



wwPDB EM Validation Summary Report ⓘ

Jul 16, 2026 – 06:20 AM JST

PDB ID : 24MC / pdb_000024mc
EMDB ID : EMD-69647
Title : Structure of oocyte cytoplasmic lattices
Authors : Liu, Q.; Gui, M.
Deposited on : 2026-03-10
Resolution : 3.40 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.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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) : 2.50

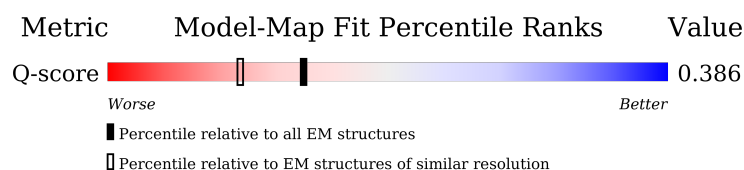
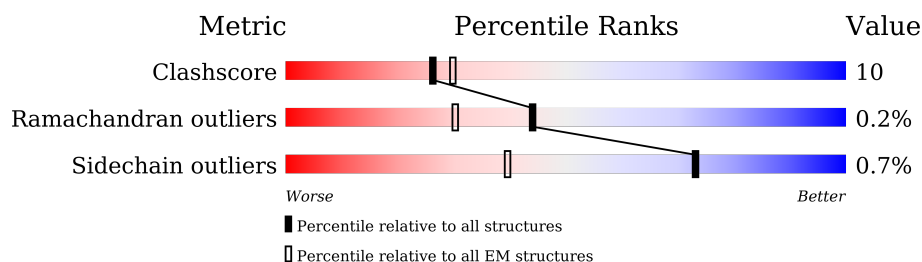
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	m	466	16% 61% 36% ..
2	p	468	11% 60% 36% ...
3	A	682	20% 74% 21% 5%
3	B	682	10% 73% 23% .

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Mol	Chain	Length	Quality of chain
3	C	682	
3	D	682	
3	E	682	
3	F	682	
3	G	682	
3	H	682	
3	I	682	
3	K	682	
4	M	937	
4	R	937	
5	N	164	
5	U	164	
6	O	346	
7	P	1163	
7	S	1163	
8	Q	581	
8	T	581	
9	V	228	
10	W	445	
10	Z	445	
11	X	449	
11	Y	449	
12	a	147	
12	c	147	
13	b	782	

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Mol	Chain	Length	Quality of chain
13	d	782	31%56%22%21%
14	e	993	42%69%28%. .
14	f	993	41%61%35%. .
15	h	163	16%57%30%13%
15	j	163	26%54%34%12%
15	l	163	46%56%25%. 18%
16	n	469	. 81%18%

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 138959 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 F-box and WD-40 domain protein 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	461	Total	C	N	O	S	0	0
			3723	2394	638	662	29		

- Molecule 2 is a protein called F-box and WD-40 domain protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	p	464	Total	C	N	O	S	0	0
			3804	2465	636	678	25		

- Molecule 3 is a protein called Inactive protein-arginine deiminase type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	651	Total	C	N	O	S	0	0
			5161	3309	846	967	39		
3	B	655	Total	C	N	O	S	0	0
			5188	3323	853	973	39		
3	C	655	Total	C	N	O	S	0	0
			5188	3323	853	973	39		
3	D	650	Total	C	N	O	S	0	0
			5154	3304	845	966	39		
3	E	655	Total	C	N	O	S	0	0
			5188	3323	853	973	39		
3	F	639	Total	C	N	O	S	0	0
			5059	3247	825	948	39		
3	G	655	Total	C	N	O	S	0	0
			5188	3323	853	973	39		
3	H	650	Total	C	N	O	S	0	0
			5148	3299	847	963	39		
3	I	651	Total	C	N	O	S	0	0
			5161	3309	846	967	39		
3	K	643	Total	C	N	O	S	0	0
			5102	3273	837	953	39		

- Molecule 4 is a protein called NLR family, pyrin domain containing 4F.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	M	88	Total	C	N	O	S	0	0
			728	470	125	130	3		
4	R	838	Total	C	N	O	S	0	0
			6735	4297	1118	1253	67		

- Molecule 5 is a protein called Oocyte-expressed protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	N	120	Total	C	N	O	S	0	0
			967	619	167	176	5		
5	U	87	Total	C	N	O	S	0	0
			701	449	120	127	5		

- Molecule 6 is a protein called Isoform 2 of KH domain-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	O	128	Total	C	N	O	S	0	0
			1066	688	191	179	8		

- Molecule 7 is a protein called NACHT, LRR and PYD domains-containing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	P	940	Total	C	N	O	S	0	0
			7419	4722	1255	1377	65		
7	S	949	Total	C	N	O	S	0	0
			7476	4757	1266	1388	65		

- Molecule 8 is a protein called Transducin-like enhancer protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Q	365	Total	C	N	O	S	0	0
			2884	1830	505	529	20		
8	T	355	Total	C	N	O	S	0	0
			2803	1778	493	512	20		

- Molecule 9 is a protein called Zinc finger BED domain-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	V	59	Total	C	N	O	S	0	0
			476	303	87	80	6		

- Molecule 10 is a protein called Tubulin beta-2A chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	W	431	Total	C	N	O	S	0	0
			3387	2125	580	656	26		
10	Z	428	Total	C	N	O	S	0	0
			3368	2115	576	651	26		

- Molecule 11 is a protein called Tubulin alpha-1C chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	X	418	Total	C	N	O	S	0	0
			3287	2083	558	624	22		
11	Y	423	Total	C	N	O	S	0	0
			3303	2091	562	628	22		

- Molecule 12 is a protein called Ubiquitin-conjugating enzyme E2 D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	a	147	Total	C	N	O	S	0	0
			1173	751	200	214	8		
12	c	147	Total	C	N	O	S	0	0
			1173	751	200	214	8		

- Molecule 13 is a protein called E3 ubiquitin-protein ligase UHRF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	b	630	Total	C	N	O	S	0	0
			5084	3180	930	941	33		
13	d	616	Total	C	N	O	S	0	0
			4985	3121	914	917	33		

- Molecule 14 is a protein called NACHT, LRR and PYD domains-containing protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	e	967	Total	C	N	O	S	0	0
			7723	4911	1322	1426	64		
14	f	963	Total	C	N	O	S	0	0
			7695	4897	1318	1416	64		

- Molecule 15 is a protein called S-phase kinase-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	h	142	Total	C	N	O	S	0	0
			1151	732	189	225	5		

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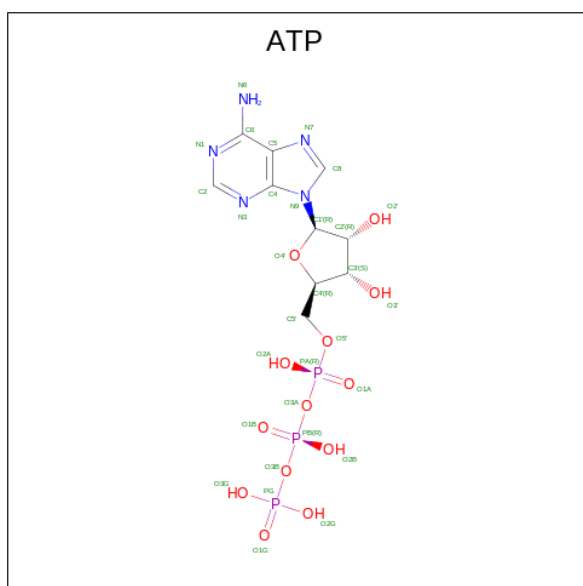
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Mol	Chain	Residues	Atoms					AltConf	Trace
15	j	144	Total	C	N	O	S	0	0
			1160	733	191	231	5		
15	l	133	Total	C	N	O	S	0	0
			1071	683	174	209	5		

- Molecule 16 is a protein called Expressed sequence C85627.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	n	467	Total	C	N	O	S	0	0
			3787	2443	629	685	30		

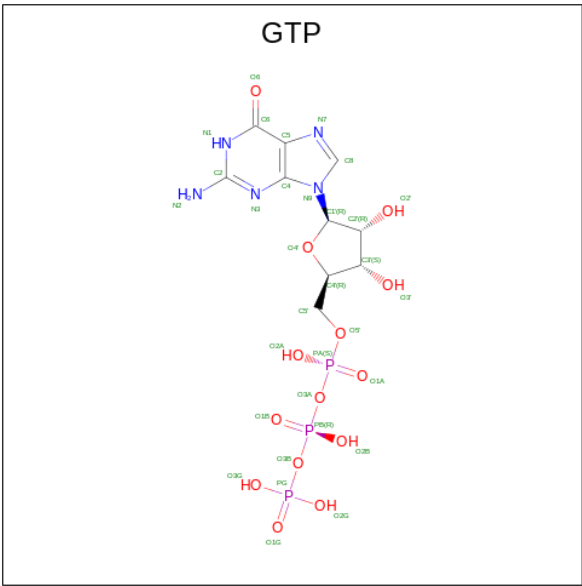
- Molecule 17 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
17	P	1	Total	C	N	O	P	0
			31	10	5	13	3	
17	R	1	Total	C	N	O	P	0
			31	10	5	13	3	
17	S	1	Total	C	N	O	P	0
			31	10	5	13	3	
17	e	1	Total	C	N	O	P	0
			31	10	5	13	3	
17	f	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 18 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$)

(labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
18	W	1	Total	C	N	O	P	0
			32	10	5	14	3	
18	X	1	Total	C	N	O	P	0
			32	10	5	14	3	
18	Y	1	Total	C	N	O	P	0
			32	10	5	14	3	
18	Z	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 19 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
19	W	1	Total	Mg	0
			1	1	
19	X	1	Total	Mg	0
			1	1	
19	Y	1	Total	Mg	0
			1	1	
19	Z	1	Total	Mg	0
			1	1	

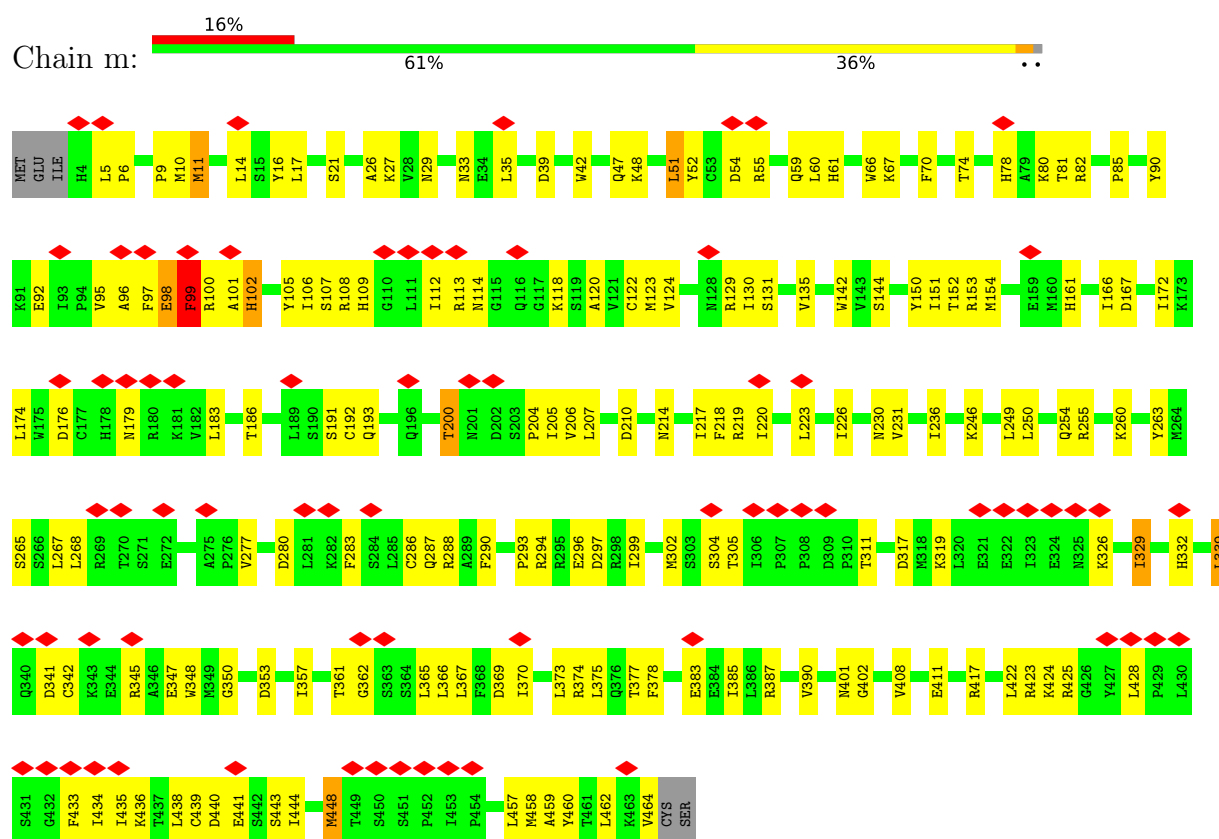
- Molecule 20 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
20	b	3	Total 3	Zn 3	0
20	d	3	Total 3	Zn 3	0

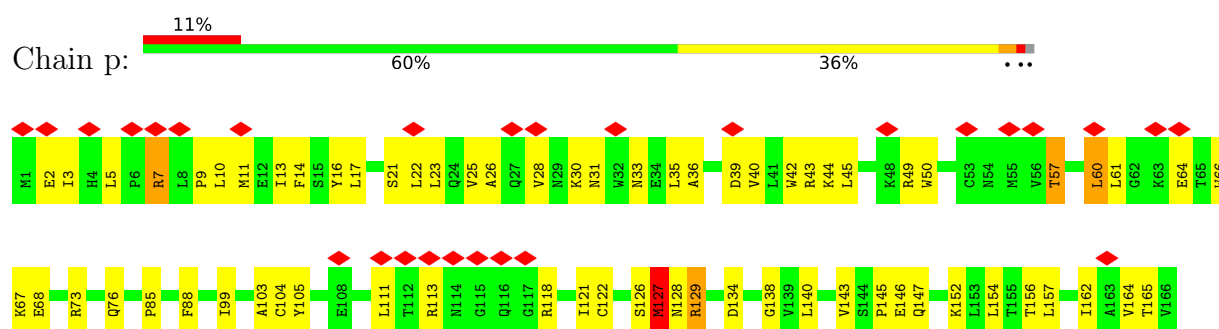
3 Residue-property plots

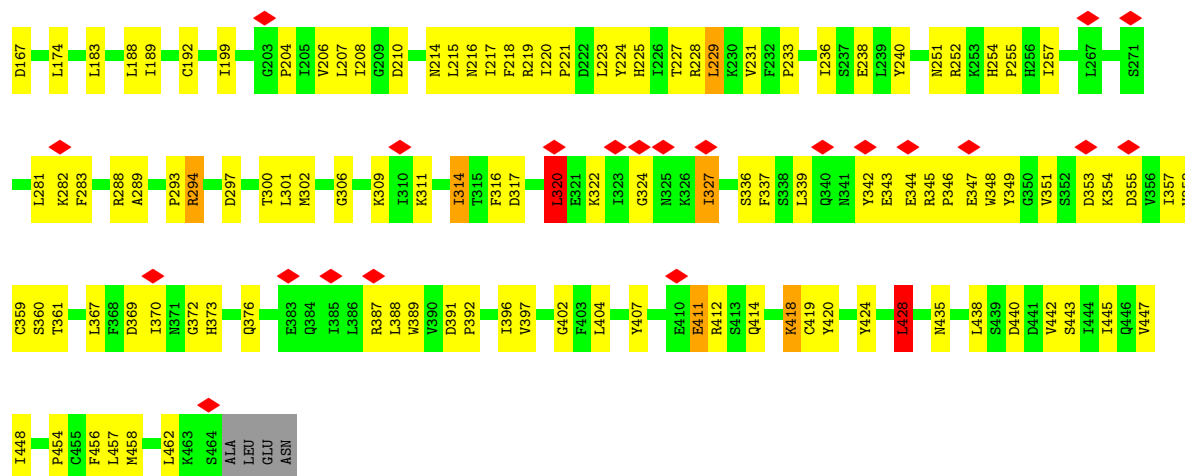
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: F-box and WD-40 domain protein 19

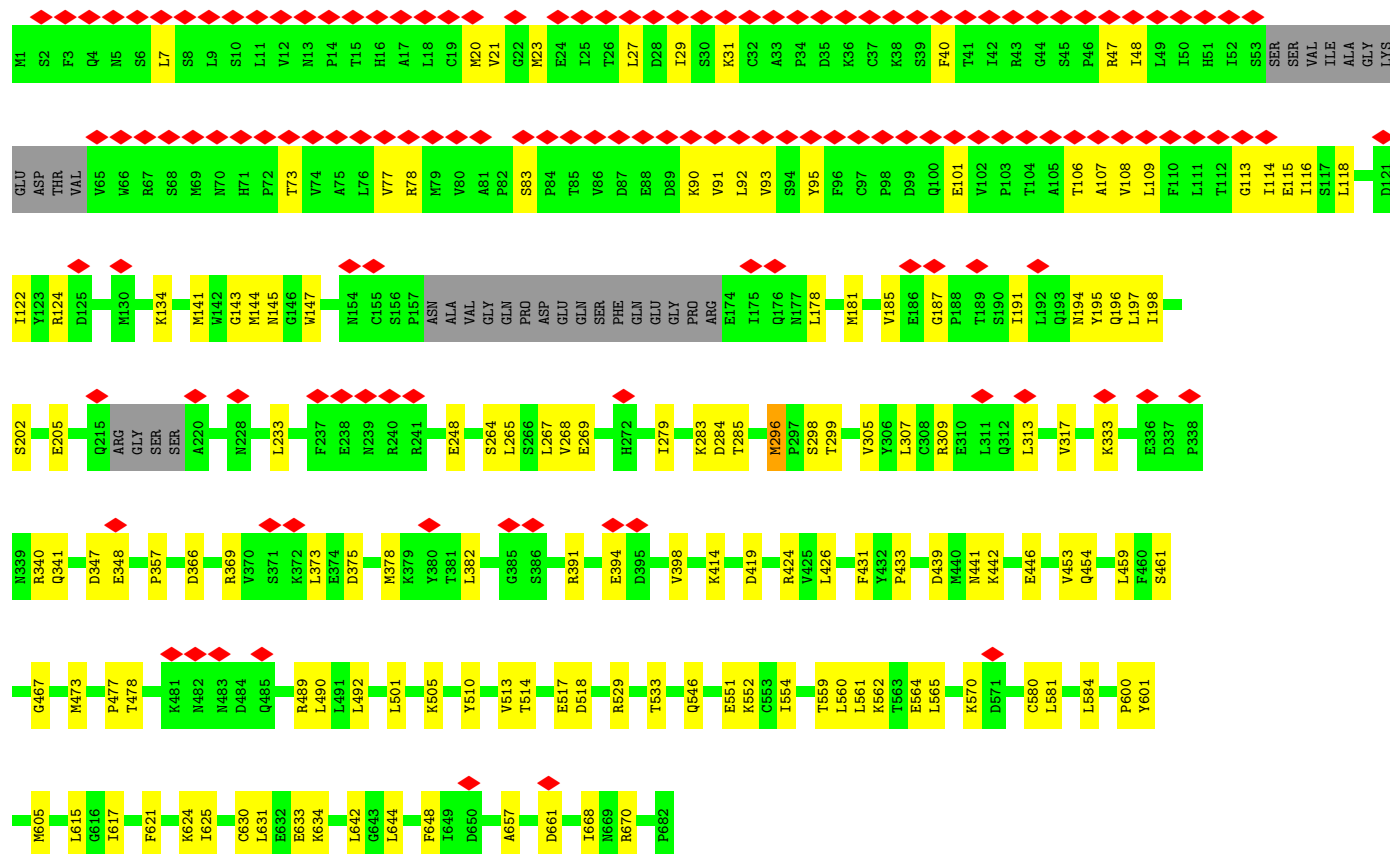
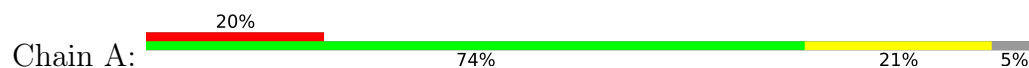


- Molecule 2: F-box and WD-40 domain protein 21

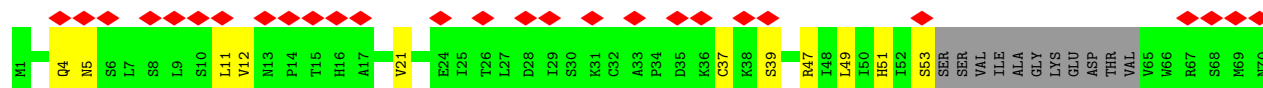


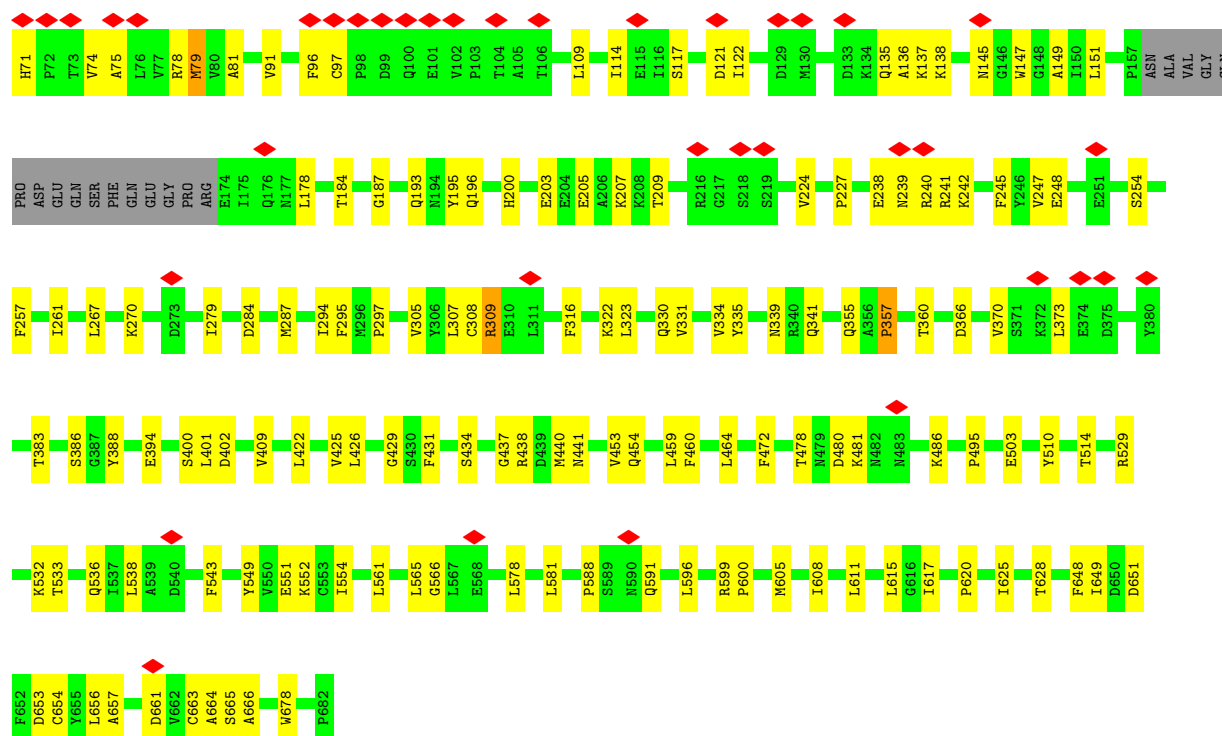


• Molecule 3: Inactive protein-arginine deiminase type-6

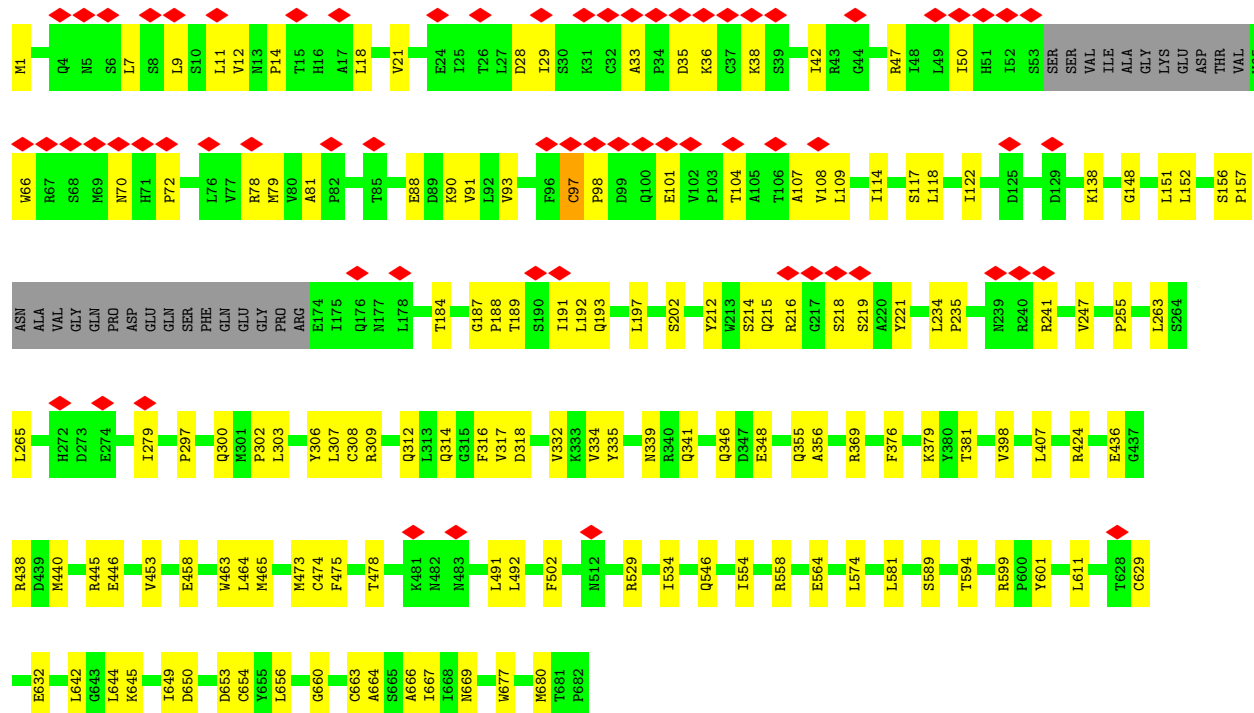
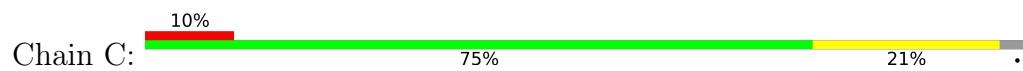


• Molecule 3: Inactive protein-arginine deiminase type-6

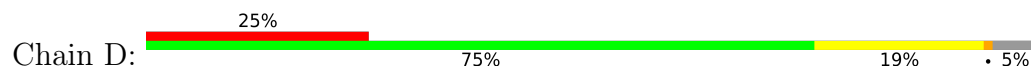


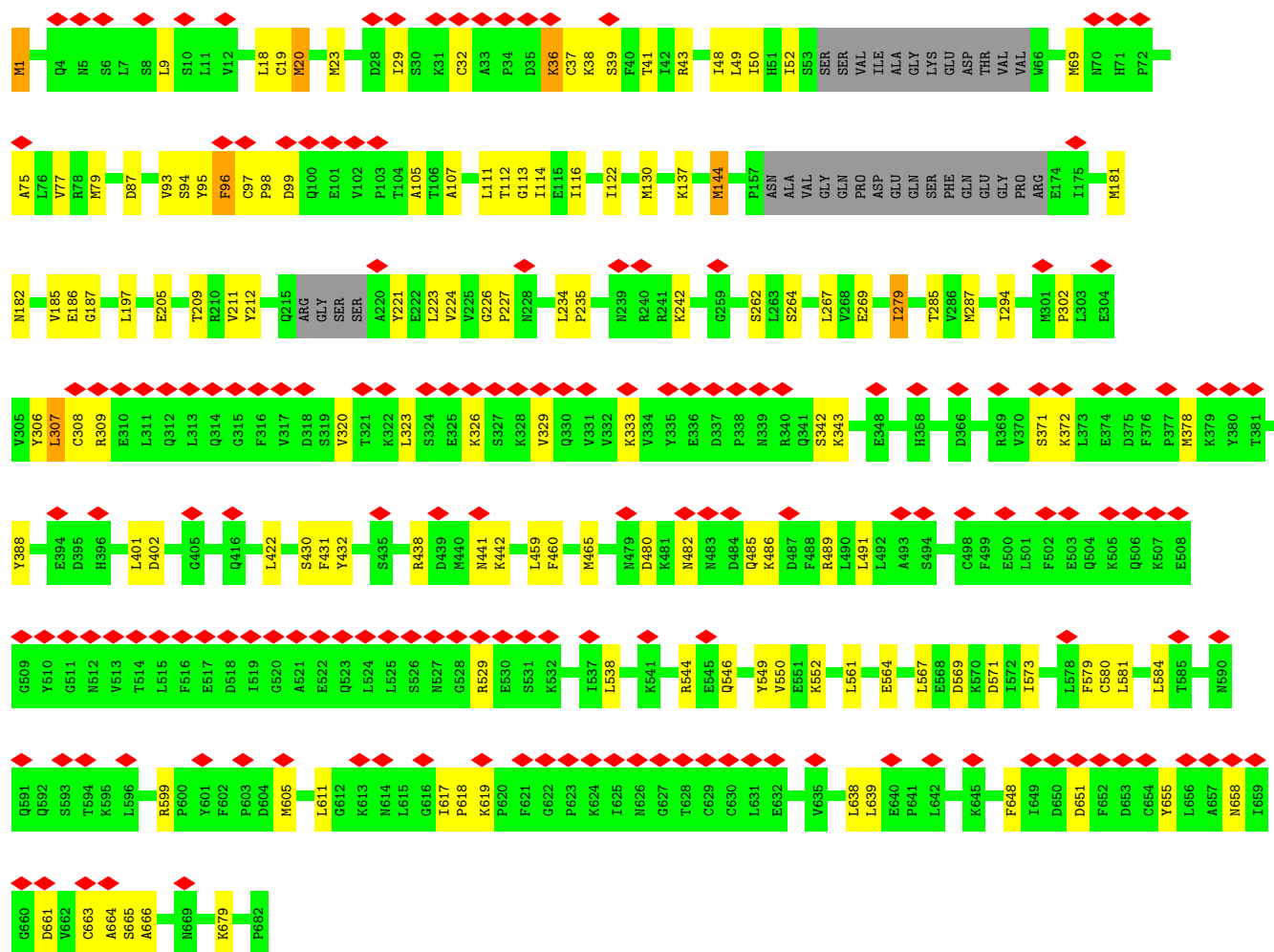


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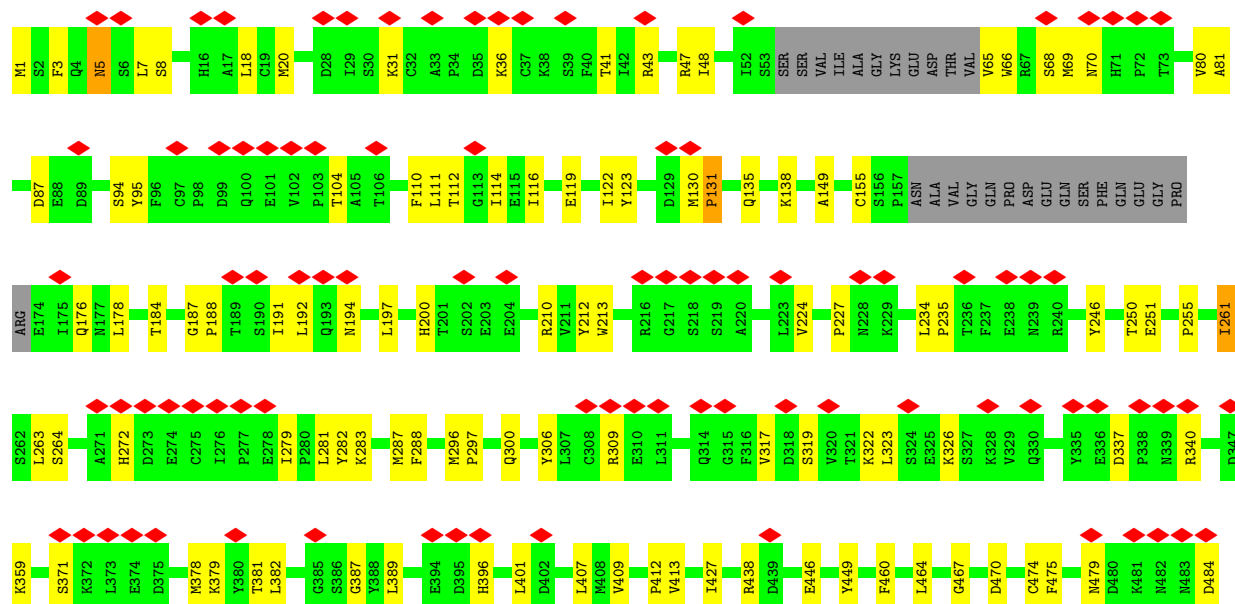
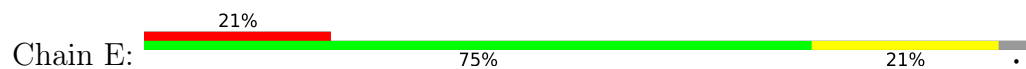


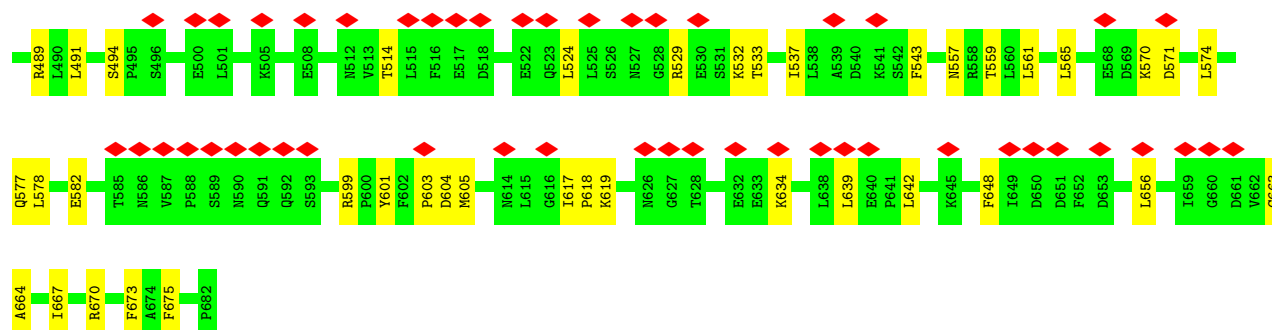
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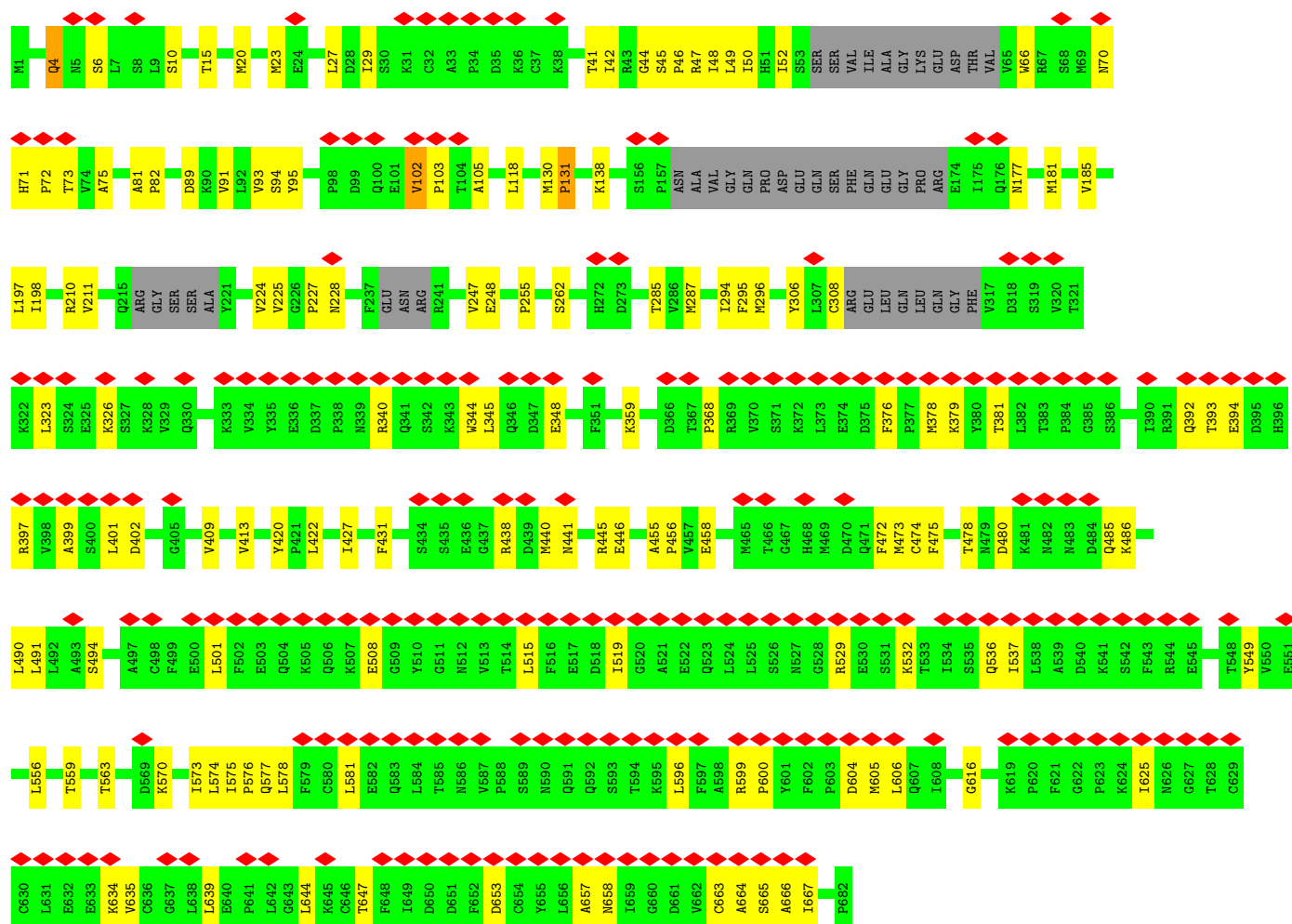
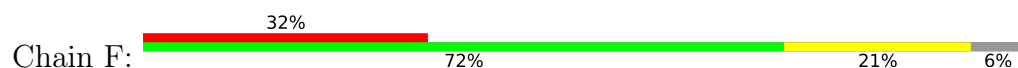


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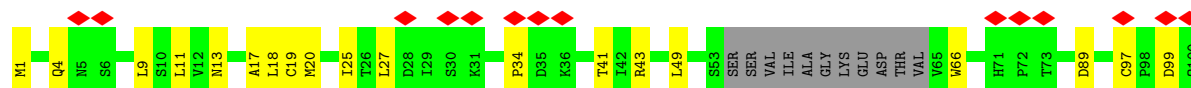
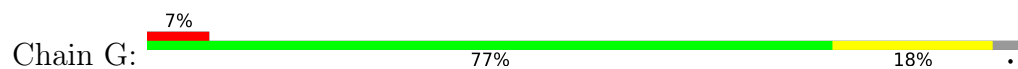


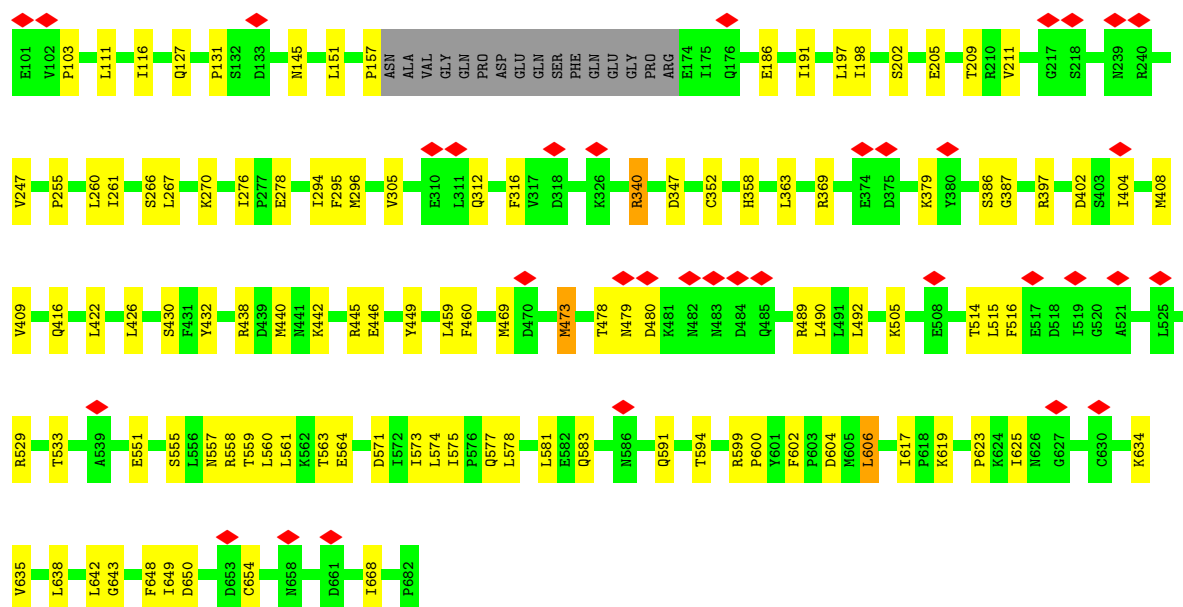


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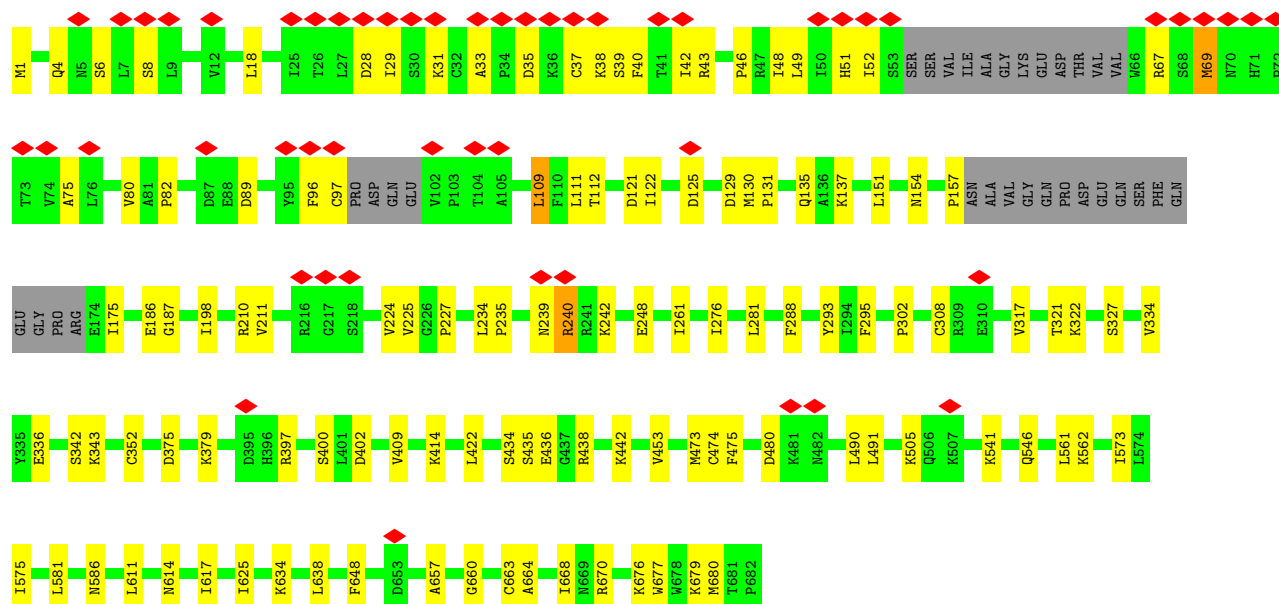
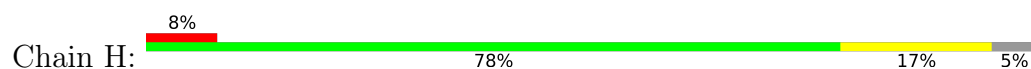


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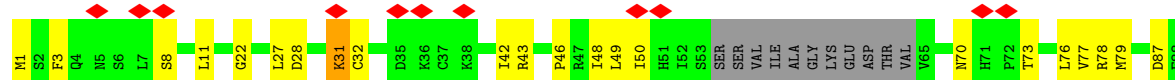


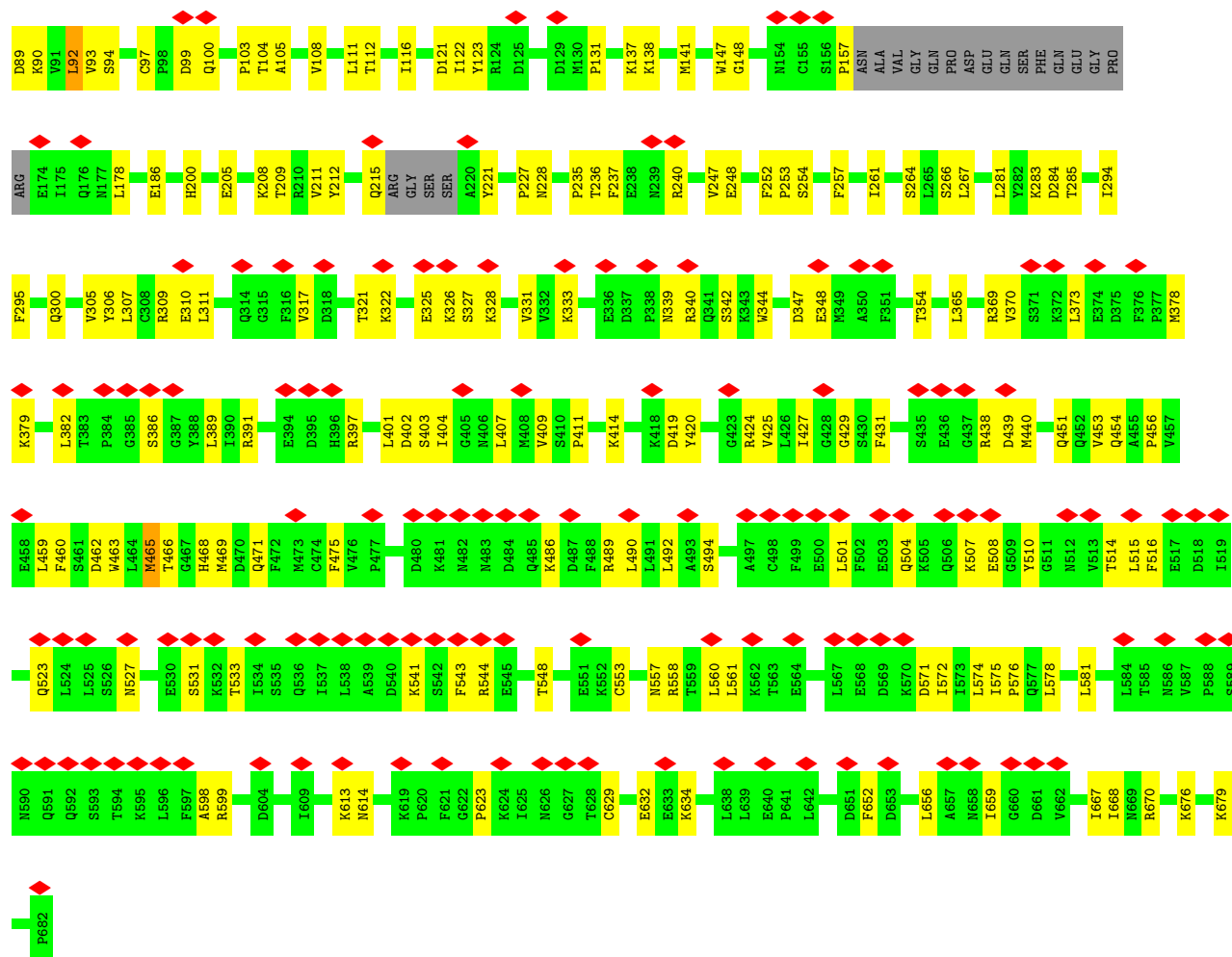


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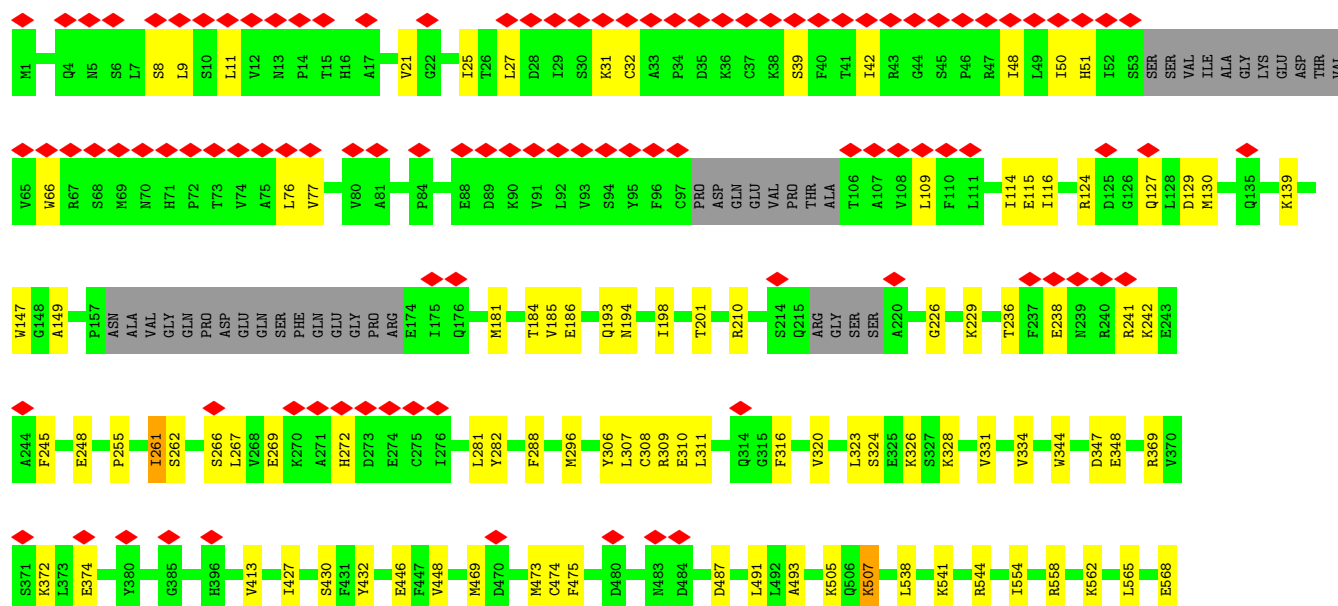
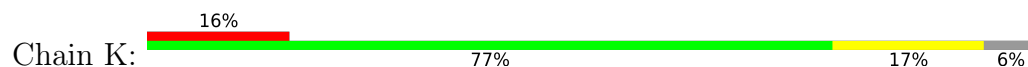


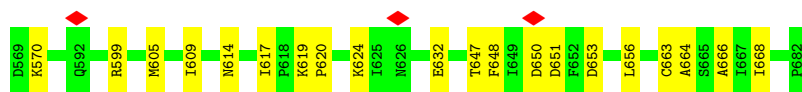
• Molecule 3: Inactive protein-arginine deiminase type-6





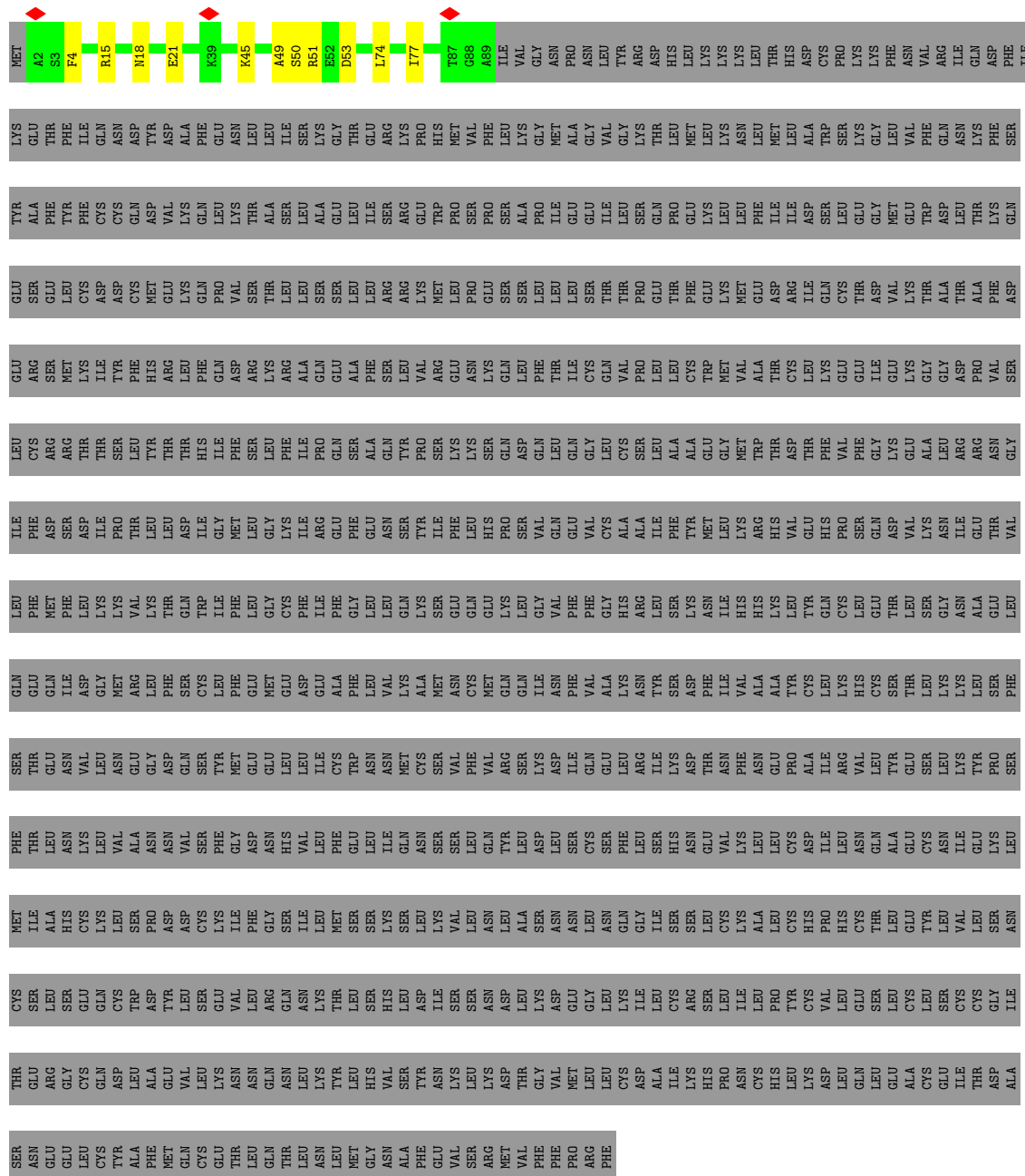
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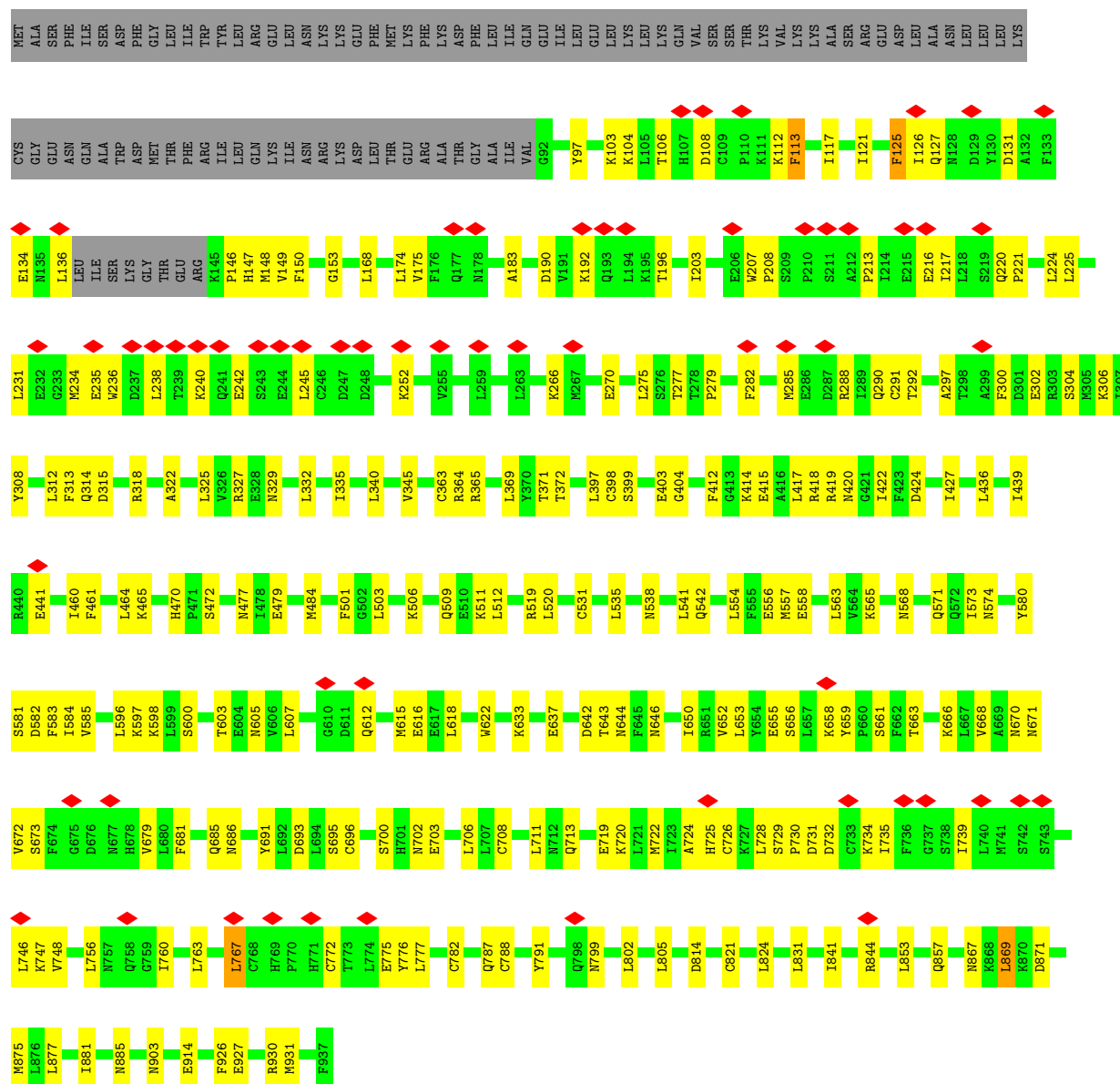
- Molecule 4: NLR family, pyrin domain containing 4F

Chain M: 8% 91%

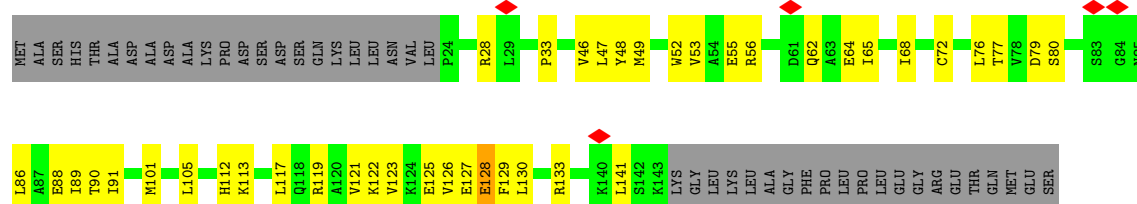


- Molecule 4: NLR family, pyrin domain containing 4F

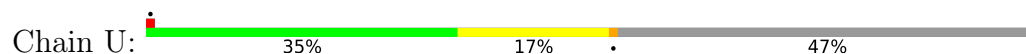
Chain R: 7% 64% 25% 11%

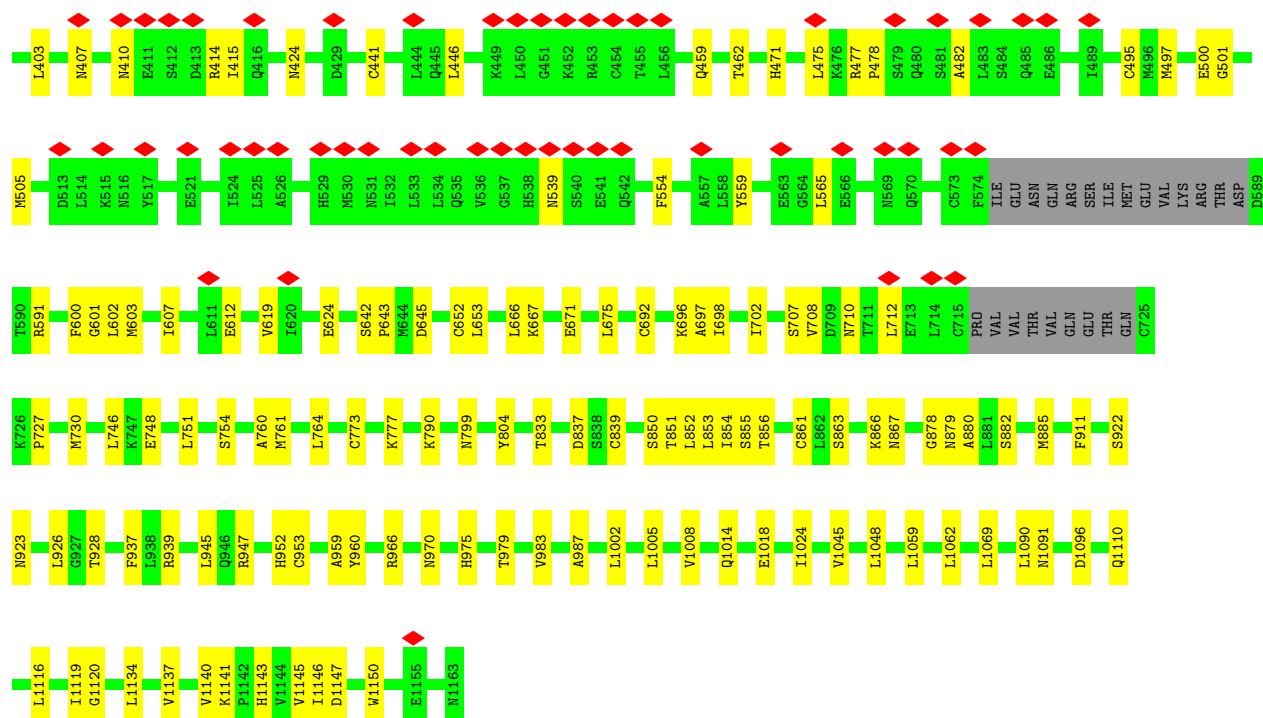


• Molecule 5: Oocyte-expressed protein homolog

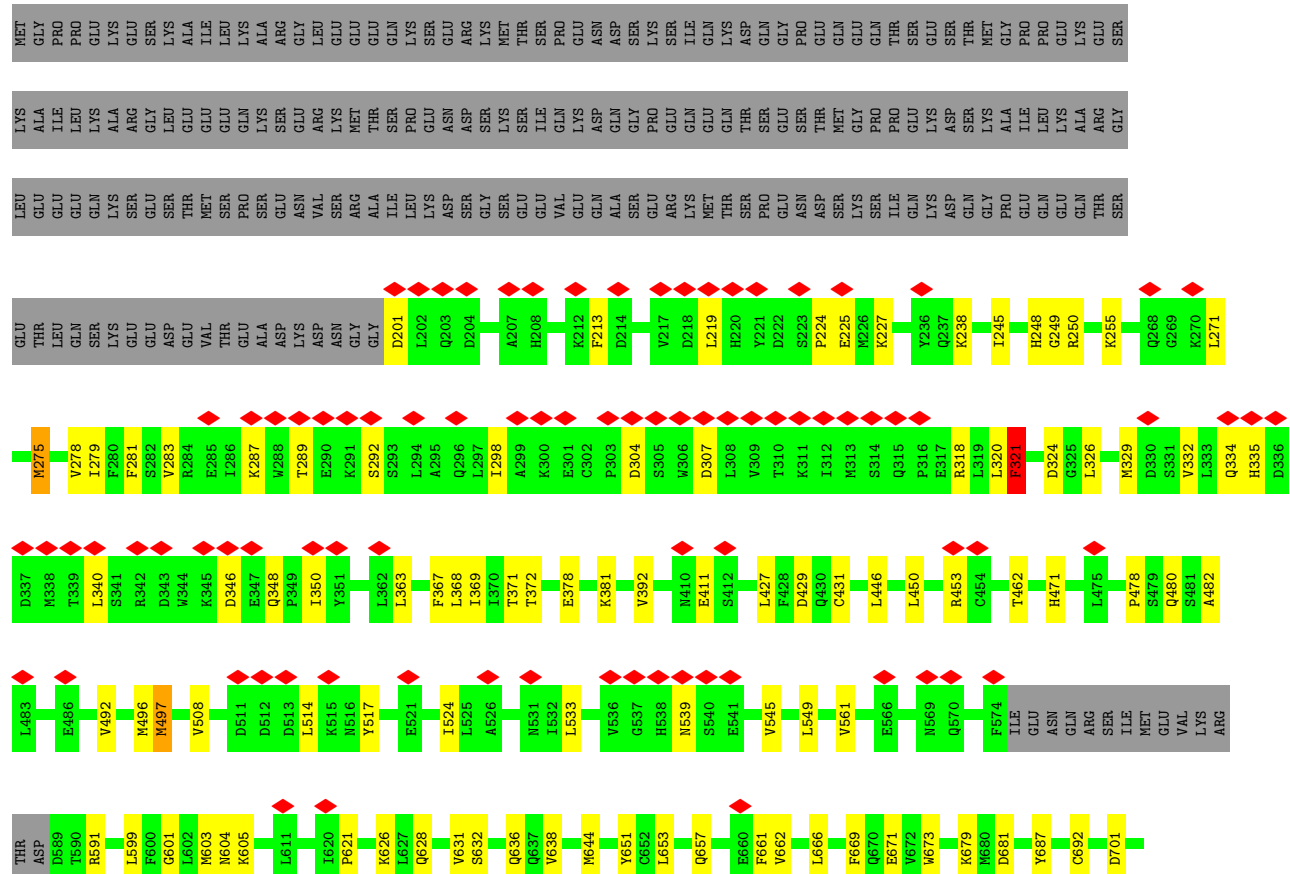


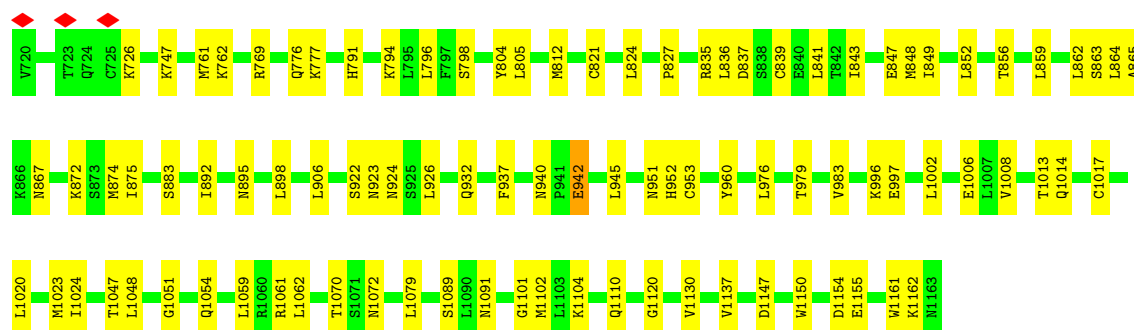
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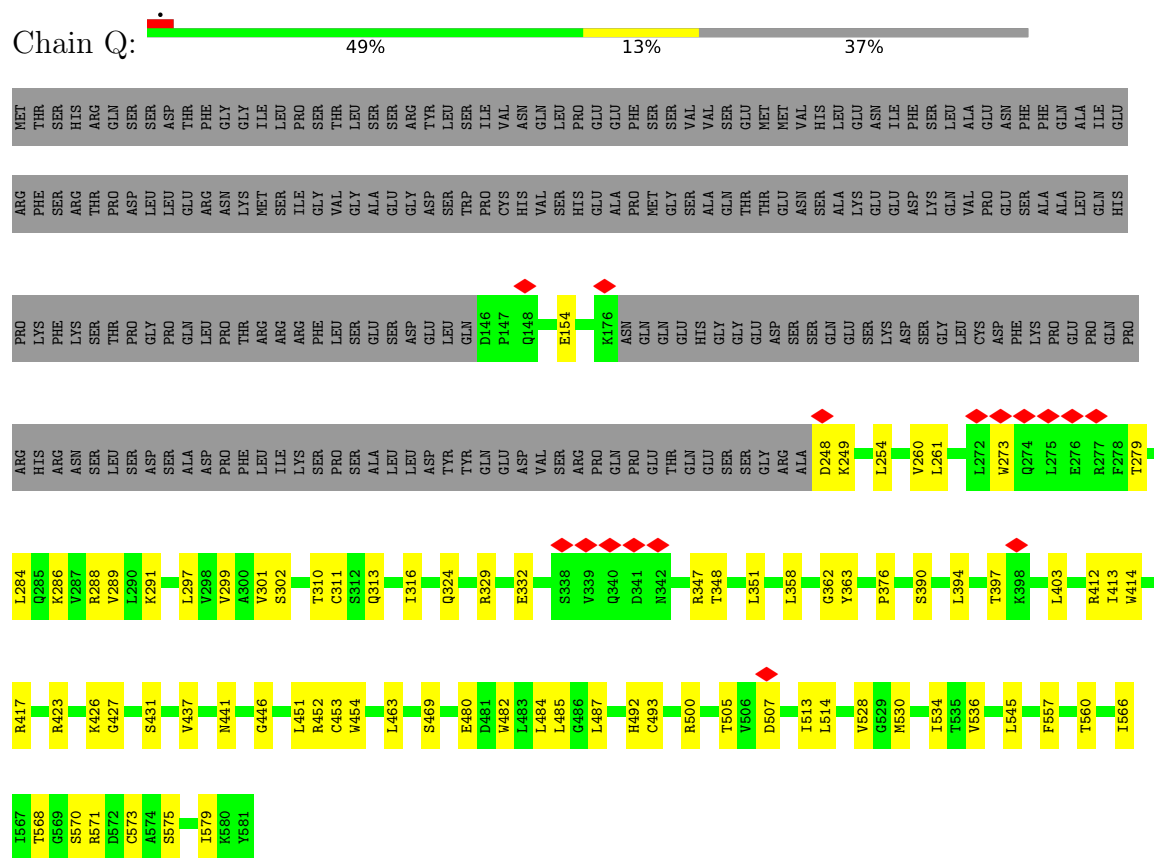


• Molecule 7: NACHT, LRR and PYD domains-containing protein 5

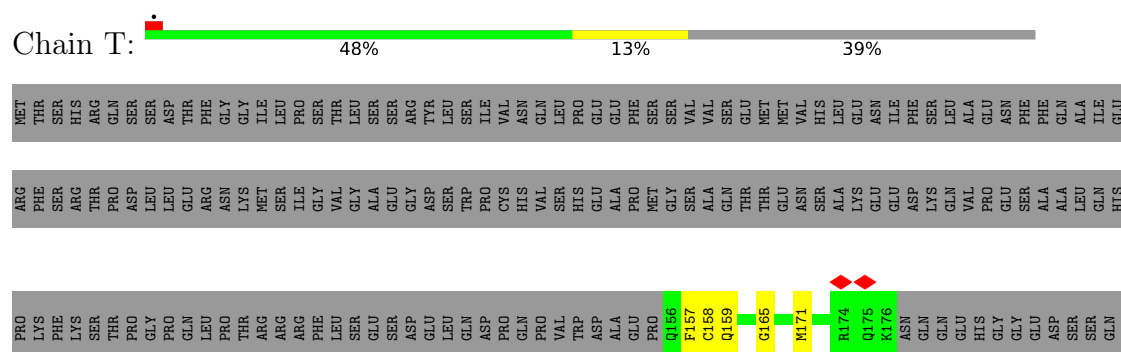


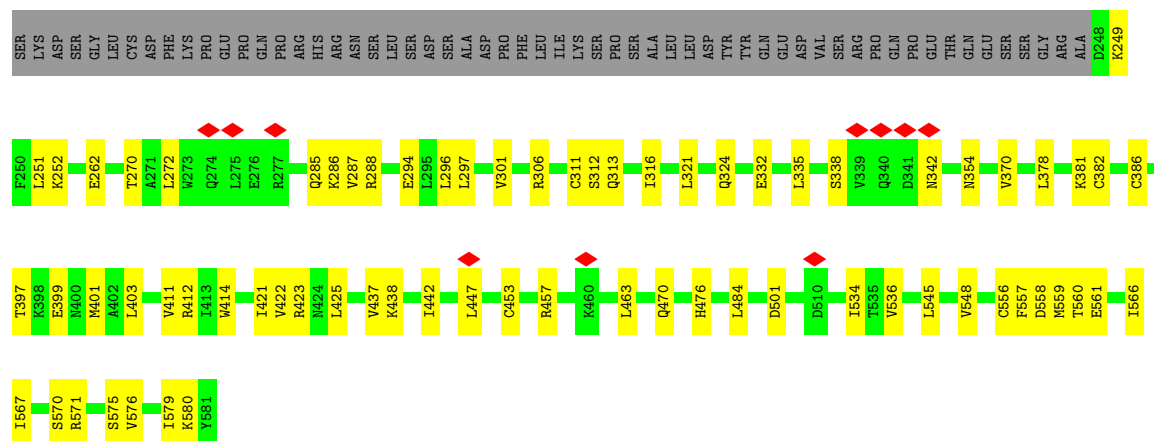


• Molecule 8: Transducin-like enhancer protein 6

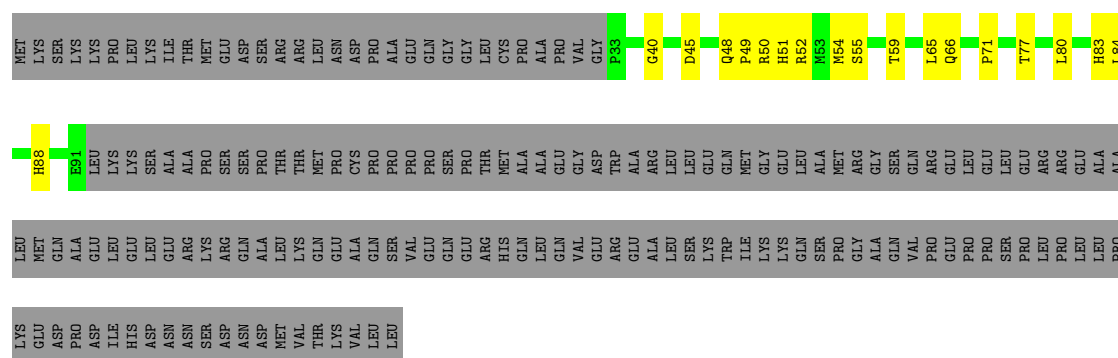


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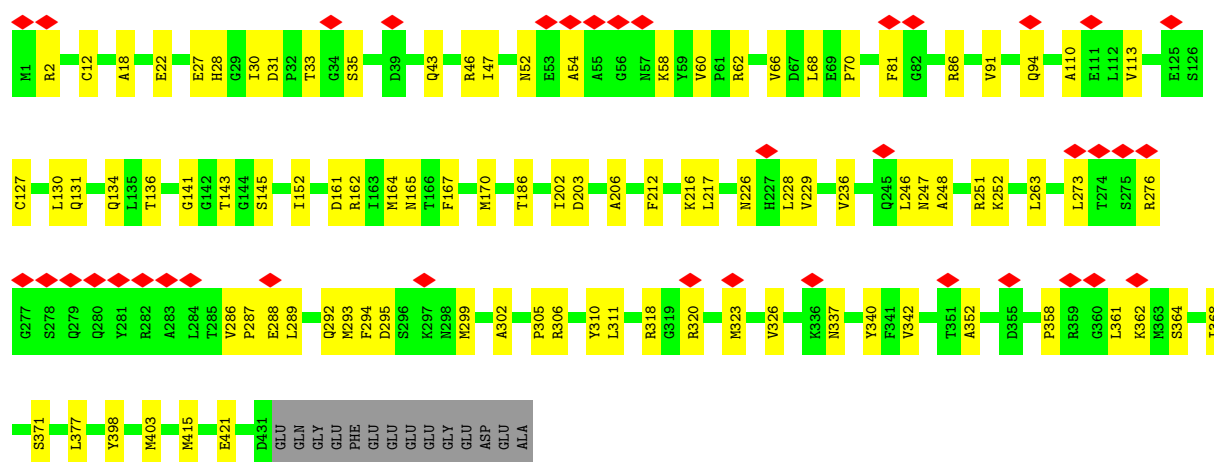
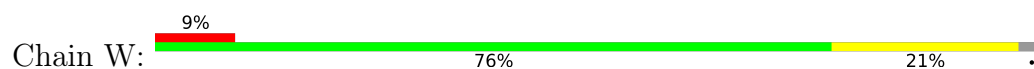




• Molecule 9: Zinc finger BED domain-containing protein 3

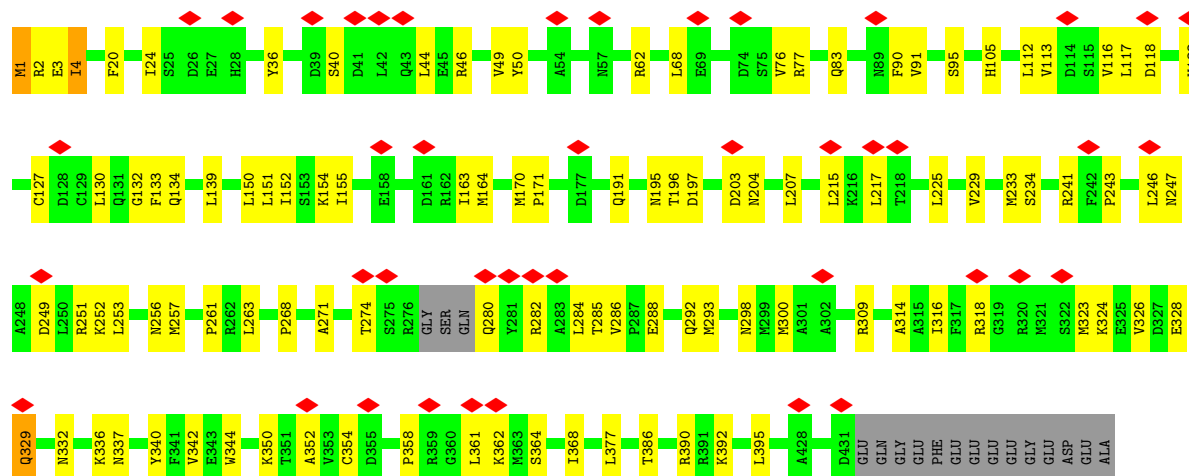


• Molecule 10: Tubulin beta-2A chain

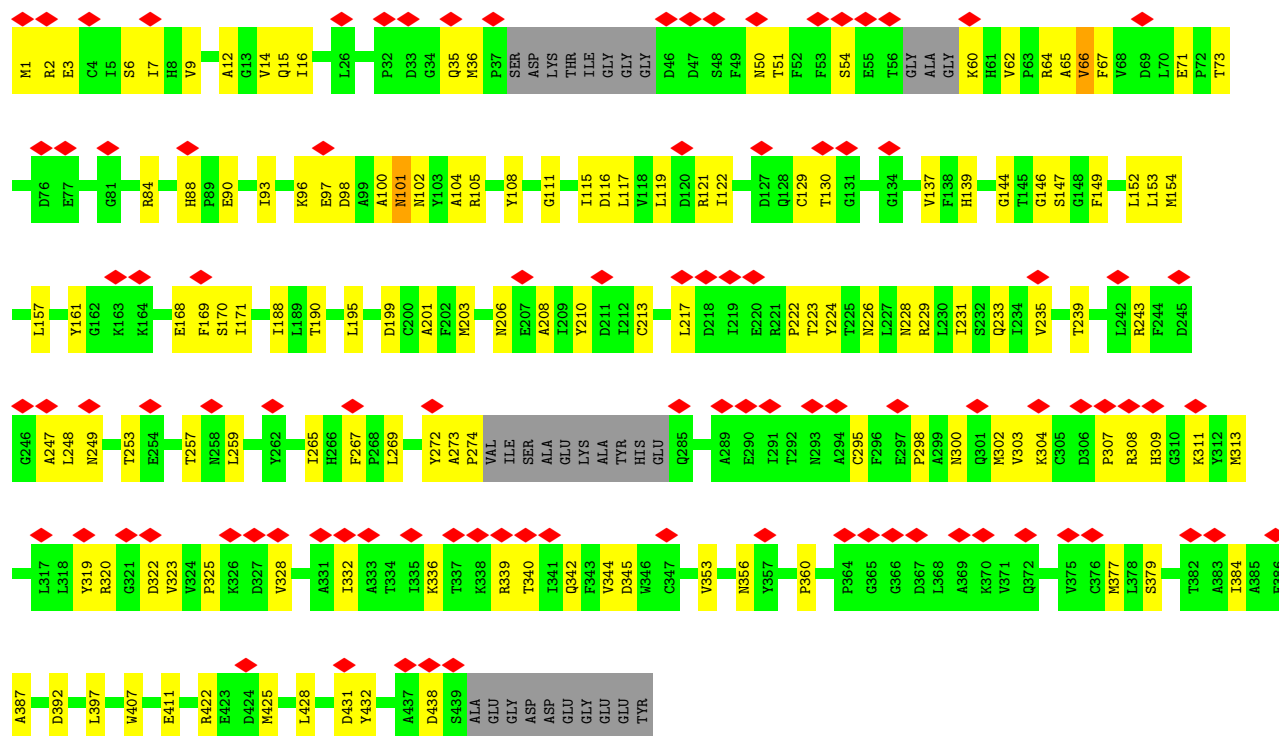


• Molecule 10: Tubulin beta-2A chain

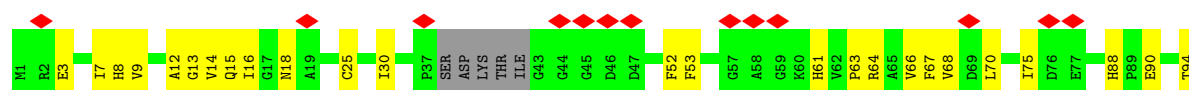


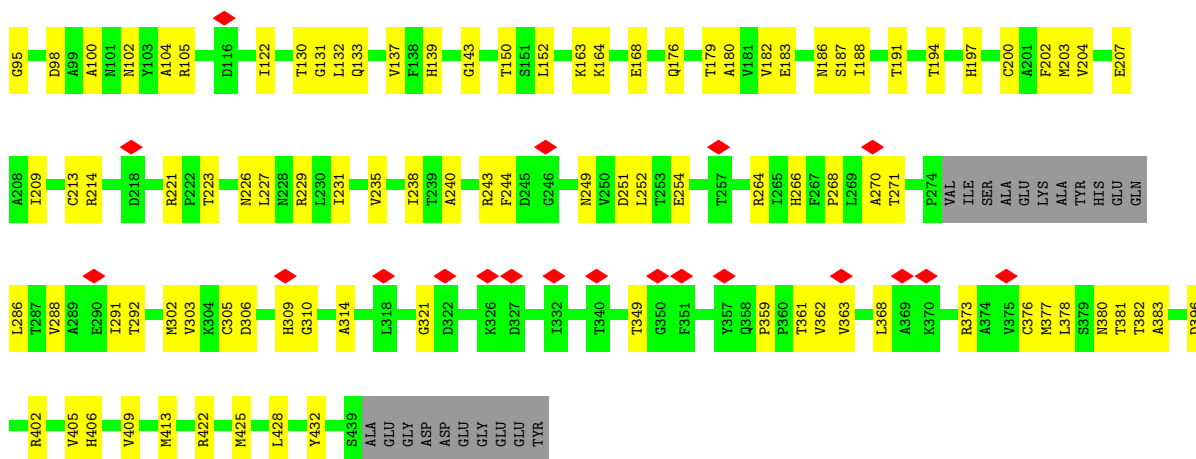


• Molecule 11: Tubulin alpha-1C chain

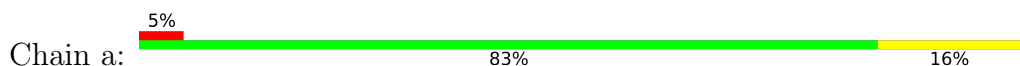


• Molecule 11: Tubulin alpha-1C chain





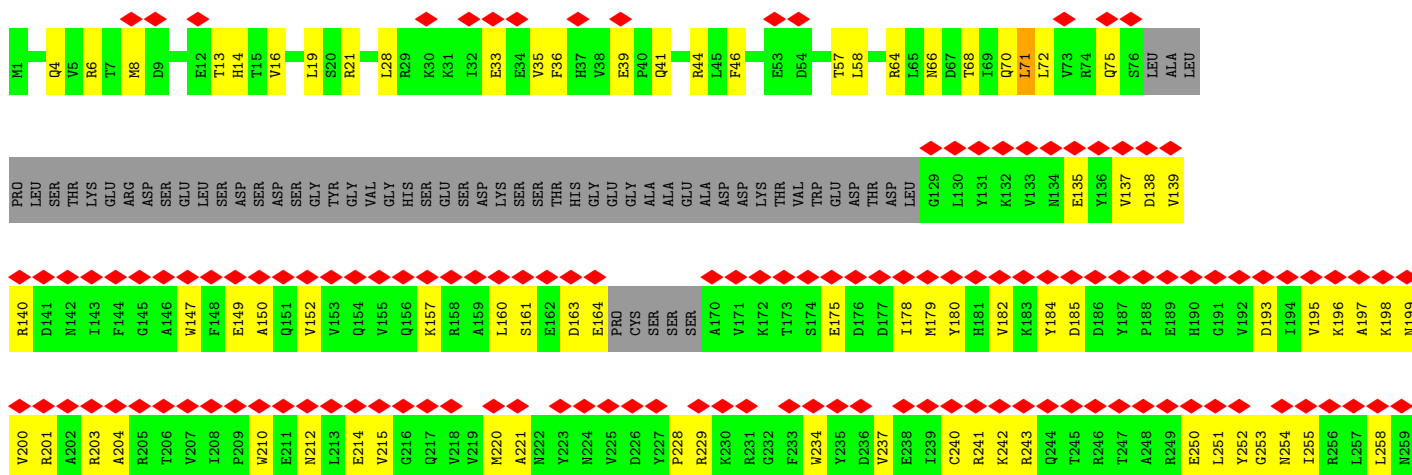
• Molecule 12: Ubiquitin-conjugating enzyme E2 D3

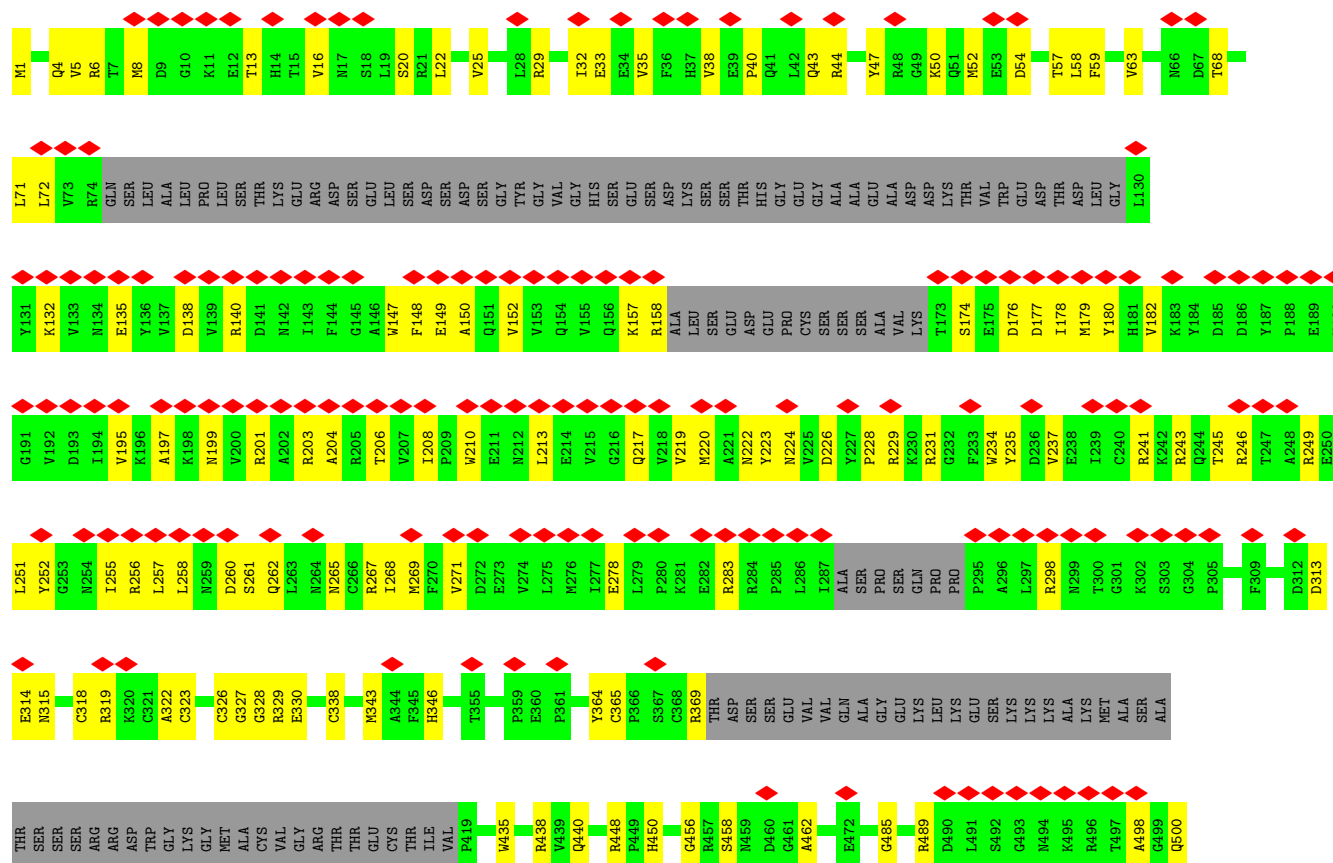


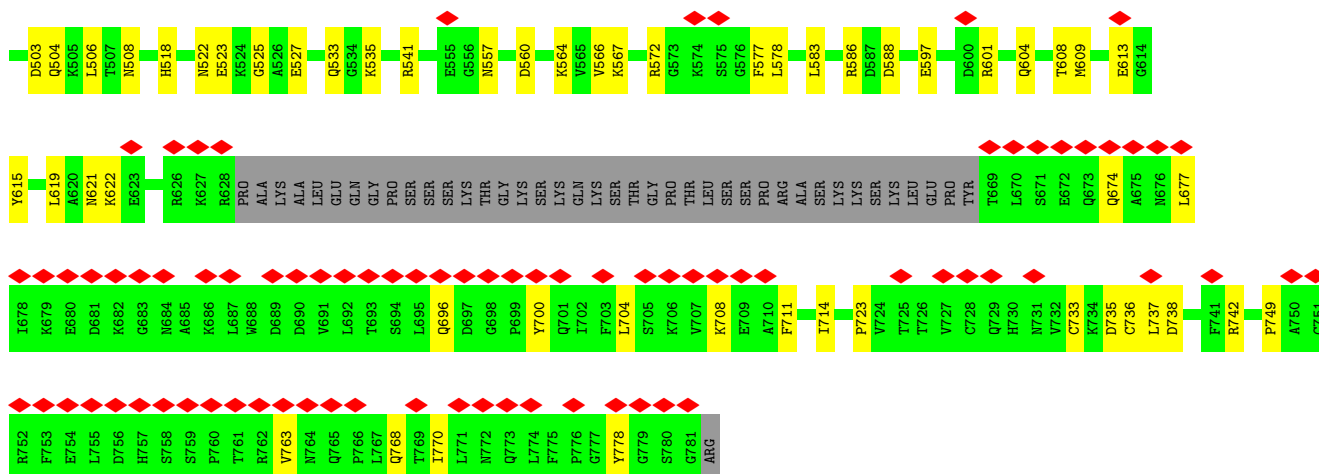
• Molecule 12: Ubiquitin-conjugating enzyme E2 D3



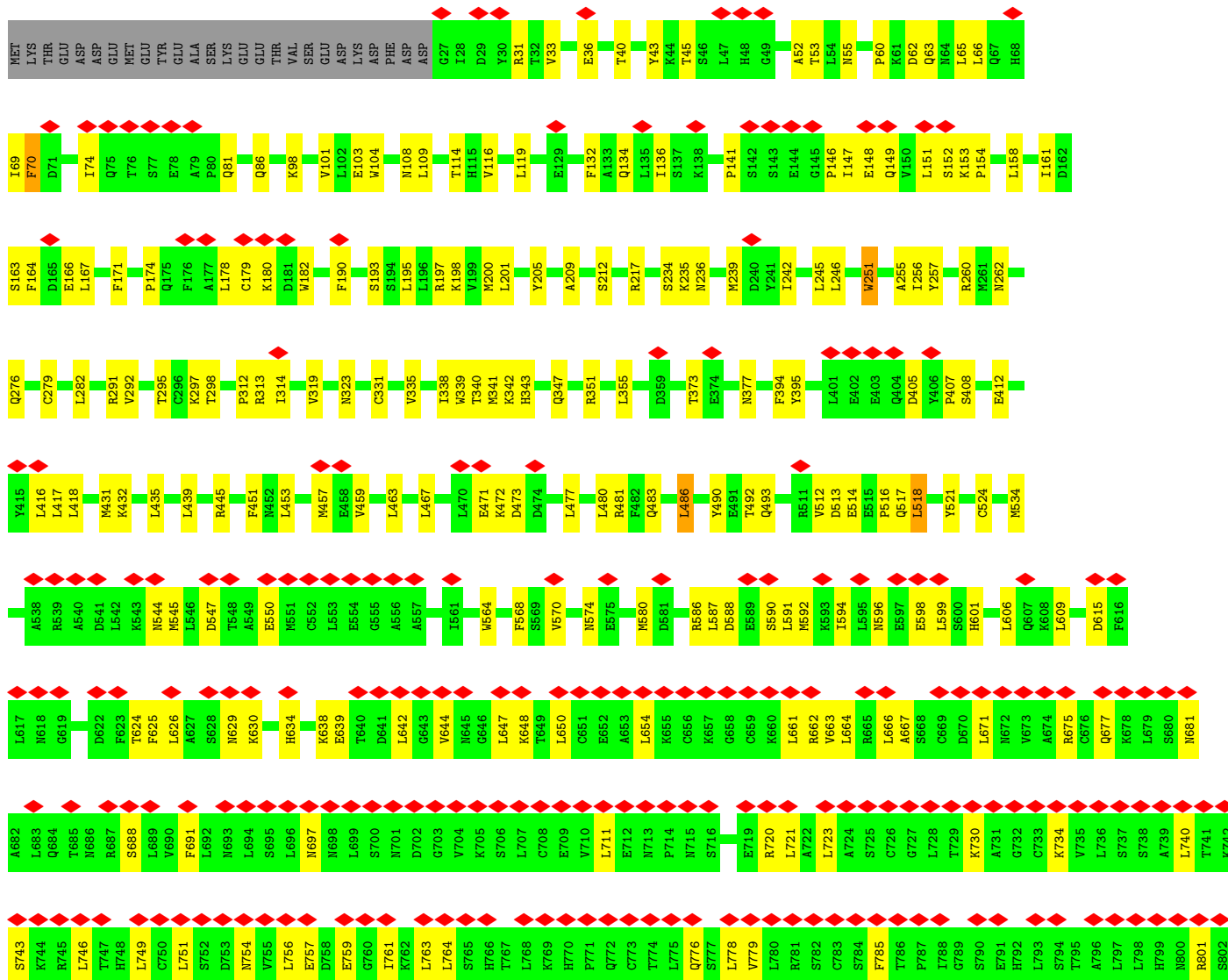
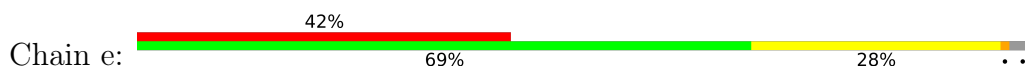
• Molecule 13: E3 ubiquitin-protein ligase UHRF1



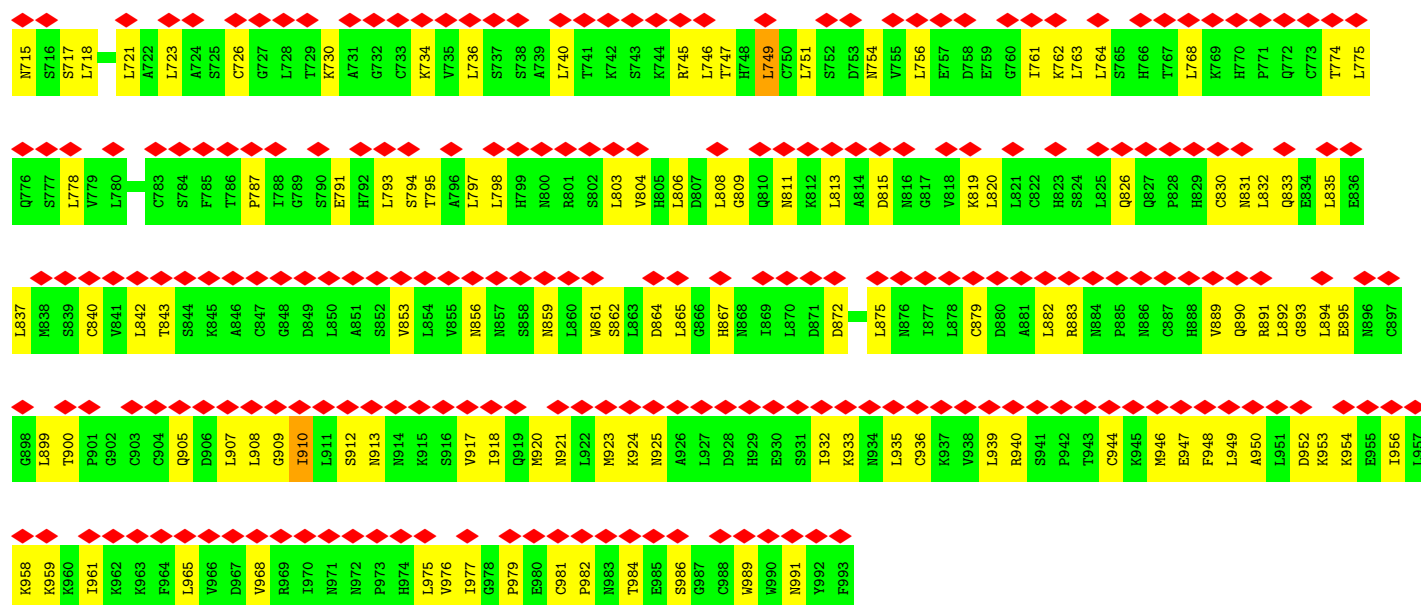




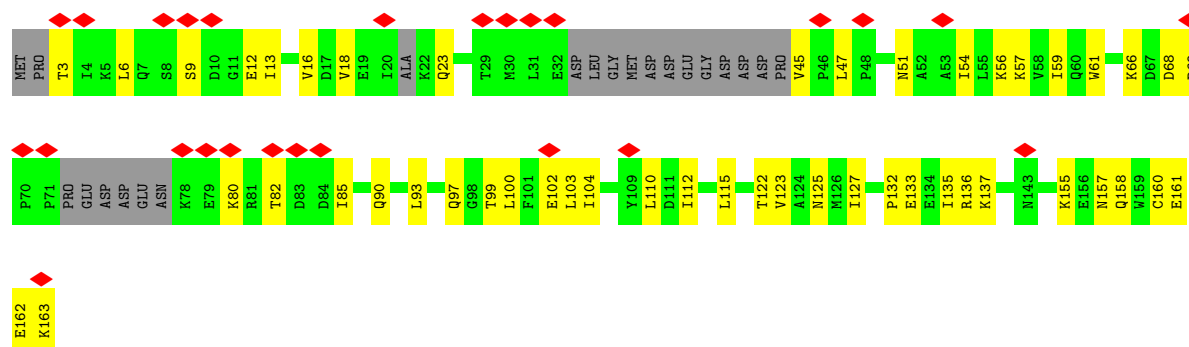
• Molecule 14: NACHT, LRR and PYD domains-containing protein 14



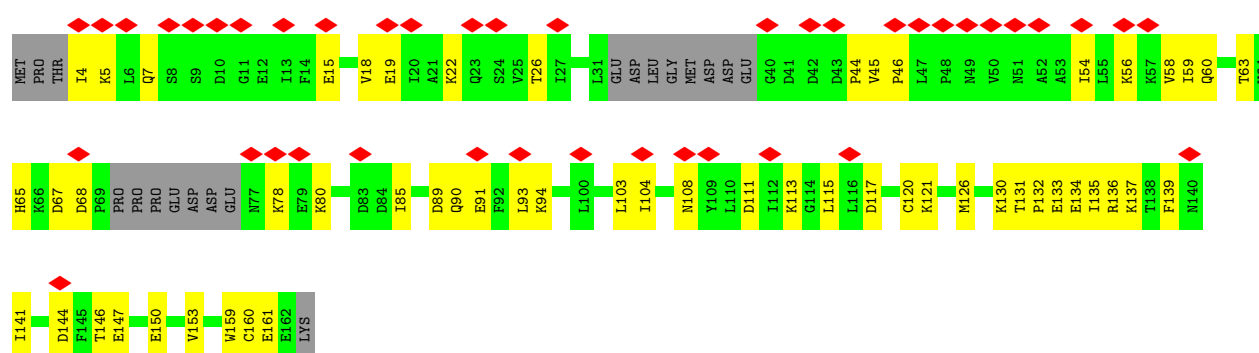




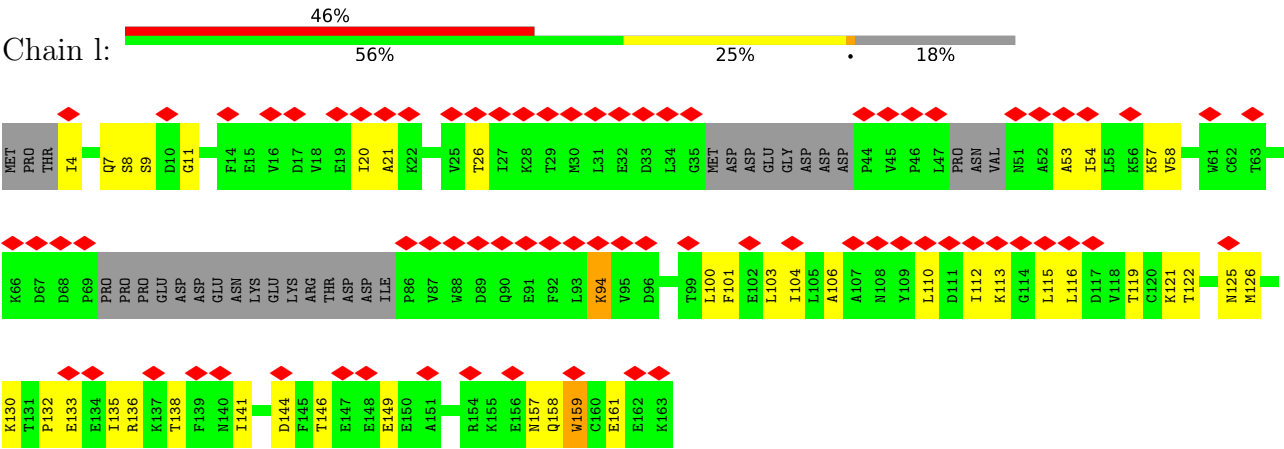
• Molecule 15: S-phase kinase-associated protein 1



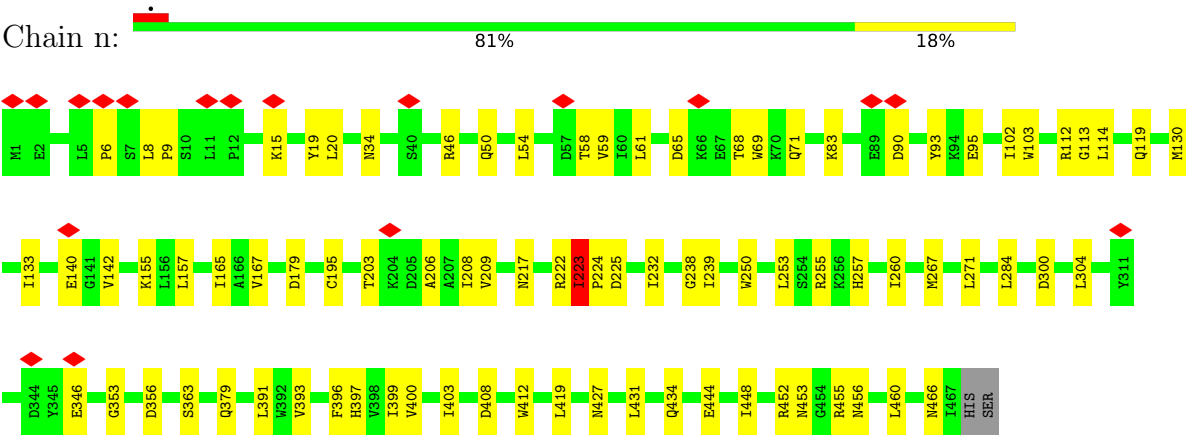
• Molecule 15: S-phase kinase-associated protein 1



• Molecule 15: S-phase kinase-associated protein 1



• Molecule 16: Expressed sequence C85627



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	288673	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)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.041	Depositor
Minimum map value	0.000	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	372.0, 372.0, 372.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ATP, GTP, ZN

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	m	0.36	0/3815	0.78	6/5180 (0.1%)
2	p	0.38	1/3906 (0.0%)	0.83	7/5299 (0.1%)
3	A	0.24	0/5278	0.58	1/7156 (0.0%)
3	B	0.25	0/5306	0.58	1/7194 (0.0%)
3	C	0.22	0/5306	0.56	2/7194 (0.0%)
3	D	0.26	0/5271	0.57	9/7146 (0.1%)
3	E	0.27	0/5306	0.64	3/7194 (0.0%)
3	F	0.25	0/5173	0.57	2/7014 (0.0%)
3	G	0.23	0/5306	0.56	1/7195 (0.0%)
3	H	0.22	0/5264	0.49	2/7134 (0.0%)
3	I	0.27	0/5278	0.61	3/7156 (0.0%)
3	K	0.21	0/5216	0.51	2/7067 (0.0%)
4	M	0.27	0/738	0.54	0/984
4	R	0.27	0/6865	0.63	6/9252 (0.1%)
5	N	0.38	0/986	0.80	2/1336 (0.1%)
5	U	0.32	0/718	0.70	1/980 (0.1%)
6	O	0.33	0/1096	0.70	2/1480 (0.1%)
7	P	0.22	0/7549	0.51	1/10205 (0.0%)
7	S	0.25	0/7608	0.57	3/10289 (0.0%)
8	Q	0.21	0/2950	0.54	1/4005 (0.0%)
8	T	0.22	0/2864	0.52	0/3883
9	V	0.25	0/494	0.55	0/672
10	W	0.27	0/3462	0.60	0/4689
10	Z	0.32	1/3442 (0.0%)	0.70	8/4661 (0.2%)
11	X	0.26	0/3360	0.58	0/4560
11	Y	0.26	0/3377	0.60	0/4583
12	a	0.25	0/1208	0.61	0/1647
12	c	0.35	0/1208	0.78	2/1647 (0.1%)
13	b	0.25	0/5196	0.56	1/7016 (0.0%)
13	d	0.29	1/5096 (0.0%)	0.62	1/6880 (0.0%)
14	e	0.26	0/7868	0.62	1/10637 (0.0%)
14	f	0.32	0/7839	0.76	6/10596 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
15	h	0.29	0/1168	0.65	0/1575
15	j	0.29	0/1177	0.69	0/1589
15	l	0.34	0/1086	0.72	1/1461 (0.1%)
16	n	0.26	1/3881 (0.0%)	0.56	2/5275 (0.0%)
All	All	0.27	4/141661 (0.0%)	0.61	77/191831 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	D	0	1
3	F	0	1
3	G	0	1
12	a	0	2
All	All	0	5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	d	283	ARG	C-N	6.39	1.43	1.32
2	p	428	LEU	C-O	5.58	1.26	1.23
16	n	223	ILE	C-N	5.50	1.41	1.34
10	Z	243	PRO	CG-CD	-5.12	1.33	1.50

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	Z	243	PRO	CA-N-CD	-13.67	92.87	112.00
3	E	131	PRO	CA-N-CD	-11.51	95.89	112.00
7	P	478	PRO	CA-N-CD	-9.75	98.35	112.00
2	p	392	PRO	CA-N-CD	-9.62	98.53	112.00
3	F	131	PRO	CA-N-CD	-9.43	98.80	112.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	36	LYS	Peptide
3	F	445	ARG	Sidechain

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Mol	Chain	Res	Type	Group
3	G	340	ARG	Sidechain
12	a	136	ARG	Sidechain
12	a	72	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	m	3723	0	3777	130	0
2	p	3804	0	3819	128	0
3	A	5161	0	5172	96	0
3	B	5188	0	5201	99	0
3	C	5188	0	5201	84	0
3	D	5154	0	5163	85	0
3	E	5188	0	5201	89	0
3	F	5059	0	5073	91	0
3	G	5188	0	5203	81	0
3	H	5148	0	5166	75	0
3	I	5161	0	5176	131	0
3	K	5102	0	5120	69	0
4	M	728	0	763	7	0
4	R	6735	0	6754	154	0
5	N	967	0	991	29	0
5	U	701	0	694	27	0
6	O	1066	0	1077	22	0
7	P	7419	0	7514	124	0
7	S	7476	0	7557	123	0
8	Q	2884	0	2862	51	0
8	T	2803	0	2795	51	0
9	V	476	0	447	16	0
10	W	3387	0	3264	62	0
10	Z	3368	0	3247	83	0
11	X	3287	0	3201	90	0
11	Y	3303	0	3214	79	0
12	a	1173	0	1159	19	0
12	c	1173	0	1159	36	0
13	b	5084	0	4971	118	0
13	d	4985	0	4876	119	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	e	7723	0	7829	193	0
14	f	7695	0	7808	241	0
15	h	1151	0	1160	33	0
15	j	1160	0	1154	39	0
15	l	1071	0	1078	35	0
16	n	3787	0	3806	52	0
17	P	31	0	12	1	0
17	R	31	0	12	2	0
17	S	31	0	12	1	0
17	e	31	0	12	0	0
17	f	31	0	12	1	0
18	W	32	0	12	2	0
18	X	32	0	12	4	0
18	Y	32	0	12	1	0
18	Z	32	0	12	0	0
19	W	1	0	0	0	0
19	X	1	0	0	0	0
19	Y	1	0	0	0	0
19	Z	1	0	0	0	0
20	b	3	0	0	0	0
20	d	3	0	0	0	0
All	All	138959	0	138760	2817	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 10.

The worst 5 of 2817 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)
13:d:733:CYS:HB2	13:d:736:CYS:SG	1.90	1.10
3:F:130:MET:HE1	3:G:43:ARG:HE	1.37	0.87
10:Z:191:GLN:O	10:Z:195:ASN:HB2	1.74	0.86
3:F:639:LEU:HB3	3:F:644:LEU:HD11	1.57	0.86
12:a:103:LEU:O	12:a:107:CYS:HB2	1.76	0.85

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	m	459/466 (98%)	425 (93%)	32 (7%)	2 (0%)	30	59
2	p	462/468 (99%)	424 (92%)	34 (7%)	4 (1%)	14	42
3	A	643/682 (94%)	609 (95%)	33 (5%)	1 (0%)	43	71
3	B	649/682 (95%)	615 (95%)	32 (5%)	2 (0%)	36	65
3	C	649/682 (95%)	626 (96%)	20 (3%)	3 (0%)	24	54
3	D	642/682 (94%)	619 (96%)	23 (4%)	0	100	100
3	E	649/682 (95%)	618 (95%)	29 (4%)	2 (0%)	36	65
3	F	627/682 (92%)	594 (95%)	31 (5%)	2 (0%)	36	65
3	G	649/682 (95%)	620 (96%)	28 (4%)	1 (0%)	43	71
3	H	642/682 (94%)	621 (97%)	21 (3%)	0	100	100
3	I	643/682 (94%)	621 (97%)	20 (3%)	2 (0%)	36	65
3	K	633/682 (93%)	606 (96%)	26 (4%)	1 (0%)	43	71
4	M	86/937 (9%)	81 (94%)	5 (6%)	0	100	100
4	R	834/937 (89%)	803 (96%)	31 (4%)	0	100	100
5	N	118/164 (72%)	115 (98%)	3 (2%)	0	100	100
5	U	85/164 (52%)	77 (91%)	8 (9%)	0	100	100
6	O	126/346 (36%)	122 (97%)	4 (3%)	0	100	100
7	P	934/1163 (80%)	898 (96%)	36 (4%)	0	100	100
7	S	945/1163 (81%)	907 (96%)	37 (4%)	1 (0%)	48	78
8	Q	361/581 (62%)	334 (92%)	25 (7%)	2 (1%)	21	50
8	T	351/581 (60%)	335 (95%)	16 (5%)	0	100	100
9	V	57/228 (25%)	53 (93%)	4 (7%)	0	100	100
10	W	429/445 (96%)	414 (96%)	15 (4%)	0	100	100
10	Z	424/445 (95%)	398 (94%)	26 (6%)	0	100	100
11	X	410/449 (91%)	397 (97%)	12 (3%)	1 (0%)	43	71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	Y	417/449 (93%)	383 (92%)	34 (8%)	0	100	100
12	a	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
12	c	145/147 (99%)	132 (91%)	12 (8%)	1 (1%)	18	47
13	b	618/782 (79%)	572 (93%)	46 (7%)	0	100	100
13	d	604/782 (77%)	565 (94%)	39 (6%)	0	100	100
14	e	965/993 (97%)	881 (91%)	83 (9%)	1 (0%)	48	78
14	f	959/993 (97%)	869 (91%)	85 (9%)	5 (0%)	24	54
15	h	134/163 (82%)	127 (95%)	7 (5%)	0	100	100
15	j	138/163 (85%)	132 (96%)	5 (4%)	1 (1%)	18	47
15	l	125/163 (77%)	117 (94%)	8 (6%)	0	100	100
16	n	465/469 (99%)	440 (95%)	23 (5%)	2 (0%)	30	59
All	All	17222/20608 (84%)	16288 (95%)	900 (5%)	34 (0%)	44	71

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	p	129	ARG
3	G	99	ASP
7	S	942	GLU
14	f	495	GLN
14	f	959	LYS

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	m	425/430 (99%)	419 (99%)	6 (1%)	59	70
2	p	428/431 (99%)	418 (98%)	10 (2%)	44	63
3	A	588/613 (96%)	587 (100%)	1 (0%)	87	85
3	B	591/613 (96%)	589 (100%)	2 (0%)	86	84
3	C	591/613 (96%)	588 (100%)	3 (0%)	81	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	587/613 (96%)	582 (99%)	5 (1%)	70	76
3	E	591/613 (96%)	587 (99%)	4 (1%)	76	78
3	F	578/613 (94%)	576 (100%)	2 (0%)	86	84
3	G	591/613 (96%)	587 (99%)	4 (1%)	76	78
3	H	586/613 (96%)	580 (99%)	6 (1%)	68	75
3	I	588/613 (96%)	585 (100%)	3 (0%)	81	81
3	K	581/613 (95%)	580 (100%)	1 (0%)	87	85
4	M	79/862 (9%)	79 (100%)	0	100	100
4	R	773/862 (90%)	768 (99%)	5 (1%)	78	80
5	N	107/143 (75%)	106 (99%)	1 (1%)	70	76
5	U	76/143 (53%)	76 (100%)	0	100	100
6	O	115/278 (41%)	114 (99%)	1 (1%)	70	76
7	P	843/1054 (80%)	842 (100%)	1 (0%)	88	89
7	S	847/1054 (80%)	839 (99%)	8 (1%)	70	76
8	Q	322/516 (62%)	322 (100%)	0	100	100
8	T	313/516 (61%)	311 (99%)	2 (1%)	78	80
9	V	50/197 (25%)	50 (100%)	0	100	100
10	W	371/382 (97%)	369 (100%)	2 (0%)	81	81
10	Z	369/382 (97%)	367 (100%)	2 (0%)	81	81
11	X	356/376 (95%)	353 (99%)	3 (1%)	73	77
11	Y	355/376 (94%)	352 (99%)	3 (1%)	73	77
12	a	132/132 (100%)	132 (100%)	0	100	100
12	c	132/132 (100%)	130 (98%)	2 (2%)	57	69
13	b	555/682 (81%)	547 (99%)	8 (1%)	59	70
13	d	544/682 (80%)	541 (99%)	3 (1%)	78	80
14	e	884/909 (97%)	876 (99%)	8 (1%)	70	76
14	f	880/909 (97%)	869 (99%)	11 (1%)	61	71
15	h	132/150 (88%)	131 (99%)	1 (1%)	73	77
15	j	132/150 (88%)	132 (100%)	0	100	100
15	l	121/150 (81%)	120 (99%)	1 (1%)	73	77
16	n	433/435 (100%)	432 (100%)	1 (0%)	87	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	15646/18463 (85%)	15536 (99%)	110 (1%)	73	78

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	S	492	VAL
11	Y	182	VAL
15	l	159	TRP
14	f	282	LEU
7	S	539	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 316 such sidechains are listed below:

Mol	Chain	Res	Type
12	a	46	GLN
14	f	273	HIS
13	b	224	ASN
13	d	773	GLN
14	f	856	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 10 are monoatomic - leaving 9 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
17	ATP	f	1001	-	29,33,33	0.29	0	44,52,52	0.61	1 (2%)
17	ATP	R	1001	-	29,33,33	0.28	0	44,52,52	0.51	1 (2%)
17	ATP	S	1201	-	29,33,33	0.29	0	44,52,52	0.46	0
18	GTP	Y	501	19	30,34,34	0.83	1 (3%)	46,54,54	1.78	11 (23%)
17	ATP	e	1001	-	29,33,33	0.28	0	44,52,52	0.46	1 (2%)
18	GTP	X	501	19	30,34,34	0.84	1 (3%)	46,54,54	1.85	11 (23%)
18	GTP	Z	501	19	30,34,34	0.86	1 (3%)	46,54,54	1.73	12 (26%)
17	ATP	P	1201	-	29,33,33	0.28	0	44,52,52	0.45	1 (2%)
18	GTP	W	501	19	30,34,34	0.85	1 (3%)	46,54,54	1.78	11 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
17	ATP	f	1001	-	-	8/22/38/38	0/3/3/3
17	ATP	R	1001	-	-	7/22/38/38	0/3/3/3
17	ATP	S	1201	-	-	5/22/38/38	0/3/3/3
18	GTP	Y	501	19	-	6/22/38/38	0/3/3/3
17	ATP	e	1001	-	-	9/22/38/38	0/3/3/3
18	GTP	X	501	19	-	3/22/38/38	0/3/3/3
18	GTP	Z	501	19	-	7/22/38/38	0/3/3/3
17	ATP	P	1201	-	-	5/22/38/38	0/3/3/3
18	GTP	W	501	19	-	3/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	Z	501	GTP	C2-N3	2.22	1.38	1.33
18	Y	501	GTP	C2-N3	2.19	1.38	1.33
18	W	501	GTP	C2-N3	2.17	1.38	1.33
18	X	501	GTP	C2-N3	2.15	1.38	1.33

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	X	501	GTP	C5-C4-N3	-5.23	119.97	128.46
18	Y	501	GTP	C5-C4-N3	-5.03	120.31	128.46
18	W	501	GTP	C5-C4-N3	-4.97	120.39	128.46
18	X	501	GTP	C2-N3-C4	4.87	120.97	112.30
18	Z	501	GTP	C5-C4-N3	-4.78	120.70	128.46

There are no chirality outliers.

5 of 53 torsion outliers are listed below:

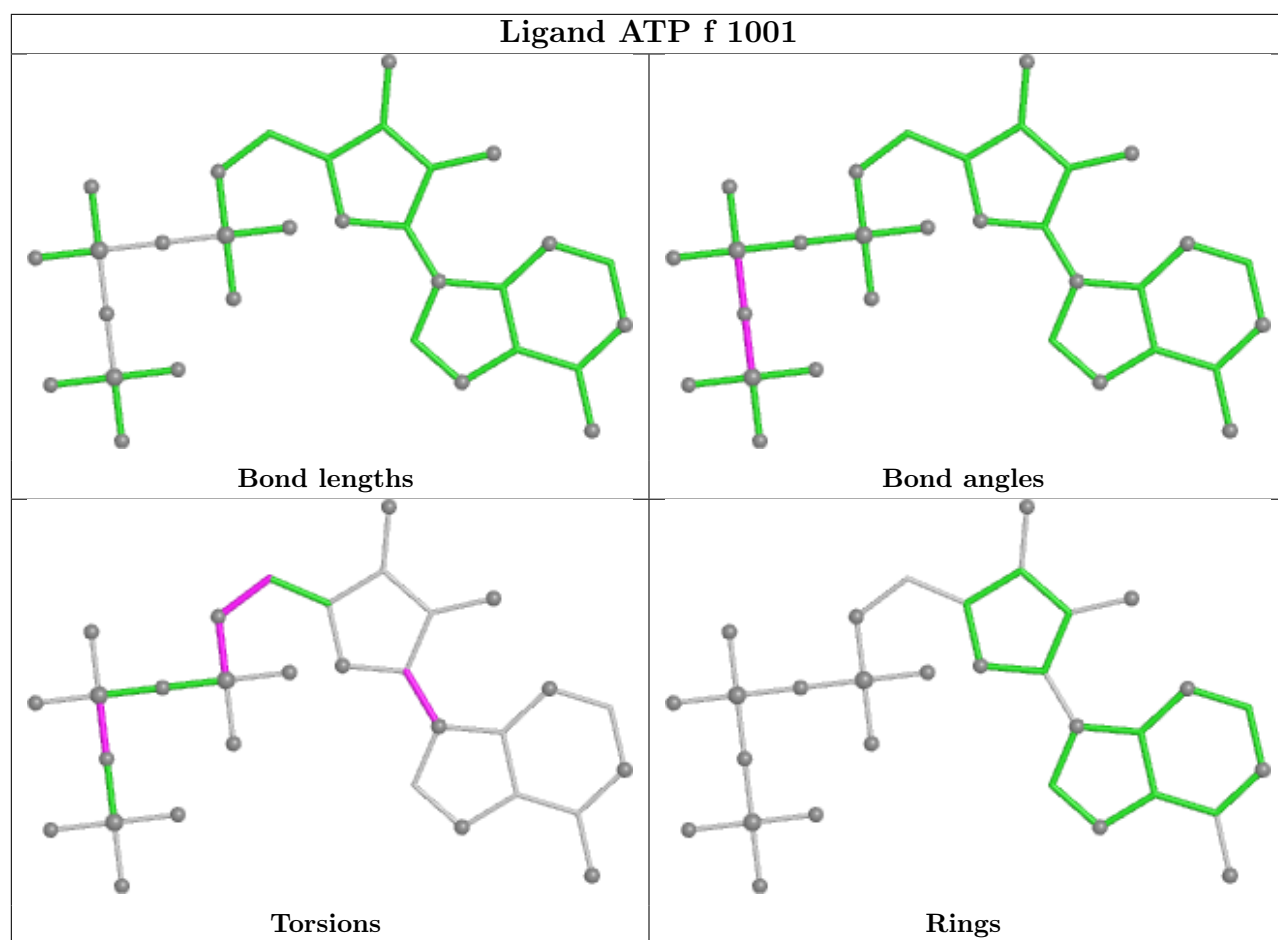
Mol	Chain	Res	Type	Atoms
17	P	1201	ATP	PB-O3B-PG-O3G
17	R	1001	ATP	C5'-O5'-PA-O1A
17	R	1001	ATP	C5'-O5'-PA-O2A
17	R	1001	ATP	C3'-C4'-C5'-O5'
17	e	1001	ATP	PB-O3B-PG-O3G

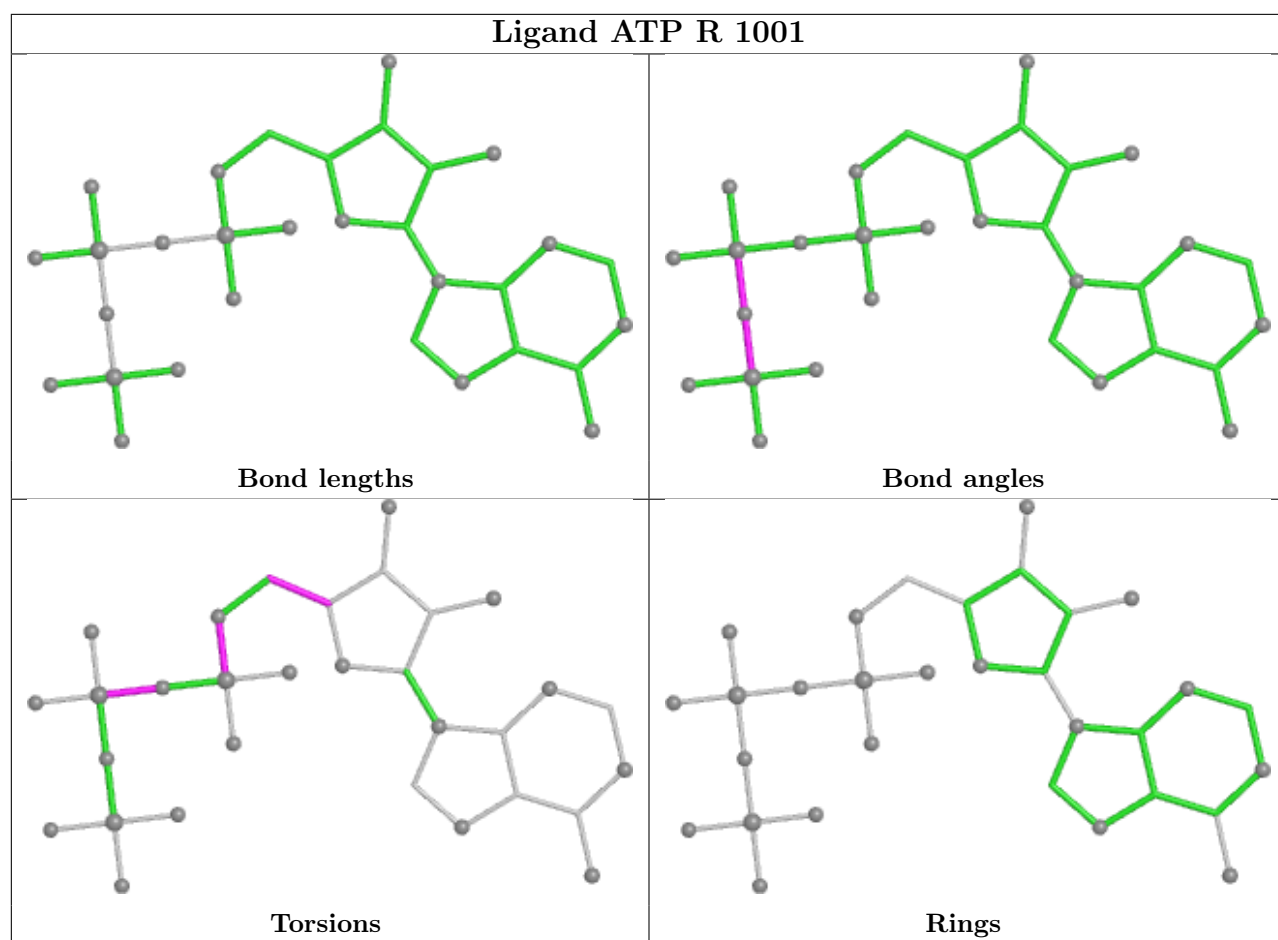
There are no ring outliers.

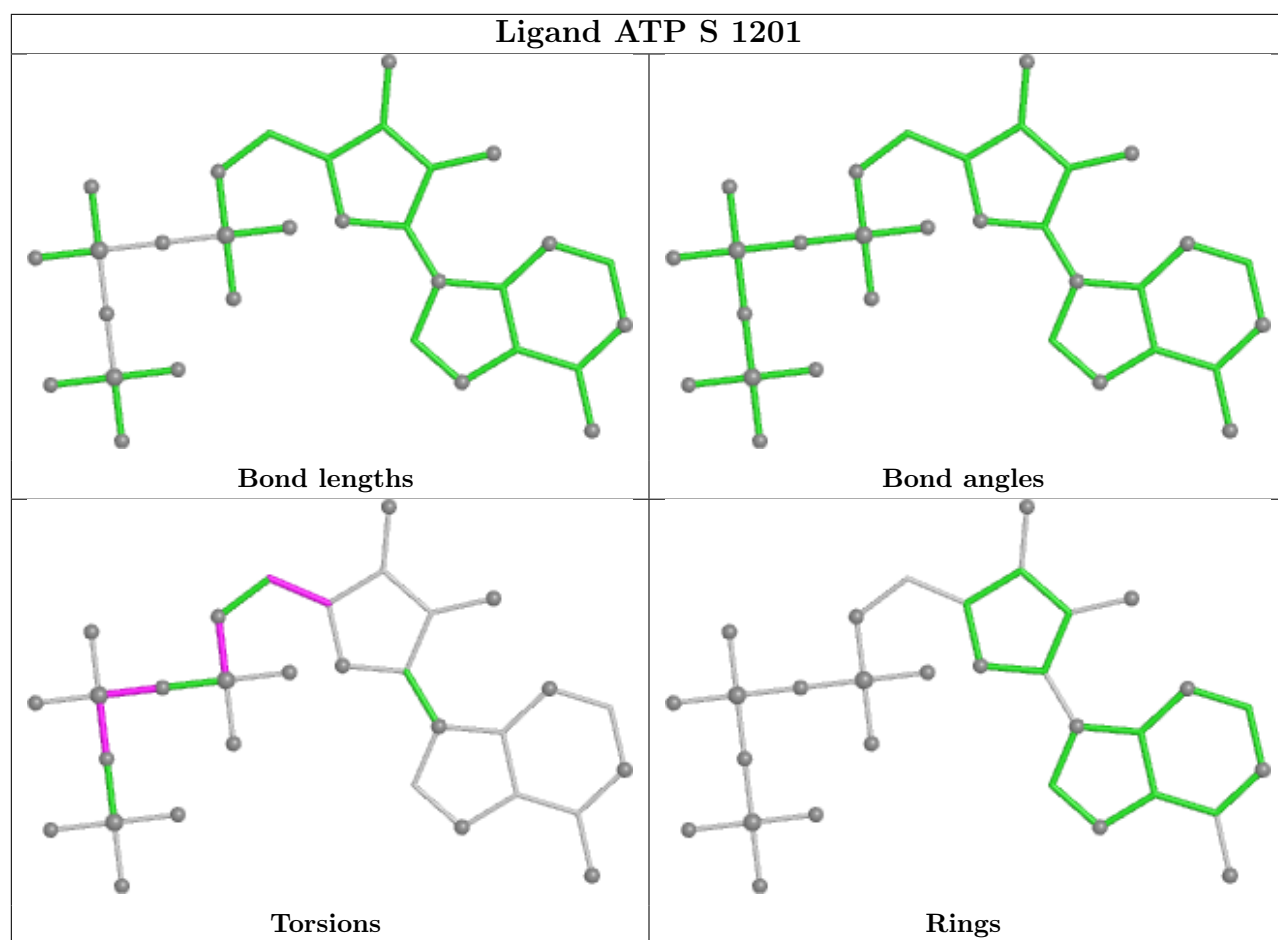
7 monomers are involved in 12 short contacts:

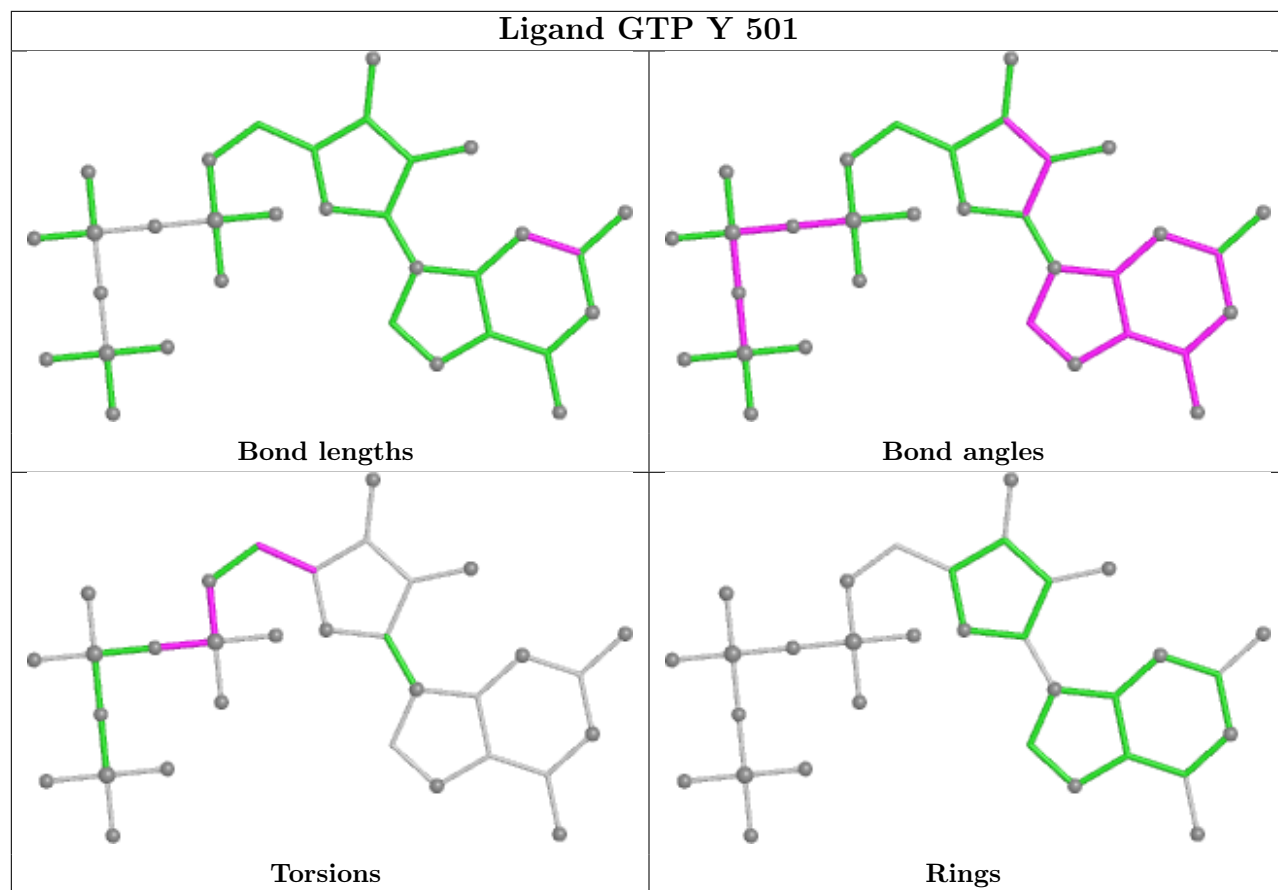
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	f	1001	ATP	1	0
17	R	1001	ATP	2	0
17	S	1201	ATP	1	0
18	Y	501	GTP	1	0
18	X	501	GTP	4	0
17	P	1201	ATP	1	0
18	W	501	GTP	2	0

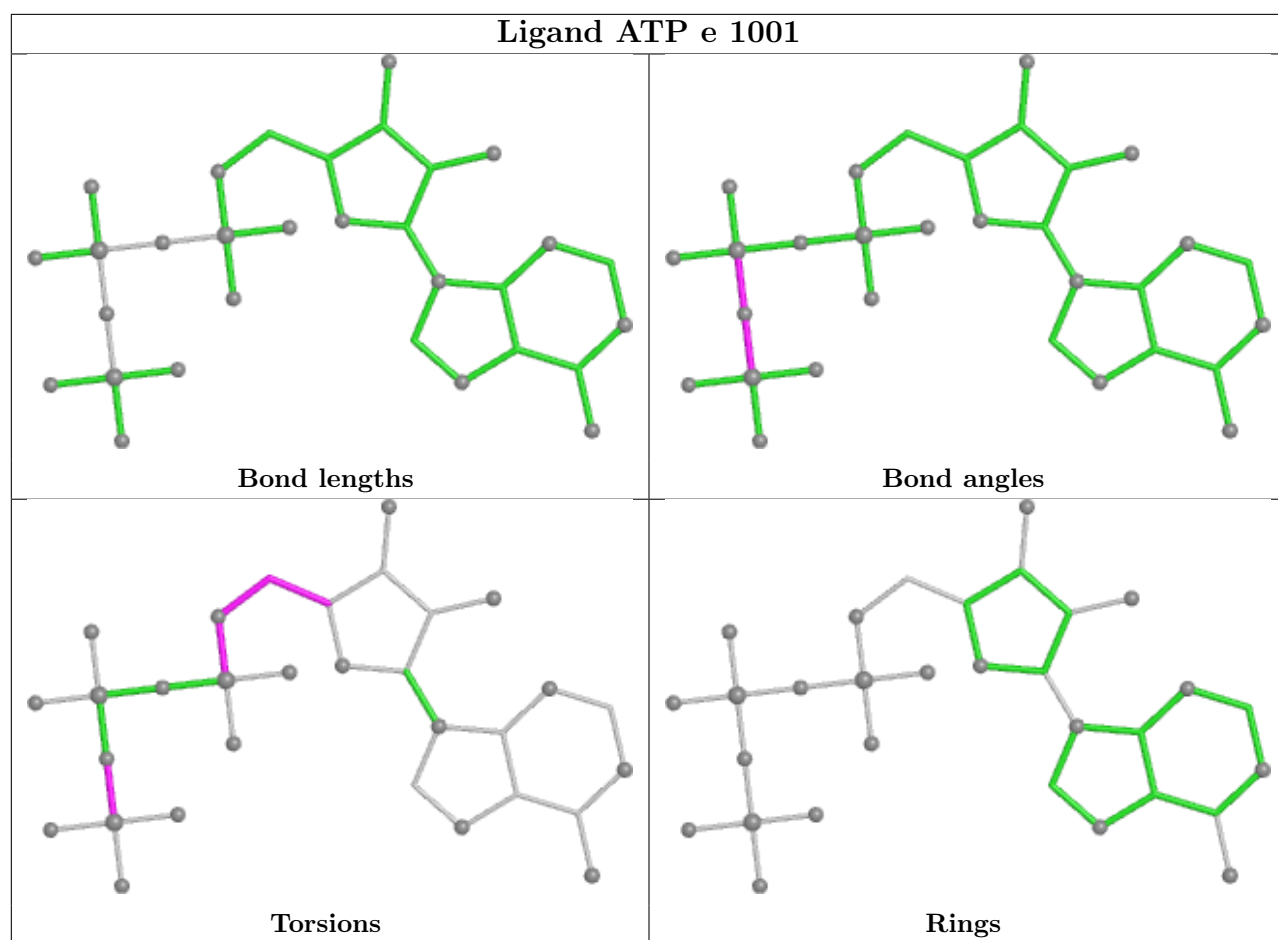
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

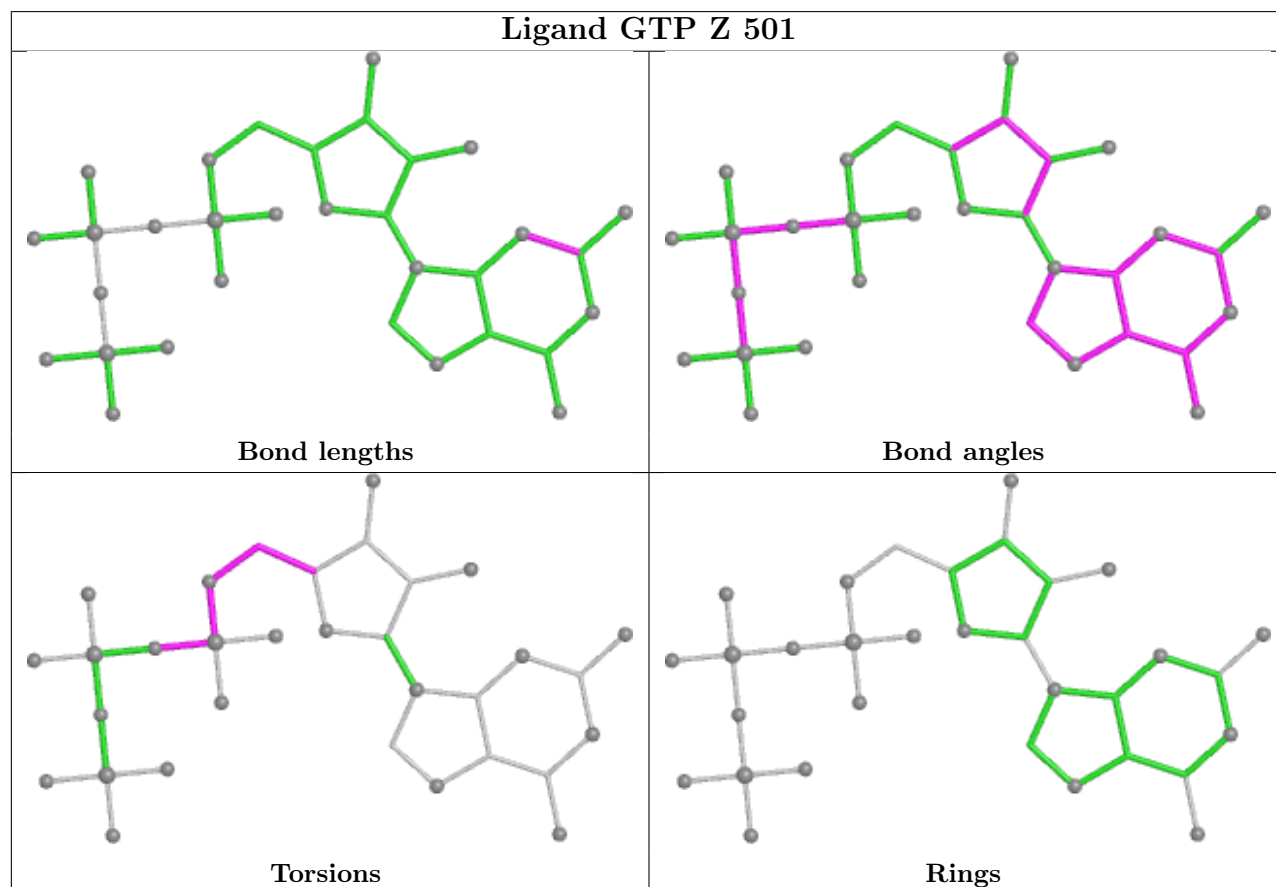
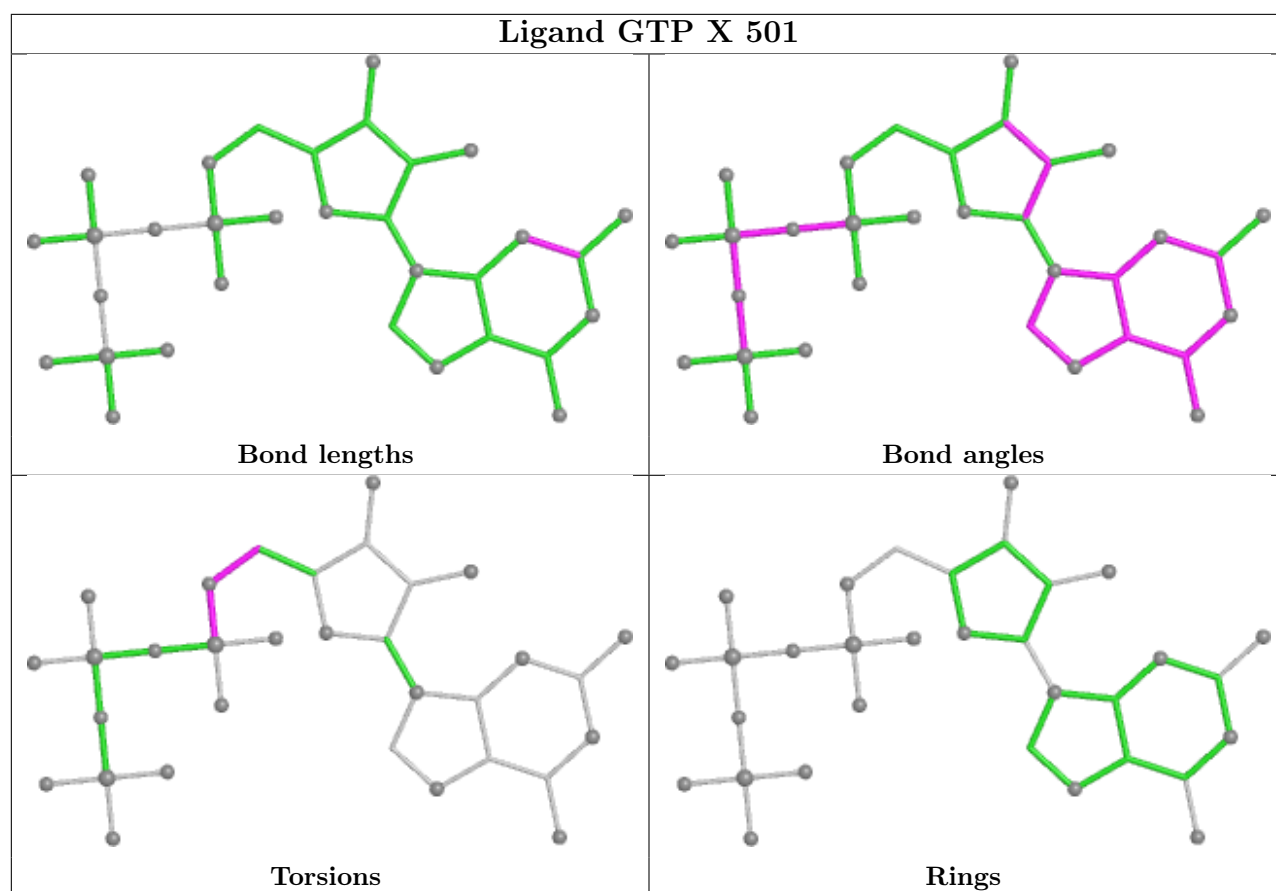


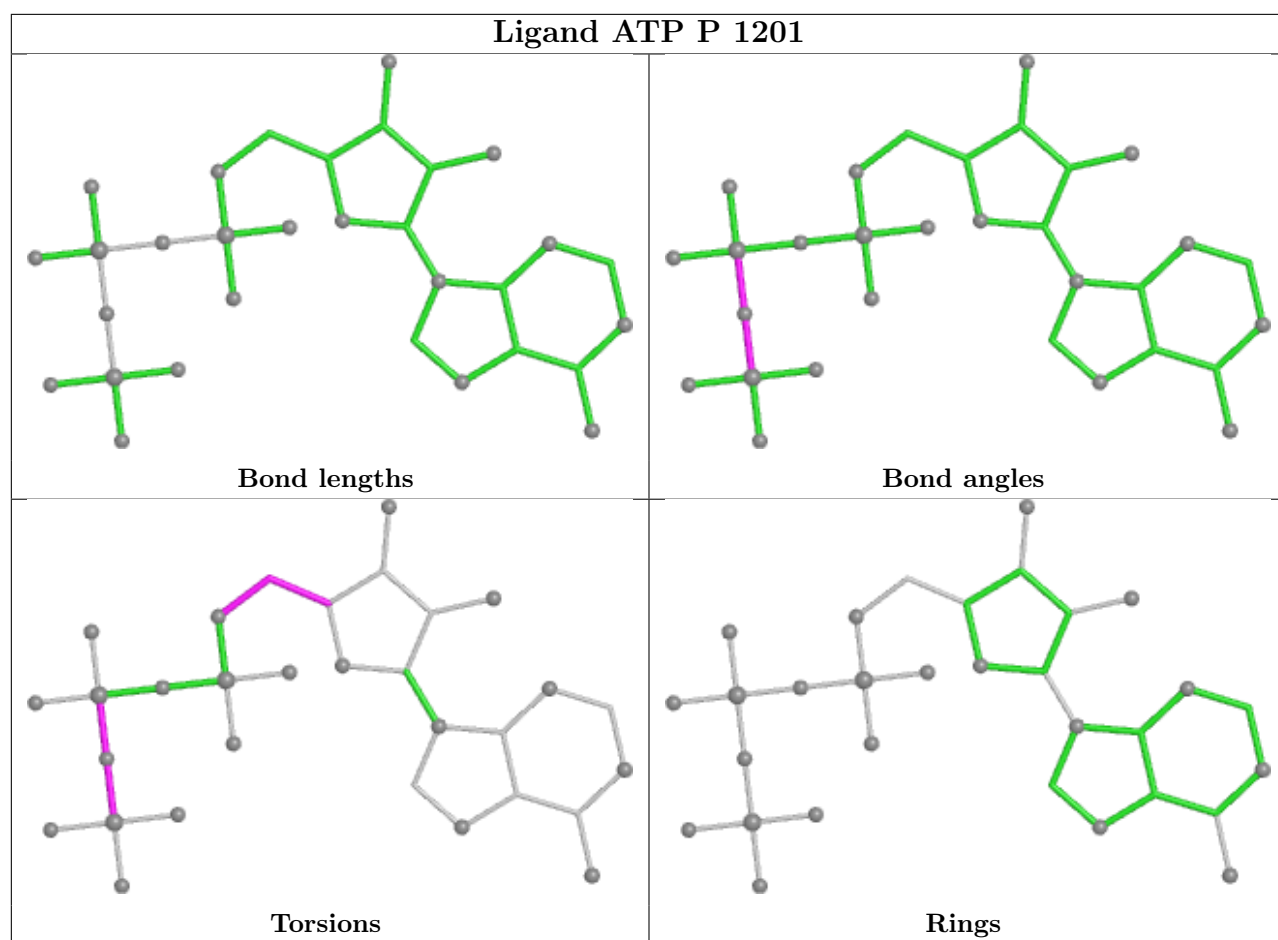


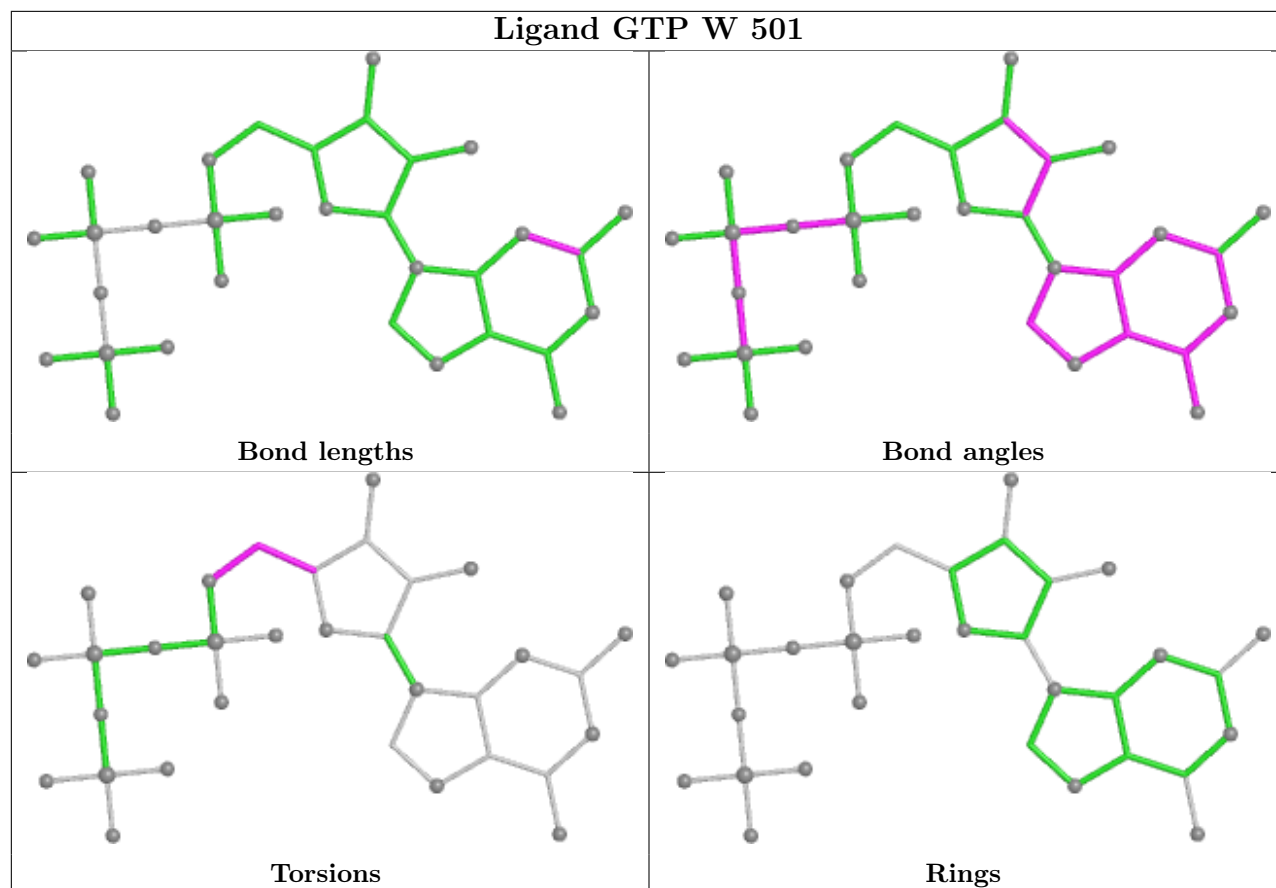












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

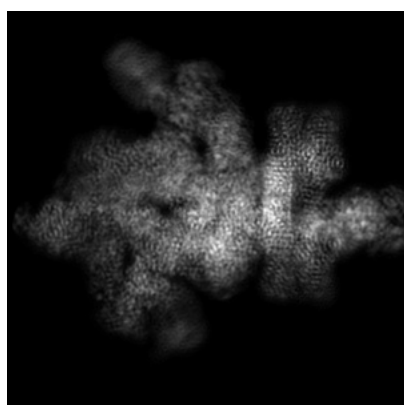
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-69647. These allow visual inspection of the internal detail of the map and identification of artifacts.

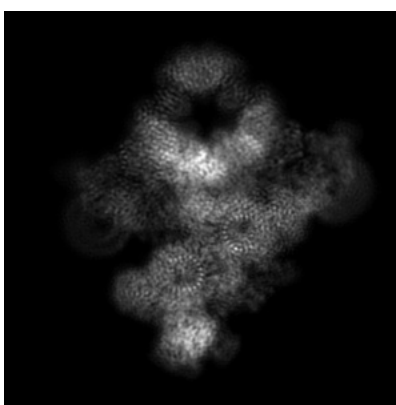
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

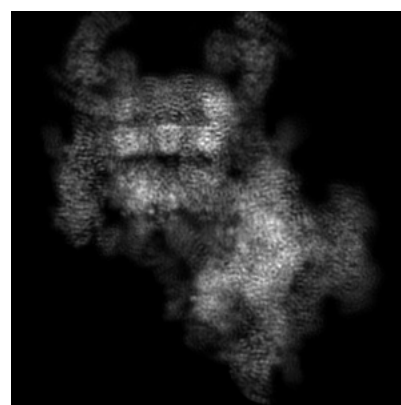
6.1.1 Primary map



X



Y

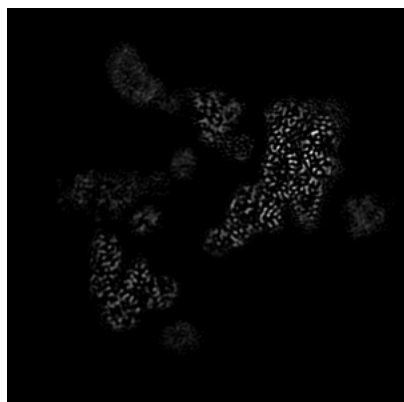


Z

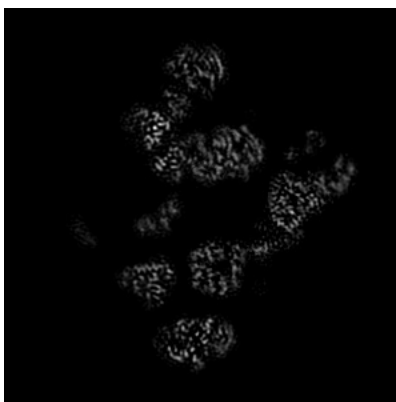
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

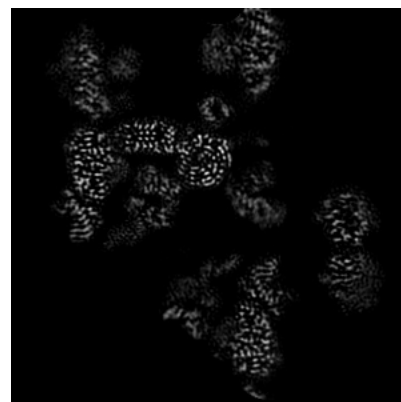
6.2.1 Primary map



X Index: 200



Y Index: 200

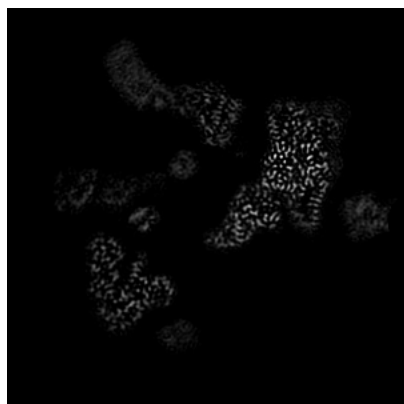


Z Index: 200

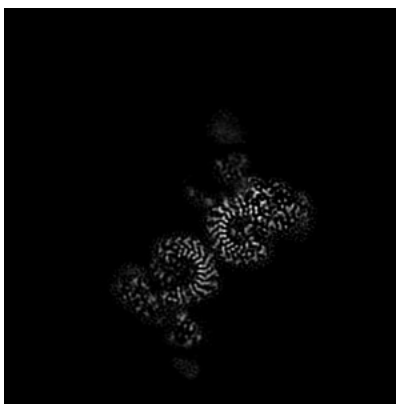
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

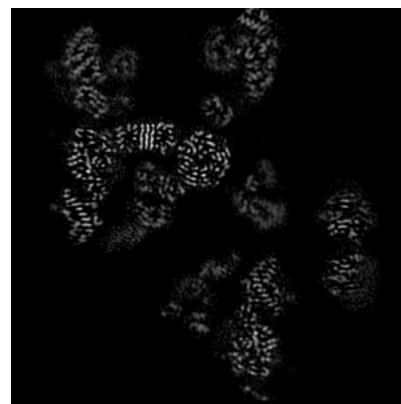
6.3.1 Primary map



X Index: 204



Y Index: 282

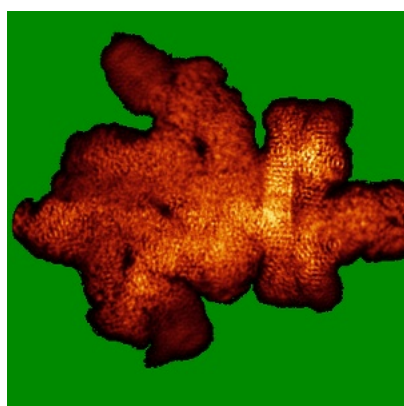


Z Index: 197

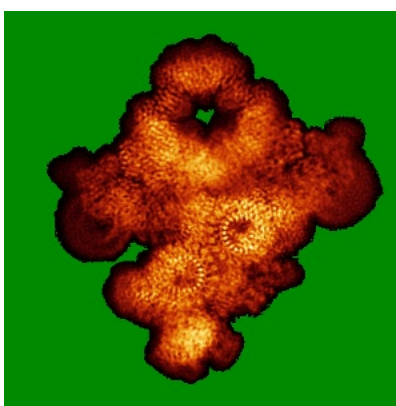
The images above show the largest variance slices of the map in three orthogonal directions.

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

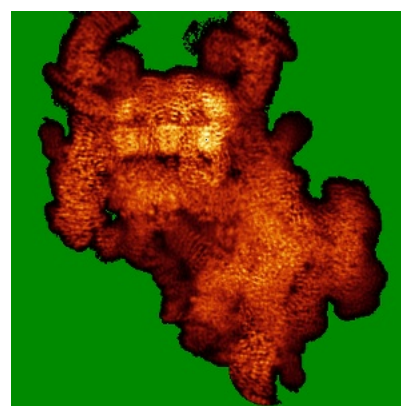
6.4.1 Primary map



X



Y

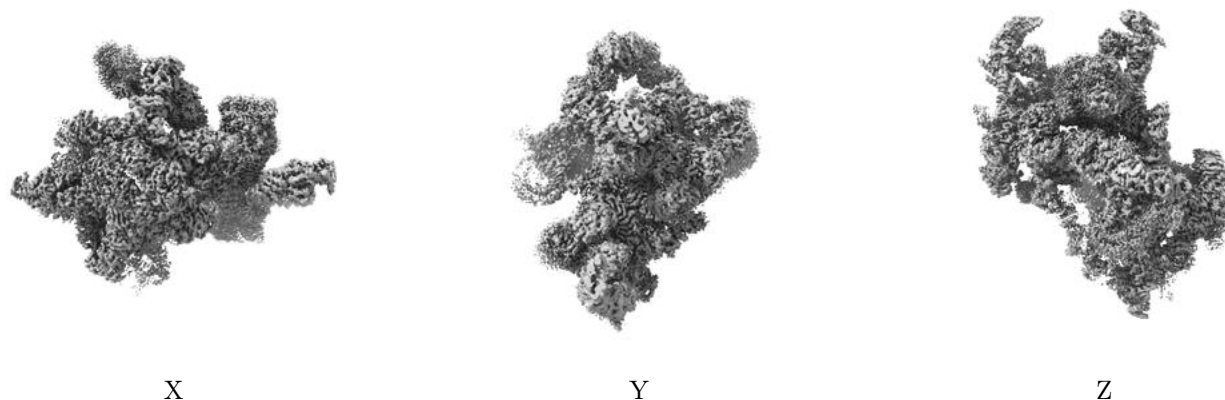


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

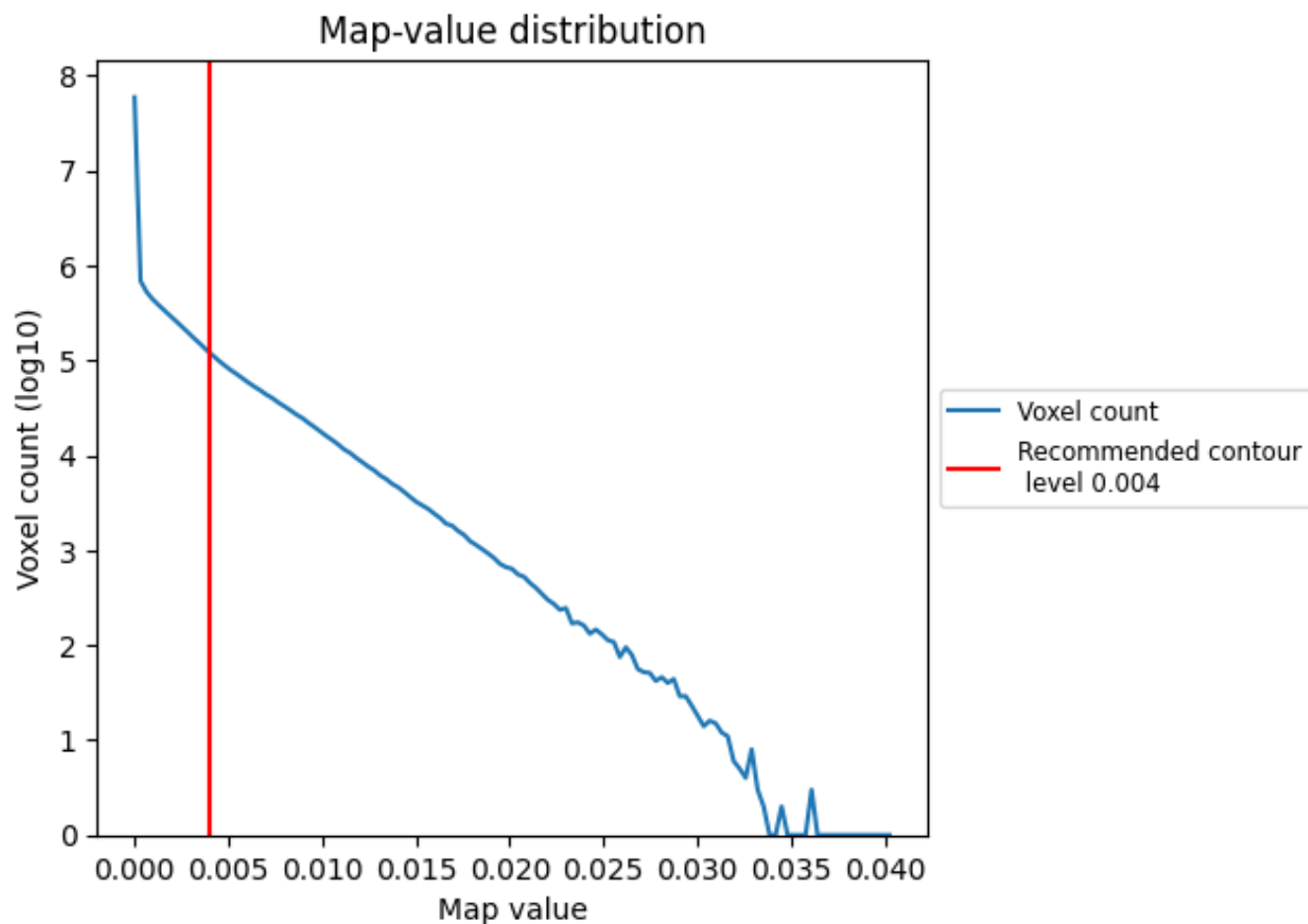
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

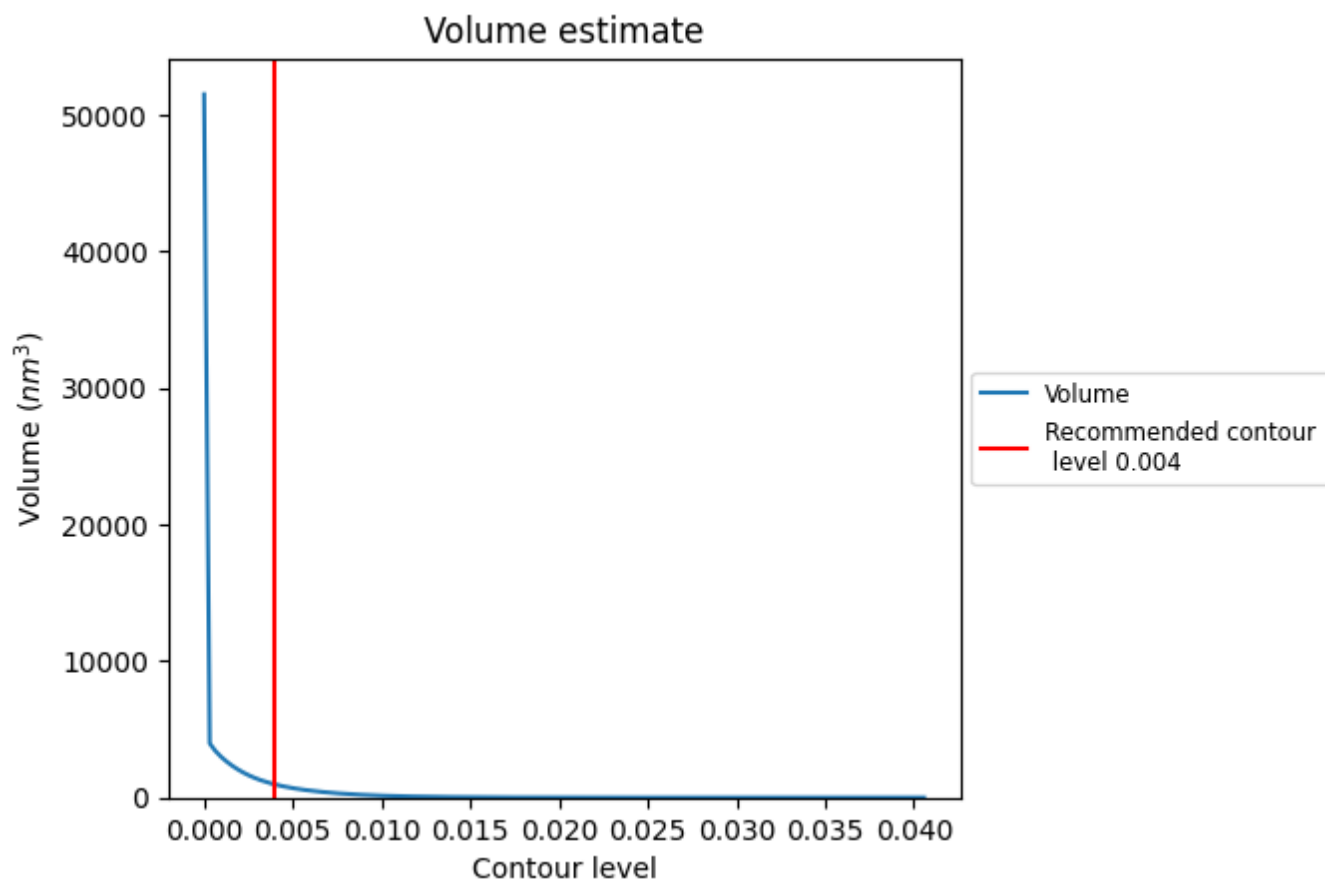
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

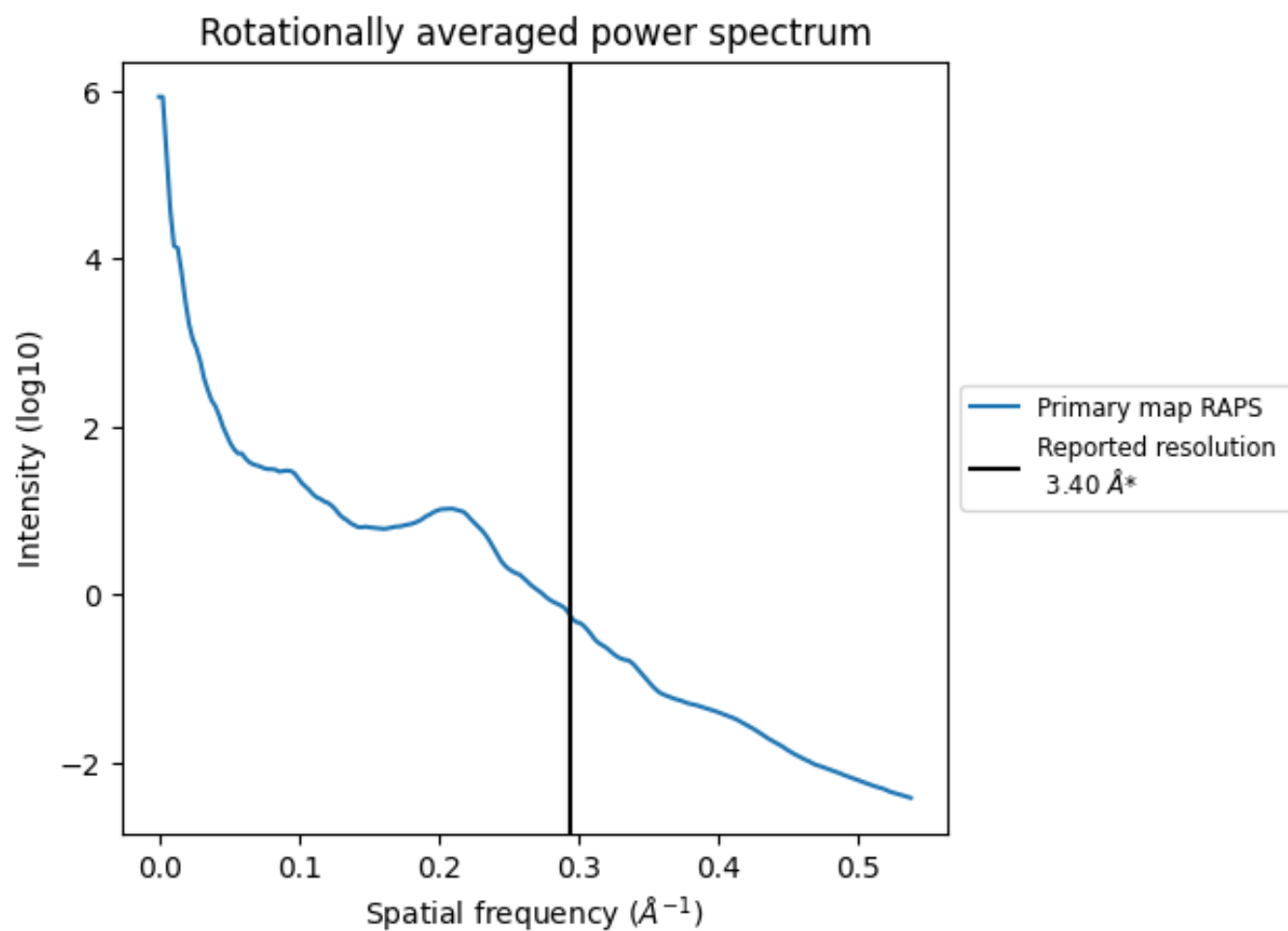
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 960 nm^3 ; this corresponds to an approximate mass of 867 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 0.294 Å⁻¹

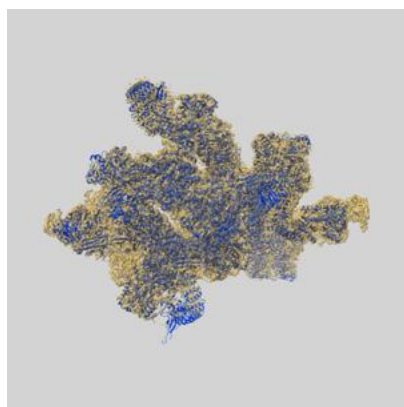
8 Fourier-Shell correlation

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

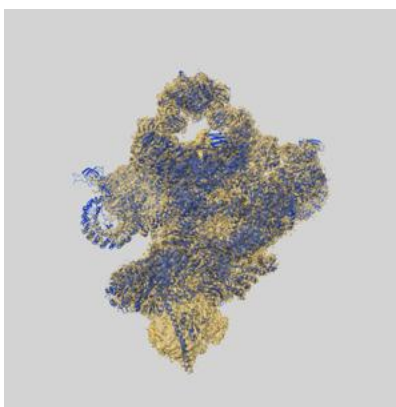
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-69647 and PDB model 24MC. Per-residue inclusion information can be found in section 3 on page 11.

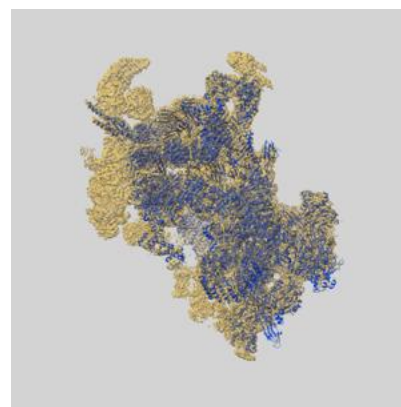
9.1 Map-model overlay [i](#)



X



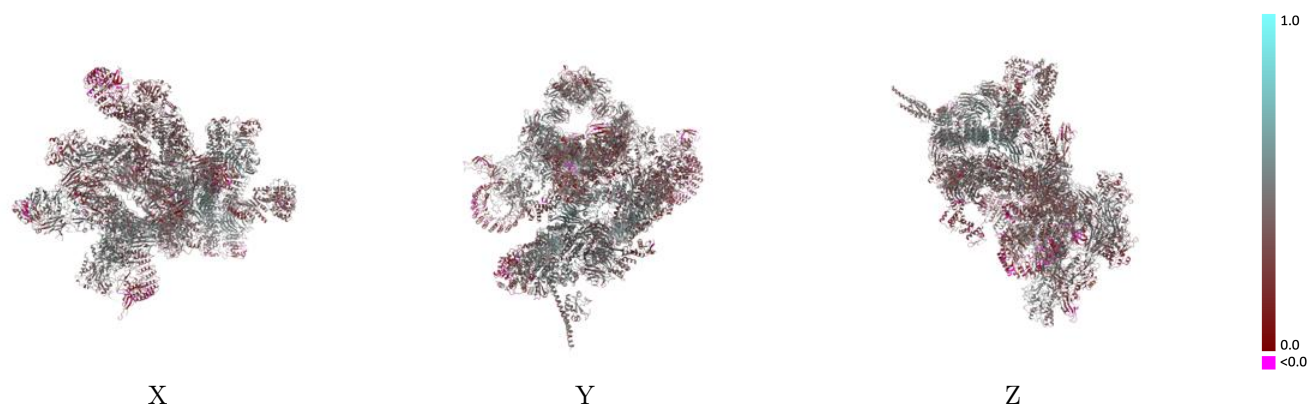
Y



Z

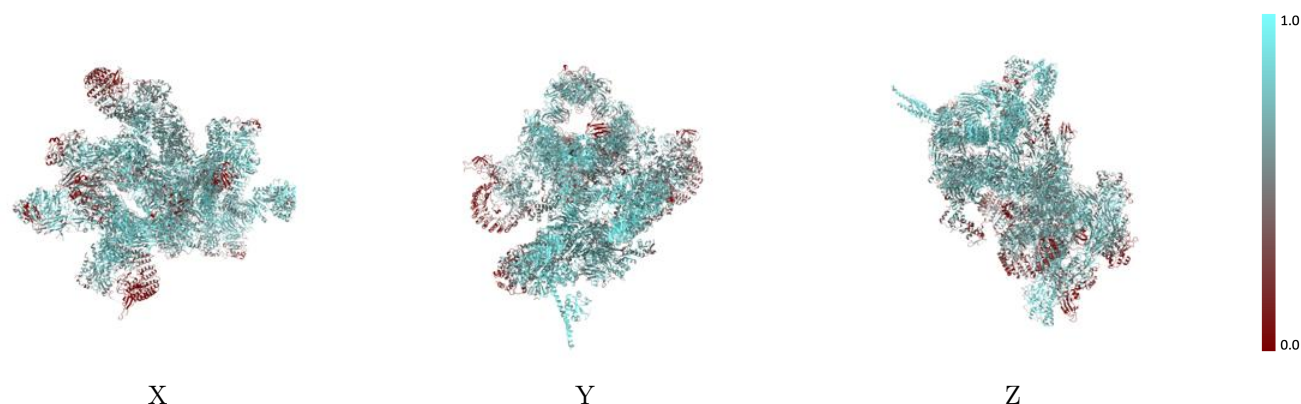
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



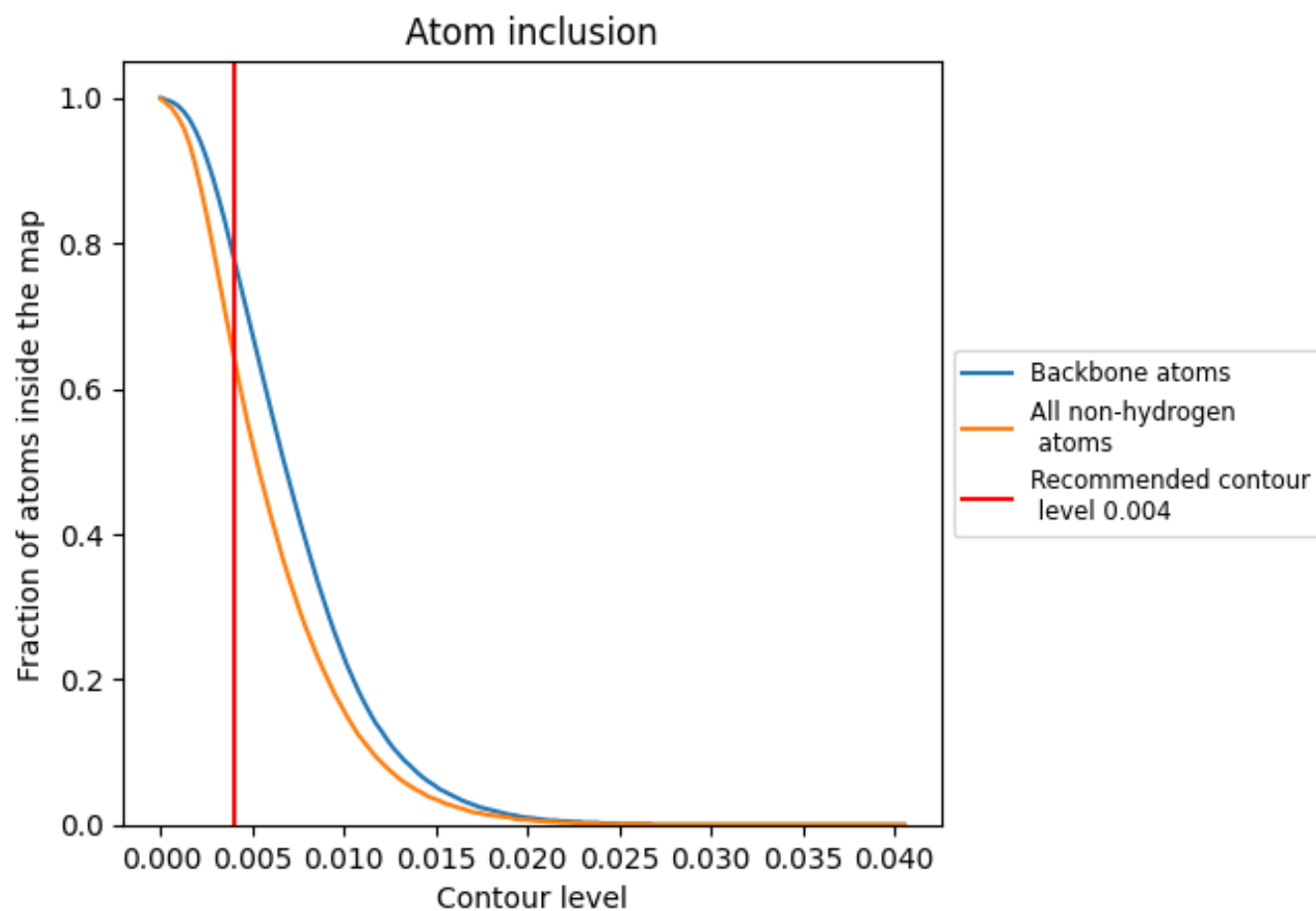
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.004).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 64% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6430	 0.3860
A	 0.6070	 0.3960
B	 0.7210	 0.4290
C	 0.7040	 0.4020
D	 0.5740	 0.3740
E	 0.6140	 0.3770
F	 0.5260	 0.3670
G	 0.7220	 0.4340
H	 0.7530	 0.4700
I	 0.5920	 0.3570
K	 0.6390	 0.3440
M	 0.7730	 0.4590
N	 0.8140	 0.4400
O	 0.8050	 0.4140
P	 0.7080	 0.4240
Q	 0.7940	 0.4770
R	 0.6930	 0.3650
S	 0.7750	 0.4600
T	 0.8340	 0.4820
U	 0.8420	 0.4610
V	 0.9070	 0.4870
W	 0.6950	 0.4190
X	 0.5720	 0.3580
Y	 0.6860	 0.3830
Z	 0.6760	 0.3830
a	 0.7800	 0.4720
b	 0.5300	 0.3730
c	 0.6610	 0.3280
d	 0.4870	 0.2720
e	 0.4480	 0.3340
f	 0.4570	 0.2700
h	 0.6090	 0.3250
j	 0.5100	 0.3120
l	 0.3600	 0.2400
m	 0.6430	 0.3930



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Chain	Atom inclusion	Q-score
n	 0.8230	 0.4820
p	 0.6730	 0.3690