



## wwPDB EM Validation Summary Report ⓘ

Jul 18, 2024 – 09:49 pm BST

PDB ID : 8RUY  
EMDB ID : EMD-19515  
Title : Structure of IFTA and IFTB in Retrograde Intraflagellar transport trains  
Authors : Lacey, S.; Pigino, G.  
Deposited on : 2024-01-31  
Resolution : 15.40 Å (reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

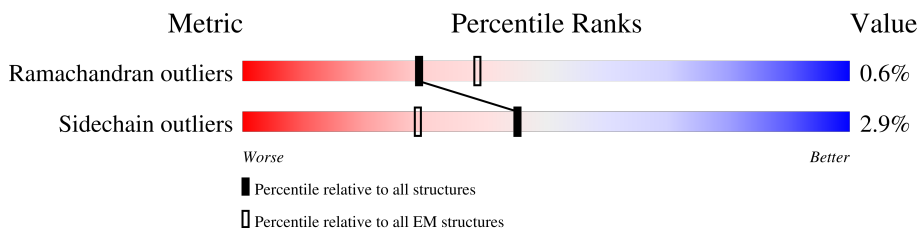
EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

# 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 15.40 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1367	16% (red), 98% (green), . (yellow)
2	B	1409	21% (red), 96% (green), .. (yellow)
3	H	454	19% (red), 93% (green), 6% (yellow)
3	h	454	13% (red), 93% (green), . . (yellow)
4	J	765	7% (red), 97% (green), . (yellow)
4	j	765	15% (red), 96% (green), . (yellow)
5	K	510	. (red), 21% (green), 79% (grey)
5	k	510	. (red), 21% (green), 79% (grey)
6	L	135	7% (red), 82% (green), . (yellow), 16% (grey)

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Mol	Chain	Length	Quality of chain
6	l	135	15% 81% 16%
7	N	443	13% 64% 32%
7	n	443	19% 66% 32%
8	O	641	28% 46% 53%
9	P	683	27% 44% 55%
10	Q	204	39% 97%
11	R	189	26% 69% 28%
12	S	344	22% 36% 61%
12	s	344	13% 41% 59%
13	T	192	28% 98%
14	I	1755	19% 95%
14	i	1755	26% 97%
15	C	1239	16% 96%
16	D	1224	11% 81% 16%
17	E	1355	17% 94%
18	F	782	6% 66% 31%
18	f	782	8% 65% 31%
19	G	647	22% 94%
19	g	647	12% 94%
20	M	469	19% 65% 34%
20	m	469	24% 64% 34%

## 2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 139391 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 Intraflagellar transport protein 144.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1367	10579	6654	1857	1998	70	0	0

- Molecule 2 is a protein called Intraflagellar transport particle protein 140.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	1374	10764	6763	1893	2029	79	0	0

- Molecule 3 is a protein called Osm-6-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	H	454	3553	2269	591	680	13	0	0
3	h	440	3443	2199	574	657	13	0	0

- Molecule 4 is a protein called Intraflagellar transport protein 80.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	J	765	6025	3807	1053	1132	33	0	0
4	j	765	6025	3807	1053	1132	33	0	0

- Molecule 5 is a protein called IFT54.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	K	106	849	524	155	164	6	0	0
5	k	106	849	524	155	164	6	0	0

- Molecule 6 is a protein called Intraflagellar transport particle protein IFT20.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	114	Total	C	N	O	S	0	0
			919	562	166	187	4		
6	l	114	Total	C	N	O	S	0	0
			919	562	166	187	4		

- Molecule 7 is a protein called Clusterin-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	N	303	Total	C	N	O	S	0	0
			2472	1547	439	476	10		
7	n	303	Total	C	N	O	S	0	0
			2472	1547	439	476	10		

- Molecule 8 is a protein called Intraflagellar transport protein 74.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	299	Total	C	N	O	S	0	0
			2411	1485	437	474	15		

- Molecule 9 is a protein called Intraflagellar transport protein 81.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	P	306	Total	C	N	O	S	0	0
			2439	1512	436	482	9		

- Molecule 10 is a protein called Intraflagellar transport protein 27.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	204	Total	C	N	O	S	0	0
			1602	1025	262	307	8		

- Molecule 11 is a protein called Intraflagellar transport protein 25.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	R	136	Total	C	N	O	S	0	0
			1086	681	190	208	7		

- Molecule 12 is a protein called Intraflagellar transport protein 46.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	S	133	1045	666	172	197	10	0	0
12	s	141	1138	727	190	213	8	0	0

- Molecule 13 is a protein called Intraflagellar transport protein 22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	T	192	1500	946	261	285	8	0	0

- Molecule 14 is a protein called Intraflagellar transport protein 172.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	i	1755	13906	8752	2439	2639	76	0	0
14	I	1714	13615	8578	2384	2577	76	0	0

- Molecule 15 is a protein called Intraflagellar transport protein 122 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	C	1210	9609	6108	1671	1773	57	0	0

- Molecule 16 is a protein called Intraflagellar transport protein 121.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	D	1027	8154	5184	1401	1509	60	0	0

- Molecule 17 is a protein called Intraflagellar transport protein 139.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	E	1325	10464	6587	1860	1956	61	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	188	GLN	GLU	variant	UNP A9XPA6

- Molecule 18 is a protein called IFT88.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	F	539	4337	2747	762	795	33	0	0
18	f	538	4328	2741	760	794	33	0	0

- Molecule 19 is a protein called IFT70.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	G	619	4978	3171	826	948	33	0	0
19	g	619	4978	3171	826	948	33	0	0

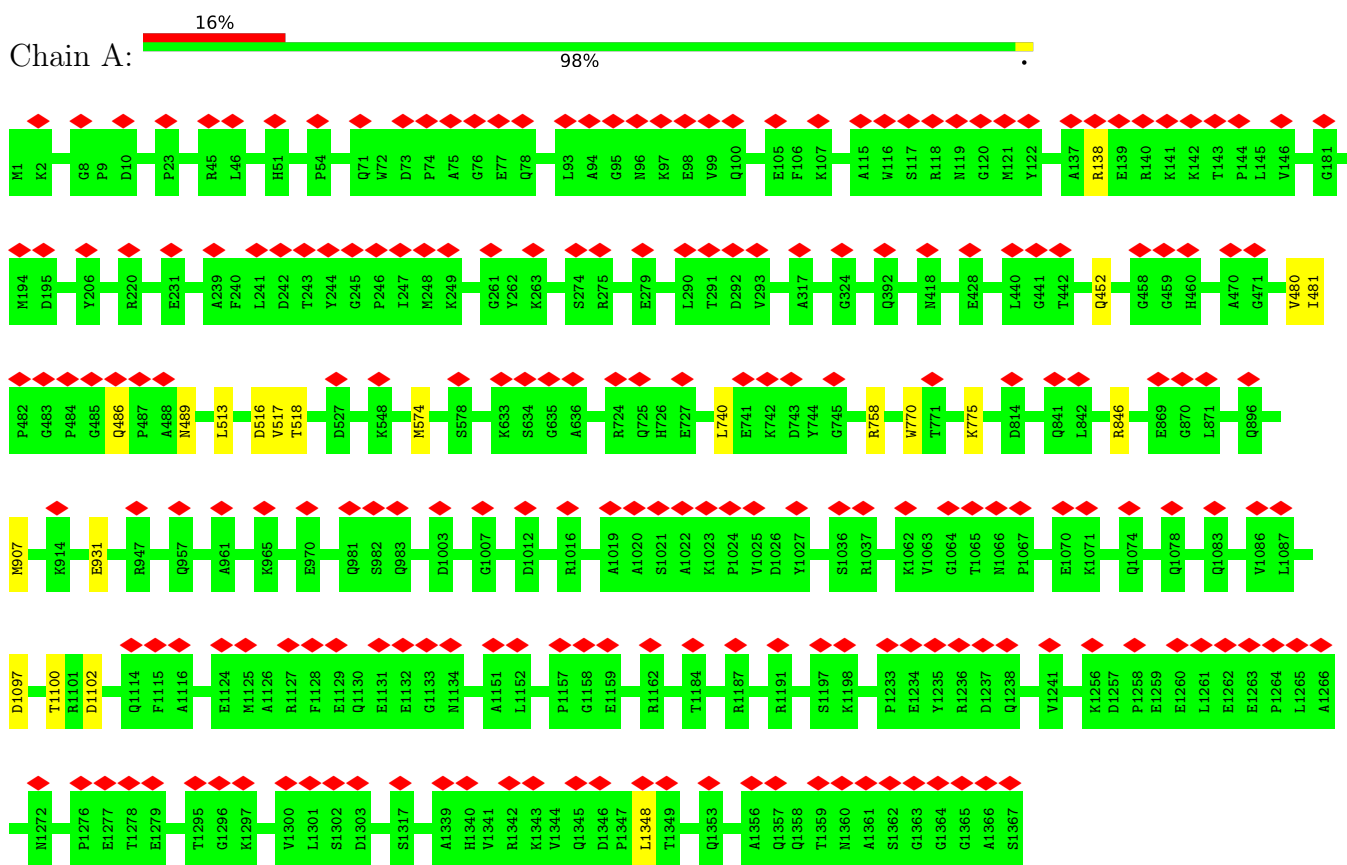
- Molecule 20 is a protein called Intraflagellar transport protein 57.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	M	309	2466	1552	438	466	10	0	0
20	m	309	2466	1552	438	466	10	0	0

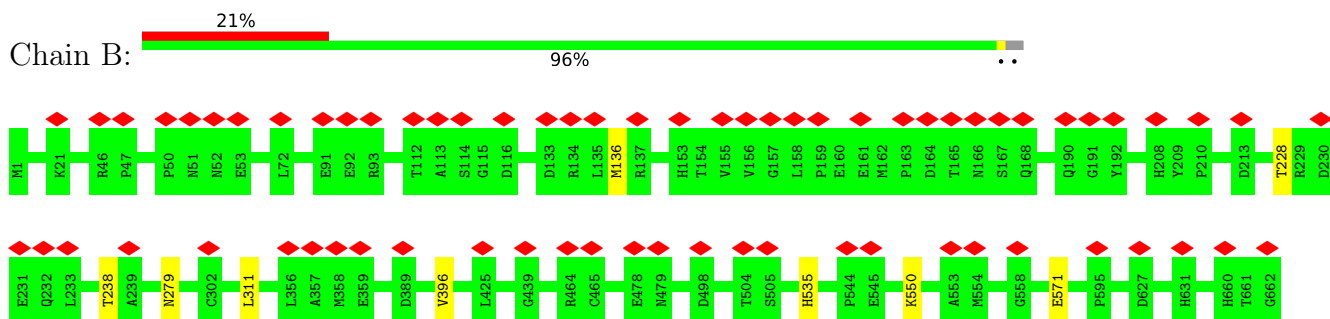
### 3 Residue-property plots [i](#)

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.

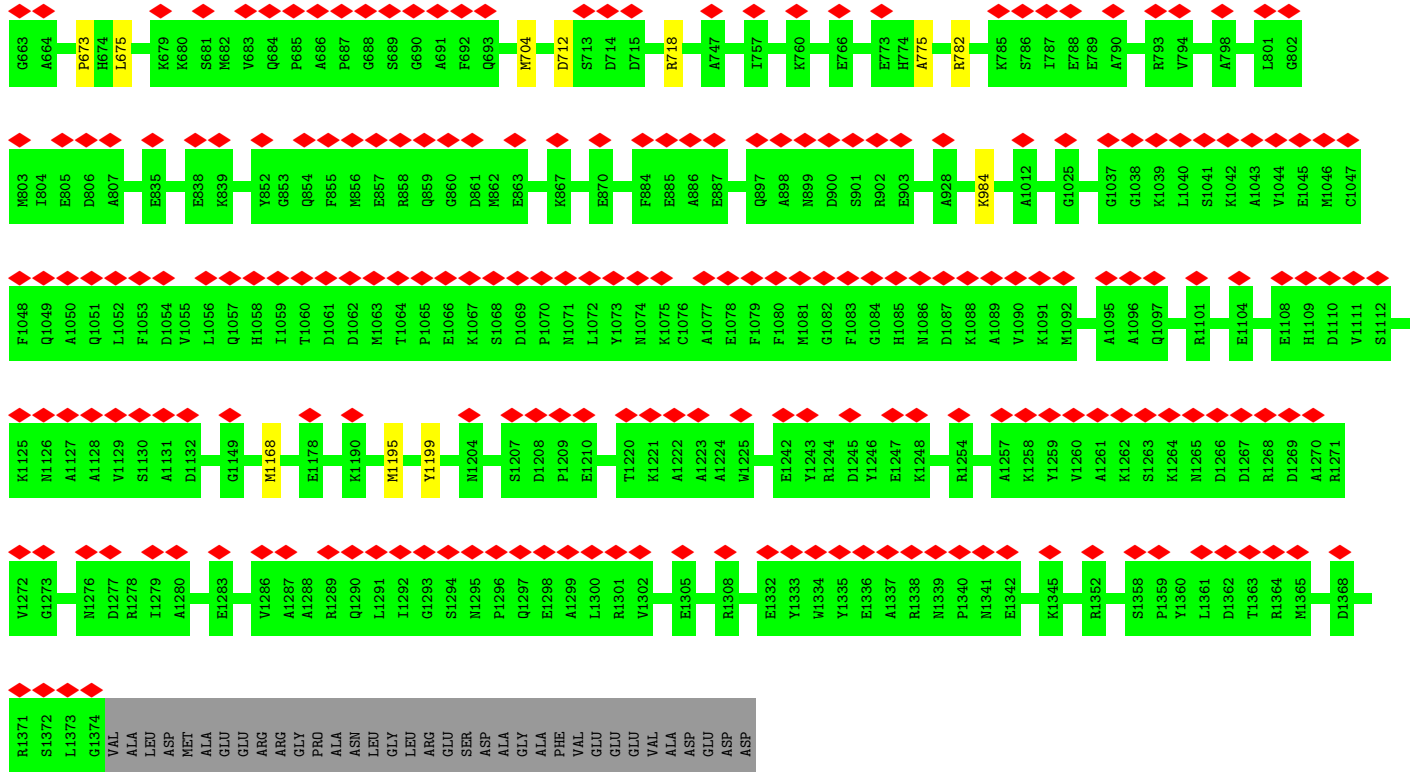
- Molecule 1: Intraflagellar transport protein 144



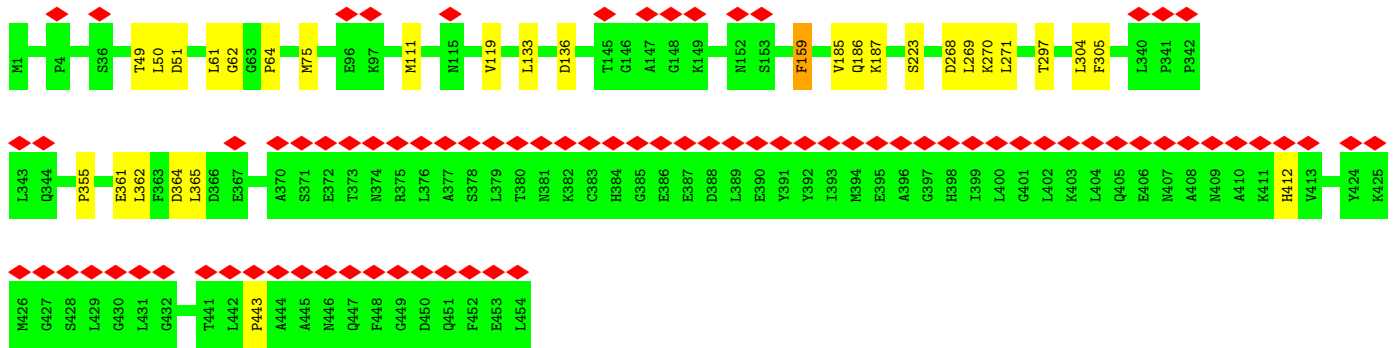
- Molecule 2: Intraflagellar transport particle protein 140



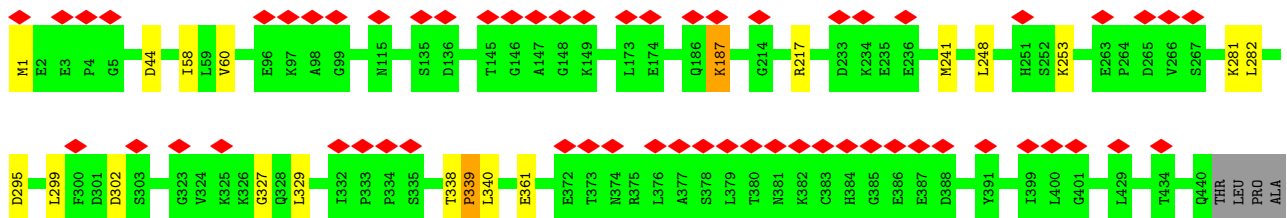




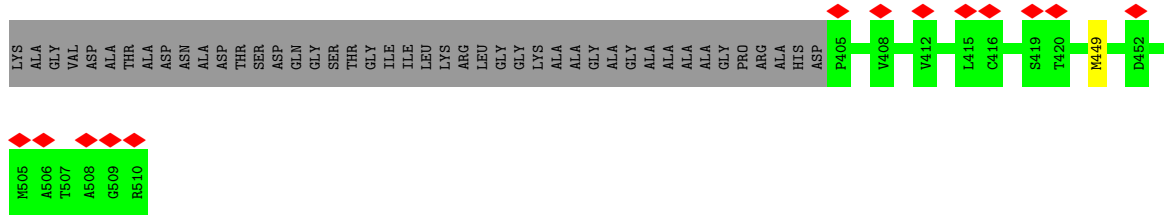
• Molecule 3: Osm-6-like protein



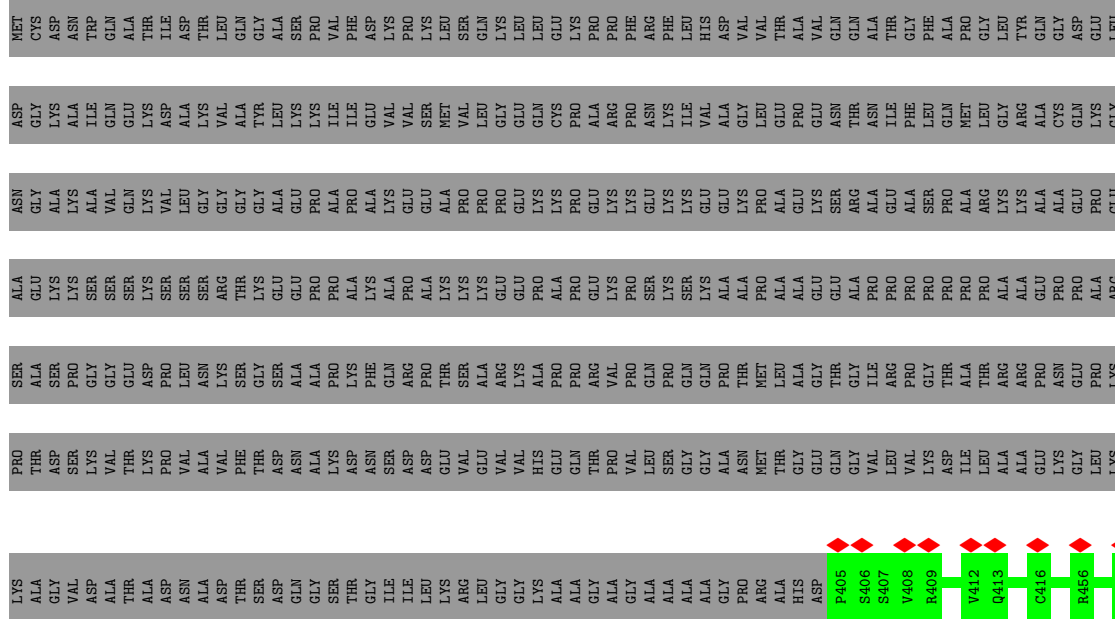
• Molecule 3: Osm-6-like protein



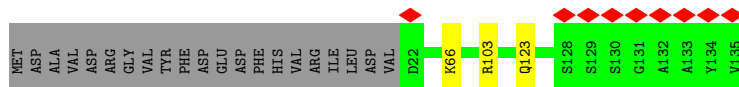
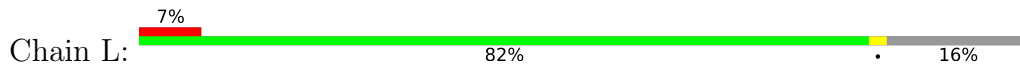




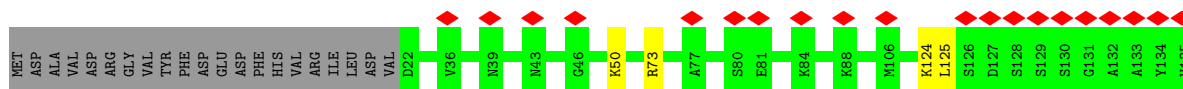
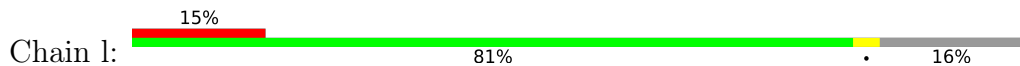
• Molecule 5: IFT54



• Molecule 6: Intraflagellar transport particle protein IFT20

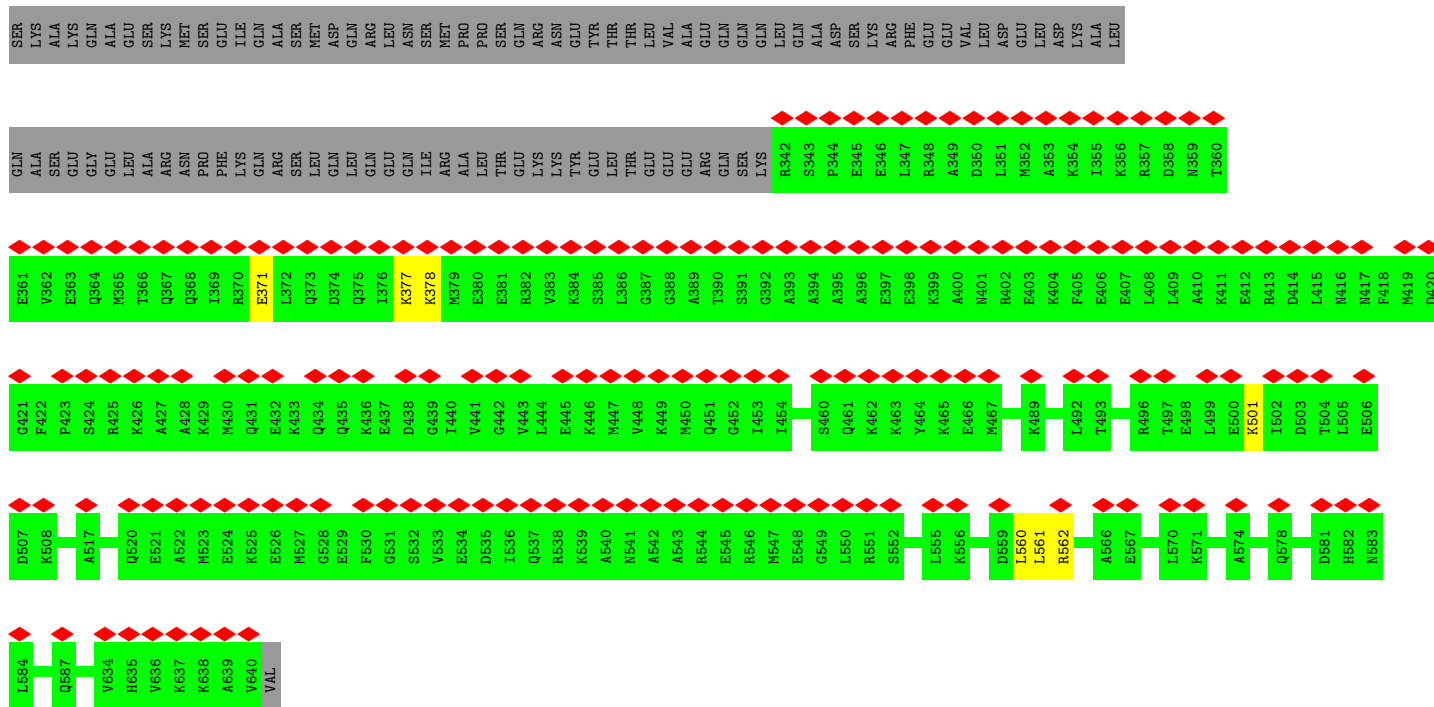


• Molecule 6: Intraflagellar transport particle protein IFT20

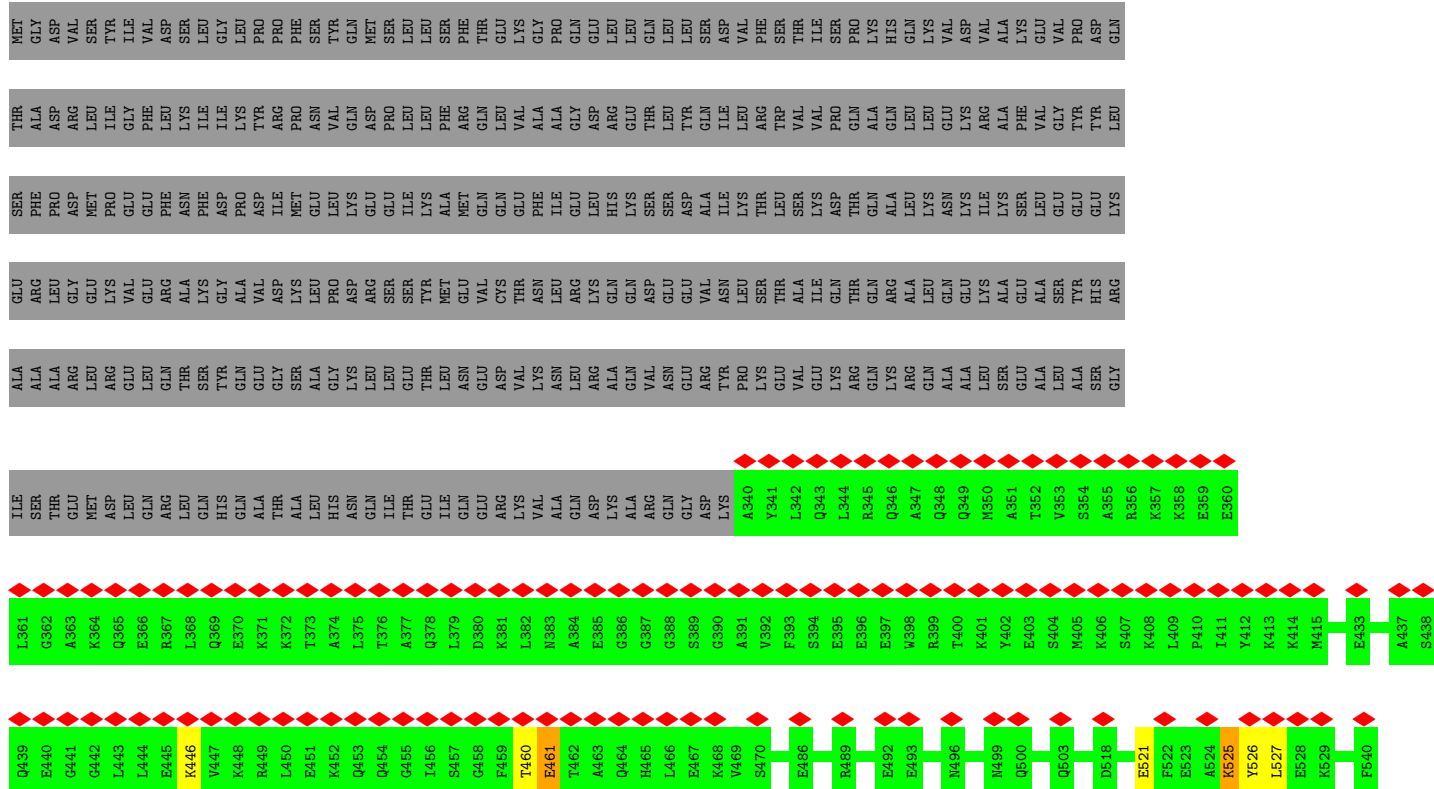


• Molecule 7: Clusterin-associated protein 1



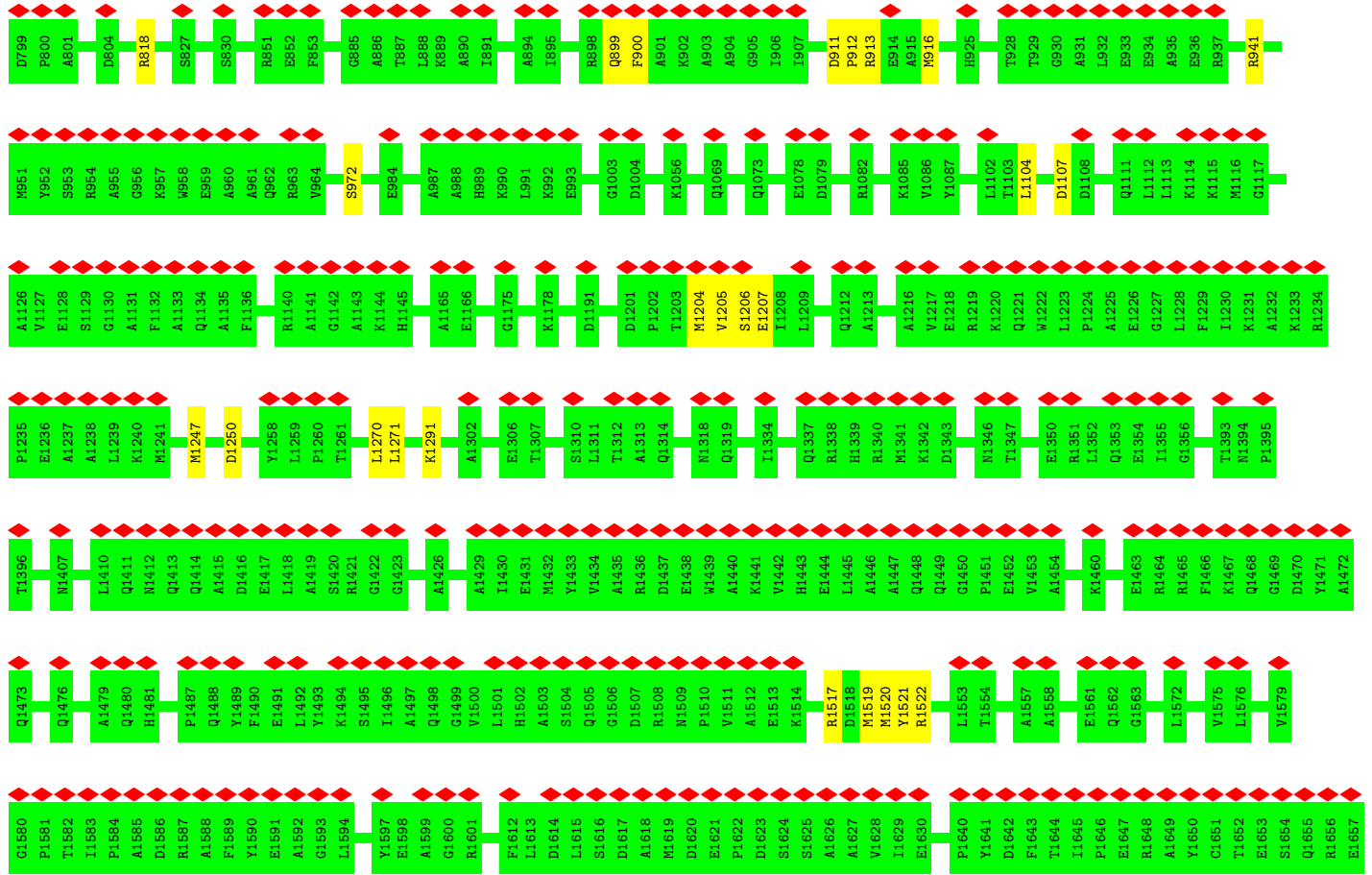


• Molecule 9: Intraflagellar transport protein 81

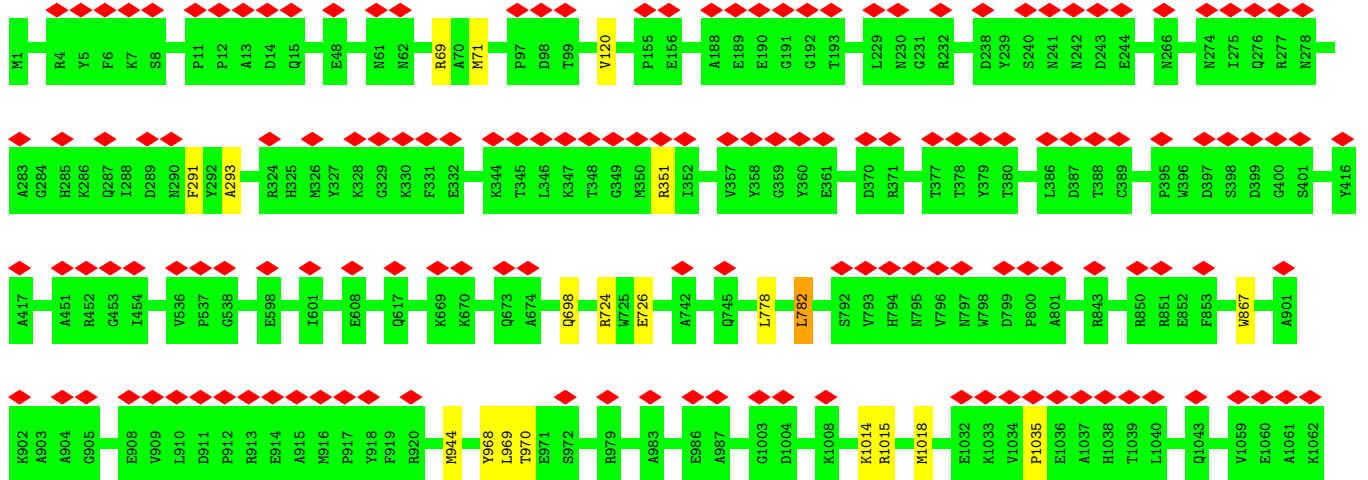
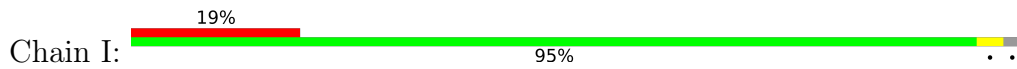




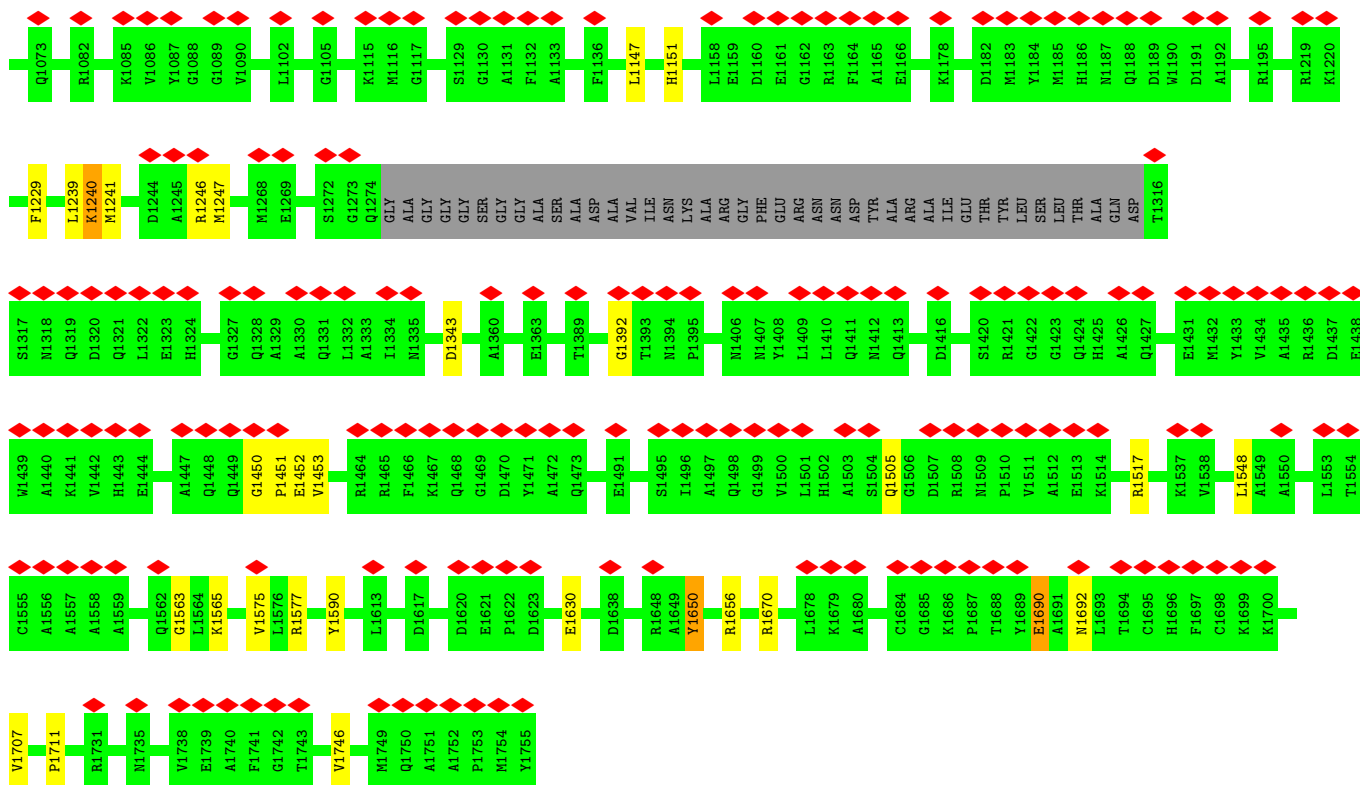




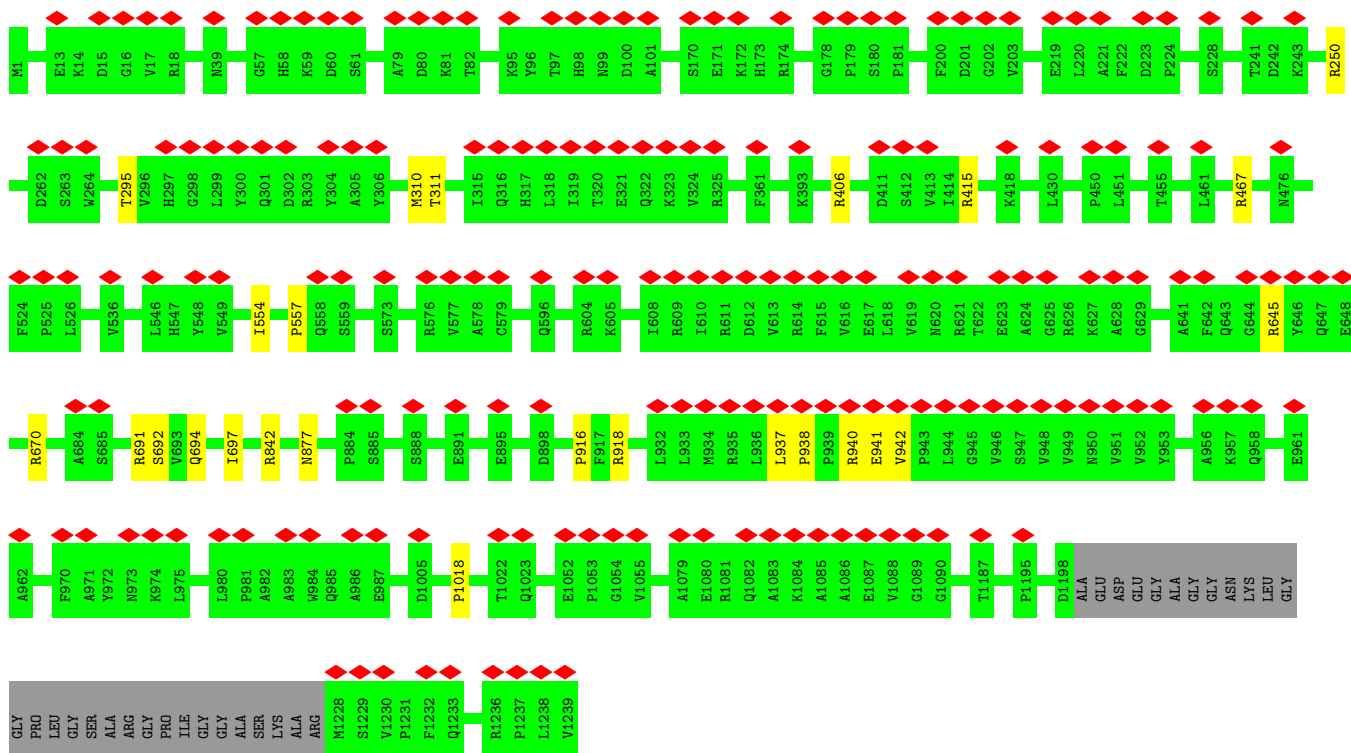
• Molecule 14: Intraflagellar transport protein 172







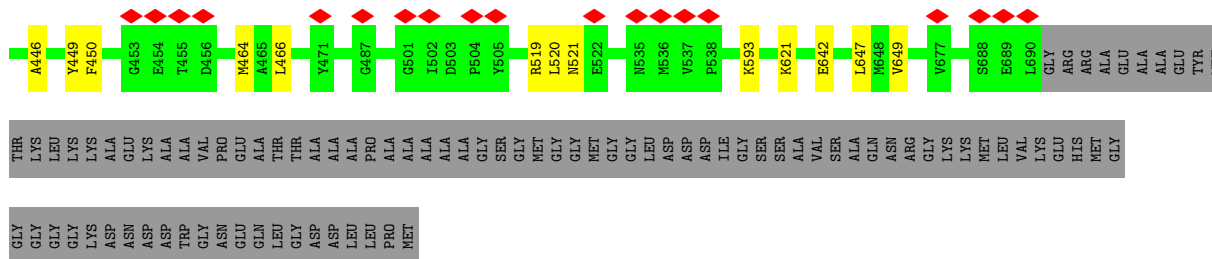
• Molecule 15: Intraflagellar transport protein 122 homolog



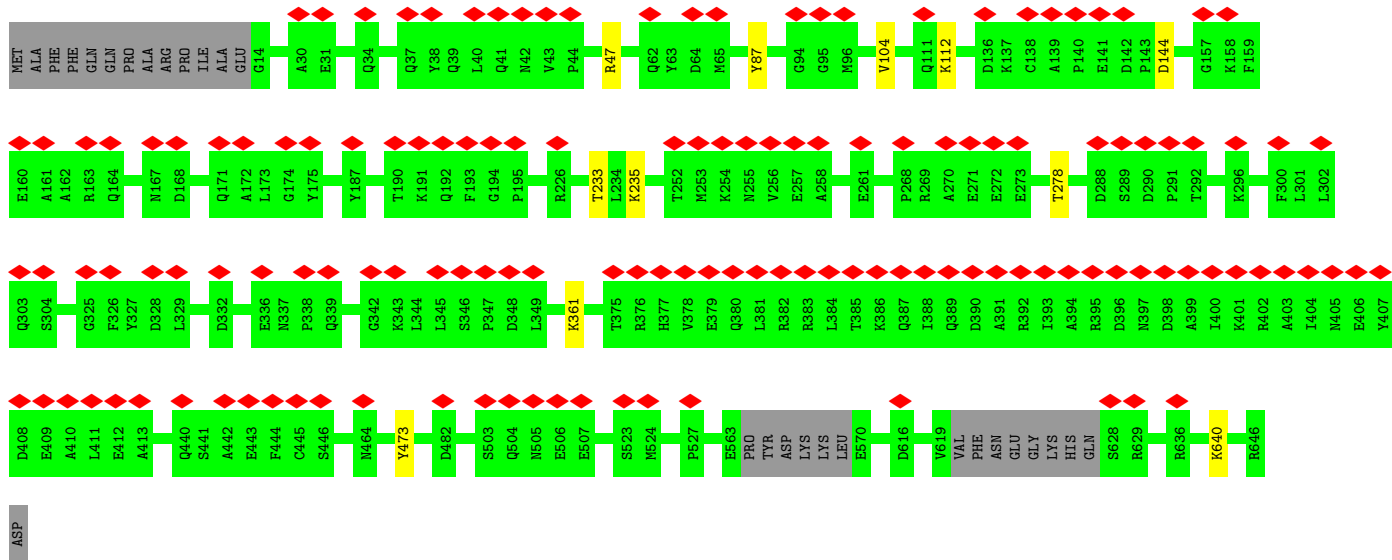
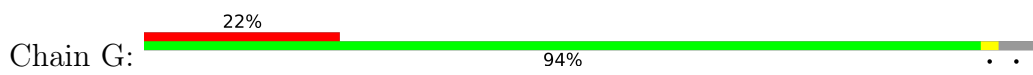
• Molecule 16: Intraflagellar transport protein 121



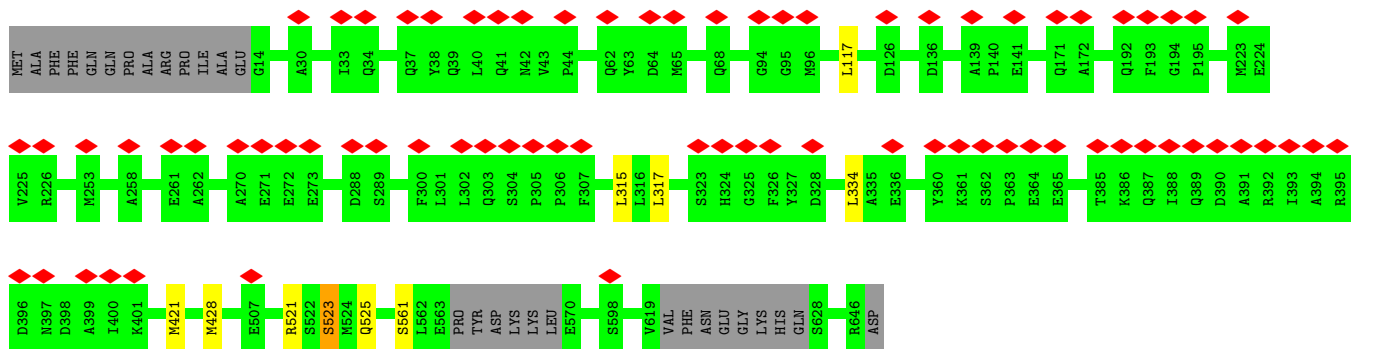
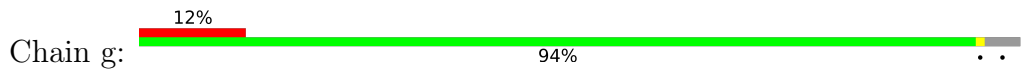




• Molecule 19: IFT70



• Molecule 19: IFT70



• Molecule 20: Intraflagellar transport protein 57





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of subtomograms used	5896	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	104	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	11.329	Depositor
Minimum map value	0.000	Depositor
Average map value	0.045	Depositor
Map value standard deviation	0.478	Depositor
Recommended contour level	4.5	Depositor
Map size ( $\text{\AA}$ )	1357.44, 2090.7, 1357.44	wwPDB
Map dimensions	224, 345, 224	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	6.06, 6.06, 6.06	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.36	0/10781	0.65	0/14601
2	B	0.36	0/10982	0.65	0/14878
3	H	0.41	0/3635	0.69	0/4918
3	h	0.39	0/3522	0.70	0/4765
4	J	0.40	0/6147	0.69	0/8333
4	j	0.37	0/6147	0.70	1/8333 (0.0%)
5	K	0.31	0/857	0.69	0/1144
5	k	0.30	0/857	0.61	0/1144
6	L	0.36	0/922	0.65	0/1226
6	l	0.37	0/922	0.63	0/1226
7	N	0.41	0/2504	0.69	0/3356
7	n	0.38	0/2504	0.66	0/3356
8	O	0.36	0/2425	0.71	0/3223
9	P	0.37	0/2462	0.67	0/3290
10	Q	0.41	0/1637	0.63	0/2224
11	R	0.36	0/1103	0.67	0/1485
12	S	0.42	0/1068	0.73	0/1441
12	s	0.31	0/1164	0.66	0/1579
13	T	0.34	0/1528	0.63	0/2066
14	I	0.40	0/13910	0.68	0/18827
14	i	0.34	0/14205	0.64	0/19226
15	C	0.34	0/9820	0.62	0/13292
16	D	0.38	0/8336	0.67	1/11273 (0.0%)
17	E	0.39	0/10649	0.69	0/14397
18	F	0.41	0/4423	0.70	0/5956
18	f	0.39	0/4414	0.67	0/5945
19	G	0.40	0/5080	0.70	0/6863
19	g	0.37	0/5080	0.65	0/6863
20	M	0.34	0/2510	0.61	0/3385
20	m	0.31	0/2510	0.61	0/3385
All	All	0.37	0/142104	0.67	2/192000 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	j	665	ARG	N-CA-C	-5.25	96.81	111.00
16	D	619	PRO	N-CA-CB	-5.09	97.00	102.60

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	A	1365/1367 (100%)	1263 (92%)	99 (7%)	3 (0%)	47	81
2	B	1372/1409 (97%)	1244 (91%)	122 (9%)	6 (0%)	34	72
3	H	452/454 (100%)	361 (80%)	80 (18%)	11 (2%)	6	33
3	h	438/454 (96%)	370 (84%)	63 (14%)	5 (1%)	14	52
4	J	763/765 (100%)	652 (86%)	107 (14%)	4 (0%)	29	69
4	j	763/765 (100%)	658 (86%)	101 (13%)	4 (0%)	29	69
5	K	104/510 (20%)	101 (97%)	3 (3%)	0	100	100
5	k	104/510 (20%)	100 (96%)	4 (4%)	0	100	100
6	L	112/135 (83%)	111 (99%)	1 (1%)	0	100	100
6	l	112/135 (83%)	107 (96%)	5 (4%)	0	100	100
7	N	301/443 (68%)	267 (89%)	32 (11%)	2 (1%)	22	63
7	n	301/443 (68%)	274 (91%)	25 (8%)	2 (1%)	22	63
8	O	297/641 (46%)	285 (96%)	12 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	P	304/683 (44%)	288 (95%)	13 (4%)	3 (1%)	15	55
10	Q	202/204 (99%)	175 (87%)	25 (12%)	2 (1%)	15	55
11	R	134/189 (71%)	119 (89%)	13 (10%)	2 (2%)	10	46
12	S	131/344 (38%)	110 (84%)	19 (14%)	2 (2%)	10	46
12	s	139/344 (40%)	131 (94%)	8 (6%)	0	100	100
13	T	190/192 (99%)	178 (94%)	11 (6%)	1 (0%)	29	69
14	I	1710/1755 (97%)	1505 (88%)	191 (11%)	14 (1%)	19	60
14	i	1753/1755 (100%)	1554 (89%)	191 (11%)	8 (0%)	29	69
15	C	1206/1239 (97%)	1076 (89%)	120 (10%)	10 (1%)	19	60
16	D	1017/1224 (83%)	872 (86%)	136 (13%)	9 (1%)	17	57
17	E	1321/1355 (98%)	1148 (87%)	165 (12%)	8 (1%)	25	66
18	F	535/782 (68%)	468 (88%)	60 (11%)	7 (1%)	12	48
18	f	534/782 (68%)	470 (88%)	62 (12%)	2 (0%)	34	72
19	G	613/647 (95%)	567 (92%)	46 (8%)	0	100	100
19	g	613/647 (95%)	544 (89%)	67 (11%)	2 (0%)	41	77
20	M	305/469 (65%)	285 (93%)	20 (7%)	0	100	100
20	m	305/469 (65%)	274 (90%)	29 (10%)	2 (1%)	22	63
All	All	17496/21111 (83%)	15557 (89%)	1830 (10%)	109 (1%)	29	66

5 of 109 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	297	THR
3	H	412	HIS
4	J	315	MET
9	P	525	LYS
3	h	187	LYS

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1119/1119 (100%)	1100 (98%)	19 (2%)	60	78
2	B	1136/1162 (98%)	1122 (99%)	14 (1%)	71	83
3	H	388/388 (100%)	368 (95%)	20 (5%)	23	48
3	h	377/388 (97%)	360 (96%)	17 (4%)	27	52
4	J	648/648 (100%)	630 (97%)	18 (3%)	43	65
4	j	648/648 (100%)	620 (96%)	28 (4%)	29	53
5	K	90/401 (22%)	89 (99%)	1 (1%)	73	84
5	k	90/401 (22%)	90 (100%)	0	100	100
6	L	101/120 (84%)	98 (97%)	3 (3%)	41	63
6	l	101/120 (84%)	97 (96%)	4 (4%)	31	55
7	N	261/358 (73%)	242 (93%)	19 (7%)	14	39
7	n	261/358 (73%)	253 (97%)	8 (3%)	40	62
8	O	260/526 (49%)	253 (97%)	7 (3%)	44	65
9	P	262/581 (45%)	255 (97%)	7 (3%)	44	65
10	Q	176/176 (100%)	172 (98%)	4 (2%)	50	70
11	R	121/147 (82%)	118 (98%)	3 (2%)	47	68
12	S	114/288 (40%)	107 (94%)	7 (6%)	18	44
12	s	128/288 (44%)	127 (99%)	1 (1%)	81	89
13	T	159/159 (100%)	156 (98%)	3 (2%)	57	75
14	I	1405/1431 (98%)	1364 (97%)	41 (3%)	42	64
14	i	1431/1431 (100%)	1389 (97%)	42 (3%)	42	64
15	C	1020/1035 (99%)	1005 (98%)	15 (2%)	65	80
16	D	865/1005 (86%)	842 (97%)	23 (3%)	44	65
17	E	1092/1114 (98%)	1050 (96%)	42 (4%)	33	57
18	F	457/627 (73%)	440 (96%)	17 (4%)	34	58
18	f	456/627 (73%)	428 (94%)	28 (6%)	18	44
19	G	534/558 (96%)	523 (98%)	11 (2%)	53	72
19	g	534/558 (96%)	525 (98%)	9 (2%)	60	78
20	M	268/381 (70%)	263 (98%)	5 (2%)	57	75
20	m	268/381 (70%)	258 (96%)	10 (4%)	34	58
All	All	14770/17424 (85%)	14344 (97%)	426 (3%)	45	64

5 of 426 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	C	645	ARG
17	E	887	LEU
18	f	519	ARG
15	C	941	GLU
16	D	1060	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
17	E	608	GLN
19	G	148	ASN
17	E	642	GLN
17	E	1278	GLN
14	I	1151	HIS

### 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 monosaccharides 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.

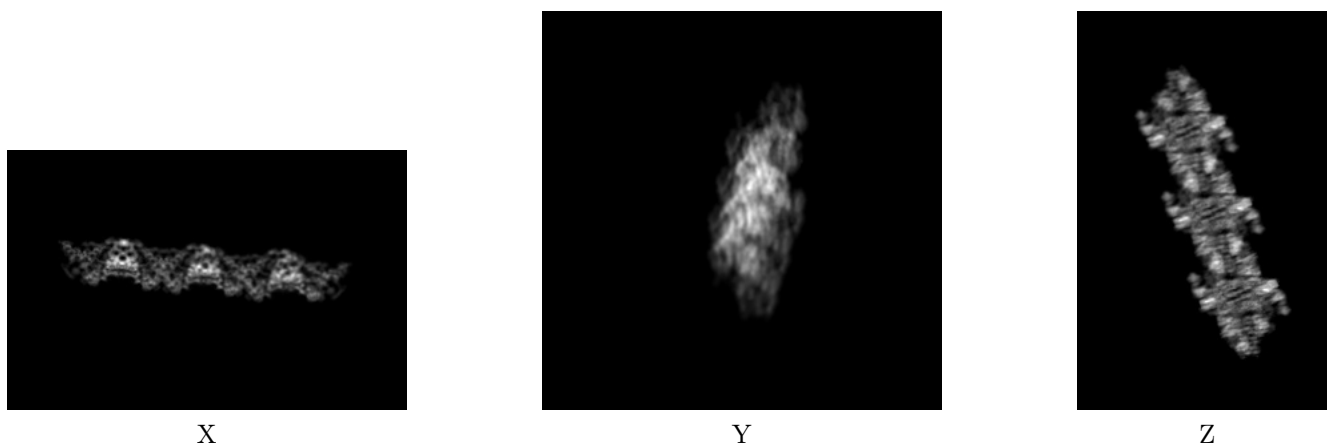
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19515. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

### 6.1 Orthogonal projections [i](#)

#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

#### 6.2.1 Primary map



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

## 6.3 Largest variance slices [\(i\)](#)

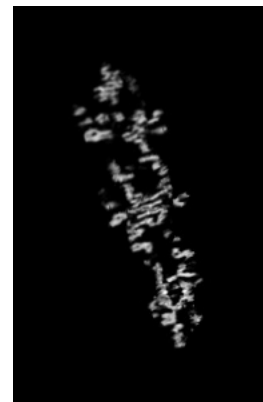
### 6.3.1 Primary map



X Index: 117



Y Index: 104

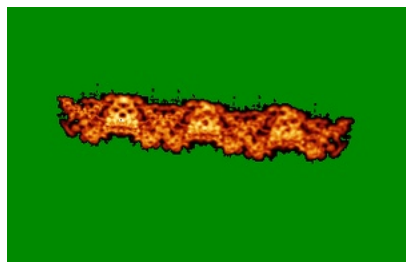


Z Index: 117

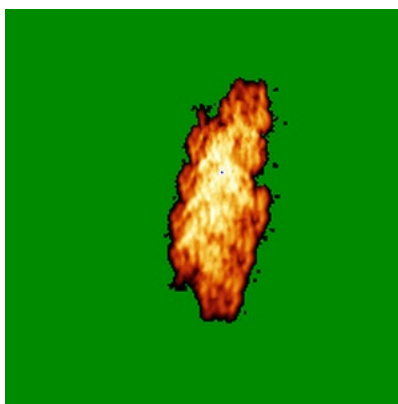
The images above show the largest variance slices of the map in three orthogonal directions.

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

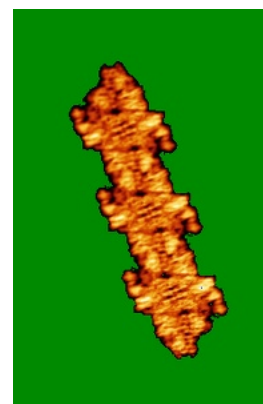
### 6.4.1 Primary map



X



Y

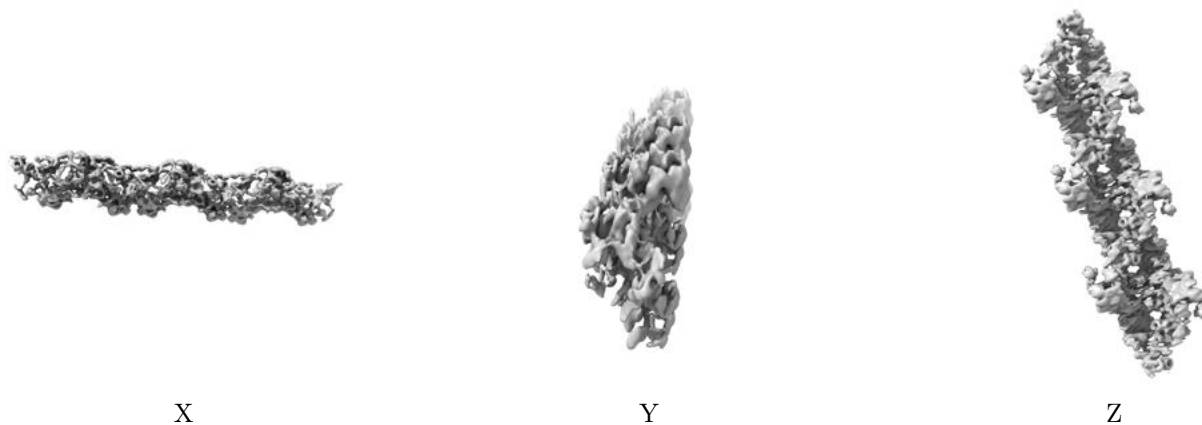


Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

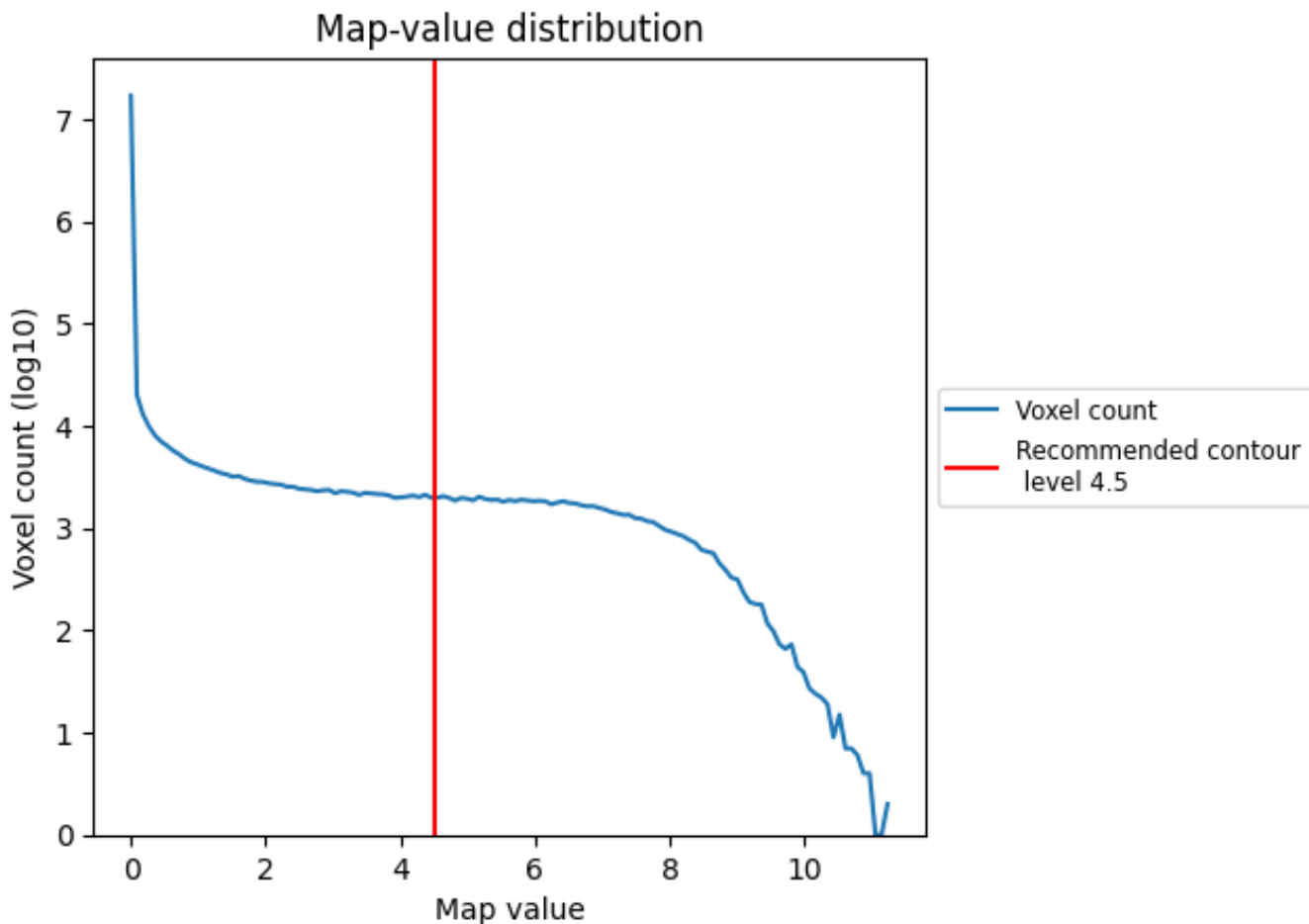
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

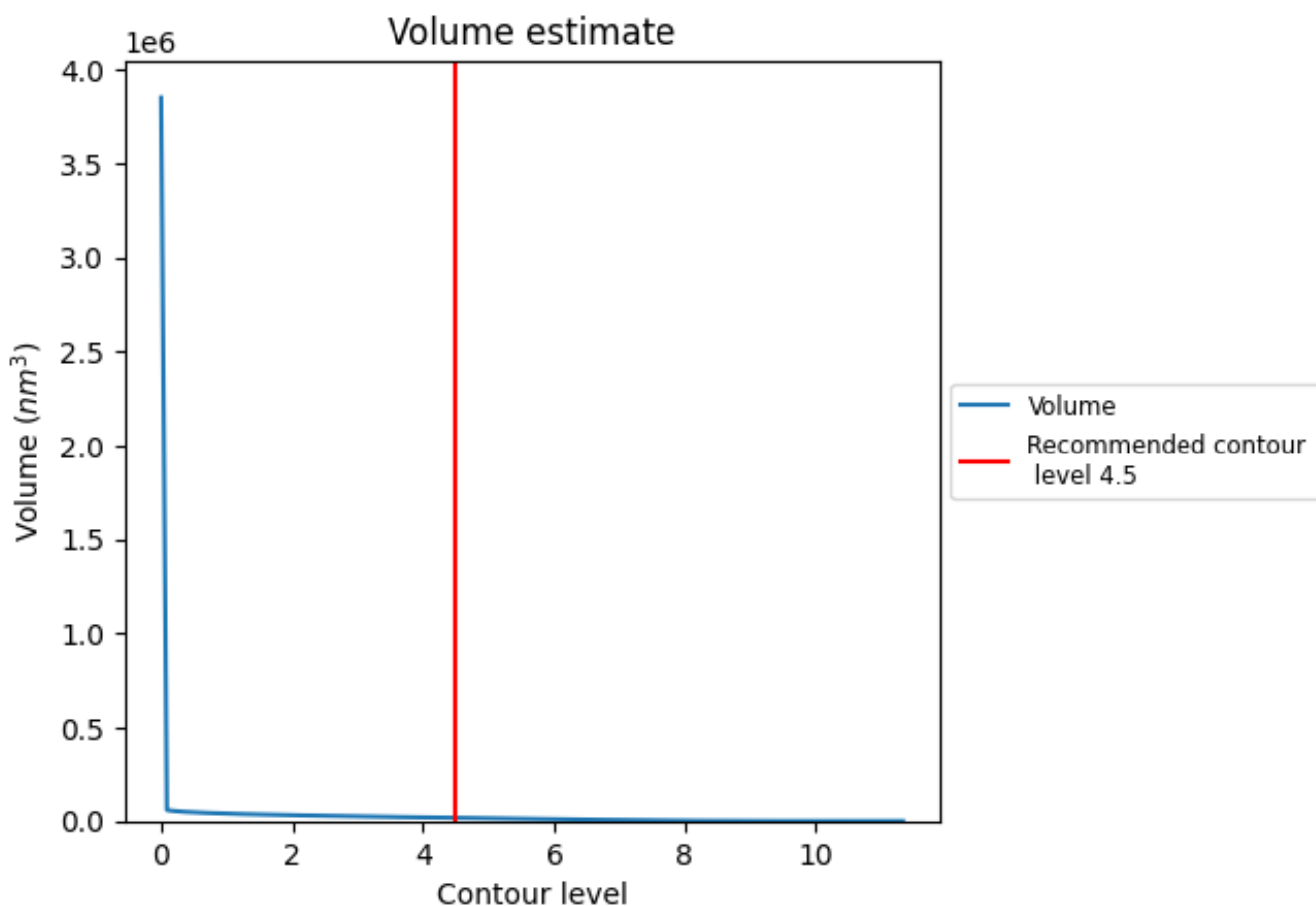
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 16773  $\text{nm}^3$ ; this corresponds to an approximate mass of 15151 kDa.

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

## 7.3 Rotationally averaged power spectrum [i](#)

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



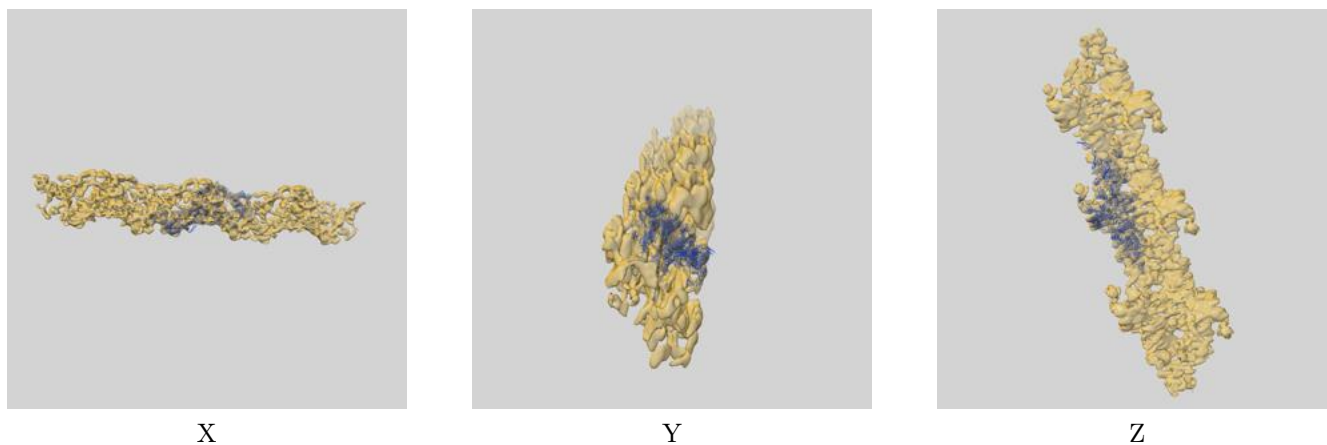
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

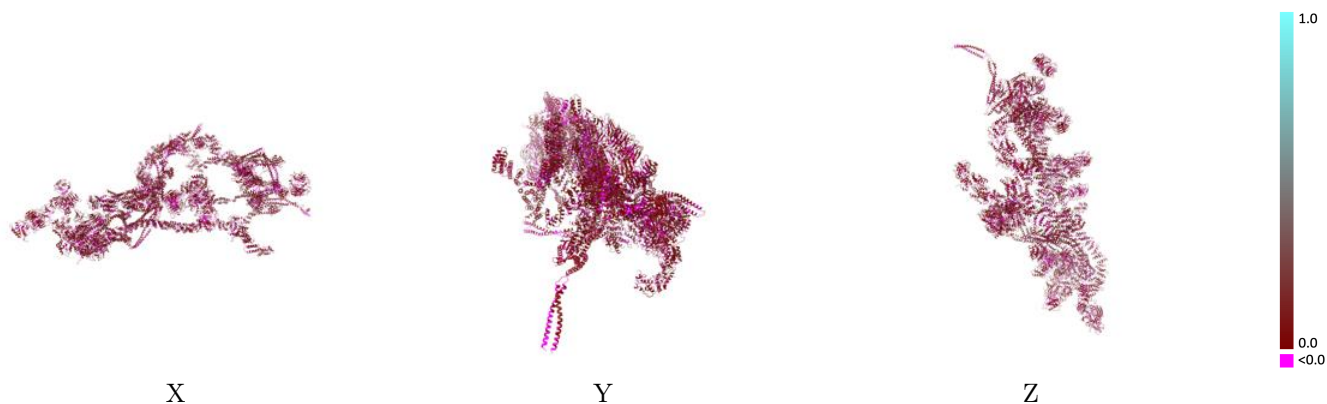
This section contains information regarding the fit between EMDB map EMD-19515 and PDB model 8RUY. Per-residue inclusion information can be found in section 3 on page 8.

### 9.1 Map-model overlay [i](#)



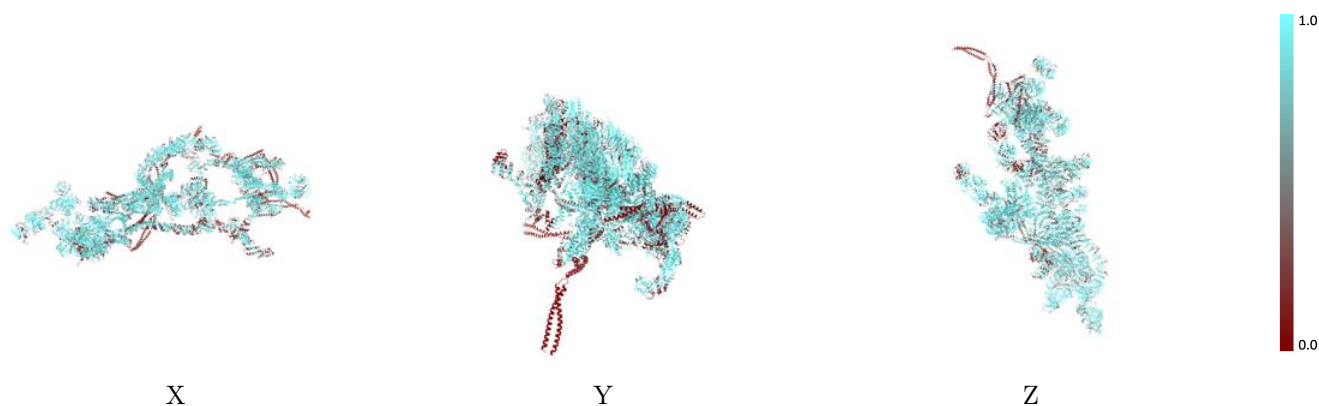
The images above show the 3D surface view of the map at the recommended contour level 4.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



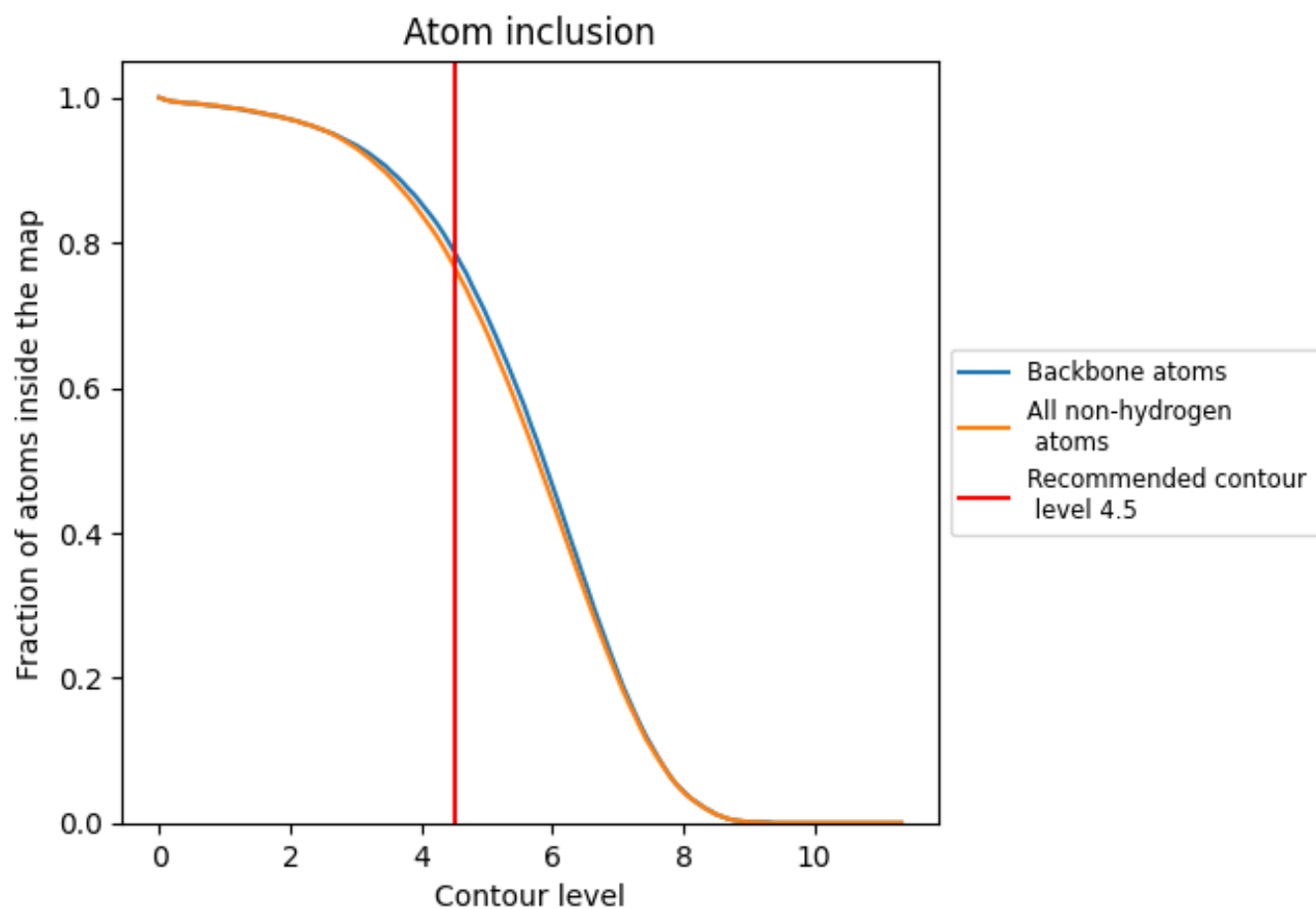
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.5).































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 77% 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 (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7680	 0.0720
A	 0.7990	 0.0770
B	 0.7640	 0.0730
C	 0.8050	 0.0670
D	 0.8520	 0.0730
E	 0.7930	 0.0780
F	 0.8880	 0.0850
G	 0.7460	 0.0680
H	 0.8080	 0.0660
I	 0.7700	 0.0700
J	 0.8970	 0.0690
K	 0.8400	 0.0750
L	 0.9110	 0.0910
M	 0.6770	 0.0720
N	 0.7590	 0.0800
O	 0.3700	 0.0650
P	 0.3780	 0.0450
Q	 0.5860	 0.0620
R	 0.5770	 0.0840
S	 0.4310	 0.0780
T	 0.6860	 0.0630
f	 0.8640	 0.0770
g	 0.8510	 0.0740
h	 0.8310	 0.0660
i	 0.7120	 0.0770
j	 0.8300	 0.0650
k	 0.8380	 0.1210
l	 0.7890	 0.0560
m	 0.6010	 0.0630
n	 0.6800	 0.0720
s	 0.6600	 0.0770

