reported value 3.54 by more than 10 %

9 Map-model fit [i](#)

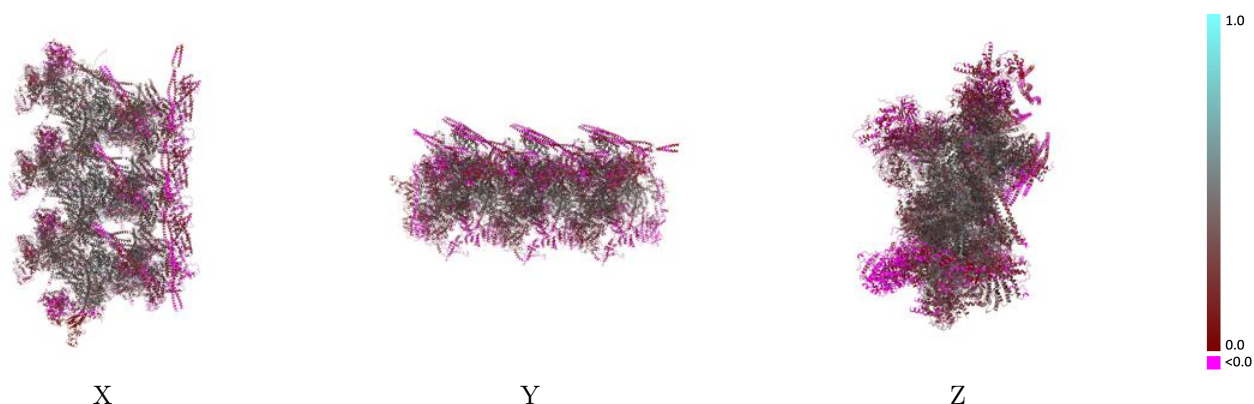
This section contains information regarding the fit between EMDB map EMD-72716 and PDB model 9YA0. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



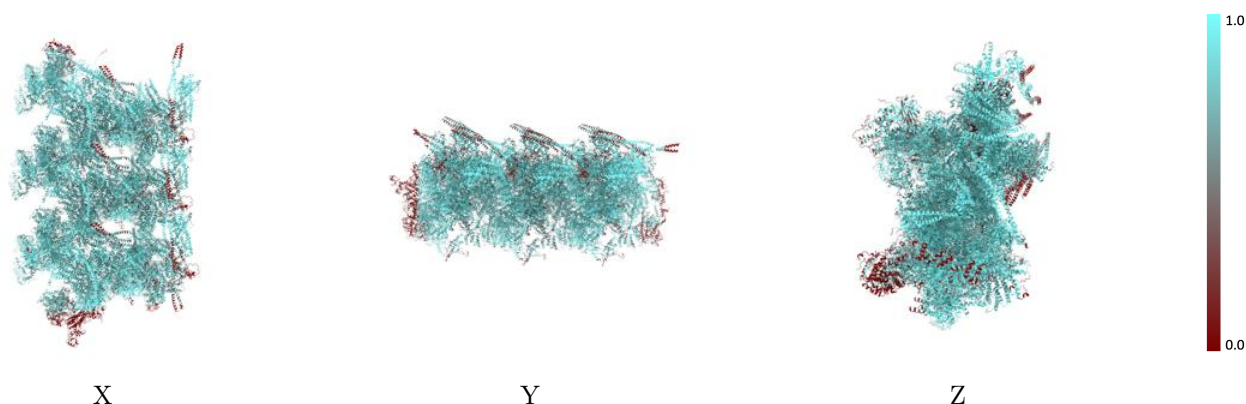
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



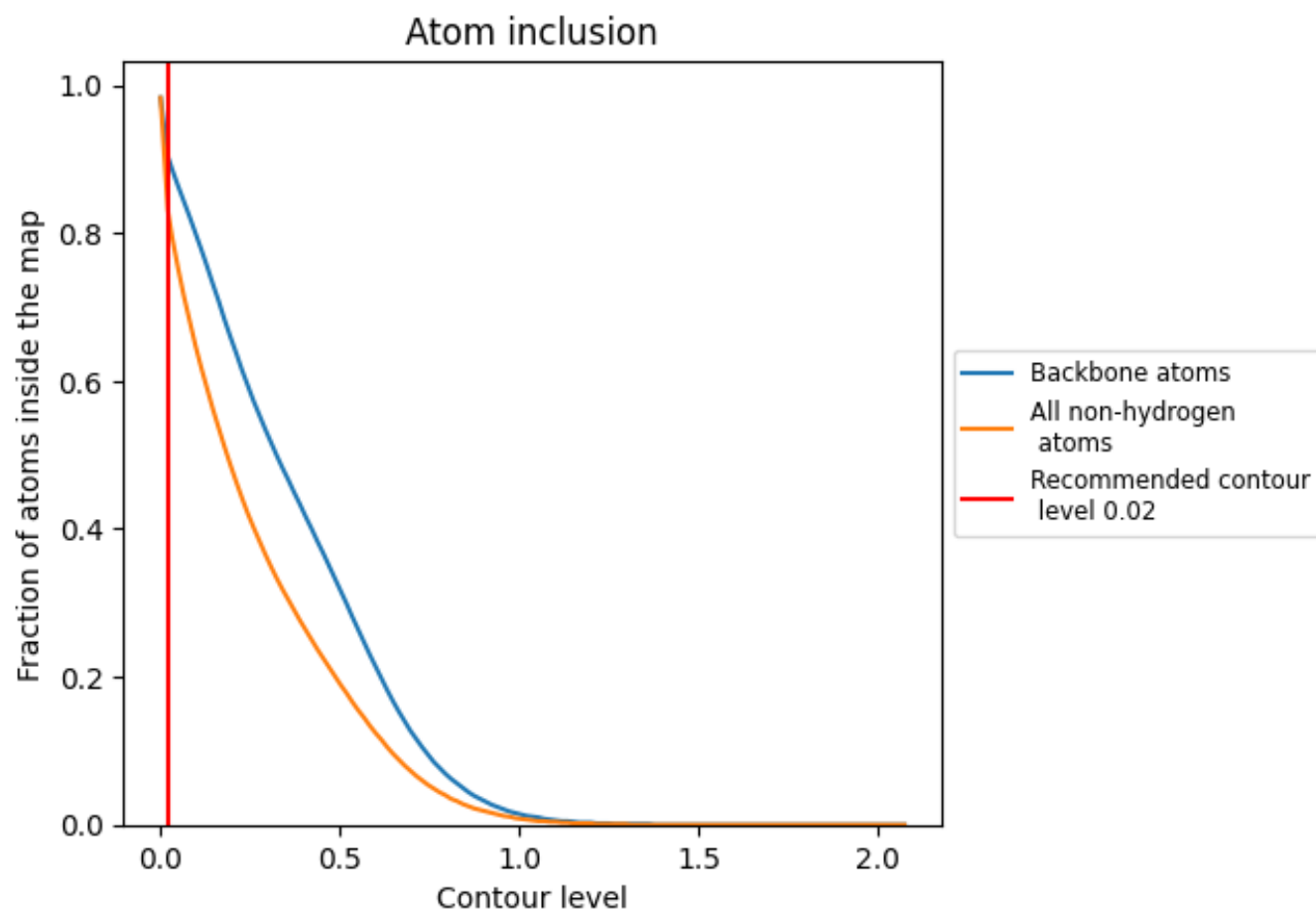
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion ⓘ



At the recommended contour level, 90% of all backbone atoms, 83% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8310	 0.2630
AA	 0.8810	 0.3180
AB	 0.9330	 0.3690
AC	 0.9200	 0.3960
AD	 0.9530	 0.4090
AE	 0.9020	 0.3070
AF	 0.9380	 0.3630
AG	 0.9310	 0.3870
AH	 0.9530	 0.4060
AI	 0.9070	 0.3080
AJ	 0.8560	 0.3270
AK	 0.8170	 0.3280
AL	 0.6320	 0.2580
BA	 0.9260	 0.3830
BB	 0.9490	 0.3730
BC	 0.9490	 0.3730
CA	 0.8220	 0.2550
CB	 0.8550	 0.2550
CC	 0.8530	 0.2500
CE	 0.7720	 0.1770
CF	 0.8240	 0.1880
CG	 0.8280	 0.1920
CI	 0.8090	 0.2280
CJ	 0.8350	 0.2300
CL	 0.8540	 0.2330
DA	 0.8870	 0.1810
DB	 0.9220	 0.1760
DC	 0.9110	 0.1670
DD	 0.8820	 0.1360
DE	 0.9150	 0.1430
DF	 0.9040	 0.1420
EA	 0.9520	 0.3910
EB	 0.9290	 0.3910
EC	 0.9460	 0.3880
FA	 0.9000	 0.3750



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Chain	Atom inclusion	Q-score
FB	 0.9120	 0.3640
FC	 0.9200	 0.3610
FD	 0.8650	 0.2500
FE	 0.8780	 0.2470
FF	 0.8540	 0.2580
GA	 0.8260	 0.3120
GB	 0.8810	 0.2880
GC	 0.8020	 0.2430
GD	 0.8730	 0.2910
GE	 0.8360	 0.2410
GF	 0.6990	 0.1670
GG	 0.8400	 0.3030
GH	 0.6860	 0.1480
GI	 0.8290	 0.2390
GJ	 0.7230	 0.1710
GK	 0.8290	 0.3120
GL	 0.7020	 0.1710
HA	 0.9060	 0.3390
HB	 0.8960	 0.3370
HC	 0.9100	 0.3600
HD	 0.8810	 0.2960
IA	 0.9190	 0.3510
IB	 0.9380	 0.3420
IC	 0.9350	 0.3450
JA	 0.8950	 0.3330
JB	 0.8520	 0.3040
JC	 0.9080	 0.3230
KA	 0.8400	 0.1560
KB	 0.8560	 0.1610
KC	 0.7530	 0.1260
KE	 0.5630	 0.0310
KF	 0.6210	 0.0460
KG	 0.6070	 0.0470
LA	 0.7380	 0.1890
LB	 0.7550	 0.1940
LC	 0.6430	 0.1780
LD	 0.6610	 0.1620
LE	 0.7910	 0.2390
LF	 0.7300	 0.2010
LG	 0.8930	 0.3760
LH	 0.9610	 0.4310
LI	 0.7700	 0.1980

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Chain	Atom inclusion	Q-score
LJ	 0.7510	 0.1710
LK	 0.6280	 0.1670
LL	 0.6600	 0.1590
LM	 0.5200	 0.0610
LN	 0.5370	 0.0240
LO	 0.5640	 0.0570
LP	 0.5260	 0.0490
MA	 0.9030	 0.2890
MB	 0.9190	 0.2890
MC	 0.7890	 0.3380
MD	 0.9200	 0.3960
ME	 0.9190	 0.2600
MF	 0.9420	 0.2670
MG	 0.8140	 0.3300
MH	 0.9440	 0.3720
MI	 0.9240	 0.2660
MJ	 0.9220	 0.2580
MK	 0.8260	 0.3310
ML	 0.9420	 0.3690
NA	 0.8300	 0.0930
NB	 0.3040	 0.0020
NC	 0.8310	 0.0940
ND	 0.3900	 0.0160
OA	 0.8440	 0.2900
OB	 0.8390	 0.2790
OC	 0.8640	 0.2850
PA	 0.7550	 0.2530
PB	 0.7980	 0.2450
PC	 0.8120	 0.2690
QA	 0.8610	 0.2020
QB	 0.5000	 0.1140
QC	 0.8330	 0.1740
QD	 0.8350	 0.2000
RA	 0.7650	 0.0940
RB	 0.6230	 0.0540
RC	 0.7670	 0.0940
RD	 0.6930	 0.1060
SA	 0.8170	 0.1530
SB	 0.4520	 0.0920
SC	 0.7500	 0.1340
SD	 0.8090	 0.1560