



wwPDB EM Validation Summary Report ⓘ

Aug 5, 2026 – 09:31 AM EDT

PDB ID : 6VZ4 / pdb_00006vz4
EMDB ID : EMD-21484
Title : Cryo-EM structure of Sth1-Arp7-Arp9-Rtt102 bound to the nucleosome in ADP Beryllium Fluoride state
Authors : Leschziner, A.E.; Baker, R.W.
Deposited on : 2020-02-27
Resolution : 3.90 Å (reported)
Based on initial models : 5TGC, 4I6M, 5Z3U

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:

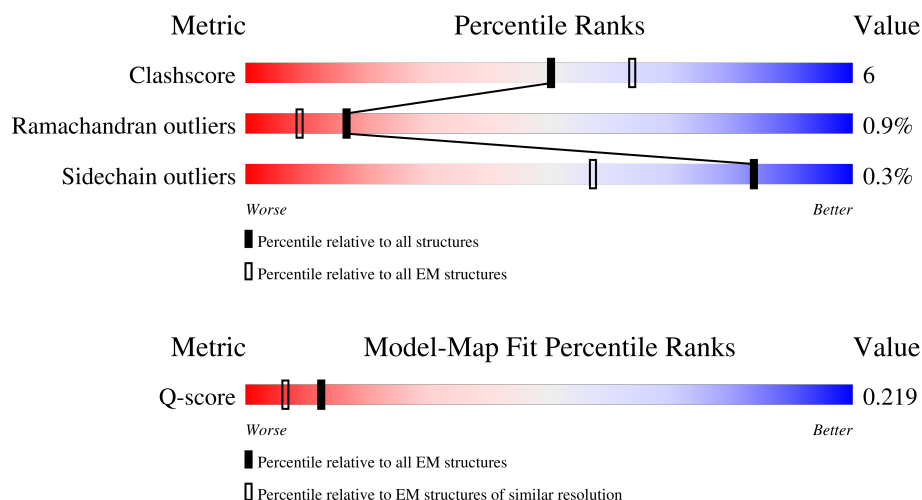
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.90 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.



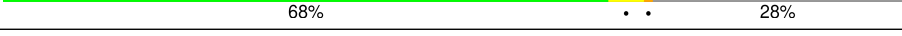
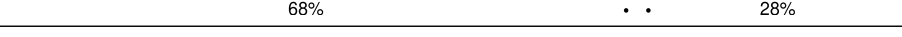
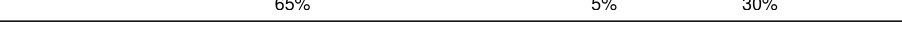
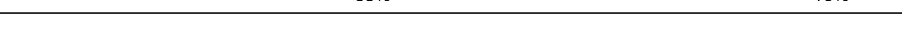
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8855 (3.40 - 4.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1-A	136	
1	1-E	136	
1	10-A	136	
1	10-E	136	

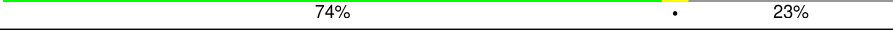
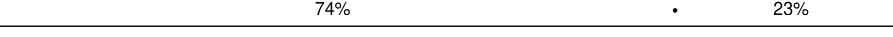
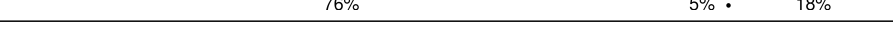
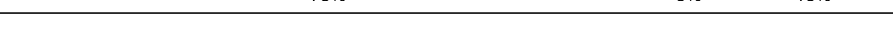
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Mol	Chain	Length	Quality of chain
1	2-A	136	
1	2-E	136	
1	3-A	136	
1	3-E	136	
1	4-A	136	
1	4-E	136	
1	5-A	136	
1	5-E	136	
1	6-A	136	
1	6-E	136	
1	7-A	136	
1	7-E	136	
1	8-A	136	
1	8-E	136	
1	9-A	136	
1	9-E	136	
2	1-B	103	
2	1-F	103	
2	10-B	103	
2	10-F	103	
2	2-B	103	
2	2-F	103	
2	3-B	103	
2	3-F	103	
2	4-B	103	

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Mol	Chain	Length	Quality of chain
2	4-F	103	
2	5-B	103	
2	5-F	103	
2	6-B	103	
2	6-F	103	
2	7-B	103	
2	7-F	103	
2	8-B	103	
2	8-F	103	
2	9-B	103	
2	9-F	103	
3	1-C	130	
3	1-G	130	
3	10-C	130	
3	10-G	130	
3	2-C	130	
3	2-G	130	
3	3-C	130	
3	3-G	130	
3	4-C	130	
3	4-G	130	
3	5-C	130	
3	5-G	130	
3	6-C	130	
3	6-G	130	

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Mol	Chain	Length	Quality of chain
3	7-C	130	
3	7-G	130	
3	8-C	130	
3	8-G	130	
3	9-C	130	
3	9-G	130	
4	1-D	125	
4	1-H	125	
4	10-D	125	
4	10-H	125	
4	2-D	125	
4	2-H	125	
4	3-D	125	
4	3-H	125	
4	4-D	125	
4	4-H	125	
4	5-D	125	
4	5-H	125	
4	6-D	125	
4	6-H	125	
4	7-D	125	
4	7-H	125	
4	8-D	125	
4	8-H	125	
4	9-D	125	

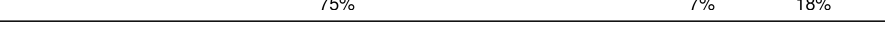
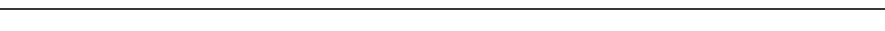
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Mol	Chain	Length	Quality of chain
4	9-H	125	
5	1-I	185	
5	10-I	185	
5	2-I	185	
5	3-I	185	
5	4-I	185	
5	5-I	185	
5	6-I	185	
5	7-I	185	
5	8-I	185	
5	9-I	185	
6	1-J	185	
6	10-J	185	
6	2-J	185	
6	3-J	185	
6	4-J	185	
6	5-J	185	
6	6-J	185	
6	7-J	185	
6	8-J	185	
6	9-J	185	
7	1-K	813	
7	10-K	813	
7	2-K	813	
7	3-K	813	

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Mol	Chain	Length	Quality of chain
7	4-K	813	
7	5-K	813	
7	6-K	813	
7	7-K	813	
7	8-K	813	
7	9-K	813	
8	1-L	477	
8	10-L	477	
8	2-L	477	
8	3-L	477	
8	4-L	477	
8	5-L	477	
8	6-L	477	
8	7-L	477	
8	8-L	477	
8	9-L	477	
9	1-M	467	
9	10-M	467	
9	2-M	467	
9	3-M	467	
9	4-M	467	
9	5-M	467	
9	6-M	467	
9	7-M	467	
9	8-M	467	

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Mol	Chain	Length	Quality of chain
9	9-M	467	
10	1-N	157	
10	10-N	157	
10	2-N	157	
10	3-N	157	
10	4-N	157	
10	5-N	157	
10	6-N	157	
10	7-N	157	
10	8-N	157	
10	9-N	157	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
13	BEF	3-K	1503	-	-	X	-
13	BEF	9-K	1503	-	-	X	-

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 239500 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 Histone H3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1-A	98	Total	C	N	O	S	0	0
			809	510	157	139	3		
1	2-A	98	Total	C	N	O	S	0	0
			809	510	157	139	3		
1	3-A	98	Total	C	N	O	S	0	0
			809	510	157	139	3		
1	4-A	98	Total	C	N	O	S	0	0
			809	510	157	139	3		
1	5-A	98	Total	C	N	O	S	0	0
			809	510	157	139	3		
1	6-A	98	Total	C	N	O	S	0	0
			809	510	157	139	3		
1	7-A	98	Total	C	N	O	S	0	0
			809	510	157	139	3		
1	8-A	98	Total	C	N	O	S	0	0
			809	510	157	139	3		
1	9-A	98	Total	C	N	O	S	0	0
			809	510	157	139	3		
1	10-A	98	Total	C	N	O	S	0	0
			809	510	157	139	3		
1	1-E	95	Total	C	N	O	S	0	0
			783	493	151	136	3		
1	2-E	95	Total	C	N	O	S	0	0
			783	493	151	136	3		
1	3-E	95	Total	C	N	O	S	0	0
			783	493	151	136	3		
1	4-E	95	Total	C	N	O	S	0	0
			783	493	151	136	3		
1	5-E	95	Total	C	N	O	S	0	0
			783	493	151	136	3		
1	6-E	95	Total	C	N	O	S	0	0
			783	493	151	136	3		
1	7-E	95	Total	C	N	O	S	0	0
			783	493	151	136	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8-E	95	Total	C	N	O	S	0	0
			783	493	151	136	3		
1	9-E	95	Total	C	N	O	S	0	0
			783	493	151	136	3		
1	10-E	95	Total	C	N	O	S	0	0
			783	493	151	136	3		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1-B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	2-B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	3-B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	4-B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	5-B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	6-B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	7-B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	8-B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	9-B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	10-B	87	Total	C	N	O	S	0	0
			703	443	142	117	1		
2	1-F	79	Total	C	N	O	S	0	0
			627	395	121	110	1		
2	2-F	79	Total	C	N	O	S	0	0
			627	395	121	110	1		
2	3-F	79	Total	C	N	O	S	0	0
			627	395	121	110	1		
2	4-F	79	Total	C	N	O	S	0	0
			627	395	121	110	1		
2	5-F	79	Total	C	N	O	S	0	0
			627	395	121	110	1		
2	6-F	79	Total	C	N	O	S	0	0
			627	395	121	110	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	7-F	79	Total	C	N	O	S	0	0
			627	395	121	110	1		
2	8-F	79	Total	C	N	O	S	0	0
			627	395	121	110	1		
2	9-F	79	Total	C	N	O	S	0	0
			627	395	121	110	1		
2	10-F	79	Total	C	N	O	S	0	0
			627	395	121	110	1		

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	1-C	107	Total	C	N	O	0	0
			823	519	161	143		
3	2-C	107	Total	C	N	O	0	0
			823	519	161	143		
3	3-C	107	Total	C	N	O	0	0
			823	519	161	143		
3	4-C	107	Total	C	N	O	0	0
			823	519	161	143		
3	5-C	107	Total	C	N	O	0	0
			823	519	161	143		
3	6-C	107	Total	C	N	O	0	0
			823	519	161	143		
3	7-C	107	Total	C	N	O	0	0
			823	519	161	143		
3	8-C	107	Total	C	N	O	0	0
			823	519	161	143		
3	9-C	107	Total	C	N	O	0	0
			823	519	161	143		
3	10-C	107	Total	C	N	O	0	0
			823	519	161	143		
3	1-G	107	Total	C	N	O	0	0
			823	519	161	143		
3	2-G	107	Total	C	N	O	0	0
			823	519	161	143		
3	3-G	107	Total	C	N	O	0	0
			823	519	161	143		
3	4-G	107	Total	C	N	O	0	0
			823	519	161	143		
3	5-G	107	Total	C	N	O	0	0
			823	519	161	143		

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Mol	Chain	Residues	Atoms				AltConf	Trace
3	6-G	107	Total	C	N	O	0	0
			823	519	161	143		
3	7-G	107	Total	C	N	O	0	0
			823	519	161	143		
3	8-G	107	Total	C	N	O	0	0
			823	519	161	143		
3	9-G	107	Total	C	N	O	0	0
			823	519	161	143		
3	10-G	107	Total	C	N	O	0	0
			823	519	161	143		

- Molecule 4 is a protein called Histone H2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1-D	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	2-D	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	3-D	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	4-D	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	5-D	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	6-D	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	7-D	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	8-D	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	9-D	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	10-D	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	1-H	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	2-H	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	3-H	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	4-H	92	Total	C	N	O	S	0	0
			719	453	129	135	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	5-H	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	6-H	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	7-H	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	8-H	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	9-H	92	Total	C	N	O	S	0	0
			719	453	129	135	2		
4	10-H	92	Total	C	N	O	S	0	0
			719	453	129	135	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	33	THR	SER	conflict	UNP Q92130
H	33	THR	SER	conflict	UNP Q92130

- Molecule 5 is a DNA chain called DNA (185-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1-I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		
5	2-I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		
5	3-I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		
5	4-I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		
5	5-I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		
5	6-I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		
5	7-I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		
5	8-I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		
5	9-I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		
5	10-I	146	Total	C	N	O	P	0	0
			2975	1413	540	876	146		

- Molecule 6 is a DNA chain called DNA (185-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1-J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		
6	2-J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		
6	3-J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		
6	4-J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		
6	5-J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		
6	6-J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		
6	7-J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		
6	8-J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		
6	9-J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		
6	10-J	146	Total	C	N	O	P	0	0
			3011	1425	564	876	146		

- Molecule 7 is a protein called Nuclear protein STH1/NPS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1-K	616	Total	C	N	O	S	0	0
			5055	3201	900	934	20		
7	2-K	616	Total	C	N	O	S	0	0
			5055	3201	900	934	20		
7	3-K	616	Total	C	N	O	S	0	0
			5055	3201	900	934	20		
7	4-K	616	Total	C	N	O	S	0	0
			5055	3201	900	934	20		
7	5-K	616	Total	C	N	O	S	0	0
			5055	3201	900	934	20		
7	6-K	616	Total	C	N	O	S	0	0
			5055	3201	900	934	20		
7	7-K	616	Total	C	N	O	S	0	0
			5055	3201	900	934	20		
7	8-K	616	Total	C	N	O	S	0	0
			5055	3201	900	934	20		
7	9-K	616	Total	C	N	O	S	0	0
			5055	3201	900	934	20		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	10-K	616	Total	C	N	O	S	0	0
			5055	3201	900	934	20		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	285	MET	-	initiating methionine	UNP P32597
K	286	GLY	-	expression tag	UNP P32597
K	287	SER	-	expression tag	UNP P32597
K	288	SER	-	expression tag	UNP P32597
K	289	HIS	-	expression tag	UNP P32597
K	290	HIS	-	expression tag	UNP P32597
K	291	HIS	-	expression tag	UNP P32597
K	292	HIS	-	expression tag	UNP P32597
K	293	HIS	-	expression tag	UNP P32597
K	294	HIS	-	expression tag	UNP P32597
K	295	SER	-	expression tag	UNP P32597
K	296	GLN	-	expression tag	UNP P32597
K	297	ASP	-	expression tag	UNP P32597
K	298	PRO	-	expression tag	UNP P32597
K	299	ASN	-	expression tag	UNP P32597
K	300	SER	-	expression tag	UNP P32597

- Molecule 8 is a protein called Actin-related protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	1-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
8	2-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
8	3-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
8	4-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
8	5-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
8	6-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
8	7-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
8	8-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	9-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		
8	10-L	393	Total	C	N	O	S	0	0
			3154	2035	514	590	15		

- Molecule 9 is a protein called Actin-like protein ARP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	1-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
9	2-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
9	3-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
9	4-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
9	5-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
9	6-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
9	7-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
9	8-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
9	9-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		
9	10-M	396	Total	C	N	O	S	0	0
			3192	2048	521	616	7		

- Molecule 10 is a protein called Regulator of Ty1 transposition protein 102.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	1-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
10	2-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
10	3-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
10	4-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
10	5-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		

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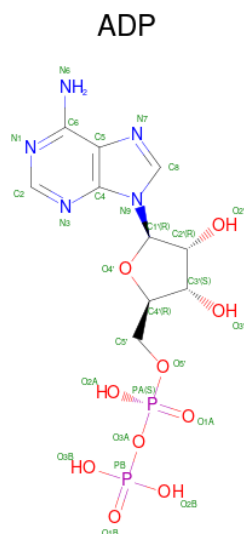
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Mol	Chain	Residues	Atoms					AltConf	Trace
10	6-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
10	7-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
10	8-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
10	9-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		
10	10-N	55	Total	C	N	O	S	0	0
			494	315	85	92	2		

- Molecule 11 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

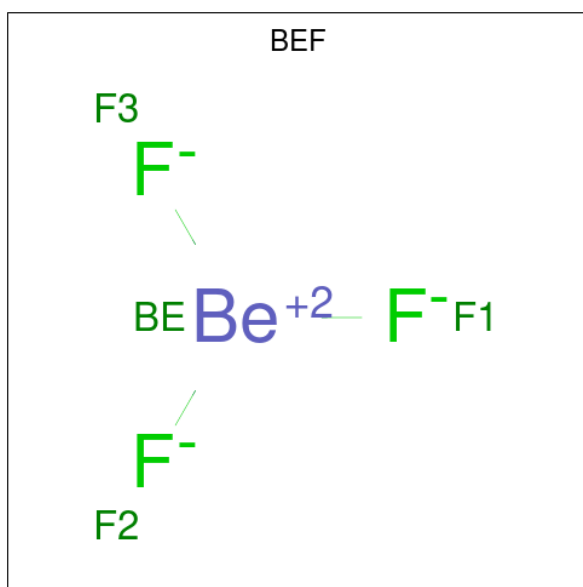
Mol	Chain	Residues	Atoms		AltConf
11	1-K	1	Total	Mg	0
			1	1	
11	2-K	1	Total	Mg	0
			1	1	
11	3-K	1	Total	Mg	0
			1	1	
11	4-K	1	Total	Mg	0
			1	1	
11	5-K	1	Total	Mg	0
			1	1	
11	6-K	1	Total	Mg	0
			1	1	
11	7-K	1	Total	Mg	0
			1	1	
11	8-K	1	Total	Mg	0
			1	1	
11	9-K	1	Total	Mg	0
			1	1	
11	10-K	1	Total	Mg	0
			1	1	

- Molecule 12 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



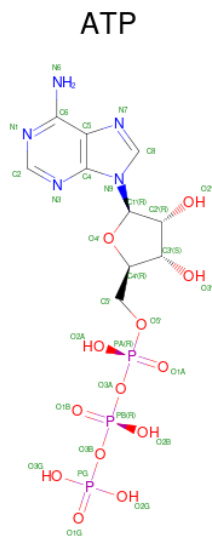
Mol	Chain	Residues	Atoms					AltConf
12	1-K	1	Total 27	C 10	N 5	O 10	P 2	0
12	2-K	1	Total 27	C 10	N 5	O 10	P 2	0
12	3-K	1	Total 27	C 10	N 5	O 10	P 2	0
12	4-K	1	Total 27	C 10	N 5	O 10	P 2	0
12	5-K	1	Total 27	C 10	N 5	O 10	P 2	0
12	6-K	1	Total 27	C 10	N 5	O 10	P 2	0
12	7-K	1	Total 27	C 10	N 5	O 10	P 2	0
12	8-K	1	Total 27	C 10	N 5	O 10	P 2	0
12	9-K	1	Total 27	C 10	N 5	O 10	P 2	0
12	10-K	1	Total 27	C 10	N 5	O 10	P 2	0

- Molecule 13 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF_3).



Mol	Chain	Residues	Atoms			AltConf
13	1-K	1	Total	Be	F	0
			4	1	3	
13	2-K	1	Total	Be	F	0
			4	1	3	
13	3-K	1	Total	Be	F	0
			4	1	3	
13	4-K	1	Total	Be	F	0
			4	1	3	
13	5-K	1	Total	Be	F	0
			4	1	3	
13	6-K	1	Total	Be	F	0
			4	1	3	
13	7-K	1	Total	Be	F	0
			4	1	3	
13	8-K	1	Total	Be	F	0
			4	1	3	
13	9-K	1	Total	Be	F	0
			4	1	3	
13	10-K	1	Total	Be	F	0
			4	1	3	

- Molecule 14 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).

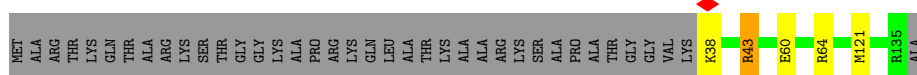


Mol	Chain	Residues	Atoms					AltConf
14	1-L	1	Total 31	C 10	N 5	O 13	P 3	0
14	2-L	1	Total 31	C 10	N 5	O 13	P 3	0
14	3-L	1	Total 31	C 10	N 5	O 13	P 3	0
14	4-L	1	Total 31	C 10	N 5	O 13	P 3	0
14	5-L	1	Total 31	C 10	N 5	O 13	P 3	0
14	6-L	1	Total 31	C 10	N 5	O 13	P 3	0
14	7-L	1	Total 31	C 10	N 5	O 13	P 3	0
14	8-L	1	Total 31	C 10	N 5	O 13	P 3	0
14	9-L	1	Total 31	C 10	N 5	O 13	P 3	0
14	10-L	1	Total 31	C 10	N 5	O 13	P 3	0

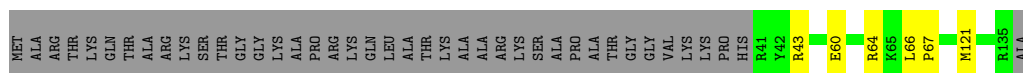
3 Residue-property plots [i](#)

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

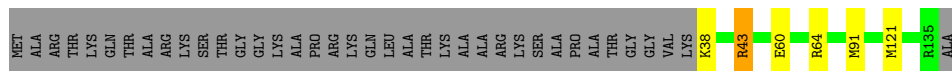
- Molecule 1: Histone H3



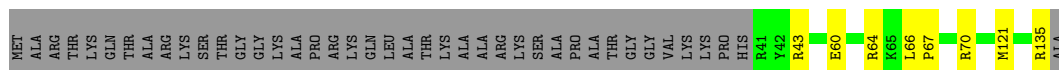
- Molecule 1: Histone H3



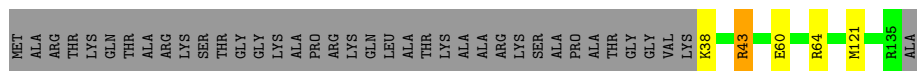
- Molecule 1: Histone H3



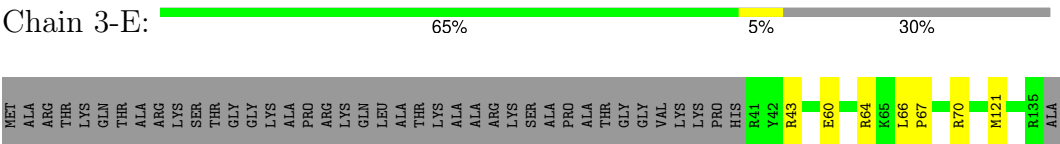
- Molecule 1: Histone H3



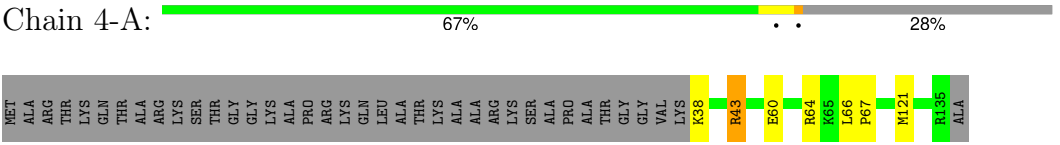
- Molecule 1: Histone H3



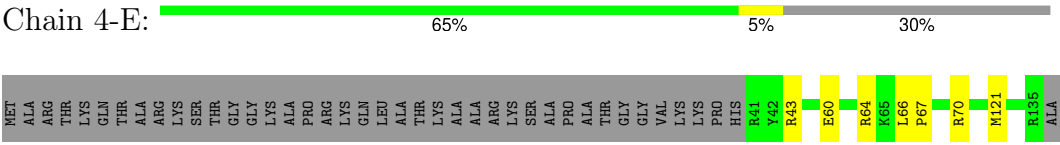
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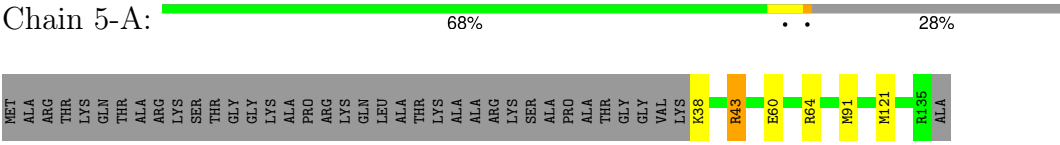
● Molecule 1: Histone H3



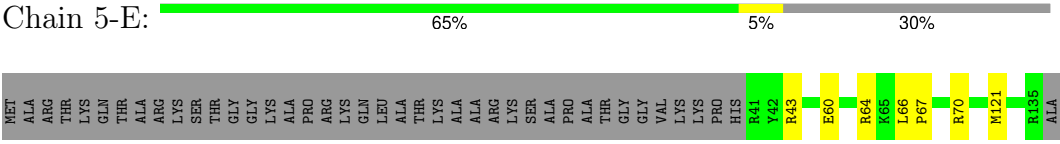
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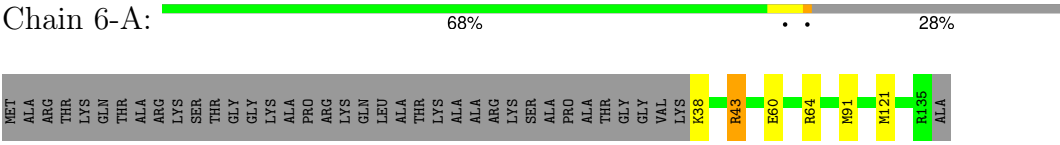
● Molecule 1: Histone H3



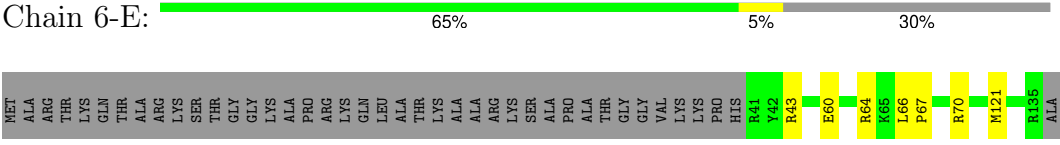
● Molecule 1: Histone H3



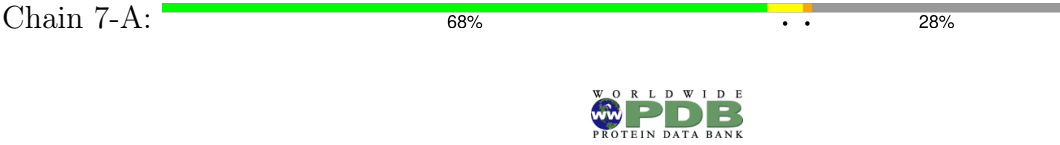
● Molecule 1: Histone H3

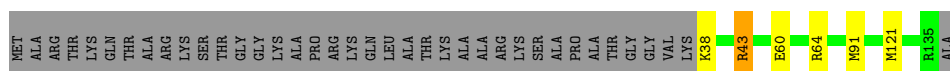


● Molecule 1: Histone H3



● Molecule 1: Histone H3





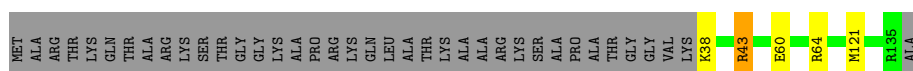
- Molecule 1: Histone H3

Chain 7-E: 65% 5% 30%



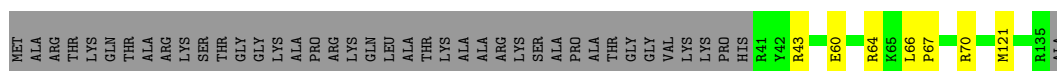
- Molecule 1: Histone H3

Chain 8-A: 68% • • 28%



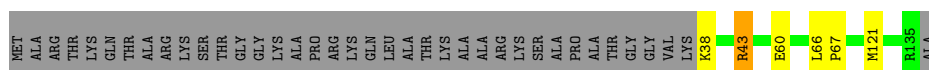
- Molecule 1: Histone H3

Chain 8-E: 65% 5% 30%



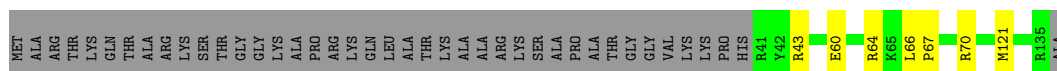
- Molecule 1: Histone H3

Chain 9-A: 68% • • 28%



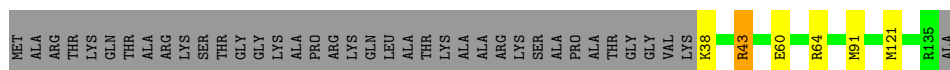
- Molecule 1: Histone H3

Chain 9-E: 65% 5% 30%



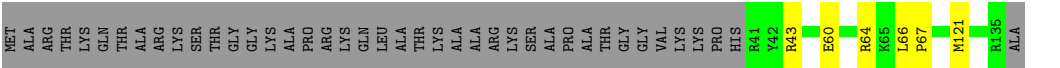
- Molecule 1: Histone H3

Chain 10-A: 68% • • 28%

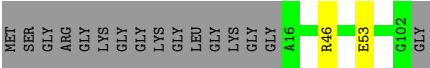
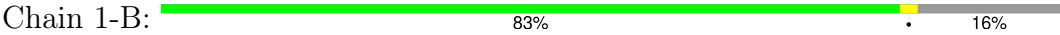


- Molecule 1: Histone H3

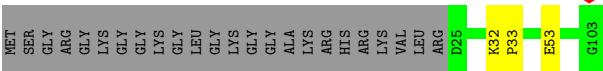
Chain 10-E: 65% • 30%



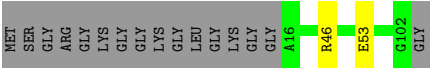
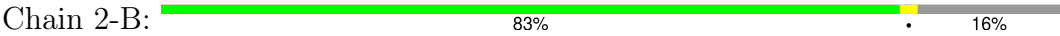
• Molecule 2: Histone H4



• Molecule 2: Histone H4



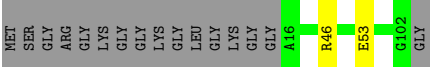
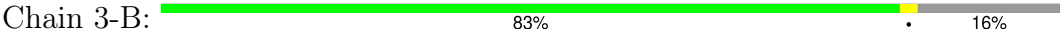
• Molecule 2: Histone H4



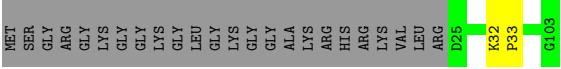
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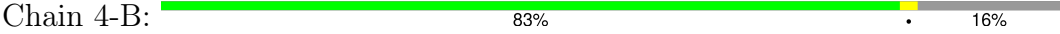
• Molecule 2: Histone H4

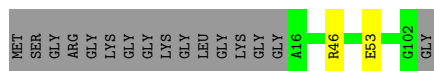


• Molecule 2: Histone H4

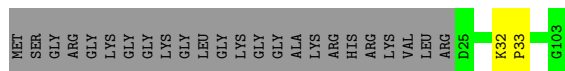
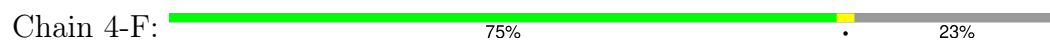


• Molecule 2: Histone H4

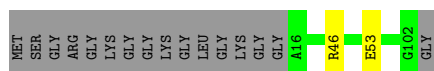
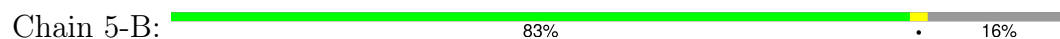




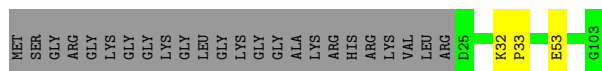
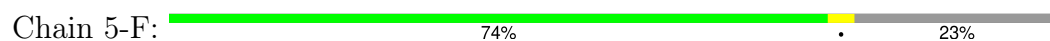
- Molecule 2: Histone H4



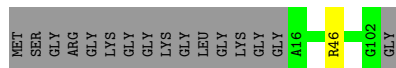
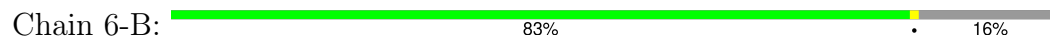
- Molecule 2: Histone H4



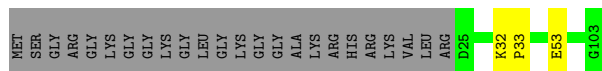
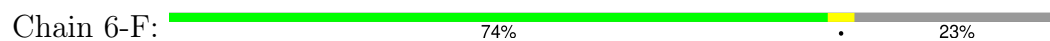
- Molecule 2: Histone H4



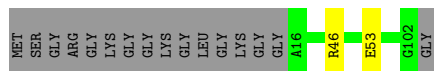
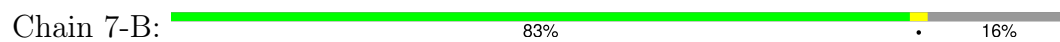
- Molecule 2: Histone H4



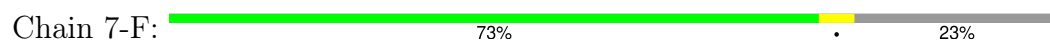
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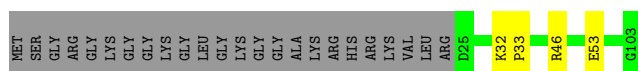


- Molecule 2: Histone H4



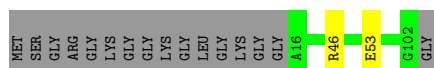
- Molecule 2: Histone H4





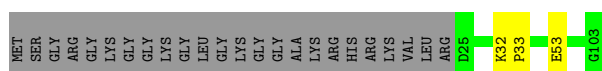
- Molecule 2: Histone H4

Chain 8-B: 83% 16%



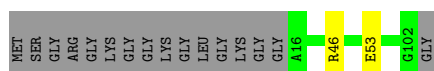
- Molecule 2: Histone H4

Chain 8-F: 74% 23%



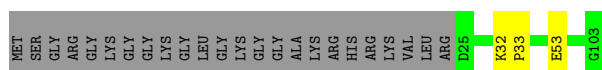
- Molecule 2: Histone H4

Chain 9-B: 83% 16%



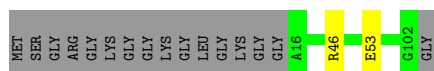
- Molecule 2: Histone H4

Chain 9-F: 74% 23%



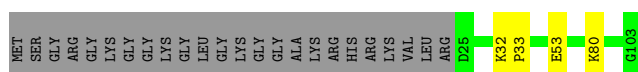
- Molecule 2: Histone H4

Chain 10-B: 83% 16%



- Molecule 2: Histone H4

Chain 10-F: 73% 23%

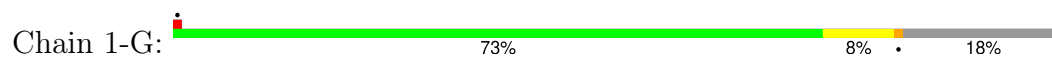


- Molecule 3: Histone H2A

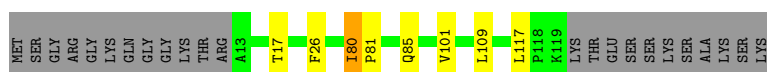
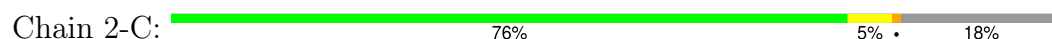
Chain 1-C: 76% 5% 18%



- Molecule 3: Histone H2A



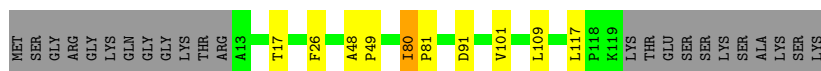
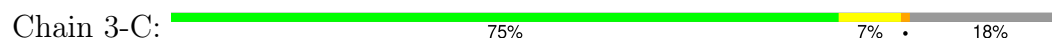
- Molecule 3: Histone H2A



- Molecule 3: Histone H2A



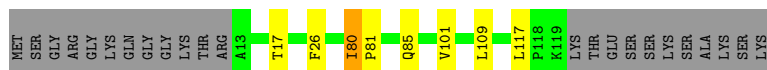
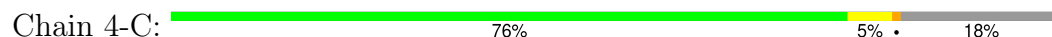
- Molecule 3: Histone H2A



- Molecule 3: Histone H2A



- Molecule 3: Histone H2A



- Molecule 3: Histone H2A





- Molecule 3: Histone H2A

Chain 5-C: 76% 5% 18%



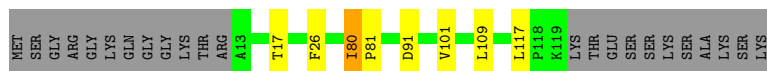
- Molecule 3: Histone H2A

Chain 5-G: 73% 8% 18%



- Molecule 3: Histone H2A

Chain 6-C: 76% 5% 18%



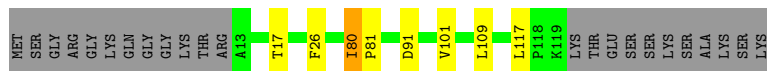
- Molecule 3: Histone H2A

Chain 6-G: 73% 8% 18%



- Molecule 3: Histone H2A

Chain 7-C: 76% 5% 18%



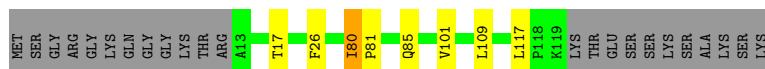
- Molecule 3: Histone H2A

Chain 7-G: 73% 8% 18%

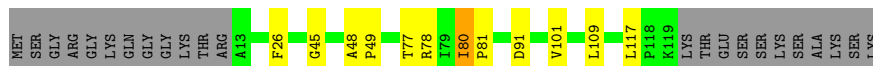


- Molecule 3: Histone H2A

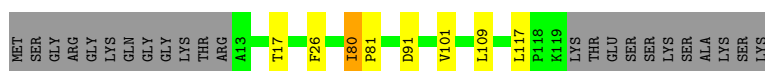
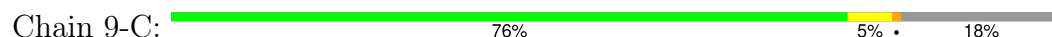
Chain 8-C: 76% 5% 18%



- Molecule 3: Histone H2A



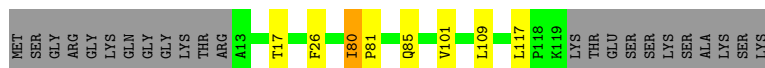
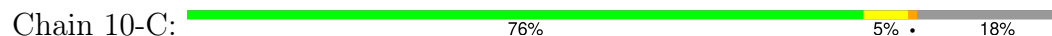
- Molecule 3: Histone H2A



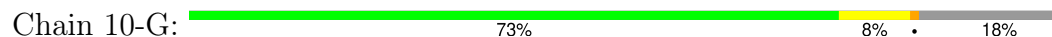
- Molecule 3: Histone H2A



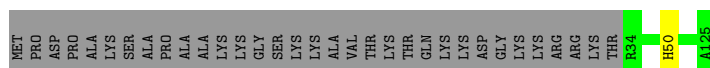
- Molecule 3: Histone H2A



- Molecule 3: Histone H2A

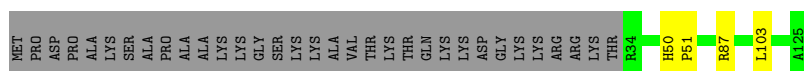


- Molecule 4: Histone H2B



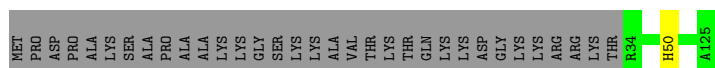
- Molecule 4: Histone H2B





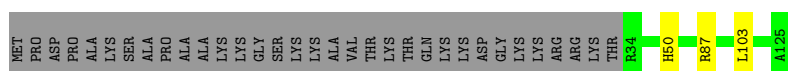
- Molecule 4: Histone H2B

Chain 2-D: 73% 26%



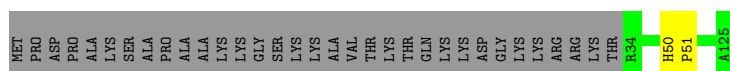
- Molecule 4: Histone H2B

Chain 2-H: 71% 26%



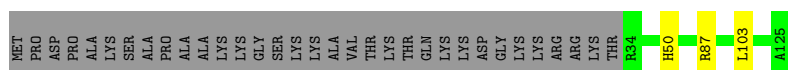
- Molecule 4: Histone H2B

Chain 3-D: 72% 26%



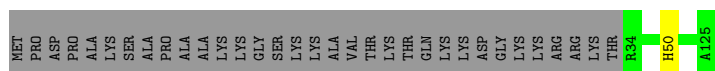
- Molecule 4: Histone H2B

Chain 3-H: 71% 26%



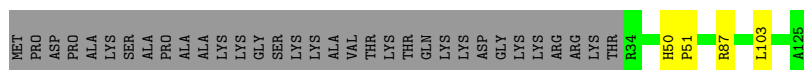
- Molecule 4: Histone H2B

Chain 4-D: 73% 26%



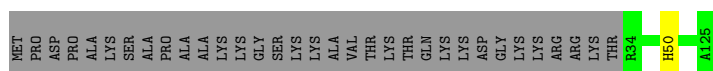
- Molecule 4: Histone H2B

Chain 4-H: 70% 26%

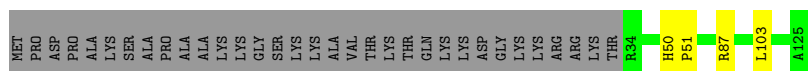


- Molecule 4: Histone H2B

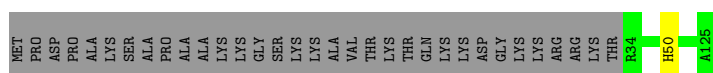
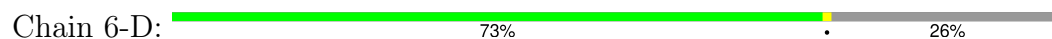
Chain 5-D: 73% 26%



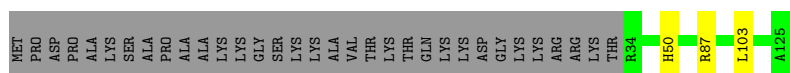
- Molecule 4: Histone H2B



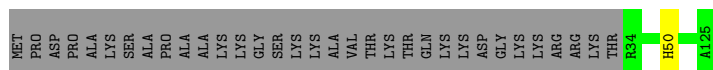
- Molecule 4: Histone H2B



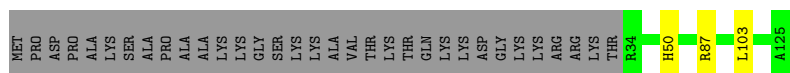
- Molecule 4: Histone H2B



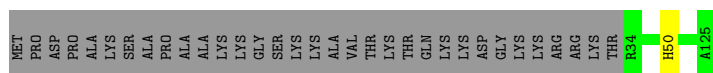
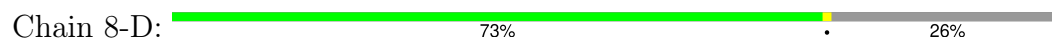
- Molecule 4: Histone H2B



- Molecule 4: Histone H2B



- Molecule 4: Histone H2B



- Molecule 4: Histone H2B



Digital Tool Type	Percentage
Digital tool	67%
Digital tool	12%
Digital tool	21%



Digital Tool	Percentage
Video conferencing tool	67%
Digital whiteboard	12%
Digital sticky note	21%



Digital Tool	Percentage
Video conferencing tool	67%
Digital whiteboard	12%
Digital sticky note	21%



Response	Percentage
U.S. should take action to protect the environment	67%
U.S. should not take action to protect the environment	12%
U.S. should not take action to protect the environment	21%



Response	Percentage
Yes, the U.S. is a democracy	66%
No, the U.S. is not a democracy	12%
Unsure	21%



Digital Tool	Percentage
Video conferencing tool	67%
Digital whiteboard	12%
Digital sticky note	21%

- Molecule 5: DNA (185-MER)



- Molecule 5: DNA (185-MER)



- Molecule 6: DNA (185-MER)



- Molecule 6: DNA (185-MER)



- Molecule 6: DNA (185-MER)



DC
DC
DT
DA
DG
DG
DT
DA
DT

- Molecule 6: DNA (185-MER)

Chain 4-J:  68% 11% 21%

DA
DT
DC
DC
DG
DG
DT
DT
DG
DG
DT
DT
DC
DC
DA
DA
DC
DC
DG
DG
DC
DC
DG
DG
DA
DA
DG
DG
T1
C20
A21
A31
G54
G55
G56
G69
G70
A91
G94
G95
G106
T107
G112
C129
G130
G131
C132
C144
G145
A146
DG
DC
DA
DA
DT
DT
DC
DC
DA
DA
DG
DG
DA
DA

DC
DC
DT
DA
DG
DG
DT
DT
DG
DG
DA
DT

- Molecule 6: DNA (185-MER)

Chain 5-J:  69% 10% 21%

DA
DT
DC
DC
DG
DG
DT
DT
DG
DG
DT
DT
DC
DC
DA
DA
DC
DC
DG
DG
DC
DC
DG
DG
DA
DA
DG
DG
T1
C20
A21
A31
G54
G55
G56
G69
G70
A91
G94
G95
G106
T107
G112
C129
G130
G131
C132
C144
G145
A146
DG
DC
DA
DA
DT
DT
DC
DC
DA
DA
DG
DG
DA
DA

DC
DT
DA
DG
DG
DT
DT
DG
DG
DA
DT

- Molecule 6: DNA (185-MER)

Chain 6-J:  68% 11% 21%

DA
DT
DC
DC
DG
DG
DT
DT
DG
DG
DT
DT
DC
DC
DA
DA
DC
DC
DG
DG
DC
DC
DG
DG
DA
DA
DG
DG
T1
C20
A21
A31
G54
G55
G56
G69
G70
A91
G94
G95
G106
T107
G112
C129
G130
G131
C132
C144
G145
A146
DG
DC
DA
DA
DT
DT
DC
DC
DA
DA
DG
DG
DA
DA

DC
DC
DT
DA
DG
DG
DT
DT
DG
DG
DA
DT

- Molecule 6: DNA (185-MER)

Chain 7-J:  68% 11% 21%

DA
DT
DC
DC
DG
DG
DT
DT
DG
DG
DT
DT
DC
DC
DA
DA
DC
DC
DG
DG
DC
DC
DG
DG
DA
DA
DG
DG
T1
C20
A21
A31
G54
G55
G56
G69
G70
A91
G94
G95
G106
T107
G112
C129
G130
G131
C132
C144
G145
A146
DG
DC
DA
DA
DT
DT
DC
DC
DA
DA
DG
DG
DA
DA

DC
DC
DT
DA
DG
DG
DT
DT
DG
DG
DA
DT

- Molecule 6: DNA (185-MER)

Chain 8-J:  68% 11% 21%

DA
DT
DC
DC
DG
DG
DT
DT
DG
DG
DT
DT
DC
DC
DA
DA
DC
DC
DG
DG
DC
DC
DG
DG
DA
DA
DG
DG
T1
C20
A21
A31
G54
G55
G56
T57
G69
G70
A91
G94
G95
G106
T107
G112
C129
G130
G131
C132
C144
G145
A146
DG
DC
DA
DA
DT
DT
DC
DC
DA
DA
DG
DG
DA
DA

DA
DC
DC
DT
DA
DG
DG
DT
DT
DG
DG
DA
DT

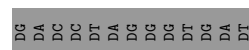
- Molecule 6: DNA (185-MER)

Response	Percentage
Doing a good job	68%
Not doing a good job	11%
Don't know	21%



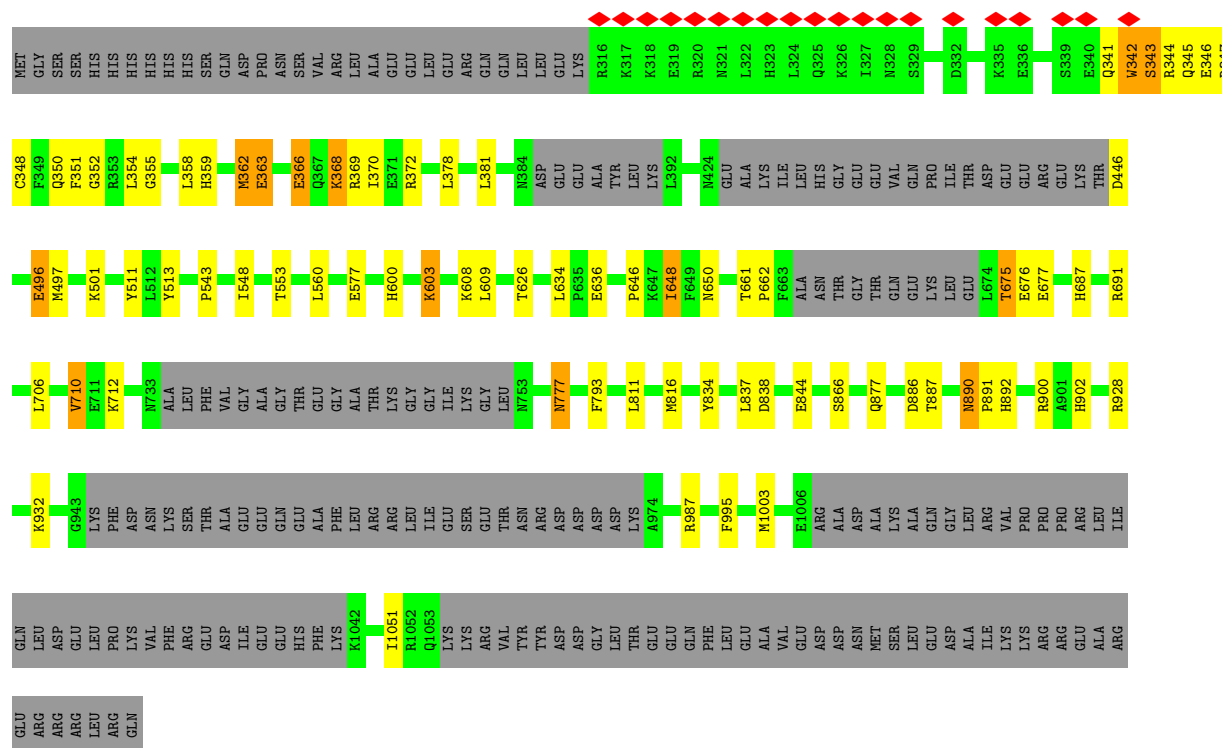
- Molecule 6: DNA (185-MER)

68% 11% 21%



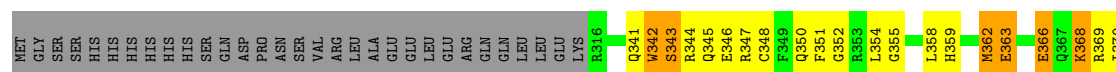
- Molecule 7: Nuclear protein STH1/NPS1

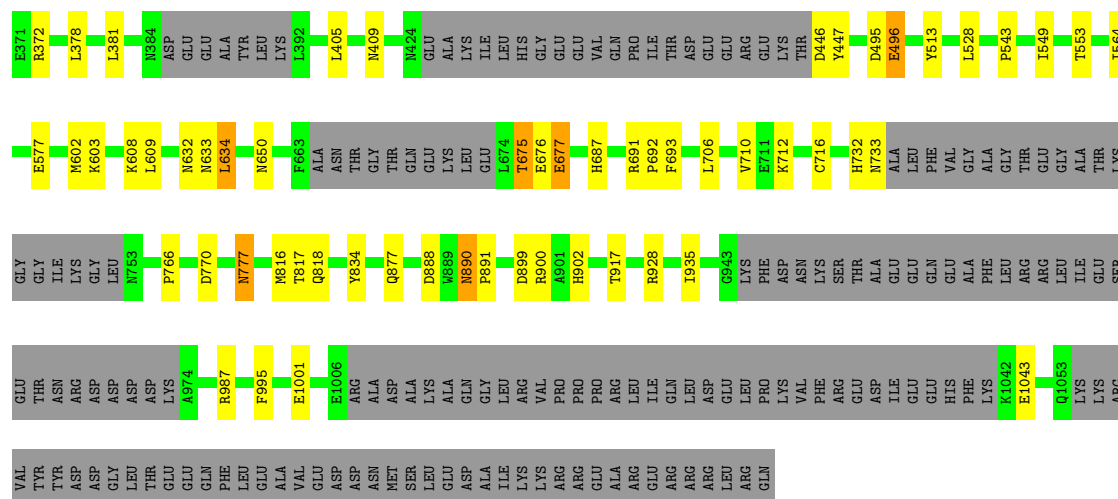
Frequency	Percentage
Daily	66%
Weekly	8%
Monthly	24%



- Molecule 7: Nuclear protein STH1/NPS1

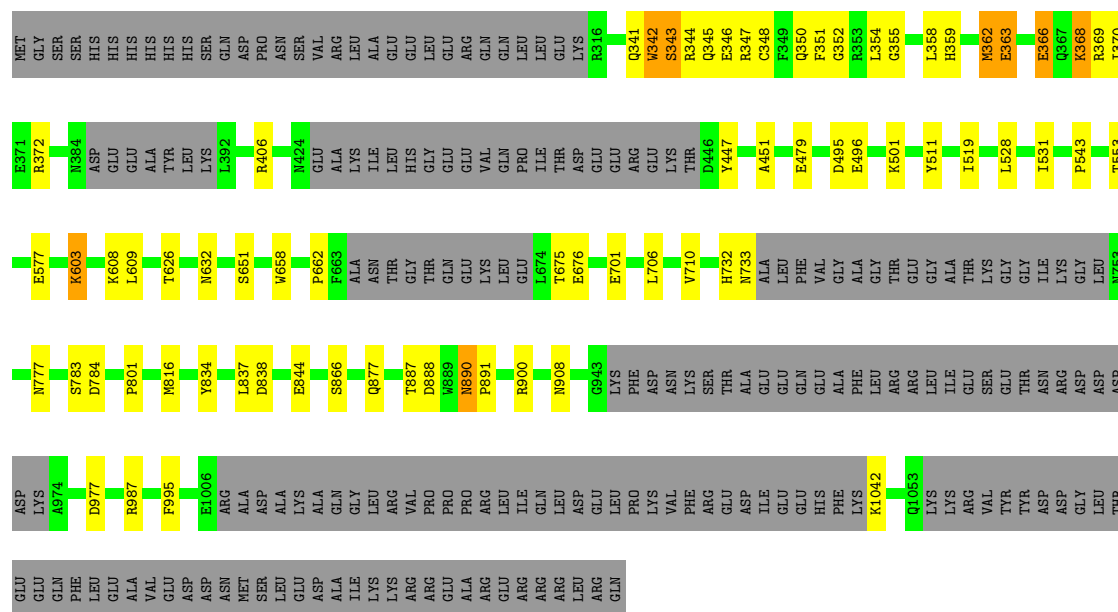
66% 8% 24%





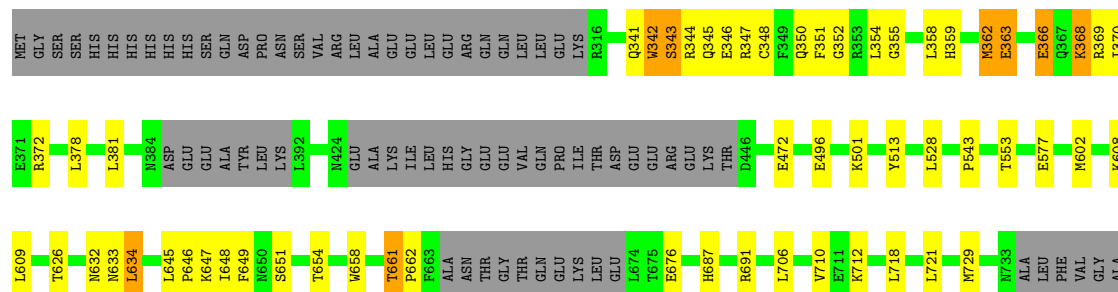
• Molecule 7: Nuclear protein STH1/NPS1

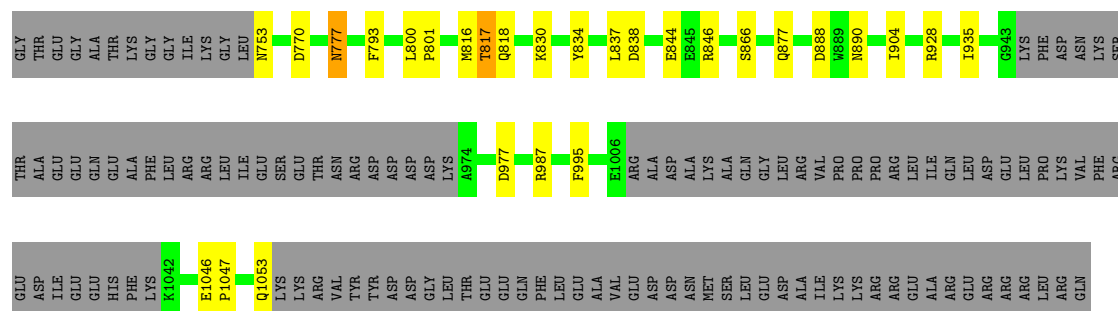
Chain 3-K: 67% 8% 24%



• Molecule 7: Nuclear protein STH1/NPS1

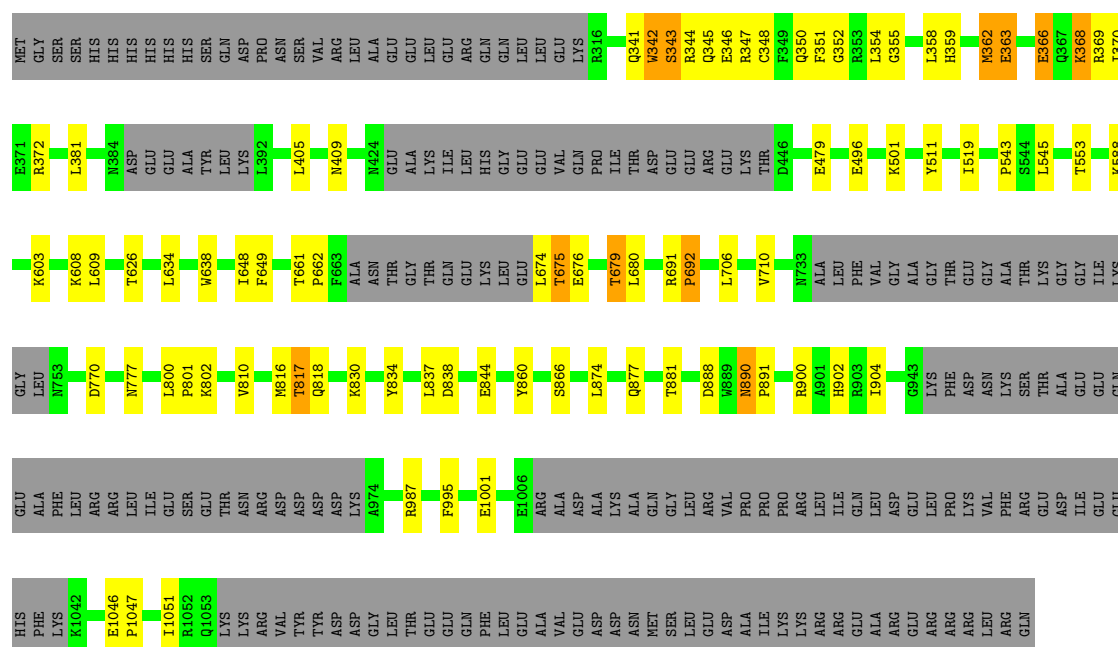
Chain 4-K: 65% 9% 24%





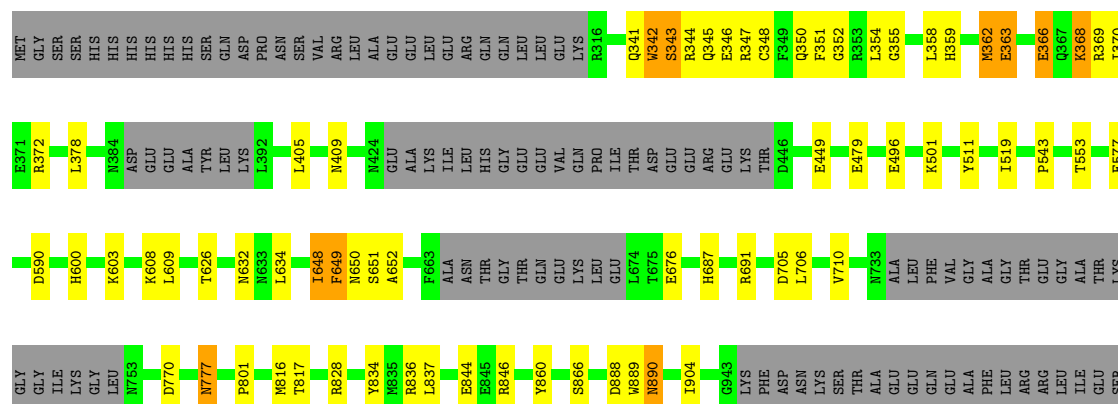
• Molecule 7: Nuclear protein STH1/NPS1

Chain 5-K: 65% 9% 24%



• Molecule 7: Nuclear protein STH1/NPS1

Chain 6-K: 66% 8% 24%

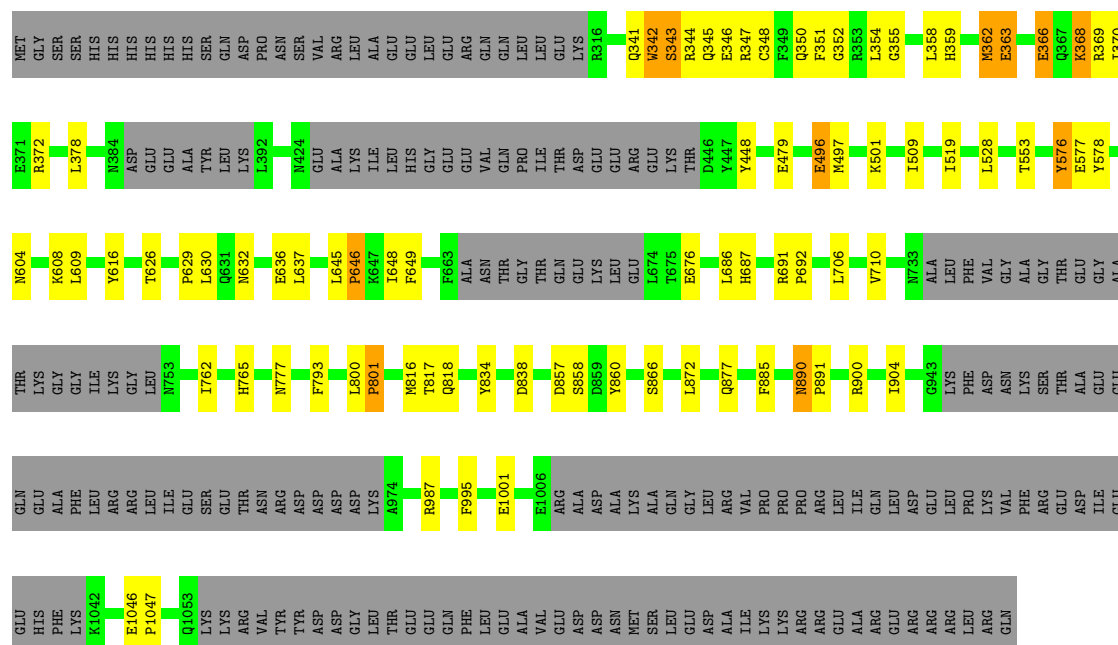




LYS
LYS
ARG
VAL
TYR
THR
ASP
GLY
THR
GLU
GLN
PHE
LEU
GLU
ALA
VAL
GLU
ASP
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ALA
ALA
ARG
GLU
ARG
GLU
ARG
LEU
ARG
GLN

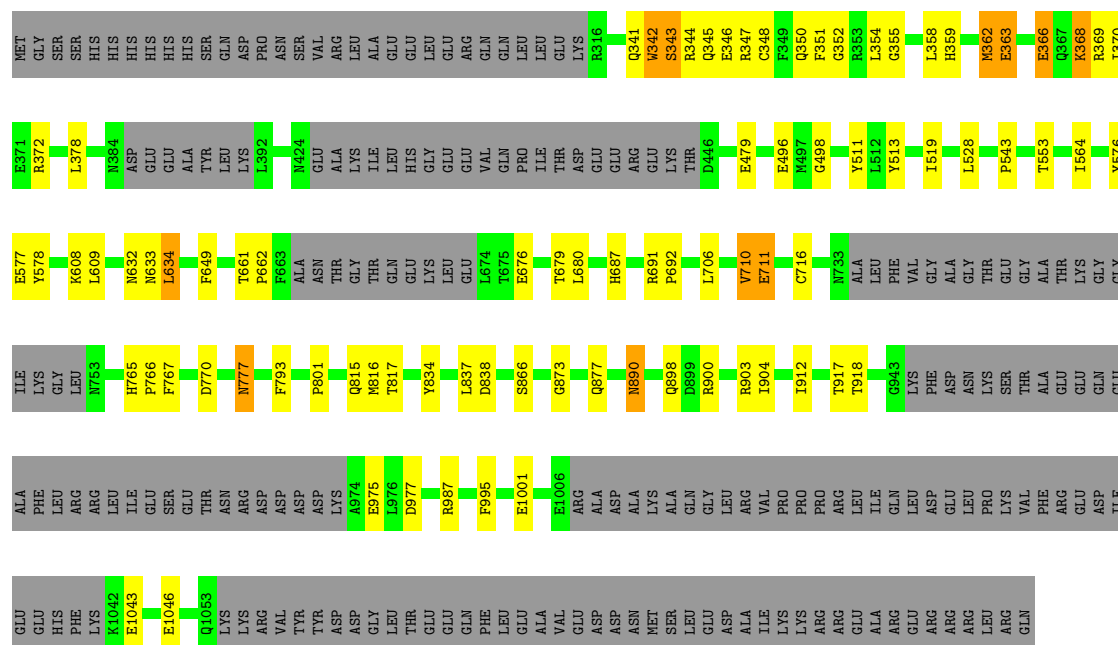
• Molecule 7: Nuclear protein STH1/NPS1

Chain 9-K: 66% 9% 24%

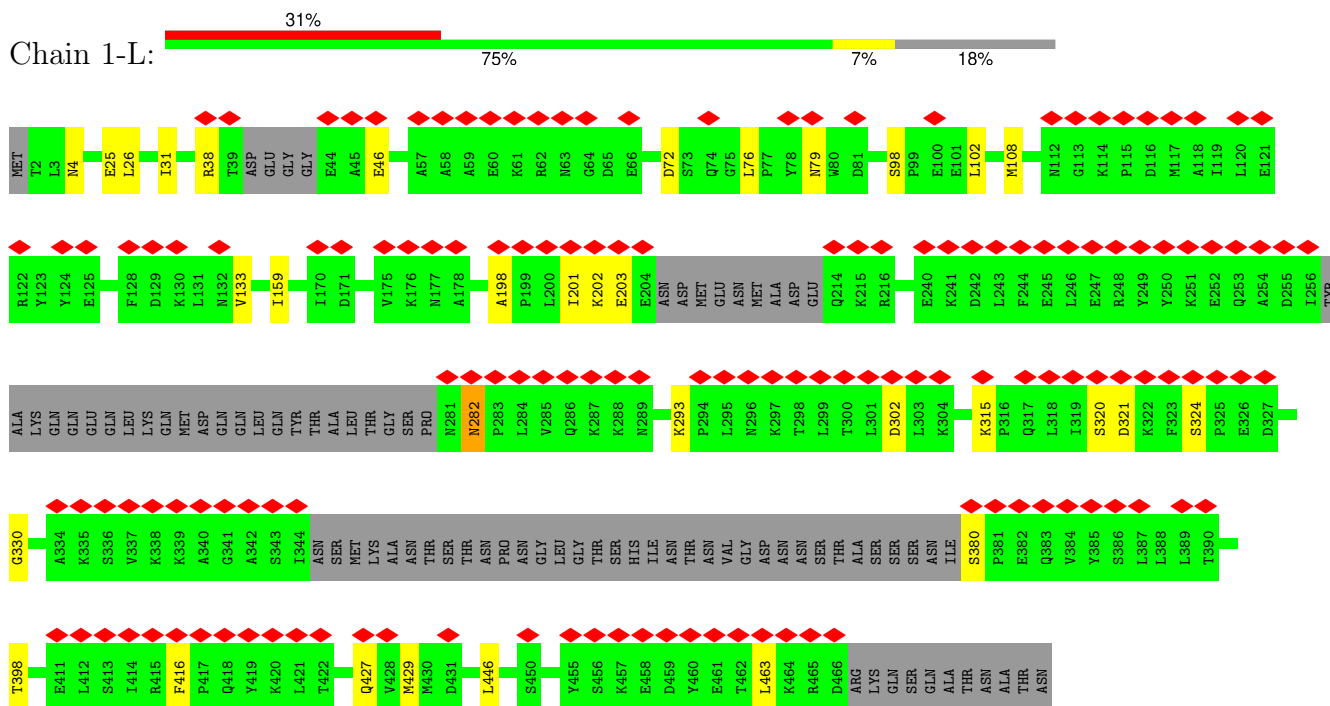


• Molecule 7: Nuclear protein STH1/NPS1

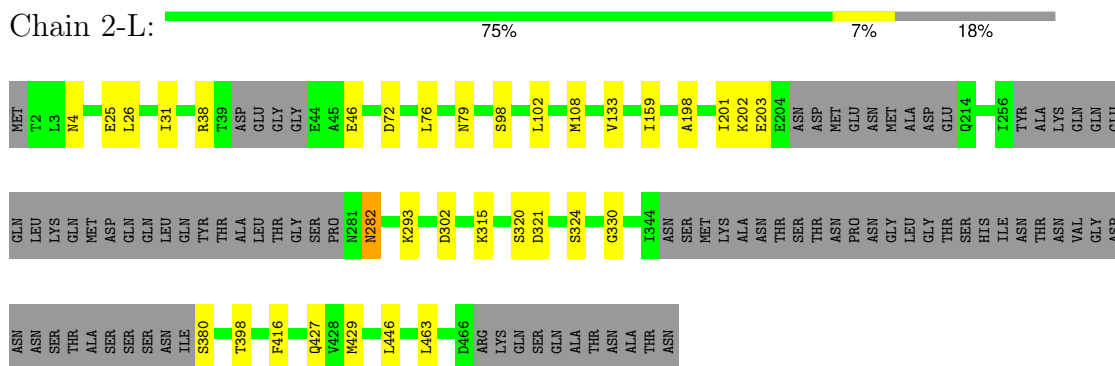
Chain 10-K: 65% 9% 24%



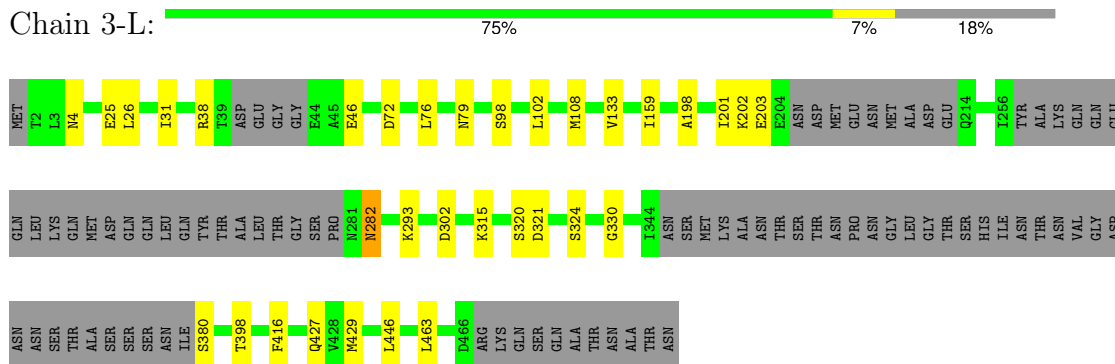
• Molecule 8: Actin-related protein 7



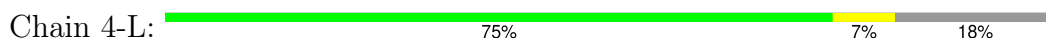
- Molecule 8: Actin-related protein 7

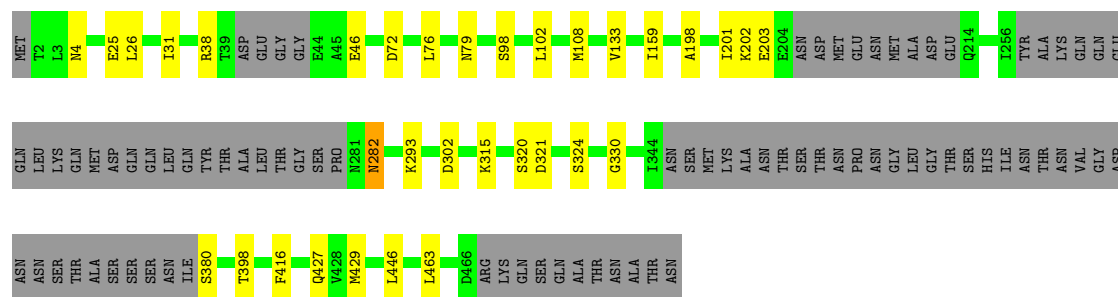


- Molecule 8: Actin-related protein 7

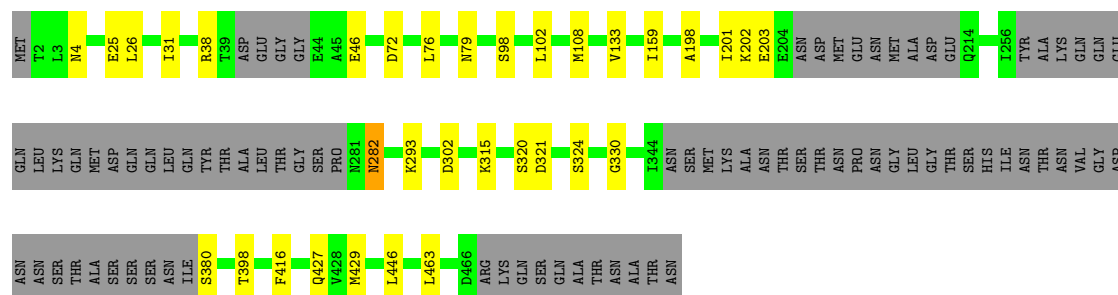
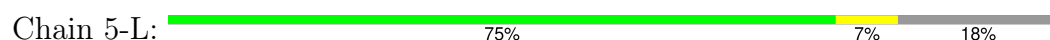


- Molecule 8: Actin-related protein 7

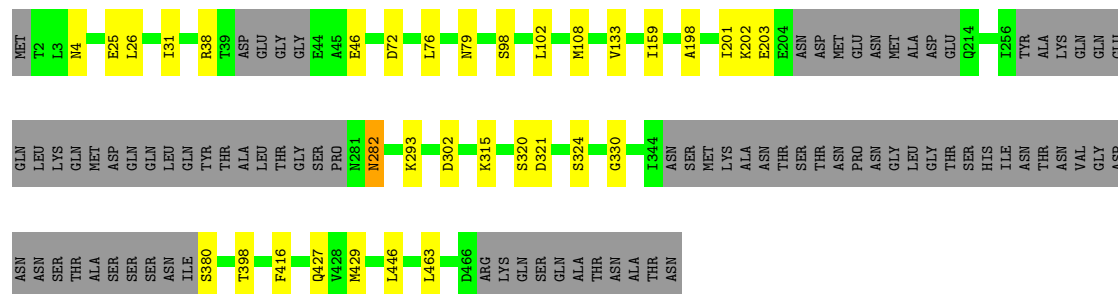
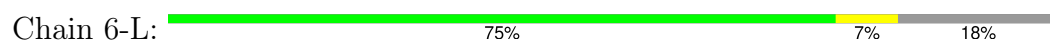




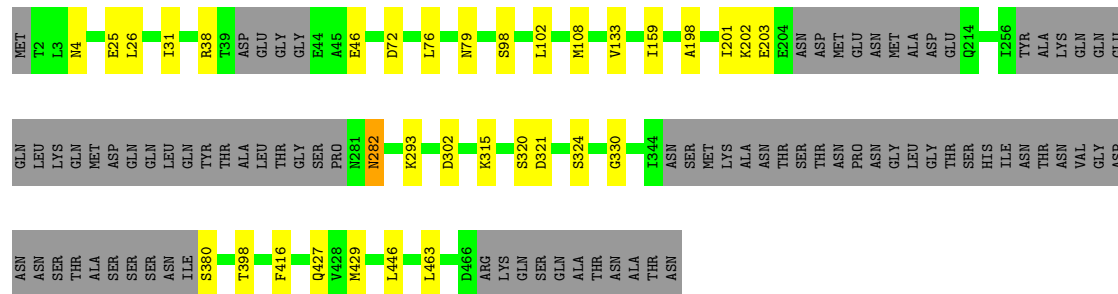
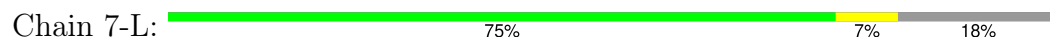
- Molecule 8: Actin-related protein 7



- Molecule 8: Actin-related protein 7

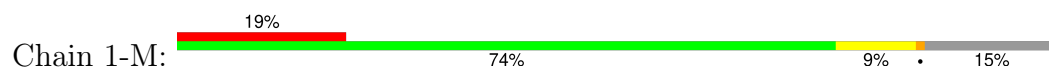


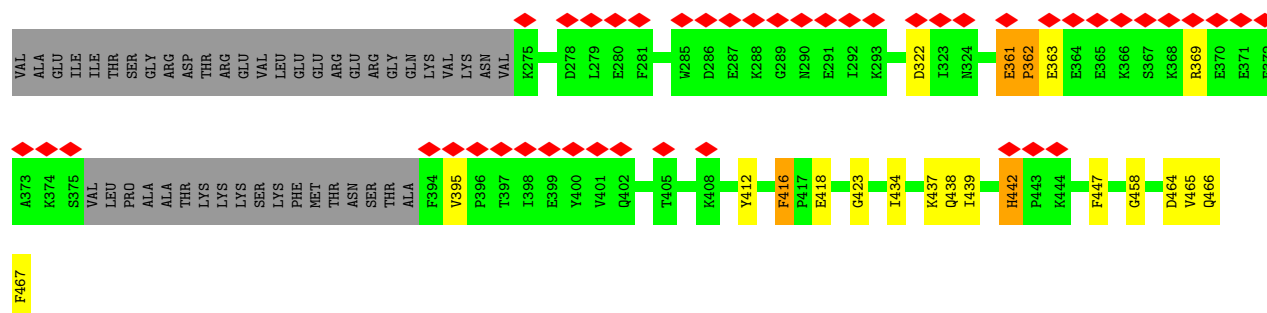
- Molecule 8: Actin-related protein 7



- Molecule 8: Actin-related protein 7

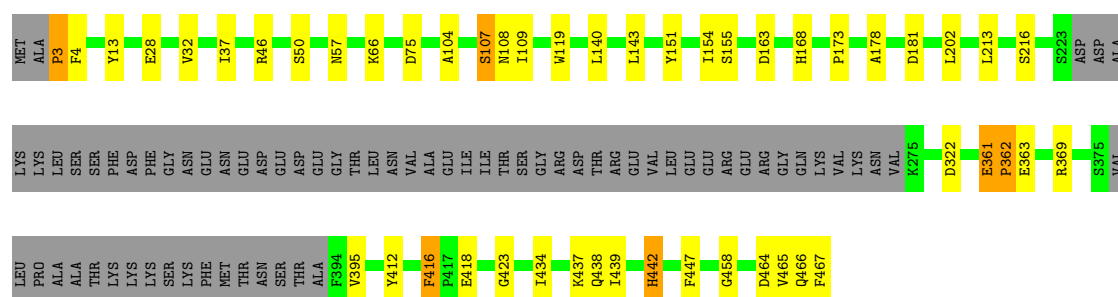
Device Type	Percentage
Smartphone	75%
Tablet	7%
Feature phone	18%





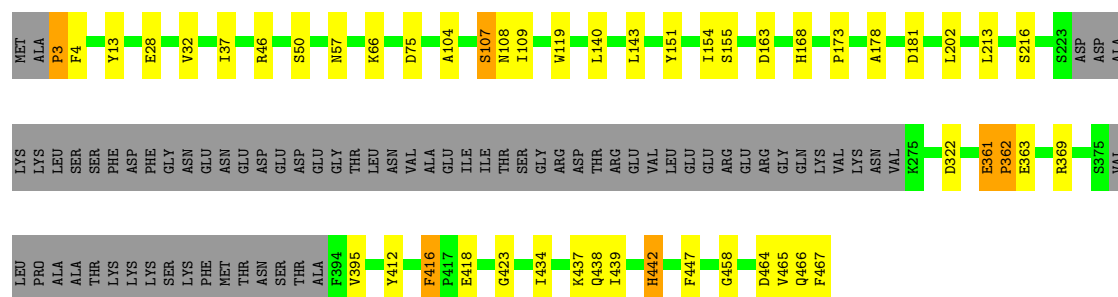
- Molecule 9: Actin-like protein ARP9

Chain 2-M: 74% 9% 15%



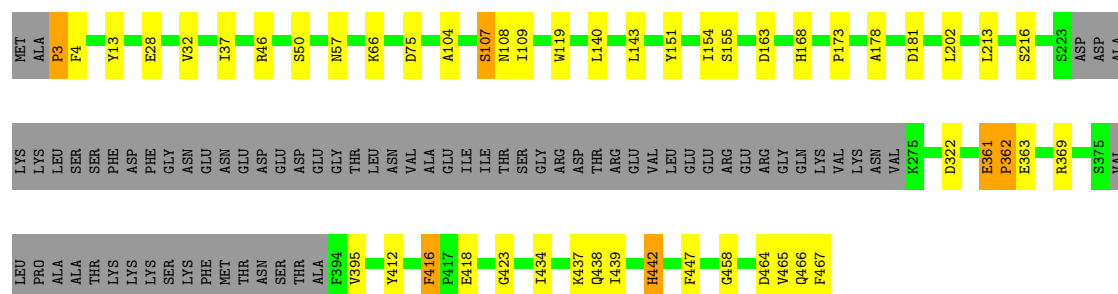
- Molecule 9: Actin-like protein ARP9

Chain 3-M: 74% 9% 15%

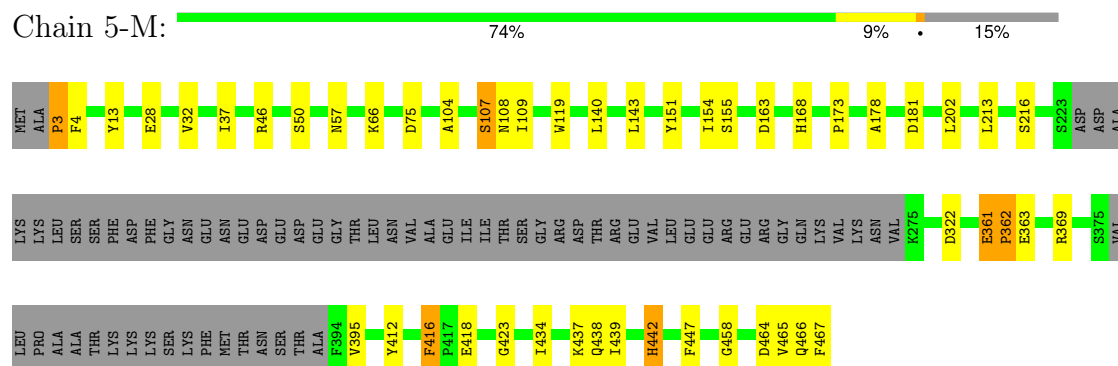


- Molecule 9: Actin-like protein ARP9

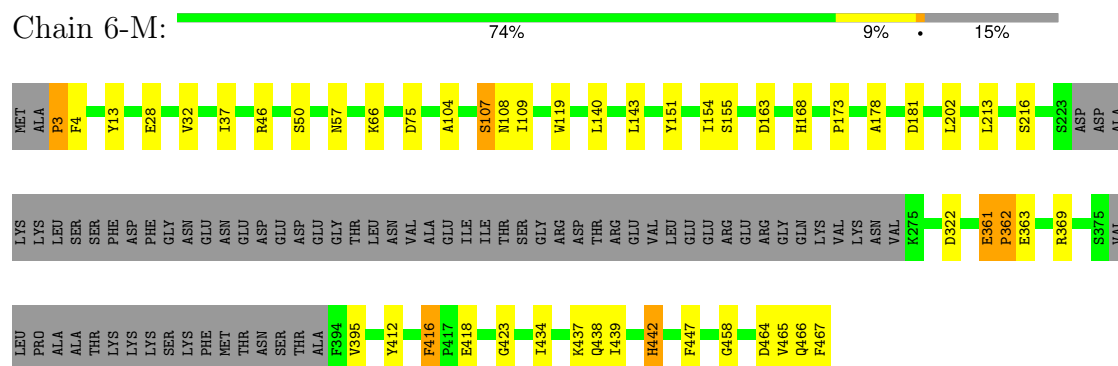
Chain 4-M: 74% 9% 15%



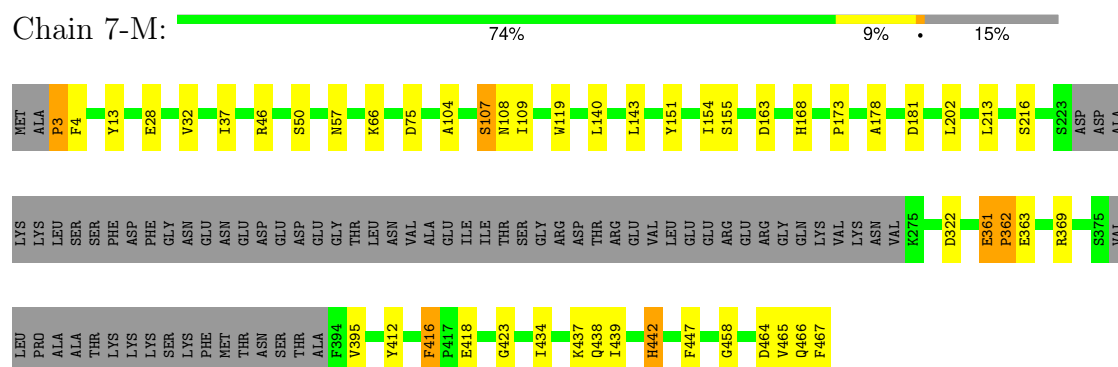
• Molecule 9: Actin-like protein ARP9



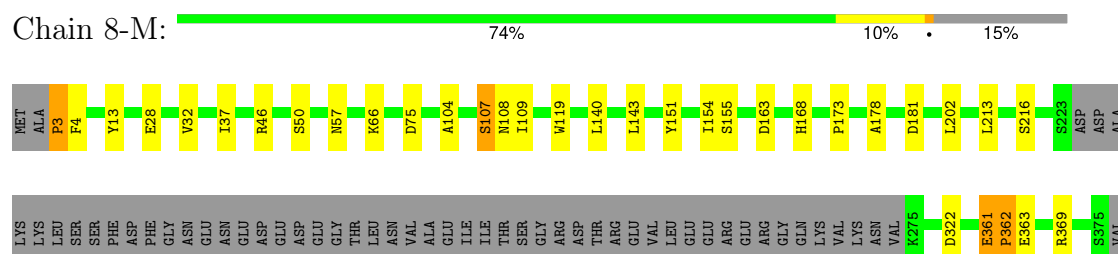
• Molecule 9: Actin-like protein ARP9



• Molecule 9: Actin-like protein ARP9



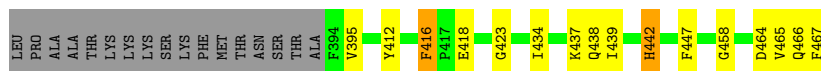
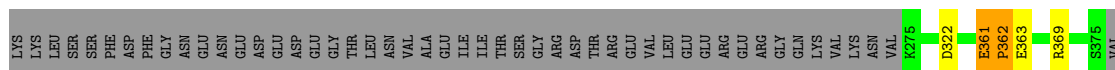
• Molecule 9: Actin-like protein ARP9





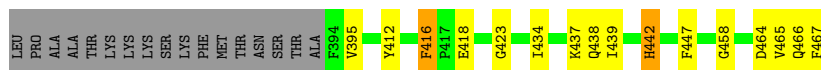
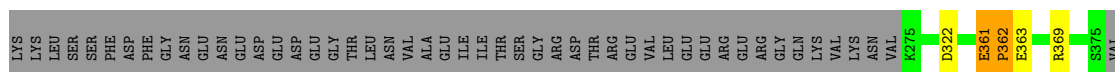
• Molecule 9: Actin-like protein ARP9

Chain 9-M: 74% 9% 15%



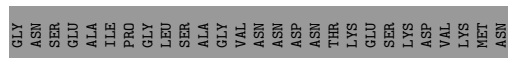
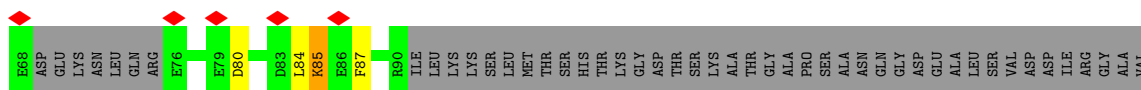
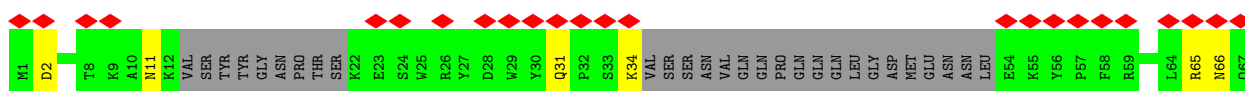
• Molecule 9: Actin-like protein ARP9

Chain 10-M: 74% 9% 15%



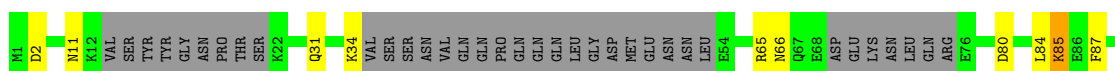
• Molecule 10: Regulator of Ty1 transposition protein 102

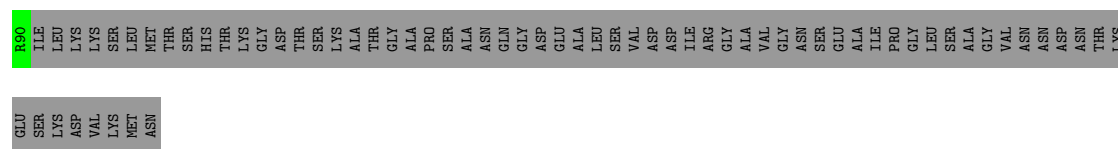
Chain 1-N: 18% 29% 6% 65%



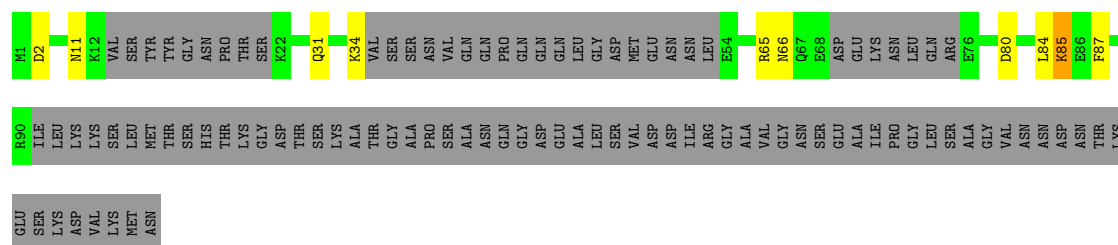
• Molecule 10: Regulator of Ty1 transposition protein 102

Chain 2-N: 29% 6% 65%

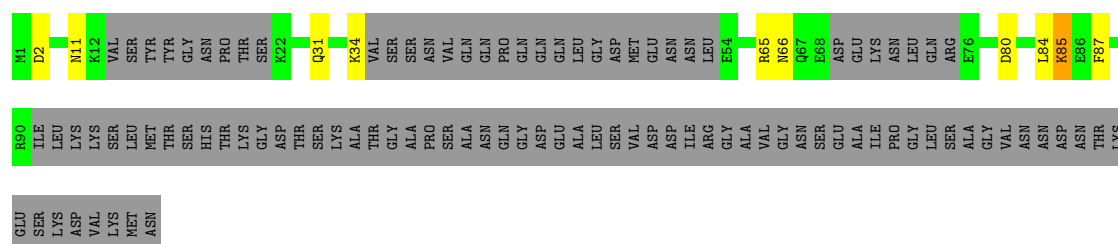




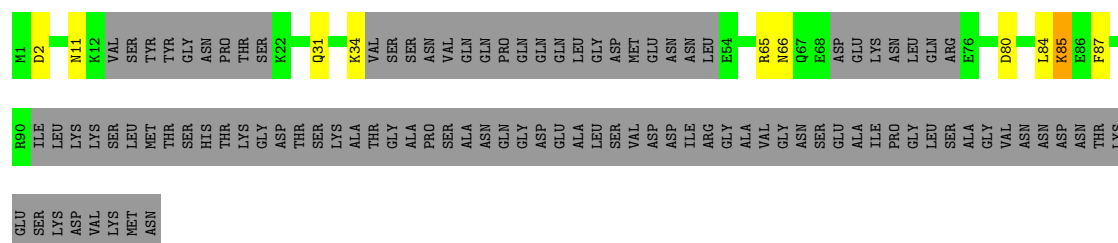
- Molecule 10: Regulator of Ty1 transposition protein 102



- Molecule 10: Regulator of Ty1 transposition protein 102



- Molecule 10: Regulator of Ty1 transposition protein 102



- Molecule 10: Regulator of Ty1 transposition protein 102



GLU
SER
LYS
ASP
VAL
LYS
MET
ASN

• Molecule 10: Regulator of Ty1 transposition protein 102

Chain 7-N: 29% 6% 65%

K1 D2 N11 K12 VAL SER TYR THR GLY ASN HIS THR PRO THR LYS SER K22 Q31 K34 VAL SER SER VAL ASN PRO ASN VAL GLN GLN GLN GLN GLN GLN LEU LEU GLY ASP MET VAL ASP ASN ASN LEU E54 R65 N66 Q67 E68 ASP GLU GLU LYS LEU ASN ARG E76 D80 L84 K85 E86 F87 LYS

GLU
SER
LYS
ASP
VAL
LYS
MET
ASN

• Molecule 10: Regulator of Ty1 transposition protein 102

Chain 8-N: 29% 6% 65%

K1 D2 N11 K12 VAL SER TYR THR GLY ASN HIS THR PRO THR LYS SER K22 Q31 K34 VAL SER SER VAL ASN PRO ASN VAL GLN GLN GLN GLN GLN GLN LEU LEU GLY ASP MET VAL ASP ASN ASN LEU E54 R65 N66 Q67 E68 ASP GLU GLU LYS LEU ASN ARG E76 D80 L84 K85 E86 F87 LYS

GLU
SER
LYS
ASP
VAL
LYS
MET
ASN

• Molecule 10: Regulator of Ty1 transposition protein 102

Chain 9-N: 29% 6% 65%

K1 D2 N11 K12 VAL SER TYR THR GLY ASN HIS THR PRO THR LYS SER K22 Q31 K34 VAL SER SER VAL ASN PRO ASN VAL GLN GLN GLN GLN GLN GLN LEU LEU GLY ASP MET VAL ASP ASN ASN LEU E54 R65 N66 Q67 E68 ASP GLU GLU LYS LEU ASN ARG E76 D80 L84 K85 E86 F87 LYS

GLU
SER
LYS
ASP
VAL
LYS
MET
ASN

• Molecule 10: Regulator of Ty1 transposition protein 102

Chain 10-N: 29% 6% 65%

K1 D2 N11 K12 VAL SER TYR THR GLY ASN HIS THR PRO THR LYS SER K22 Q31 K34 VAL SER SER VAL ASN PRO ASN VAL GLN GLN GLN GLN GLN GLN LEU LEU GLY ASP MET VAL ASP ASN ASN LEU E54 R65 N66 Q67 E68 ASP GLU GLU LYS LEU ASN ARG E76 D80 L84 K85 E86 F87 LYS

GLU
SER
LYS
ASP
VAL
LYS
MET
ASN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	293940	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.055	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	348.0, 348.0, 348.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	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, BEF, ADP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1-A	0.91	0/821	0.94	6/1100 (0.5%)
1	1-E	0.92	0/793	0.91	4/1062 (0.4%)
1	2-A	0.91	0/821	0.94	6/1100 (0.5%)
1	2-E	0.92	0/793	0.91	4/1062 (0.4%)
1	3-A	0.91	0/821	0.94	6/1100 (0.5%)
1	3-E	0.92	0/793	0.91	4/1062 (0.4%)
1	4-A	0.91	0/821	0.94	6/1100 (0.5%)
1	4-E	0.92	0/793	0.91	4/1062 (0.4%)
1	5-A	0.91	0/821	0.94	6/1100 (0.5%)
1	5-E	0.92	0/793	0.91	4/1062 (0.4%)
1	6-A	0.91	0/821	0.94	6/1100 (0.5%)
1	6-E	0.92	0/793	0.91	4/1062 (0.4%)
1	7-A	0.91	0/821	0.94	6/1100 (0.5%)
1	7-E	0.92	0/793	0.91	4/1062 (0.4%)
1	8-A	0.91	0/821	0.94	6/1100 (0.5%)
1	8-E	0.92	0/793	0.91	4/1062 (0.4%)
1	9-A	0.91	0/821	0.94	6/1100 (0.5%)
1	9-E	0.92	0/793	0.91	4/1062 (0.4%)
1	10-A	0.91	0/821	0.94	6/1100 (0.5%)
1	10-E	0.92	0/793	0.91	4/1062 (0.4%)
2	1-B	0.87	0/711	0.73	0/950
2	1-F	0.88	0/634	0.77	0/848
2	2-B	0.87	0/711	0.73	0/950
2	2-F	0.88	0/634	0.77	0/848
2	3-B	0.87	0/711	0.73	0/950
2	3-F	0.88	0/634	0.77	0/848
2	4-B	0.87	0/711	0.73	0/950
2	4-F	0.88	0/634	0.77	0/848
2	5-B	0.87	0/711	0.73	0/950
2	5-F	0.88	0/634	0.77	0/848
2	6-B	0.87	0/711	0.73	0/950
2	6-F	0.88	0/634	0.77	0/848

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	7-B	0.87	0/711	0.73	0/950
2	7-F	0.88	0/634	0.77	0/848
2	8-B	0.87	0/711	0.73	0/950
2	8-F	0.88	0/634	0.77	0/848
2	9-B	0.87	0/711	0.73	0/950
2	9-F	0.88	0/634	0.77	0/848
2	10-B	0.87	0/711	0.73	0/950
2	10-F	0.88	0/634	0.77	0/848
3	1-C	0.87	0/833	0.92	9/1124 (0.8%)
3	1-G	0.88	0/833	0.97	9/1124 (0.8%)
3	2-C	0.87	0/833	0.92	9/1124 (0.8%)
3	2-G	0.88	0/833	0.97	9/1124 (0.8%)
3	3-C	0.87	0/833	0.92	9/1124 (0.8%)
3	3-G	0.88	0/833	0.97	9/1124 (0.8%)
3	4-C	0.87	0/833	0.92	9/1124 (0.8%)
3	4-G	0.88	0/833	0.97	9/1124 (0.8%)
3	5-C	0.87	0/833	0.92	9/1124 (0.8%)
3	5-G	0.88	0/833	0.97	9/1124 (0.8%)
3	6-C	0.87	0/833	0.92	9/1124 (0.8%)
3	6-G	0.88	0/833	0.97	9/1124 (0.8%)
3	7-C	0.87	0/833	0.92	9/1124 (0.8%)
3	7-G	0.88	0/833	0.97	9/1124 (0.8%)
3	8-C	0.87	0/833	0.92	9/1124 (0.8%)
3	8-G	0.88	0/833	0.97	9/1124 (0.8%)
3	9-C	0.87	0/833	0.92	9/1124 (0.8%)
3	9-G	0.88	0/833	0.97	9/1124 (0.8%)
3	10-C	0.87	0/833	0.92	9/1124 (0.8%)
3	10-G	0.88	0/833	0.97	9/1124 (0.8%)
4	1-D	0.93	0/730	0.78	2/983 (0.2%)
4	1-H	0.94	0/730	0.84	4/983 (0.4%)
4	2-D	0.93	0/730	0.78	2/983 (0.2%)
4	2-H	0.94	0/730	0.84	4/983 (0.4%)
4	3-D	0.93	0/730	0.78	2/983 (0.2%)
4	3-H	0.94	0/730	0.84	4/983 (0.4%)
4	4-D	0.93	0/730	0.78	2/983 (0.2%)
4	4-H	0.94	0/730	0.84	4/983 (0.4%)
4	5-D	0.93	0/730	0.78	2/983 (0.2%)
4	5-H	0.94	0/730	0.84	4/983 (0.4%)
4	6-D	0.93	0/730	0.78	2/983 (0.2%)
4	6-H	0.94	0/730	0.84	4/983 (0.4%)
4	7-D	0.93	0/730	0.78	2/983 (0.2%)
4	7-H	0.94	0/730	0.84	4/983 (0.4%)
4	8-D	0.93	0/730	0.78	2/983 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	8-H	0.94	0/730	0.84	4/983 (0.4%)
4	9-D	0.93	0/730	0.78	2/983 (0.2%)
4	9-H	0.94	0/730	0.84	4/983 (0.4%)
4	10-D	0.93	0/730	0.78	2/983 (0.2%)
4	10-H	0.94	0/730	0.84	4/983 (0.4%)
5	1-I	0.39	0/3333	0.50	0/5137
5	2-I	0.39	0/3333	0.50	0/5137
5	3-I	0.39	0/3333	0.50	0/5137
5	4-I	0.39	0/3333	0.50	0/5137
5	5-I	0.39	0/3333	0.50	0/5137
5	6-I	0.39	0/3333	0.50	0/5137
5	7-I	0.39	0/3333	0.50	0/5137
5	8-I	0.39	0/3333	0.50	0/5137
5	9-I	0.39	0/3333	0.50	0/5137
5	10-I	0.39	0/3333	0.50	0/5137
6	1-J	0.40	0/3381	0.49	0/5221
6	2-J	0.40	0/3381	0.49	0/5221
6	3-J	0.40	0/3381	0.49	0/5221
6	4-J	0.40	0/3381	0.49	0/5221
6	5-J	0.40	0/3381	0.49	0/5221
6	6-J	0.40	0/3381	0.49	0/5221
6	7-J	0.40	0/3381	0.49	0/5221
6	8-J	0.40	0/3381	0.49	0/5221
6	9-J	0.40	0/3381	0.49	0/5221
6	10-J	0.40	0/3381	0.49	0/5221
7	1-K	0.63	2/5138 (0.0%)	0.69	18/6910 (0.3%)
7	2-K	0.63	2/5138 (0.0%)	0.69	18/6910 (0.3%)
7	3-K	0.63	2/5138 (0.0%)	0.69	18/6910 (0.3%)
7	4-K	0.63	2/5138 (0.0%)	0.69	18/6910 (0.3%)
7	5-K	0.63	2/5138 (0.0%)	0.69	18/6910 (0.3%)
7	6-K	0.63	2/5138 (0.0%)	0.69	18/6910 (0.3%)
7	7-K	0.63	2/5138 (0.0%)	0.69	18/6910 (0.3%)
7	8-K	0.63	2/5138 (0.0%)	0.69	18/6910 (0.3%)
7	9-K	0.63	2/5138 (0.0%)	0.69	18/6910 (0.3%)
7	10-K	0.63	2/5138 (0.0%)	0.69	18/6910 (0.3%)
8	1-L	0.93	0/3220	1.12	32/4355 (0.7%)
8	2-L	0.93	0/3220	1.12	32/4355 (0.7%)
8	3-L	0.93	0/3220	1.12	32/4355 (0.7%)
8	4-L	0.93	0/3220	1.12	32/4355 (0.7%)
8	5-L	0.93	0/3220	1.12	32/4355 (0.7%)
8	6-L	0.93	0/3220	1.12	32/4355 (0.7%)
8	7-L	0.93	0/3220	1.12	32/4355 (0.7%)
8	8-L	0.93	0/3220	1.12	32/4355 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	9-L	0.93	0/3220	1.12	32/4355 (0.7%)
8	10-L	0.93	0/3220	1.12	32/4355 (0.7%)
9	1-M	0.92	0/3259	1.11	32/4417 (0.7%)
9	2-M	0.92	0/3259	1.11	32/4417 (0.7%)
9	3-M	0.92	0/3259	1.11	32/4417 (0.7%)
9	4-M	0.92	0/3259	1.11	32/4417 (0.7%)
9	5-M	0.92	0/3259	1.11	32/4417 (0.7%)
9	6-M	0.92	0/3259	1.11	32/4417 (0.7%)
9	7-M	0.92	0/3259	1.11	32/4417 (0.7%)
9	8-M	0.92	0/3259	1.11	32/4417 (0.7%)
9	9-M	0.92	0/3259	1.11	32/4417 (0.7%)
9	10-M	0.92	0/3259	1.11	32/4417 (0.7%)
10	1-N	0.82	0/505	1.11	6/674 (0.9%)
10	2-N	0.82	0/505	1.11	6/674 (0.9%)
10	3-N	0.82	0/505	1.11	6/674 (0.9%)
10	4-N	0.82	0/505	1.11	6/674 (0.9%)
10	5-N	0.82	0/505	1.11	6/674 (0.9%)
10	6-N	0.82	0/505	1.11	6/674 (0.9%)
10	7-N	0.82	0/505	1.11	6/674 (0.9%)
10	8-N	0.82	0/505	1.11	6/674 (0.9%)
10	9-N	0.82	0/505	1.11	6/674 (0.9%)
10	10-N	0.82	0/505	1.11	6/674 (0.9%)
All	All	0.75	20/249210 (0.0%)	0.82	1220/348880 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	6-K	0	2
9	1-M	0	2
9	2-M	0	2
9	3-M	0	2
9	4-M	0	2
9	5-M	0	2
9	6-M	0	2
9	7-M	0	2
9	8-M	0	2
9	9-M	0	2
9	10-M	0	2
All	All	0	22

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	1-K	342	TRP	C-N	14.11	1.53	1.33
7	2-K	342	TRP	C-N	14.11	1.53	1.33
7	3-K	342	TRP	C-N	14.11	1.53	1.33
7	4-K	342	TRP	C-N	14.11	1.53	1.33
7	5-K	342	TRP	C-N	14.11	1.53	1.33

The worst 5 of 1220 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	1-K	342	TRP	CA-C-N	17.78	155.50	121.54
7	1-K	342	TRP	C-N-CA	17.78	155.50	121.54
7	2-K	342	TRP	CA-C-N	17.78	155.50	121.54
7	2-K	342	TRP	C-N-CA	17.78	155.50	121.54
7	3-K	342	TRP	CA-C-N	17.78	155.50	121.54

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	1-M	3	PRO	Peptide,Mainchain
9	2-M	3	PRO	Peptide,Mainchain
9	3-M	3	PRO	Peptide,Mainchain
9	4-M	3	PRO	Peptide,Mainchain
9	5-M	3	PRO	Mainchain

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	1-A	809	0	849	3	0
1	1-E	783	0	822	3	0
1	2-A	809	0	849	4	0
1	2-E	783	0	822	5	0
1	3-A	809	0	849	3	0
1	3-E	783	0	822	4	0
1	4-A	809	0	849	4	0

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Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	4-E	783	0	822	4	0
1	5-A	809	0	849	4	0
1	5-E	783	0	822	4	0
1	6-A	809	0	849	4	0
1	6-E	783	0	822	4	0
1	7-A	809	0	849	5	0
1	7-E	783	0	822	4	0
1	8-A	809	0	849	3	0
1	8-E	783	0	822	4	0
1	9-A	809	0	849	3	0
1	9-E	783	0	822	4	0
1	10-A	809	0	849	4	0
1	10-E	783	0	822	3	0
2	1-B	703	0	757	3	0
2	1-F	627	0	663	2	0
2	2-B	703	0	757	2	0
2	2-F	627	0	663	1	0
2	3-B	703	0	757	2	0
2	3-F	627	0	663	1	0
2	4-B	703	0	757	3	0
2	4-F	627	0	663	1	0
2	5-B	703	0	757	3	0
2	5-F	627	0	663	2	0
2	6-B	703	0	757	2	0
2	6-F	627	0	663	2	0
2	7-B	703	0	757	3	0
2	7-F	627	0	663	3	0
2	8-B	703	0	757	2	0
2	8-F	627	0	663	2	0
2	9-B	703	0	757	2	0
2	9-F	627	0	663	2	0
2	10-B	703	0	757	2	0
2	10-F	627	0	663	3	0
3	1-C	823	0	882	3	0
3	1-G	823	0	882	8	0
3	2-C	823	0	882	3	0
3	2-G	823	0	882	8	0
3	3-C	823	0	882	4	0
3	3-G	823	0	882	8	0
3	4-C	823	0	882	3	0
3	4-G	823	0	882	8	0
3	5-C	823	0	882	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	5-G	823	0	882	8	0
3	6-C	823	0	882	3	0
3	6-G	823	0	882	8	0
3	7-C	823	0	882	3	0
3	7-G	823	0	882	8	0
3	8-C	823	0	882	3	0
3	8-G	823	0	882	8	0
3	9-C	823	0	882	3	0
3	9-G	823	0	882	8	0
3	10-C	823	0	882	3	0
3	10-G	823	0	882	8	0
4	1-D	719	0	740	0	0
4	1-H	719	0	740	2	0
4	2-D	719	0	740	0	0
4	2-H	719	0	740	2	0
4	3-D	719	0	740	0	0
4	3-H	719	0	740	2	0
4	4-D	719	0	740	0	0
4	4-H	719	0	740	2	0
4	5-D	719	0	740	0	0
4	5-H	719	0	740	2	0
4	6-D	719	0	740	0	0
4	6-H	719	0	740	2	0
4	7-D	719	0	740	0	0
4	7-H	719	0	740	2	0
4	8-D	719	0	740	0	0
4	8-H	719	0	740	2	0
4	9-D	719	0	740	0	0
4	9-H	719	0	740	2	0
4	10-D	719	0	740	0	0
4	10-H	719	0	740	2	0
5	1-I	2975	0	1639	20	0
5	2-I	2975	0	1639	18	0
5	3-I	2975	0	1639	28	0
5	4-I	2975	0	1639	23	0
5	5-I	2975	0	1639	22	0
5	6-I	2975	0	1639	26	0
5	7-I	2975	0	1639	29	0
5	8-I	2975	0	1639	34	0
5	9-I	2975	0	1639	22	0
5	10-I	2975	0	1639	30	0
6	1-J	3011	0	1639	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	2-J	3011	0	1639	18	0
6	3-J	3011	0	1639	18	0
6	4-J	3011	0	1639	27	0
6	5-J	3011	0	1639	19	0
6	6-J	3011	0	1639	20	0
6	7-J	3011	0	1639	21	0
6	8-J	3011	0	1639	20	0
6	9-J	3011	0	1639	23	0
6	10-J	3011	0	1639	20	0
7	1-K	5055	0	5102	173	0
7	2-K	5055	0	5102	173	0
7	3-K	5055	0	5102	170	0
7	4-K	5055	0	5102	187	0
7	5-K	5055	0	5102	177	0
7	6-K	5055	0	5102	187	0
7	7-K	5055	0	5102	185	0
7	8-K	5055	0	5102	201	0
7	9-K	5055	0	5102	187	0
7	10-K	5055	0	5102	186	0
8	1-L	3154	0	3173	13	0
8	2-L	3154	0	3173	13	0
8	3-L	3154	0	3173	13	0
8	4-L	3154	0	3173	13	0
8	5-L	3154	0	3173	13	0
8	6-L	3154	0	3173	13	0
8	7-L	3154	0	3173	13	0
8	8-L	3154	0	3173	13	0
8	9-L	3154	0	3173	13	0
8	10-L	3154	0	3173	13	0
9	1-M	3192	0	3180	126	0
9	2-M	3192	0	3180	126	0
9	3-M	3192	0	3180	126	0
9	4-M	3192	0	3180	126	0
9	5-M	3192	0	3180	126	0
9	6-M	3192	0	3180	126	0
9	7-M	3192	0	3180	126	0
9	8-M	3192	0	3180	134	0
9	9-M	3192	0	3180	126	0
9	10-M	3192	0	3180	126	0
10	1-N	494	0	473	6	0
10	2-N	494	0	473	6	0
10	3-N	494	0	473	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	4-N	494	0	473	6	0
10	5-N	494	0	473	6	0
10	6-N	494	0	473	6	0
10	7-N	494	0	473	6	0
10	8-N	494	0	473	6	0
10	9-N	494	0	473	6	0
10	10-N	494	0	473	6	0
11	1-K	1	0	0	0	0
11	2-K	1	0	0	0	0
11	3-K	1	0	0	0	0
11	4-K	1	0	0	0	0
11	5-K	1	0	0	0	0
11	6-K	1	0	0	0	0
11	7-K	1	0	0	0	0
11	8-K	1	0	0	0	0
11	9-K	1	0	0	0	0
11	10-K	1	0	0	0	0
12	1-K	27	0	12	3	0
12	2-K	27	0	12	1	0
12	3-K	27	0	12	5	0
12	4-K	27	0	12	3	0
12	5-K	27	0	12	2	0
12	6-K	27	0	12	2	0
12	7-K	27	0	12	1	0
12	8-K	27	0	12	2	0
12	9-K	27	0	12	3	0
12	10-K	27	0	12	4	0
13	1-K	4	0	0	0	0
13	2-K	4	0	0	0	0
13	3-K	4	0	0	3	0
13	4-K	4	0	0	0	0
13	5-K	4	0	0	0	0
13	6-K	4	0	0	1	0
13	7-K	4	0	0	0	0
13	8-K	4	0	0	0	0
13	9-K	4	0	0	2	0
13	10-K	4	0	0	0	0
14	1-L	31	0	12	1	0
14	2-L	31	0	12	1	0
14	3-L	31	0	12	1	0
14	4-L	31	0	12	1	0
14	5-L	31	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	6-L	31	0	12	1	0
14	7-L	31	0	12	1	0
14	8-L	31	0	12	1	0
14	9-L	31	0	12	1	0
14	10-L	31	0	12	1	0
All	All	239500	0	215650	2562	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 6.

The worst 5 of 2562 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)
7:K:351:PHE:CE1	9:M:467:PHE:CE2	1.78	1.70
7:K:351:PHE:CE1	9:M:467:PHE:CE2	1.78	1.70
7:K:351:PHE:CE1	9:M:467:PHE:CE2	1.78	1.70
7:K:351:PHE:CE1	9:M:467:PHE:CE2	1.78	1.70
7:K:351:PHE:CE1	9:M:467:PHE:CE2	1.78	1.70

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1-A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
1	1-E	93/136 (68%)	92 (99%)	1 (1%)	0	100	100
1	2-A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
1	2-E	93/136 (68%)	92 (99%)	1 (1%)	0	100	100
1	3-A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3-E	93/136 (68%)	92 (99%)	1 (1%)	0	100	100
1	4-A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
1	4-E	93/136 (68%)	92 (99%)	1 (1%)	0	100	100
1	5-A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
1	5-E	93/136 (68%)	92 (99%)	1 (1%)	0	100	100
1	6-A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
1	6-E	93/136 (68%)	93 (100%)	0	0	100	100
1	7-A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
1	7-E	93/136 (68%)	92 (99%)	1 (1%)	0	100	100
1	8-A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
1	8-E	93/136 (68%)	91 (98%)	2 (2%)	0	100	100
1	9-A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
1	9-E	93/136 (68%)	92 (99%)	1 (1%)	0	100	100
1	10-A	96/136 (71%)	95 (99%)	1 (1%)	0	100	100
1	10-E	93/136 (68%)	92 (99%)	1 (1%)	0	100	100
2	1-B	85/103 (82%)	83 (98%)	2 (2%)	0	100	100
2	1-F	77/103 (75%)	76 (99%)	1 (1%)	0	100	100
2	2-B	85/103 (82%)	83 (98%)	2 (2%)	0	100	100
2	2-F	77/103 (75%)	76 (99%)	1 (1%)	0	100	100
2	3-B	85/103 (82%)	83 (98%)	2 (2%)	0	100	100
2	3-F	77/103 (75%)	76 (99%)	1 (1%)	0	100	100
2	4-B	85/103 (82%)	83 (98%)	2 (2%)	0	100	100
2	4-F	77/103 (75%)	76 (99%)	1 (1%)	0	100	100
2	5-B	85/103 (82%)	83 (98%)	2 (2%)	0	100	100
2	5-F	77/103 (75%)	76 (99%)	1 (1%)	0	100	100
2	6-B	85/103 (82%)	82 (96%)	3 (4%)	0	100	100
2	6-F	77/103 (75%)	76 (99%)	1 (1%)	0	100	100
2	7-B	85/103 (82%)	82 (96%)	3 (4%)	0	100	100
2	7-F	77/103 (75%)	76 (99%)	1 (1%)	0	100	100
2	8-B	85/103 (82%)	83 (98%)	2 (2%)	0	100	100
2	8-F	77/103 (75%)	76 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	9-B	85/103 (82%)	83 (98%)	2 (2%)	0	100	100
2	9-F	77/103 (75%)	76 (99%)	1 (1%)	0	100	100
2	10-B	85/103 (82%)	83 (98%)	2 (2%)	0	100	100
2	10-F	77/103 (75%)	75 (97%)	2 (3%)	0	100	100
3	1-C	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	1-G	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	2-C	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	2-G	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	3-C	105/130 (81%)	103 (98%)	2 (2%)	0	100	100
3	3-G	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	4-C	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	4-G	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	5-C	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	5-G	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	6-C	105/130 (81%)	103 (98%)	2 (2%)	0	100	100
3	6-G	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	7-C	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	7-G	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	8-C	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	8-G	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	9-C	105/130 (81%)	103 (98%)	2 (2%)	0	100	100
3	9-G	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	10-C	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
3	10-G	105/130 (81%)	102 (97%)	3 (3%)	0	100	100
4	1-D	90/125 (72%)	85 (94%)	5 (6%)	0	100	100
4	1-H	90/125 (72%)	88 (98%)	1 (1%)	1 (1%)	11	43
4	2-D	90/125 (72%)	86 (96%)	4 (4%)	0	100	100
4	2-H	90/125 (72%)	89 (99%)	1 (1%)	0	100	100
4	3-D	90/125 (72%)	86 (96%)	3 (3%)	1 (1%)	11	43
4	3-H	90/125 (72%)	88 (98%)	2 (2%)	0	100	100
4	4-D	90/125 (72%)	85 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	4-H	90/125 (72%)	89 (99%)	0	1 (1%)	11	43
4	5-D	90/125 (72%)	85 (94%)	5 (6%)	0	100	100
4	5-H	90/125 (72%)	88 (98%)	1 (1%)	1 (1%)	11	43
4	6-D	90/125 (72%)	86 (96%)	4 (4%)	0	100	100
4	6-H	90/125 (72%)	89 (99%)	1 (1%)	0	100	100
4	7-D	90/125 (72%)	85 (94%)	5 (6%)	0	100	100
4	7-H	90/125 (72%)	89 (99%)	1 (1%)	0	100	100
4	8-D	90/125 (72%)	85 (94%)	5 (6%)	0	100	100
4	8-H	90/125 (72%)	89 (99%)	0	1 (1%)	11	43
4	9-D	90/125 (72%)	87 (97%)	3 (3%)	0	100	100
4	9-H	90/125 (72%)	89 (99%)	0	1 (1%)	11	43
4	10-D	90/125 (72%)	85 (94%)	5 (6%)	0	100	100
4	10-H	90/125 (72%)	88 (98%)	1 (1%)	1 (1%)	11	43
7	1-K	602/813 (74%)	566 (94%)	24 (4%)	12 (2%)	6	32
7	2-K	602/813 (74%)	564 (94%)	25 (4%)	13 (2%)	5	31
7	3-K	602/813 (74%)	560 (93%)	30 (5%)	12 (2%)	6	32
7	4-K	602/813 (74%)	566 (94%)	24 (4%)	12 (2%)	6	32
7	5-K	602/813 (74%)	560 (93%)	30 (5%)	12 (2%)	6	32
7	6-K	602/813 (74%)	558 (93%)	32 (5%)	12 (2%)	6	32
7	7-K	602/813 (74%)	560 (93%)	31 (5%)	11 (2%)	6	34
7	8-K	602/813 (74%)	558 (93%)	36 (6%)	8 (1%)	9	40
7	9-K	602/813 (74%)	559 (93%)	32 (5%)	11 (2%)	6	34
7	10-K	602/813 (74%)	561 (93%)	29 (5%)	12 (2%)	6	32
8	1-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	69
8	2-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	69
8	3-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	69
8	4-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	69
8	5-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	69
8	6-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	69
8	7-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	69
8	8-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	9-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	69
8	10-L	383/477 (80%)	371 (97%)	11 (3%)	1 (0%)	36	69
9	1-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	37
9	2-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	37
9	3-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	37
9	4-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	37
9	5-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	37
9	6-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	37
9	7-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	37
9	8-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	37
9	9-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	37
9	10-M	390/467 (84%)	371 (95%)	13 (3%)	6 (2%)	8	37
10	1-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	31
10	2-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	31
10	3-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	31
10	4-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	31
10	5-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	31
10	6-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	31
10	7-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	31
10	8-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	31
10	9-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	31
10	10-N	47/157 (30%)	44 (94%)	2 (4%)	1 (2%)	5	31
All	All	21630/29020 (74%)	20713 (96%)	715 (3%)	202 (1%)	16	47

5 of 202 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	1-K	343	SER
7	1-K	496	GLU
7	1-K	634	LEU
8	1-L	202	LYS
9	1-M	155	SER

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	1-A	86/111 (78%)	86 (100%)	0	100	100
1	1-E	83/111 (75%)	83 (100%)	0	100	100
1	2-A	86/111 (78%)	86 (100%)	0	100	100
1	2-E	83/111 (75%)	83 (100%)	0	100	100
1	3-A	86/111 (78%)	86 (100%)	0	100	100
1	3-E	83/111 (75%)	83 (100%)	0	100	100
1	4-A	86/111 (78%)	86 (100%)	0	100	100
1	4-E	83/111 (75%)	83 (100%)	0	100	100
1	5-A	86/111 (78%)	86 (100%)	0	100	100
1	5-E	83/111 (75%)	83 (100%)	0	100	100
1	6-A	86/111 (78%)	86 (100%)	0	100	100
1	6-E	83/111 (75%)	83 (100%)	0	100	100
1	7-A	86/111 (78%)	86 (100%)	0	100	100
1	7-E	83/111 (75%)	83 (100%)	0	100	100
1	8-A	86/111 (78%)	86 (100%)	0	100	100
1	8-E	83/111 (75%)	83 (100%)	0	100	100
1	9-A	86/111 (78%)	86 (100%)	0	100	100
1	9-E	83/111 (75%)	83 (100%)	0	100	100
1	10-A	86/111 (78%)	86 (100%)	0	100	100
1	10-E	83/111 (75%)	83 (100%)	0	100	100
2	1-B	72/79 (91%)	72 (100%)	0	100	100
2	1-F	64/79 (81%)	64 (100%)	0	100	100
2	2-B	72/79 (91%)	72 (100%)	0	100	100
2	2-F	64/79 (81%)	64 (100%)	0	100	100
2	3-B	72/79 (91%)	72 (100%)	0	100	100
2	3-F	64/79 (81%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	4-B	72/79 (91%)	72 (100%)	0	100	100
2	4-F	64/79 (81%)	64 (100%)	0	100	100
2	5-B	72/79 (91%)	72 (100%)	0	100	100
2	5-F	64/79 (81%)	64 (100%)	0	100	100
2	6-B	72/79 (91%)	72 (100%)	0	100	100
2	6-F	64/79 (81%)	64 (100%)	0	100	100
2	7-B	72/79 (91%)	72 (100%)	0	100	100
2	7-F	64/79 (81%)	64 (100%)	0	100	100
2	8-B	72/79 (91%)	72 (100%)	0	100	100
2	8-F	64/79 (81%)	64 (100%)	0	100	100
2	9-B	72/79 (91%)	72 (100%)	0	100	100
2	9-F	64/79 (81%)	64 (100%)	0	100	100
2	10-B	72/79 (91%)	72 (100%)	0	100	100
2	10-F	64/79 (81%)	64 (100%)	0	100	100
3	1-C	84/102 (82%)	84 (100%)	0	100	100
3	1-G	84/102 (82%)	84 (100%)	0	100	100
3	2-C	84/102 (82%)	84 (100%)	0	100	100
3	2-G	84/102 (82%)	84 (100%)	0	100	100
3	3-C	84/102 (82%)	84 (100%)	0	100	100
3	3-G	84/102 (82%)	84 (100%)	0	100	100
3	4-C	84/102 (82%)	84 (100%)	0	100	100
3	4-G	84/102 (82%)	84 (100%)	0	100	100
3	5-C	84/102 (82%)	84 (100%)	0	100	100
3	5-G	84/102 (82%)	84 (100%)	0	100	100
3	6-C	84/102 (82%)	84 (100%)	0	100	100
3	6-G	84/102 (82%)	84 (100%)	0	100	100
3	7-C	84/102 (82%)	84 (100%)	0	100	100
3	7-G	84/102 (82%)	84 (100%)	0	100	100
3	8-C	84/102 (82%)	84 (100%)	0	100	100
3	8-G	84/102 (82%)	84 (100%)	0	100	100
3	9-C	84/102 (82%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	9-G	84/102 (82%)	84 (100%)	0	100	100
3	10-C	84/102 (82%)	84 (100%)	0	100	100
3	10-G	84/102 (82%)	84 (100%)	0	100	100
4	1-D	78/104 (75%)	78 (100%)	0	100	100
4	1-H	78/104 (75%)	78 (100%)	0	100	100
4	2-D	78/104 (75%)	78 (100%)	0	100	100
4	2-H	78/104 (75%)	78 (100%)	0	100	100
4	3-D	78/104 (75%)	78 (100%)	0	100	100
4	3-H	78/104 (75%)	78 (100%)	0	100	100
4	4-D	78/104 (75%)	78 (100%)	0	100	100
4	4-H	78/104 (75%)	78 (100%)	0	100	100
4	5-D	78/104 (75%)	78 (100%)	0	100	100
4	5-H	78/104 (75%)	78 (100%)	0	100	100
4	6-D	78/104 (75%)	78 (100%)	0	100	100
4	6-H	78/104 (75%)	78 (100%)	0	100	100
4	7-D	78/104 (75%)	78 (100%)	0	100	100
4	7-H	78/104 (75%)	78 (100%)	0	100	100
4	8-D	78/104 (75%)	78 (100%)	0	100	100
4	8-H	78/104 (75%)	78 (100%)	0	100	100
4	9-D	78/104 (75%)	78 (100%)	0	100	100
4	9-H	78/104 (75%)	78 (100%)	0	100	100
4	10-D	78/104 (75%)	78 (100%)	0	100	100
4	10-H	78/104 (75%)	78 (100%)	0	100	100
7	1-K	558/735 (76%)	553 (99%)	5 (1%)	70	75
7	2-K	558/735 (76%)	553 (99%)	5 (1%)	70	75
7	3-K	558/735 (76%)	553 (99%)	5 (1%)	70	75
7	4-K	558/735 (76%)	553 (99%)	5 (1%)	70	75
7	5-K	558/735 (76%)	553 (99%)	5 (1%)	70	75
7	6-K	558/735 (76%)	553 (99%)	5 (1%)	70	75
7	7-K	558/735 (76%)	553 (99%)	5 (1%)	70	75
7	8-K	558/735 (76%)	553 (99%)	5 (1%)	70	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	9-K	558/735 (76%)	553 (99%)	5 (1%)	70	75
7	10-K	558/735 (76%)	553 (99%)	5 (1%)	70	75
8	1-L	349/420 (83%)	349 (100%)	0	100	100
8	2-L	349/420 (83%)	349 (100%)	0	100	100
8	3-L	349/420 (83%)	349 (100%)	0	100	100
8	4-L	349/420 (83%)	349 (100%)	0	100	100
8	5-L	349/420 (83%)	349 (100%)	0	100	100
8	6-L	349/420 (83%)	349 (100%)	0	100	100
8	7-L	349/420 (83%)	349 (100%)	0	100	100
8	8-L	349/420 (83%)	349 (100%)	0	100	100
8	9-L	349/420 (83%)	349 (100%)	0	100	100
8	10-L	349/420 (83%)	349 (100%)	0	100	100
9	1-M	362/423 (86%)	362 (100%)	0	100	100
9	2-M	362/423 (86%)	362 (100%)	0	100	100
9	3-M	362/423 (86%)	362 (100%)	0	100	100
9	4-M	362/423 (86%)	362 (100%)	0	100	100
9	5-M	362/423 (86%)	362 (100%)	0	100	100
9	6-M	362/423 (86%)	362 (100%)	0	100	100
9	7-M	362/423 (86%)	362 (100%)	0	100	100
9	8-M	362/423 (86%)	362 (100%)	0	100	100
9	9-M	362/423 (86%)	362 (100%)	0	100	100
9	10-M	362/423 (86%)	362 (100%)	0	100	100
10	1-N	54/140 (39%)	54 (100%)	0	100	100
10	2-N	54/140 (39%)	54 (100%)	0	100	100
10	3-N	54/140 (39%)	54 (100%)	0	100	100
10	4-N	54/140 (39%)	54 (100%)	0	100	100
10	5-N	54/140 (39%)	54 (100%)	0	100	100
10	6-N	54/140 (39%)	54 (100%)	0	100	100
10	7-N	54/140 (39%)	54 (100%)	0	100	100
10	8-N	54/140 (39%)	54 (100%)	0	100	100
10	9-N	54/140 (39%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	10-N	54/140 (39%)	54 (100%)	0	100	100
All	All	19520/25100 (78%)	19470 (100%)	50 (0%)	84	85

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	6-K	368	LYS
7	8-K	362	MET
7	10-K	370	ILE
7	6-K	370	ILE
7	7-K	366	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 100 such sidechains are listed below:

Mol	Chain	Res	Type
8	6-L	194	HIS
7	8-K	361	GLN
9	10-M	17	GLN
9	6-M	17	GLN
8	7-L	74	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 40 ligands modelled in this entry, 10 are monoatomic - leaving 30 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
12	ADP	3-K	1502	13	28,29,29	1.39	5 (17%)	43,45,45	1.89	9 (20%)
13	BEF	4-K	1503	12	0,3,3	-	-	-		
13	BEF	1-K	1503	12	0,3,3	-	-	-		
14	ATP	8-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
12	ADP	7-K	1502	13	28,29,29	1.36	5 (17%)	43,45,45	1.99	9 (20%)
13	BEF	3-K	1503	12	0,3,3	-	-	-		
14	ATP	4-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
13	BEF	2-K	1503	12	0,3,3	-	-	-		
14	ATP	9-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
14	ATP	10-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
12	ADP	10-K	1502	13	28,29,29	1.47	6 (21%)	43,45,45	1.89	12 (27%)
12	ADP	8-K	1502	13	28,29,29	1.47	6 (21%)	43,45,45	1.96	10 (23%)
14	ATP	3-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
14	ATP	6-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
12	ADP	5-K	1502	13	28,29,29	1.46	6 (21%)	43,45,45	1.96	11 (25%)
14	ATP	2-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
14	ATP	1-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
14	ATP	5-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
13	BEF	9-K	1503	12	0,3,3	-	-	-		
12	ADP	1-K	1502	13	28,29,29	1.40	5 (17%)	43,45,45	2.02	10 (23%)
12	ADP	9-K	1502	13	28,29,29	1.36	5 (17%)	43,45,45	1.92	9 (20%)
13	BEF	5-K	1503	12	0,3,3	-	-	-		
13	BEF	7-K	1503	12	0,3,3	-	-	-		
12	ADP	4-K	1502	13	28,29,29	1.39	5 (17%)	43,45,45	1.91	11 (25%)
12	ADP	2-K	1502	13	28,29,29	1.45	6 (21%)	43,45,45	1.94	11 (25%)
13	BEF	10-K	1503	12	0,3,3	-	-	-		
14	ATP	7-L	501	-	32,33,33	1.49	8 (25%)	48,52,52	1.85	10 (20%)
13	BEF	6-K	1503	12	0,3,3	-	-	-		
12	ADP	6-K	1502	13	28,29,29	1.37	4 (14%)	43,45,45	1.91	10 (23%)
13	BEF	8-K	1503	12	0,3,3	-	-	-		

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
12	ADP	3-K	1502	13	-	7/16/32/32	0/3/3/3
14	ATP	8-L	501	-	-	2/22/38/38	0/3/3/3
12	ADP	7-K	1502	13	-	4/16/32/32	0/3/3/3
14	ATP	4-L	501	-	-	2/22/38/38	0/3/3/3
14	ATP	9-L	501	-	-	2/22/38/38	0/3/3/3
14	ATP	10-L	501	-	-	2/22/38/38	0/3/3/3
12	ADP	10-K	1502	13	-	5/16/32/32	0/3/3/3
12	ADP	8-K	1502	13	-	4/16/32/32	0/3/3/3
14	ATP	3-L	501	-	-	2/22/38/38	0/3/3/3
14	ATP	6-L	501	-	-	2/22/38/38	0/3/3/3
12	ADP	5-K	1502	13	-	4/16/32/32	0/3/3/3
14	ATP	2-L	501	-	-	2/22/38/38	0/3/3/3
14	ATP	1-L	501	-	-	2/22/38/38	0/3/3/3
14	ATP	5-L	501	-	-	2/22/38/38	0/3/3/3
12	ADP	1-K	1502	13	-	3/16/32/32	0/3/3/3
12	ADP	9-K	1502	13	-	4/16/32/32	0/3/3/3
12	ADP	4-K	1502	13	-	3/16/32/32	0/3/3/3
12	ADP	2-K	1502	13	-	2/16/32/32	0/3/3/3
14	ATP	7-L	501	-	-	2/22/38/38	0/3/3/3
12	ADP	6-K	1502	13	-	4/16/32/32	0/3/3/3

The worst 5 of 133 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	10-K	1502	ADP	C5-C4	4.39	1.46	1.39
12	5-K	1502	ADP	C5-C4	4.37	1.46	1.39
12	6-K	1502	ADP	C5-C4	4.27	1.46	1.39
12	1-K	1502	ADP	C5-C4	4.21	1.46	1.39
12	3-K	1502	ADP	C5-C4	4.18	1.46	1.39

The worst 5 of 202 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	1-L	501	ATP	C5-C4-N3	-6.24	118.13	126.72
14	2-L	501	ATP	C5-C4-N3	-6.24	118.13	126.72
14	3-L	501	ATP	C5-C4-N3	-6.24	118.13	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	4-L	501	ATP	C5-C4-N3	-6.24	118.13	126.72
14	5-L	501	ATP	C5-C4-N3	-6.24	118.13	126.72

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	1-K	1502	ADP	C5'-O5'-PA-O1A
12	1-K	1502	ADP	C4'-C5'-O5'-PA
12	2-K	1502	ADP	C5'-O5'-PA-O1A
12	3-K	1502	ADP	PA-O3A-PB-O2B
12	3-K	1502	ADP	PA-O3A-PB-O3B

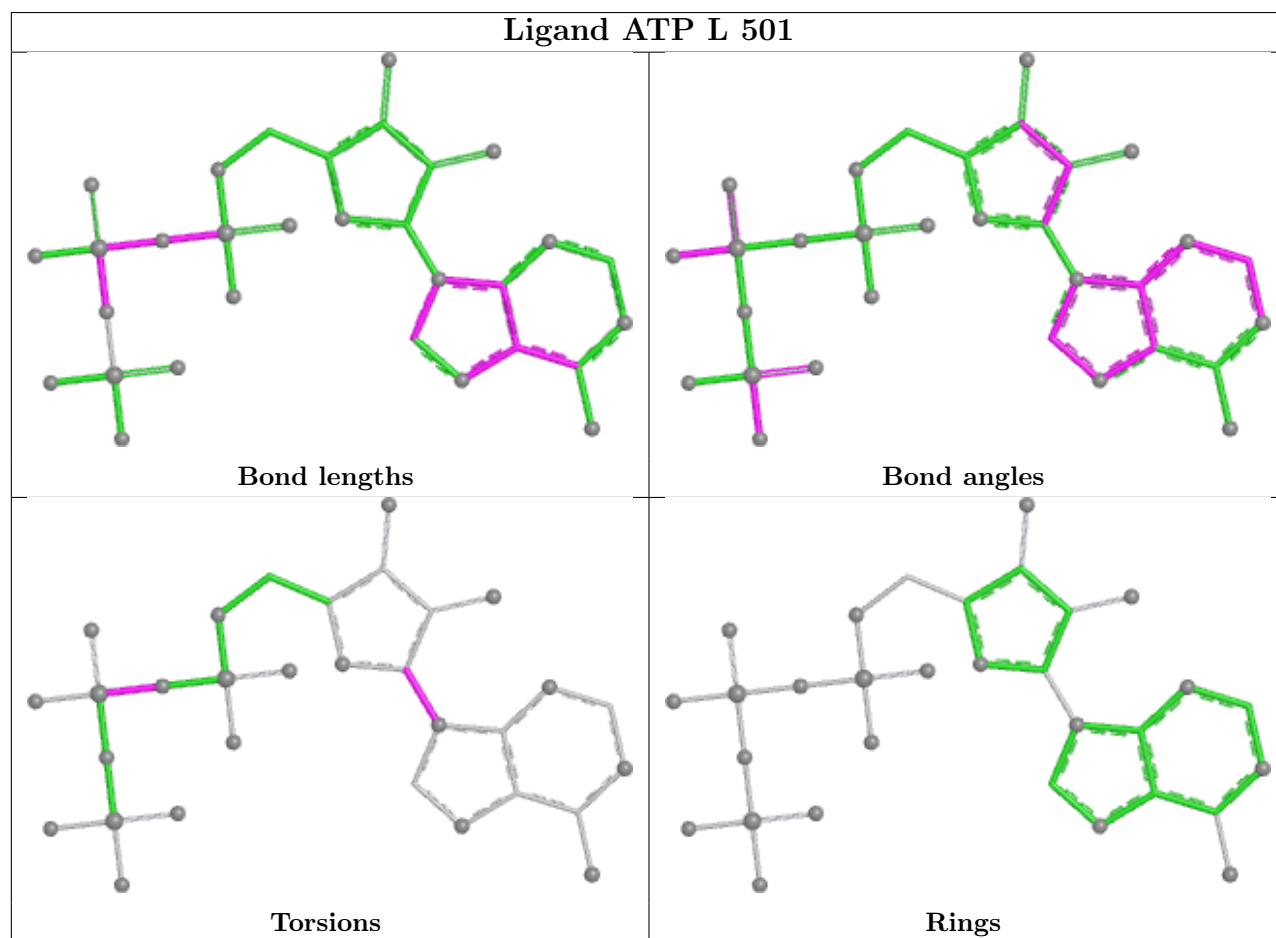
There are no ring outliers.

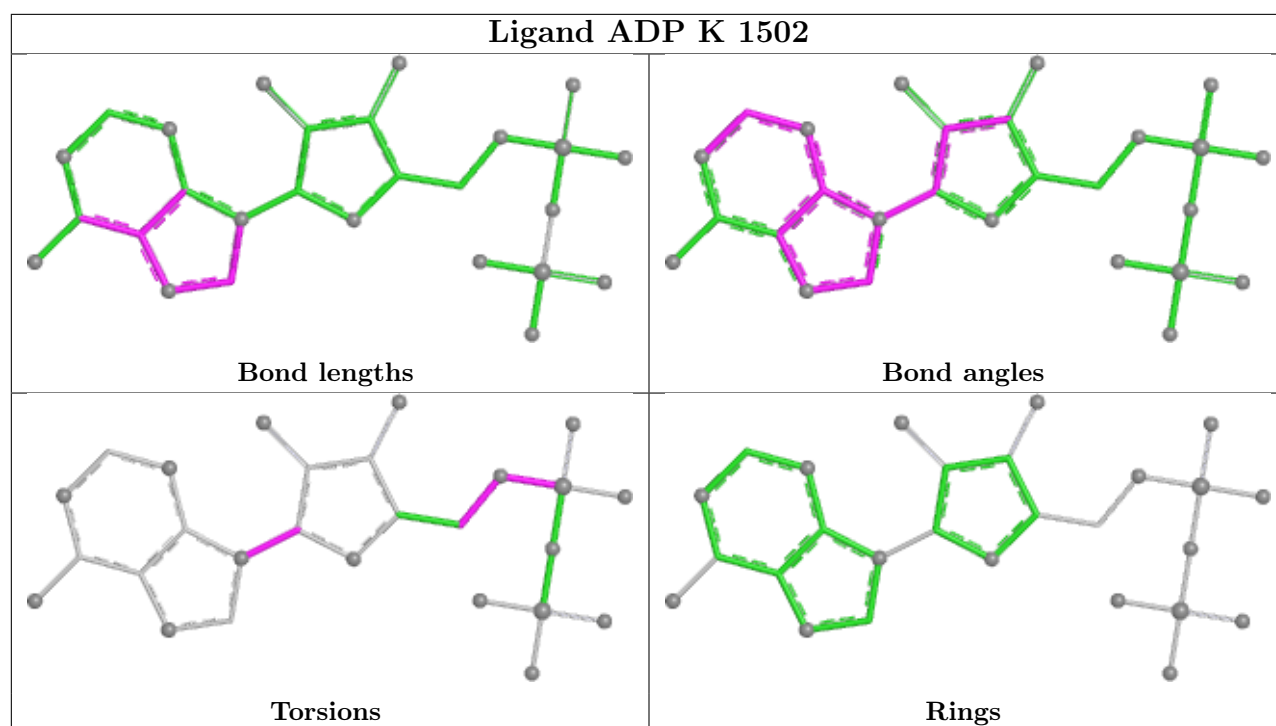
23 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	3-K	1502	ADP	5	0
14	8-L	501	ATP	1	0
12	7-K	1502	ADP	1	0
13	3-K	1503	BEF	3	0
14	4-L	501	ATP	1	0
14	9-L	501	ATP	1	0
14	10-L	501	ATP	1	0
12	10-K	1502	ADP	4	0
12	8-K	1502	ADP	2	0
14	3-L	501	ATP	1	0
14	6-L	501	ATP	1	0
12	5-K	1502	ADP	2	0
14	2-L	501	ATP	1	0
14	1-L	501	ATP	1	0
14	5-L	501	ATP	1	0
13	9-K	1503	BEF	2	0
12	1-K	1502	ADP	3	0
12	9-K	1502	ADP	3	0
12	4-K	1502	ADP	3	0
12	2-K	1502	ADP	1	0
14	7-L	501	ATP	1	0
13	6-K	1503	BEF	1	0
12	6-K	1502	ADP	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.

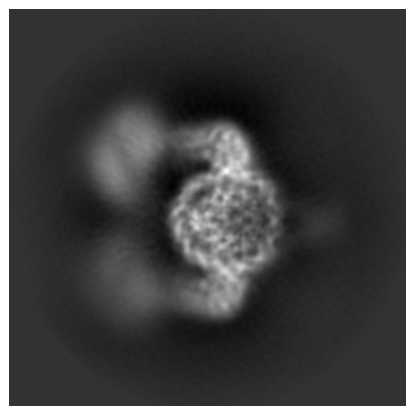
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21484. These allow visual inspection of the internal detail of the map and identification of artifacts.

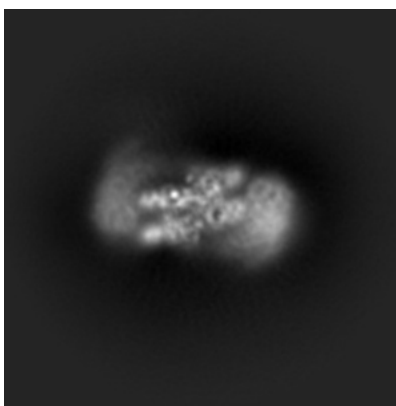
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

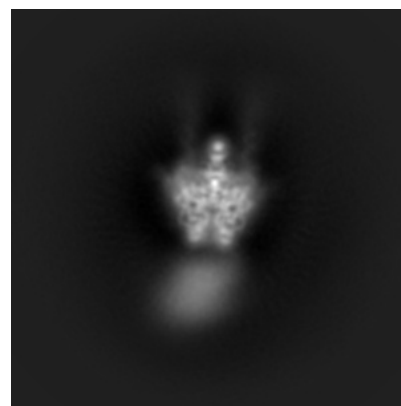
6.1.1 Primary map



X

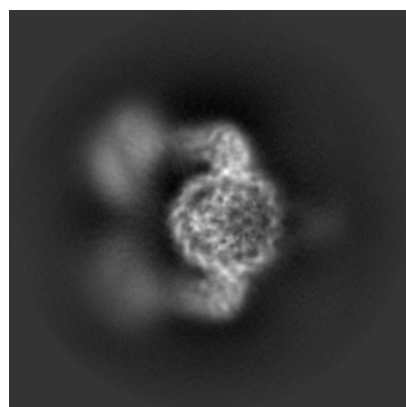


Y

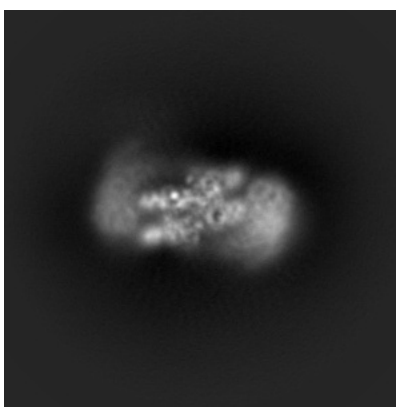


Z

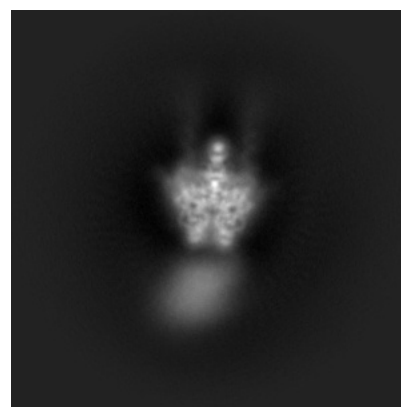
6.1.2 Raw map



X



Y

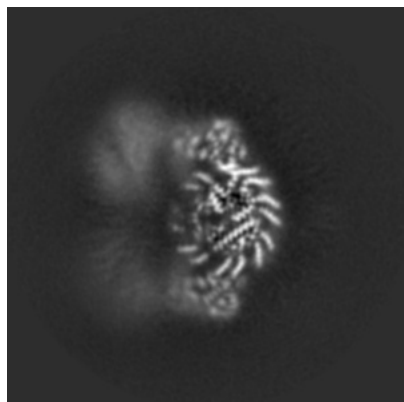


Z

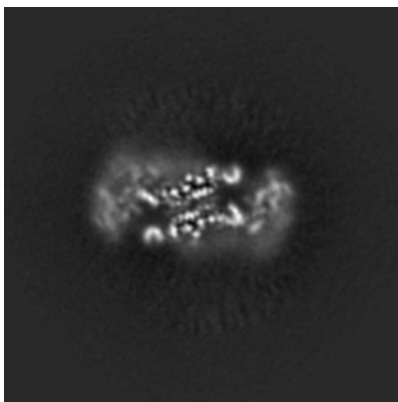
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

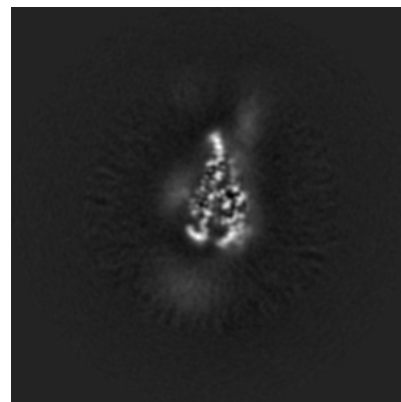
6.2.1 Primary map



X Index: 150

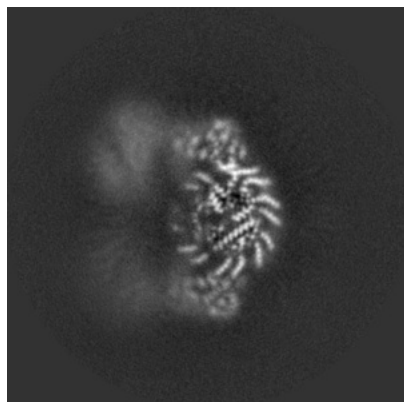


Y Index: 150

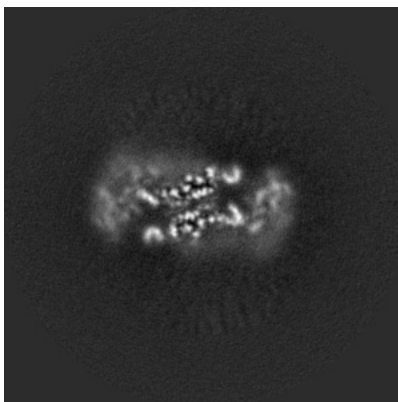


Z Index: 150

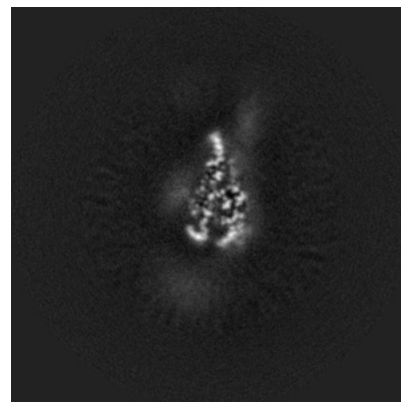
6.2.2 Raw map



X Index: 150



Y Index: 150

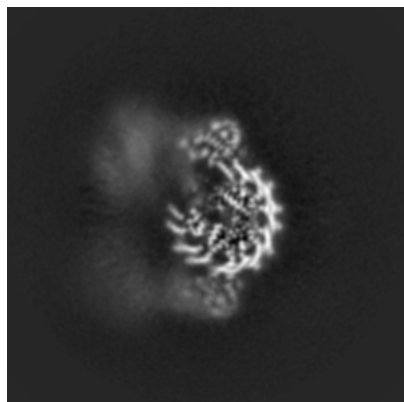


Z Index: 150

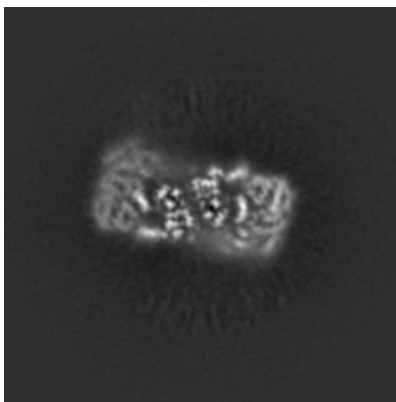
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

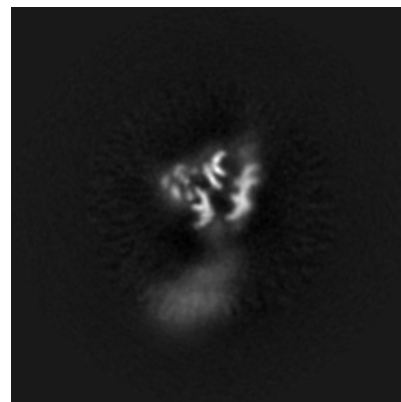
6.3.1 Primary map



X Index: 154

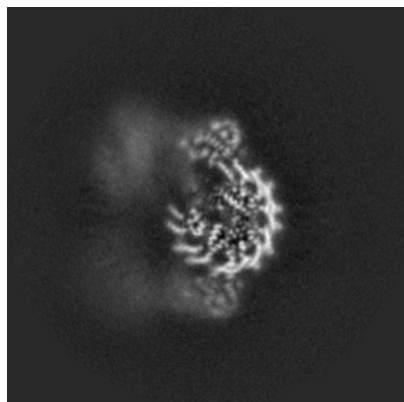


Y Index: 163

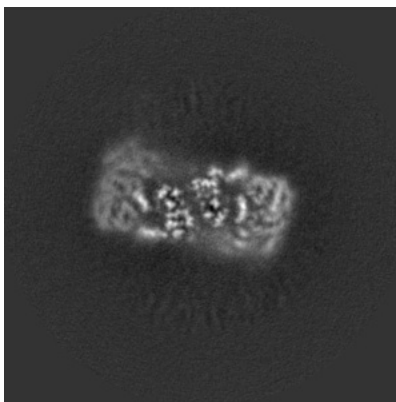


Z Index: 174

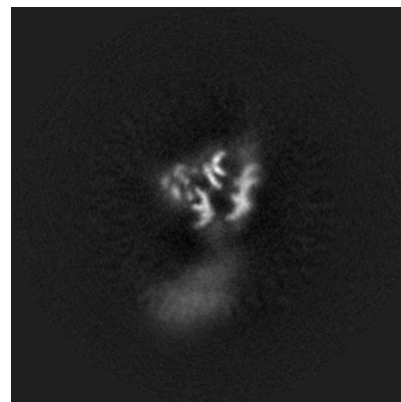
6.3.2 Raw map



X Index: 154



Y Index: 163

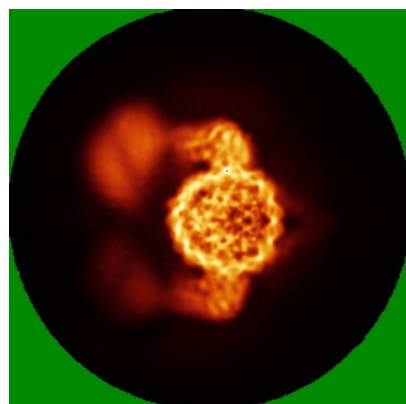


Z Index: 174

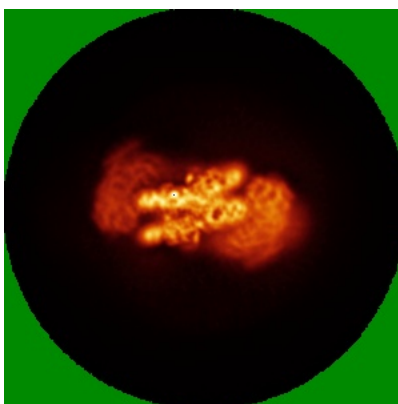
The images above show the largest variance slices of the map in three orthogonal directions.

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

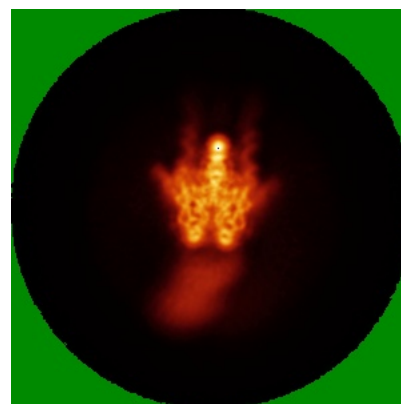
6.4.1 Primary map



X

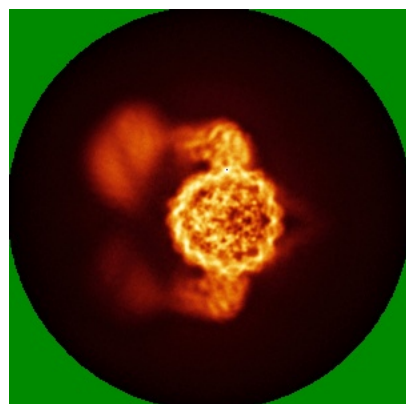


Y

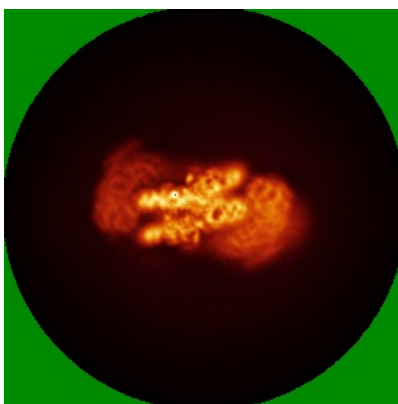


Z

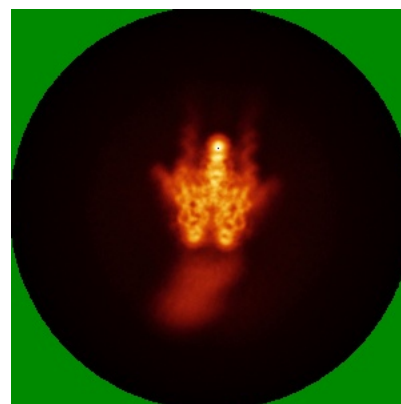
6.4.2 Raw map



X



Y

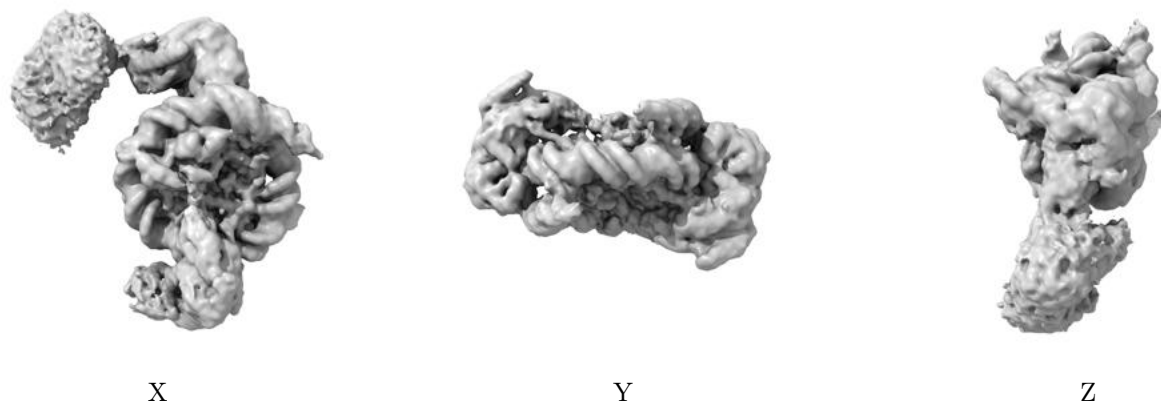


Z

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.

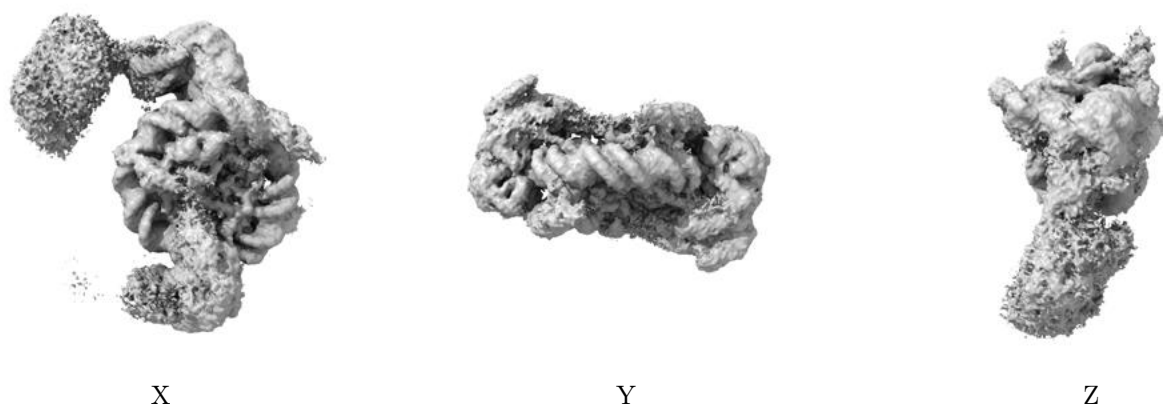
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

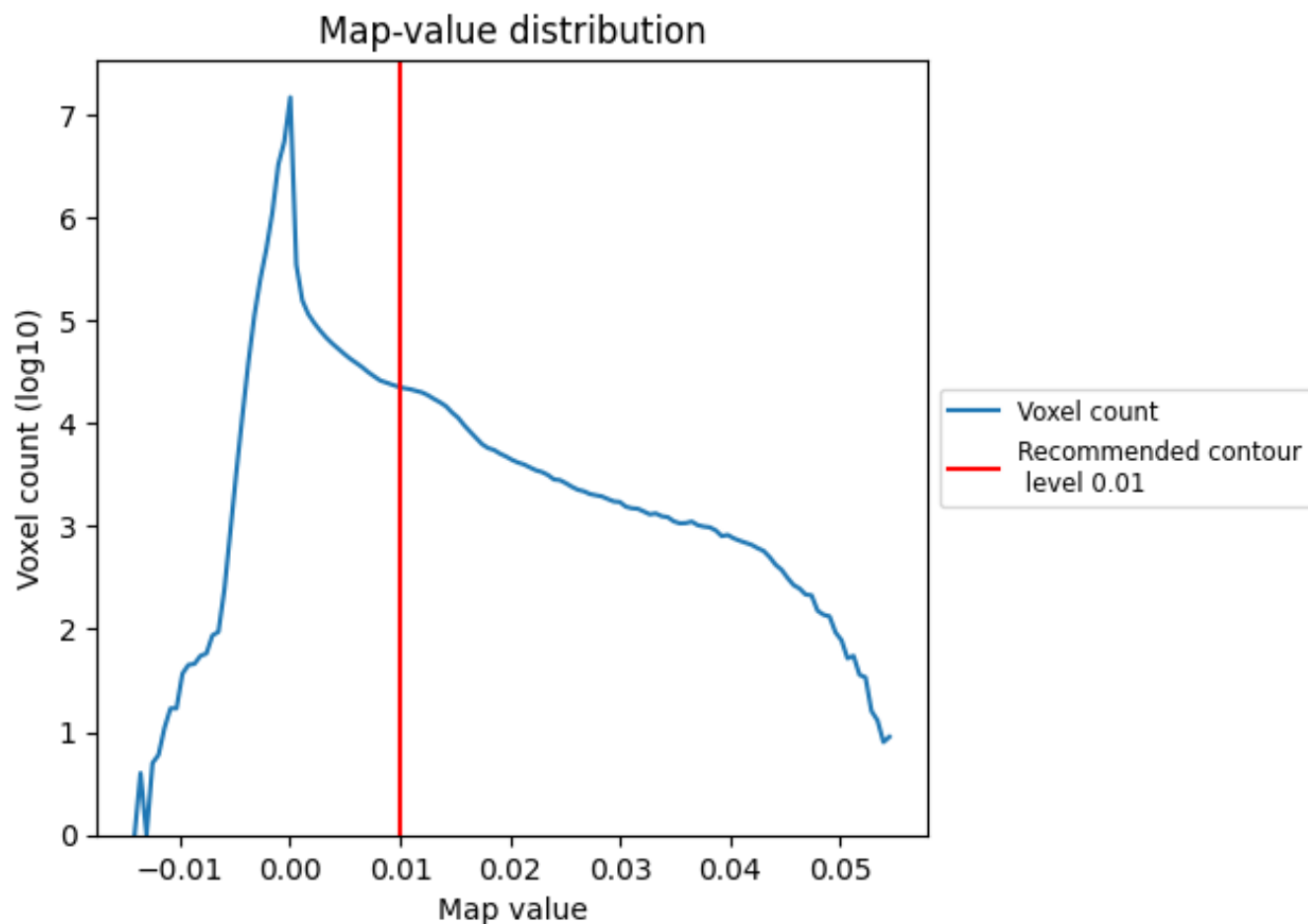
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

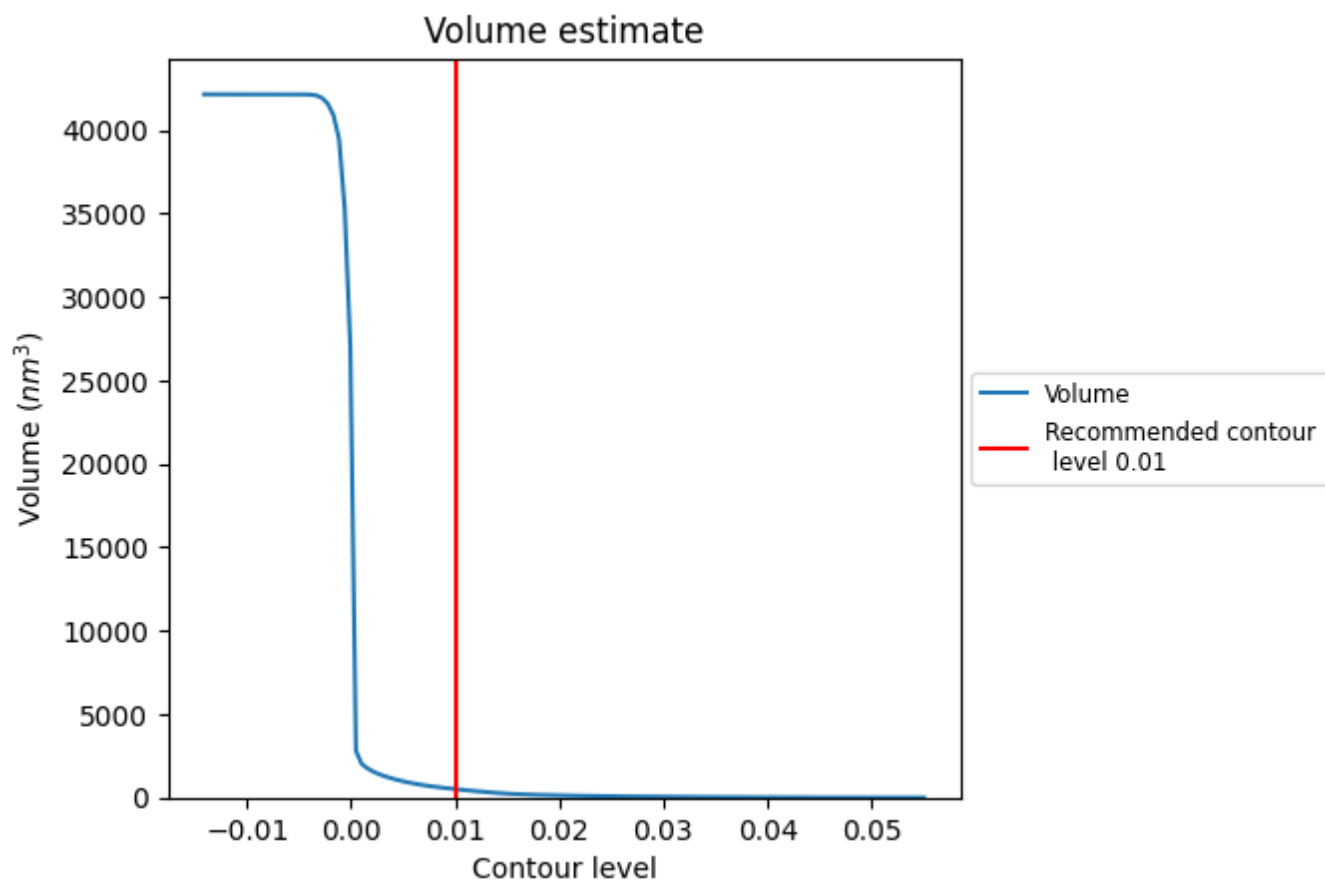
This section contains the results of statistical analysis of the map.

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.

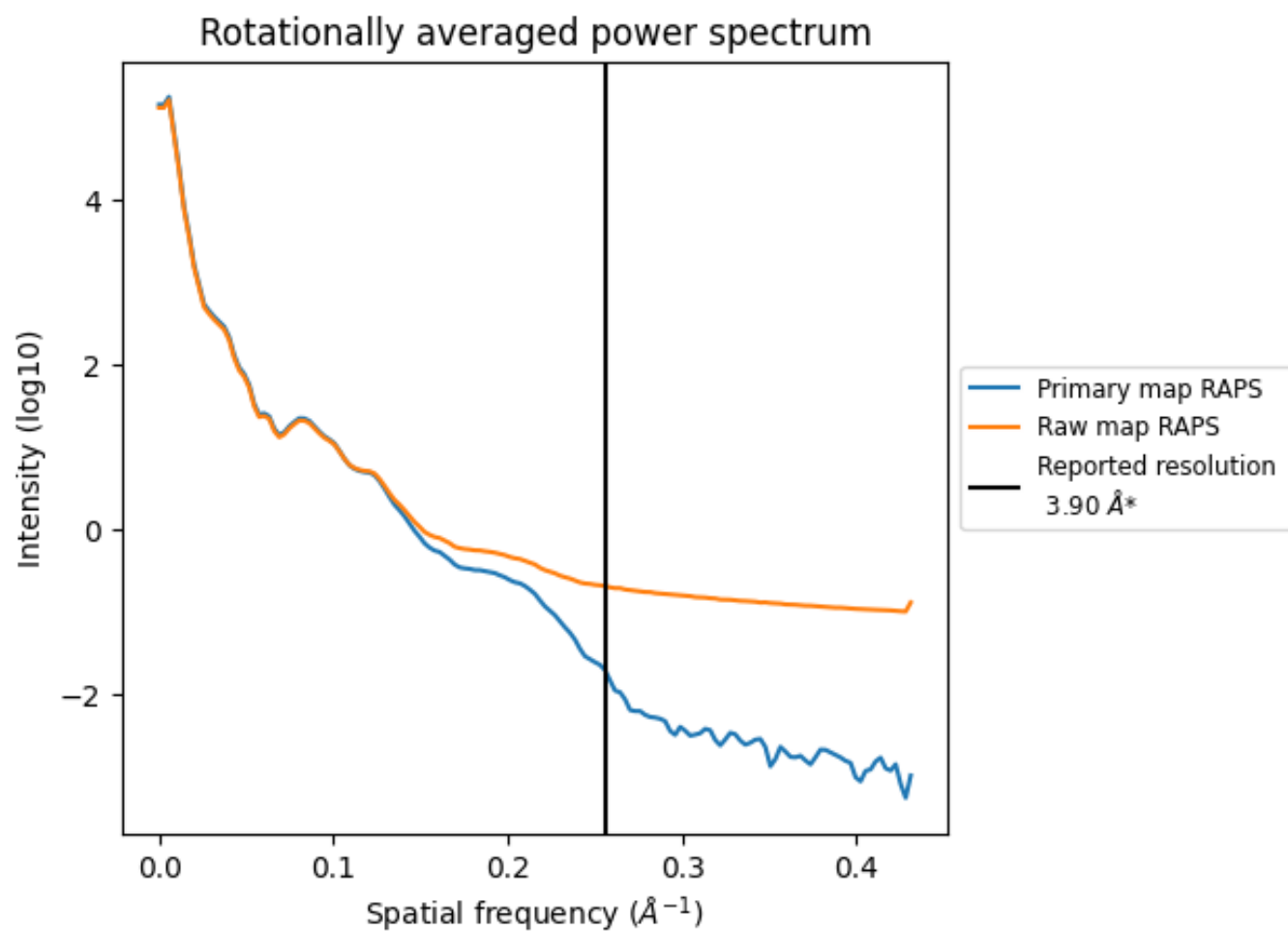
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 505 nm^3 ; this corresponds to an approximate mass of 456 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 ⓘ

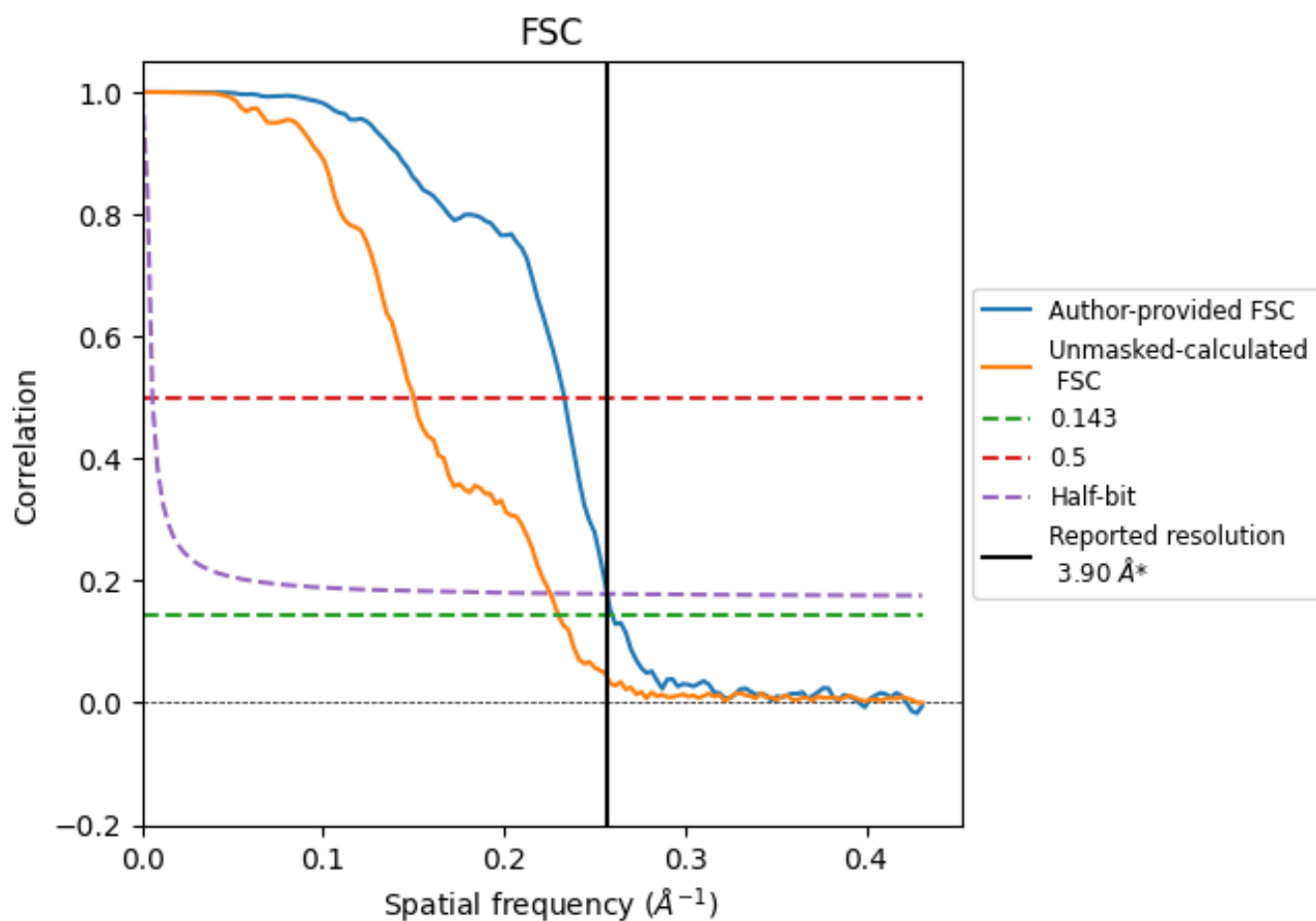


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.256 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

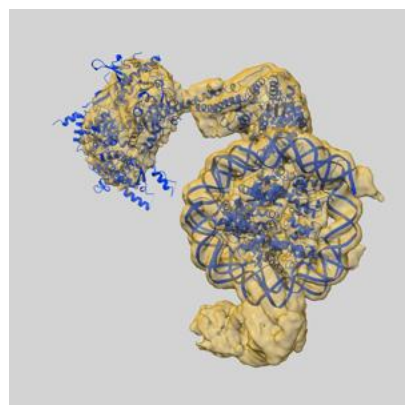
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.85	4.29	3.89
Unmasked-calculated*	4.35	6.67	4.43

*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 4.35 differs from the reported value 3.9 by more than 10 %

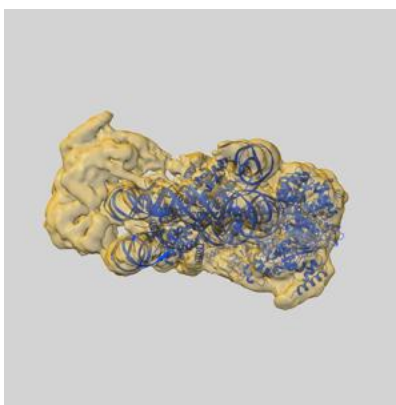
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21484 and PDB model 6VZ4. Per-residue inclusion information can be found in section [3](#) on page [21](#).

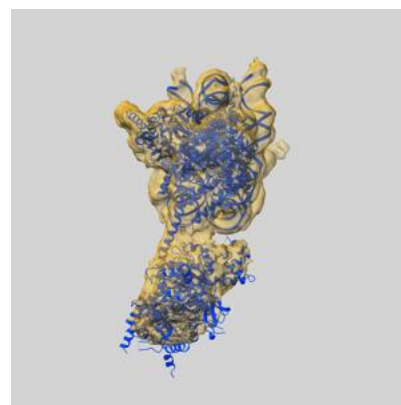
9.1 Map-model overlay [i](#)



X



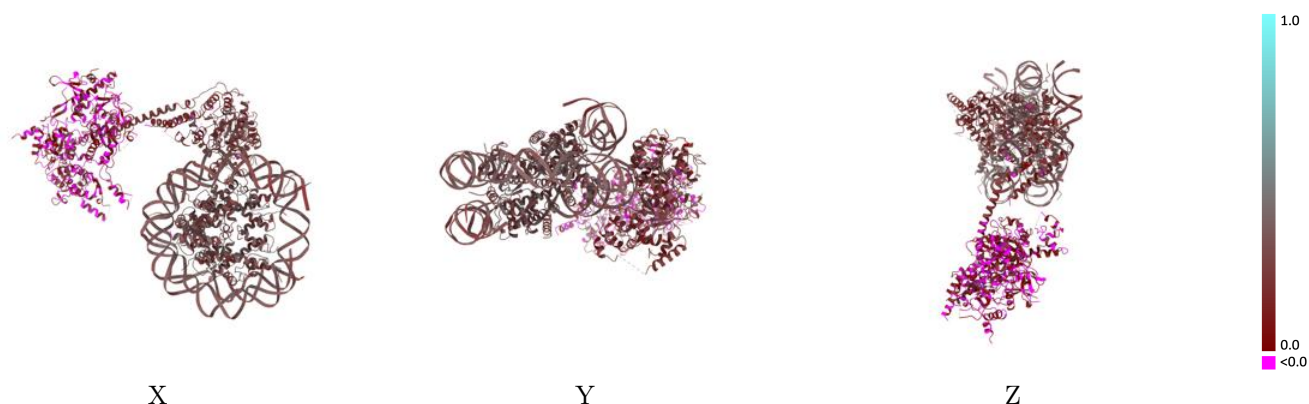
Y



Z

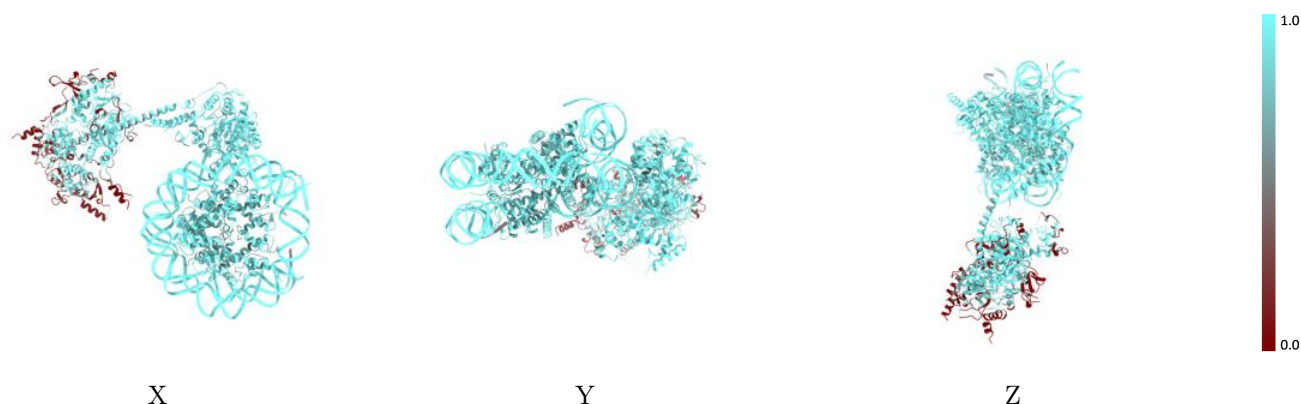
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



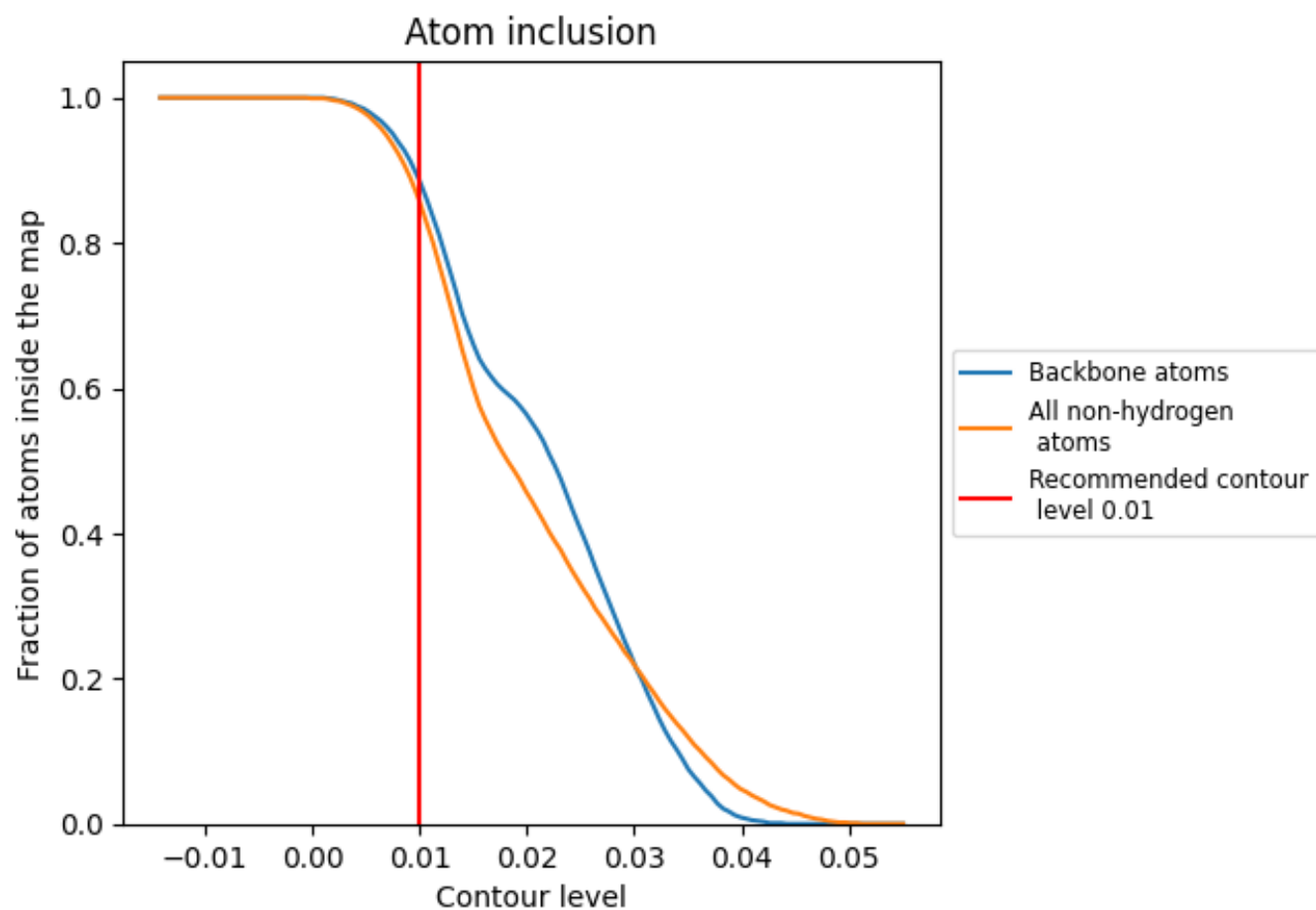
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 86% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8580	0.2190
A	0.9150	0.3120
B	0.9170	0.3220
C	0.8930	0.3230
D	0.9330	0.3190
E	0.9120	0.3180
F	0.9140	0.3260
G	0.9100	0.3240
H	0.9300	0.3200
I	0.9930	0.3280
J	0.9910	0.3260
K	0.9210	0.2080
L	0.5700	0.0480
M	0.7540	0.0420
N	0.4050	0.0380

1.0

0.0

<0.0