



wwPDB EM Validation Summary Report ⓘ

Jun 13, 2026 – 07:46 am BST

PDB ID : 9SFP / pdb_00009sfp
EMDB ID : EMD-54838
Title : Native cytoplasmic lattices from mouse oocytes
Authors : Kilic, Z.I.; van Loenhout, J.; Chaillet, M.; Noteborn, W.E.M.; Leung, M.R.
Deposited on : 2025-08-20
Resolution : 4.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

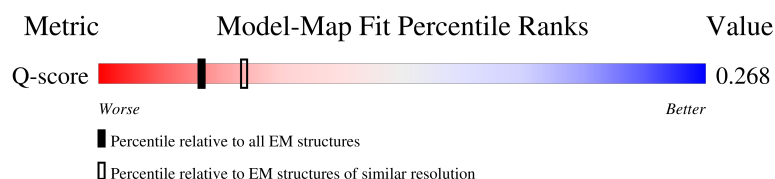
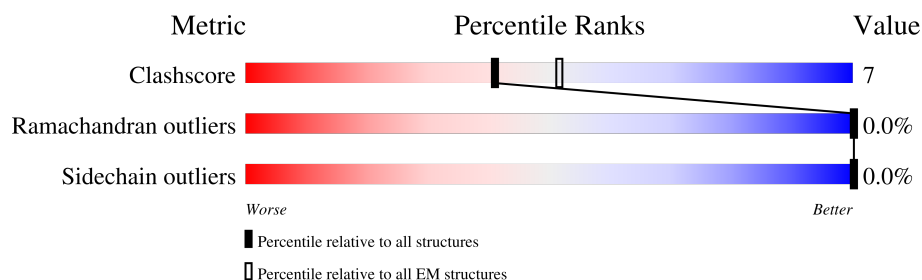
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	A	468	5% 83% 16% .
1	B	468	16% 82% 18%
2	C	440	21% 8% 71%
3	D	937	23% 76% 21% .

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Mol	Chain	Length	Quality of chain
3	F	937	
4	H	1163	
4	I	1163	
5	J	993	
6	K	164	
6	L	164	
7	M	682	
7	N	682	
7	O	682	
7	P	682	
7	Q	682	
7	R	682	
7	S	682	
7	T	682	
7	U	682	
7	V	682	
8	W	581	
8	Y	581	
9	a	451	
10	b	445	
11	c	147	
12	d	782	
13	e	228	

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 117354 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 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	465	Total	C	N	O	S	0	0
			3764	2426	631	676	31		
1	B	468	Total	C	N	O	S	0	0
			3791	2444	637	679	31		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	127	Total	C	N	O	S	0	0
			1056	682	189	177	8		

- Molecule 3 is a protein called NLR family, pyrin domain containing 4F.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	907	Total	C	N	O	S	0	0
			7303	4665	1210	1359	69		
3	F	918	Total	C	N	O	S	0	0
			7387	4719	1226	1372	70		

- Molecule 4 is a protein called NACHT, LRR and PYD domains-containing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	949	Total	C	N	O	S	0	0
			7518	4783	1269	1398	68		
4	I	949	Total	C	N	O	S	0	0
			7518	4783	1269	1398	68		

- Molecule 5 is a protein called NACHT, LRR and PYD domains-containing protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	955	Total	C	N	O	S	0	0
			7628	4849	1307	1408	64		

- Molecule 6 is a protein called Oocyte-expressed protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	121	Total	C	N	O	S	0	0
			973	622	169	177	5		
6	L	86	Total	C	N	O	S	0	0
			694	443	118	128	5		

- Molecule 7 is a protein called Inactive protein-arginine deiminase type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	682	Total	C	N	O	S	0	0
			5388	3442	888	1019	39		
7	N	682	Total	C	N	O	S	0	0
			5388	3442	888	1019	39		
7	O	682	Total	C	N	O	S	0	0
			5388	3442	888	1019	39		
7	P	682	Total	C	N	O	S	0	0
			5388	3442	888	1019	39		
7	Q	665	Total	C	N	O	S	0	0
			5256	3364	864	989	39		
7	R	671	Total	C	N	O	S	0	0
			5300	3389	874	998	39		
7	S	682	Total	C	N	O	S	0	0
			5388	3442	888	1019	39		
7	T	682	Total	C	N	O	S	0	0
			5388	3442	888	1019	39		
7	U	682	Total	C	N	O	S	0	0
			5388	3442	888	1019	39		
7	V	682	Total	C	N	O	S	0	0
			5388	3442	888	1019	39		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	W	339	Total	C	N	O	S	0	0
			2679	1697	473	490	19		
8	Y	339	Total	C	N	O	S	0	0
			2679	1697	473	490	19		

- Molecule 9 is a protein called Tubulin alpha-1A chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	438	Total	C	N	O	S	0	0
			3423	2167	582	652	22		

- Molecule 10 is a protein called Tubulin beta-4B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	430	Total	C	N	O	S	0	0
			3373	2119	578	650	26		

- Molecule 11 is a protein called Ubiquitin-conjugating enzyme E2 D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	147	Total	C	N	O	S	0	0
			1174	751	200	215	8		

- Molecule 12 is a protein called E3 ubiquitin-protein ligase UHRF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	282	Total	C	N	O	S	0	0
			2278	1419	430	422	7		

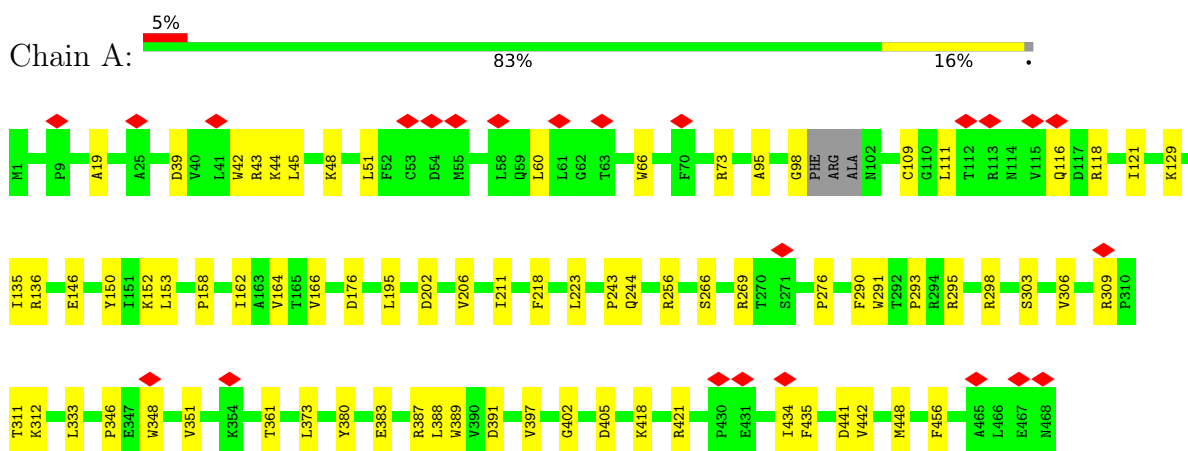
- Molecule 13 is a protein called Zinc finger BED domain-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	e	57	Total	C	N	O	S	0	0
			456	289	85	76	6		

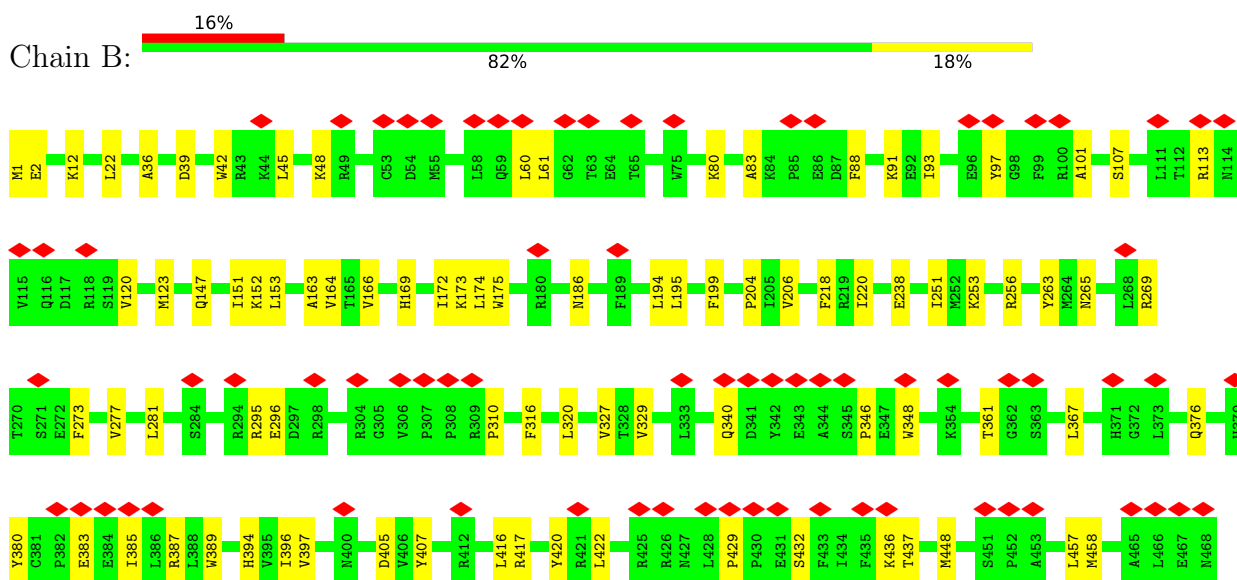
3 Residue-property plots

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 12

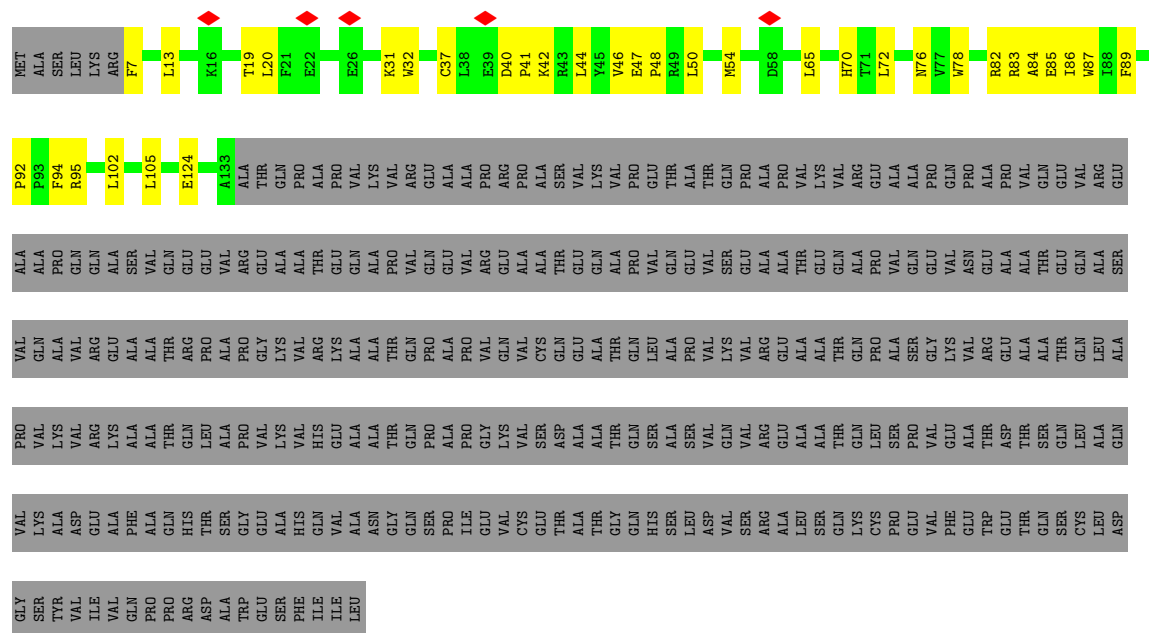


- Molecule 1: F-box and WD-40 domain protein 12

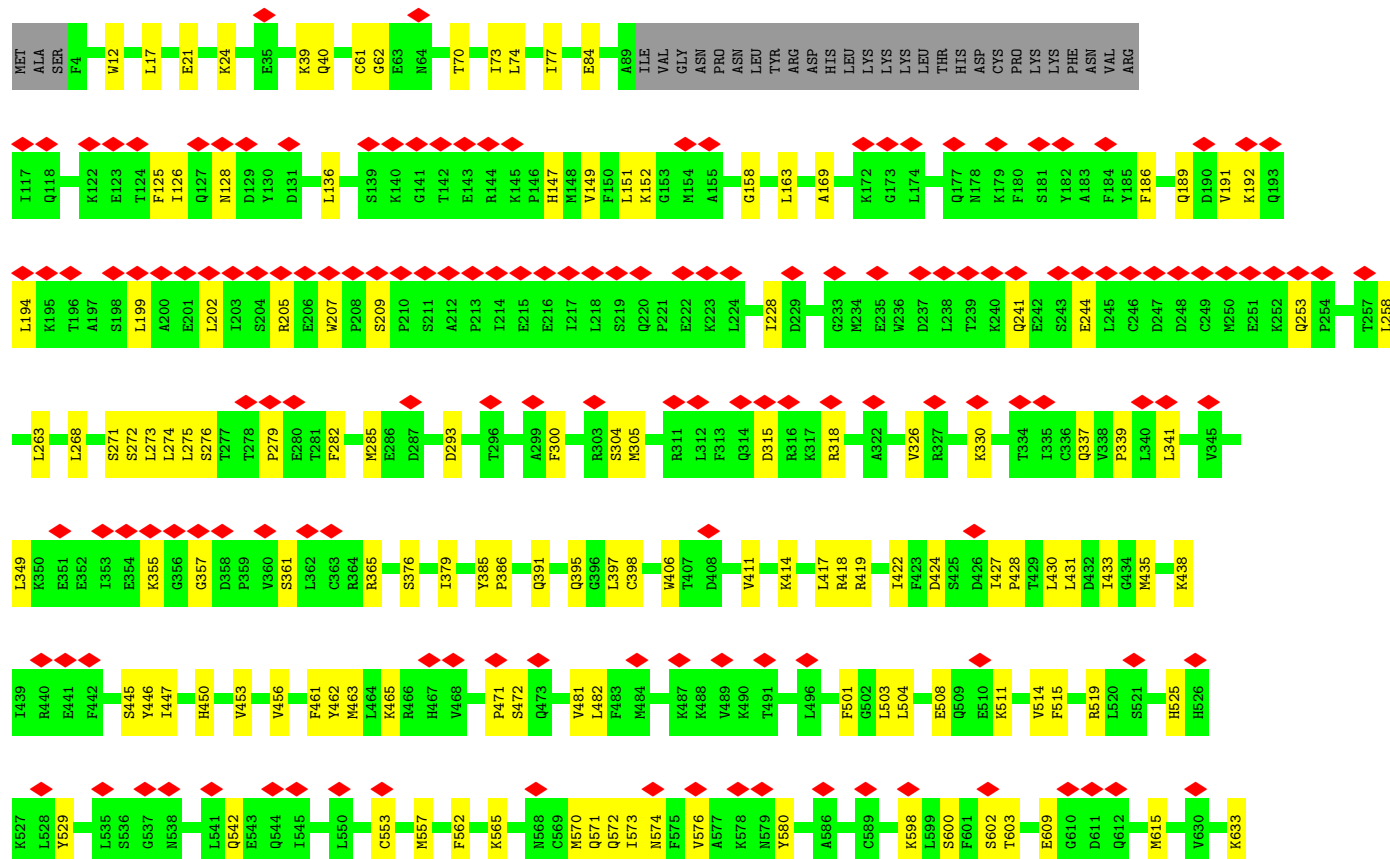
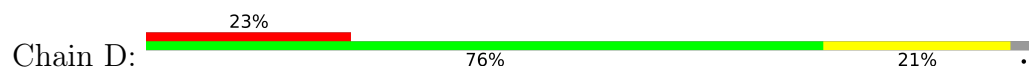


- Molecule 2: KH domain-containing protein 3

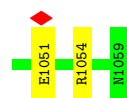




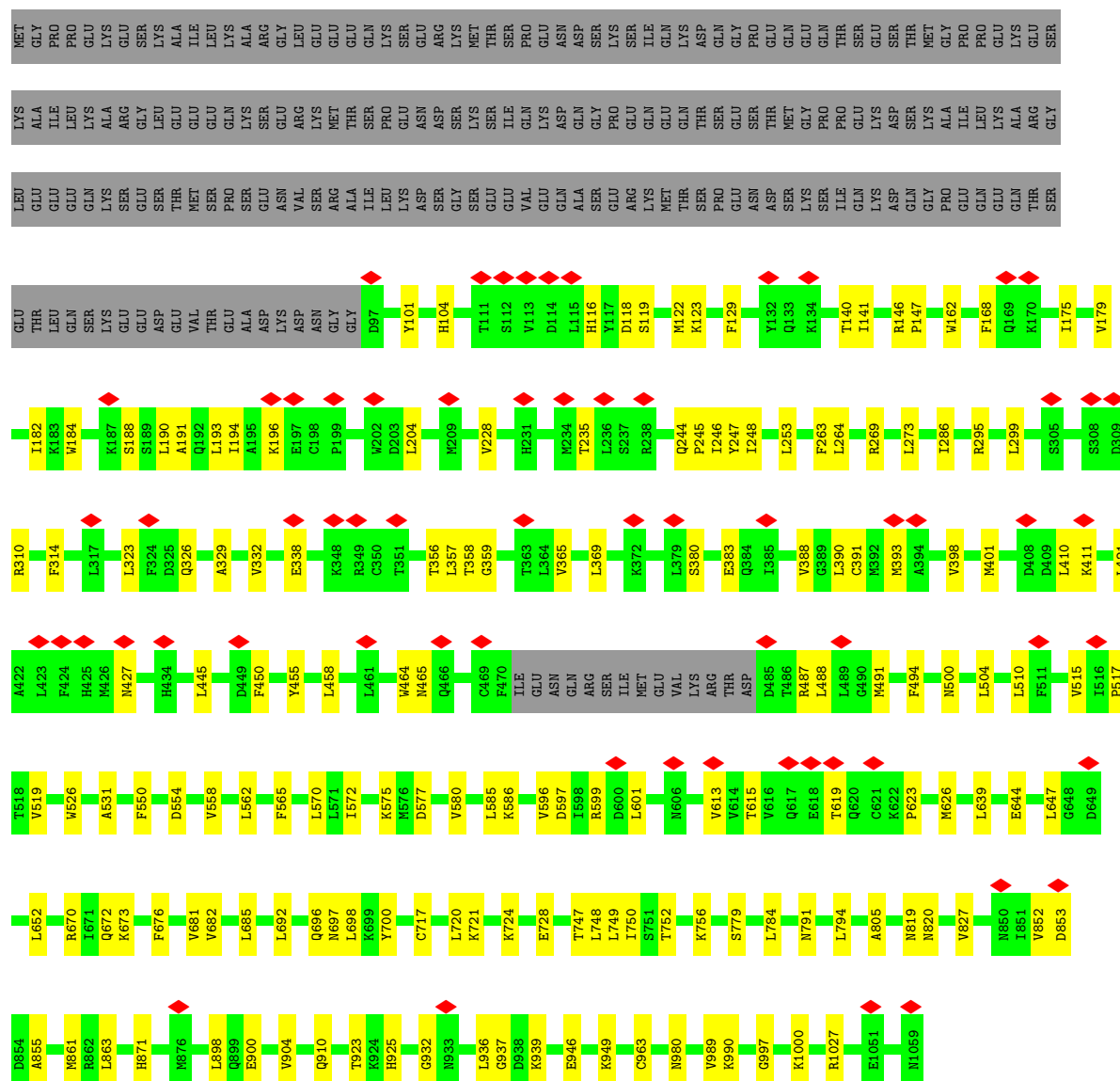
- Molecule 3: NLR family, pyrin domain containing 4F



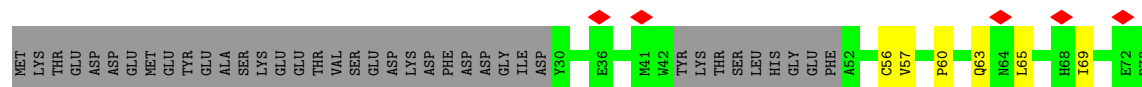
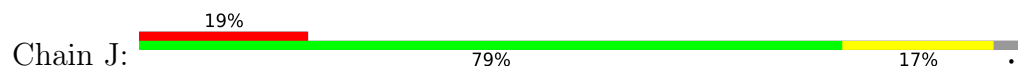


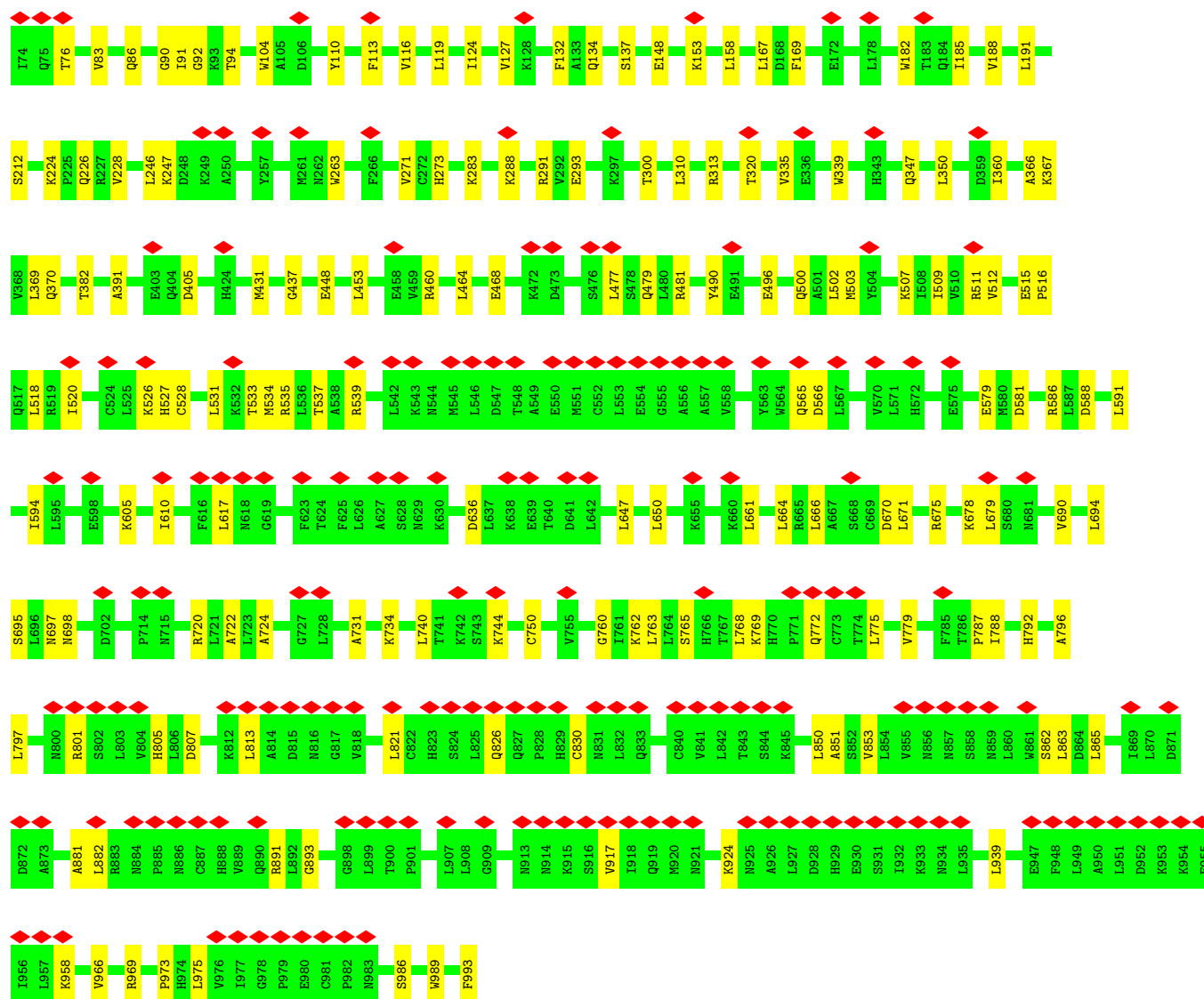


• Molecule 4: NACHT, LRR and PYD domains-containing protein 5

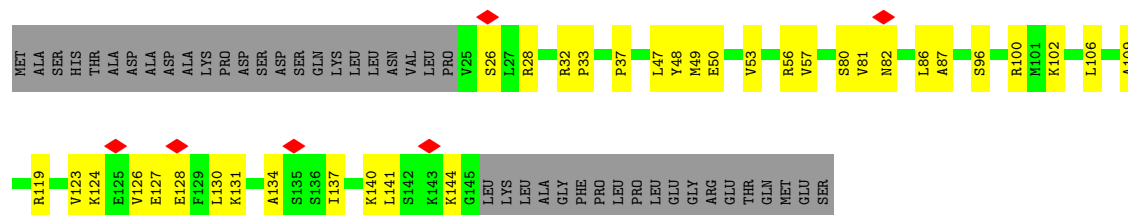


• Molecule 5: NACHT, LRR and PYD domains-containing protein 14



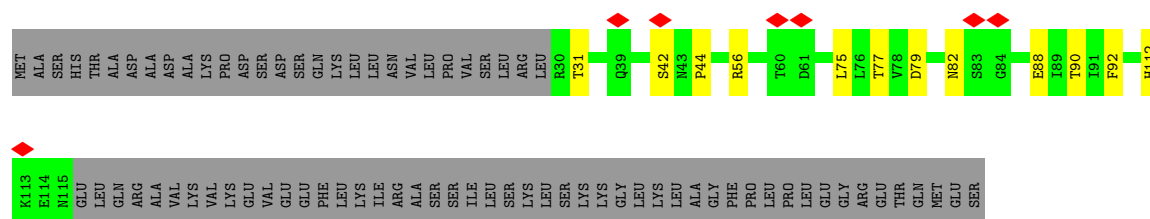


• Molecule 6: Oocyte-expressed protein homolog

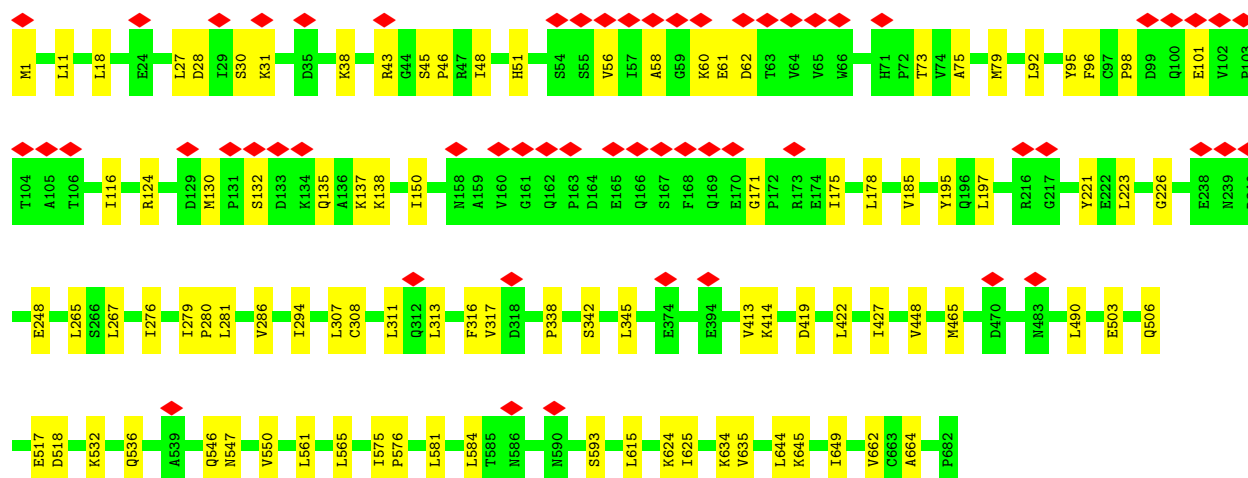
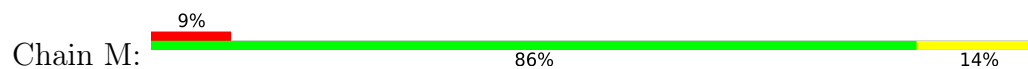


• Molecule 6: Oocyte-expressed protein homolog

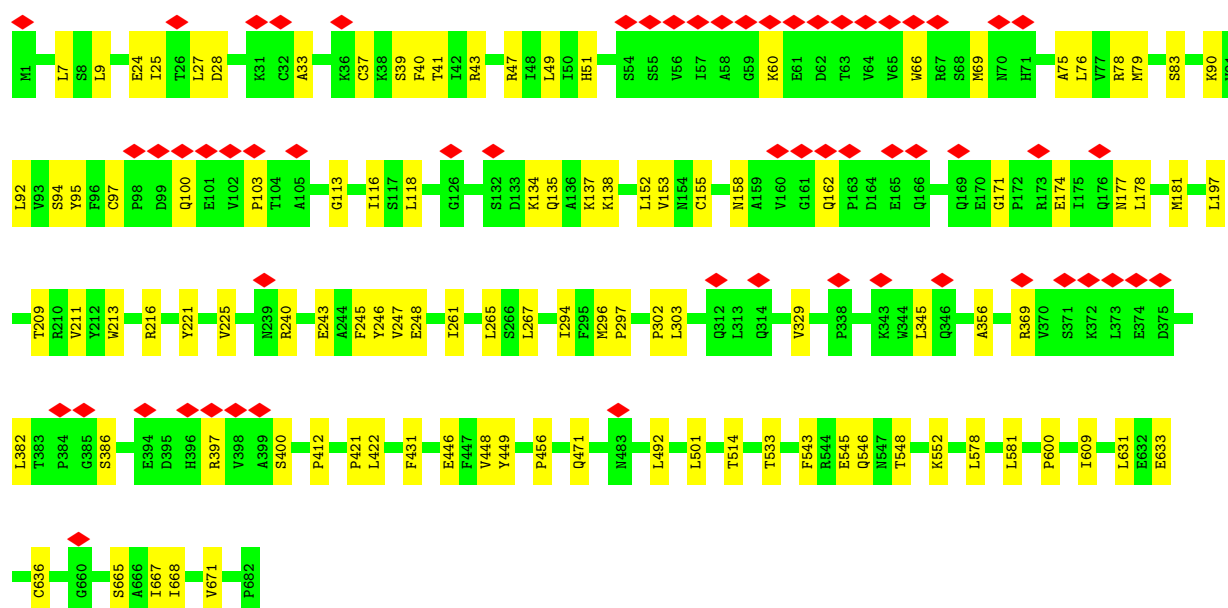
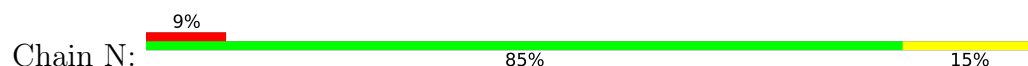




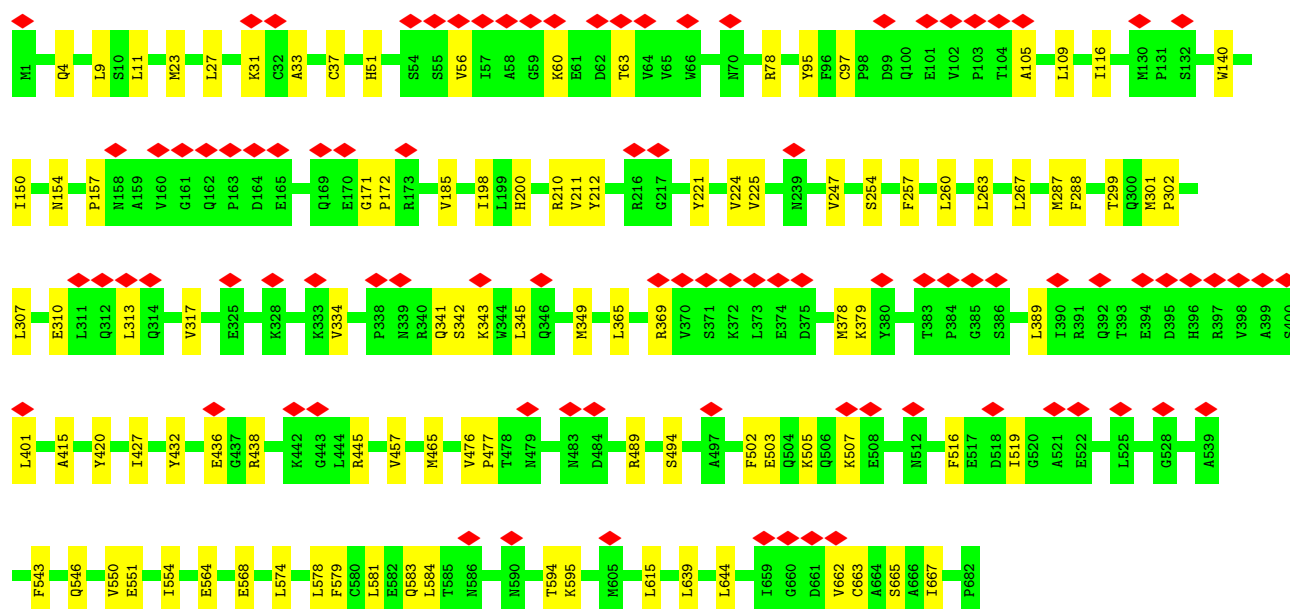
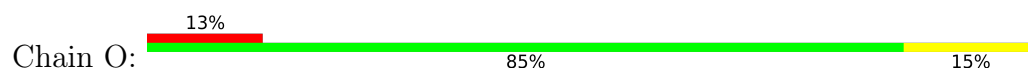
• Molecule 7: Inactive protein-arginine deiminase type-6



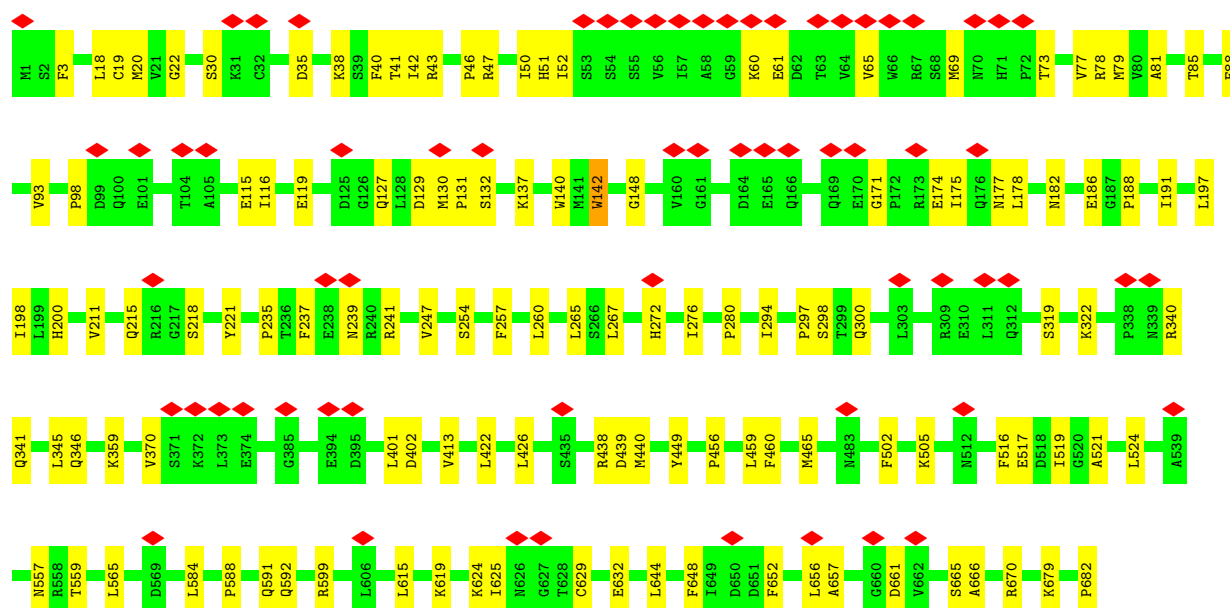
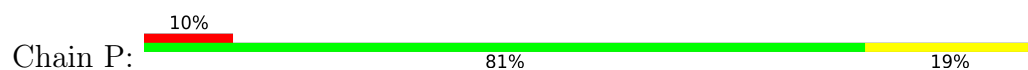
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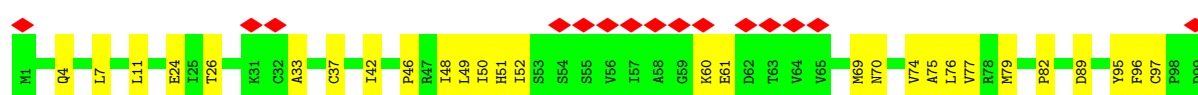
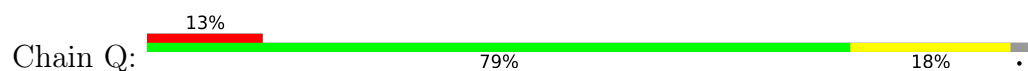
• Molecule 7: Inactive protein-arginine deiminase type-6

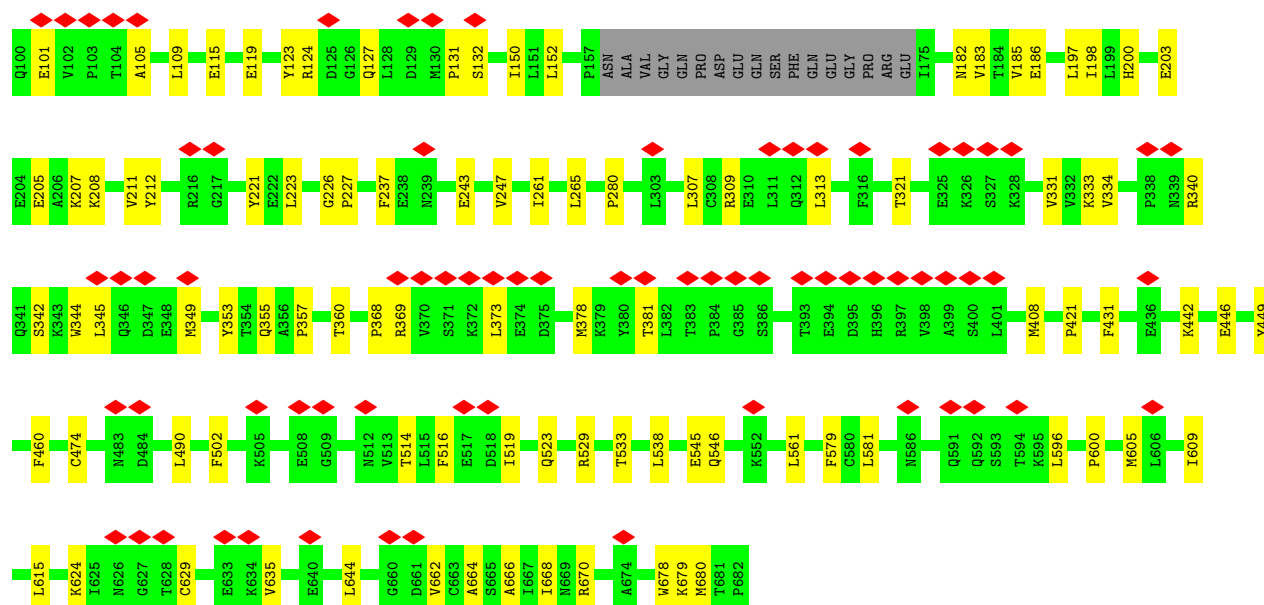


• Molecule 7: Inactive protein-arginine deiminase type-6

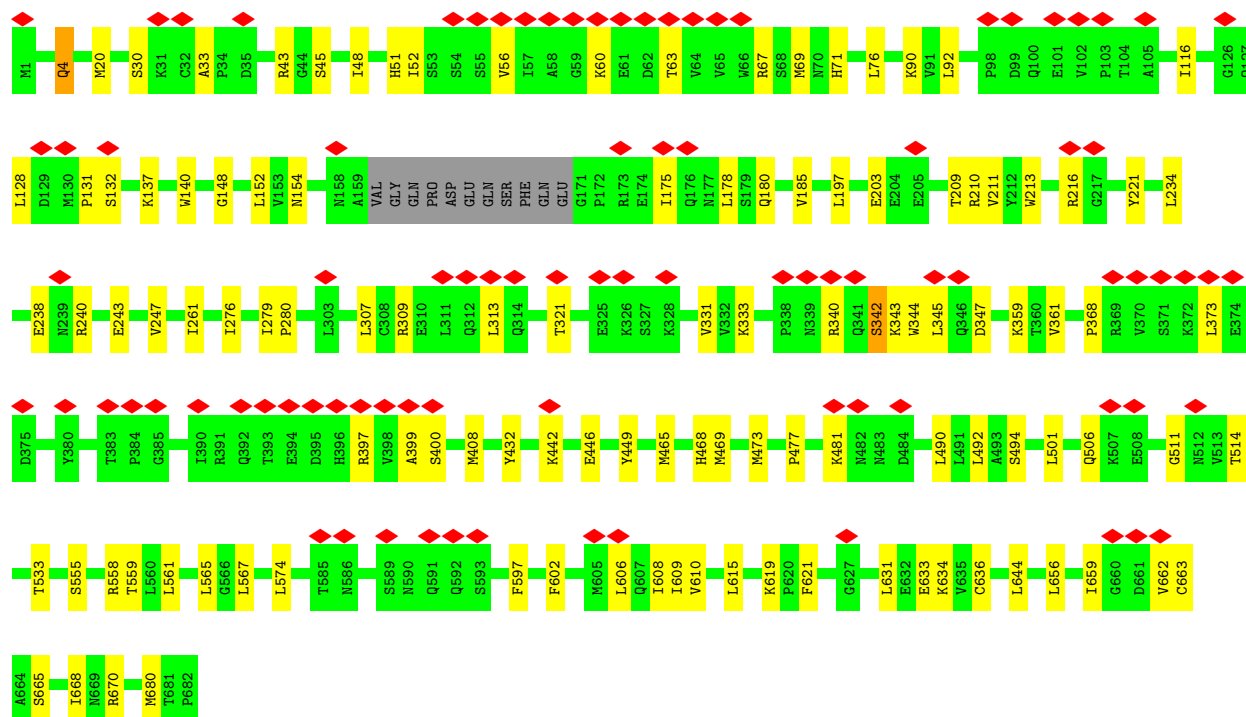
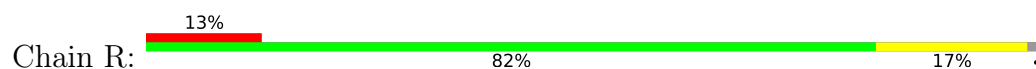


• Molecule 7: Inactive protein-arginine deiminase type-6

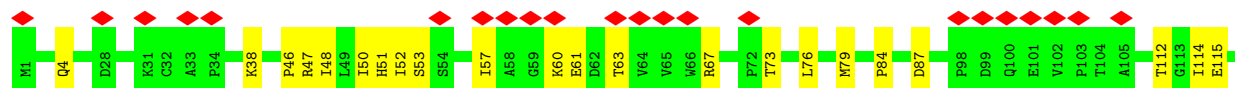
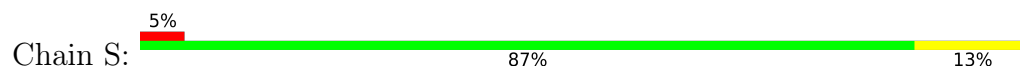


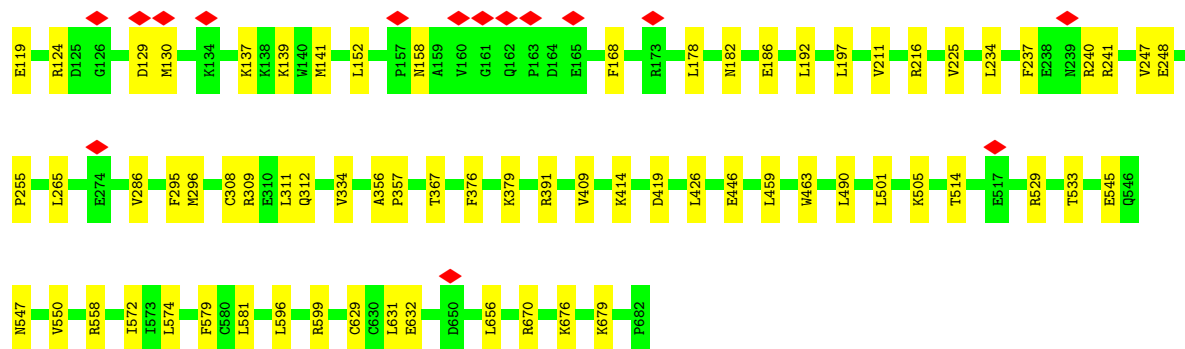


• Molecule 7: Inactive protein-arginine deiminase type-6

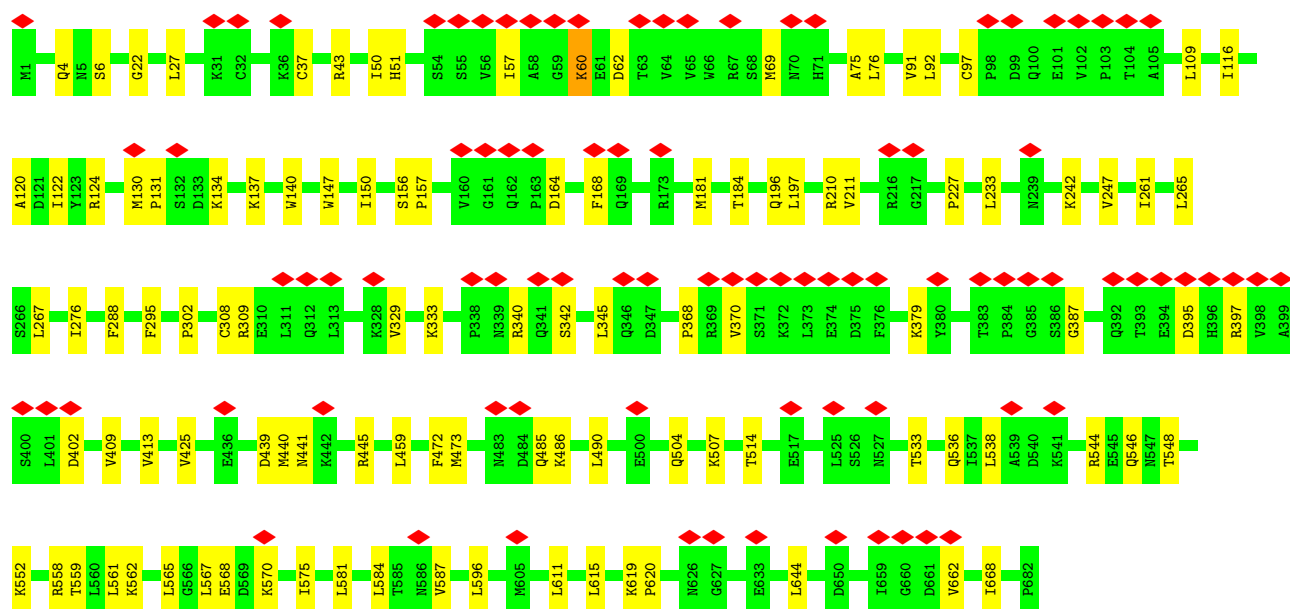
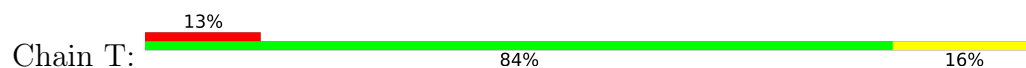


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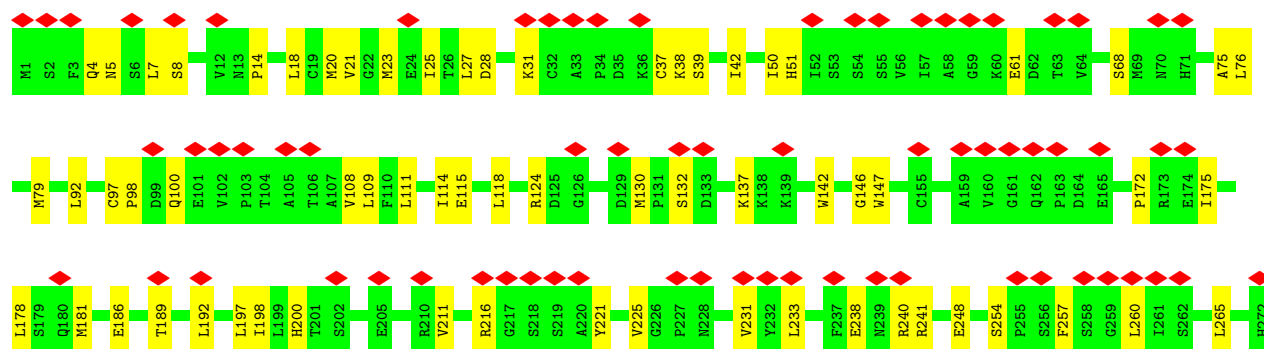
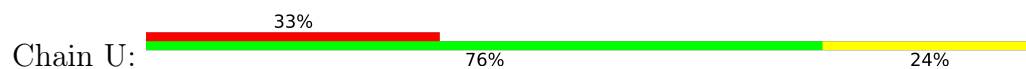


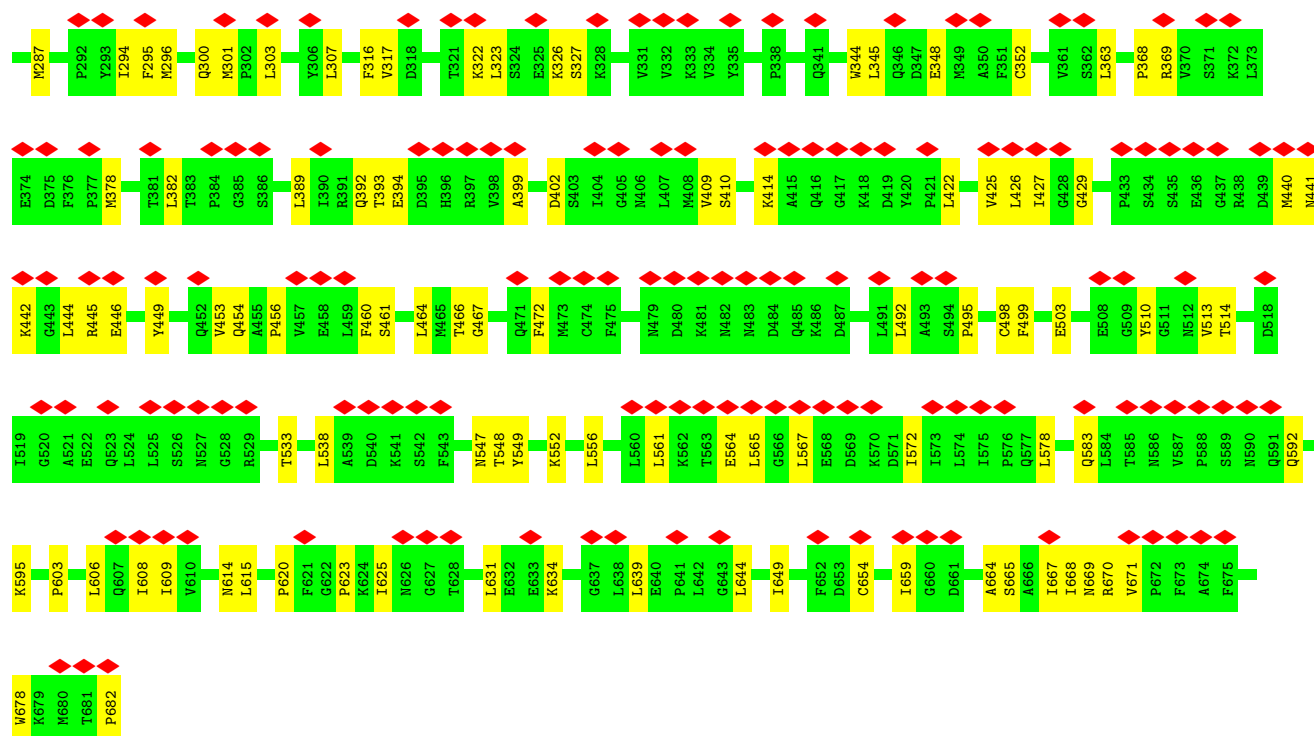


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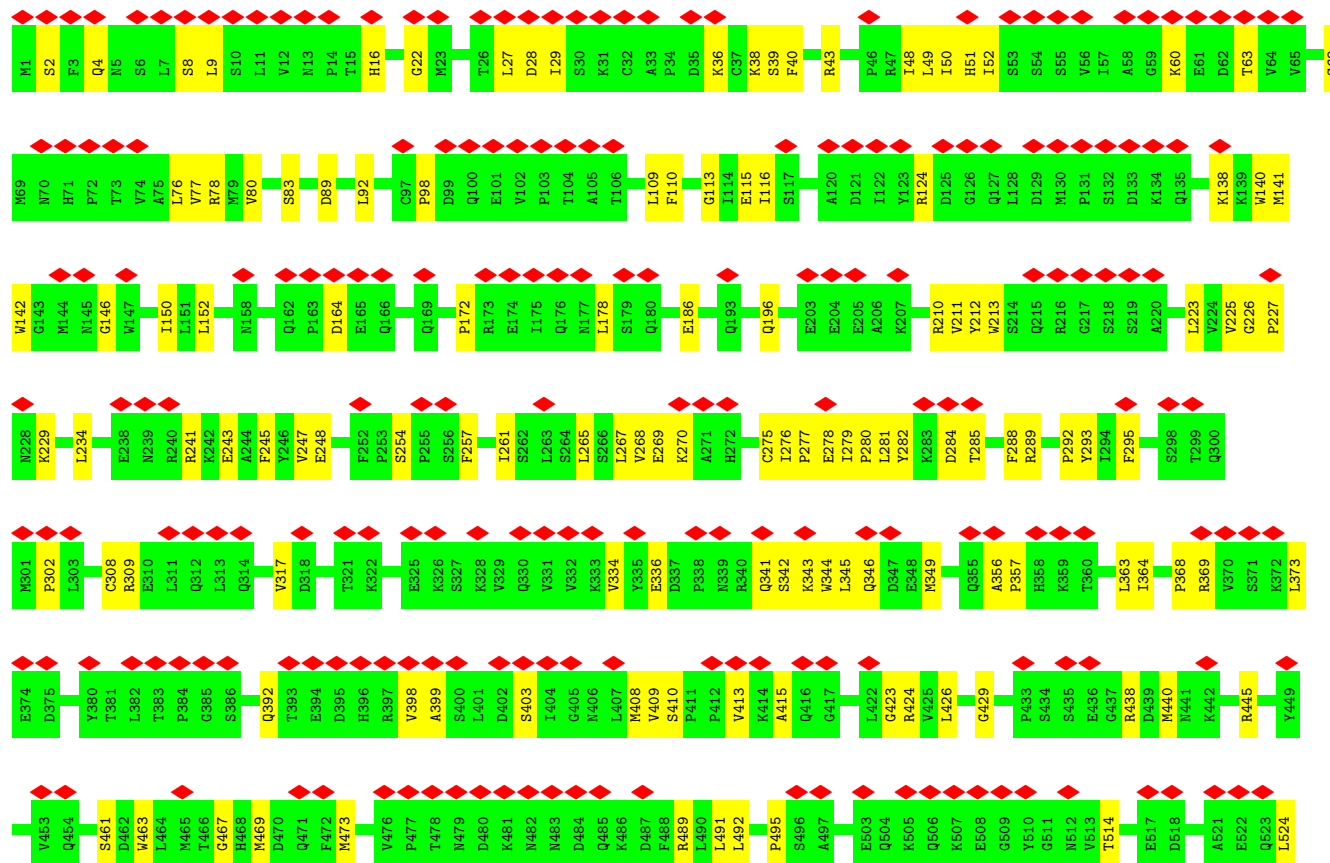
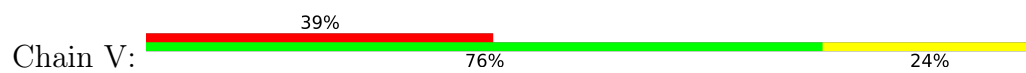


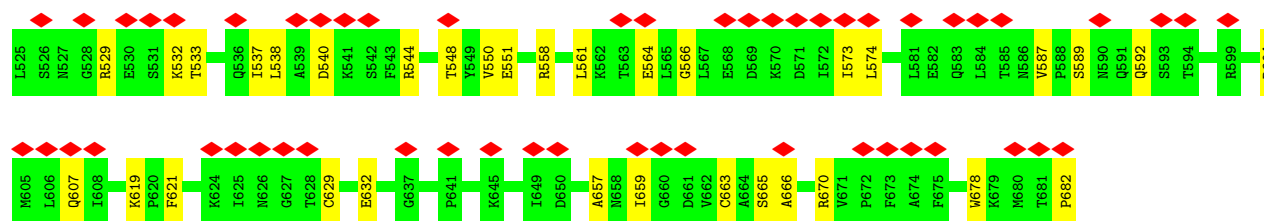
• Molecule 7: Inactive protein-arginine deiminase type-6



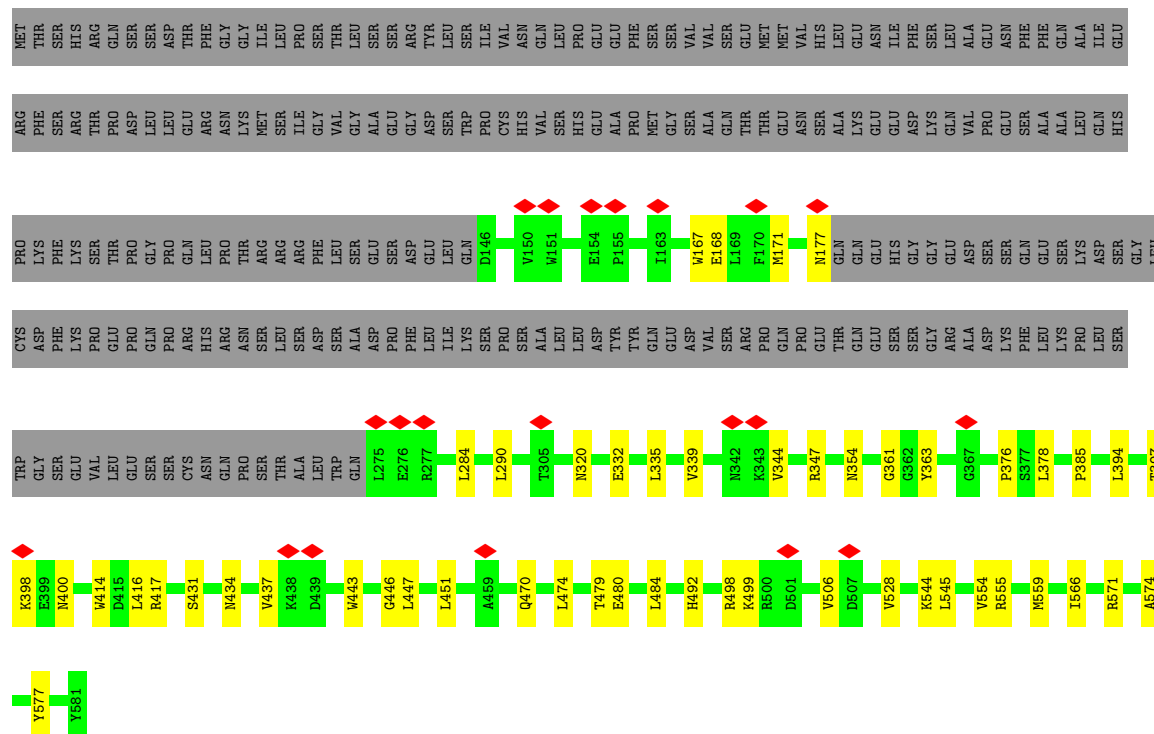


• Molecule 7: Inactive protein-arginine deiminase type-6

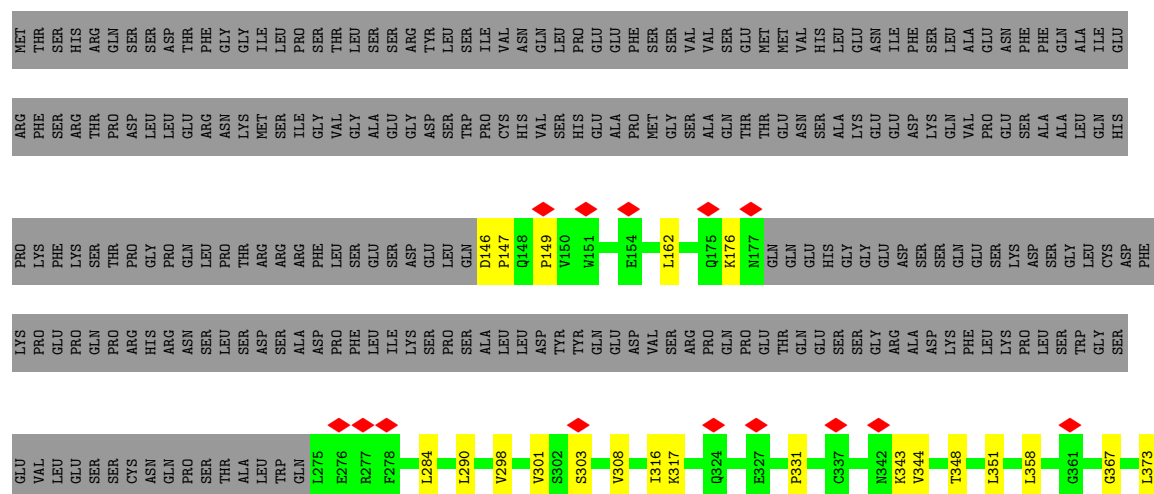


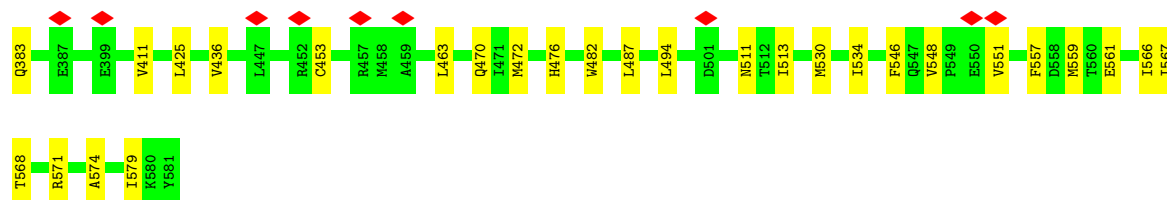


• Molecule 8: Transducin-like enhancer protein 6

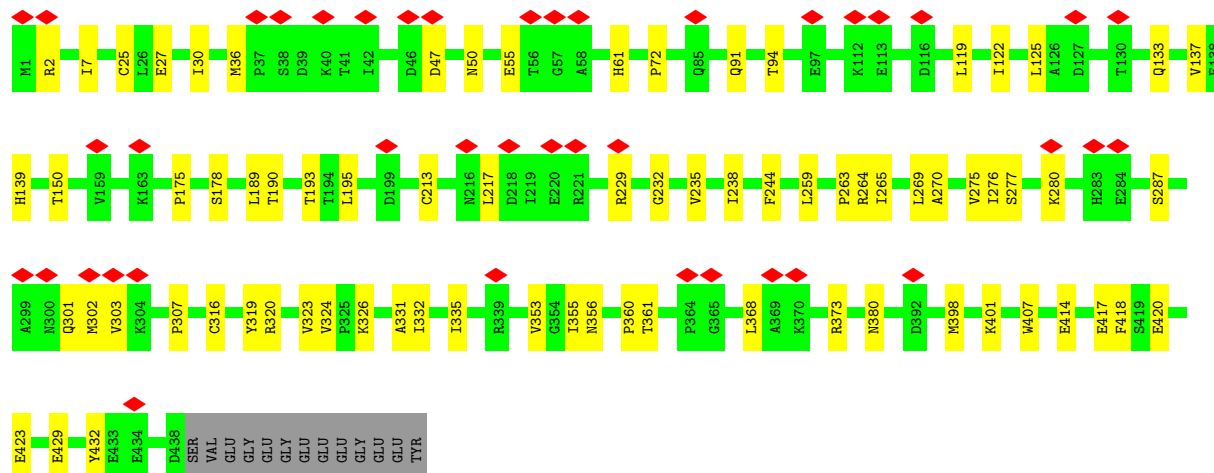
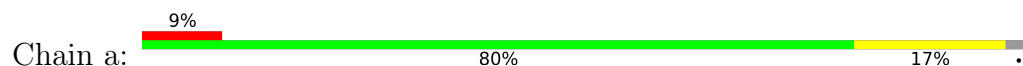


• Molecule 8: Transducin-like enhancer protein 6

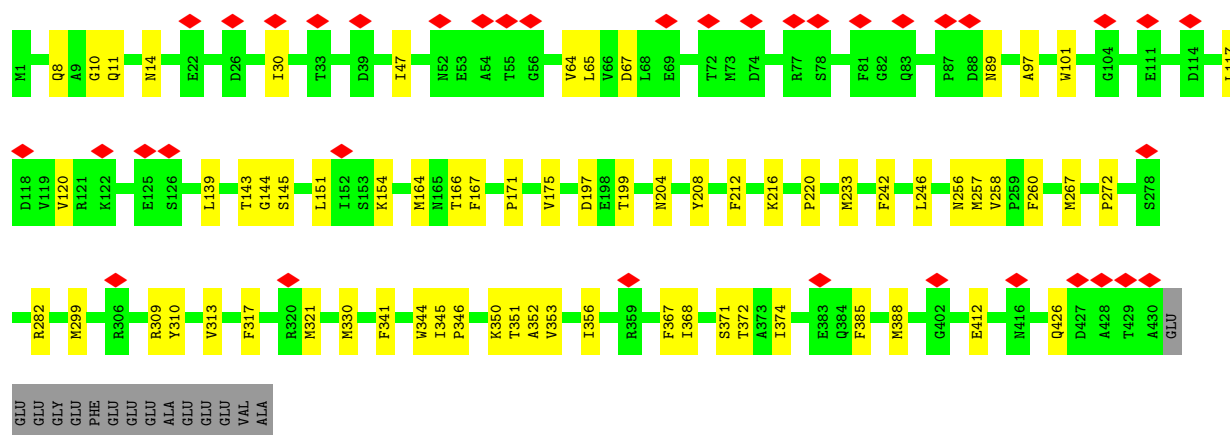
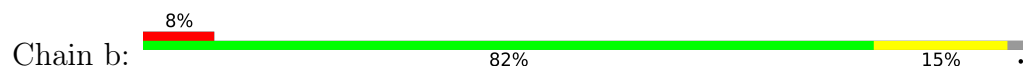




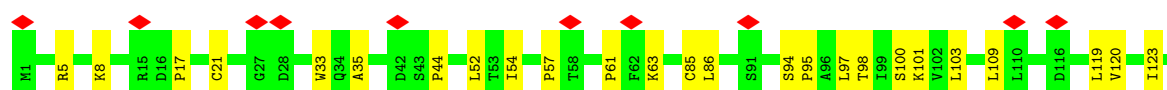
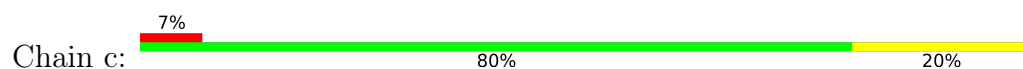
• Molecule 9: Tubulin alpha-1A chain

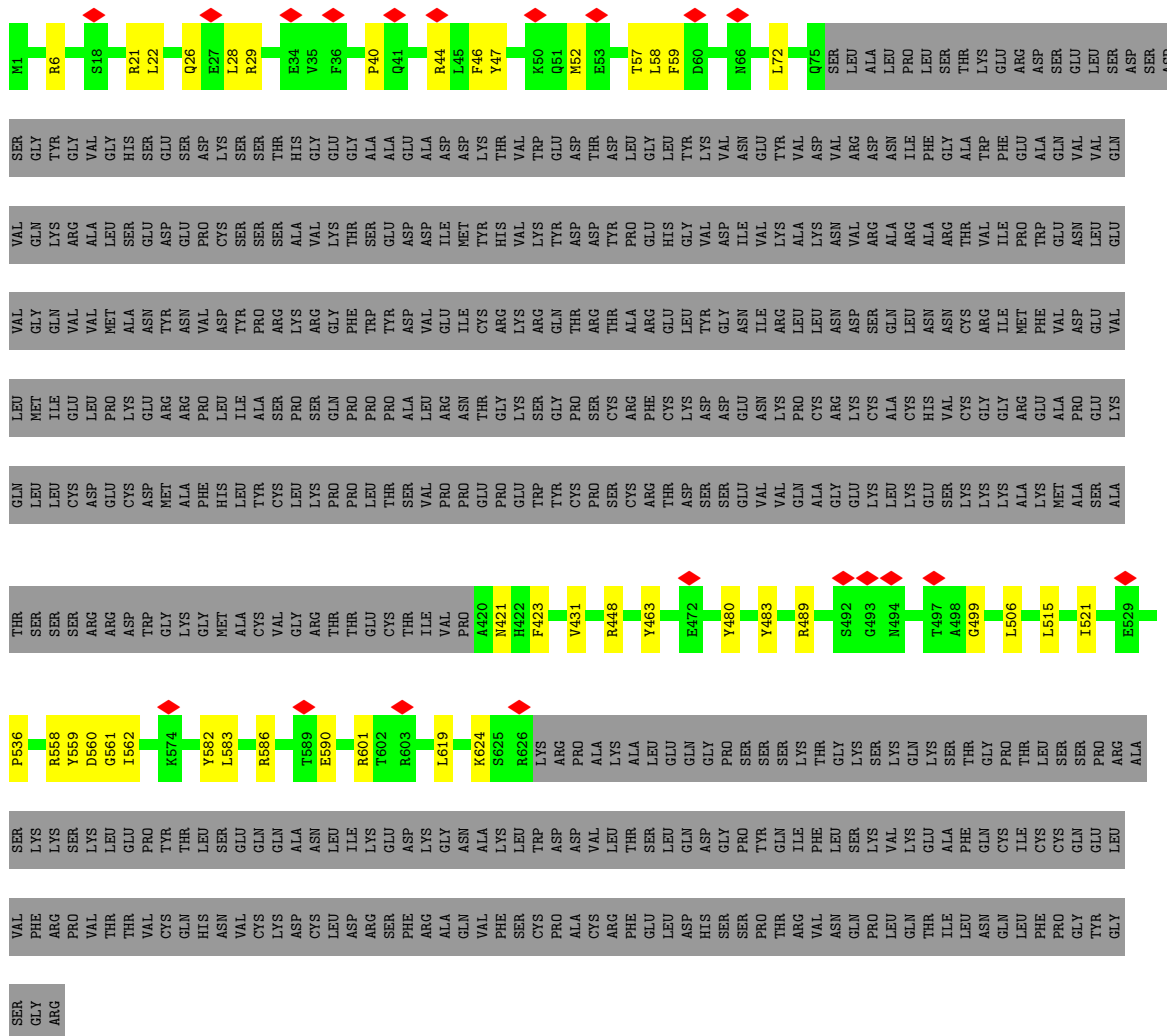


• Molecule 10: Tubulin beta-4B chain

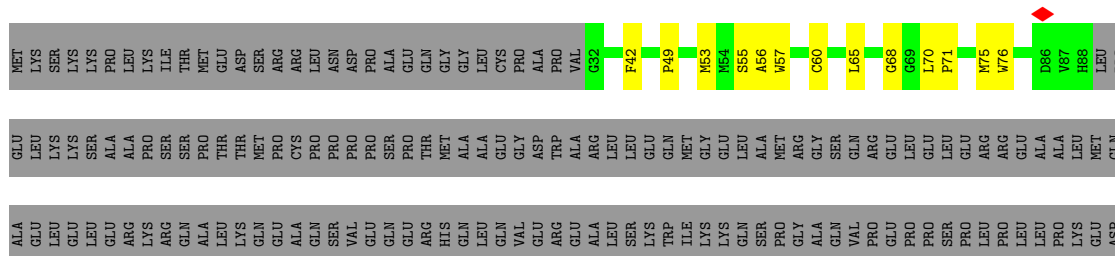


• Molecule 11: Ubiquitin-conjugating enzyme E2 D3





- Molecule 13: Zinc finger BED domain-containing protein 3



PRO
ASP
ILE
HIS
ASP
ASN
ASN
SER
ASP
ASN
ASP
MET
VAL
THR
LYS
VAL
LEU
LEU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	424595	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)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.438	Depositor
Minimum map value	0.000	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	683.69995, 619.04, 551.19995	wwPDB
Map dimensions	645, 584, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	A	0.17	0/3859	0.46	0/5240
1	B	0.15	0/3888	0.42	0/5280
2	C	0.27	0/1087	0.68	1/1469 (0.1%)
3	D	0.18	0/7438	0.48	0/10015
3	F	0.18	0/7523	0.48	0/10128
4	H	0.17	0/7652	0.48	1/10345 (0.0%)
4	I	0.17	0/7652	0.46	1/10345 (0.0%)
5	J	0.18	0/7769	0.50	5/10502 (0.0%)
6	K	0.26	0/991	0.61	0/1341
6	L	0.22	0/711	0.64	0/970
7	M	0.17	0/5511	0.41	0/7475
7	N	0.16	0/5511	0.43	0/7475
7	O	0.17	0/5511	0.44	0/7475
7	P	0.17	0/5511	0.45	0/7475
7	Q	0.16	0/5375	0.44	0/7289
7	R	0.17	0/5420	0.46	0/7350
7	S	0.17	0/5511	0.41	0/7475
7	T	0.17	0/5511	0.46	0/7475
7	U	0.18	0/5511	0.48	1/7475 (0.0%)
7	V	0.18	0/5511	0.48	0/7475
8	W	0.16	0/2738	0.41	0/3714
8	Y	0.16	0/2738	0.40	0/3714
9	a	0.18	0/3501	0.44	0/4753
10	b	0.19	0/3448	0.50	0/4673
11	c	0.18	0/1209	0.53	0/1647
12	d	0.16	0/2329	0.43	2/3139 (0.1%)
13	e	0.25	0/473	0.68	0/643
All	All	0.17	0/119889	0.46	11/162357 (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
7	O	0	1
7	P	0	1
7	R	0	1
7	S	0	1
7	T	0	1
7	U	0	2
7	V	0	1
All	All	0	8

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	405	ASP	CA-C-N	9.68	148.45	120.97
5	J	405	ASP	C-N-CA	9.68	148.45	120.97
4	H	990	LYS	CA-CB-CG	5.77	125.65	114.10
12	d	558	ARG	CA-C-N	5.59	132.21	121.54
12	d	558	ARG	C-N-CA	5.59	132.21	121.54

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	O	568	GLU	Peptide
7	P	142	TRP	Peptide
7	R	342	SER	Peptide
7	S	130	MET	Peptide
7	T	60	LYS	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	A	3764	0	3785	47	0
1	B	3791	0	3813	52	0
2	C	1056	0	1060	25	0
3	D	7303	0	7357	118	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	7387	0	7452	141	0
4	H	7518	0	7632	114	0
4	I	7518	0	7632	102	0
5	J	7628	0	7740	104	0
6	K	973	0	999	29	0
6	L	694	0	679	8	0
7	M	5388	0	5389	65	0
7	N	5388	0	5389	60	0
7	O	5388	0	5389	58	0
7	P	5388	0	5389	80	0
7	Q	5256	0	5275	77	0
7	R	5300	0	5315	79	0
7	S	5388	0	5389	55	0
7	T	5388	0	5389	65	0
7	U	5388	0	5389	114	0
7	V	5388	0	5389	115	0
8	W	2679	0	2665	33	0
8	Y	2679	0	2665	29	0
9	a	3423	0	3335	47	0
10	b	3373	0	3257	41	0
11	c	1174	0	1161	17	0
12	d	2278	0	2226	23	0
13	e	456	0	425	9	0
All	All	117354	0	117585	1610	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 7.

The worst 5 of 1610 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)
5:J:539:ARG:HA	5:J:586:ARG:H	1.51	0.76
7:S:53:SER:HB2	7:S:67:ARG:HH12	1.53	0.74
11:c:17:PRO:HG2	12:d:624:LYS:HE2	1.70	0.74
10:b:30:ILE:HD11	10:b:47:ILE:HD11	1.69	0.73
4:H:223:ASP:HA	4:H:269:ARG:HH22	1.54	0.73

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	A	461/468 (98%)	429 (93%)	32 (7%)	0	100	100
1	B	466/468 (100%)	445 (96%)	21 (4%)	0	100	100
2	C	125/440 (28%)	115 (92%)	10 (8%)	0	100	100
3	D	903/937 (96%)	866 (96%)	37 (4%)	0	100	100
3	F	914/937 (98%)	867 (95%)	47 (5%)	0	100	100
4	H	945/1163 (81%)	894 (95%)	51 (5%)	0	100	100
4	I	945/1163 (81%)	890 (94%)	55 (6%)	0	100	100
5	J	951/993 (96%)	894 (94%)	56 (6%)	1 (0%)	48	82
6	K	119/164 (73%)	112 (94%)	7 (6%)	0	100	100
6	L	84/164 (51%)	81 (96%)	3 (4%)	0	100	100
7	M	680/682 (100%)	654 (96%)	26 (4%)	0	100	100
7	N	680/682 (100%)	650 (96%)	30 (4%)	0	100	100
7	O	680/682 (100%)	653 (96%)	27 (4%)	0	100	100
7	P	680/682 (100%)	651 (96%)	29 (4%)	0	100	100
7	Q	661/682 (97%)	627 (95%)	34 (5%)	0	100	100
7	R	667/682 (98%)	632 (95%)	35 (5%)	0	100	100
7	S	680/682 (100%)	660 (97%)	20 (3%)	0	100	100
7	T	680/682 (100%)	645 (95%)	35 (5%)	0	100	100
7	U	680/682 (100%)	642 (94%)	38 (6%)	0	100	100
7	V	680/682 (100%)	643 (95%)	37 (5%)	0	100	100
8	W	335/581 (58%)	314 (94%)	21 (6%)	0	100	100
8	Y	335/581 (58%)	318 (95%)	17 (5%)	0	100	100
9	a	436/451 (97%)	423 (97%)	13 (3%)	0	100	100
10	b	428/445 (96%)	410 (96%)	18 (4%)	0	100	100
11	c	145/147 (99%)	138 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	d	278/782 (36%)	266 (96%)	11 (4%)	1 (0%)	30	66
13	e	55/228 (24%)	47 (86%)	8 (14%)	0	100	100
All	All	14693/16932 (87%)	13966 (95%)	725 (5%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	J	57	VAL
12	d	560	ASP

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	A	427/429 (100%)	427 (100%)	0	100	100
1	B	429/429 (100%)	429 (100%)	0	100	100
2	C	113/357 (32%)	113 (100%)	0	100	100
3	D	834/862 (97%)	834 (100%)	0	100	100
3	F	843/862 (98%)	843 (100%)	0	100	100
4	H	861/1054 (82%)	860 (100%)	1 (0%)	88	88
4	I	861/1054 (82%)	861 (100%)	0	100	100
5	J	874/909 (96%)	874 (100%)	0	100	100
6	K	107/143 (75%)	107 (100%)	0	100	100
6	L	75/143 (52%)	75 (100%)	0	100	100
7	M	613/613 (100%)	613 (100%)	0	100	100
7	N	613/613 (100%)	613 (100%)	0	100	100
7	O	613/613 (100%)	613 (100%)	0	100	100
7	P	613/613 (100%)	613 (100%)	0	100	100
7	Q	599/613 (98%)	599 (100%)	0	100	100
7	R	603/613 (98%)	602 (100%)	1 (0%)	87	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	S	613/613 (100%)	613 (100%)	0	100	100
7	T	613/613 (100%)	612 (100%)	1 (0%)	87	85
7	U	613/613 (100%)	613 (100%)	0	100	100
7	V	613/613 (100%)	613 (100%)	0	100	100
8	W	298/516 (58%)	298 (100%)	0	100	100
8	Y	298/516 (58%)	298 (100%)	0	100	100
9	a	368/378 (97%)	368 (100%)	0	100	100
10	b	368/380 (97%)	368 (100%)	0	100	100
11	c	132/132 (100%)	132 (100%)	0	100	100
12	d	240/682 (35%)	240 (100%)	0	100	100
13	e	47/197 (24%)	47 (100%)	0	100	100
All	All	13281/15173 (88%)	13278 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	H	230	GLN
7	R	4	GLN
7	T	536	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 181 such sidechains are listed below:

Mol	Chain	Res	Type
7	R	177	ASN
7	V	392	GLN
7	R	441	ASN
7	S	527	ASN
8	W	156	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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.

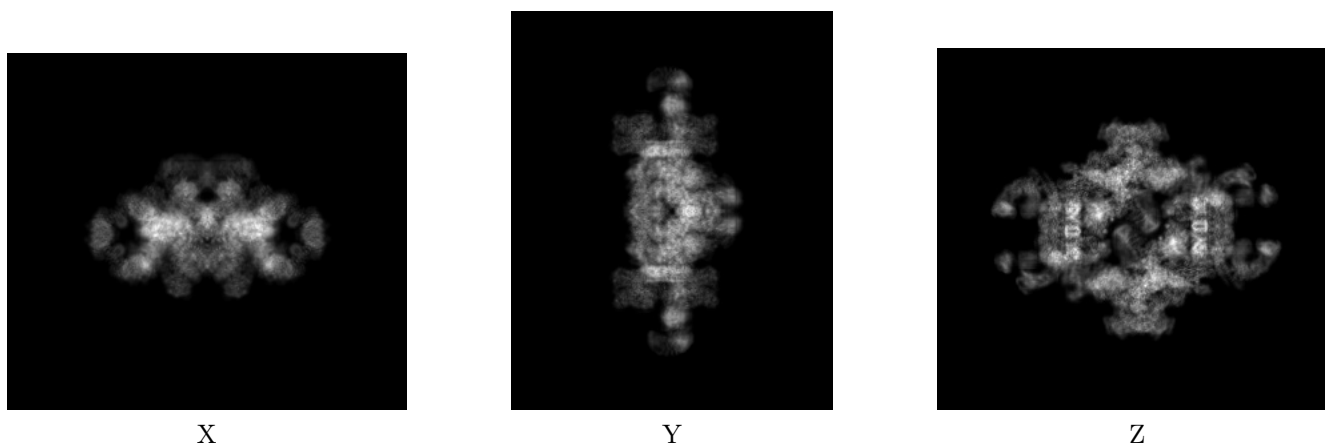
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-54838. 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](#)

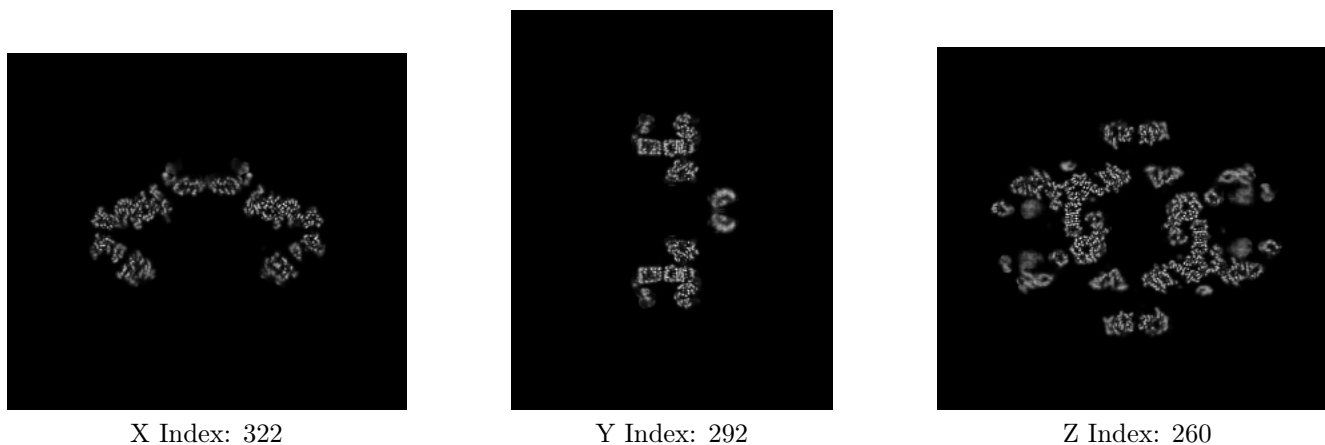
6.1.1 Primary map



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

6.2 Central slices [i](#)

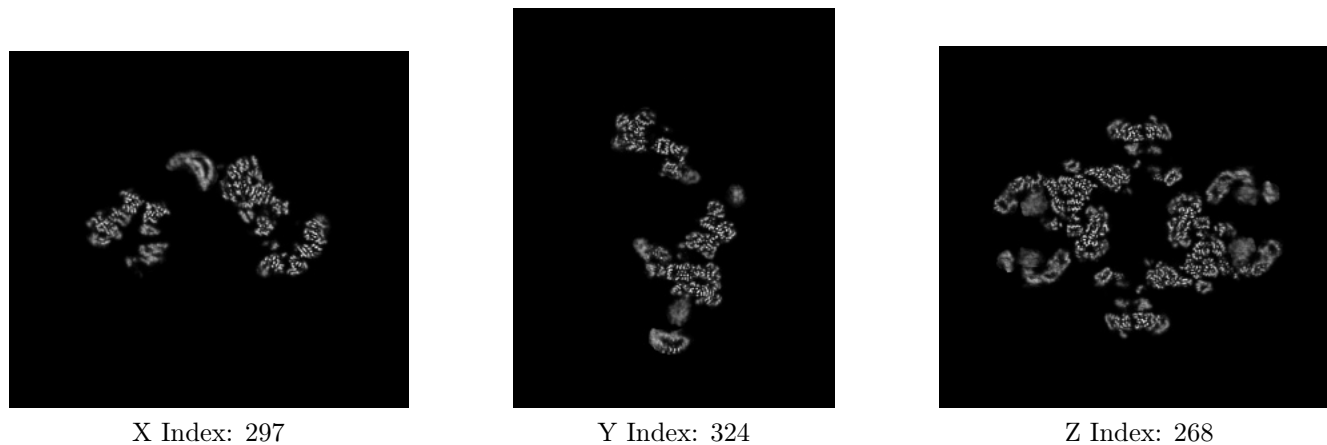
6.2.1 Primary map



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

6.3 Largest variance slices [i](#)

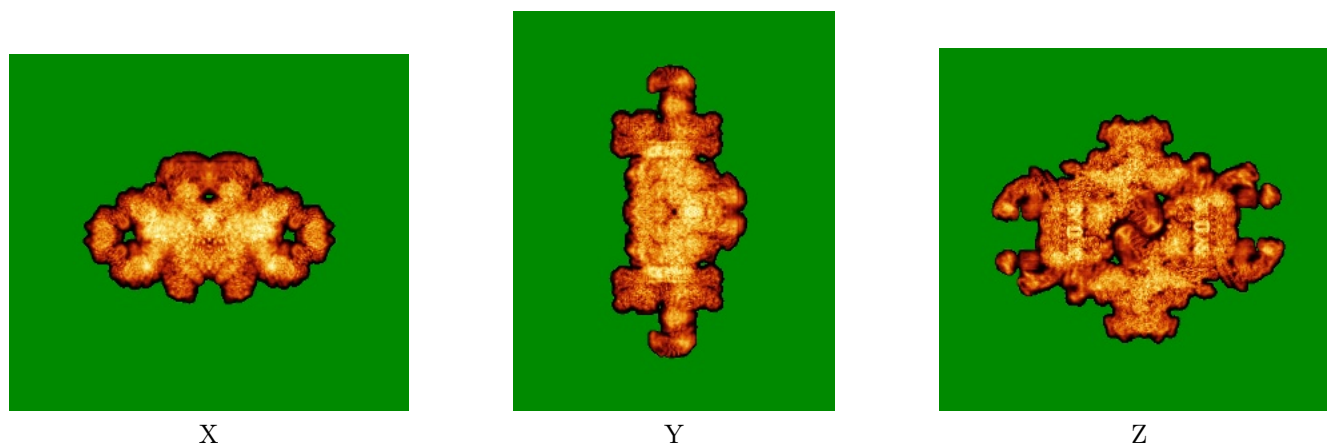
6.3.1 Primary map



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

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

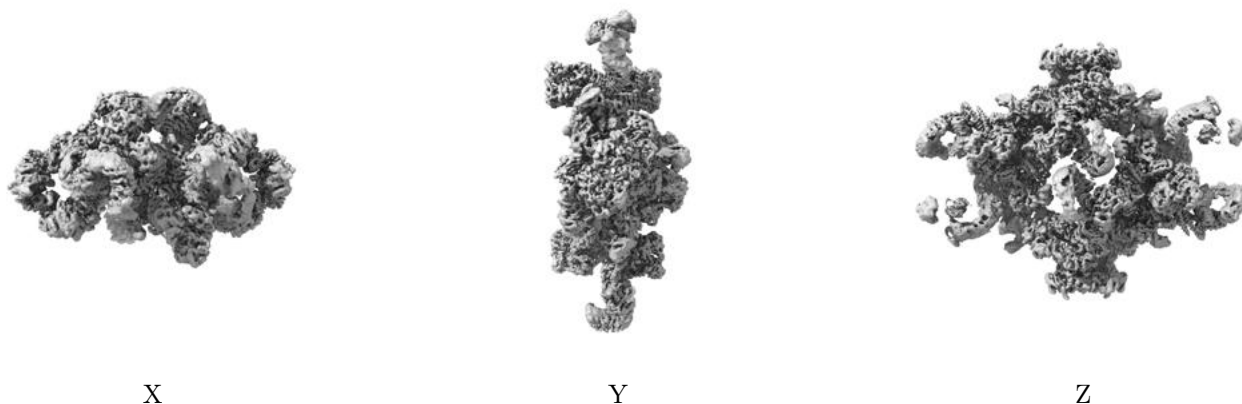
6.4.1 Primary map



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 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

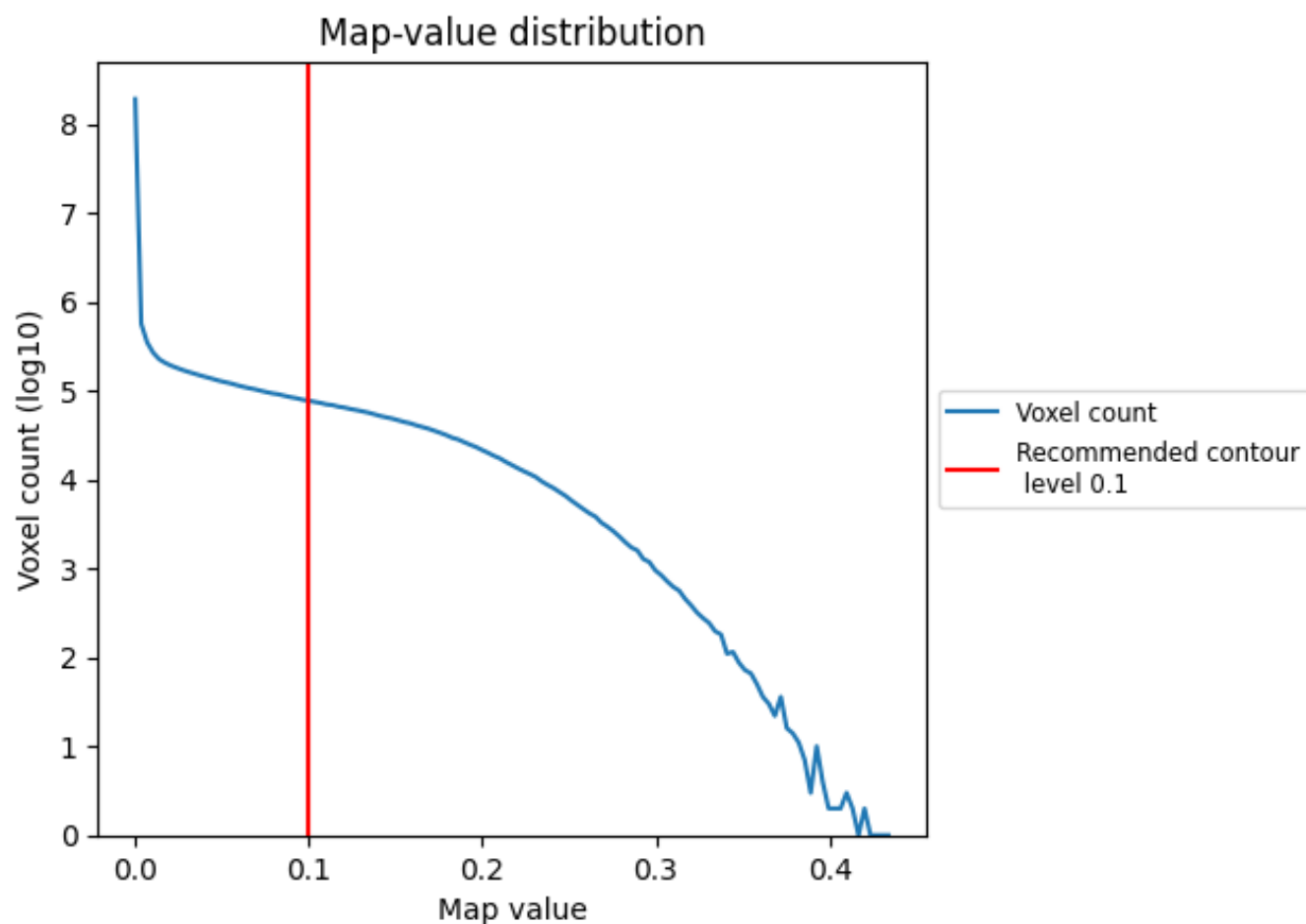
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

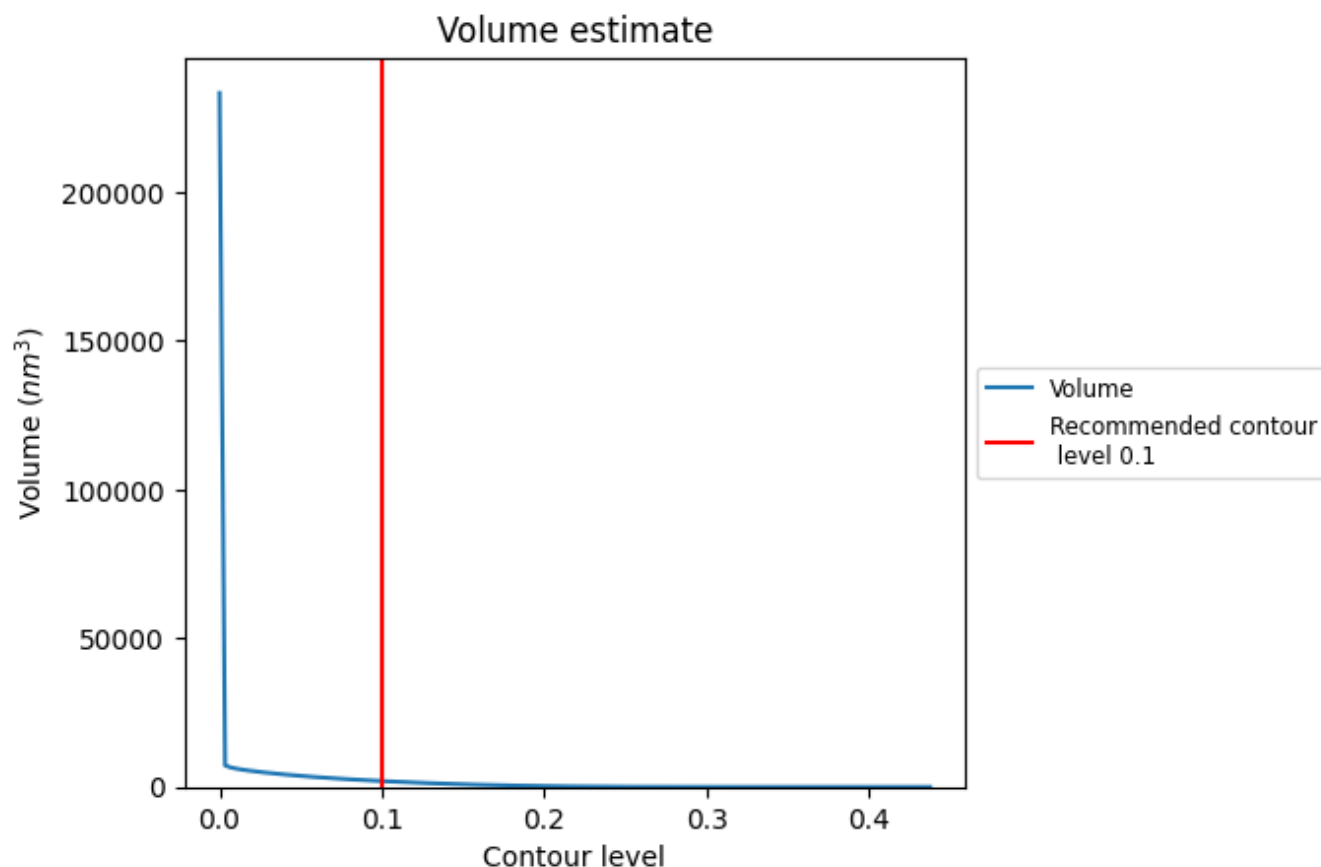
This section contains the results of statistical analysis of the map.

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 1978 nm³; this corresponds to an approximate mass of 1786 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

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

8 Fourier-Shell correlation

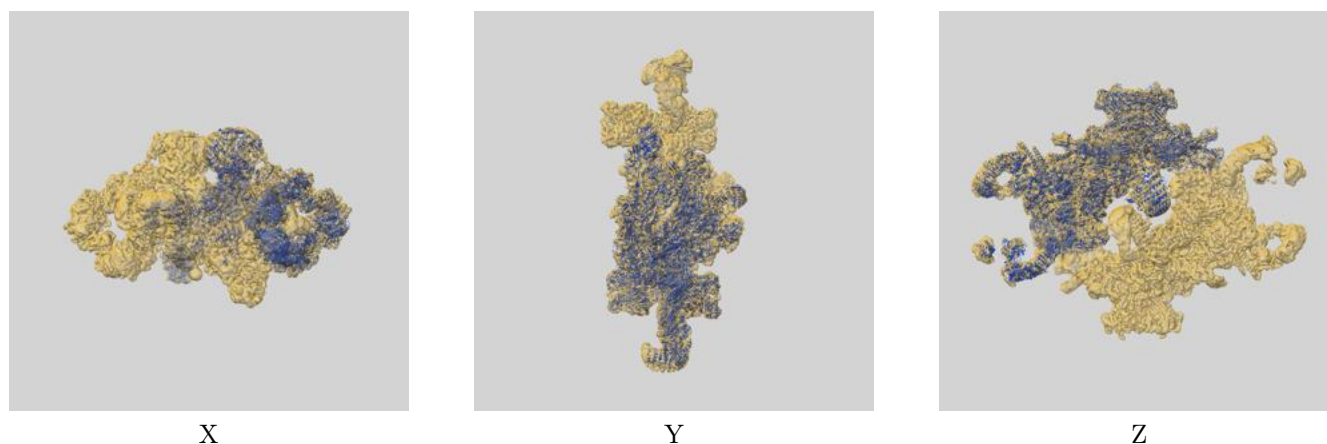
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

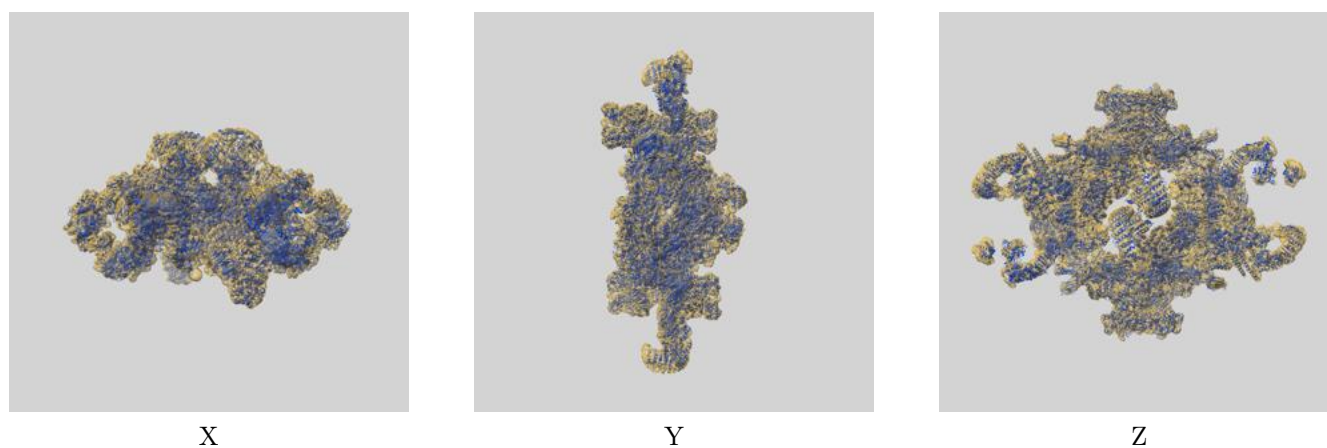
This section contains information regarding the fit between EMDB map EMD-54838 and PDB model 9SFP. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

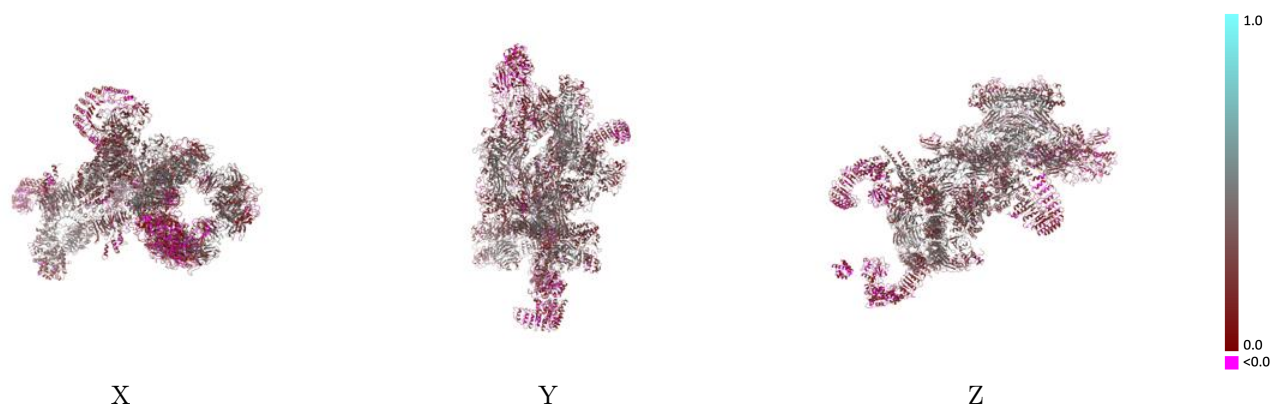


9.1.2 Map-model assembly overlay [i](#)



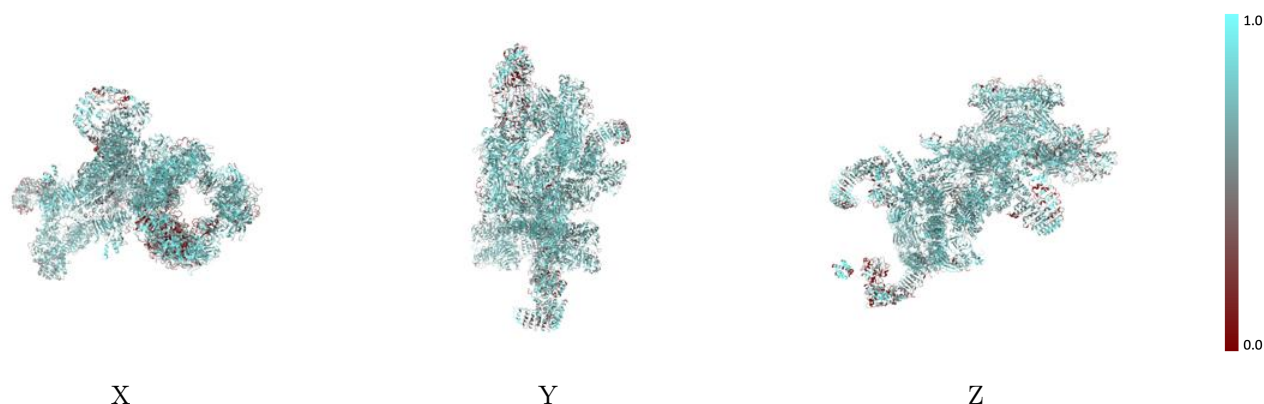
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



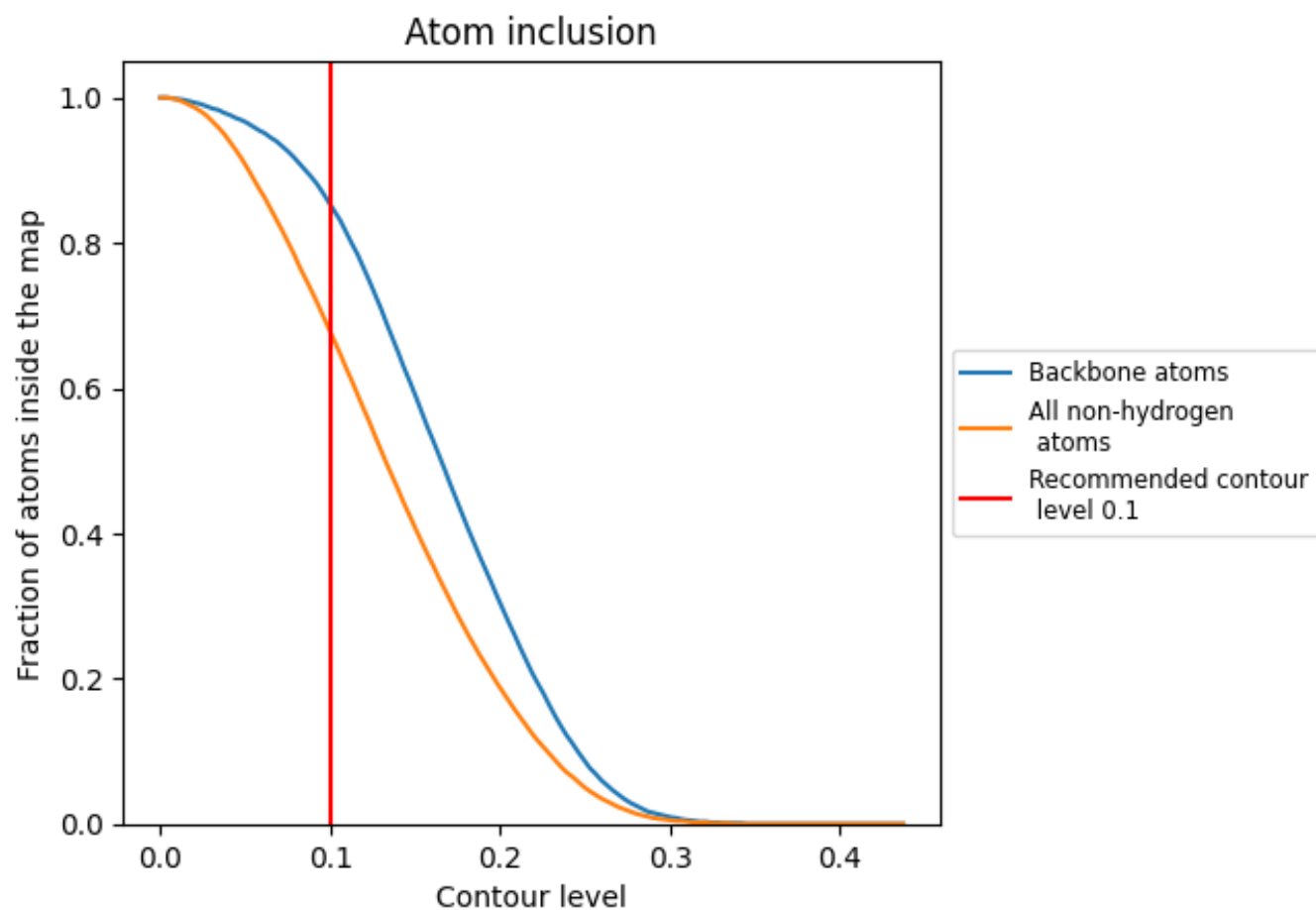
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 68% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6780	 0.2680
A	 0.7710	 0.3060
B	 0.6860	 0.2280
C	 0.7430	 0.3180
D	 0.6160	 0.1470
F	 0.5290	 0.1220
H	 0.7120	 0.3040
I	 0.7240	 0.3100
J	 0.6220	 0.2080
K	 0.7640	 0.3600
L	 0.7530	 0.3580
M	 0.7430	 0.3630
N	 0.7470	 0.3320
O	 0.6840	 0.3060
P	 0.7120	 0.3200
Q	 0.6860	 0.2990
R	 0.6740	 0.2990
S	 0.7920	 0.3730
T	 0.6920	 0.3140
U	 0.5640	 0.1250
V	 0.5100	 0.1010
W	 0.7450	 0.3500
Y	 0.7400	 0.3290
a	 0.6950	 0.3060
b	 0.7040	 0.2890
c	 0.7220	 0.3330
d	 0.7400	 0.3270
e	 0.7950	 0.3460

