wwPDB EM Validation Summary Report (i)

Oct 12, 2026 – 01:53 pm BST

PDB ID	:	9SWW / pdb_00009sww
EMDB ID	:	EMD-55327
Title	:	GFAP intermediate filament
Authors	:	Beales, C.T.; Eibauer, M.; Medalia, O.
Deposited on	:	2025-10-07
Resolution	:	7.40 Å(reported)
Based on initial models	:	6A9P, .

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 (i) 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 (i)) were used in the production of this report:

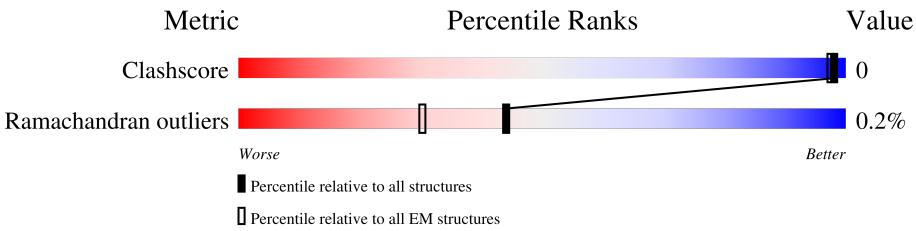
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

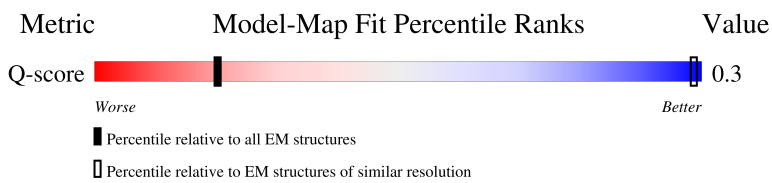
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 7.40 Å.

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





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	412 (6.90 - 7.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	0	430	10% 90%
1	6	430	98%
1	9	430	5% 95%
1	A	430	36% 64%
1	AC	430	16% 84%

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Mol	Chain	Length	Quality of chain
1	AD	430	19% 80%
1	AG	430	26% 74%
1	AH	430	30% 70%
1	AK	430	35% 65%
1	AL	430	37% 63%
1	AM	430	5% 95%
1	AN	430	7% 93%
1	AO	430	37% 63%
1	AP	430	36% 64%
1	AQ	430	14% 85%
1	AR	430	14% 84%
1	AS	430	36% 64%
1	AT	430	37% 63%
1	AU	430	25% 74%
1	AV	430	23% 74%
1	B	430	36% 64%
1	C	430	35% 64%
1	D	430	34% 63%
1	E	430	37% 63%
1	F	430	36% 63%
1	G	430	5% 37% 63%
1	H	430	36% 64%
1	I	430	30% 70%
1	J	430	31% 69%
1	K	430	5% 37% 62%

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Mol	Chain	Length	Quality of chain
1	L	430	37% 63%
1	M	430	19% 81%
1	N	430	19% 79%
1	O	430	5% 37% 62%
1	P	430	37% 63%
1	Q	430	9% 91%
1	R	430	10% 89%
1	S	430	6% 37% 63%
1	T	430	36% 63%
1	V	430	99%
1	W	430	30% 70%
1	X	430	33% 66%
1	a	430	20% 80%
1	b	430	21% 77%
1	e	430	10% 90%
1	f	430	12% 87%
1	j	430	96%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 30815 atoms, of which 10295 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 Glial fibrillary acidic protein.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	0	43	Total C H N O 258 86 86 43 43	0	0
1	6	8	Total C H N O 48 16 16 8 8	0	0
1	9	23	Total C H N O 139 46 47 23 23	0	0
1	A	156	Total C H N O 935 312 311 156 156	0	0
1	AC	69	Total C H N O 416 138 140 69 69	0	0
1	AD	84	Total C H N O 505 168 169 84 84	0	0
1	AG	111	Total C H N O 669 222 225 111 111	0	0
1	AH	127	Total C H N O 764 254 256 127 127	0	0
1	AK	150	Total C H N O 902 300 302 150 150	0	0
1	AL	158	Total C H N O 949 316 317 158 158	0	0
1	AM	23	Total C H N O 139 46 47 23 23	0	0
1	AN	31	Total C H N O 187 62 63 31 31	0	0
1	AO	157	Total C H N O 943 314 315 157 157	0	0
1	AP	156	Total C H N O 937 312 313 156 156	0	0
1	AQ	64	Total C H N O 384 128 128 64 64	0	0
1	AR	69	Total C H N O 414 138 138 69 69	0	0
1	AS	156	Total C H N O 937 312 313 156 156	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
1	AT	158	949	316	317	158	158	0	0
			Total	C	H	N	O		
1	AU	111	667	222	223	111	111	0	0
			Total	C	H	N	O		
1	AV	112	673	224	225	112	112	0	0
			Total	C	H	N	O		
1	B	156	935	312	311	156	156	0	0
			Total	C	H	N	O		
1	C	153	919	306	307	153	153	0	0
			Total	C	H	N	O		
1	D	158	949	316	317	158	158	0	0
			Total	C	H	N	O		
1	E	161	966	322	322	161	161	0	0
			Total	C	H	N	O		
1	F	160	960	320	320	160	160	0	0
			Total	C	H	N	O		
1	G	161	965	322	321	161	161	0	0
			Total	C	H	N	O		
1	H	155	929	310	309	155	155	0	0
			Total	C	H	N	O		
1	I	127	762	254	254	127	127	0	0
			Total	C	H	N	O		
1	J	134	805	268	269	134	134	0	0
			Total	C	H	N	O		
1	K	162	972	324	324	162	162	0	0
			Total	C	H	N	O		
1	L	161	966	322	322	161	161	0	0
			Total	C	H	N	O		
1	M	81	485	162	161	81	81	0	0
			Total	C	H	N	O		
1	N	89	534	178	178	89	89	0	0
			Total	C	H	N	O		
1	O	162	972	324	324	162	162	0	0
			Total	C	H	N	O		
1	P	158	948	316	316	158	158	0	0
			Total	C	H	N	O		
1	Q	40	240	80	80	40	40	0	0
			Total	C	H	N	O		
1	R	48	289	96	97	48	48	0	0
			Total	C	H	N	O		
1	S	161	968	322	324	161	161	0	0

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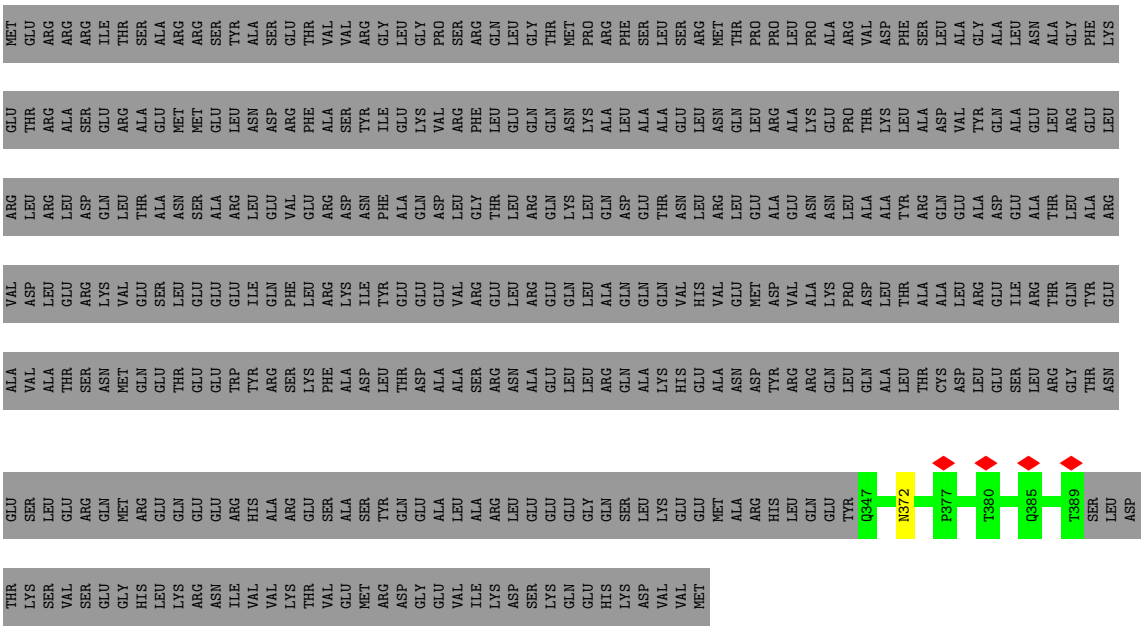
Mol	Chain	Residues	Atoms	AltConf	Trace
1	T	157	Total C H N O 944 314 316 157 157	0	0
1	V	5	Total C H N O 31 10 11 5 5	0	0
1	W	128	Total C H N O 771 256 259 128 128	0	0
1	X	145	Total C H N O 872 290 292 145 145	0	0
1	a	86	Total C H N O 519 172 175 86 86	0	0
1	b	100	Total C H N O 602 200 202 100 100	0	0
1	e	41	Total C H N O 247 82 83 41 41	0	0
1	f	58	Total C H N O 349 116 117 58 58	0	0
1	j	17	Total C H N O 101 34 33 17 17	0	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.

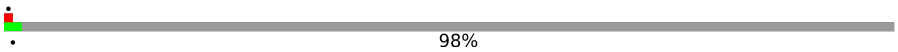
- Molecule 1: Glial fibrillary acidic protein

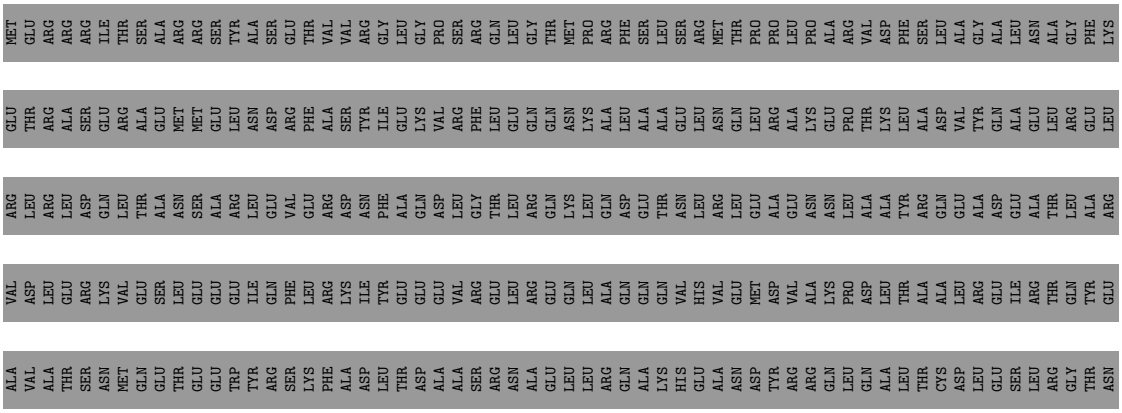
Chain 0:

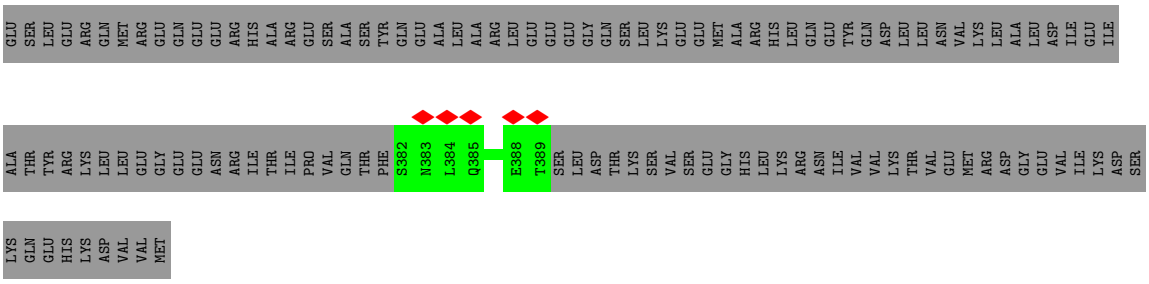


- Molecule 1: Glial fibrillary acidic protein

Chain 6:

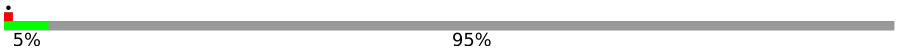


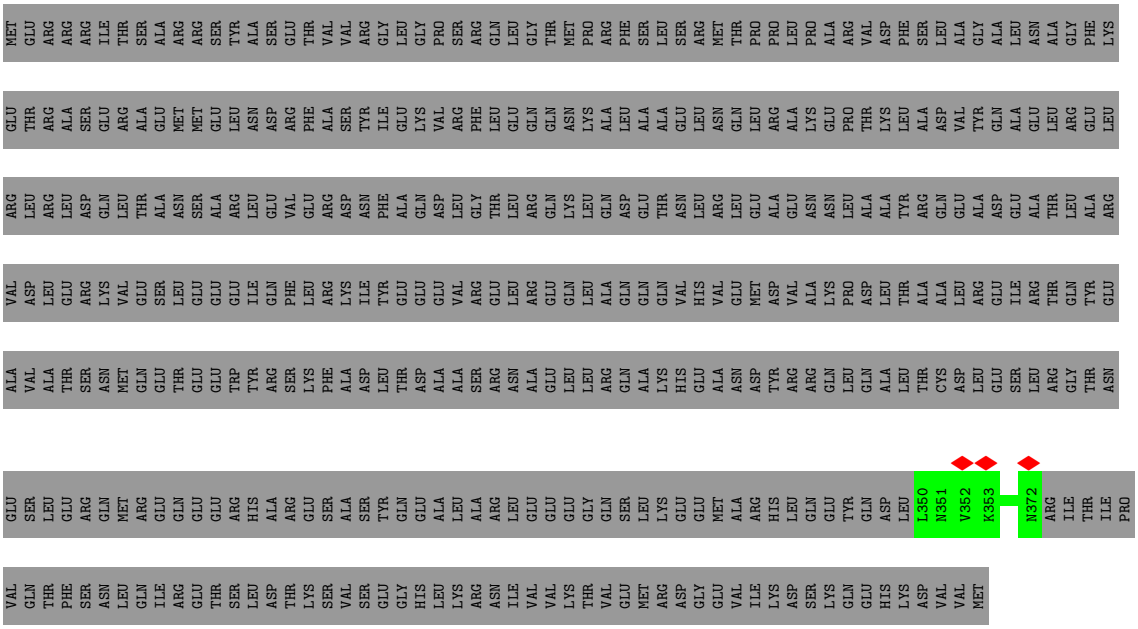




- Molecule 1: Glial fibrillary acidic protein

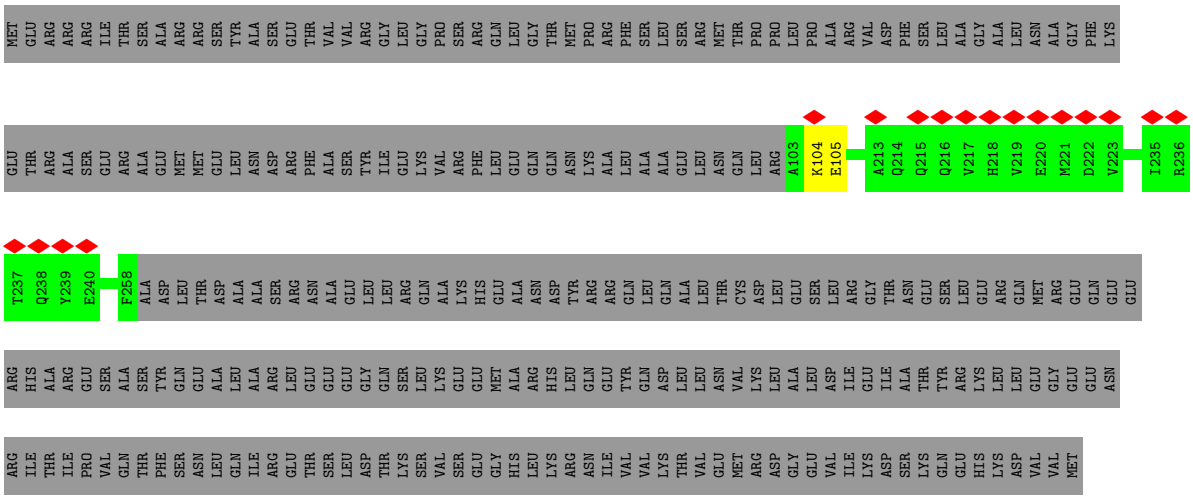
Chain 9:





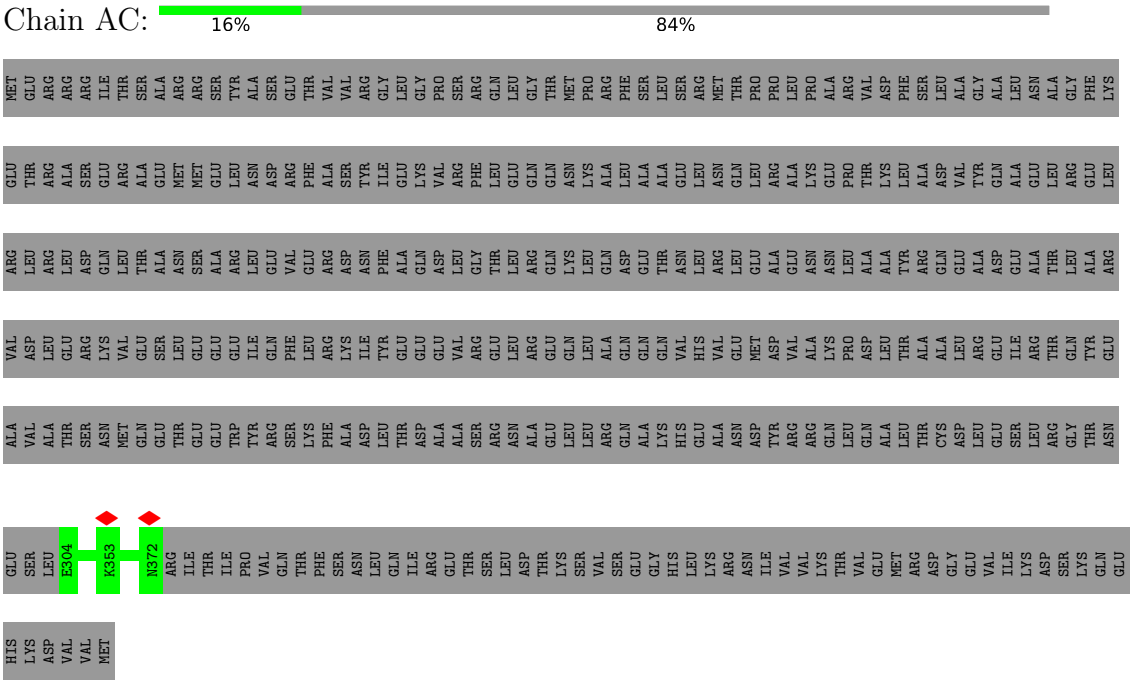
- Molecule 1: Glial fibrillary acidic protein

Chain A:



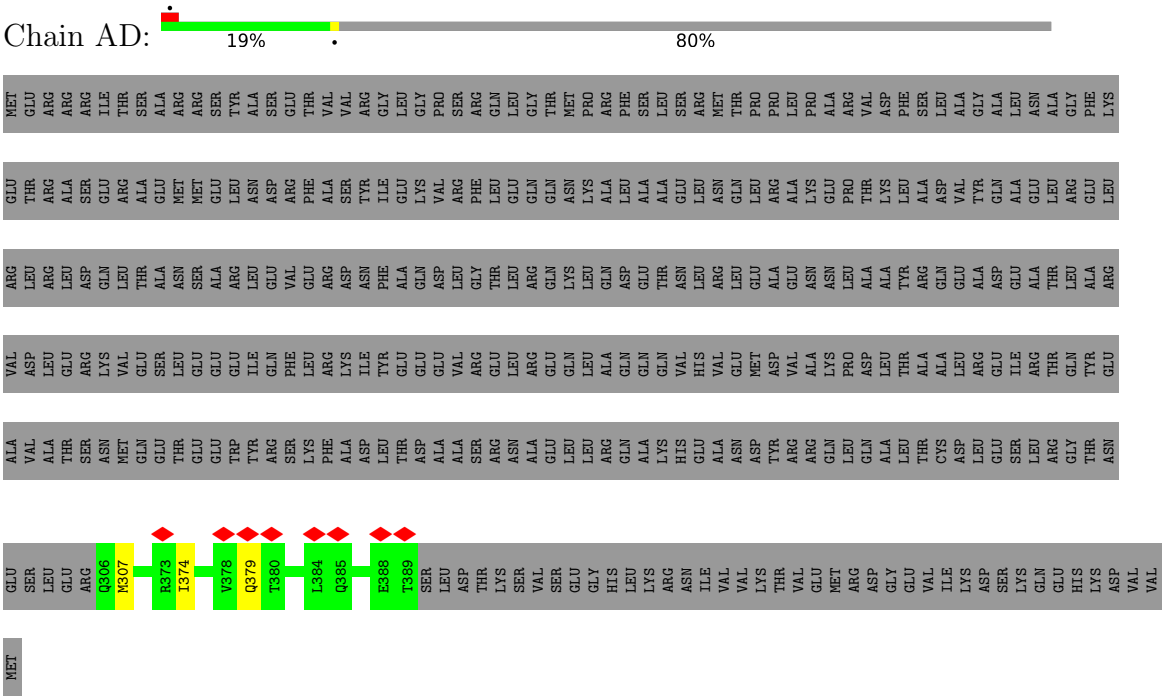
- Molecule 1: Glial fibrillary acidic protein

Chain AC:



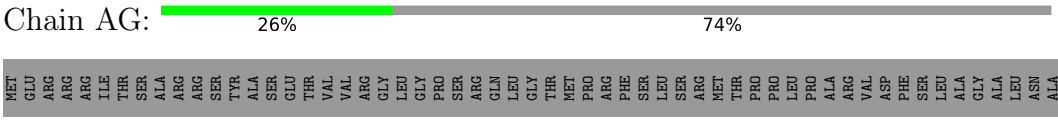
• Molecule 1: Glial fibrillary acidic protein

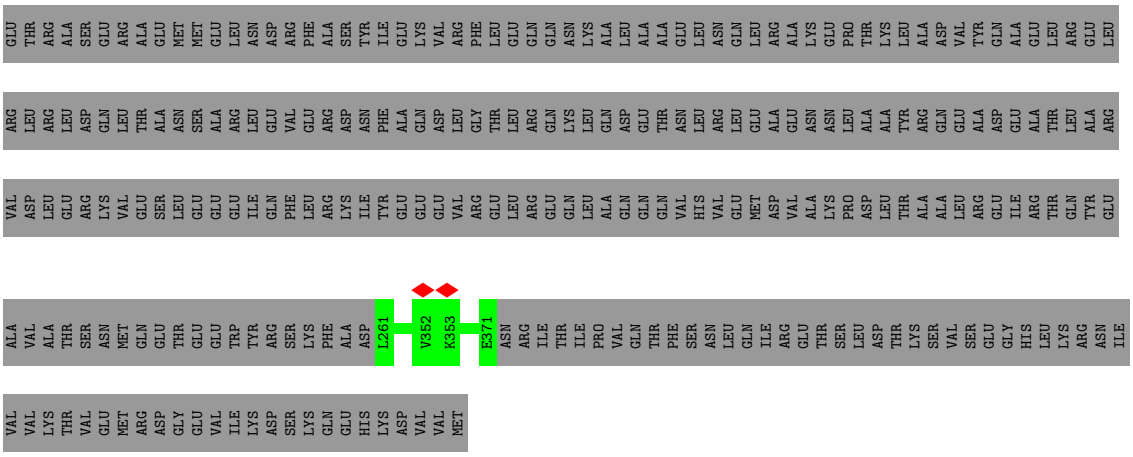
Chain AD:



• Molecule 1: Glial fibrillary acidic protein

Chain AG:



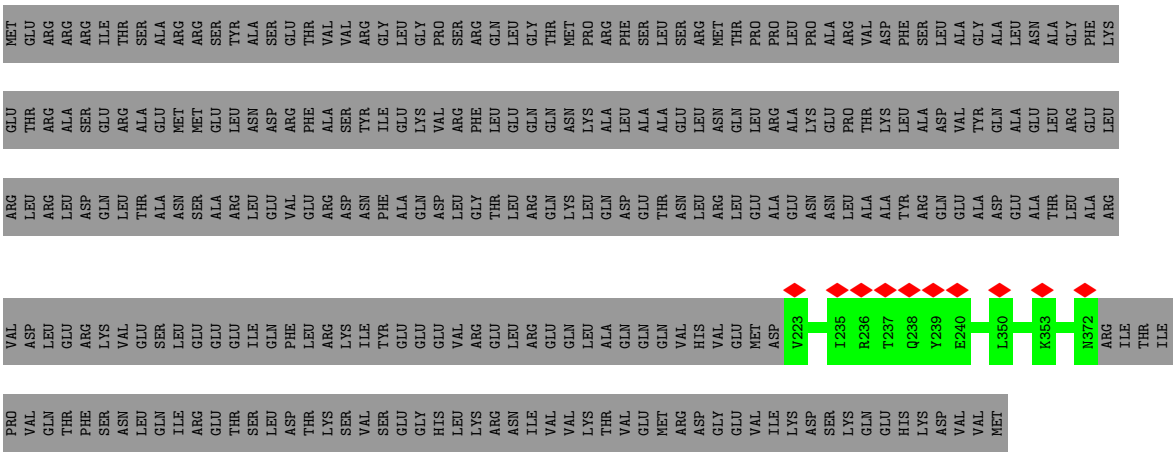


• Molecule 1: Glial fibrillary acidic protein

Chain AH:

• Molecule 1: Glial fibrillary acidic protein

Chain AK:



- Molecule 1: Glial fibrillary acidic protein

Chain AL: 37% 63%

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

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

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

VAL ASP LEU GLU ARG LYS VAL GLU SER LEU GLU GLU ILE GLN PHE LEU ARG LYS ILE TYR GLU GLU GLU VAL ARG GLU LEU ARG GLU GLN GLN GLN VAL HIS VAL GLU MET ASP V223 A224 K225 I374 P377 V378 Q379 T380 PHE SER ASN LEU GLN ILE ARG GLU

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

- Molecule 1: Glial fibrillary acidic protein

Chain AM: 5% 95%

MET GLU ARG ARG ARG ILE THR SER ALA ARG ARG SER TYR ALA SER GLU THR VAL VAL ARG GLY LEU GLY PRO SER ARG GLN LEU GLY THR MET PRO ARG PHE SER LEU SER ARG MET THR PRO PRO LEU PRO ALA ARG VAL ASP PHE SER LEU ALA GLY ALA LEU ASN A57 G58 F59

S79 TYR ILE GLU LYS VAL ARG PHE LEU GLU GLN GLN ASN LYS ALA LEU ALA ALA GLU LEU ASN GLN LEU ARG ALA LYS GLU PRO THR LYS LEU ALA ASP VAL TYR GLN ALA GLU LEU ARG GLU GLU LEU ARG LEU ARG LEU ASP GLN LEU THR ALA ASN SER ALA ARG LEU GLU VAL GLU ARG

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

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

ALA ASP LEU THR ASP ALA ALA SER ARG ASN ALA GLU LEU LEU ARG GLN ALA LYS HIS GLU ALA ASN ASP TYR ARG ARG GLN LEU GLN ALA LEU THR CYS ASP LEU GLU SER LEU ARG GLY THR ASN GLU SER LEU GLU ARG GLN MET ARG GLU GLN GLU GLU ARG HIS ALA ARG GLU SER

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

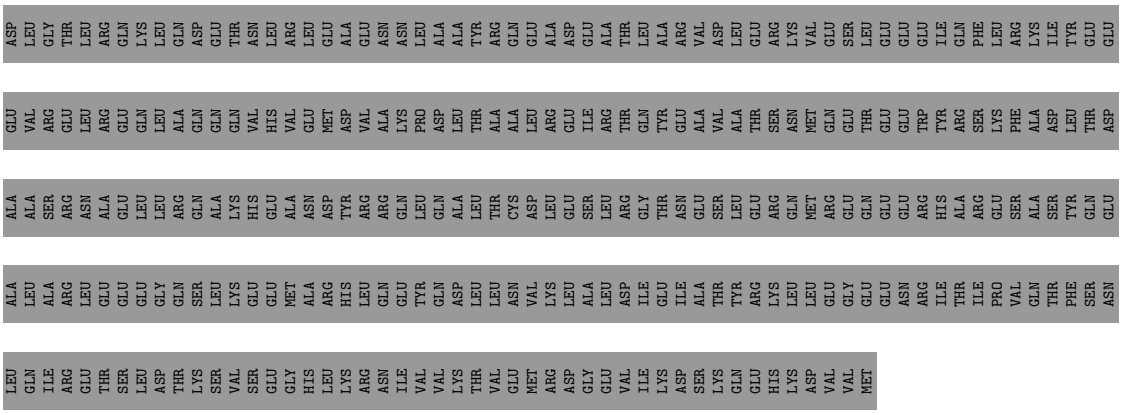
GLN THR PHE SER ASN LEU GLN ILE ARG GLU THR SER LEU ASP THR LYS SER VAL SER GLU GLU GLY HIS LEU LYS ARG ASN ILE VAL VAL LYS THR VAL GLU MET ARG ASP GLY GLU VAL ILE LYS ASP SER LYS GLN GLU HIS LYS ASP VAL VAL MET

- Molecule 1: Glial fibrillary acidic protein

Chain AN: 7% 93%

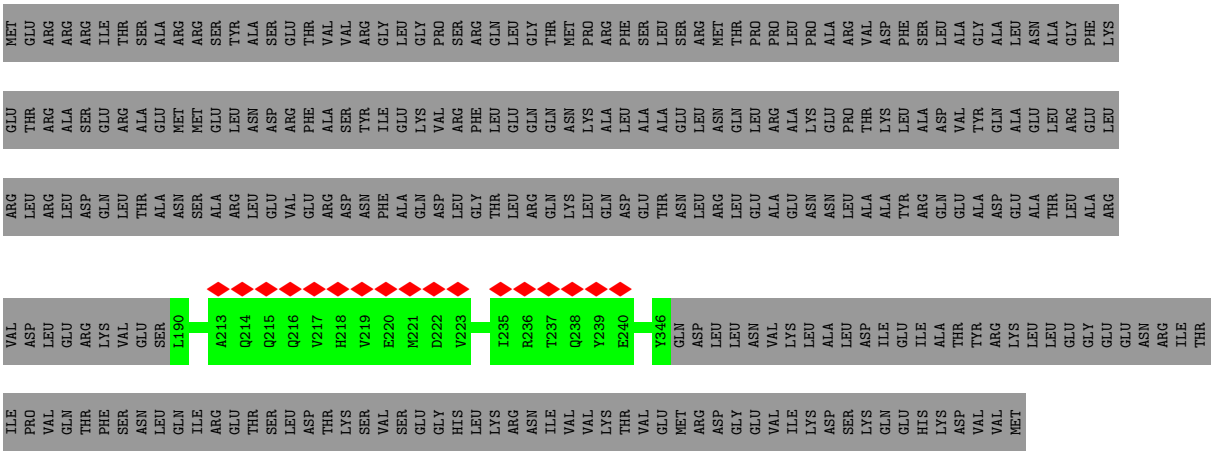
MET GLU ARG ARG ARG ILE THR SER ALA ARG ARG SER TYR ALA SER GLU THR VAL VAL ARG GLY LEU GLY PRO SER ARG GLN LEU GLY THR MET PRO ARG PHE SER LEU SER ARG MET THR PRO PRO LEU PRO ALA ARG VAL ASP PHE SER LEU ALA GLY A54 K60 E61 E69

V84 ARG PHE LEU GLU GLN GLN ASN LYS ALA LEU ALA ALA GLU LEU ASN GLN LEU ARG ALA LYS GLU PRO THR LYS LEU ALA ASP VAL TYR GLN ALA GLU LEU ARG GLU LEU ARG LEU ARG LEU ASP GLN LEU THR ALA ASN SER ALA ARG LEU GLU VAL GLU ARG ASP ASN PHE ALA GLN



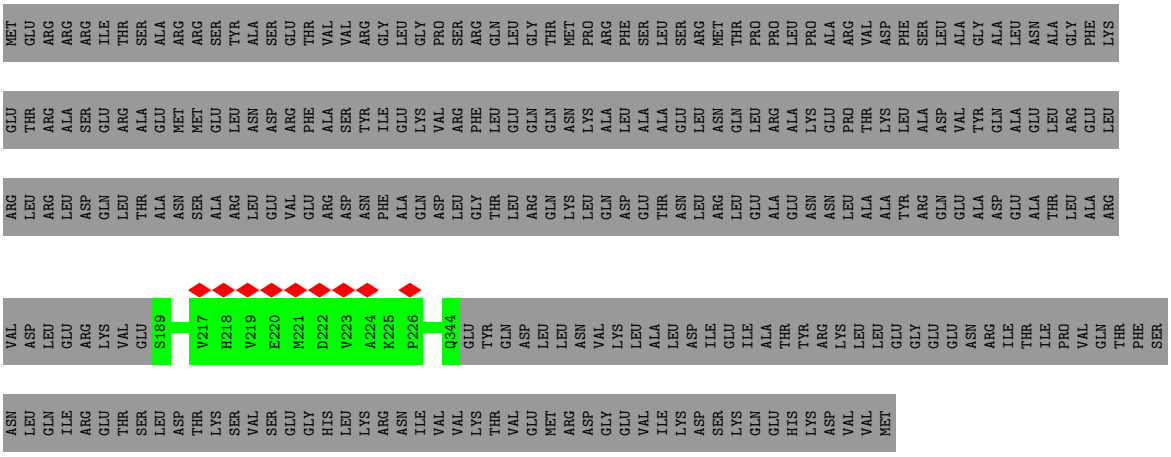
- Molecule 1: Glial fibrillary acidic protein

Chain AO:



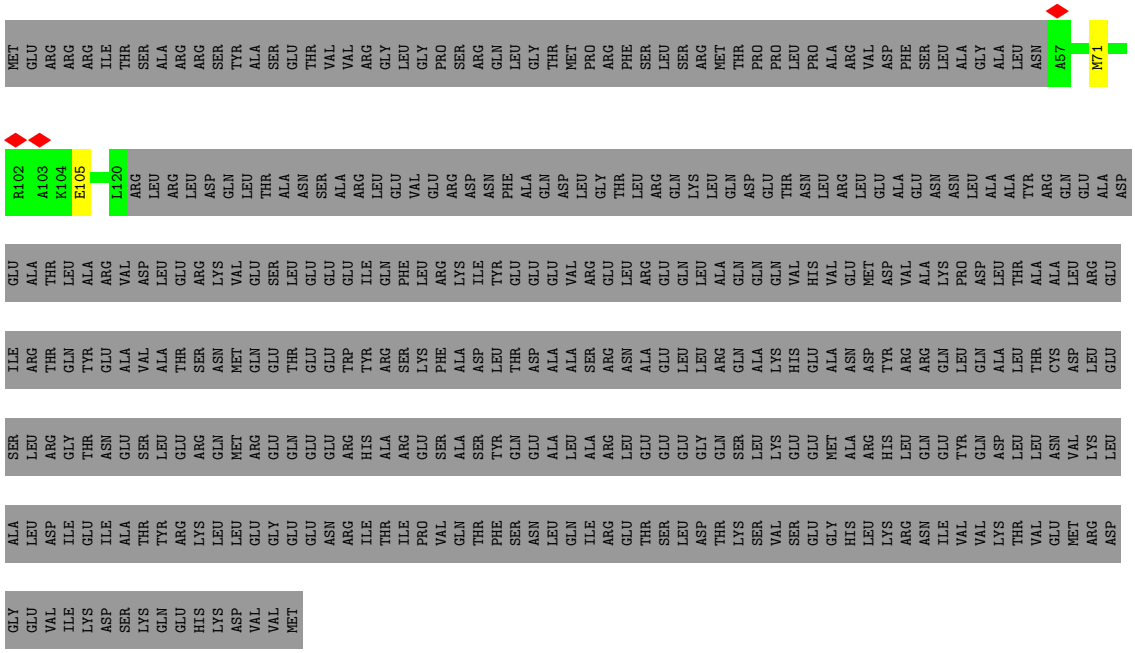
- Molecule 1: Glial fibrillary acidic protein

Chain AP:



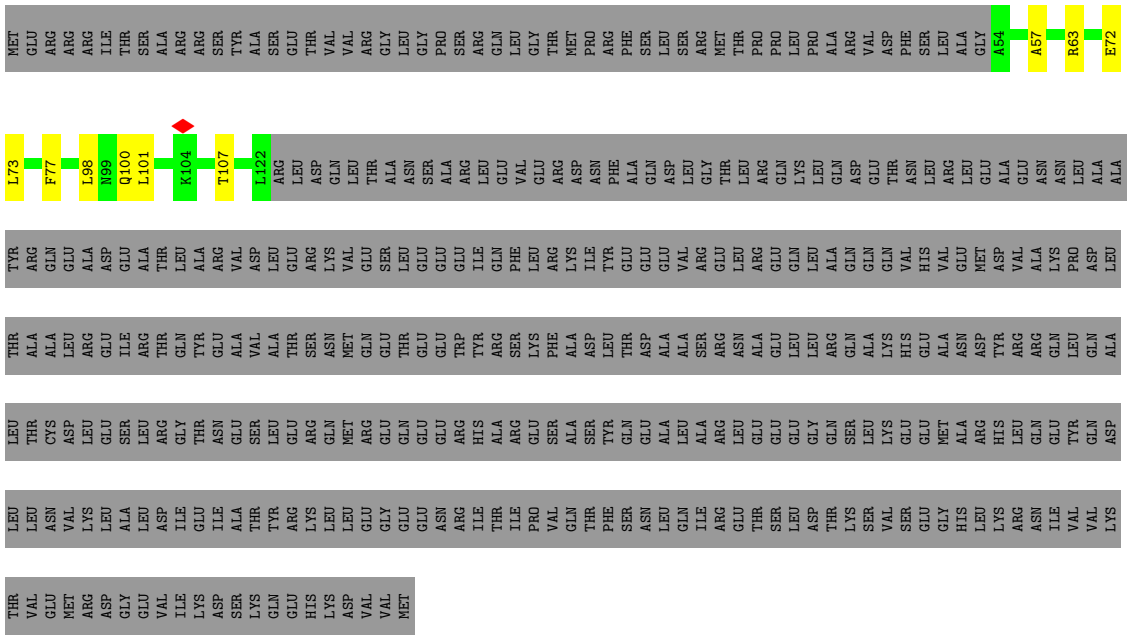
- Molecule 1: Glial fibrillary acidic protein

Chain AQ:



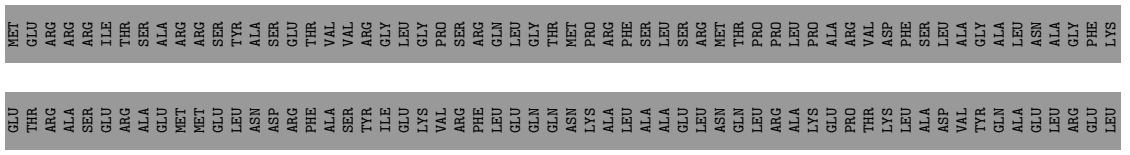
• Molecule 1: Glial fibrillary acidic protein

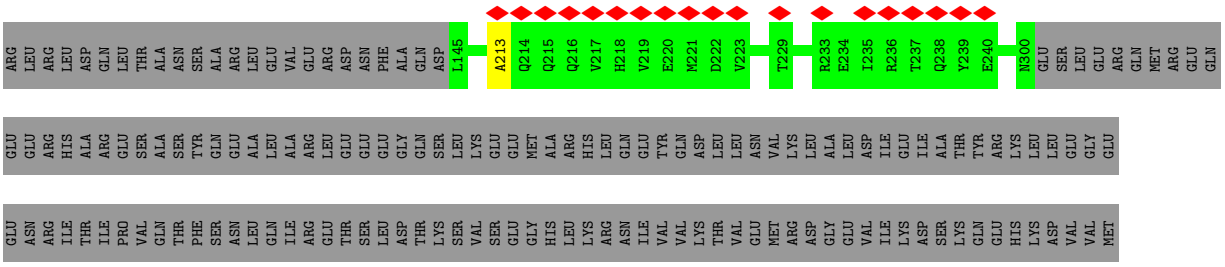
Chain AR:



• Molecule 1: Glial fibrillary acidic protein

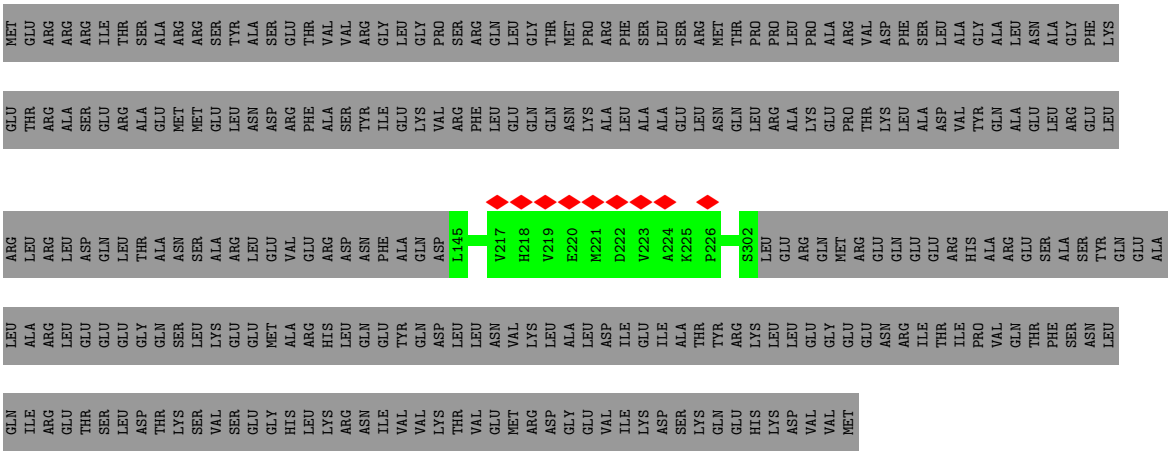
Chain AS:





• Molecule 1: Glial fibrillary acidic protein

Chain AT:



• Molecule 1: Glial fibrillary acidic protein

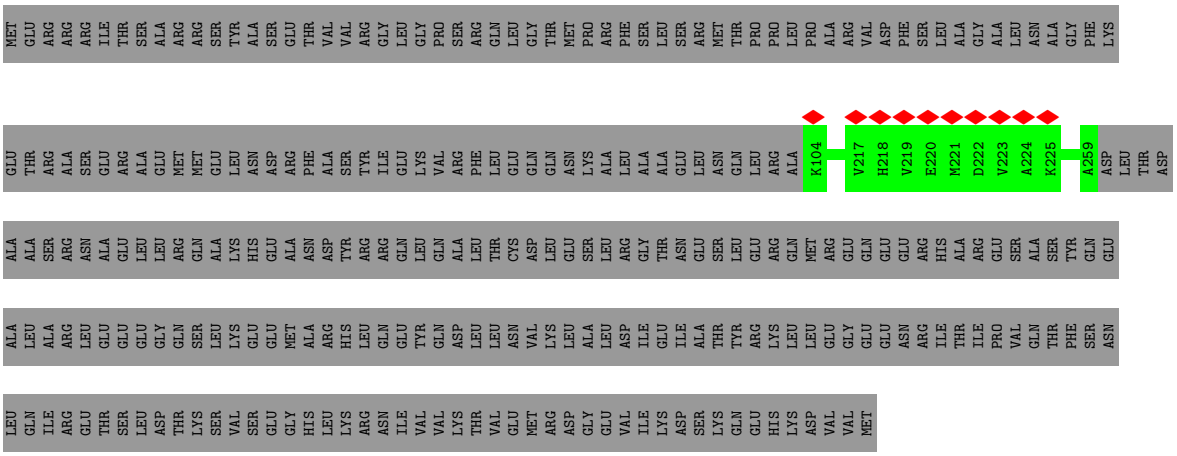
Chain AU:

• Molecule 1: Glial fibrillary acidic protein

Chain AV:

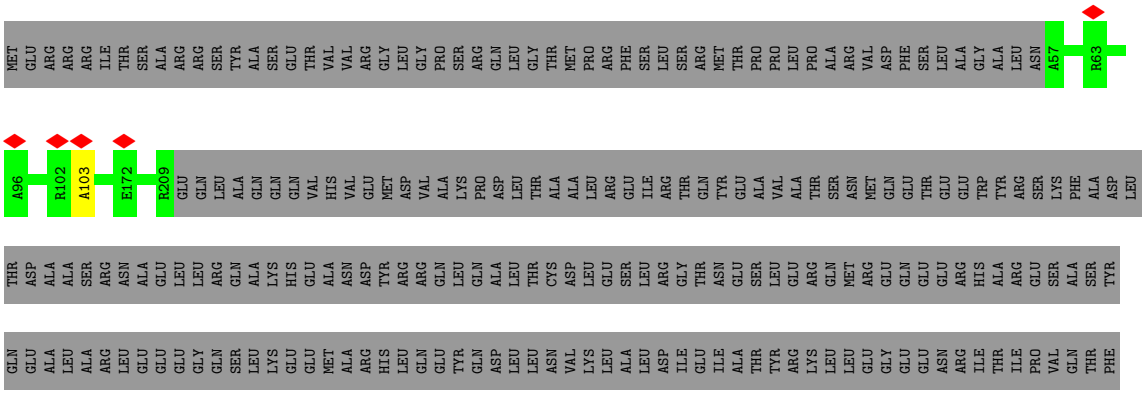
• Molecule 1: Glial fibrillary acidic protein

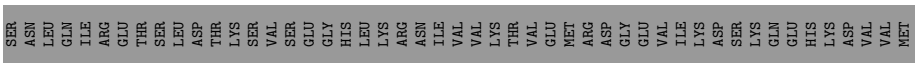
Chain B:



• Molecule 1: Glial fibrillary acidic protein

Chain C:



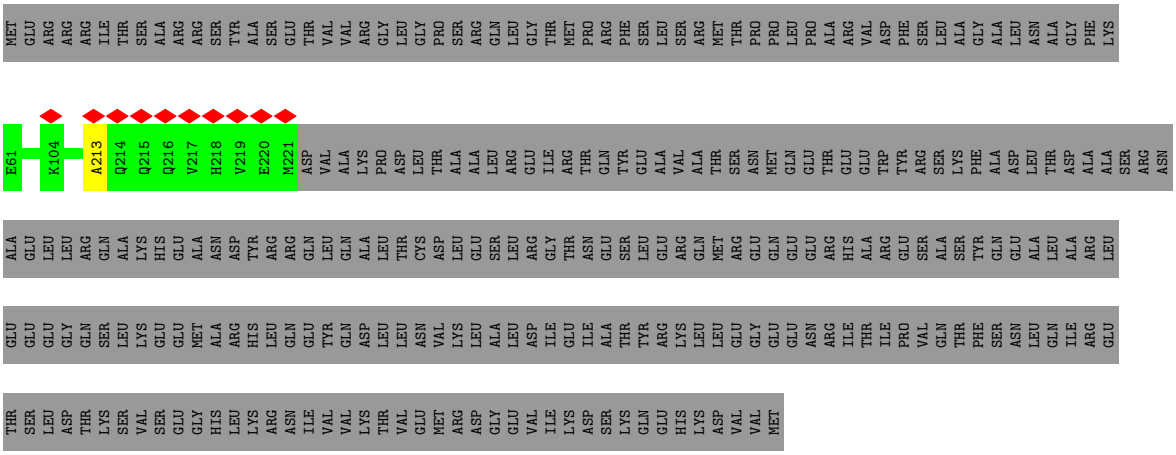


- Molecule 1: Glial fibrillary acidic protein

Chain D:

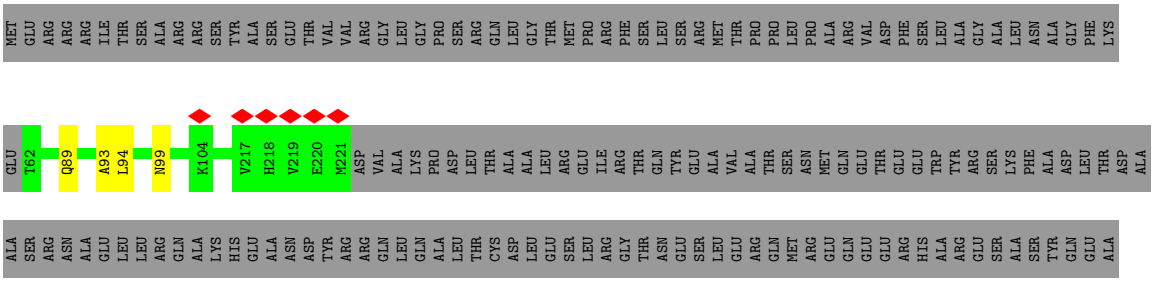
- Molecule 1: Glial fibrillary acidic protein

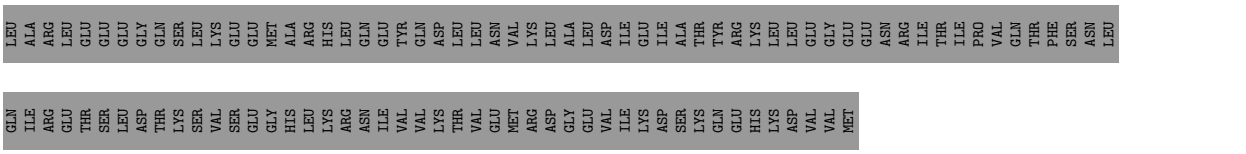
Chain E:



- Molecule 1: Glial fibrillary acidic protein

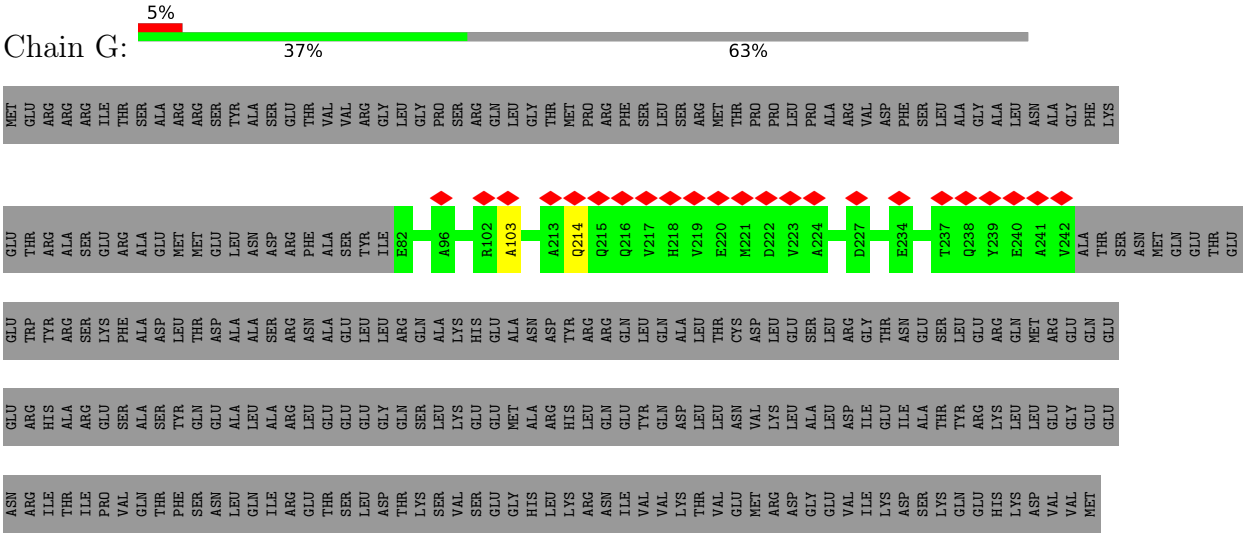
Chain F:





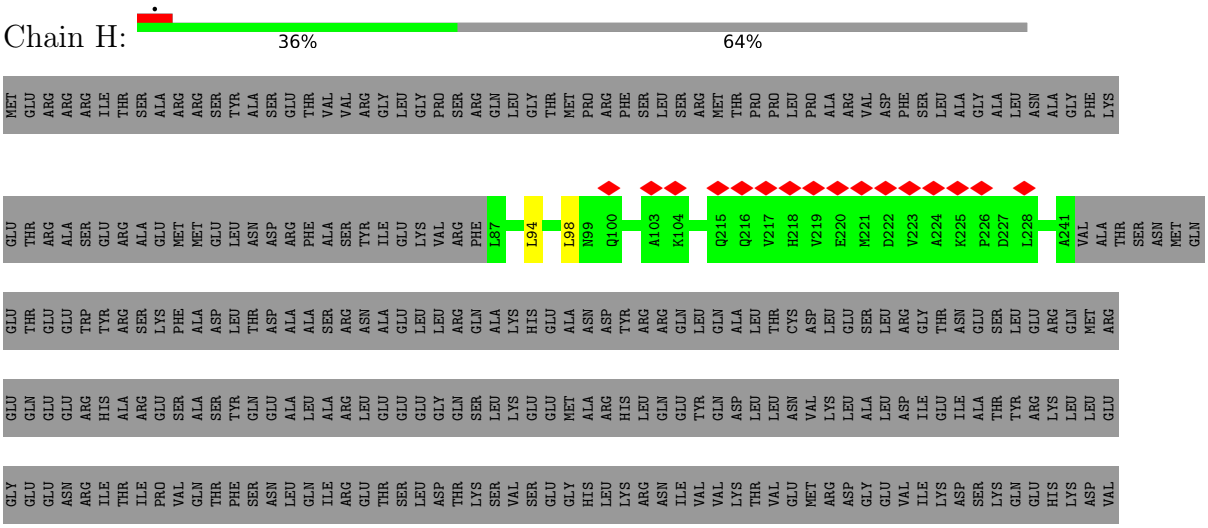
• Molecule 1: Glial fibrillary acidic protein

Chain G:



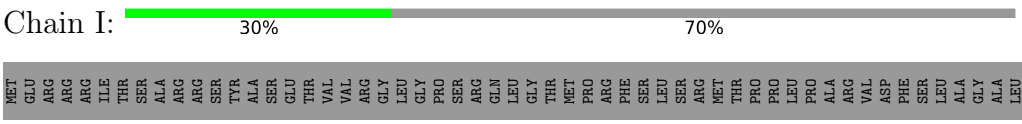
• Molecule 1: Glial fibrillary acidic protein

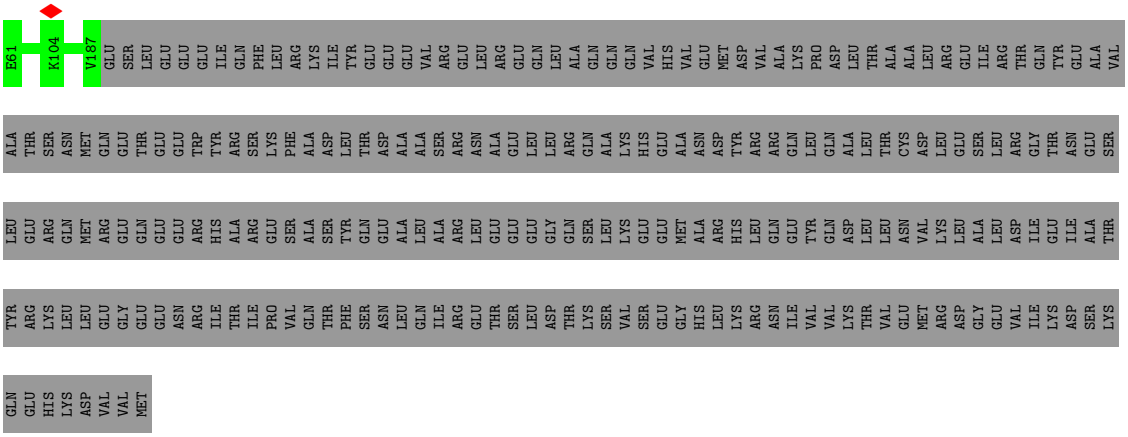
Chain H:



• Molecule 1: Glial fibrillary acidic protein

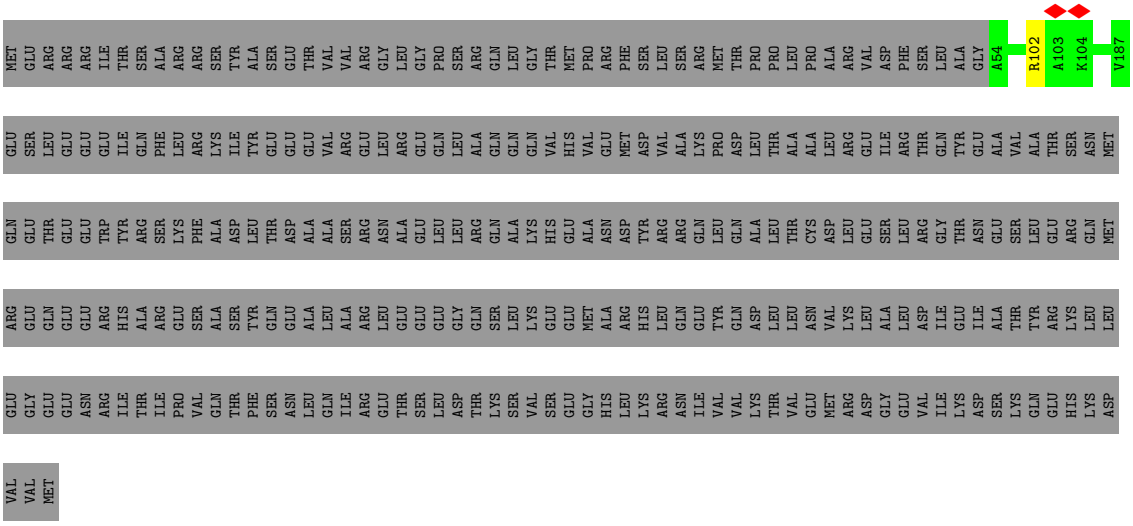
Chain I:





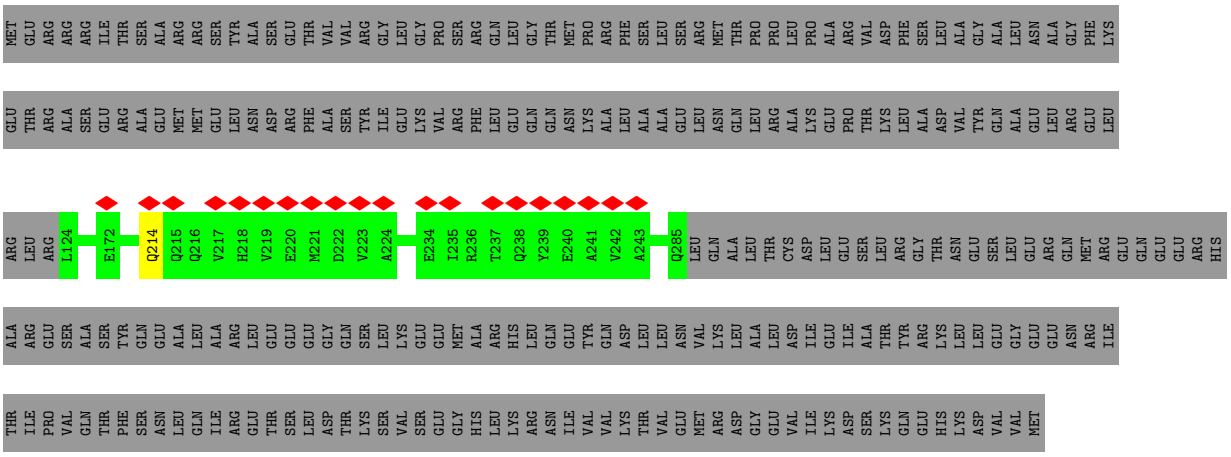
- Molecule 1: Glial fibrillary acidic protein

Chain J:



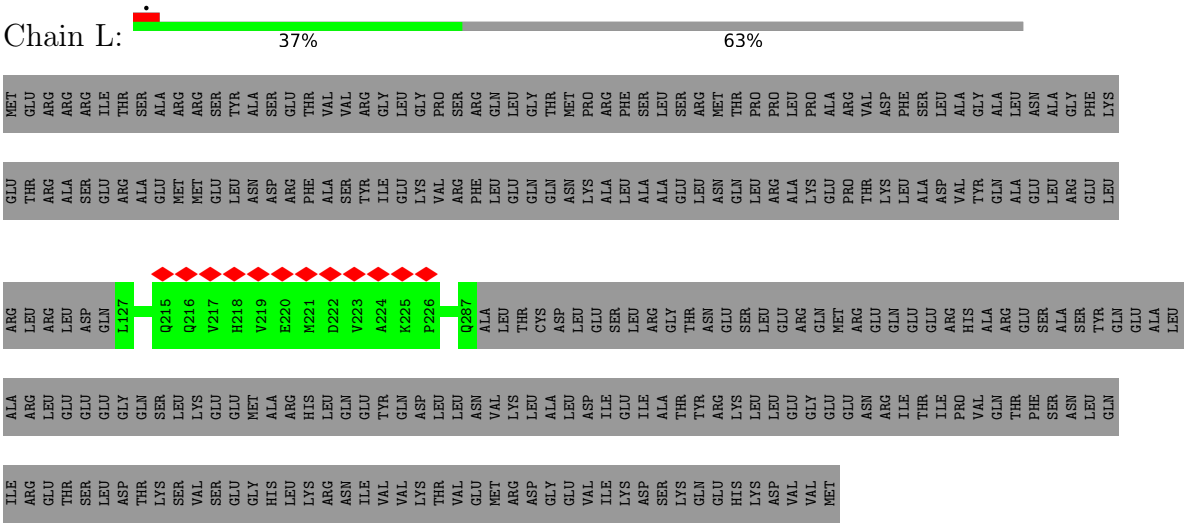
- Molecule 1: Glial fibrillary acidic protein

Chain K:



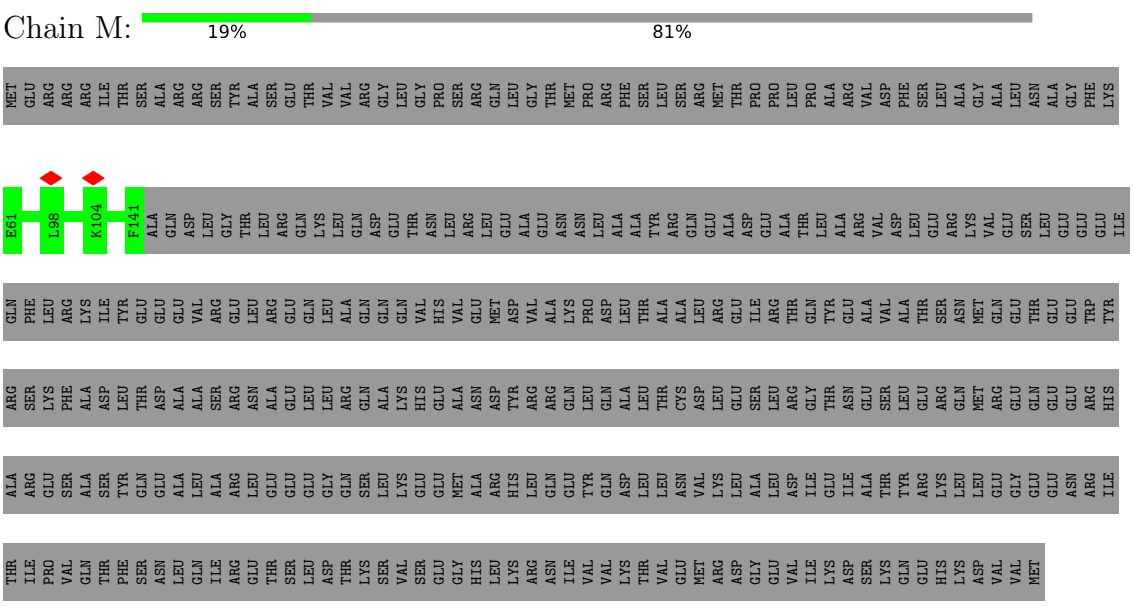
- Molecule 1: Glial fibrillary acidic protein

Chain L:



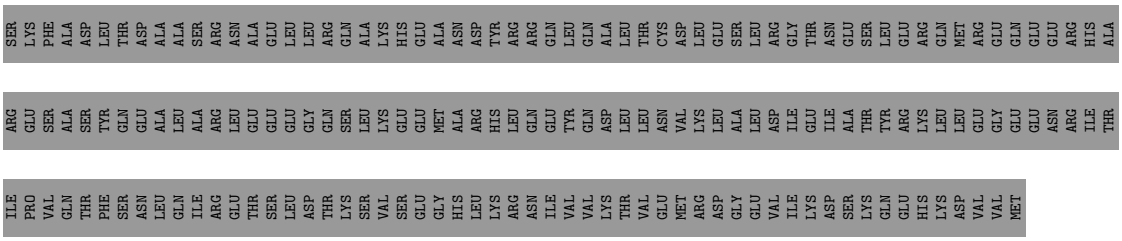
- Molecule 1: Glial fibrillary acidic protein

Chain M:



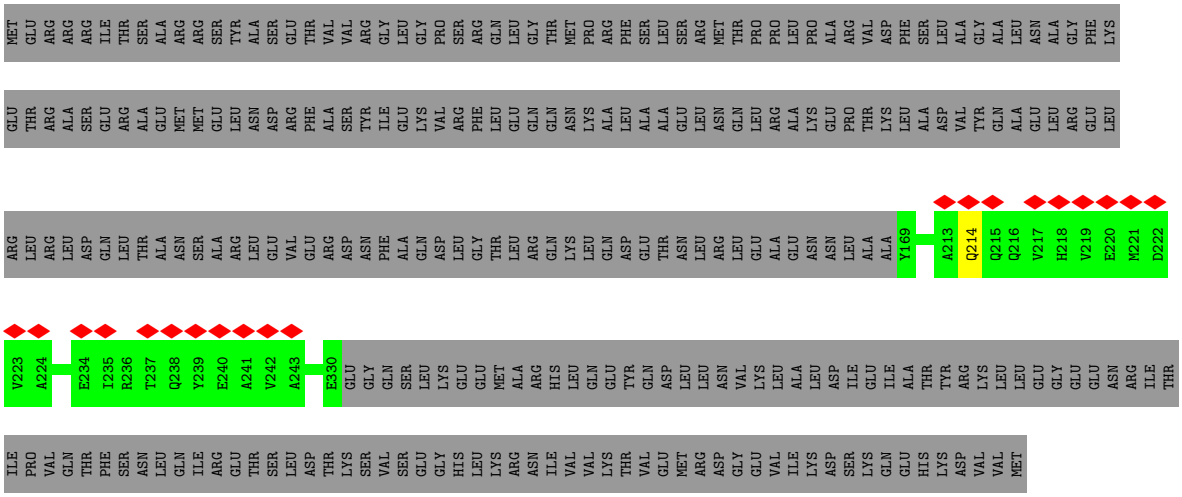
- Molecule 1: Glial fibrillary acidic protein

Chain N:



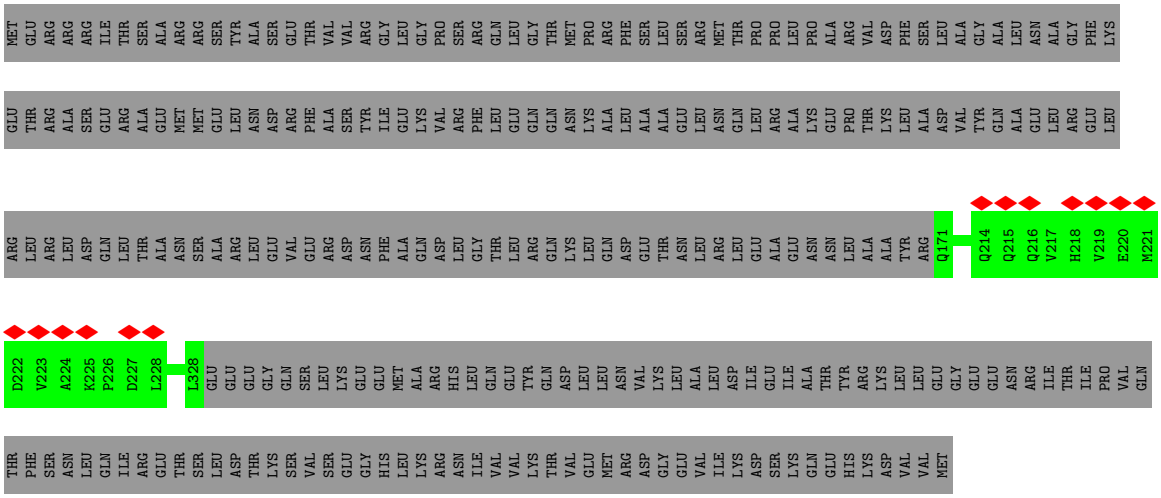
• Molecule 1: Glial fibrillary acidic protein

Chain O:



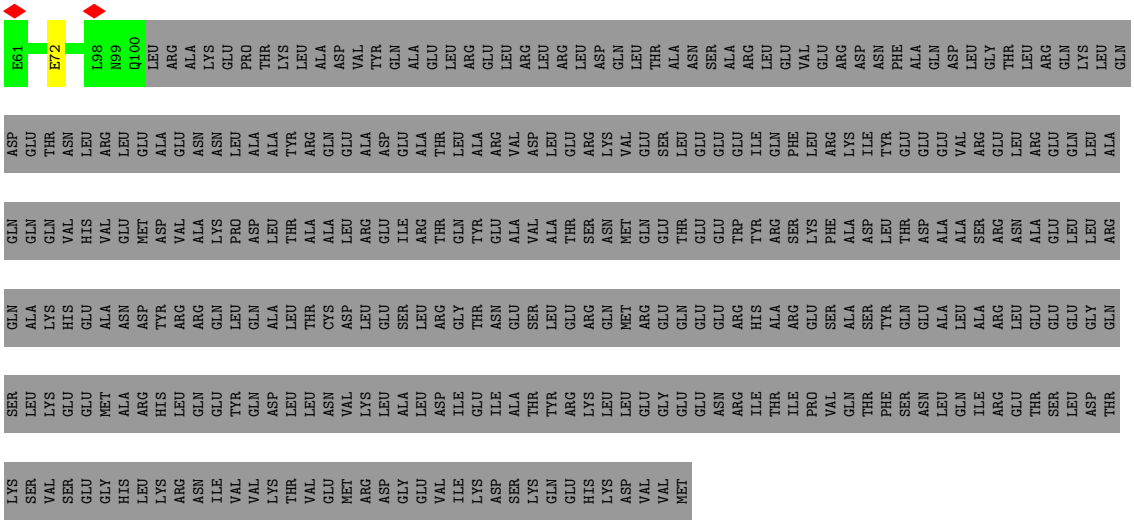
• Molecule 1: Glial fibrillary acidic protein

Chain P:



• Molecule 1: Glial fibrillary acidic protein

Chain Q:

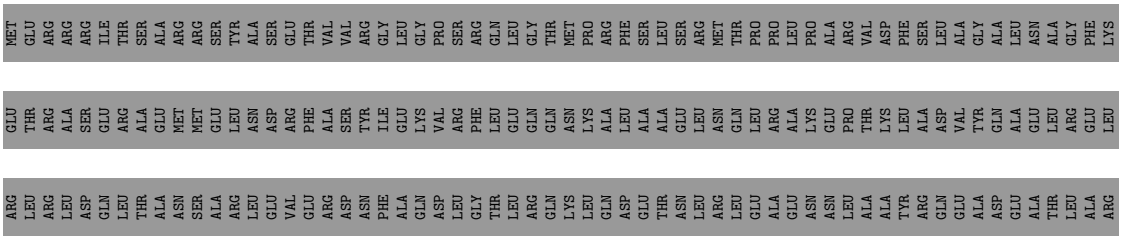


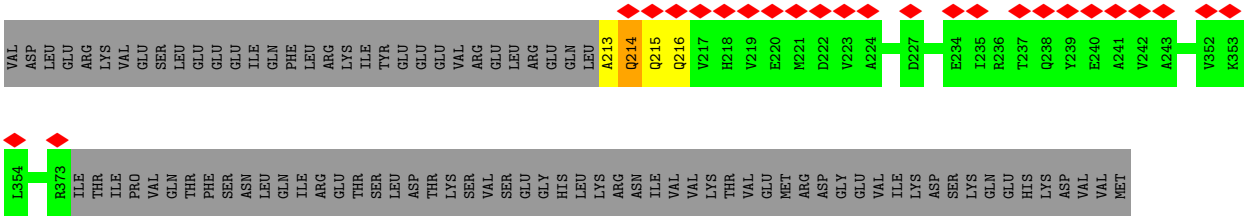
• Molecule 1: Glial fibrillary acidic protein

Chain R:

• Molecule 1: Glial fibrillary acidic protein

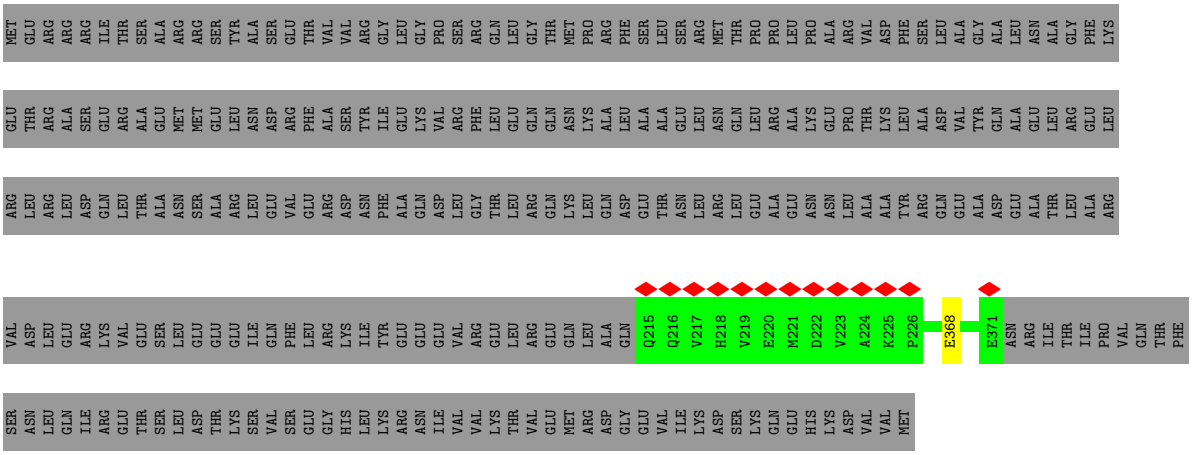
Chain S:





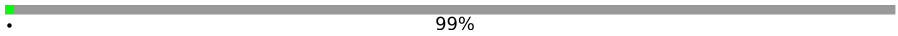
• Molecule 1: Glial fibrillary acidic protein

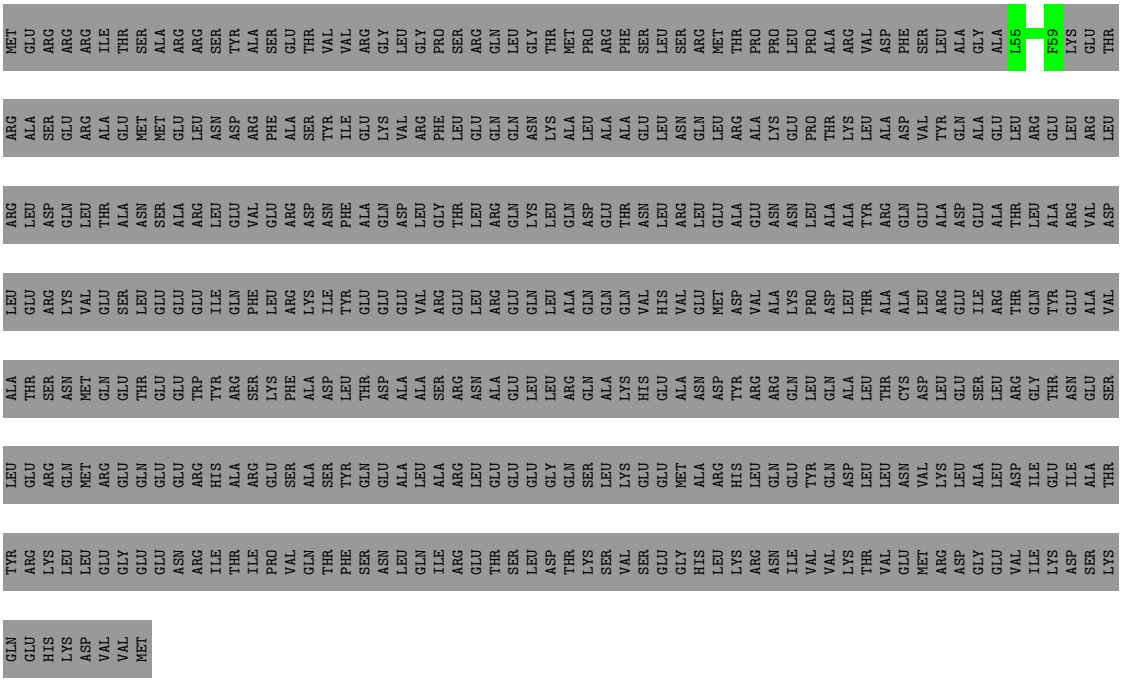
Chain T:



• Molecule 1: Glial fibrillary acidic protein

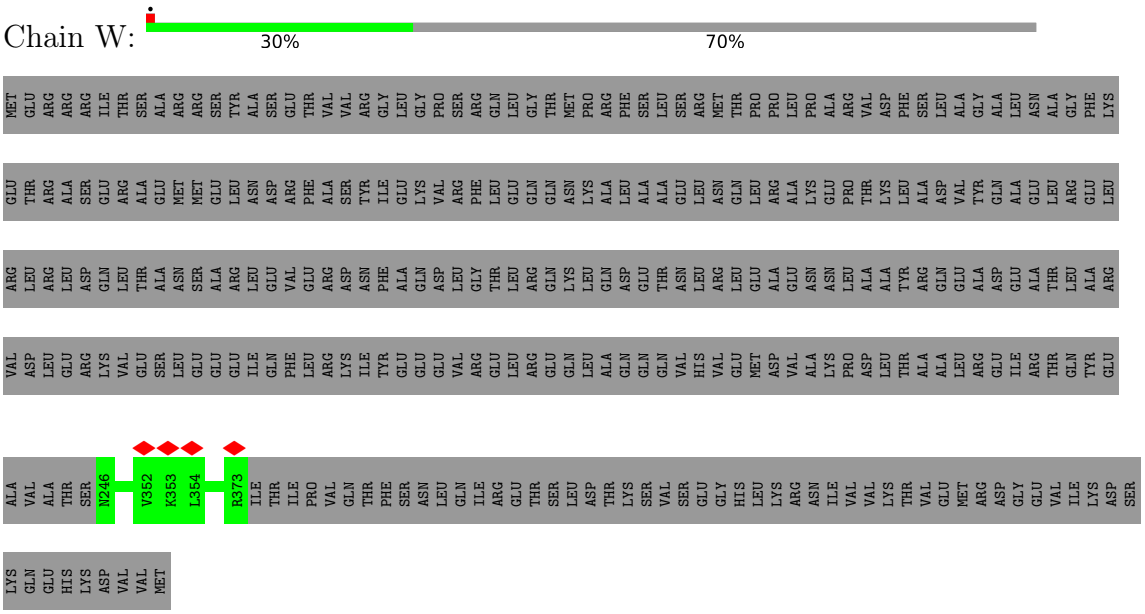
Chain V:





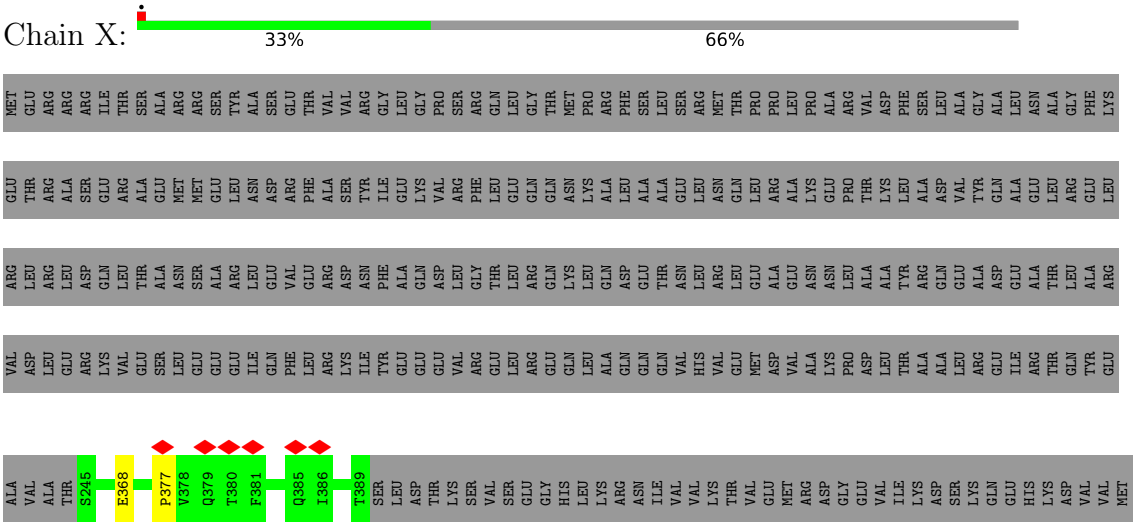
• Molecule 1: Glial fibrillary acidic protein

Chain W:



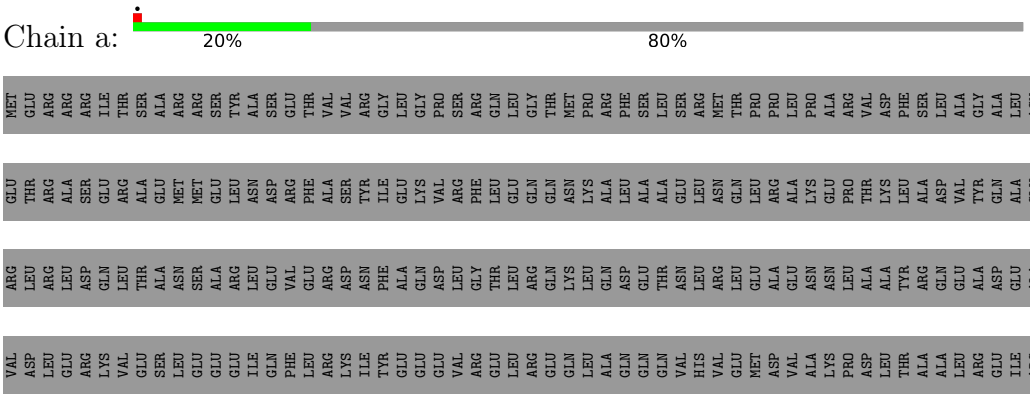
- Molecule 1: Glial fibrillary acidic protein

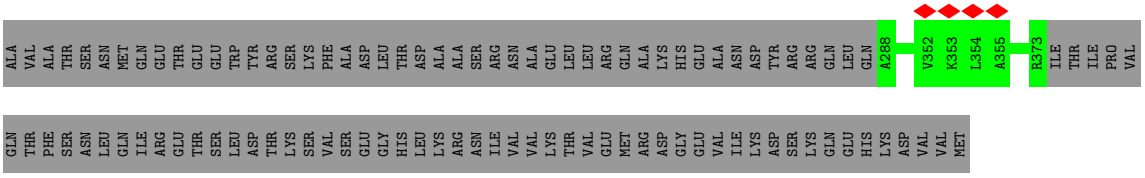
Chain X:



- Molecule 1: Glial fibrillary acidic protein

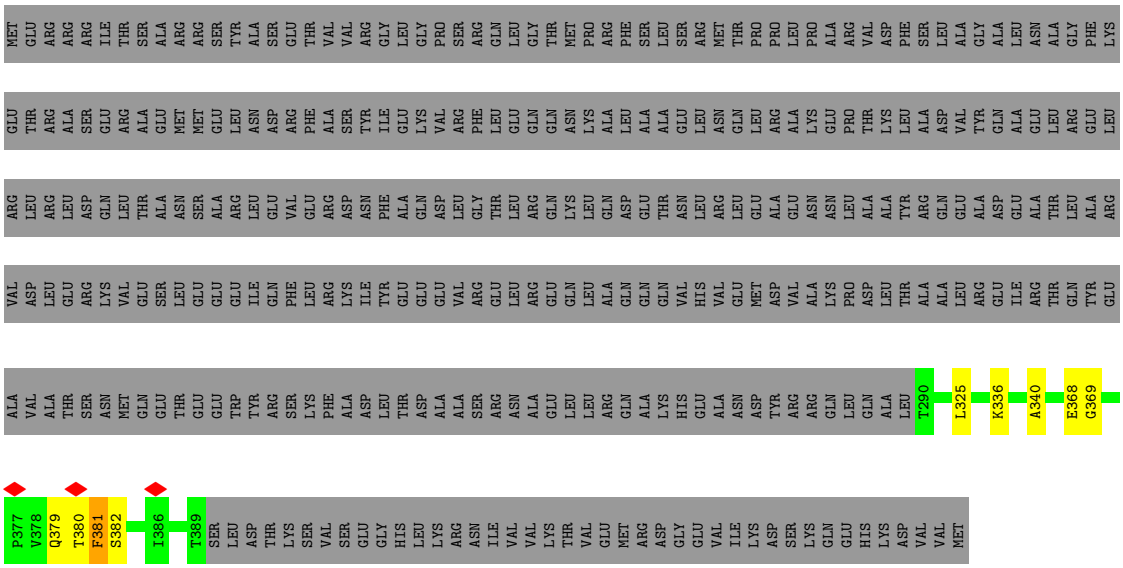
Chain a:





• Molecule 1: Glial fibrillary acidic protein

Chain b:

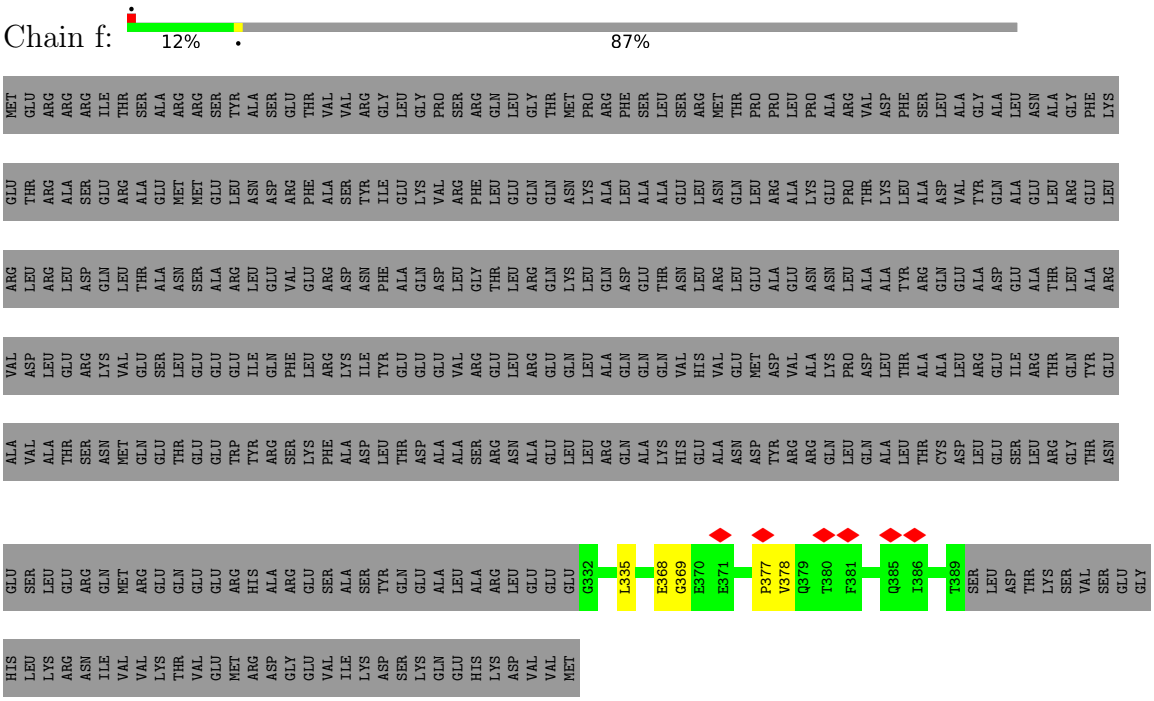


• Molecule 1: Glial fibrillary acidic protein

Chain e:

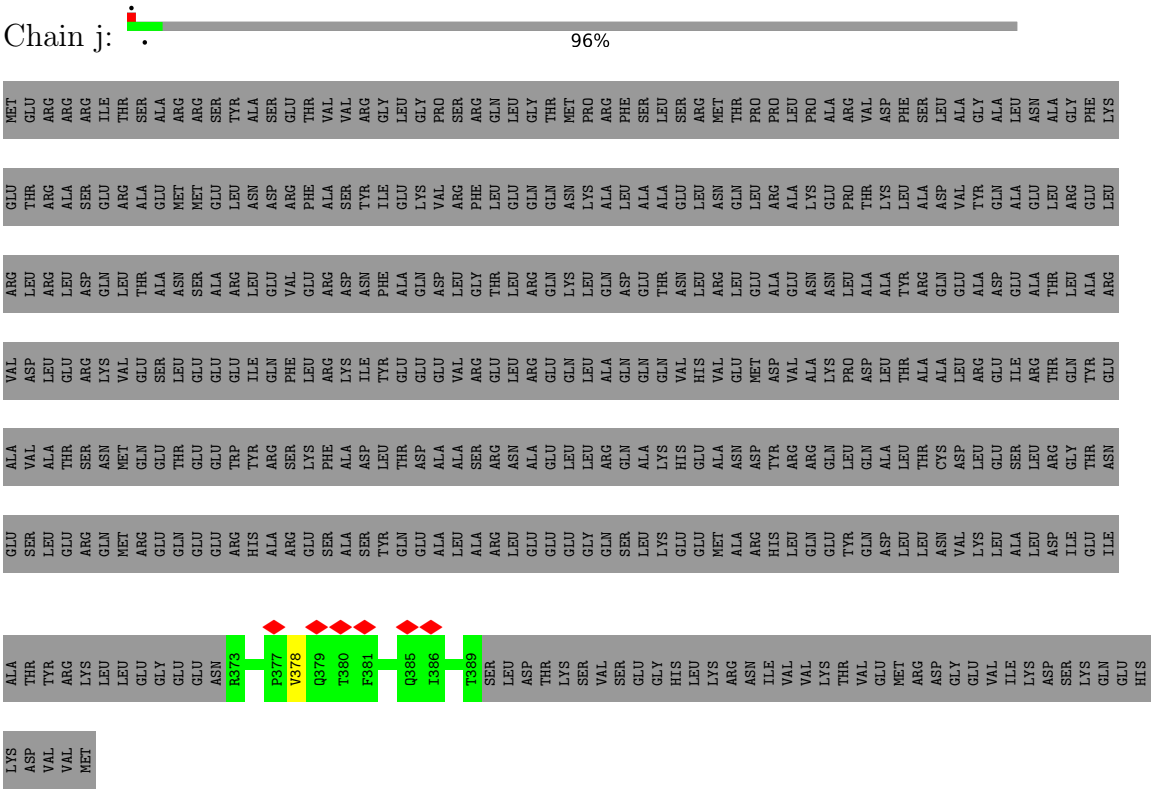
• Molecule 1: Glial fibrillary acidic protein

Chain f:



• Molecule 1: Glial fibrillary acidic protein

Chain j:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=127°, rise=63.3 Å, axial sym=C1	Depositor
Number of segments used	236160	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.021	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	311.80798, 311.80798, 311.80798	wwPDB
Map dimensions	232, 232, 232	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.344, 1.344, 1.344	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	0	0.83	0/171	1.61	1/212 (0.5%)
1	6	0.28	0/31	0.73	0/37
1	9	0.66	0/91	1.25	0/112
1	A	0.66	0/623	1.29	5/777 (0.6%)
1	AC	0.63	0/275	1.38	0/342
1	AD	0.68	0/335	1.22	2/417 (0.5%)
1	AG	0.64	0/443	1.23	0/552
1	AH	0.72	0/507	1.23	0/632
1	AK	0.62	0/599	1.14	0/747
1	AL	0.69	0/631	1.20	0/787
1	AM	0.88	0/91	1.61	0/112
1	AN	1.63	1/123 (0.8%)	1.80	1/152 (0.7%)
1	AO	0.59	0/627	1.13	0/782
1	AP	0.59	0/623	1.13	0/777
1	AQ	0.88	0/255	1.43	2/317 (0.6%)
1	AR	1.26	1/275 (0.4%)	1.87	5/342 (1.5%)
1	AS	0.58	0/623	1.09	1/777 (0.1%)
1	AT	0.61	0/631	1.15	0/787
1	AU	0.82	0/443	1.38	2/552 (0.4%)
1	AV	1.16	1/447 (0.2%)	1.70	7/557 (1.3%)
1	B	0.65	0/623	1.23	0/777
1	C	0.74	0/611	1.34	1/762 (0.1%)
1	D	1.14	2/631 (0.3%)	1.55	11/787 (1.4%)
1	E	0.70	0/643	1.28	1/802 (0.1%)
1	F	0.79	1/639 (0.2%)	1.41	4/797 (0.5%)
1	G	0.71	0/643	1.24	1/802 (0.1%)
1	H	0.81	0/619	1.30	3/772 (0.4%)
1	I	0.73	0/507	1.36	0/632
1	J	0.79	0/535	1.39	0/667
1	K	0.61	0/647	1.12	1/807 (0.1%)
1	L	0.58	0/643	1.11	0/802
1	M	0.78	0/323	1.43	0/402
1	N	1.08	0/355	1.70	9/442 (2.0%)
1	O	0.64	0/647	1.17	1/807 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	P	0.58	0/631	1.13	0/787
1	Q	0.76	0/159	1.38	2/197 (1.0%)
1	R	0.90	0/191	1.63	1/237 (0.4%)
1	S	0.65	0/643	1.22	2/802 (0.2%)
1	T	0.72	0/627	1.35	1/782 (0.1%)
1	V	0.74	0/19	1.78	0/22
1	W	0.64	0/511	1.24	0/637
1	X	0.85	1/579 (0.2%)	1.39	1/722 (0.1%)
1	a	0.60	0/343	1.12	0/427
1	b	1.03	2/399 (0.5%)	1.57	6/497 (1.2%)
1	e	0.65	0/163	1.31	0/202
1	f	0.94	0/231	1.65	3/287 (1.0%)
1	j	1.14	0/67	1.20	0/82
All	All	0.76	9/20473 (0.0%)	1.31	74/25509 (0.3%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	89	GLN	C-O	-5.88	1.17	1.24
1	D	98	LEU	C-O	5.84	1.31	1.24
1	AN	61	GLU	C-O	5.73	1.31	1.24
1	b	325	LEU	C-O	5.72	1.30	1.24
1	D	68	ALA	C-O	5.65	1.30	1.24

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	0	372	ASN	N-CA-C	10.29	122.38	107.88
1	S	215	GLN	N-CA-C	-9.59	101.34	113.43
1	F	93	ALA	N-CA-C	-8.29	102.33	111.36
1	b	369	GLY	N-CA-C	8.22	123.71	114.67
1	f	335	LEU	N-CA-C	-8.10	102.39	111.71

There are no chirality outliers.

There are no planarity outliers.

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	0	172	86	43	0	0
1	6	32	16	7	0	0
1	9	92	47	24	0	0
1	A	624	311	155	0	0
1	AC	276	140	72	0	0
1	AD	336	169	86	1	0
1	AG	444	225	116	0	0
1	AH	508	256	131	0	0
1	AK	600	302	154	0	0
1	AL	632	317	161	0	0
1	AM	92	47	24	0	0
1	AN	124	63	32	0	0
1	AO	628	315	159	0	0
1	AP	624	313	158	0	0
1	AQ	256	128	64	0	0
1	AR	276	138	69	2	0
1	AS	624	313	158	0	0
1	AT	632	317	160	0	0
1	AU	444	223	113	0	0
1	AV	448	225	114	3	0
1	B	624	311	155	0	0
1	C	612	307	155	0	0
1	D	632	317	160	1	0
1	E	644	322	161	0	0
1	F	640	320	160	0	0
1	G	644	321	160	0	0
1	H	620	309	154	1	0
1	I	508	254	127	0	0
1	J	536	269	136	1	0
1	K	648	324	162	0	0
1	L	644	322	161	0	0
1	M	324	161	79	0	0
1	N	356	178	89	0	0
1	O	648	324	162	0	0
1	P	632	316	158	0	0
1	Q	160	80	39	0	0
1	R	192	97	49	1	0
1	S	644	324	165	1	0
1	T	628	316	161	0	0
1	V	20	11	6	0	0
1	W	512	259	133	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	X	580	292	149	0	0
1	a	344	175	91	0	0
1	b	400	202	104	1	0
1	e	164	83	42	0	0
1	f	232	117	60	1	0
1	j	68	33	15	1	0
All	All	20520	10295	5193	11	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 0.

The worst 5 of 11 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)
1:S:213:ALA:O	1:S:214:GLN:C	2.24	0.81
1:AD:379:GLN:CA	1:J:102:ARG:CA	2.82	0.57
1:R:101:LEU:O	1:R:102:ARG:C	2.50	0.54
1:AR:100:GLN:O	1:AR:101:LEU:C	2.51	0.52
1:b:381:PHE:O	1:b:382:SER:C	2.54	0.50

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	0	41/430 (10%)	38 (93%)	3 (7%)	0	100	100
1	6	6/430 (1%)	5 (83%)	1 (17%)	0	100	100
1	9	21/430 (5%)	21 (100%)	0	0	100	100
1	A	154/430 (36%)	153 (99%)	1 (1%)	0	100	100
1	AC	67/430 (16%)	67 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AD	82/430 (19%)	76 (93%)	5 (6%)	1 (1%)	10	44
1	AG	109/430 (25%)	109 (100%)	0	0	100	100
1	AH	125/430 (29%)	121 (97%)	4 (3%)	0	100	100
1	AK	148/430 (34%)	148 (100%)	0	0	100	100
1	AL	156/430 (36%)	152 (97%)	3 (2%)	1 (1%)	21	59
1	AM	21/430 (5%)	20 (95%)	1 (5%)	0	100	100
1	AN	29/430 (7%)	28 (97%)	1 (3%)	0	100	100
1	AO	155/430 (36%)	155 (100%)	0	0	100	100
1	AP	154/430 (36%)	153 (99%)	1 (1%)	0	100	100
1	AQ	62/430 (14%)	61 (98%)	0	1 (2%)	7	38
1	AR	67/430 (16%)	64 (96%)	3 (4%)	0	100	100
1	AS	154/430 (36%)	154 (100%)	0	0	100	100
1	AT	156/430 (36%)	155 (99%)	1 (1%)	0	100	100
1	AU	109/430 (25%)	106 (97%)	3 (3%)	0	100	100
1	AV	110/430 (26%)	103 (94%)	5 (4%)	2 (2%)	6	34
1	B	154/430 (36%)	152 (99%)	2 (1%)	0	100	100
1	C	151/430 (35%)	147 (97%)	4 (3%)	0	100	100
1	D	156/430 (36%)	150 (96%)	3 (2%)	3 (2%)	6	32
1	E	159/430 (37%)	158 (99%)	1 (1%)	0	100	100
1	F	158/430 (37%)	151 (96%)	7 (4%)	0	100	100
1	G	159/430 (37%)	156 (98%)	2 (1%)	1 (1%)	21	59
1	H	153/430 (36%)	150 (98%)	3 (2%)	0	100	100
1	I	125/430 (29%)	124 (99%)	1 (1%)	0	100	100
1	J	132/430 (31%)	130 (98%)	2 (2%)	0	100	100
1	K	160/430 (37%)	159 (99%)	1 (1%)	0	100	100
1	L	159/430 (37%)	157 (99%)	2 (1%)	0	100	100
1	M	79/430 (18%)	77 (98%)	2 (2%)	0	100	100
1	N	87/430 (20%)	83 (95%)	4 (5%)	0	100	100
1	O	160/430 (37%)	159 (99%)	1 (1%)	0	100	100
1	P	156/430 (36%)	154 (99%)	2 (1%)	0	100	100
1	Q	38/430 (9%)	38 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	46/430 (11%)	46 (100%)	0	0	100	100
1	S	159/430 (37%)	157 (99%)	1 (1%)	1 (1%)	21	59
1	T	155/430 (36%)	154 (99%)	1 (1%)	0	100	100
1	V	3/430 (1%)	3 (100%)	0	0	100	100
1	W	126/430 (29%)	126 (100%)	0	0	100	100
1	X	143/430 (33%)	142 (99%)	1 (1%)	0	100	100
1	a	84/430 (20%)	84 (100%)	0	0	100	100
1	b	98/430 (23%)	94 (96%)	3 (3%)	1 (1%)	12	48
1	e	39/430 (9%)	39 (100%)	0	0	100	100
1	f	56/430 (13%)	53 (95%)	2 (4%)	1 (2%)	6	34
1	j	15/430 (4%)	14 (93%)	1 (7%)	0	100	100
All	All	5036/20210 (25%)	4946 (98%)	78 (2%)	12 (0%)	44	78

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AQ	105	GLU
1	AV	105	GLU
1	D	93	ALA
1	D	103	ALA
1	S	214	GLN

5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

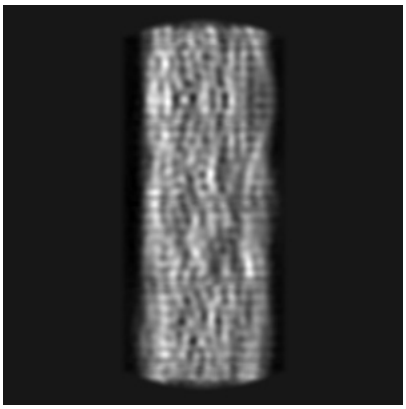
6 Map visualisation (i)

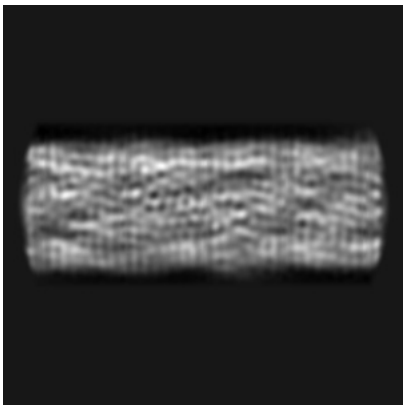
This section contains visualisations of the EMDB entry EMD-55327. These allow visual inspection of the internal detail of the map and identification of artifacts.

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)

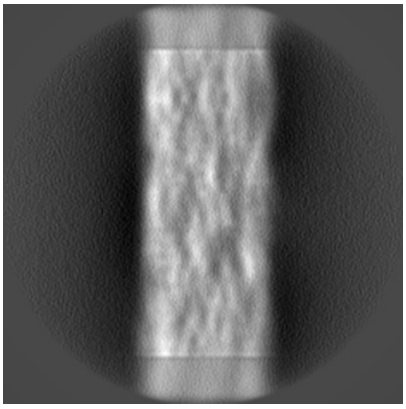
6.1.1 Primary map

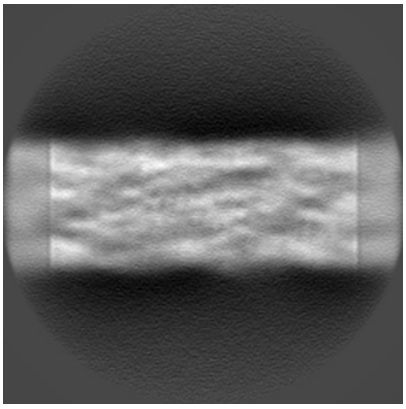

X

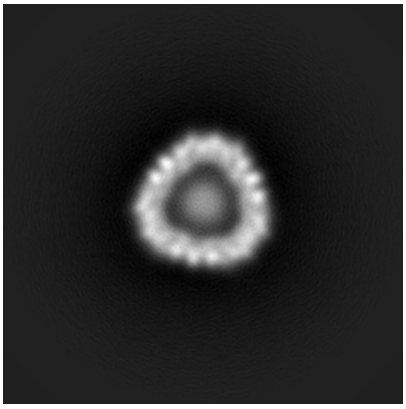

Y

Z

6.1.2 Raw map


X

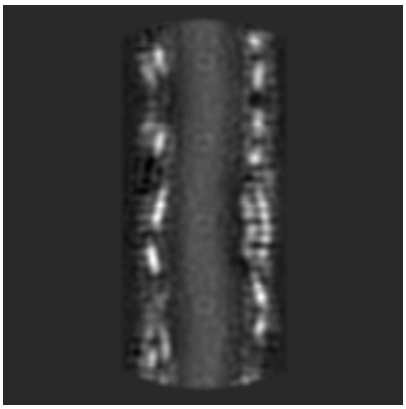

Y

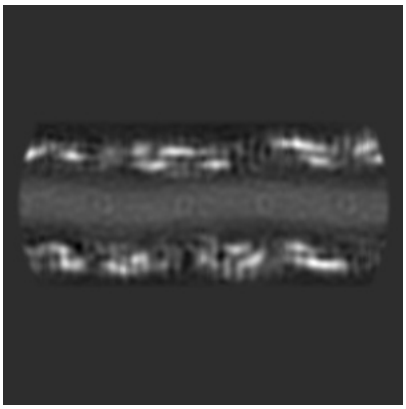

Z

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

6.2 Central slices (i)

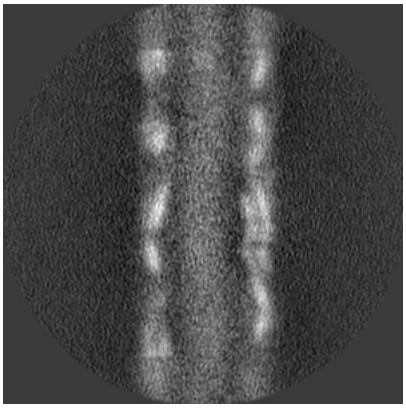
6.2.1 Primary map

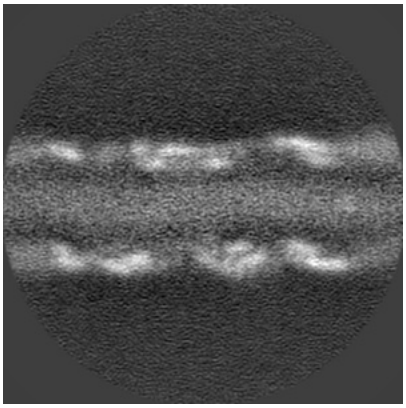

X Index: 116

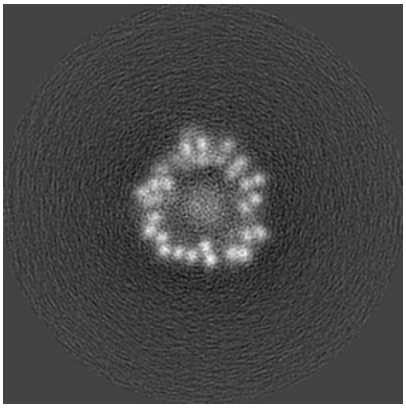

Y Index: 116

Z Index: 116

6.2.2 Raw map


X Index: 116

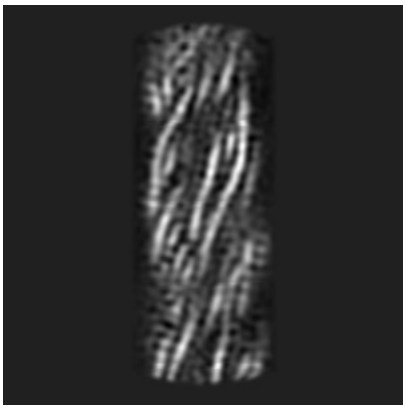

Y Index: 116

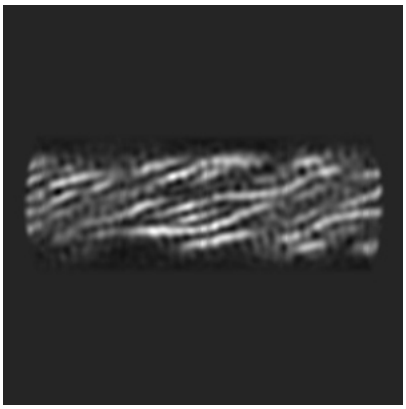

Z Index: 116

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

6.3 Largest variance slices (i)

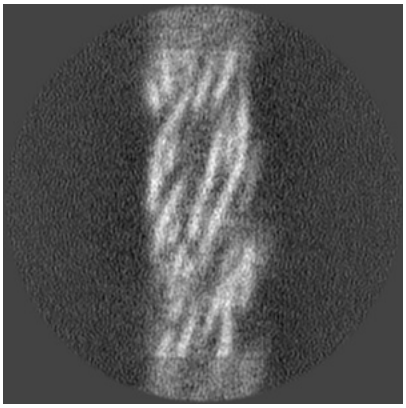
6.3.1 Primary map

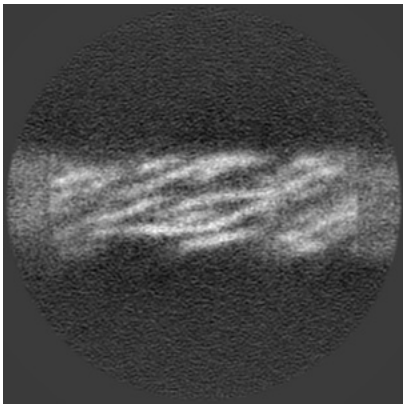

X Index: 140

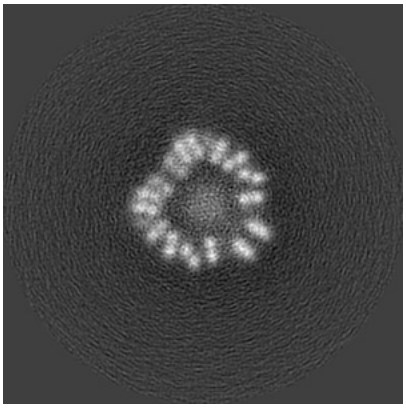

Y Index: 88

Z Index: 82

6.3.2 Raw map


X Index: 141

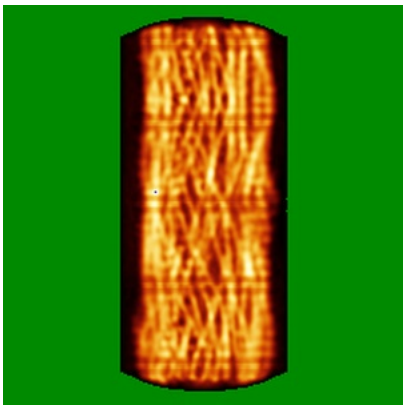

Y Index: 88

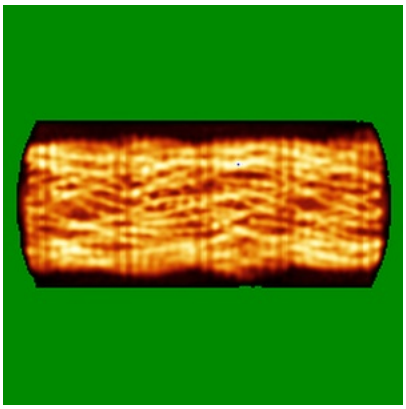

Z Index: 129

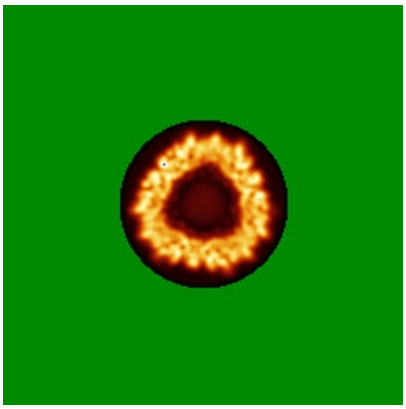
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

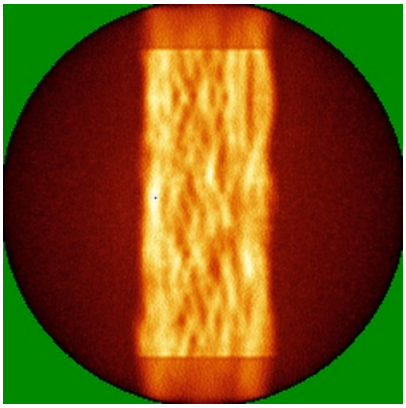
6.4.1 Primary map

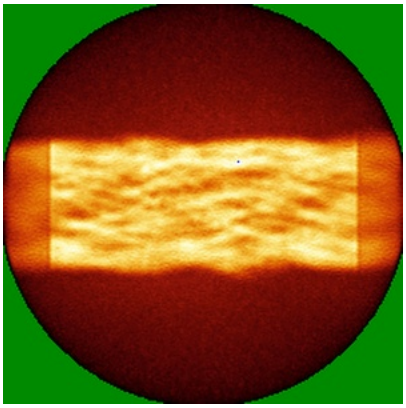

X

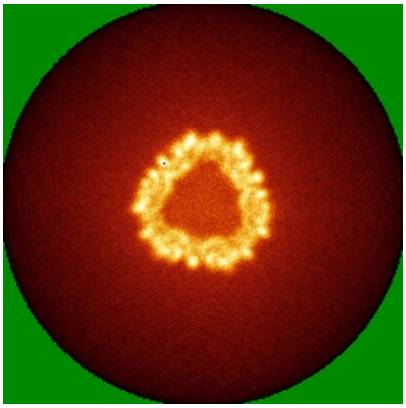

Y


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.

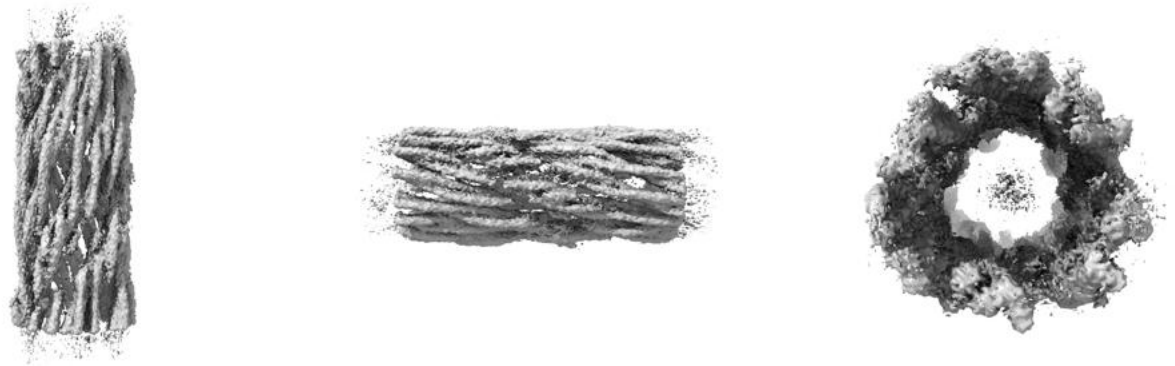
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.007. 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



X Y Z

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.

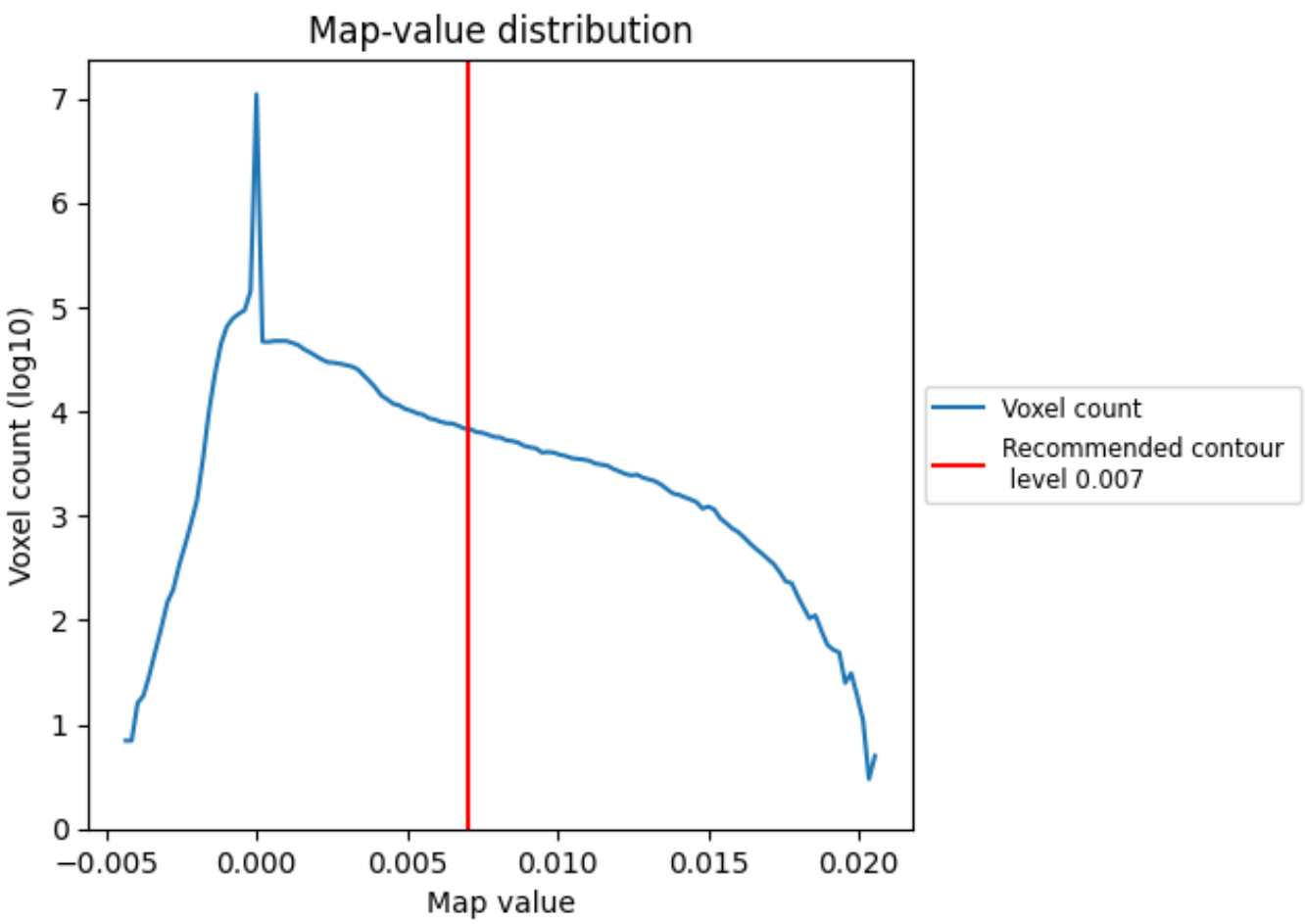
6.6 Mask visualisation (i)

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

7 Map analysis (i)

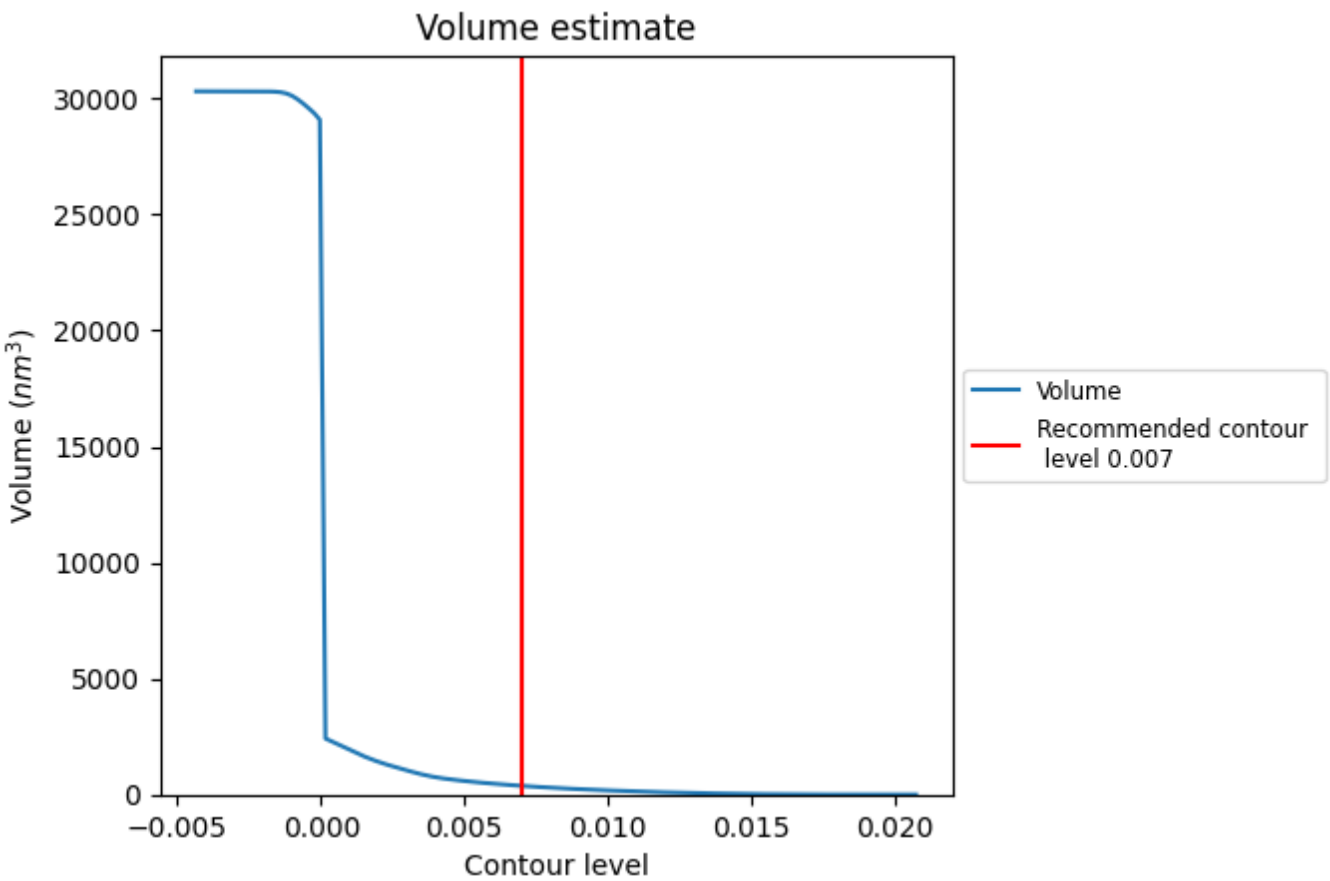
This section contains the results of statistical analysis of the map.

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.

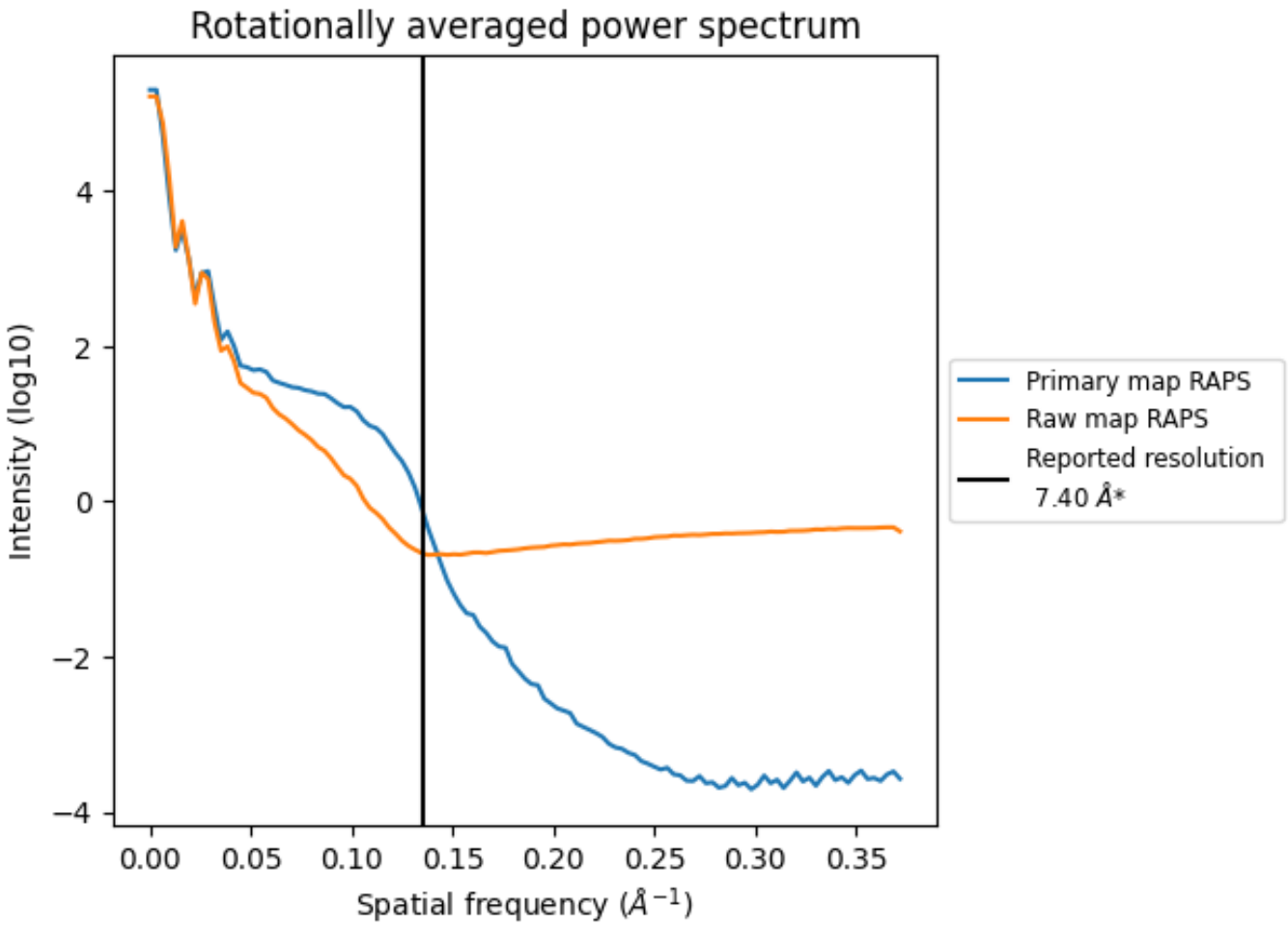
7.2 Volume estimate (i)



The volume at the recommended contour level is 375 nm^3; this corresponds to an approximate mass of 339 kDa.

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

7.3 Rotationally averaged power spectrum (i)

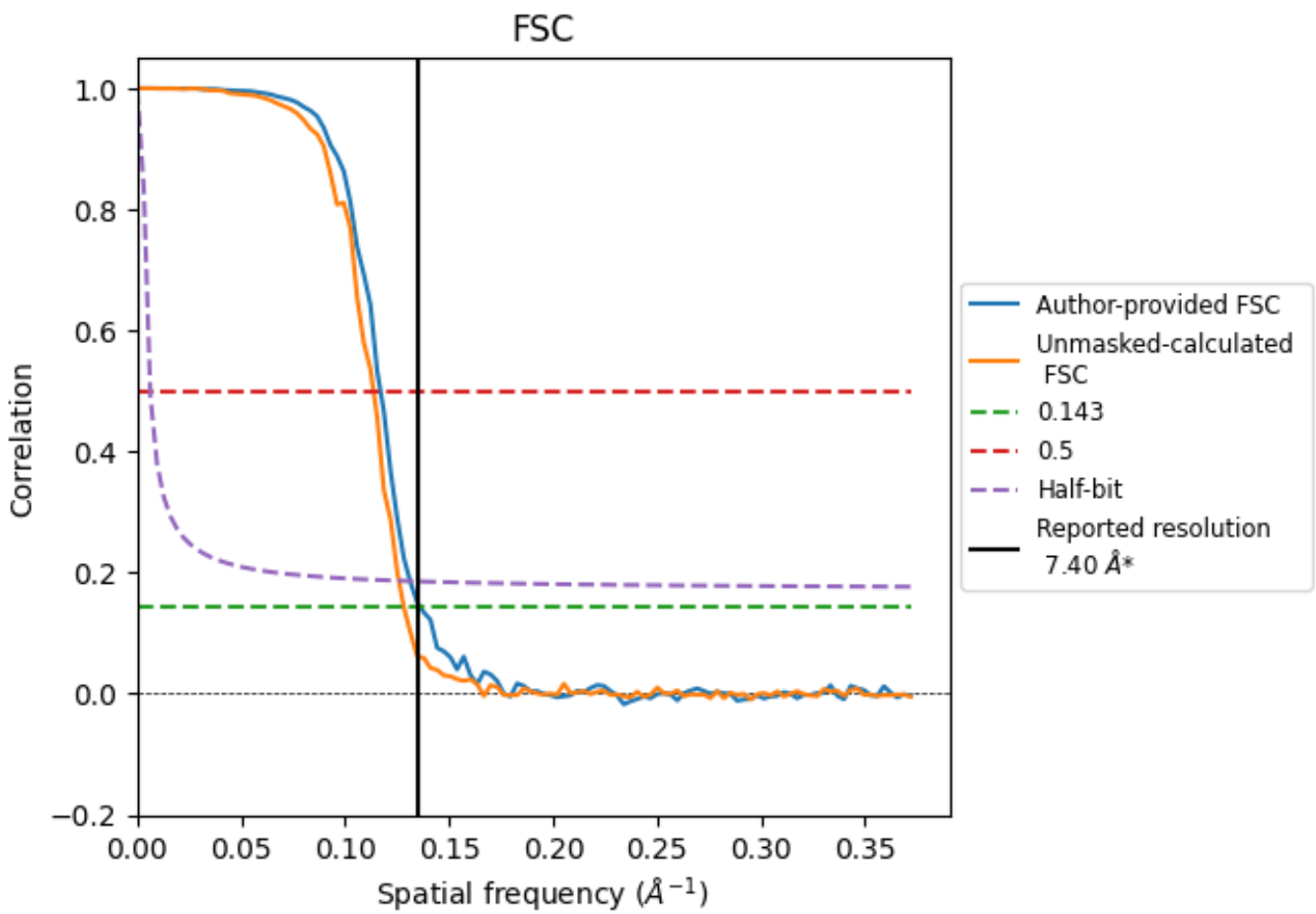


*Reported resolution corresponds to spatial frequency of 0.135 Å^{-1}

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 0.135 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.40	-	-
Author-provided FSC curve	7.34	8.55	7.62
Unmasked-calculated*	7.79	8.80	7.94

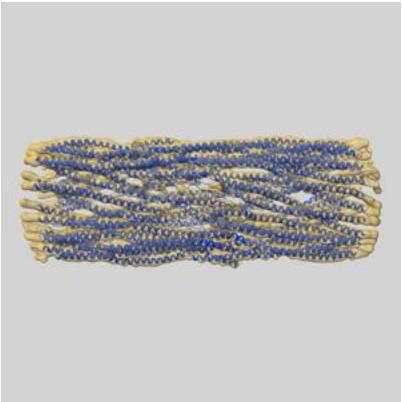
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit (i)

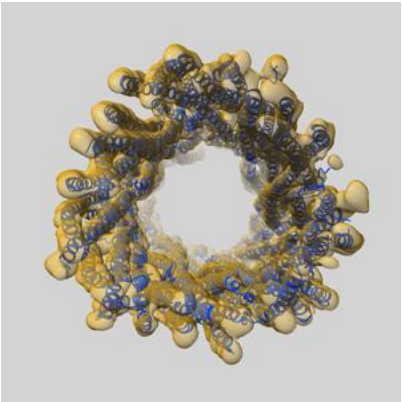
This section contains information regarding the fit between EMDB map EMD-55327 and PDB model 9SWW. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay (i)

X



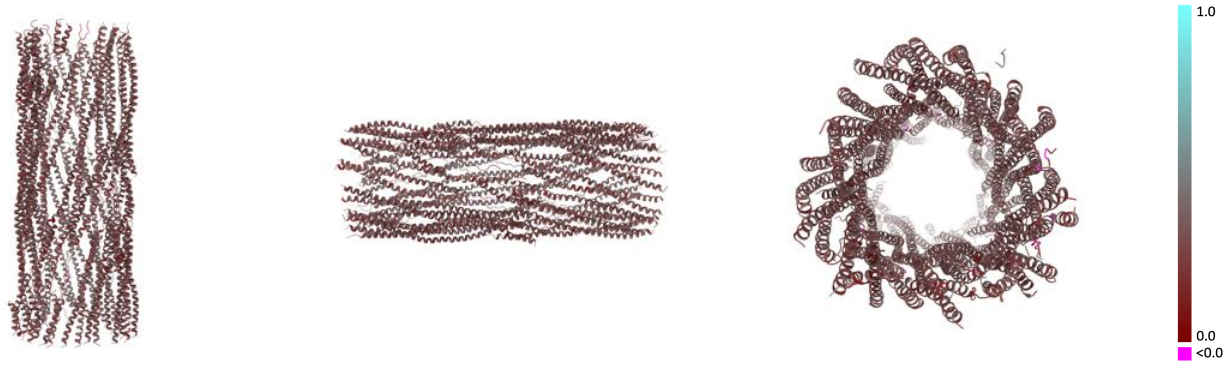
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.007 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.

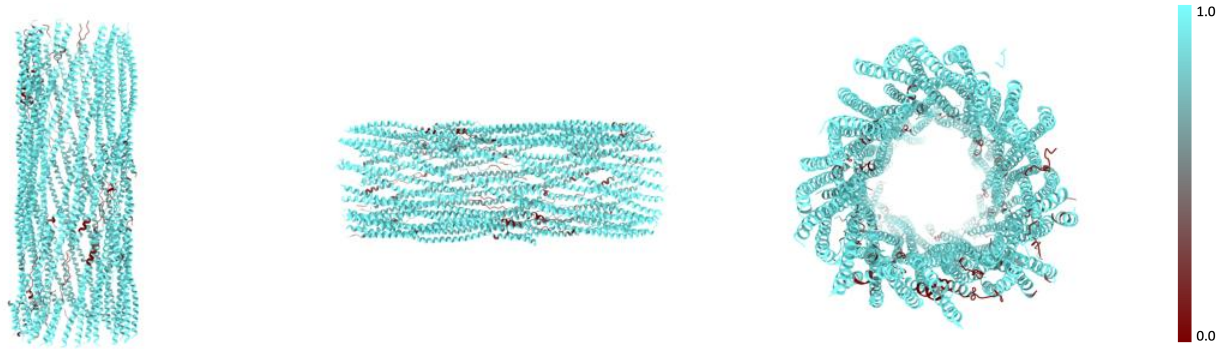
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

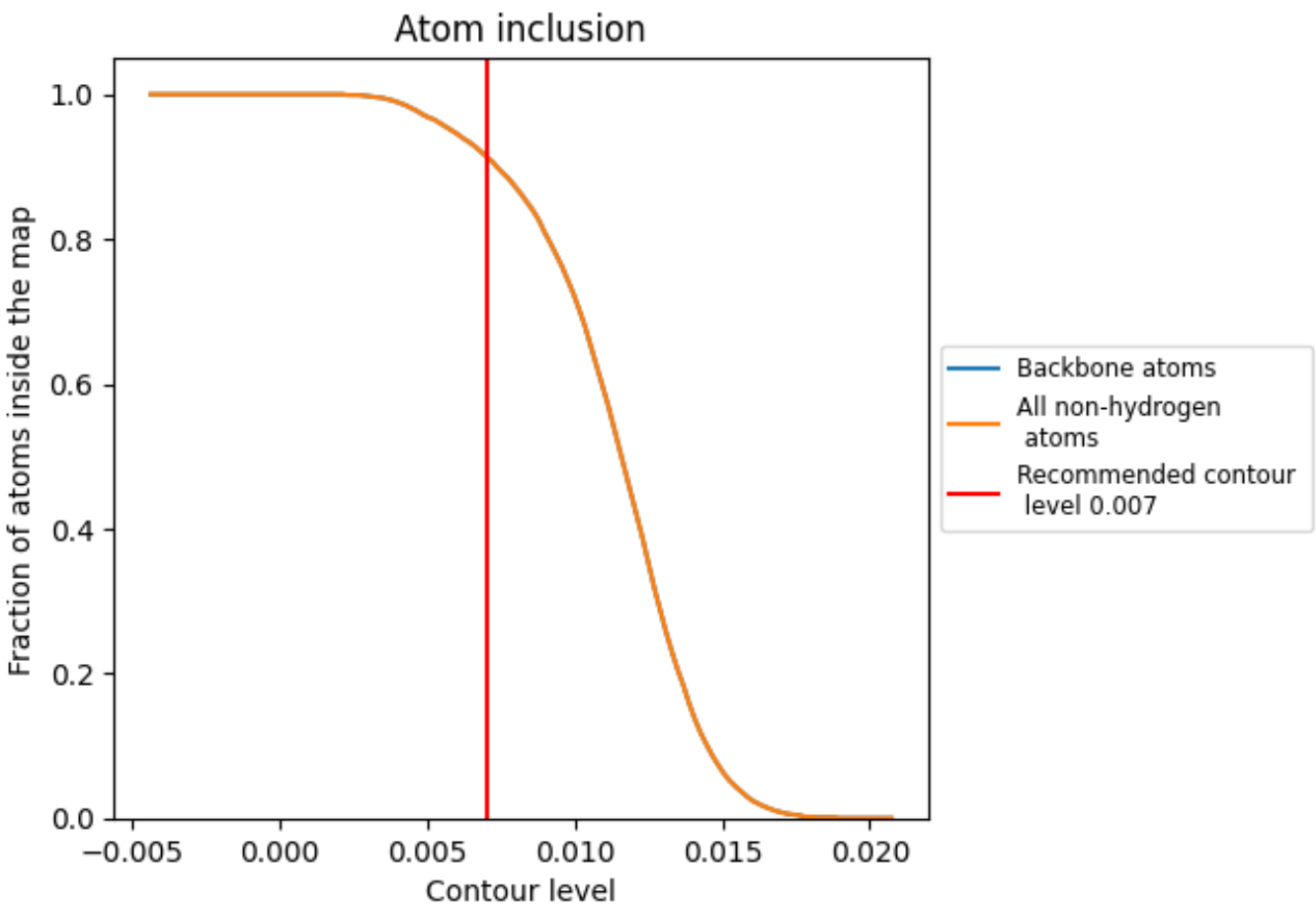
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.007).

9.4 Atom inclusion (i)



At the recommended contour level, 92% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9150	0.3000
0	0.8720	0.3030
6	0.3750	0.2420
9	0.8480	0.2730
A	0.8700	0.2940
AC	0.9350	0.2940
AD	0.8810	0.2870
AG	0.9690	0.2960
AH	0.9210	0.3000
AK	0.9150	0.2960
AL	0.9590	0.3060
AM	0.8700	0.2810
AN	0.9520	0.3160
AO	0.8770	0.2990
AP	0.9260	0.3140
AQ	0.9020	0.2740
AR	0.9640	0.3180
AS	0.8700	0.2990
AT	0.9330	0.3060
AU	0.9460	0.2940
AV	0.9710	0.2950
B	0.9280	0.3030
C	0.9510	0.2970
D	0.9780	0.3050
E	0.9220	0.2910
F	0.9440	0.2990
G	0.8370	0.2890
H	0.8850	0.2940
I	0.9720	0.3100
J	0.9800	0.3100
K	0.8570	0.2970
L	0.9150	0.3040
M	0.9540	0.2970
N	0.9580	0.3080
O	0.8600	0.3020

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
P	0.9110	0.3150
Q	0.9440	0.2960
R	0.9740	0.3100
S	0.8280	0.2900
T	0.9120	0.3000
V	1.0000	0.4070
W	0.9590	0.3030
X	0.9430	0.3000
a	0.9540	0.2990
b	0.9380	0.3080
e	0.8780	0.2970
f	0.8450	0.2790
j	0.5740	0.2140