Full wwPDB EM Validation Report ⓘ

Dec 19, 2022 – 01:26 PM EST

PDB ID	:	7NAD
EMDB ID	:	EMD-24270
Title	:	State E2 nucleolar 60S ribosomal biogenesis intermediate - Spb4 local refinement model
Authors	:	Cruz, V.E.; Sekulski, K.; Peddada, N.; Erzberger, J.P.
Deposited on	:	2021-06-21
Resolution	:	3.04 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

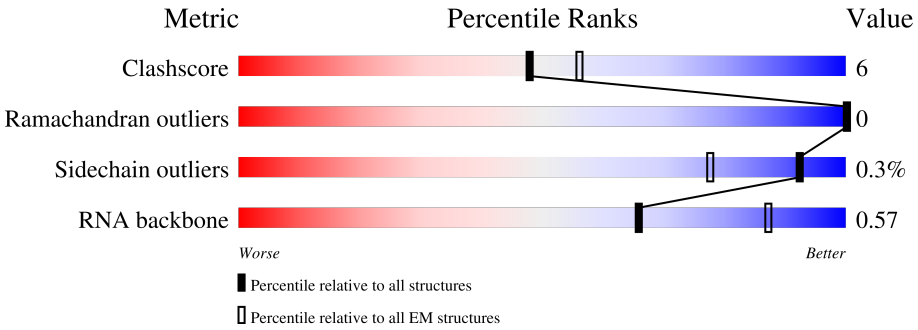
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance

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

The reported resolution of this entry is 3.04 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1	697	20% 62% 34%
2	2	72	46% 50% 28% 18%
3	5	235	35% 48% 5% 48%
4	8	710	7% 92%
5	B	387	98%
6	G	256	5% 93%
7	I	663	15% 43% 7% 50%

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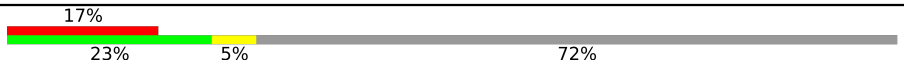
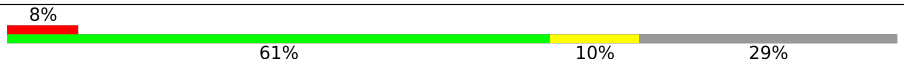
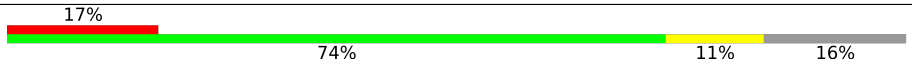
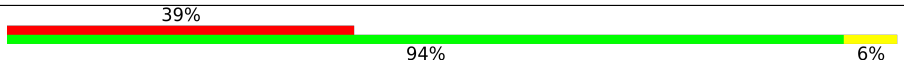
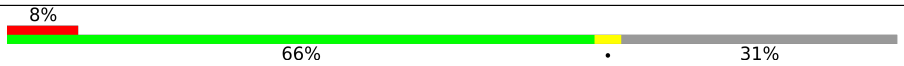
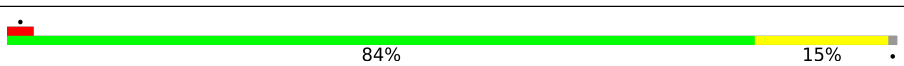
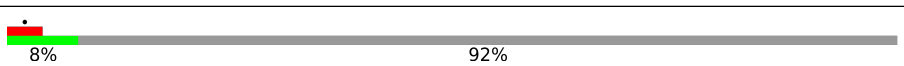
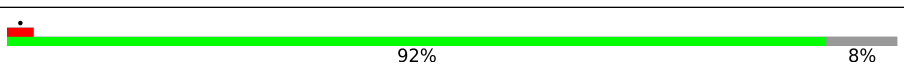
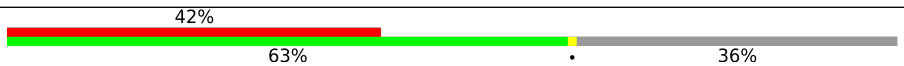
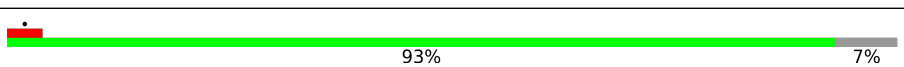
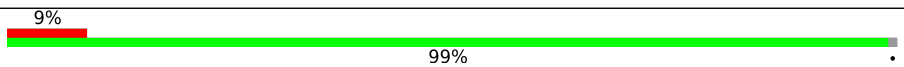
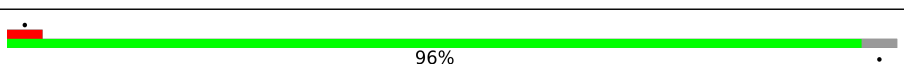
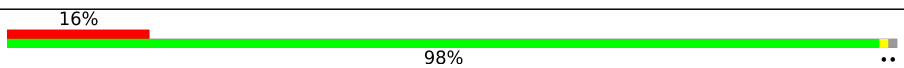
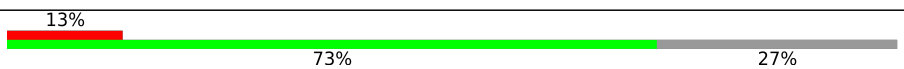
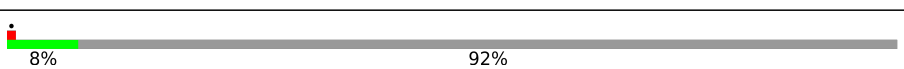
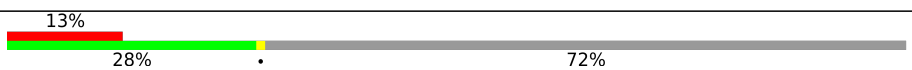
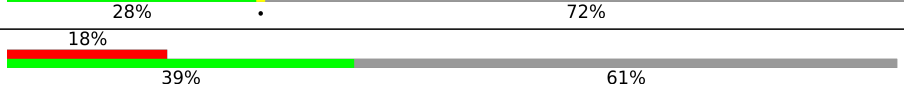
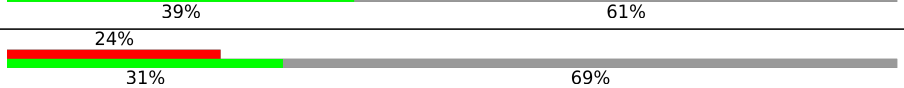
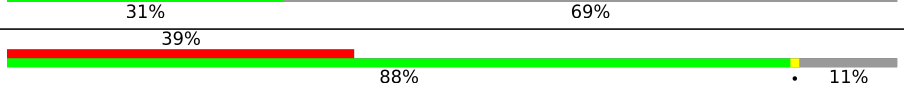
Mol	Chain	Length	Quality of chain
8	P	184	
9	R	189	
10	U	121	
11	V	36	
12	X	142	
13	Z	136	
14	b	647	
15	c	105	
16	d	113	
17	g	121	
18	k	78	
19	m	429	
20	n	104	
21	p	460	
22	t	322	
23	u	199	
24	w	841	
25	j	88	
26	x	606	

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 43123 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 RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	697	14914	6657	2688	4872	697	0	0

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	59	1255	560	222	414	59	0	0

- Molecule 3 is a protein called RRP17 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	5	123	1061	660	196	204	1	0	0

- Molecule 4 is a protein called NOC2 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	8	58	480	290	103	87	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	9	72	48	11	12	1	0	0

- Molecule 6 is a protein called RPL8A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	G	19	175	115	34	26	0	0

- Molecule 7 is a protein called NOC3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	334	Total	C	N	O	S	0	0
			2675	1691	467	507	10		

- Molecule 8 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	P	51	Total	C	N	O	0	0
			433	269	92	72		

- Molecule 9 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	R	134	Total	C	N	O	0	0
			1082	679	220	183		

- Molecule 10 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	U	102	Total	C	N	O	0	0
			808	524	132	152		

- Molecule 11 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	V	36	Total	C	N	O	S	0	0
			277	176	50	47	4		

- Molecule 12 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	X	98	Total	C	N	O	S	0	0
			786	502	138	144	2		

- Molecule 13 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 14 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	b	53	Total	C	N	O	S	0	0
			431	267	86	74	4		

- Molecule 15 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 16 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	d	72	Total	C	N	O	S	0	0
			593	384	115	93	1		

- Molecule 17 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 18 is a protein called RPL38 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 19 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	m	412	Total	C	N	O	S	0	0
			3302	2123	583	586	10		

- Molecule 20 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	n	103	Total	C	N	O	S	0	0
			861	544	164	148	5		

- Molecule 21 is a protein called YTM1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	p	337	Total	C	N	O	S	0	0
			2628	1633	470	518	7		

- Molecule 22 is a protein called RLP7 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	t	26	Total	C	N	O	0	0
			221	132	49	40		

- Molecule 23 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	u	56	Total	C	N	O	S	0	0
			481	303	98	79	1		

- Molecule 24 is a protein called SPB1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	w	328	Total	C	N	O	S	0	0
			2707	1698	489	510	10		

- Molecule 25 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	j	27	Total	C	N	O	S	0	0
			212	127	45	36	4		

- Molecule 26 is a protein called SPB4 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	x	539	Total	C	N	O	S	0	0
			4340	2781	744	795	20		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	405	ALA	THR	conflict	UNP A0A8H8UL81

- Molecule 27 is ZINC ION (three-letter code: ZN) (formula: Zn).

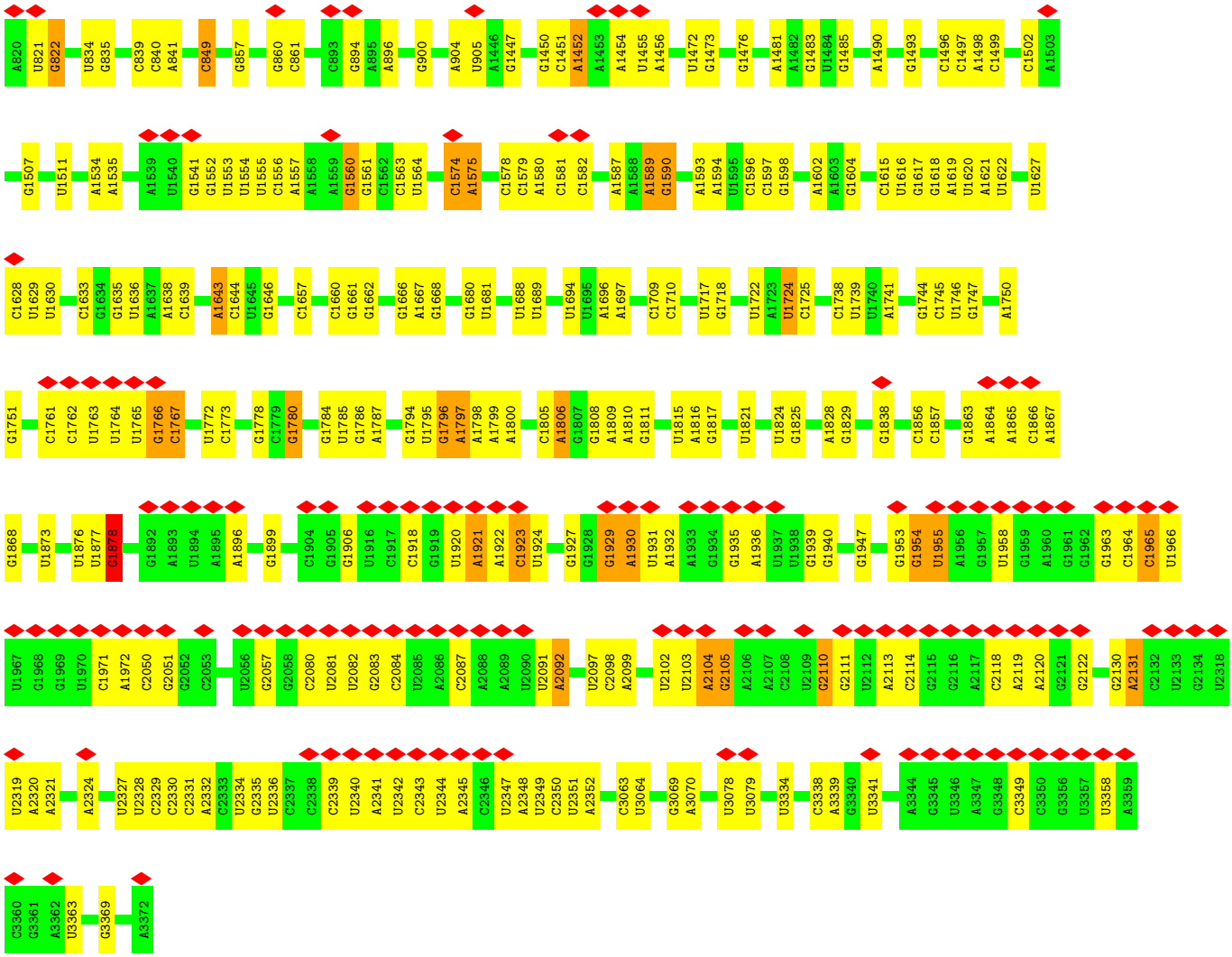
Mol	Chain	Residues	Atoms		AltConf
27	g	1	Total	Zn	0
			1	1	

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.

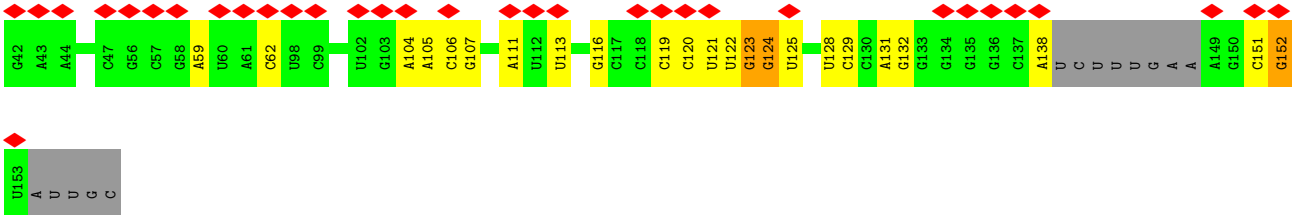
- Molecule 1: 25S rRNA

Chain 1:



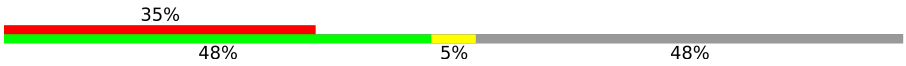
- Molecule 2: 5.8S rRNA

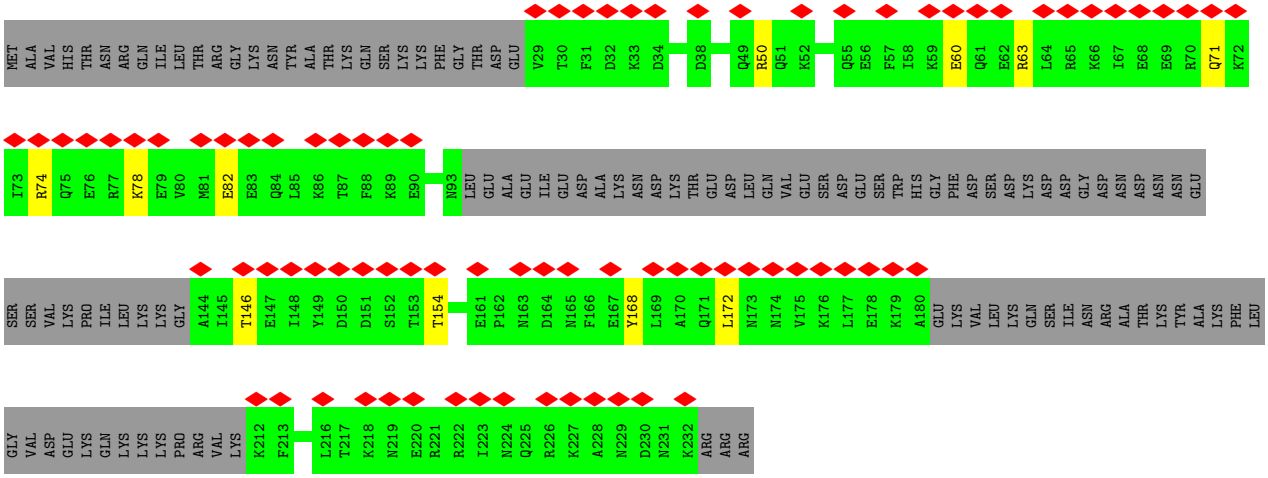
Chain 2:



• Molecule 3: RRP17 isoform 1

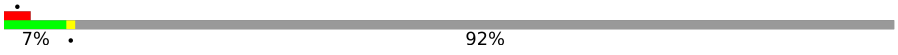
Chain 5:

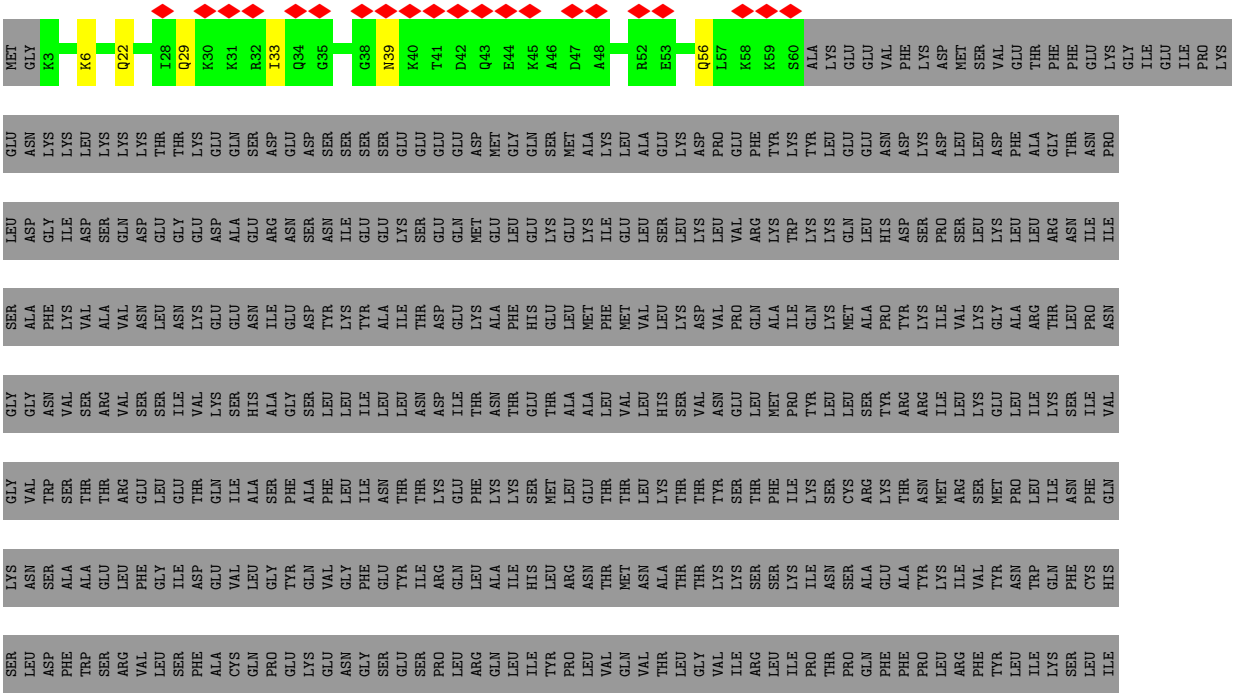


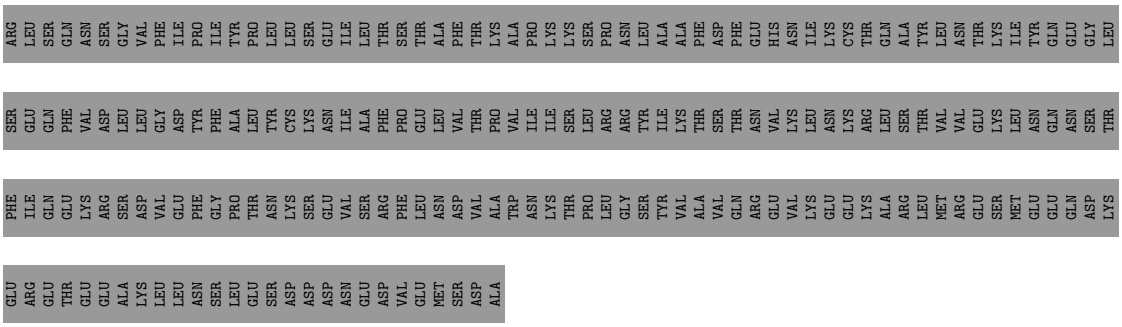


• Molecule 4: NOC2 isoform 1

Chain 8:

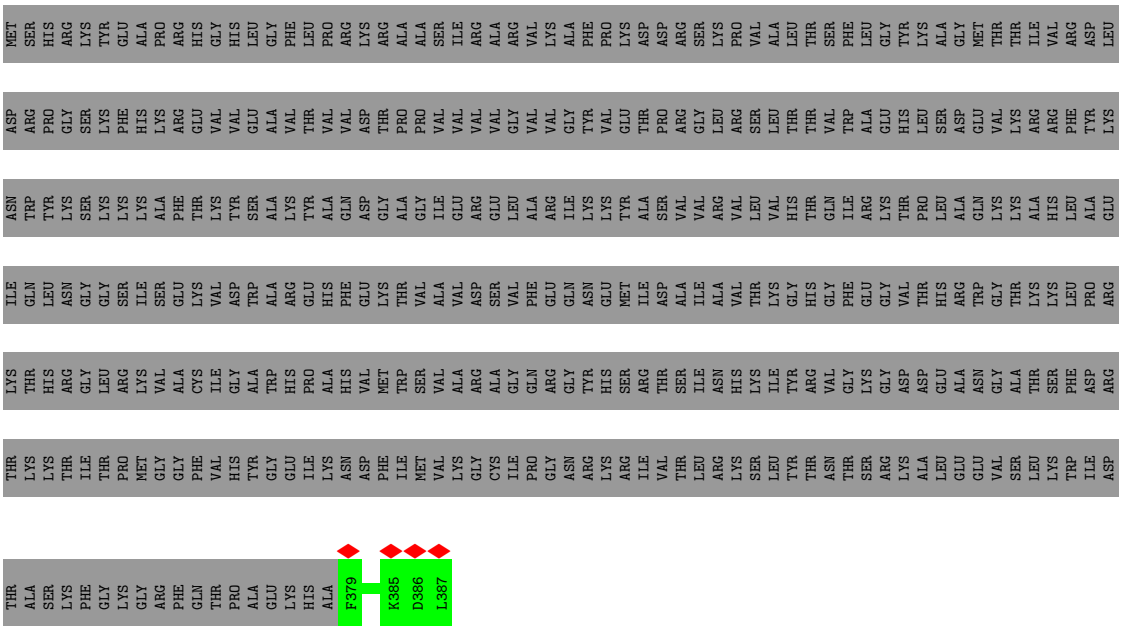






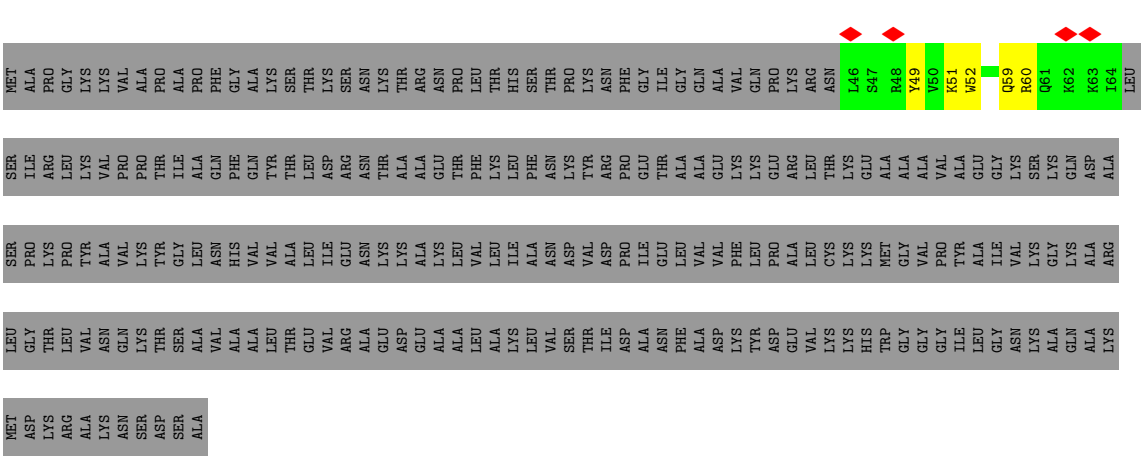
• Molecule 5: 60S ribosomal protein L3

Chain B: 98%

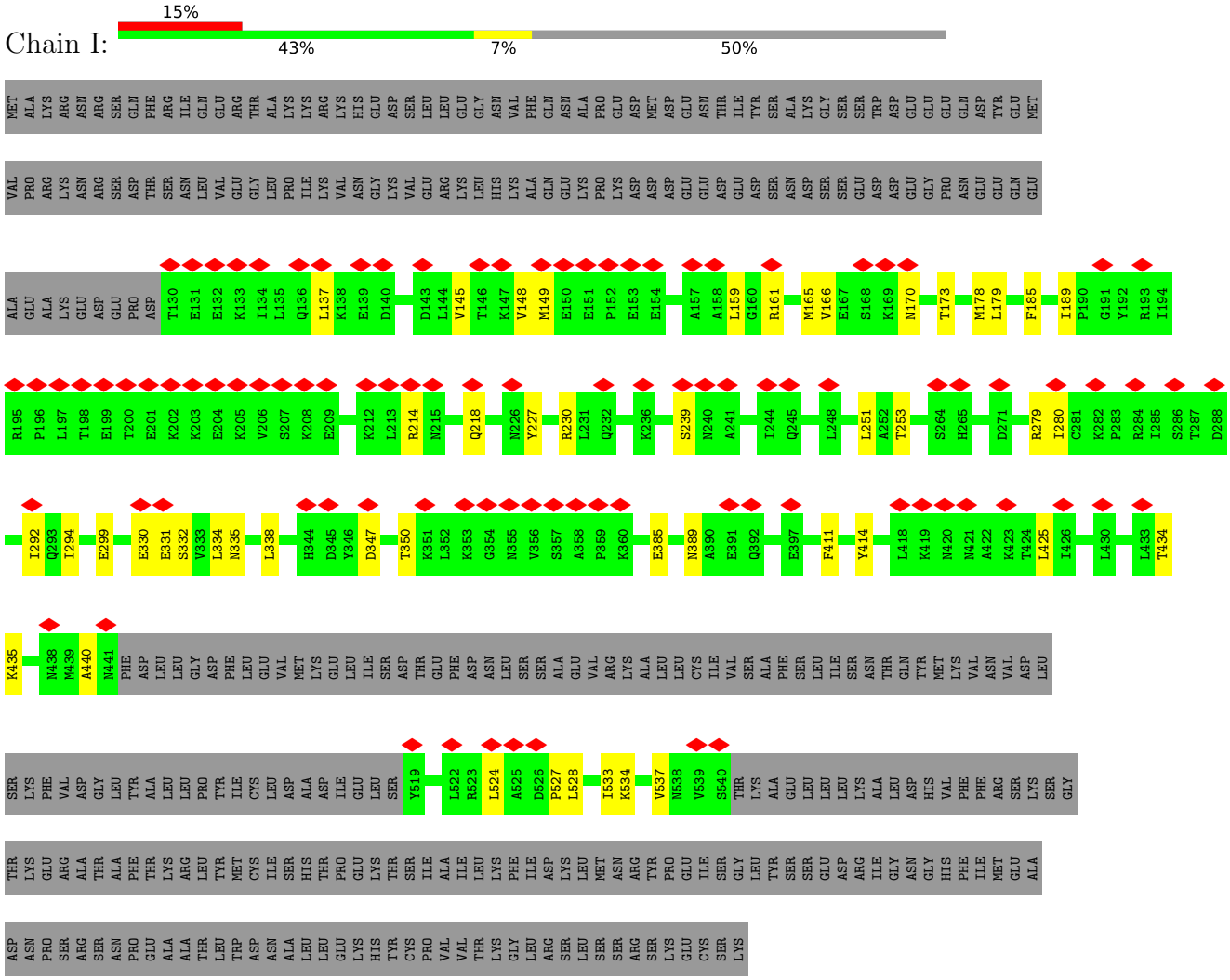


• Molecule 6: RPL8A isoform 1

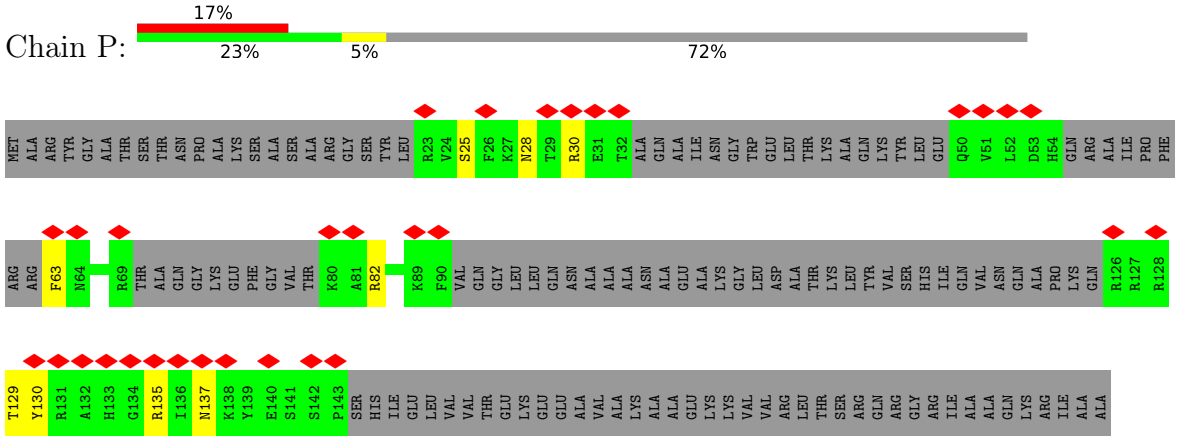
Chain G: 5% 93%



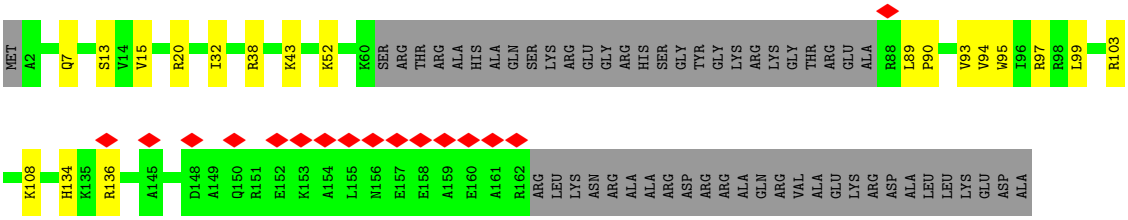
• Molecule 7: NOC3 isoform 1



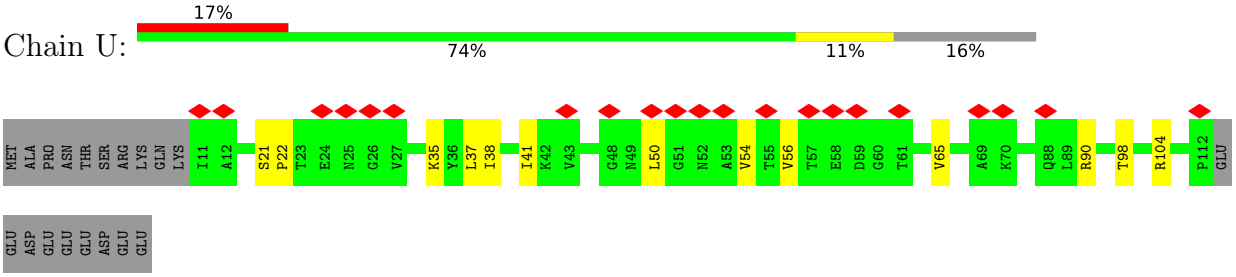
• Molecule 8: 60S ribosomal protein L17-A



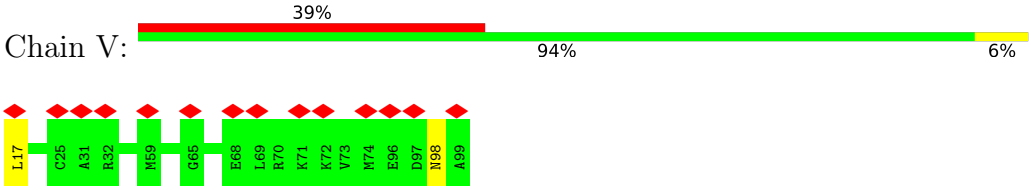
• Molecule 9: 60S ribosomal protein L19-A



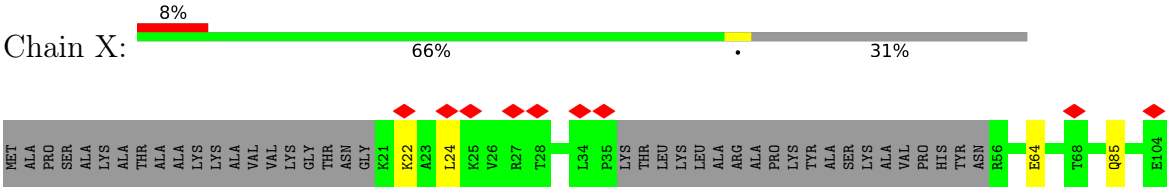
• Molecule 10: 60S ribosomal protein L22-A



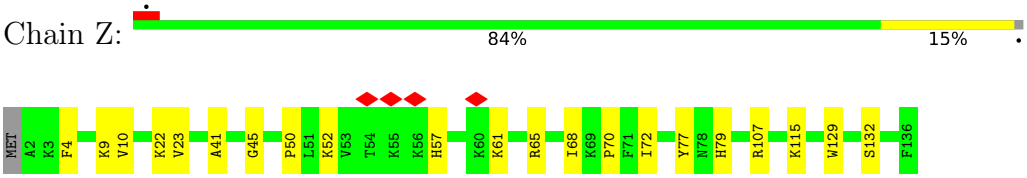
• Molecule 11: 60S ribosomal protein L23-A



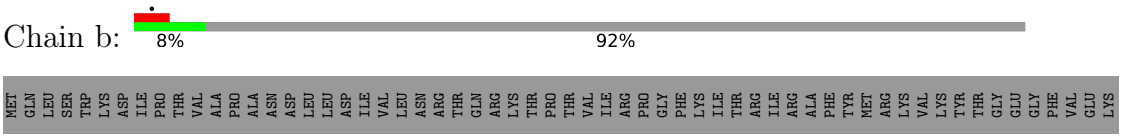
• Molecule 12: 60S ribosomal protein L25

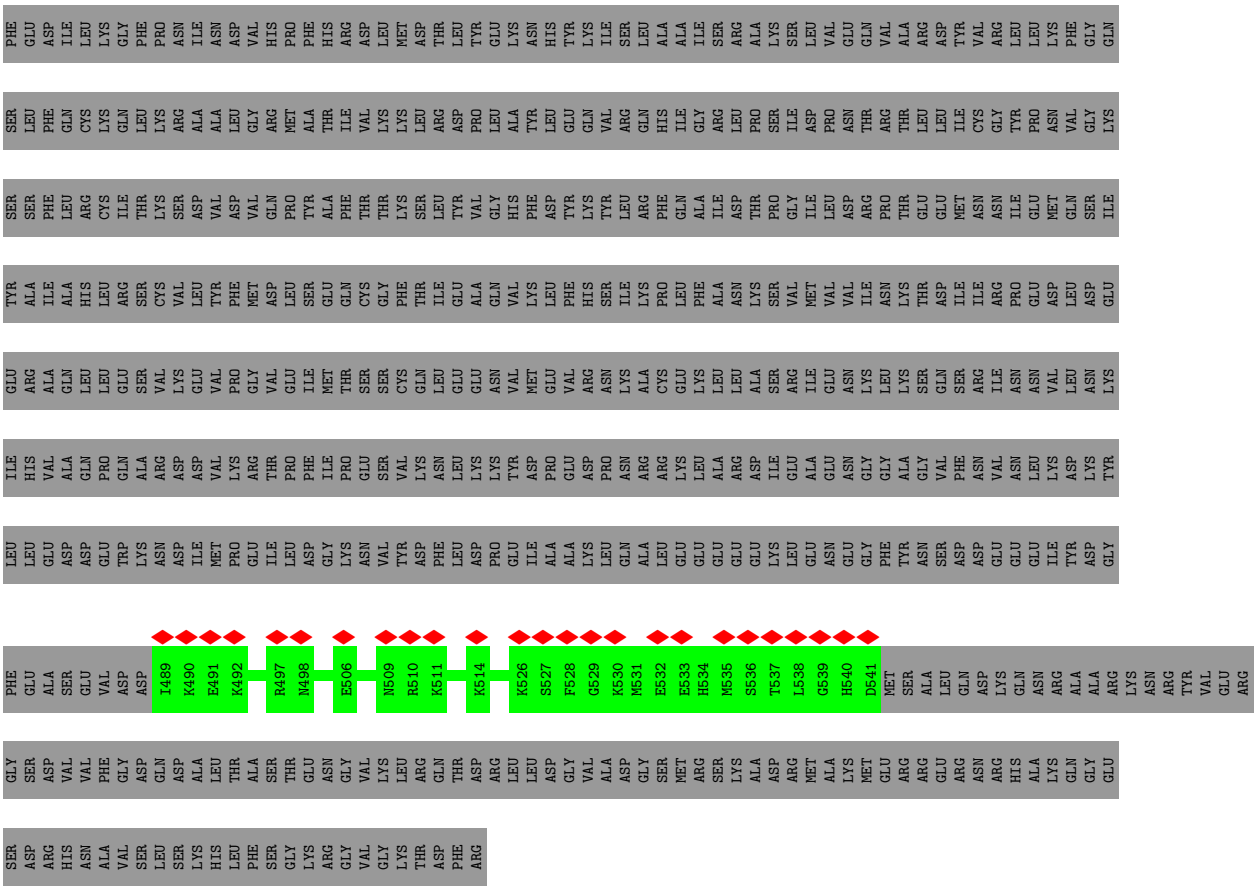


• Molecule 13: 60S ribosomal protein L27-A



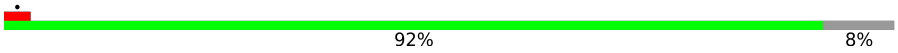
• Molecule 14: Nucleolar GTP-binding protein 1

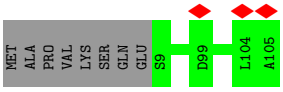




• Molecule 15: 60S ribosomal protein L30

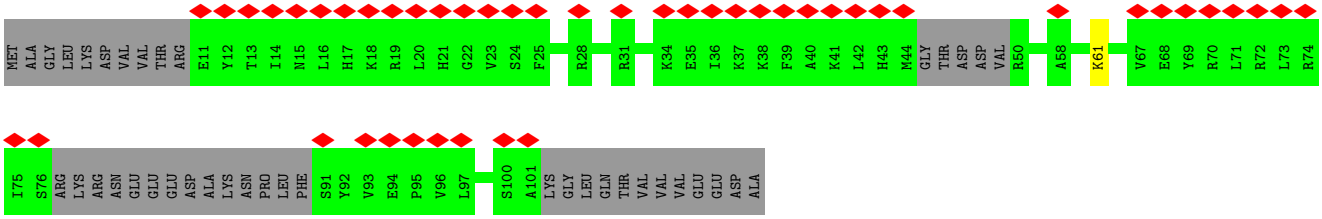
Chain c:





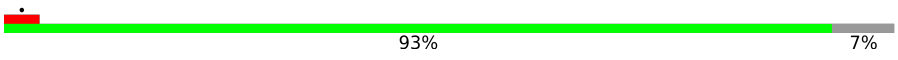
• Molecule 16: 60S ribosomal protein L31-A

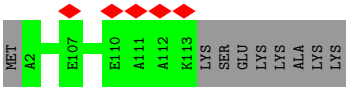
Chain d:



• Molecule 17: 60S ribosomal protein L34-A

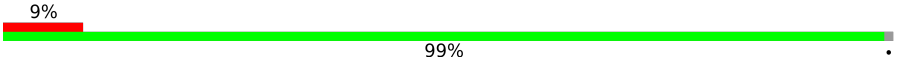
Chain g:

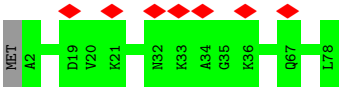




• Molecule 18: RPL38 isoform 1

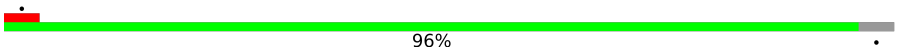
Chain k:

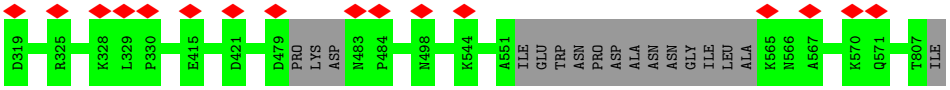




• Molecule 19: Ribosome biogenesis protein ERB1

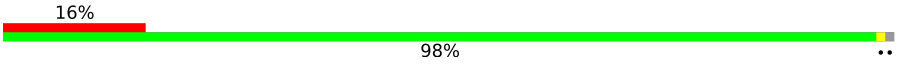
Chain m:

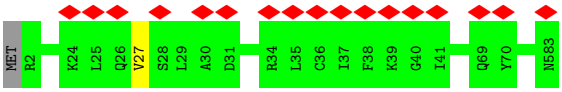




• Molecule 20: Pescadillo homolog

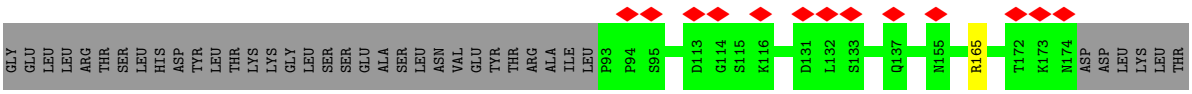
Chain n:

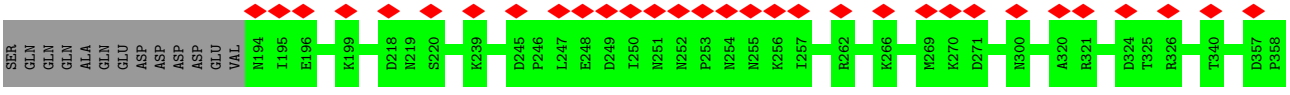


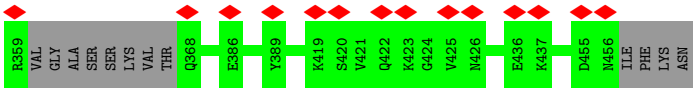


• Molecule 21: YTM1 isoform 1

Chain p:

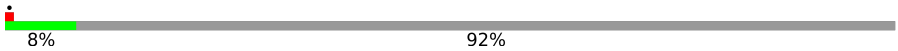


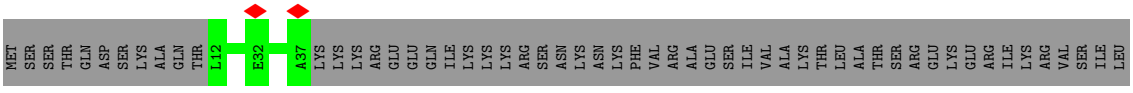


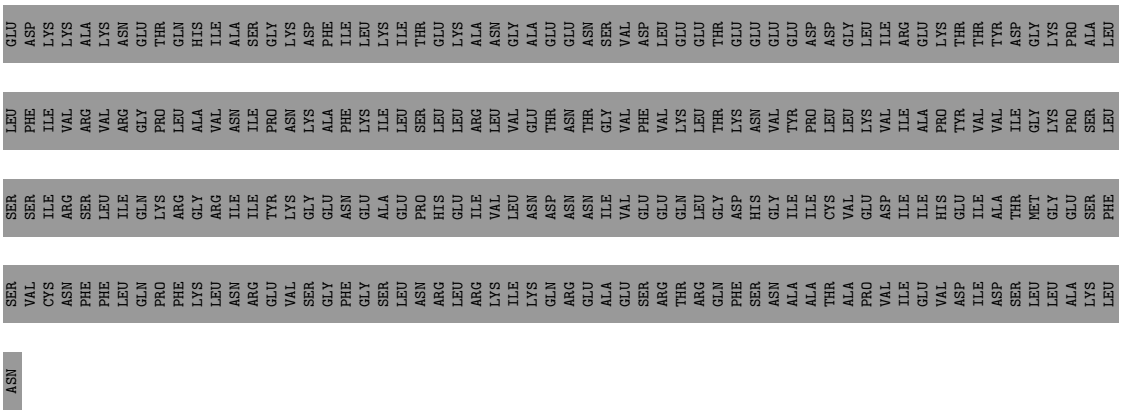


• Molecule 22: RLP7 isoform 1

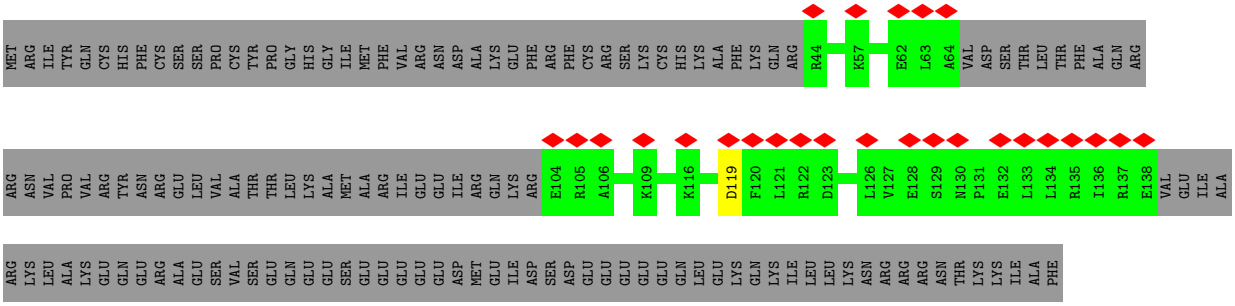
Chain t:



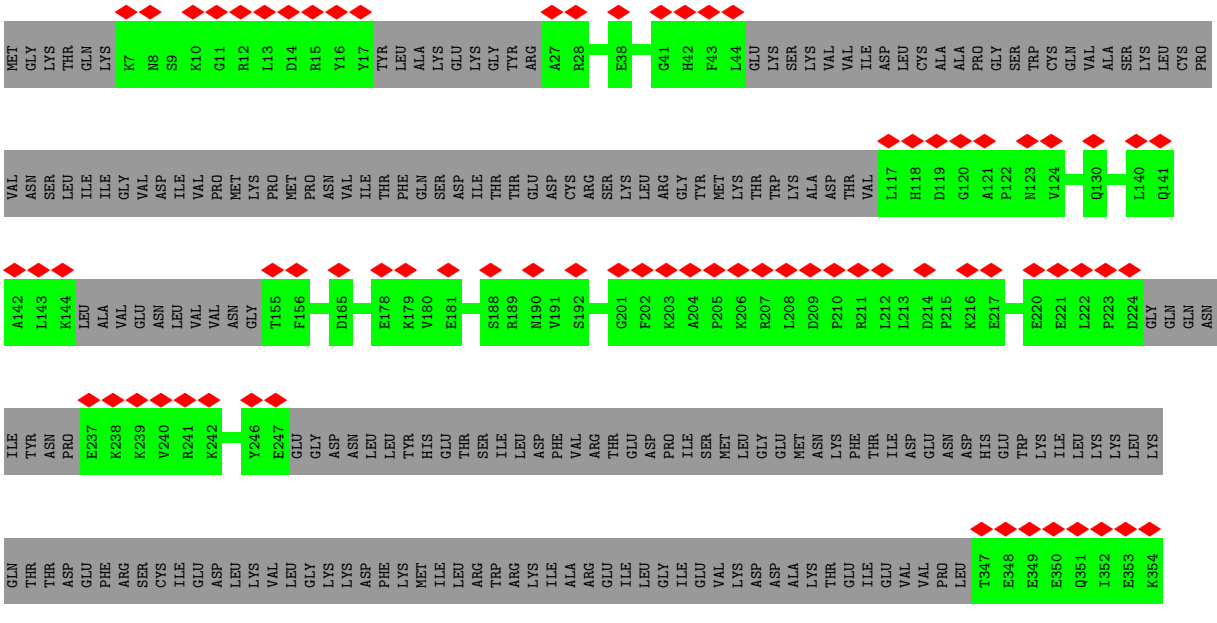


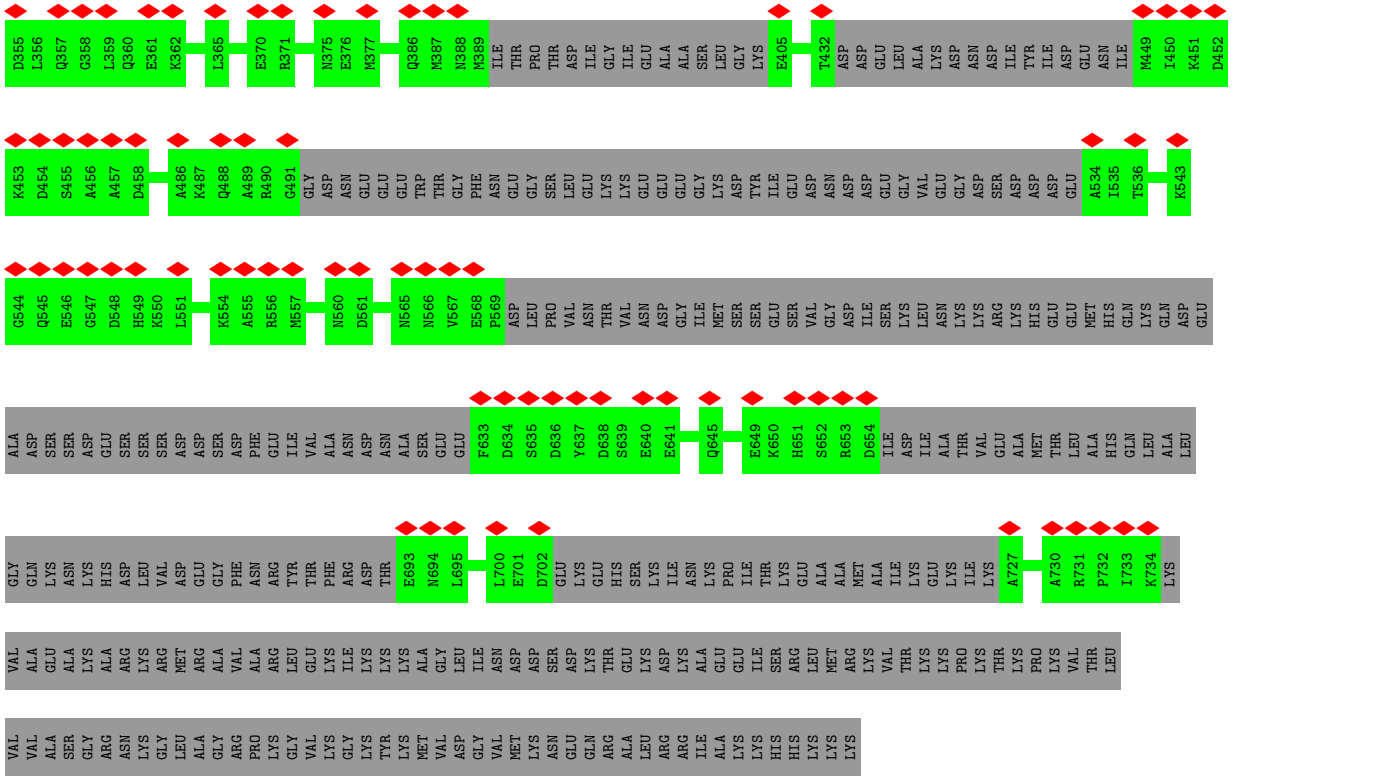


• Molecule 23: Ribosome biogenesis protein RLP24



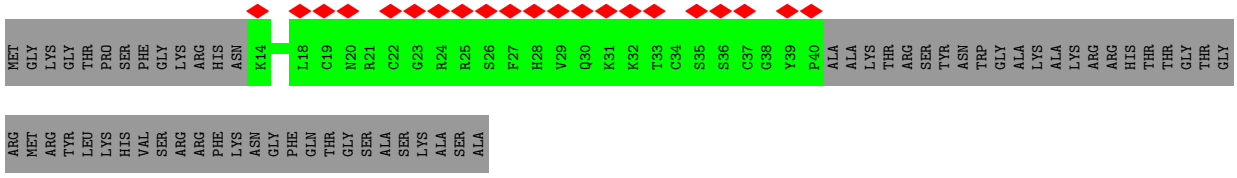
• Molecule 24: SPB1 isoform 1





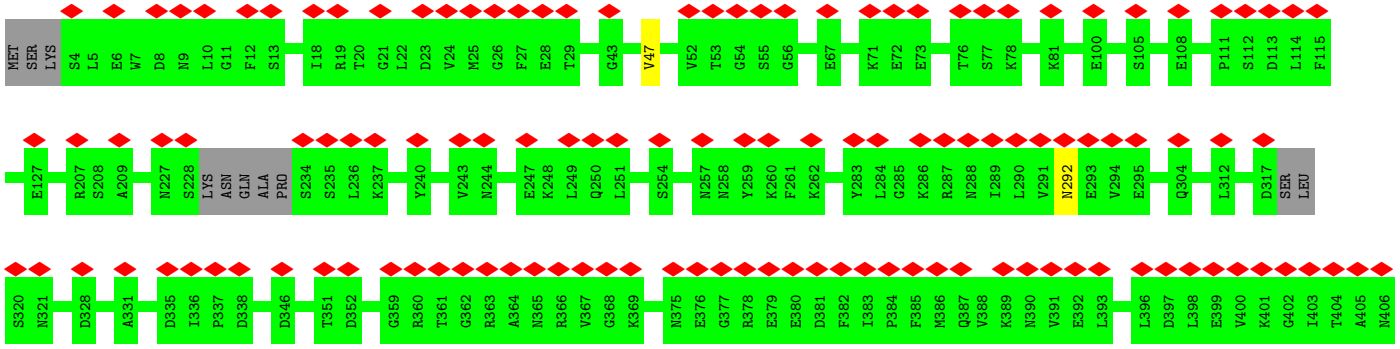
• Molecule 25: 60S ribosomal protein L37-A

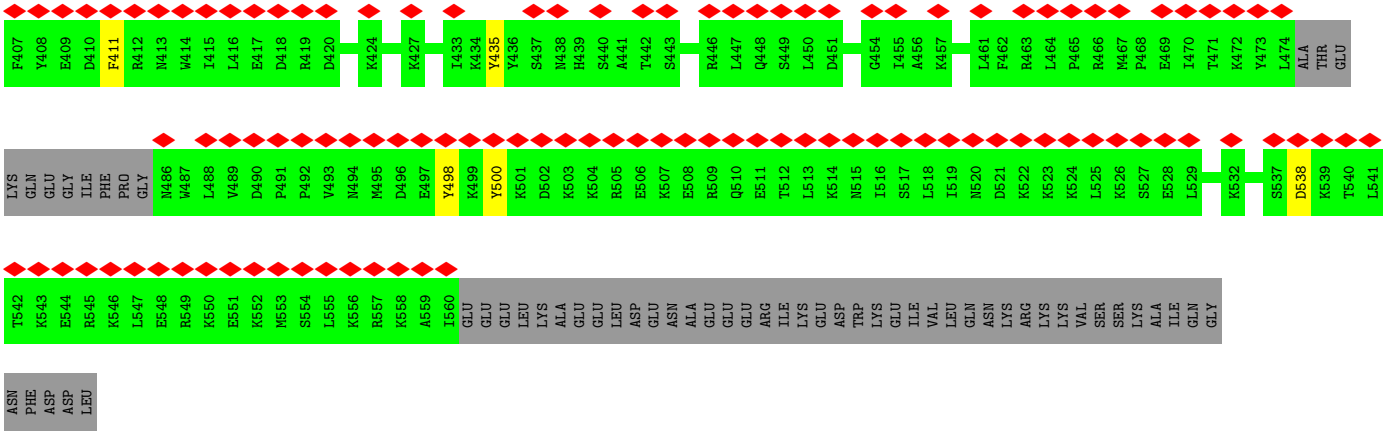
Chain j:



• Molecule 26: SPB4 isoform 1

Chain x:




F407 Y408 E409 D410 F411 R412 N413 W414 I415 L416 E417 D418 R419 D420 K424 K427 I433 K434 Y435 Y436 S437 N438 H439 S440 A441 T442 S443 R446 L447 Q448 S449 L450 D451 G454 I455 A456 K457 L461 F462 R463 L464 P465 R466 M467 P468 E469 I470 T471 K472 Y473 L474 ALA THR GLU
LYS GLN GLU GLY ILE PHE PRO GLY N486 W487 L488 V489 D490 P491 P492 V493 N494 M495 D496 E497 Y498 K499 Y500 K501 D502 K503 K504 R505 E506 K507 E508 R509 Q510 E511 T512 L513 K514 N515 I516 S517 L518 I519 N520 D521 K522 K523 K524 L525 K526 S527 E528 L529 K532 S537 D538 K539 T540 L541
T542 K543 E544 R545 K546 L547 E548 R549 K550 E551 K552 M553 S554 L555 K556 R557 K558 A559 I560 GLU GLU GLU LEU LYS ALA GLU GLU LEU ASP GLU ASN ALA GLU GLU GLU ARG ILE LYS GLU ASP TRP LYS GLU ILE VAL LEU GLN ASN LYS ARG LYS LYS VAL SER SER LYS ALA ILE GLN GLY
ASN PHE ASP ASP LEU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	198000	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 ($e^-/Å^2$)	1.2	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.152	Depositor
Minimum map value	-0.089	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.023	Depositor
Map size (Å)	453.6, 453.6, 453.6	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	1	0.21	0/16678	0.78	5/25974 (0.0%)
2	2	0.24	0/1398	0.73	0/2169
3	5	0.25	0/1070	0.49	0/1421
4	8	0.23	0/482	0.50	0/630
5	B	0.23	0/72	0.35	0/93
6	G	0.23	0/179	0.52	0/239
7	I	0.24	0/2708	0.46	0/3643
8	P	0.22	0/439	0.55	0/579
9	R	0.27	0/1095	0.52	0/1465
10	U	0.25	0/825	0.47	0/1120
11	V	0.25	0/276	0.47	0/363
12	X	0.24	0/794	0.49	0/1066
13	Z	0.25	0/1118	0.46	0/1497
14	b	0.22	0/436	0.49	0/575
15	c	0.25	0/751	0.44	0/1008
16	d	0.24	0/603	0.52	0/804
17	g	0.25	0/891	0.54	0/1191
18	k	0.25	0/618	0.52	0/826
19	m	0.24	0/3387	0.50	0/4594
20	n	0.24	0/872	0.46	0/1151
21	p	0.25	0/2674	0.53	0/3623
22	t	0.22	0/221	0.60	0/294
23	u	0.25	0/487	0.60	1/641 (0.2%)
24	w	0.24	0/2741	0.47	0/3644
25	j	0.25	0/216	0.58	0/286
26	x	0.26	0/4419	0.50	0/5958
All	All	0.24	0/45450	0.63	6/64854 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	1560	G	C8-N9-C1'	5.21	133.78	127.00
23	u	119	ASP	CB-CG-OD2	5.21	122.98	118.30
1	1	1496	C	C2-N1-C1'	5.15	124.47	118.80
1	1	1878	G	C4-N9-C1'	5.11	133.14	126.50
1	1	1923	C	C2-N1-C1'	5.10	124.41	118.80
1	1	1560	G	C4-N9-C1'	-5.08	119.89	126.50

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	1	14914	0	7510	145	0
2	2	1255	0	640	10	0
3	5	1061	0	1076	8	0
4	8	480	0	518	5	0
5	B	72	0	79	0	0
6	G	175	0	188	4	0
7	I	2675	0	2797	27	0
8	P	433	0	434	5	0
9	R	1082	0	1160	12	0
10	U	808	0	822	8	0
11	V	277	0	302	1	0
12	X	786	0	841	2	0
13	Z	1092	0	1155	13	0
14	b	431	0	460	0	0
15	c	743	0	797	0	0
16	d	593	0	640	0	0
17	g	881	0	945	0	0
18	k	612	0	682	0	0
19	m	3302	0	3354	0	0
20	n	861	0	920	0	0
21	p	2628	0	2612	0	0
22	t	221	0	233	0	0
23	u	481	0	511	0	0
24	w	2707	0	2719	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	j	212	0	210	0	0
26	x	4340	0	4468	0	0
27	g	1	0	0	0	0
All	All	43123	0	36073	222	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (222) 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)
1:1:1661:G:H2'	1:1:1662:G:C8	2.22	0.74
1:1:894:G:OP2	1:1:894:G:N2	2.17	0.74
1:1:2082:U:H2'	1:1:2083:G:H8	1.59	0.68
3:5:60:GLU:OE2	3:5:63:ARG:NH2	2.24	0.68
1:1:849:C:H5'	3:5:74:ARG:HH11	1.57	0.68
1:1:1635:G:N2	1:1:1638:A:OP2	2.24	0.68
1:1:1947:G:OP2	1:1:1947:G:N2	2.23	0.67
1:1:1799:A:H2'	1:1:1800:A:H8	1.60	0.66
1:1:1924:U:H1'	1:1:2110:G:N2	2.11	0.66
1:1:1896:A:H61	1:1:2339:C:H42	1.44	0.65
13:Z:23:VAL:HG12	13:Z:45:GLY:HA3	1.77	0.65
1:1:1929:G:H21	9:R:108:LYS:HE2	1.61	0.65
1:1:1493:G:OP2	1:1:1493:G:N2	2.26	0.64
8:P:130:TYR:HD1	8:P:135:ARG:O	1.80	0.64
1:1:1574:C:H2'	1:1:1575:A:C8	2.33	0.64
1:1:1574:C:H2'	1:1:1575:A:H8	1.63	0.63
7:I:280:ILE:HD11	7:I:294:ILE:HB	1.81	0.63
1:1:1809:A:OP2	13:Z:65:ARG:NH1	2.33	0.62
1:1:1799:A:H2'	1:1:1800:A:C8	2.36	0.61
9:R:13:SER:OG	9:R:38:ARG:NH2	2.33	0.60
1:1:1447:G:N7	8:P:25:SER:OG	2.31	0.60
1:1:1596:C:H2'	1:1:1597:C:C6	2.38	0.59
1:1:1954:G:O2'	1:1:1955:U:OP1	2.21	0.58
7:I:299:GLU:HB3	7:I:528:LEU:HD22	1.86	0.58
1:1:1786:G:H2'	1:1:1787:A:C8	2.39	0.57
1:1:2097:U:H2'	1:1:2098:C:C6	2.40	0.57
10:U:37:LEU:O	10:U:41:ILE:HG12	2.05	0.56
1:1:1896:A:H61	1:1:2339:C:N4	2.03	0.56
7:I:338:LEU:HD12	7:I:435:LYS:HD3	1.88	0.56
1:1:2321:A:OP1	3:5:50:ARG:NH2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1657:C:O2'	1:1:1796:G:O2'	2.20	0.55
1:1:1798:A:H2'	1:1:1799:A:C8	2.40	0.55
1:1:2131:A:H61	1:1:2321:A:H61	1.54	0.55
7:I:166:VAL:HG12	7:I:230:ARG:HG2	1.89	0.55
9:R:134:HIS:CE1	9:R:136:ARG:HB2	2.42	0.55
1:1:1696:A:H2'	1:1:1697:A:C8	2.41	0.55
1:1:1972:A:N6	1:1:2051:G:O6	2.39	0.55
1:1:1766:G:HO2'	1:1:1767:C:H6	1.55	0.54
10:U:35:LYS:HD3	10:U:38:ILE:HD11	1.90	0.54
1:1:1497:C:O2'	1:1:1602:A:N3	2.35	0.54
1:1:1620:U:H2'	1:1:1621:A:C8	2.43	0.53
1:1:1920:U:H3'	1:1:1921:A:H8	1.73	0.53
13:Z:50:PRO:HD3	13:Z:68:ILE:HG12	1.90	0.53
13:Z:52:LYS:O	13:Z:65:ARG:NH2	2.42	0.53
1:1:1765:U:O2'	1:1:1766:G:O4'	2.26	0.53
2:2:151:C:H2'	2:2:151:C:O2	2.08	0.53
9:R:89:LEU:HD23	9:R:94:VAL:HG22	1.90	0.53
13:Z:72:ILE:HD11	13:Z:107:ARG:HG3	1.91	0.52
1:1:840:C:H2'	1:1:841:A:H8	1.73	0.52
1:1:1615:C:H2'	1:1:1616:U:C6	2.45	0.52
1:1:1724:U:H1'	1:1:1725:C:C5	2.44	0.51
1:1:1643:A:H5"	1:1:1644:C:C4	2.45	0.51
1:1:1724:U:H1'	1:1:1725:C:C6	2.44	0.51
1:1:1810:A:H2'	1:1:1811:G:C8	2.46	0.51
1:1:1857:C:OP1	4:8:6:LYS:NZ	2.38	0.51
1:1:1717:U:H2'	1:1:1718:G:C8	2.46	0.51
7:I:292:ILE:HD11	7:I:524:LEU:HD12	1.92	0.51
1:1:900:G:H1'	1:1:1589:A:N6	2.26	0.51
1:1:1452:A:N6	1:1:1507:G:O2'	2.34	0.51
1:1:849:C:H5'	3:5:74:ARG:NH1	2.25	0.51
1:1:1618:G:H2'	1:1:1619:A:C8	2.46	0.51
1:1:1899:G:O2'	1:1:2334:U:O4	2.22	0.51
11:V:17:LEU:HD11	11:V:98:ASN:HB3	1.93	0.51
1:1:1680:G:OP2	10:U:90:ARG:NH2	2.44	0.51
8:P:129:THR:O	8:P:137:ASN:HB2	2.10	0.51
7:I:145:VAL:O	7:I:149:MET:HB2	2.11	0.50
2:2:152:G:H5'	6:G:59:GLN:HG3	1.92	0.50
1:1:1797:A:H2'	1:1:1798:A:C8	2.45	0.50
1:1:1877:U:H4'	1:1:1878:G:C5	2.47	0.50
1:1:894:G:N2	4:8:39:ASN:OD1	2.43	0.50
3:5:78:LYS:O	3:5:82:GLU:HG2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2328:U:H2'	1:1:2329:C:H6	1.77	0.49
1:1:1554:U:H4'	1:1:1555:U:H5'	1.93	0.49
1:1:1717:U:H2'	1:1:1718:G:H8	1.77	0.49
1:1:1643:A:H2'	1:1:1644:C:C2	2.48	0.49
1:1:1965:C:H2'	1:1:1966:U:O4'	2.12	0.49
1:1:1722:U:OP2	9:R:103:ARG:NH1	2.46	0.49
1:1:1616:U:H2'	1:1:1617:G:C8	2.47	0.49
1:1:1896:A:N6	1:1:2339:C:H42	2.11	0.49
1:1:1873:U:OP2	9:R:20:ARG:NH2	2.46	0.48
1:1:1553:U:H4'	1:1:1554:U:H5'	1.94	0.48
1:1:1498:A:H2'	1:1:1499:C:C6	2.49	0.48
2:2:131:A:H2'	2:2:132:G:H8	1.78	0.48
1:1:1667:A:H2'	1:1:1668:G:H8	1.78	0.48
1:1:2050:C:O2	1:1:2050:C:H2'	2.13	0.48
7:I:178:MET:O	7:I:227:TYR:OH	2.32	0.48
2:2:152:G:OP2	6:G:60:ARG:NE	2.47	0.48
7:I:334:LEU:HD21	7:I:414:TYR:HE1	1.77	0.48
1:1:1497:C:H2'	1:1:1498:A:H8	1.79	0.48
1:1:1590:G:O2'	1:1:1797:A:N6	2.47	0.48
1:1:1646:G:H1'	1:1:1809:A:N6	2.29	0.48
2:2:123:G:H2'	2:2:124:G:C8	2.49	0.48
7:I:179:LEU:HD21	7:I:251:LEU:HD12	1.95	0.48
10:U:56:VAL:HG22	10:U:65:VAL:HG22	1.96	0.48
1:1:1680:G:H2'	1:1:1681:U:H6	1.77	0.47
1:1:1824:U:H2'	1:1:1825:G:H8	1.79	0.47
1:1:1954:G:HO2'	1:1:1955:U:P	2.36	0.47
1:1:2340:U:H2'	1:1:2341:A:H8	1.79	0.47
1:1:1560:G:O2'	1:1:1561:G:O4'	2.16	0.47
1:1:2082:U:H2'	1:1:2083:G:C8	2.44	0.47
1:1:839:C:H4'	1:1:1724:U:H2'	1.95	0.47
13:Z:70:PRO:HG3	13:Z:115:LYS:HB2	1.95	0.47
1:1:1578:C:H2'	1:1:1579:C:C6	2.48	0.47
1:1:1660:C:H2'	1:1:1661:G:H8	1.79	0.47
1:1:1688:U:H2'	1:1:1689:U:C6	2.50	0.47
1:1:1805:C:H2'	1:1:1806:A:H8	1.79	0.47
9:R:89:LEU:HD12	9:R:90:PRO:HD2	1.98	0.46
1:1:2327:U:H2'	1:1:2328:U:H6	1.80	0.46
1:1:2083:G:H2'	1:1:2084:C:C6	2.50	0.46
1:1:2104:A:H4'	1:1:2105:G:H4'	1.97	0.46
7:I:148:VAL:HG21	7:I:159:LEU:HB2	1.98	0.46
12:X:64:GLU:OE1	12:X:85:GLN:NE2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1828:A:H2'	1:1:1829:G:C8	2.49	0.46
1:1:2342:U:H2'	1:1:2343:C:H6	1.80	0.46
3:5:146:THR:OG1	3:5:154:THR:OG1	2.32	0.46
4:8:29:GLN:O	4:8:33:ILE:HG12	2.16	0.46
1:1:3338:C:H2'	1:1:3339:A:H8	1.81	0.46
10:U:21:SER:HB3	10:U:22:PRO:HD3	1.97	0.46
1:1:1936:A:N3	1:1:1936:A:H2'	2.31	0.46
7:I:185:PHE:O	7:I:189:ILE:HG12	2.16	0.46
7:I:330:GLU:HG2	7:I:332:SER:H	1.80	0.46
12:X:22:LYS:HD3	12:X:24:LEU:HD23	1.98	0.46
1:1:2351:U:H2'	1:1:2352:A:H8	1.81	0.45
7:I:347:ASP:O	7:I:350:THR:HG23	2.16	0.45
1:1:1856:C:H2'	1:1:1857:C:H6	1.82	0.45
6:G:51:LYS:HG3	6:G:52:TRP:CD1	2.52	0.45
1:1:1472:U:H2'	1:1:1473:G:H8	1.82	0.45
1:1:1746:U:H2'	1:1:1747:G:H8	1.81	0.45
1:1:2331:C:H2'	1:1:2332:A:C8	2.51	0.45
1:1:1497:C:H2'	1:1:1498:A:C8	2.52	0.45
1:1:1534:A:H2'	1:1:1535:A:C8	2.52	0.45
1:1:2328:U:H2'	1:1:2329:C:C6	2.51	0.45
7:I:214:ARG:O	7:I:218:GLN:HG2	2.16	0.45
13:Z:10:VAL:HG11	13:Z:129:TRP:HZ3	1.81	0.45
13:Z:41:ALA:HB2	13:Z:77:TYR:HE1	1.82	0.44
1:1:1557:A:OP1	6:G:49:TYR:OH	2.23	0.44
1:1:2331:C:H2'	1:1:2332:A:H8	1.82	0.44
1:1:1621:A:H2'	1:1:1622:U:C6	2.52	0.44
13:Z:57:HIS:HD2	13:Z:61:LYS:HG2	1.83	0.44
10:U:50:LEU:HD22	10:U:54:VAL:HB	1.99	0.44
1:1:2130:G:H2'	1:1:2131:A:C8	2.51	0.44
1:1:2344:U:H2'	1:1:2345:A:C8	2.53	0.44
7:I:385:GLU:OE2	7:I:389:ASN:ND2	2.47	0.44
2:2:119:C:H2'	2:2:120:C:C6	2.53	0.44
7:I:332:SER:O	7:I:335:ASN:HB2	2.18	0.44
9:R:93:VAL:HG12	9:R:97:ARG:HE	1.82	0.44
1:1:1643:A:H5"	1:1:1644:C:C5	2.53	0.44
1:1:1502:C:C5	1:1:1511:U:H5"	2.52	0.44
1:1:2083:G:H2'	1:1:2084:C:H6	1.82	0.44
1:1:1964:C:H3'	1:1:1965:C:H5"	2.00	0.44
10:U:35:LYS:HA	10:U:38:ILE:HG12	2.00	0.44
1:1:1636:U:O2'	13:Z:79:HIS:ND1	2.48	0.43
4:8:56:GLN:HG2	7:I:533:ILE:HD11	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:R:7:GLN:HG2	9:R:32:ILE:HG22	2.00	0.43
1:1:1930:A:H3'	1:1:1931:U:C6	2.53	0.43
1:1:3069:G:C2	1:1:3070:A:C8	3.07	0.43
13:Z:4:PHE:HB2	13:Z:9:LYS:NZ	2.34	0.43
7:I:434:THR:HG21	7:I:537:VAL:HG21	2.01	0.43
1:1:840:C:H2'	1:1:841:A:C8	2.52	0.43
1:1:1667:A:H2'	1:1:1668:G:C8	2.53	0.43
1:1:1778:G:O2'	1:1:1780:G:OP2	2.24	0.43
1:1:1563:C:H2'	1:1:1564:U:C6	2.54	0.43
1:1:1563:C:H2'	1:1:1564:U:H6	1.83	0.43
7:I:534:LYS:HD3	7:I:534:LYS:HA	1.72	0.43
1:1:1560:G:H2'	1:1:1561:G:C8	2.54	0.43
1:1:1616:U:H2'	1:1:1617:G:H8	1.84	0.43
8:P:28:ASN:OD1	8:P:82:ARG:NH1	2.52	0.43
1:1:1593:A:H2'	1:1:1594:A:C8	2.54	0.42
1:1:1666:G:H2'	1:1:1667:A:H8	1.84	0.42
1:1:2342:U:H2'	1:1:2343:C:C6	2.54	0.42
1:1:1963:G:H2'	1:1:1964:C:C6	2.54	0.42
2:2:107:G:H4'	2:2:138:A:H5'	2.00	0.42
2:2:121:U:H2'	2:2:122:U:C6	2.54	0.42
2:2:128:U:OP1	2:2:129:C:N4	2.48	0.42
1:1:834:U:H2'	1:1:835:G:O4'	2.19	0.42
1:1:2097:U:H2'	1:1:2098:C:H6	1.82	0.42
1:1:2327:U:H2'	1:1:2328:U:C6	2.54	0.42
3:5:71:GLN:O	3:5:74:ARG:HG2	2.19	0.42
1:1:1930:A:H3'	1:1:1931:U:H6	1.83	0.42
1:1:1597:C:H2'	1:1:1598:G:C8	2.54	0.42
7:I:253:THR:OG1	7:I:279:ARG:NH2	2.53	0.42
1:1:1680:G:H2'	1:1:1681:U:C6	2.53	0.42
7:I:137:LEU:HD21	7:I:173:THR:HA	2.02	0.42
7:I:331:GLU:HA	7:I:425:LEU:HD23	2.02	0.42
1:1:1660:C:H2'	1:1:1661:G:C8	2.54	0.41
7:I:161:ARG:O	7:I:165:MET:HG3	2.19	0.41
9:R:95:TRP:CZ2	9:R:99:LEU:HD22	2.54	0.41
1:1:3063:C:H2'	1:1:3064:U:H6	1.86	0.41
2:2:122:U:H2'	2:2:123:G:C8	2.56	0.41
3:5:168:TYR:HE1	3:5:172:LEU:HD11	1.85	0.41
1:1:1661:G:H2'	1:1:1662:G:H8	1.77	0.41
1:1:1772:U:H5'	1:1:1773:C:H5'	2.01	0.41
7:I:170:ASN:HB3	7:I:173:THR:OG1	2.20	0.41
1:1:1456:A:N1	1:1:1476:G:O2'	2.42	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1490:A:H61	1:1:1838:G:H1'	1.85	0.41
1:1:1472:U:H2'	1:1:1473:G:C8	2.55	0.41
1:1:1784:G:H2'	1:1:1785:U:O4'	2.21	0.41
1:1:2330:C:H2'	1:1:2331:C:H6	1.86	0.41
7:I:239:SER:O	7:I:239:SER:OG	2.34	0.41
7:I:411:PHE:HE2	7:I:440:ALA:HB2	1.86	0.41
13:Z:22:LYS:NZ	13:Z:132:SER:O	2.36	0.41
10:U:98:THR:HG22	10:U:104:ARG:HE	1.86	0.41
1:1:1597:C:H5'	1:1:1696:A:H1'	2.03	0.40
1:1:1709:C:H2'	1:1:1710:C:H6	1.85	0.40
1:1:1953:G:O4'	1:1:2092:A:N6	2.55	0.40
1:1:1744:G:H2'	1:1:1745:C:C6	2.56	0.40
1:1:2080:C:H2'	1:1:2081:U:C6	2.56	0.40
1:1:2347:U:C2	1:1:2348:A:C8	3.09	0.40
1:1:3338:C:H2'	1:1:3339:A:C8	2.56	0.40
7:I:335:ASN:ND2	7:I:527:PRO:HG3	2.36	0.40
8:P:30:ARG:HD2	8:P:63:PHE:HE2	1.87	0.40
9:R:15:VAL:HG11	9:R:52:LYS:HB2	2.04	0.40
1:1:821:U:H2'	1:1:822:G:C4'	2.51	0.40
1:1:896:A:N3	4:8:22:GLN:NE2	2.67	0.40
1:1:2349:U:H2'	1:1:2350:C:C6	2.56	0.40
9:R:43:LYS:HE3	9:R:43:LYS:HB2	1.78	0.40
1:1:1541:G:O6	1:1:1552:G:N2	2.34	0.40
1:1:1738:C:H2'	1:1:1739:U:C6	2.56	0.40
1:1:1794:G:H2'	1:1:1794:G:N3	2.36	0.40
1:1:1809:A:P	13:Z:65:ARG:HH12	2.44	0.40
1:1:1958:U:H3	1:1:2083:G:H1	1.68	0.40
1:1:2098:C:H2'	1:1:2099:A:O4'	2.22	0.40

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	
3	5	117/235 (50%)	114 (97%)	3 (3%)	0	100	100
4	8	56/710 (8%)	55 (98%)	1 (2%)	0	100	100
5	B	7/387 (2%)	7 (100%)	0	0	100	100
6	G	17/256 (7%)	17 (100%)	0	0	100	100
7	I	330/663 (50%)	317 (96%)	13 (4%)	0	100	100
8	P	41/184 (22%)	38 (93%)	3 (7%)	0	100	100
9	R	130/189 (69%)	129 (99%)	1 (1%)	0	100	100
10	U	100/121 (83%)	96 (96%)	4 (4%)	0	100	100
11	V	28/36 (78%)	28 (100%)	0	0	100	100
12	X	94/142 (66%)	93 (99%)	1 (1%)	0	100	100
13	Z	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
14	b	51/647 (8%)	49 (96%)	2 (4%)	0	100	100
15	c	95/105 (90%)	95 (100%)	0	0	100	100
16	d	66/113 (58%)	66 (100%)	0	0	100	100
17	g	110/121 (91%)	109 (99%)	1 (1%)	0	100	100
18	k	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
19	m	404/429 (94%)	387 (96%)	17 (4%)	0	100	100
20	n	99/104 (95%)	96 (97%)	3 (3%)	0	100	100
21	p	331/460 (72%)	306 (92%)	25 (8%)	0	100	100
22	t	24/322 (8%)	23 (96%)	1 (4%)	0	100	100
23	u	52/199 (26%)	52 (100%)	0	0	100	100
24	w	304/841 (36%)	293 (96%)	11 (4%)	0	100	100
25	j	25/88 (28%)	24 (96%)	1 (4%)	0	100	100
26	x	531/606 (88%)	510 (96%)	21 (4%)	0	100	100
All	All	3220/7172 (45%)	3109 (97%)	111 (3%)	0	100	100

There are no Ramachandran outliers to report.

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
3	5	117/217 (54%)	117 (100%)	0	100 100
4	8	52/647 (8%)	52 (100%)	0	100 100
5	B	8/323 (2%)	8 (100%)	0	100 100
6	G	19/208 (9%)	19 (100%)	0	100 100
7	I	306/602 (51%)	306 (100%)	0	100 100
8	P	46/146 (32%)	46 (100%)	0	100 100
9	R	112/154 (73%)	112 (100%)	0	100 100
10	U	89/107 (83%)	89 (100%)	0	100 100
11	V	30/30 (100%)	30 (100%)	0	100 100
12	X	87/118 (74%)	87 (100%)	0	100 100
13	Z	115/116 (99%)	115 (100%)	0	100 100
14	b	46/573 (8%)	46 (100%)	0	100 100
15	c	81/88 (92%)	81 (100%)	0	100 100
16	d	62/97 (64%)	61 (98%)	1 (2%)	62 85
17	g	95/103 (92%)	95 (100%)	0	100 100
18	k	68/69 (99%)	68 (100%)	0	100 100
19	m	367/381 (96%)	367 (100%)	0	100 100
20	n	92/93 (99%)	91 (99%)	1 (1%)	73 90
21	p	300/413 (73%)	299 (100%)	1 (0%)	92 97
22	t	24/287 (8%)	24 (100%)	0	100 100
23	u	49/180 (27%)	49 (100%)	0	100 100
24	w	294/745 (40%)	294 (100%)	0	100 100
25	j	25/71 (35%)	25 (100%)	0	100 100
26	x	489/548 (89%)	482 (99%)	7 (1%)	67 86
All	All	2973/6316 (47%)	2963 (100%)	10 (0%)	92 97

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	d	61	LYS
20	n	27	VAL
21	p	165	ARG
26	x	47	VAL

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Mol	Chain	Res	Type
26	x	292	ASN
26	x	411	PHE
26	x	435	TYR
26	x	498	TYR
26	x	500	TYR
26	x	538	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	684/697 (98%)	106 (15%)	2 (0%)
2	2	55/72 (76%)	11 (20%)	1 (1%)
All	All	739/769 (96%)	117 (15%)	3 (0%)

All (117) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	822	G
1	1	849	C
1	1	857	G
1	1	860	G
1	1	861	C
1	1	904	A
1	1	905	U
1	1	1450	G
1	1	1451	C
1	1	1452	A
1	1	1454	A
1	1	1455	U
1	1	1481	A
1	1	1483	G
1	1	1485	G
1	1	1556	C
1	1	1575	A
1	1	1580	A
1	1	1581	C
1	1	1582	C
1	1	1587	A

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Mol	Chain	Res	Type
1	1	1589	A
1	1	1590	G
1	1	1604	G
1	1	1627	U
1	1	1628	C
1	1	1629	U
1	1	1630	U
1	1	1633	C
1	1	1639	C
1	1	1643	A
1	1	1694	U
1	1	1724	U
1	1	1741	A
1	1	1750	A
1	1	1751	G
1	1	1761	C
1	1	1762	C
1	1	1763	U
1	1	1764	U
1	1	1766	G
1	1	1767	C
1	1	1780	G
1	1	1795	U
1	1	1796	G
1	1	1797	A
1	1	1806	A
1	1	1808	G
1	1	1815	U
1	1	1816	A
1	1	1817	G
1	1	1821	U
1	1	1863	G
1	1	1864	A
1	1	1865	A
1	1	1866	C
1	1	1867	A
1	1	1868	G
1	1	1876	U
1	1	1878	G
1	1	1906	G
1	1	1918	C
1	1	1921	A

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Mol	Chain	Res	Type
1	1	1922	A
1	1	1923	C
1	1	1927	G
1	1	1929	G
1	1	1930	A
1	1	1932	A
1	1	1935	G
1	1	1939	G
1	1	1940	G
1	1	1954	G
1	1	1955	U
1	1	1965	C
1	1	1971	C
1	1	2057	G
1	1	2087	C
1	1	2091	U
1	1	2092	A
1	1	2102	U
1	1	2103	U
1	1	2104	A
1	1	2105	G
1	1	2110	G
1	1	2111	G
1	1	2113	A
1	1	2114	C
1	1	2118	C
1	1	2119	A
1	1	2120	A
1	1	2122	G
1	1	2131	A
1	1	2319	U
1	1	2320	A
1	1	2324	A
1	1	2335	G
1	1	2336	U
1	1	3078	U
1	1	3079	U
1	1	3334	U
1	1	3341	U
1	1	3349	C
1	1	3358	U
1	1	3363	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	3369	G
2	2	59	A
2	2	62	C
2	2	104	A
2	2	105	A
2	2	106	C
2	2	111	A
2	2	113	U
2	2	116	G
2	2	124	G
2	2	125	U
2	2	152	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1574	C
1	1	1954	G
2	2	123	G

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)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	1	13
11	V	3
2	2	2
20	n	1
19	m	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	905:U	O3'	1446:A	P	67.50
1	n	70:TYR	C	550:GLU	N	61.88
1	1	2356:A	O3'	3061:G	P	60.66
1	1	1906:G	O3'	1916:U	P	41.20
1	1	864:G	O3'	893:C	P	34.94
1	1	1884:A	O3'	1892:G	P	27.85
1	V	74:MET	C	96:GLU	N	22.75
1	2	62:C	O3'	98:U	P	20.83
1	1	2058:G	O3'	2080:C	P	18.58
1	1	1541:G	O3'	1552:G	P	18.29
1	1	3081:C	O3'	3333:G	P	17.92
1	2	47:C	O3'	56:G	P	17.79
1	1	1566:A	O3'	1574:C	P	17.24
1	1	1972:A	O3'	2050:C	P	16.94
1	m	330:PRO	C	392:LEU	N	16.87
1	1	3350:C	O3'	3356:G	P	14.97
1	1	2134:G	O3'	2318:U	P	13.42
1	1	1838:G	O3'	1853:U	P	9.56
1	V	25:CYS	C	31:ALA	N	7.34
1	V	37:ILE	C	59:MET	N	5.87

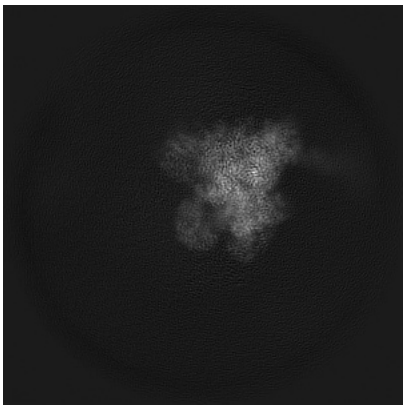
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-24270. These allow visual inspection of the internal detail of the map and identification of artifacts.

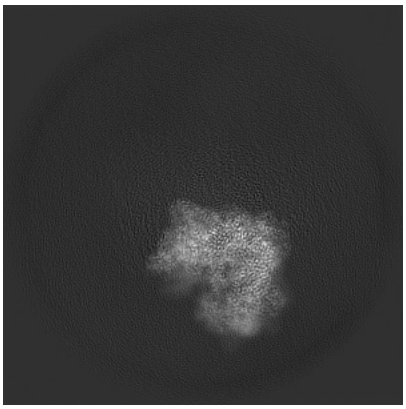
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

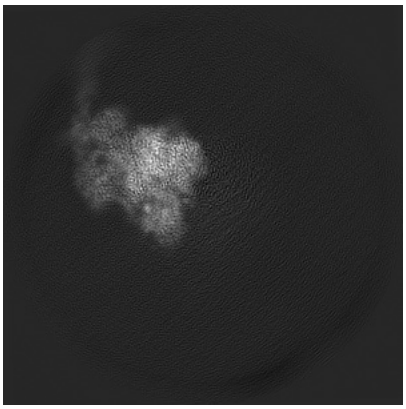
6.1.1 Primary map



X

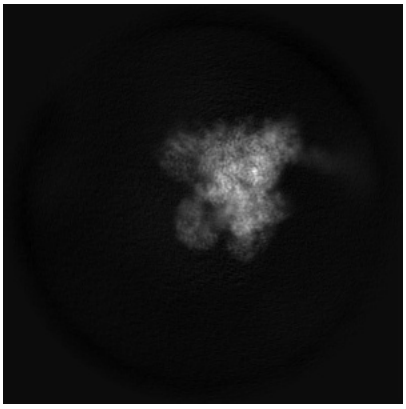


Y

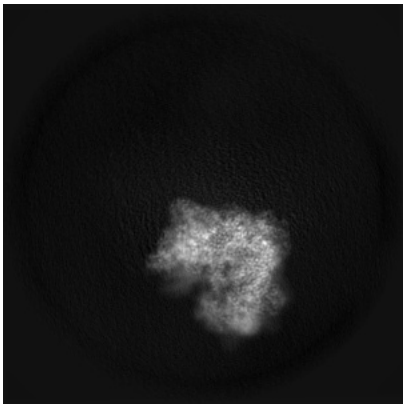


Z

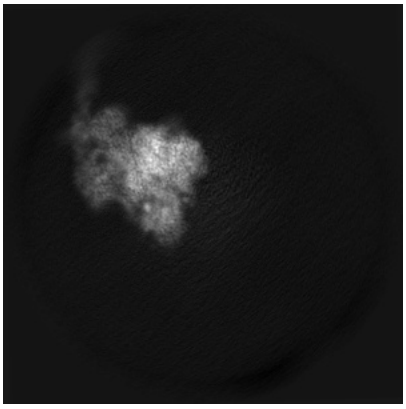
6.1.2 Raw map



X



Y

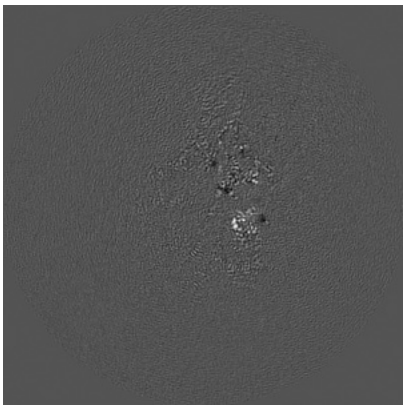


Z

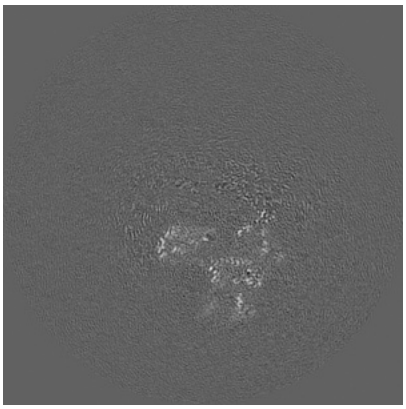
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

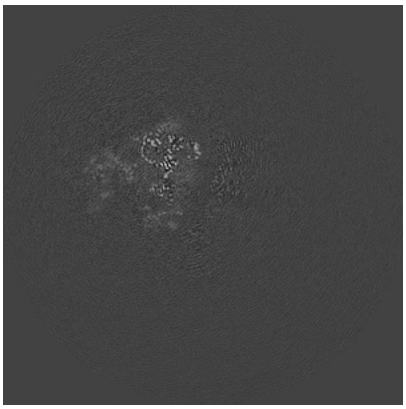
6.2.1 Primary map



X Index: 210

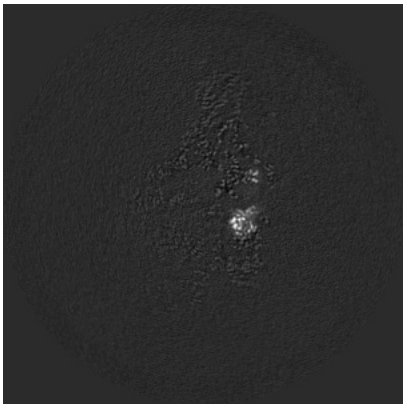


Y Index: 210

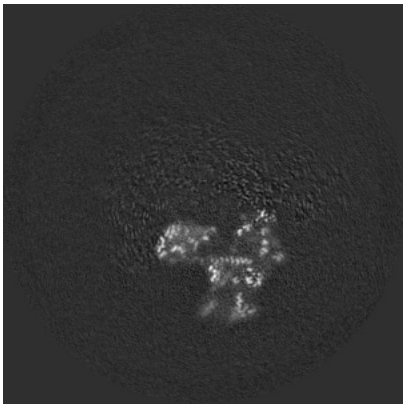


Z Index: 210

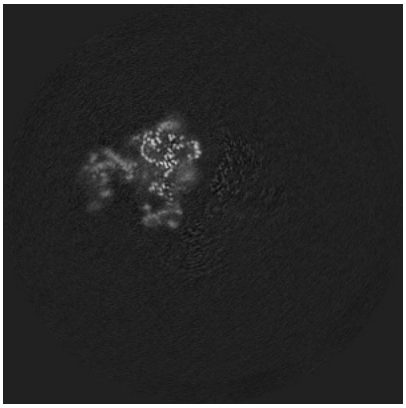
6.2.2 Raw map



X Index: 210



Y Index: 210

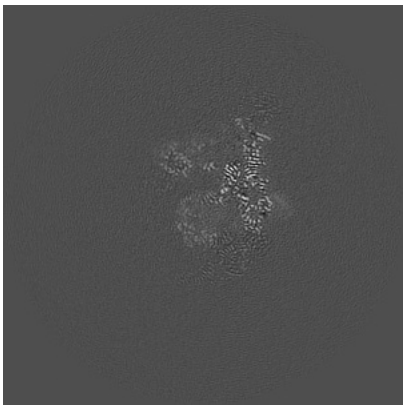


Z Index: 210

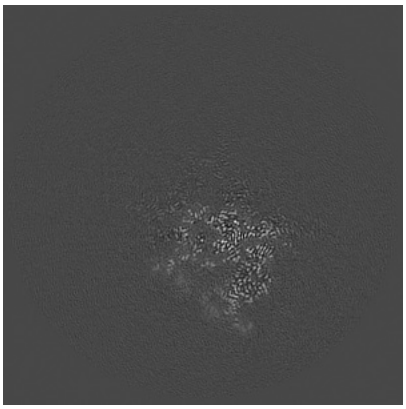
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

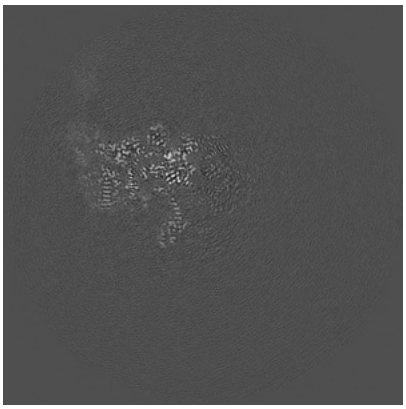
6.3.1 Primary map



X Index: 178

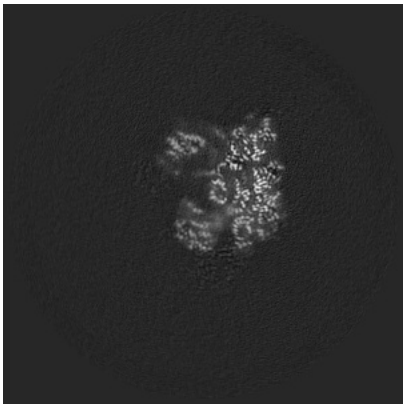


Y Index: 263

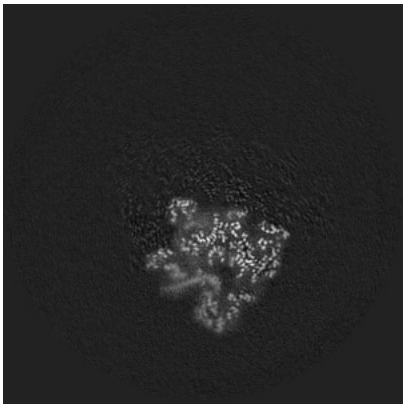


Z Index: 247

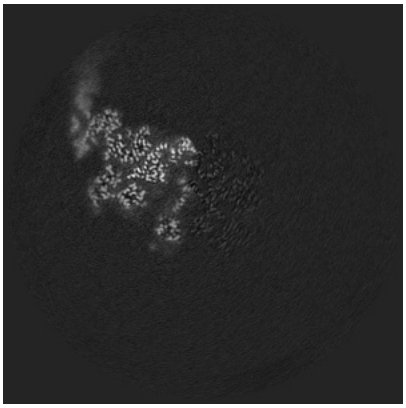
6.3.2 Raw map



X Index: 161



Y Index: 248



Z Index: 258

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

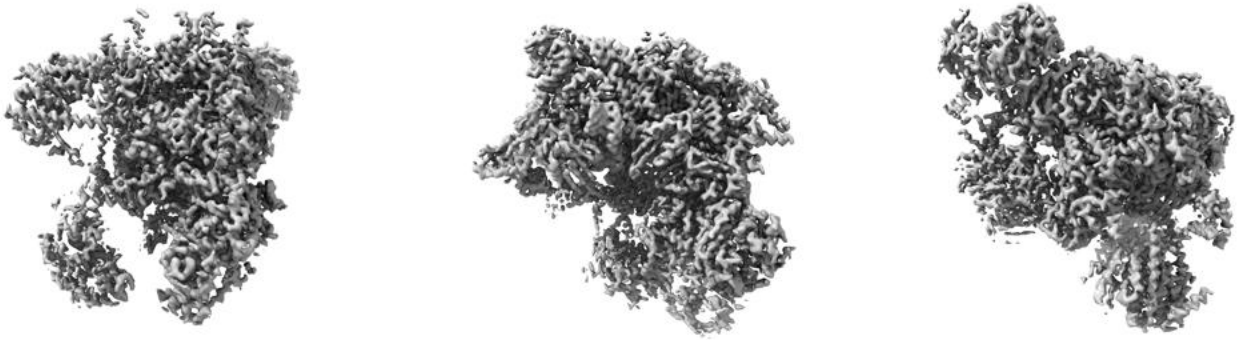
6.4 Orthogonal surface views (i)

6.4.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.023. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

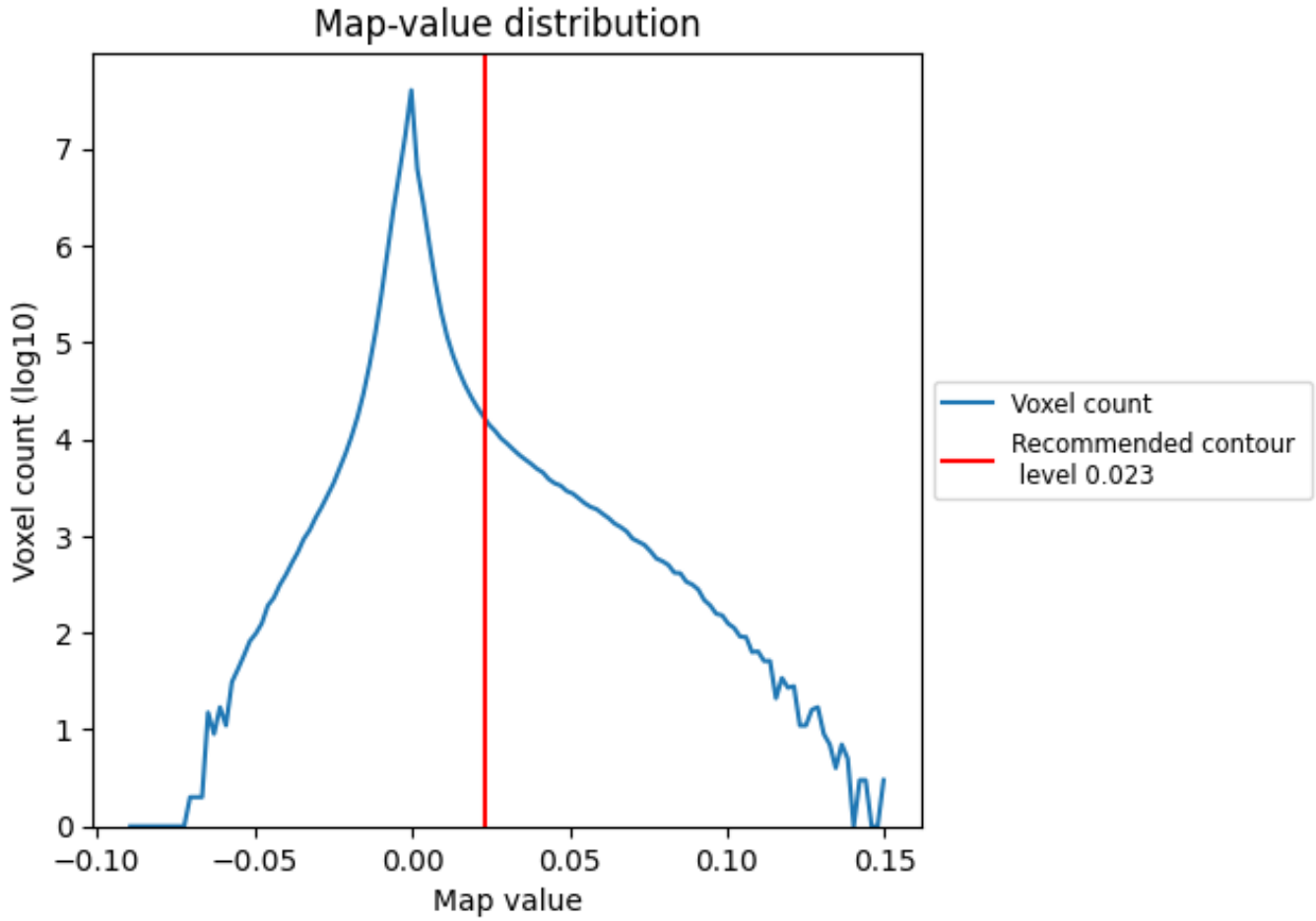
6.5 Mask visualisation (i)

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

7 Map analysis

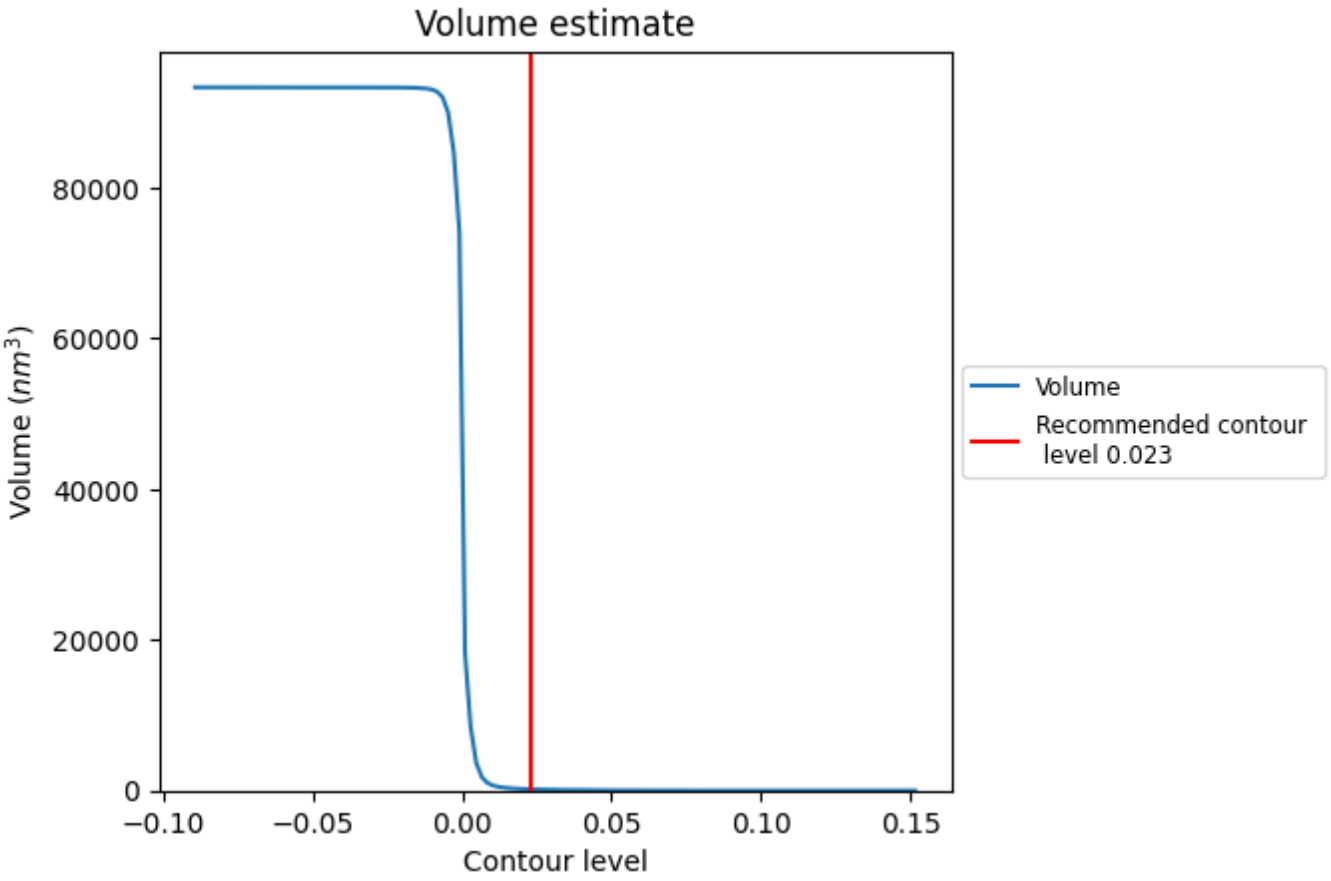
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

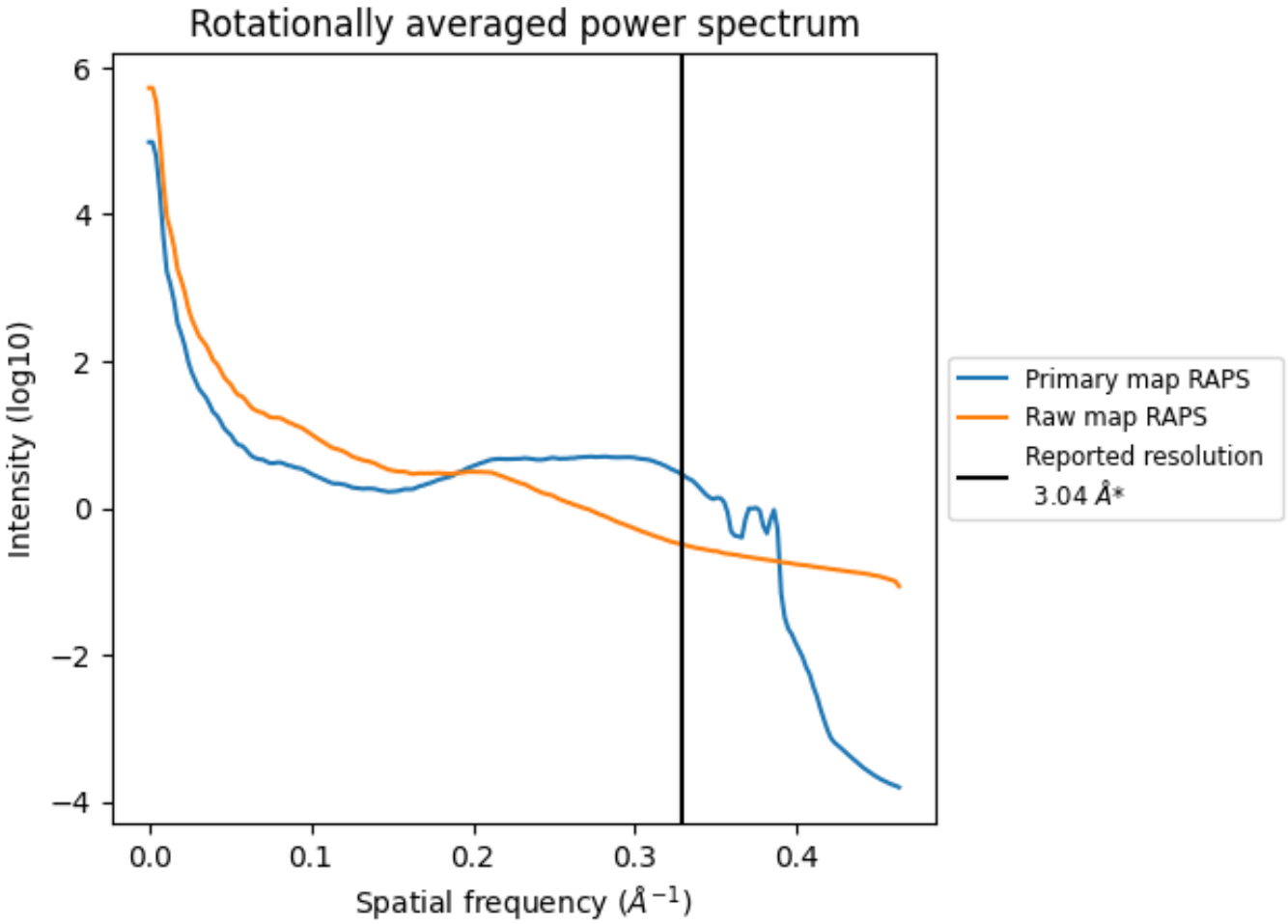
7.2 Volume estimate



The volume at the recommended contour level is 169 nm^3; this corresponds to an approximate mass of 153 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)

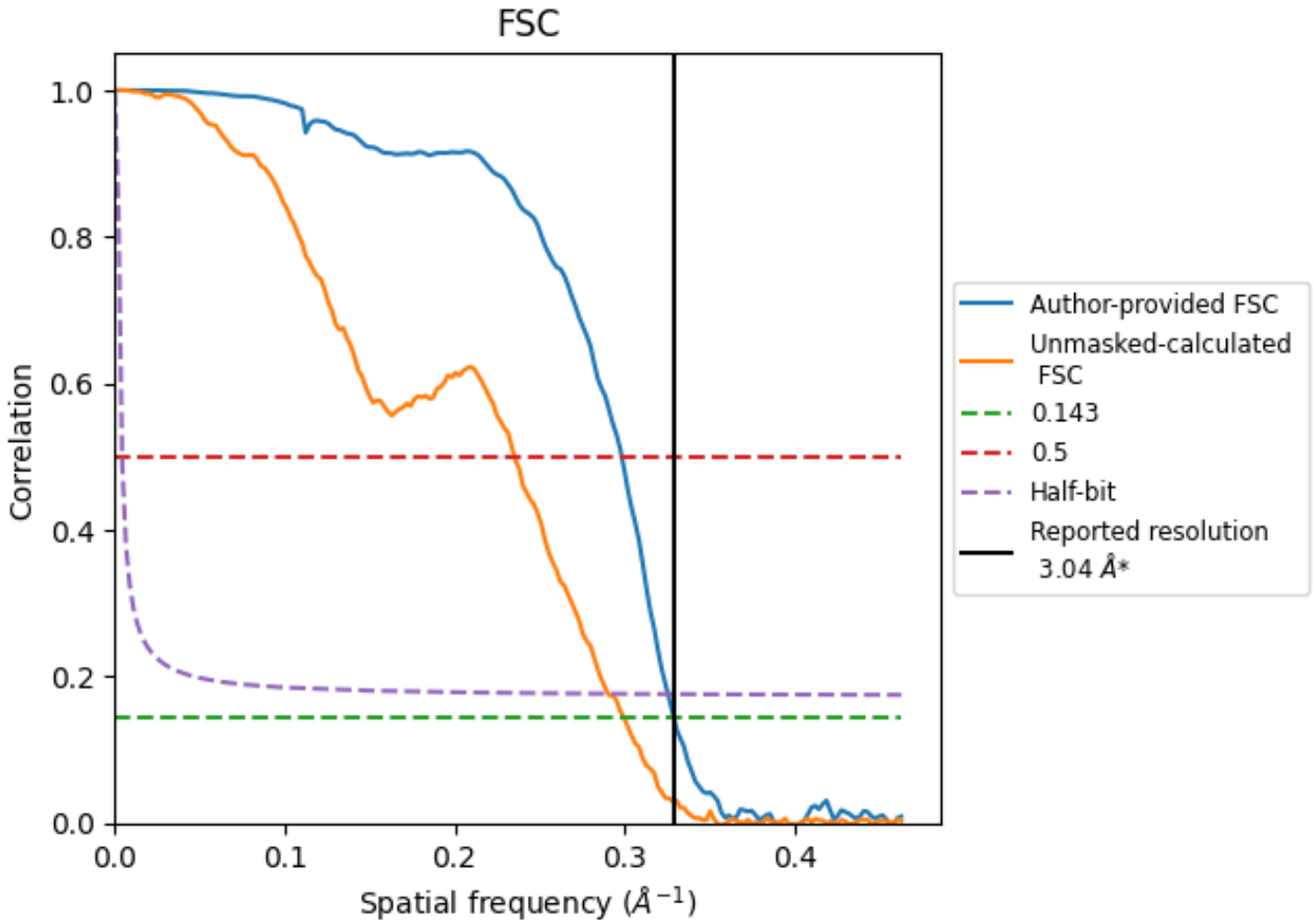


*Reported resolution corresponds to spatial frequency of 0.329 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.329 Å^{-1}

8.2 Resolution estimates (i)

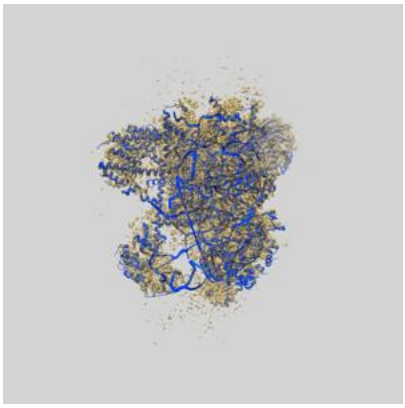
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.04	-	-
Author-provided FSC curve	3.04	3.35	3.07
Unmasked-calculated*	3.33	4.25	3.44

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

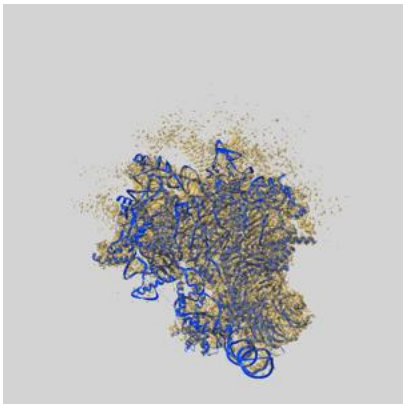
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-24270 and PDB model 7NAD. Per-residue inclusion information can be found in section 3 on page 9.

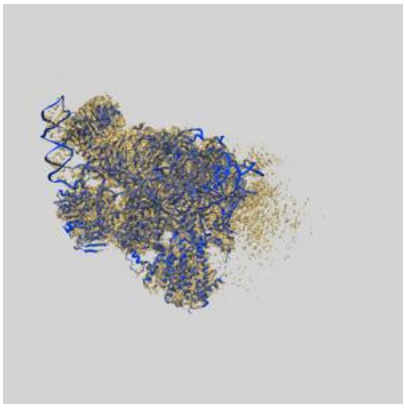
9.1 Map-model overlay



X



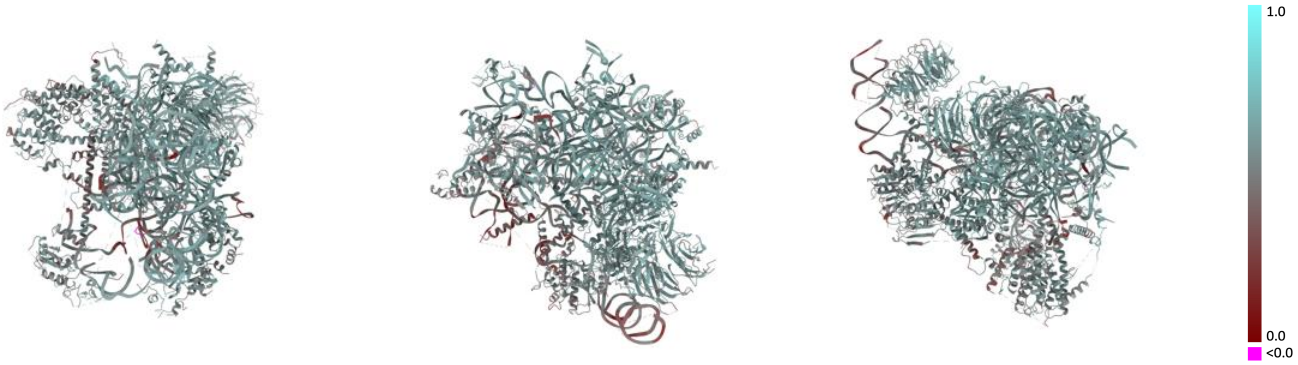
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.023 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.

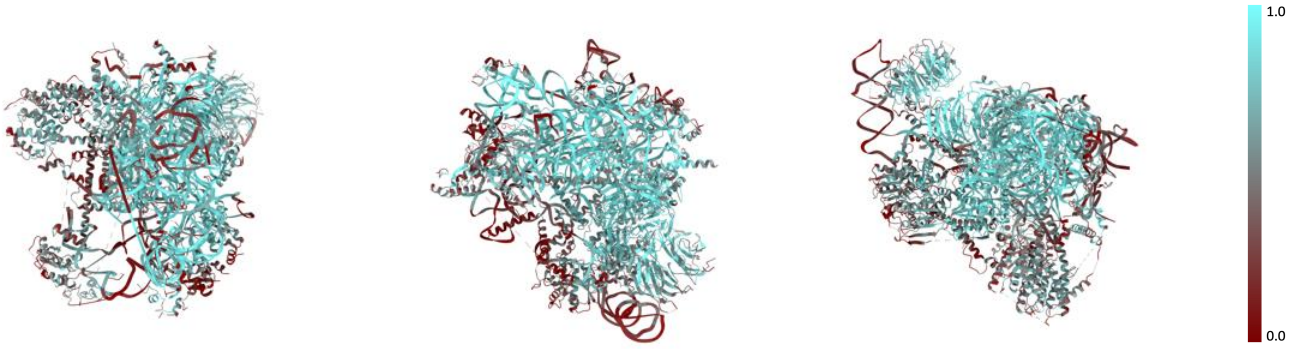
9.2 Q-score mapped to coordinate model (i)



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.

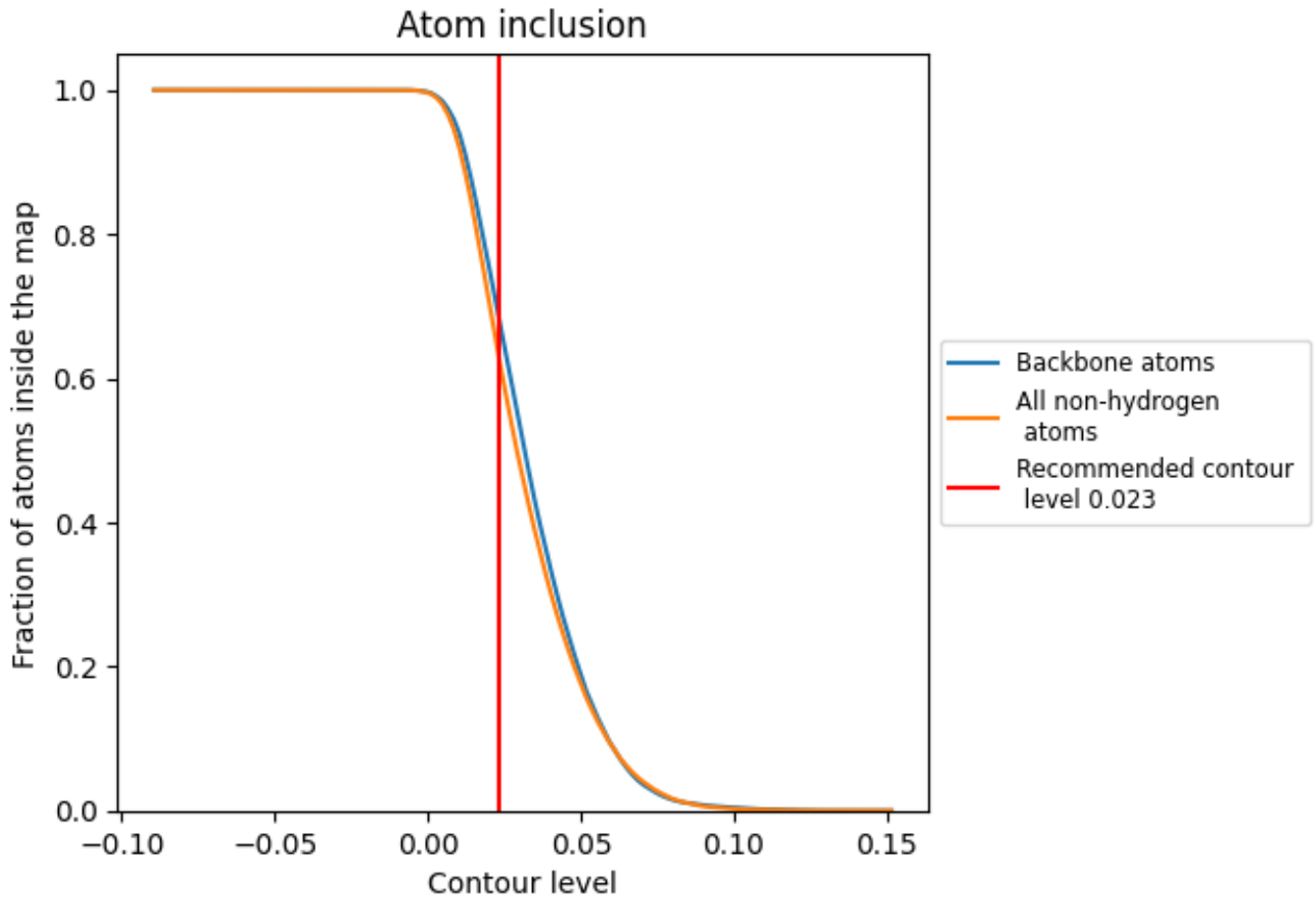
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.023).

9.4 Atom inclusion (i)



At the recommended contour level, 69% of all backbone atoms, 64% 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 (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6351	0.5470
1	0.7286	0.5420
2	0.4367	0.5640
5	0.3311	0.4720
8	0.5577	0.5400
B	0.5000	0.5110
G	0.6687	0.5740
I	0.5228	0.5160
P	0.3374	0.5030
R	0.7182	0.5720
U	0.6448	0.5640
V	0.4926	0.5350
X	0.7282	0.5900
Z	0.8226	0.6070
b	0.4238	0.5000
c	0.7934	0.5920
d	0.3264	0.5720
g	0.8570	0.6140
j	0.2293	0.5560
k	0.7112	0.5760
m	0.8245	0.6080
n	0.6906	0.5890
p	0.6540	0.5570
t	0.6890	0.5930
u	0.4967	0.4990
w	0.4230	0.5100
x	0.4470	0.5110