



## wwPDB EM Validation Summary Report ⓘ

Nov 29, 2022 – 03:55 PM JST

PDB ID : 7WKK  
EMDB ID : EMD-32566  
Title : Cryo-EM structure of the IR subunit from *X. laevis* NPC  
Authors : Huang, G.; Zhan, X.; Shi, Y.  
Deposited on : 2022-01-10  
Resolution : 4.20 Å (reported)

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

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

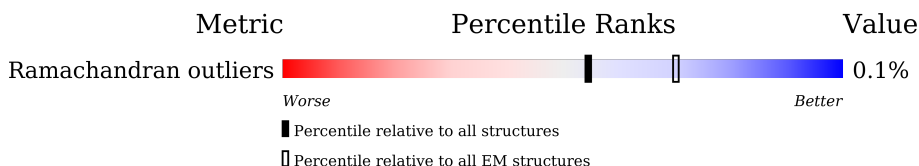
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 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 4.20 Å.

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






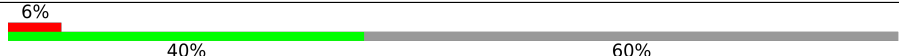
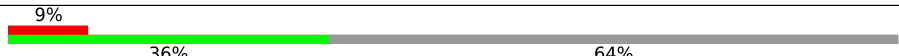
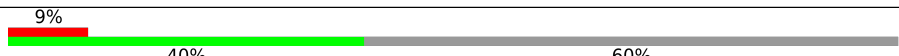
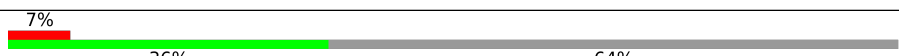




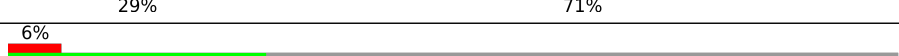

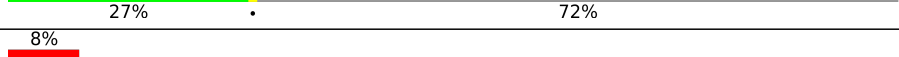





Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023

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	2011	84% 16%
1	a	2011	83% 17%
2	B	1739	85% 15%
2	b	1739	85% 15%
3	C	820	77% 23% 5%
3	E	820	76% 24%
3	c	820	77% 23%
3	e	820	76% 24%
4	D	1388	80% 20%
4	F	1388	79% 21%
4	M	1388	62% 37% 12%

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Mol	Chain	Length	Quality of chain
4	d	1388	 81% 19%
4	f	1388	 79% 21%
4	m	1388	 62% 37%
5	G	535	 40% 60%
5	J	535	 36% 64%
5	g	535	 40% 60%
5	j	535	 36% 64%
6	H	547	 30% 70%
6	L	547	 29% 71%
6	h	547	 30% 70%
6	l	547	 29% 71%
7	I	599	 29% 71%
7	K	599	 27% 72%
7	i	599	 29% 71%
7	k	599	 27% 72%
8	O	523	 70% 30%
8	o	523	 70% 30%
9	N	660	 65% 35%
9	n	660	 65% 35%

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 92821 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 MGC83295 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	1684	Total	C	N	O	0	0
			8339	4971	1684	1684		
1	a	1669	Total	C	N	O	0	0
			8268	4930	1669	1669		

- Molecule 2 is a protein called Nup188 domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	1482	Total	C	N	O	0	0
			7347	4383	1482	1482		
2	b	1482	Total	C	N	O	0	0
			7347	4383	1482	1482		

- Molecule 3 is a protein called Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	C	633	Total	C	N	O	0	0
			3144	1878	633	633		
3	E	625	Total	C	N	O	0	0
			3105	1855	625	625		
3	c	633	Total	C	N	O	0	0
			3144	1878	633	633		
3	e	625	Total	C	N	O	0	0
			3105	1855	625	625		

- Molecule 4 is a protein called Nup155-prov protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D	1115	Total	C	N	O	0	0
			5524	3294	1115	1115		
4	F	1094	Total	C	N	O	0	0
			5417	3229	1094	1094		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	M	869	Total	C	N	O	0	0
			4296	2558	869	869		
4	d	1123	Total	C	N	O	0	0
			5563	3317	1123	1123		
4	f	1097	Total	C	N	O	0	0
			5432	3238	1097	1097		
4	m	869	Total	C	N	O	0	0
			4296	2558	869	869		

- Molecule 5 is a protein called Nup54.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	215	Total	C	N	O	0	0
			1063	633	215	215		
5	J	195	Total	C	N	O	0	0
			963	573	195	195		
5	g	215	Total	C	N	O	0	0
			1063	633	215	215		
5	j	195	Total	C	N	O	0	0
			963	573	195	195		

- Molecule 6 is a protein called IL4I1 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	H	163	Total	C	N	O	0	0
			813	487	163	163		
6	L	156	Total	C	N	O	0	0
			778	466	156	156		
6	h	163	Total	C	N	O	0	0
			813	487	163	163		
6	l	156	Total	C	N	O	0	0
			778	466	156	156		

- Molecule 7 is a protein called MGC84997 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	I	171	Total	C	N	O	0	0
			853	511	171	171		
7	K	166	Total	C	N	O	0	0
			829	497	166	166		
7	i	171	Total	C	N	O	0	0
			853	511	171	171		

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	k	166	829	497	166	166	0	0

- Molecule 8 is a protein called Aaas-prov protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	O	367	1805	1071	367	367	0	0
8	o	367	1805	1071	367	367	0	0

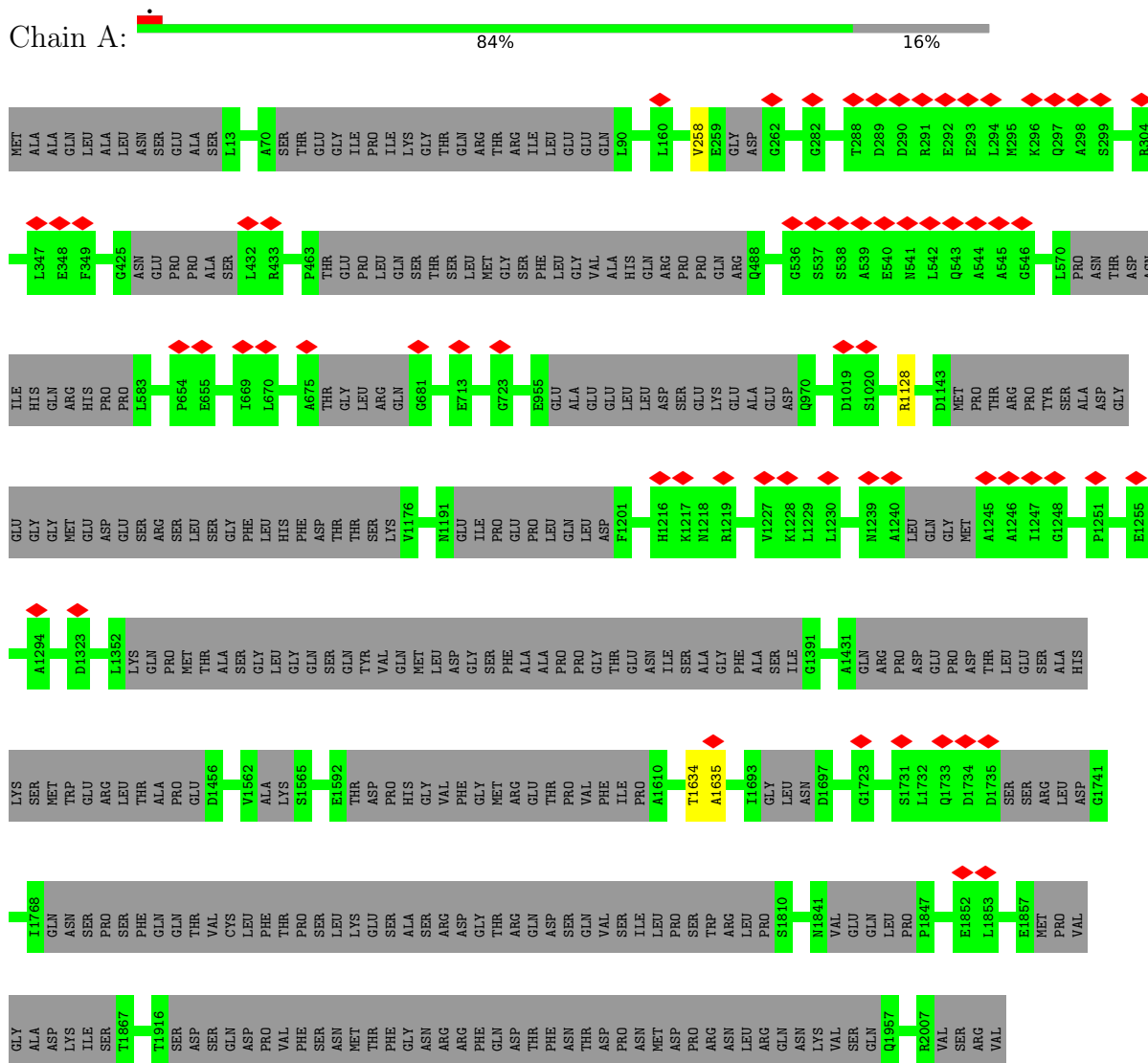
- Molecule 9 is a protein called Nucleoporin NDC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	N	431	2143	1281	431	431	0	0
9	n	431	2143	1281	431	431	0	0

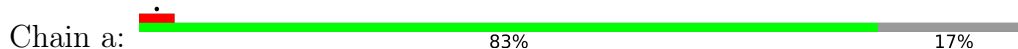
### 3 Residue-property plots [i](#)

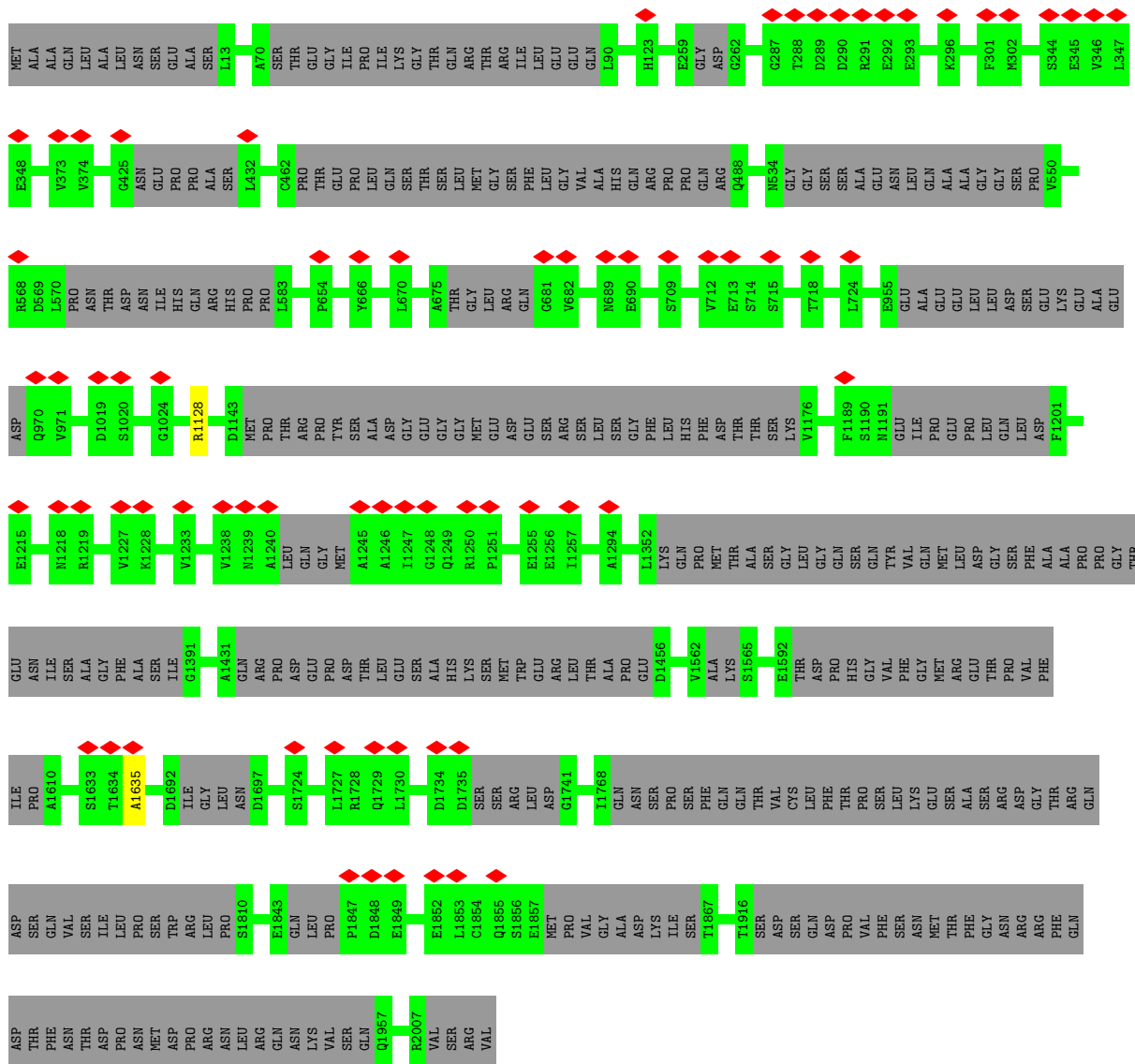
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: MGC83295 protein

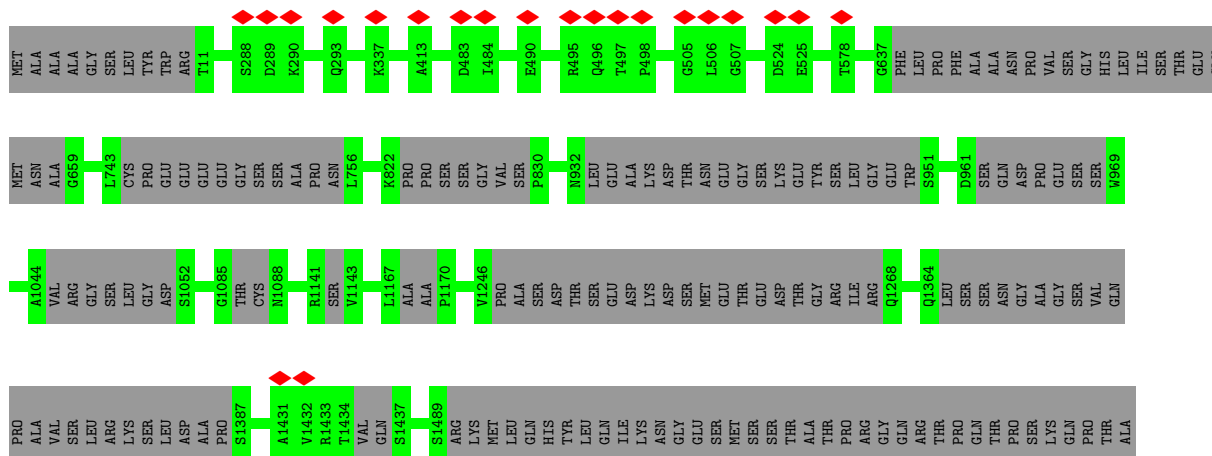
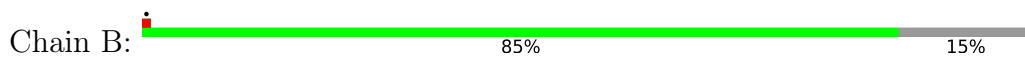


- Molecule 1: MGC83295 protein

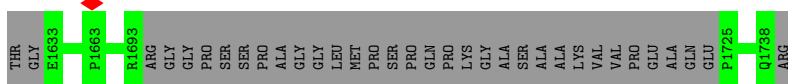
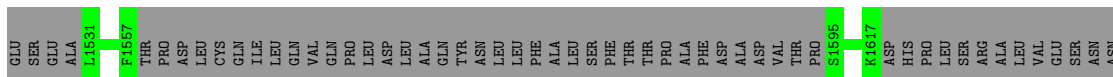




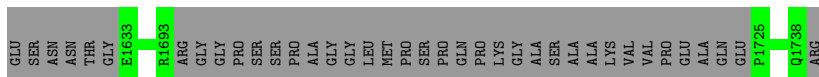
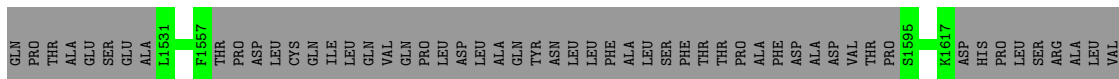
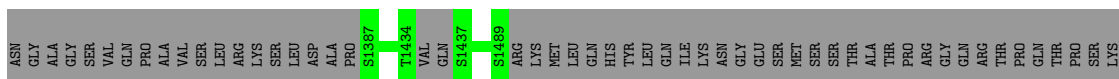
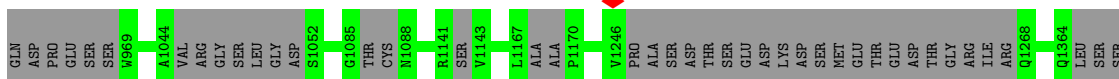
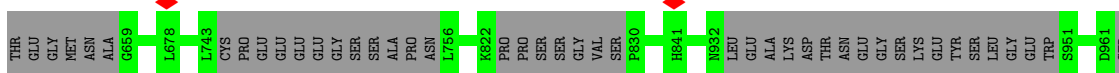
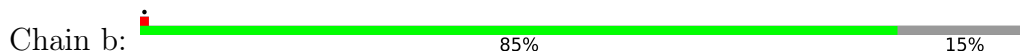
• Molecule 2: Nup188 domain-containing protein



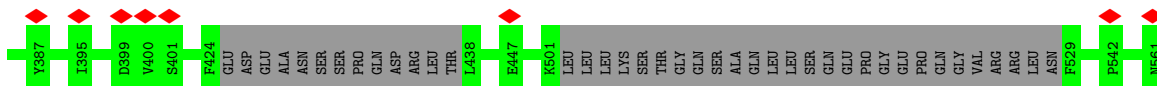
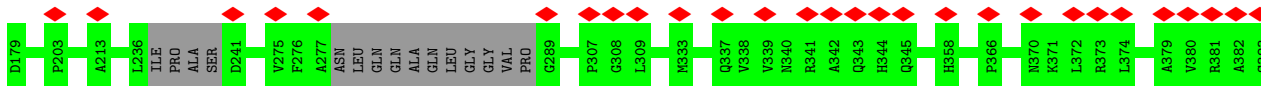
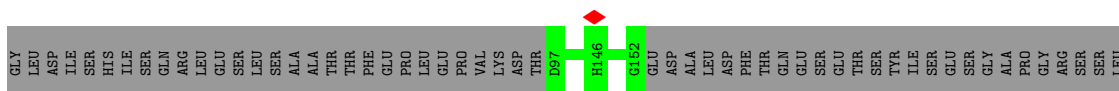
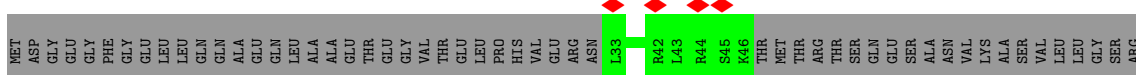
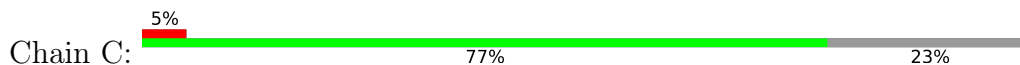




• Molecule 2: Nup188 domain-containing protein

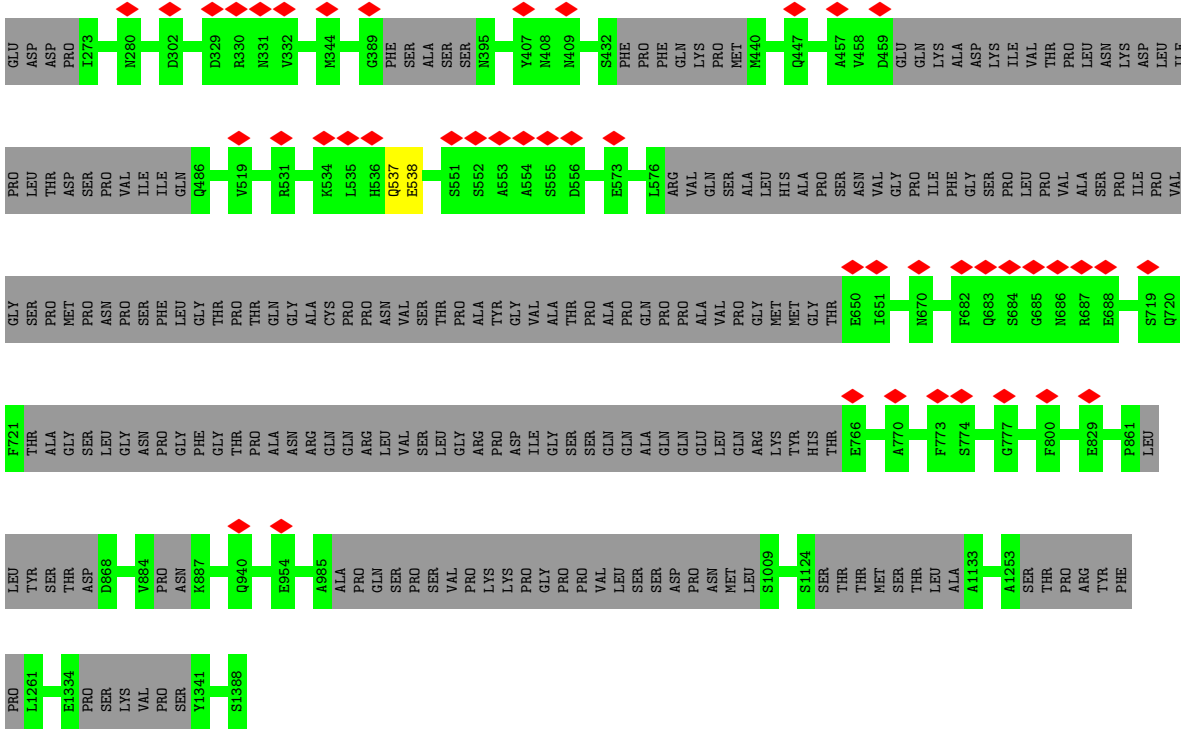


• Molecule 3: Nuclear pore complex protein Nup93

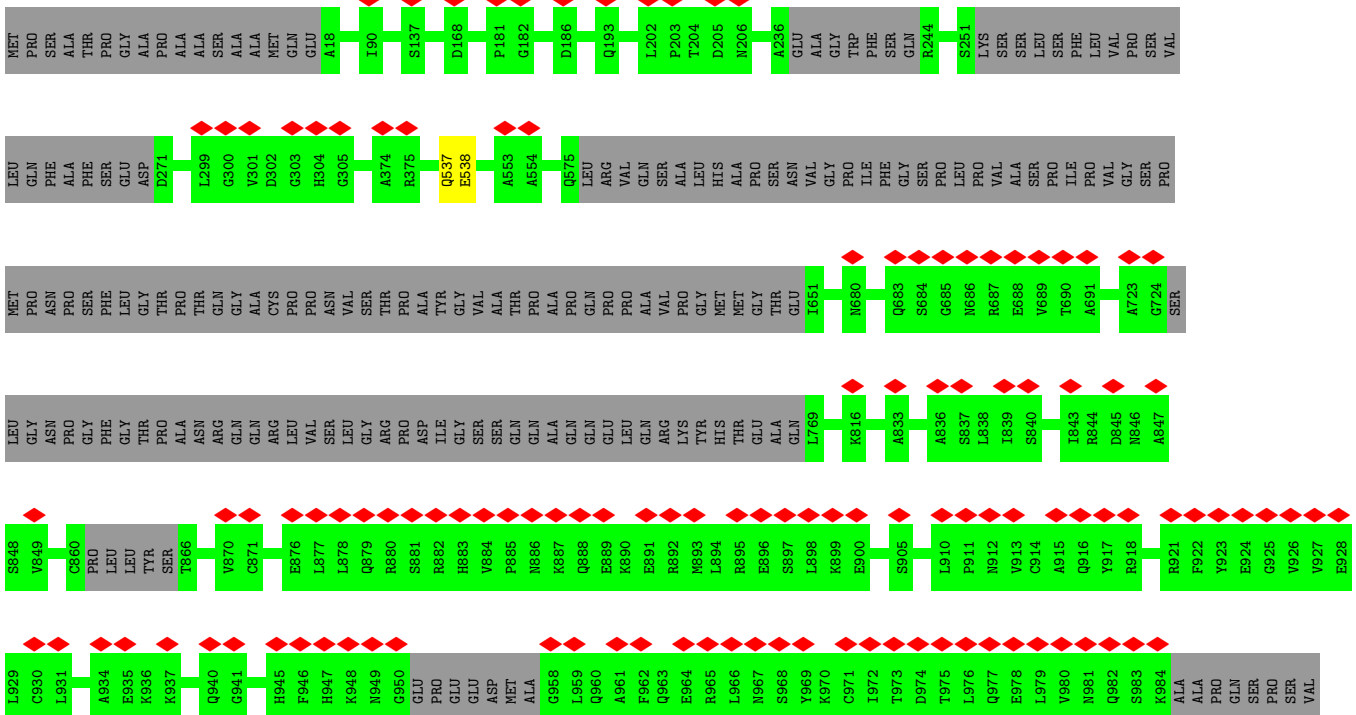


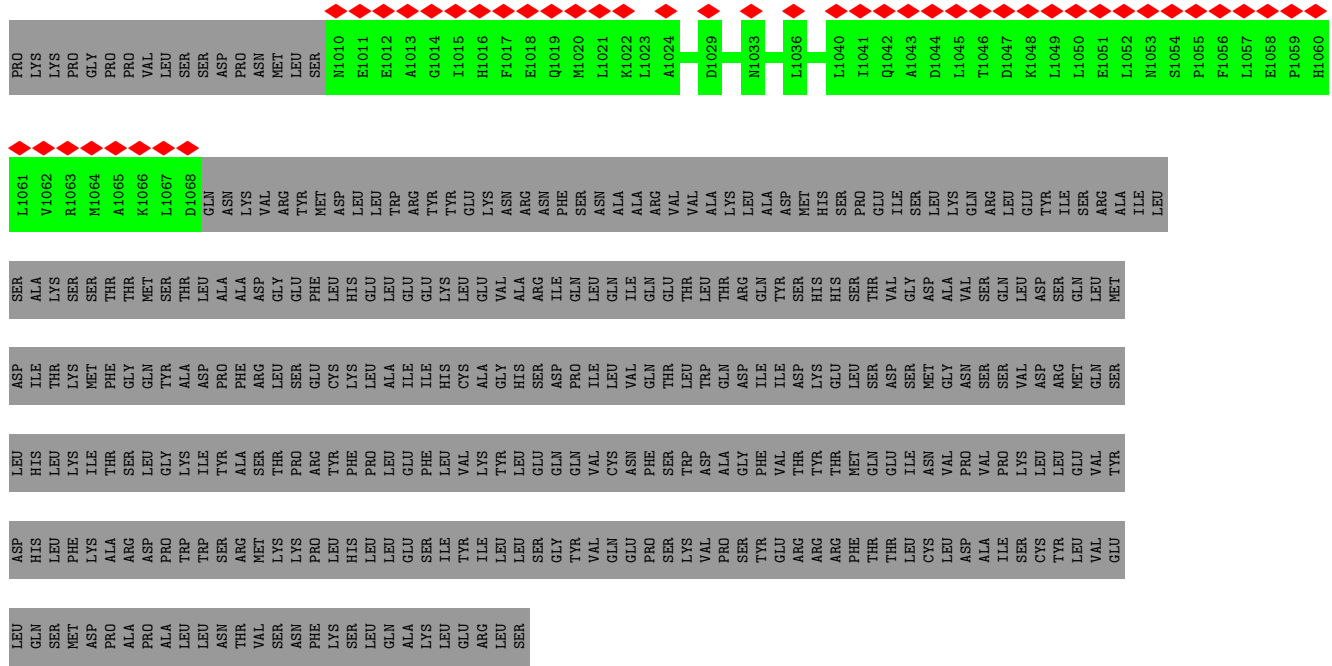




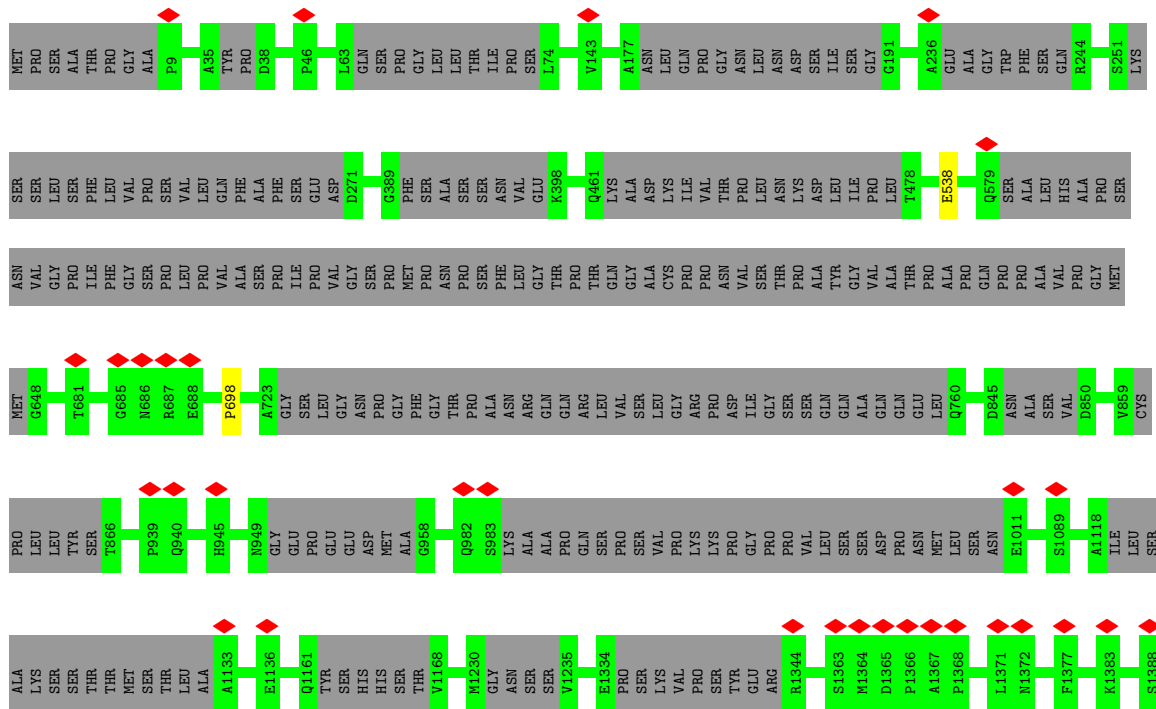
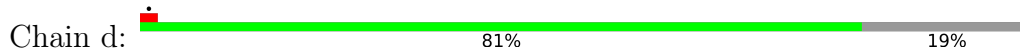


● Molecule 4: Nup155-prov protein

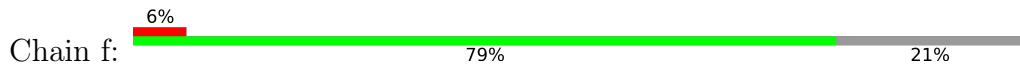


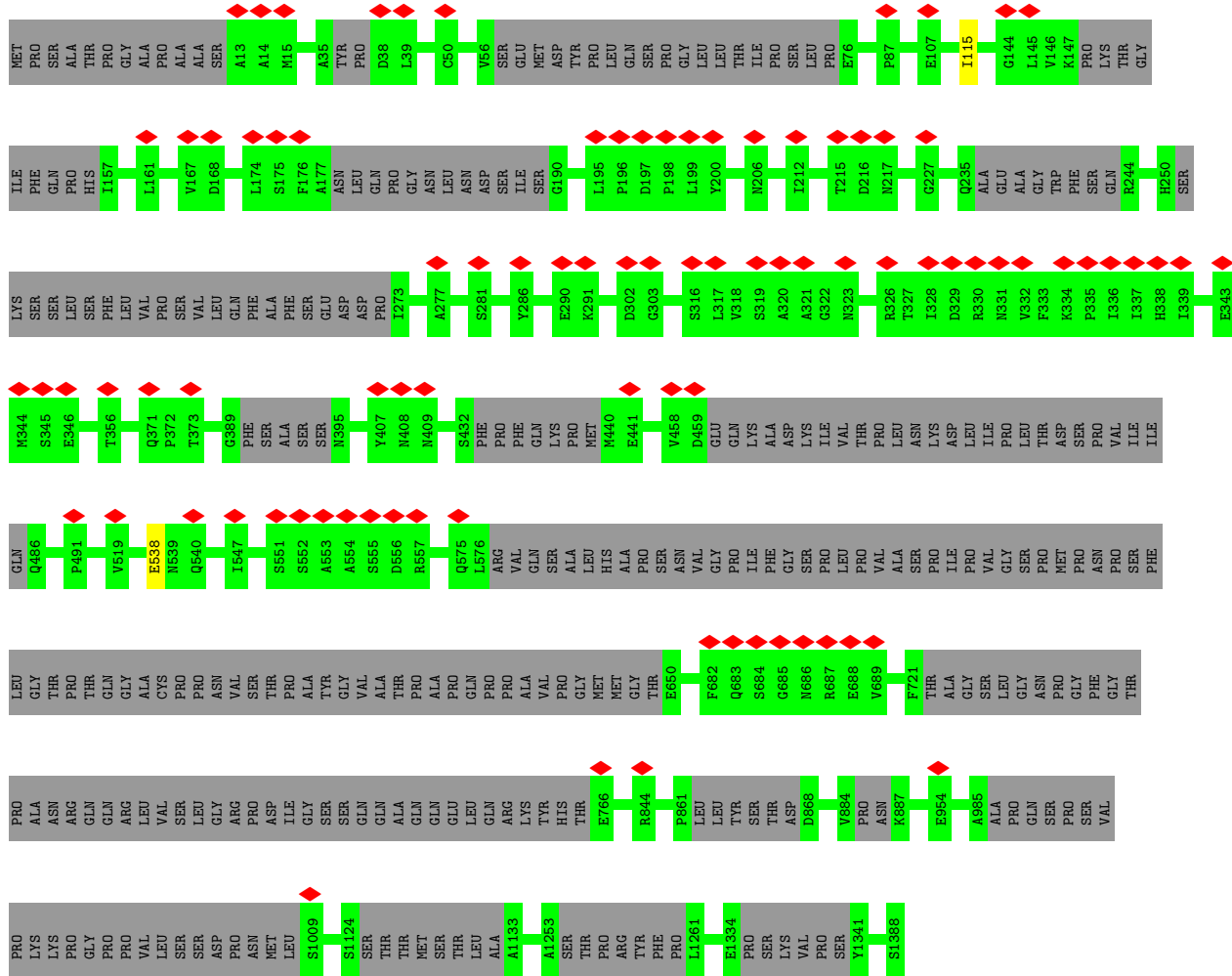


• Molecule 4: Nup155-prov protein

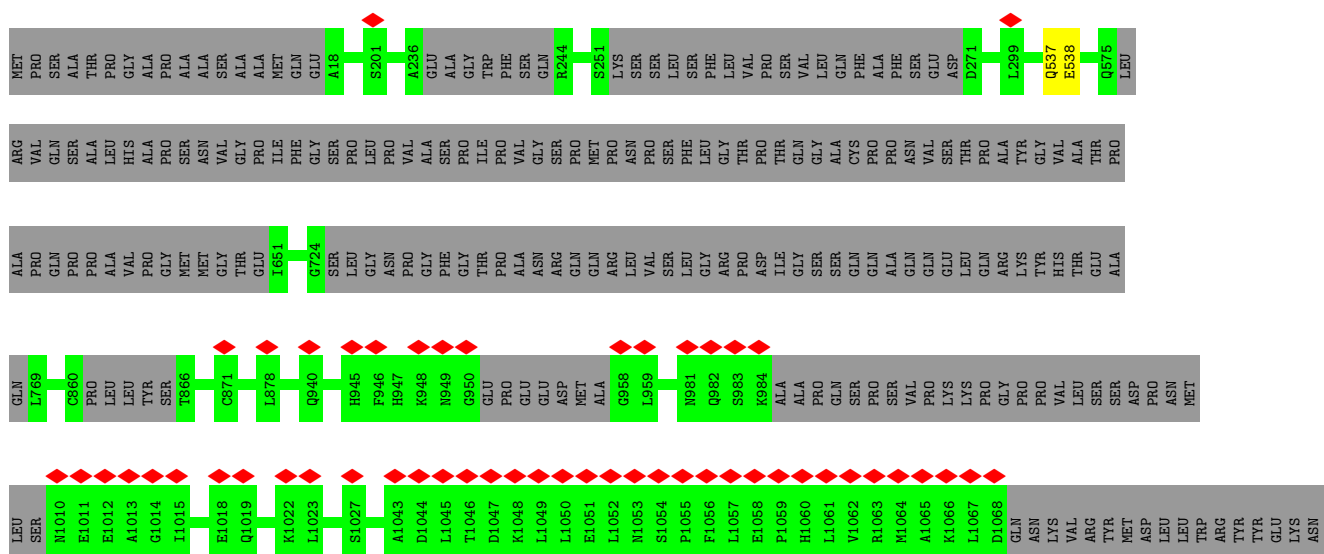


• Molecule 4: Nup155-prov protein





● Molecule 4: Nup155-prov protein



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

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• Molecule 5: Nup54



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

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1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350
1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370
1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386
1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400
1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415
1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430
1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445
1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460
1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474
1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488
1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500

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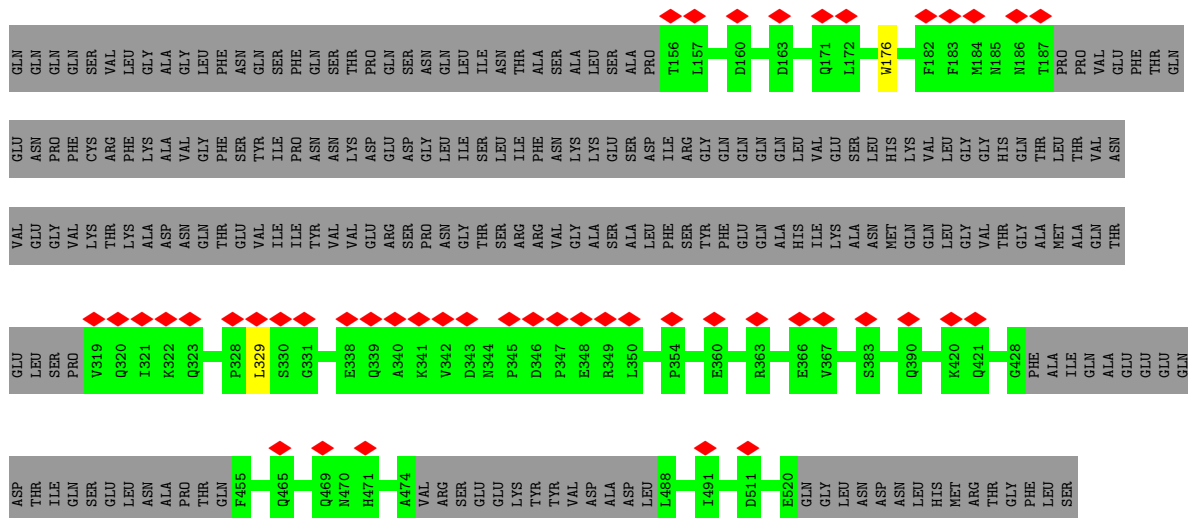
• Molecule 5: Nup54



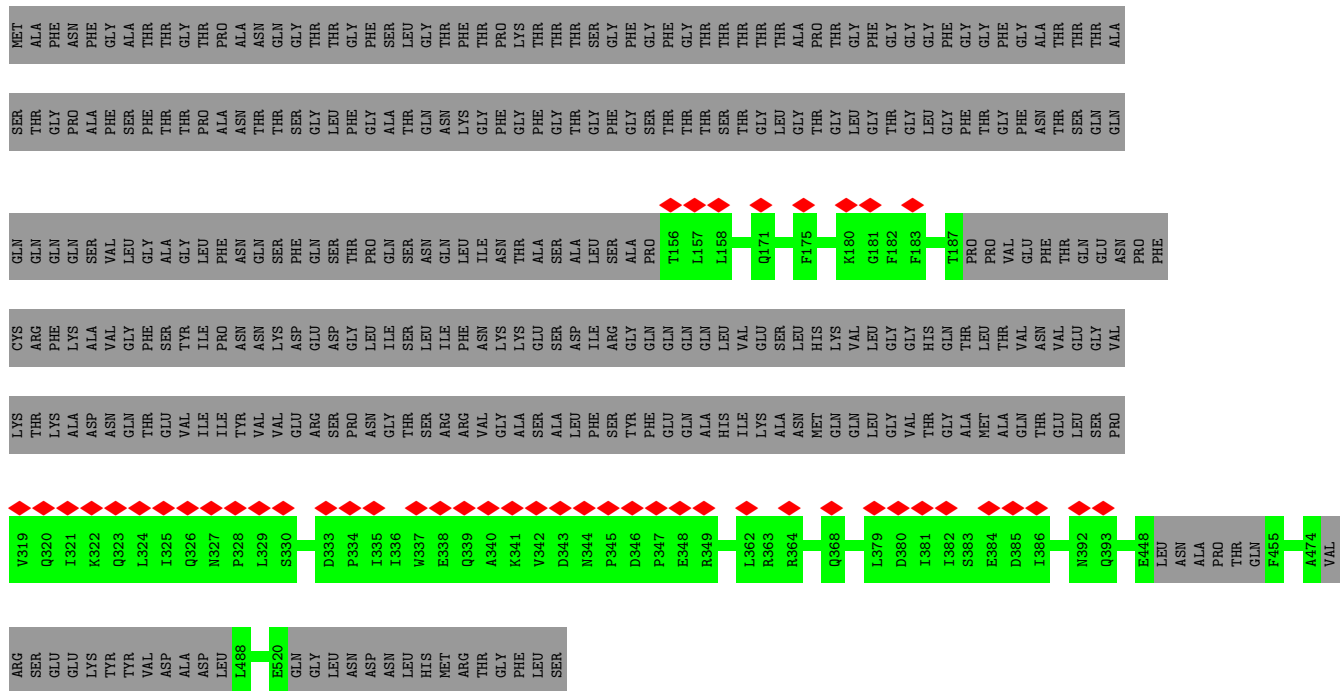
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MET ALA PHE PHE PHE PHE PHE PHE PHE PHE PHE PHE PHE PHE PHE PHE PHE
SER THR PRO ASN ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP
GLY TYR THR THR THR THR THR THR THR THR THR THR THR THR THR THR THR
SER THR THR THR THR THR THR THR THR THR THR THR THR THR THR THR THR

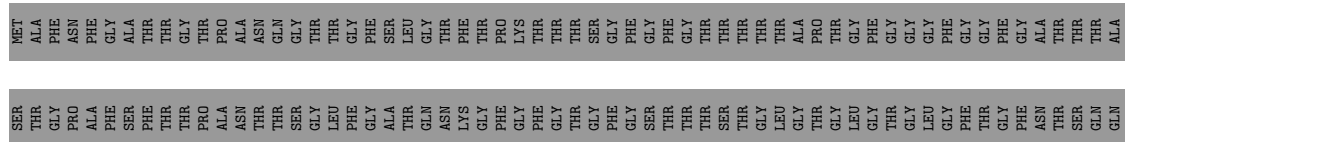
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• Molecule 5: Nup54



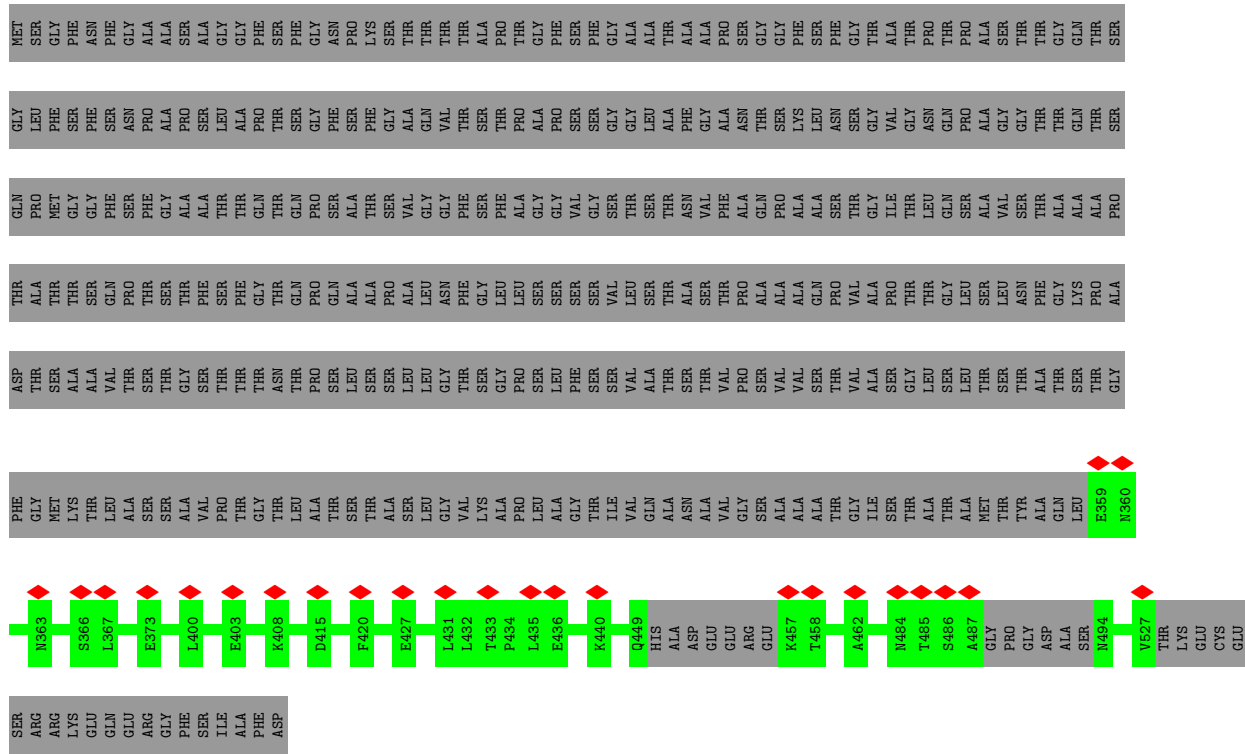
• Molecule 5: Nup54



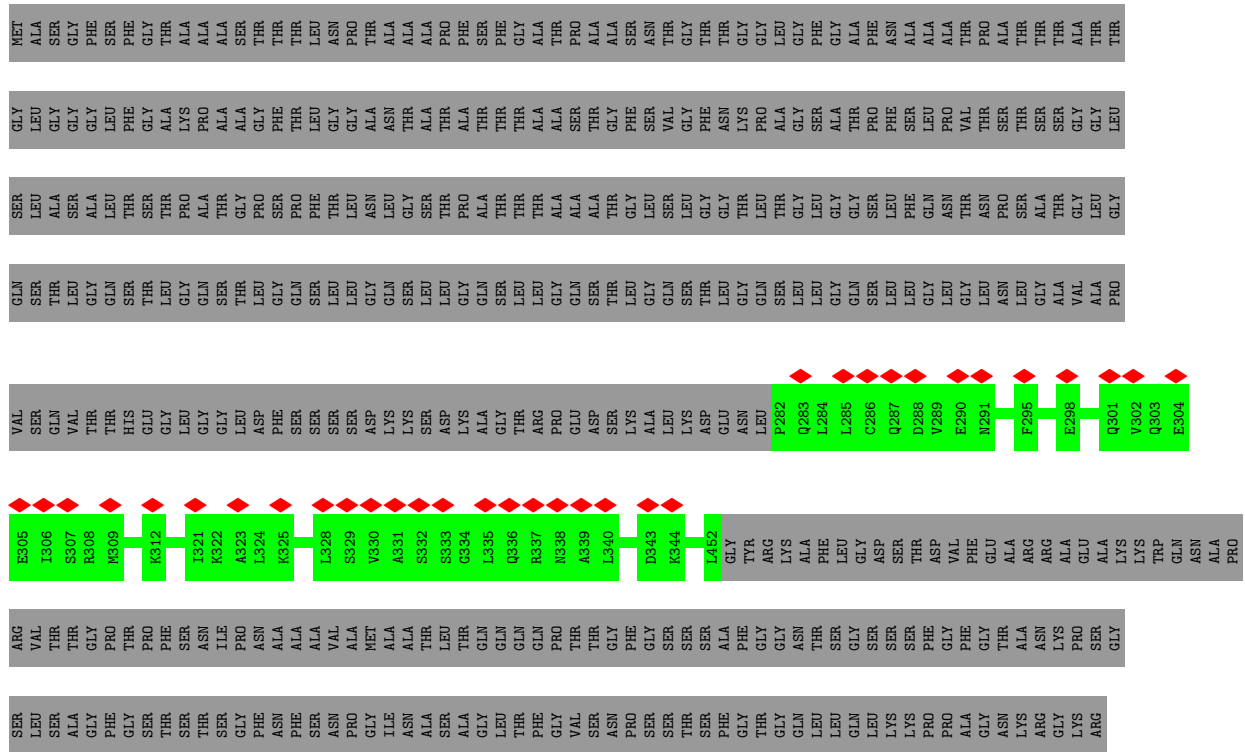








• Molecule 7: MGC84997 protein



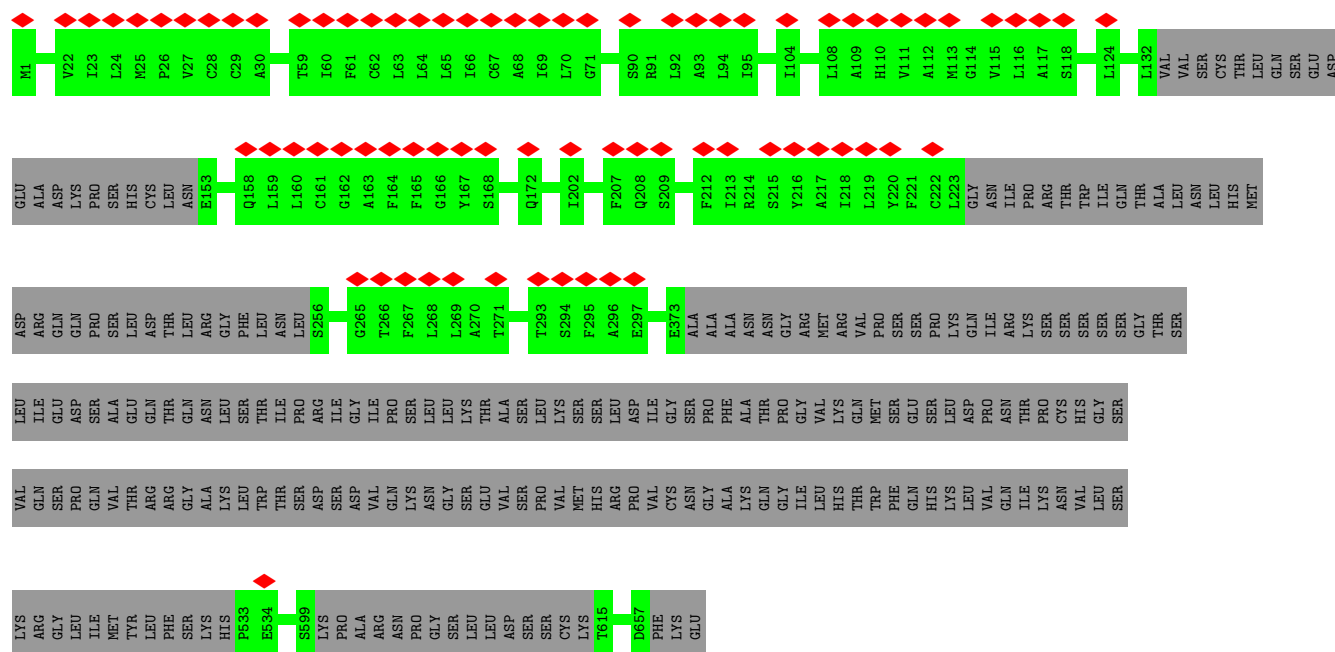
• Molecule 7: MGC84997 protein







● Molecule 9: Nucleoporin NDC1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	2093631	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.038	Depositor
Minimum map value	-0.020	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size ( $\text{\AA}$ )	710.144, 710.144, 710.144	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.387, 1.387, 1.387	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	0.30	0/8318	0.40	0/11563
1	a	0.29	0/8246	0.40	0/11463
2	B	0.25	0/7330	0.38	0/10197
2	b	0.25	0/7330	0.38	0/10197
3	C	0.25	0/3134	0.37	0/4359
3	E	0.33	0/3093	0.41	0/4299
3	c	0.25	0/3134	0.38	0/4359
3	e	0.32	0/3093	0.42	0/4299
4	D	0.29	0/5506	0.43	0/7649
4	F	0.28	0/5399	0.42	0/7498
4	M	0.25	0/4288	0.43	0/5961
4	d	0.29	0/5545	0.44	0/7703
4	f	0.28	0/5414	0.42	0/7519
4	m	0.25	0/4288	0.43	0/5961
5	G	0.26	0/1059	0.41	0/1469
5	J	0.25	0/959	0.39	0/1329
5	g	0.26	0/1059	0.41	0/1469
5	j	0.26	0/959	0.40	0/1329
6	H	0.26	0/811	0.35	0/1131
6	L	0.35	0/775	0.38	0/1079
6	h	0.27	0/811	0.34	0/1131
6	l	0.34	0/775	0.37	0/1079
7	I	0.26	0/852	0.37	0/1190
7	K	0.41	1/827 (0.1%)	0.40	1/1154 (0.1%)
7	i	0.27	0/852	0.36	0/1190
7	k	0.30	0/827	0.37	0/1154
8	O	0.29	0/1799	0.49	0/2491
8	o	0.29	0/1799	0.49	0/2491
9	N	0.26	0/2138	0.36	0/2978
9	n	0.26	0/2138	0.36	0/2978
All	All	0.28	1/92558 (0.0%)	0.41	1/128669 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
4	F	0	1
4	M	0	1
4	f	0	1
4	m	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	K	415	SER	C-N	7.98	1.49	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	K	415	SER	C-N-CA	5.52	145.19	122.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1634	THR	Peptide
4	F	537	GLN	Peptide
4	M	537	GLN	Peptide
4	f	115	ILE	Peptide
4	m	537	GLN	Peptide

## 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	1642/2011 (82%)	1523 (93%)	116 (7%)	3 (0%)	47	80
1	a	1625/2011 (81%)	1509 (93%)	114 (7%)	2 (0%)	51	85
2	B	1448/1739 (83%)	1406 (97%)	42 (3%)	0	100	100
2	b	1448/1739 (83%)	1407 (97%)	41 (3%)	0	100	100
3	C	613/820 (75%)	593 (97%)	20 (3%)	0	100	100
3	E	601/820 (73%)	542 (90%)	59 (10%)	0	100	100
3	c	613/820 (75%)	592 (97%)	21 (3%)	0	100	100
3	e	601/820 (73%)	547 (91%)	54 (9%)	0	100	100
4	D	1079/1388 (78%)	1020 (94%)	58 (5%)	1 (0%)	51	85
4	F	1058/1388 (76%)	1018 (96%)	39 (4%)	1 (0%)	51	85
4	M	853/1388 (62%)	823 (96%)	29 (3%)	1 (0%)	51	85
4	d	1087/1388 (78%)	1029 (95%)	56 (5%)	2 (0%)	47	80
4	f	1061/1388 (76%)	1014 (96%)	46 (4%)	1 (0%)	51	85
4	m	853/1388 (62%)	823 (96%)	29 (3%)	1 (0%)	51	85
5	G	207/535 (39%)	193 (93%)	14 (7%)	0	100	100
5	J	187/535 (35%)	178 (95%)	7 (4%)	2 (1%)	14	52
5	g	207/535 (39%)	192 (93%)	15 (7%)	0	100	100
5	j	187/535 (35%)	174 (93%)	12 (6%)	1 (0%)	29	68
6	H	159/547 (29%)	154 (97%)	5 (3%)	0	100	100
6	L	150/547 (27%)	150 (100%)	0	0	100	100
6	h	159/547 (29%)	153 (96%)	6 (4%)	0	100	100
6	l	150/547 (27%)	148 (99%)	2 (1%)	0	100	100
7	I	169/599 (28%)	162 (96%)	7 (4%)	0	100	100
7	K	162/599 (27%)	154 (95%)	6 (4%)	2 (1%)	13	50
7	i	169/599 (28%)	159 (94%)	10 (6%)	0	100	100
7	k	162/599 (27%)	156 (96%)	4 (2%)	2 (1%)	13	50
8	O	355/523 (68%)	339 (96%)	16 (4%)	0	100	100
8	o	355/523 (68%)	339 (96%)	16 (4%)	0	100	100
9	N	421/660 (64%)	412 (98%)	9 (2%)	0	100	100
9	n	421/660 (64%)	412 (98%)	9 (2%)	0	100	100

*Continued on next page...*

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	18202/28198 (65%)	17321 (95%)	862 (5%)	19 (0%)	54 85

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1635	ALA
1	a	1635	ALA
1	A	258	VAL
4	F	538	GLU
5	J	176	TRP

### 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 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.

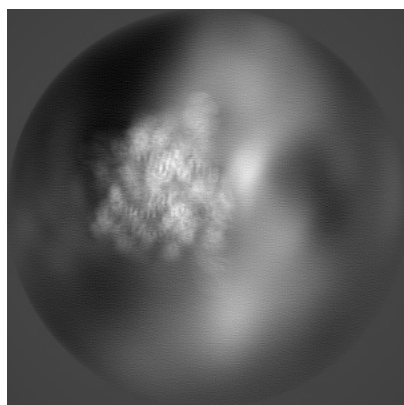
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32566. These allow visual inspection of the internal detail of the map and identification of artifacts.

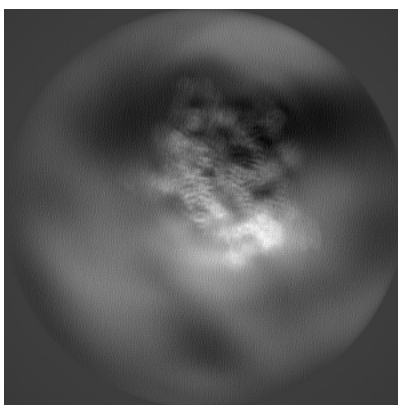
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

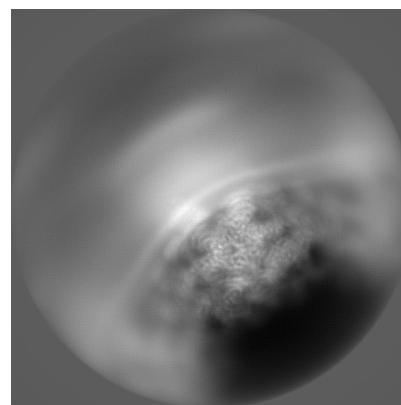
#### 6.1.1 Primary map



X



Y

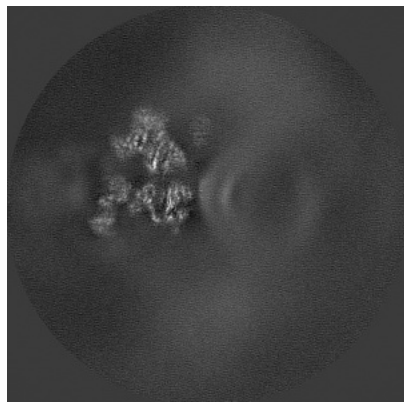


Z

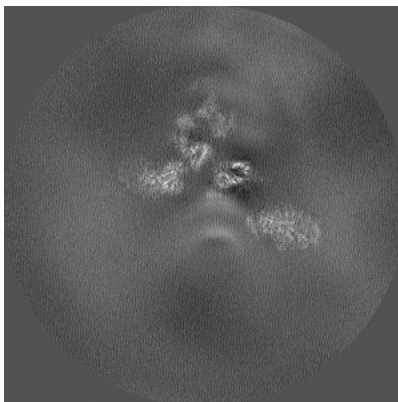
The images above show the map projected in three orthogonal directions.

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

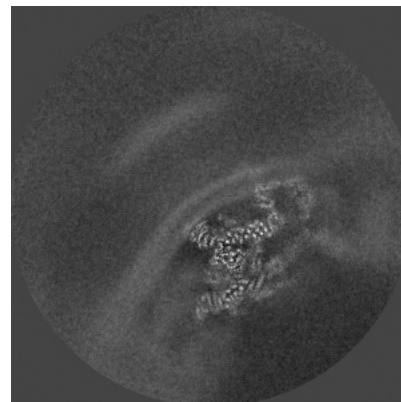
#### 6.2.1 Primary map



X Index: 256



Y Index: 256

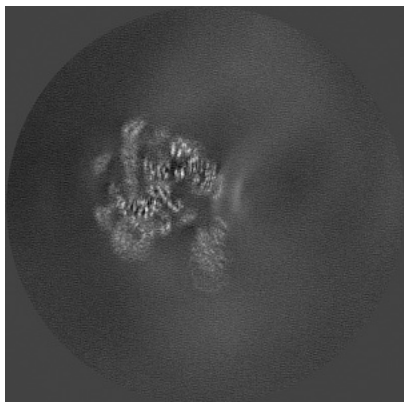


Z Index: 256

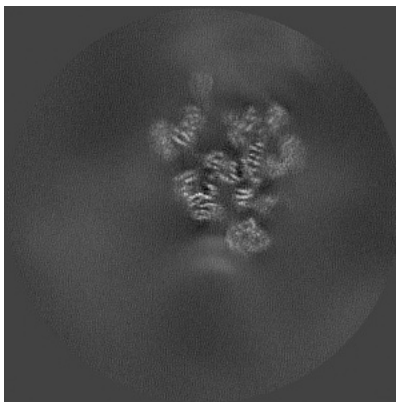
The images above show central slices of the map in three orthogonal directions.

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

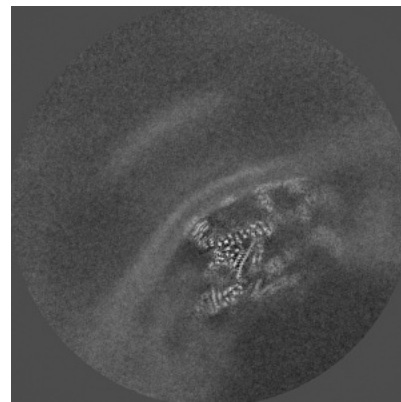
### 6.3.1 Primary map



X Index: 293



Y Index: 206



Z Index: 260

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

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

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

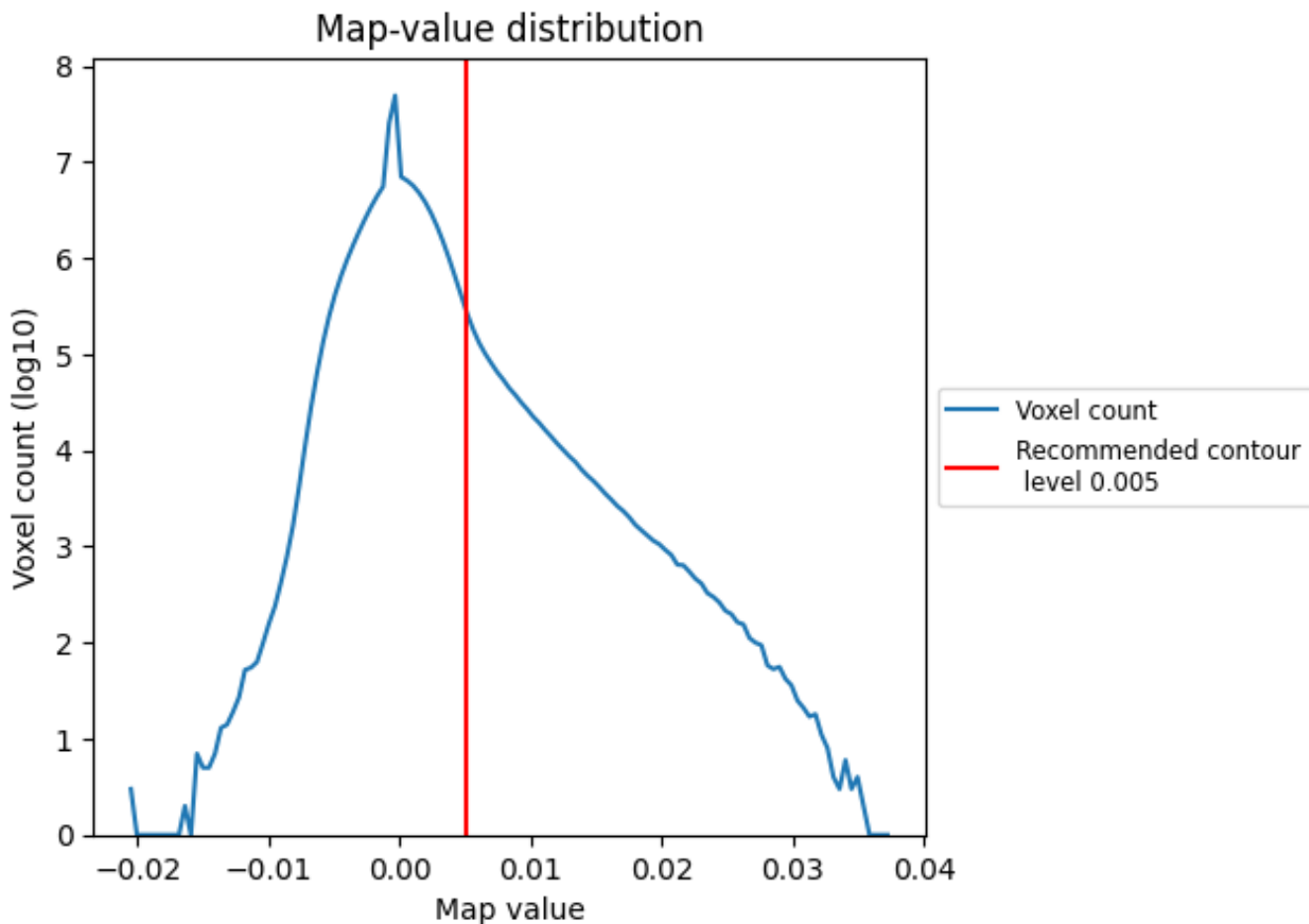
## 6.5 Mask visualisation

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.

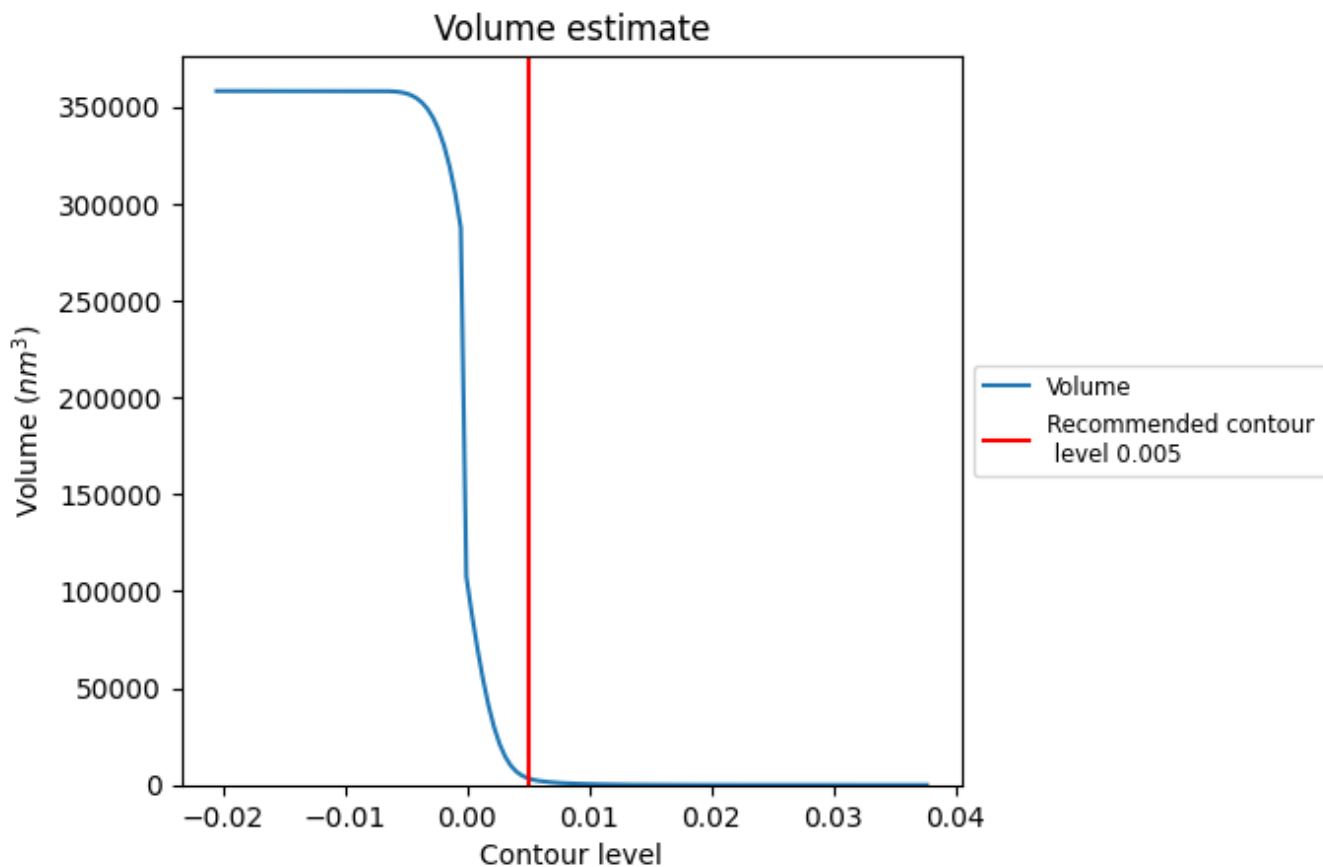
### 7.1 Map-value distribution [i](#)



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.



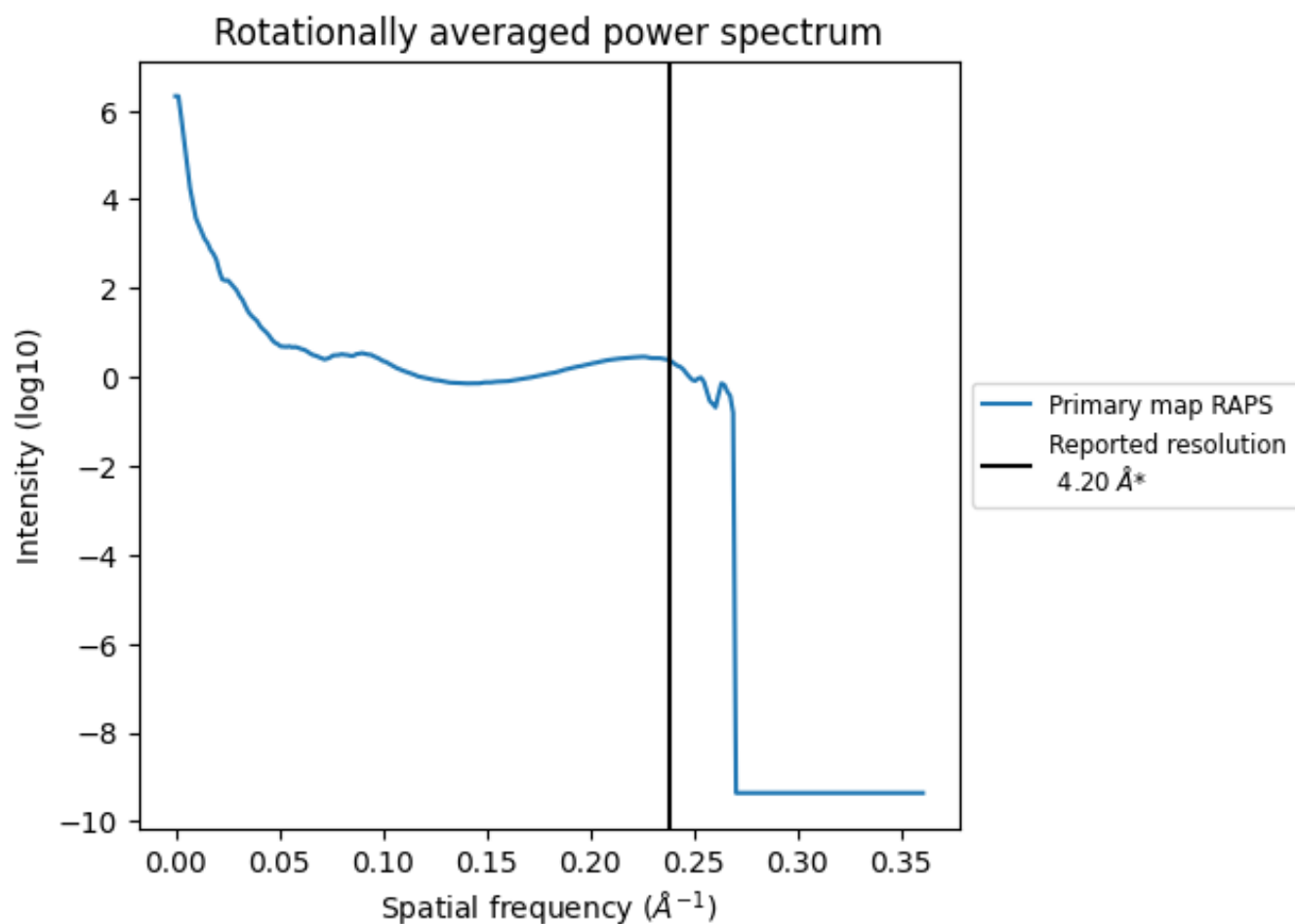
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3486 nm<sup>3</sup>; this corresponds to an approximate mass of 3149 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 0.238 Å<sup>-1</sup>

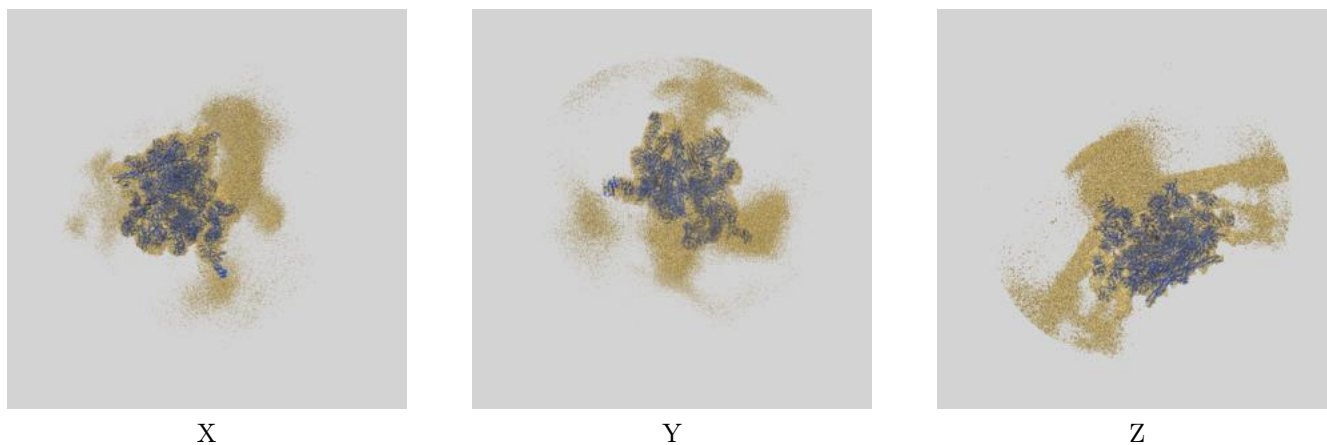
## 8 Fourier-Shell correlation

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

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

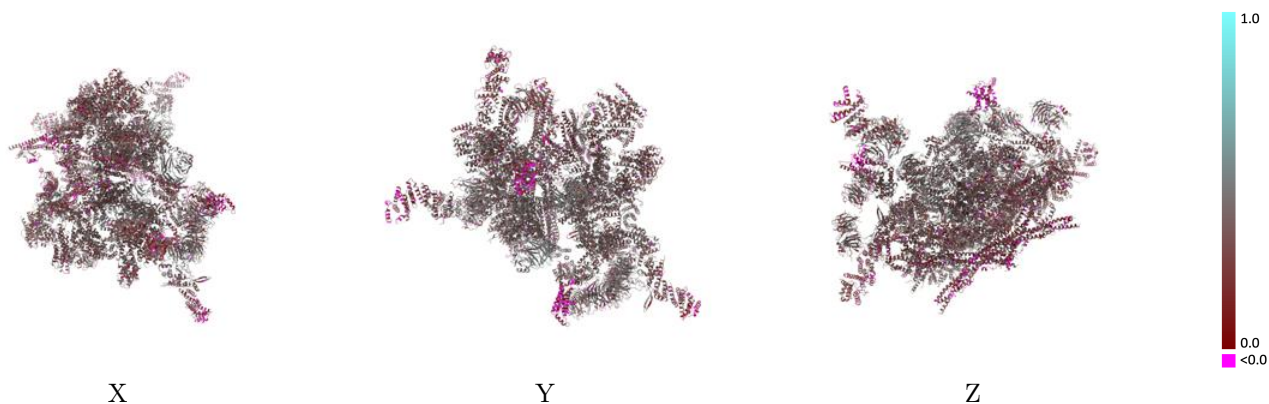
This section contains information regarding the fit between EMDB map EMD-32566 and PDB model 7WKK. Per-residue inclusion information can be found in section 3 on page 7.

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



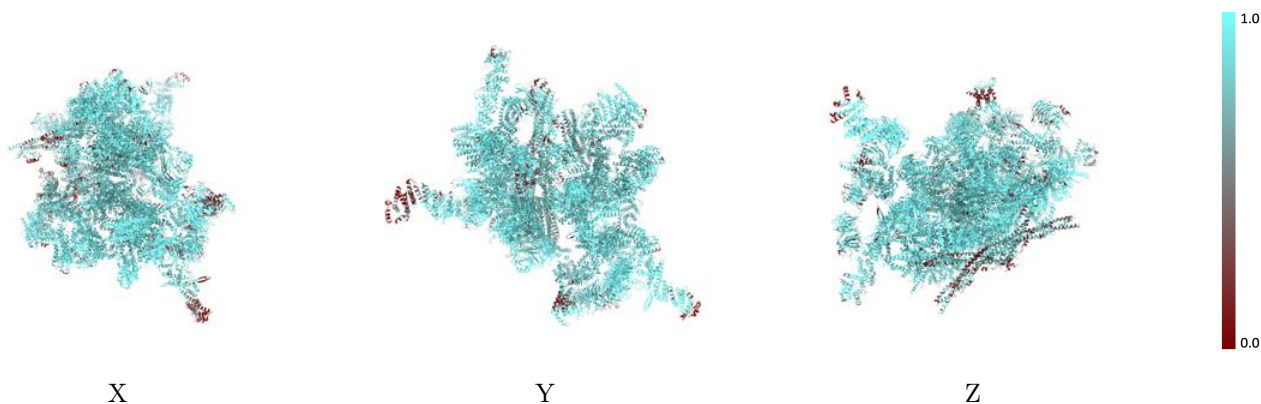
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



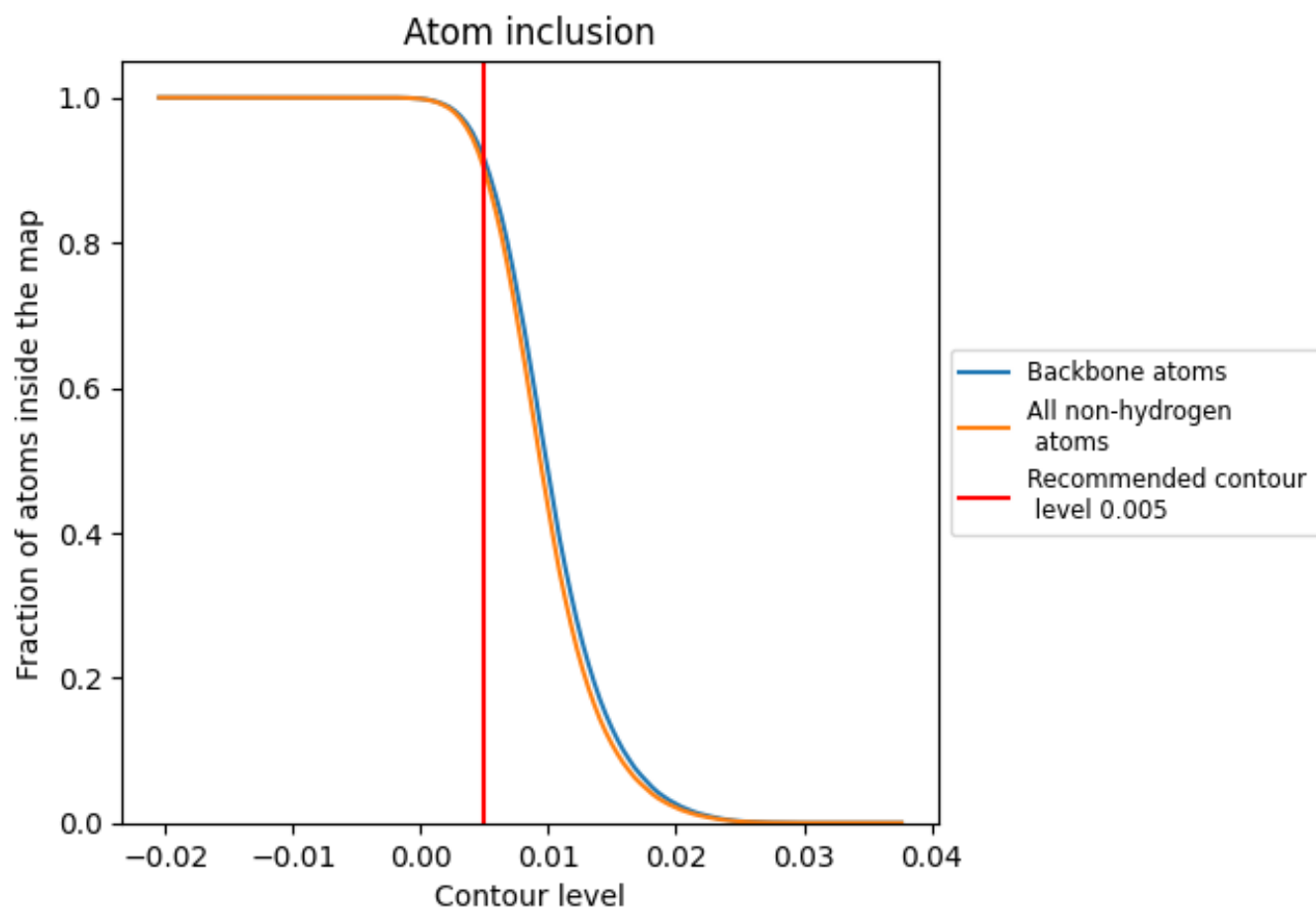
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9000	 0.3490
A	 0.9403	 0.3610
B	 0.9650	 0.3500
C	 0.8979	 0.3010
D	 0.9712	 0.4130
E	 0.9758	 0.4020
F	 0.9225	 0.3760
G	 0.8071	 0.3160
H	 0.7171	 0.2640
I	 0.7691	 0.2870
J	 0.7300	 0.2680
K	 0.6791	 0.2380
L	 0.7198	 0.2520
M	 0.7907	 0.3620
N	 0.7639	 0.2400
O	 0.8343	 0.3690
a	 0.9274	 0.3590
b	 0.9641	 0.3420
c	 0.9170	 0.3040
d	 0.9543	 0.4020
e	 0.9723	 0.3950
f	 0.8951	 0.3660
g	 0.7291	 0.2720
h	 0.7466	 0.2870
i	 0.6917	 0.2760
j	 0.7591	 0.2820
k	 0.7370	 0.2500
l	 0.7763	 0.2530
m	 0.9232	 0.3720
n	 0.8087	 0.2360
o	 0.8255	 0.3550

