



wwPDB EM Validation Summary Report ⓘ

Jun 17, 2026 – 05:49 pm BST

PDB ID : 6GB2 / pdb_00006gb2
EMDB ID : EMD-4370
Title : Unique features of mammalian mitochondrial translation initiation revealed by cryo-EM. This file contains the 39S ribosomal subunit.
Authors : Kummer, E.; Leibundgut, M.; Boehringer, D.; Ban, N.
Deposited on : 2018-04-13
Resolution : 3.20 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

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:

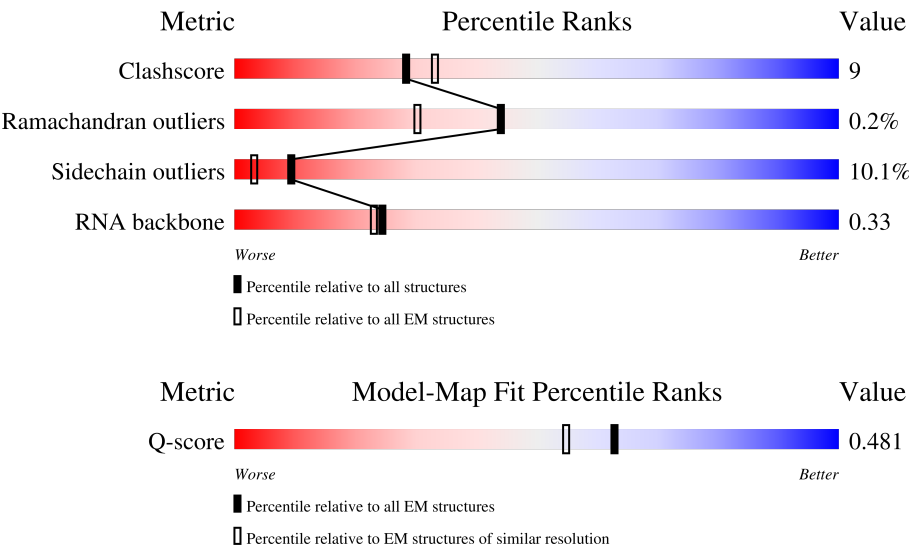
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.20 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	BL	198	35% 28%7% 65%
1	CL	198	23% 15%7% 77%
1	DL	198	14% 10% 86%

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Mol	Chain	Length	Quality of chain
1	EL	198	
1	FL	198	
1	GL	198	
1	HL	198	
2	B0	148	
3	B1	256	
4	B2	252	
5	B3	161	
6	B4	126	
7	B5	188	
8	B6	65	
9	B7	95	
10	B8	188	
11	B9	100	
12	BA	1571	
13	BB	73	
14	BC	657	
15	BD	306	
16	BE	348	
17	BF	294	
18	BI	268	
19	BJ	262	
20	BK	192	
21	BN	178	
22	BO	145	

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Mol	Chain	Length	Quality of chain
23	BP	296	
24	BQ	251	
25	BR	169	
26	BS	180	
27	BT	292	
28	BU	149	
29	BV	209	
30	BW	210	
31	BX	150	
32	BY	216	
33	Ba	423	
34	Bb	380	
35	Bc	334	
36	Bd	206	
37	Be	135	
38	Bf	142	
39	Bg	159	
40	Bh	332	
41	Bi	306	
42	Bj	279	
43	Bk	212	
44	Bl	166	
45	Bm	159	
46	Bn	128	
47	Bo	124	

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Mol	Chain	Length	Quality of chain
48	Bp	112	
49	Bq	138	
50	Bt	102	
51	Bu	205	
52	Bv	222	
53	Bw	433	
54	Bx	196	
55	Bz	82	
56	AV	71	

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 111109 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 Mitochondrial ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	CL	45	Total	C	N	O	0	0
			317	203	52	62		
1	DL	27	Total	C	N	O	0	0
			213	137	33	43		
1	EL	28	Total	C	N	O	0	0
			222	143	35	44		
1	FL	27	Total	C	N	O	0	0
			213	137	33	43		
1	GL	27	Total	C	N	O	0	0
			213	137	33	43		
1	HL	26	Total	C	N	O	0	0
			205	131	32	42		
1	BL	70	Total	C	N	O	0	0
			537	346	93	98		

- Molecule 2 is a protein called Mitochondrial ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B0	110	Total	C	N	O	S	0	0
			857	553	156	145	3		

- Molecule 3 is a protein called Mitochondrial ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B1	244	Total	C	N	O	S	0	0
			2036	1315	363	353	5		

- Molecule 4 is a protein called Mitochondrial ribosomal protein L47.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B2	179	Total	C	N	O	S	0	0
			1548	992	290	260	6		

- Molecule 5 is a protein called 'Mitochondrial ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B3	118	Total	C	N	O	S	0	0
			968	622	178	165	3		

- Molecule 6 is a protein called 'Mitochondrial ribosomal protein L55.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B4	45	Total	C	N	O	S	0	0
			381	239	77	62	3		

- Molecule 7 is a protein called Mitochondrial ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B5	110	Total	C	N	O	S	0	0
			902	553	181	162	6		

- Molecule 8 is a protein called Mitochondrial ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B6	52	Total	C	N	O	S	0	0
			425	274	78	71	2		

- Molecule 9 is a protein called Mitochondrial ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B7	46	Total	C	N	O	S	0	0
			387	239	89	58	1		

- Molecule 10 is a protein called Mitochondrial ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B8	95	Total	C	N	O	S	0	0
			833	539	163	129	2		

- Molecule 11 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B9	38	Total	C	N	O	S	0	0
			335	214	70	47	4		

- Molecule 12 is a RNA chain called 16S ribosomal RNA, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BA	1549	Total	C	N	O	P	0	0
			32950	14798	5993	10610	1549		

- Molecule 13 is a RNA chain called CP tRNAPhe, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BB	67	Total	C	N	O	P	0	0
			1427	640	261	459	67		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	72	C	-	insertion	GB 76262549
BB	73	A	-	insertion	GB 76262549

- Molecule 14 is a protein called Translation initiation factor IF-2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BC	571	Total	C	N	O	S	0	0
			4364	2743	765	839	17		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BC	71	SER	-	expression tag	UNP P46199
BC	72	GLY	-	expression tag	UNP P46199
BC	73	GLY	-	expression tag	UNP P46199
BC	74	SER	-	expression tag	UNP P46199
BC	75	GLY	-	expression tag	UNP P46199
BC	76	SER	-	expression tag	UNP P46199
BC	77	GLY	-	expression tag	UNP P46199

- Molecule 15 is a protein called Mitochondrial ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BD	240	Total	C	N	O	S	0	0
			1860	1160	371	319	10		

- Molecule 16 is a protein called ICT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BE	307	Total	C	N	O	S	0	0
			2420	1554	426	430	10		

- Molecule 17 is a protein called Mitochondrial ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BF	250	Total	C	N	O	S	0	0
			2011	1294	367	344	6		

- Molecule 18 is a protein called Mitochondrial ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BI	98	Total	C	N	O		0	0
			805	509	155	141			

- Molecule 19 is a protein called Mitochondrial ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BJ	212	Total	C	N	O	S	0	0
			1705	1100	306	290	9		

- Molecule 20 is a protein called Mitochondrial ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BK	176	Total	C	N	O	S	0	0
			1303	830	236	235	2		

- Molecule 21 is a protein called Mitochondrial ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BN	177	Total	C	N	O	S	0	0
			1444	926	258	253	7		

- Molecule 22 is a protein called Mitochondrial ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BO	115	Total	C	N	O	S	0	0
			896	562	176	154	4		

- Molecule 23 is a protein called Mitochondrial ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BP	288	Total	C	N	O	S	0	0
			2312	1473	430	403	6		

- Molecule 24 is a protein called Mitochondrial ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BQ	222	Total	C	N	O	S	0	0
			1803	1156	331	306	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BQ	237	HIS	TYR	conflict	UNP F1RI89

- Molecule 25 is a protein called Mitochondrial ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BR	153	Total	C	N	O	S	0	0
			1240	777	236	222	5		

- Molecule 26 is a protein called Mitochondrial ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BS	143	Total	C	N	O	S	0	0
			1168	733	227	204	4		

- Molecule 27 is a protein called Mitochondrial ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BT	223	Total	C	N	O	S	0	0
			1845	1181	319	336	9		

- Molecule 28 is a protein called Mitochondrial ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BU	140	Total	C	N	O	S	0	0
			1159	732	239	185	3		

- Molecule 29 is a protein called Mitochondrial ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BV	155	Total	C	N	O	S	0	0
			1231	789	219	219	4		

- Molecule 30 is a protein called Mitochondrial ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BW	166	Total	C	N	O	S	0	0
			1374	876	258	234	6		

- Molecule 31 is a protein called Mitochondrial ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BX	149	Total	C	N	O	S	0	0
			1181	752	227	200	2		

- Molecule 32 is a protein called Mitochondrial ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BY	206	Total	C	N	O	S	0	0
			1678	1056	308	309	5		

- Molecule 33 is a protein called Mitochondrial ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ba	393	Total	C	N	O	S	0	0
			3173	2040	556	565	12		

- Molecule 34 is a protein called Mitochondrial ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Bb	354	Total	C	N	O	S	0	0
			2952	1876	542	525	9		

- Molecule 35 is a protein called Mitochondrial ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Bc	295	Total	C	N	O	S	0	0
			2408	1541	410	441	16		

- Molecule 36 is a protein called Mitochondrial ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Bd	99	Total	C	N	O	S	0	0
			832	528	148	155	1		

- Molecule 37 is a protein called Mitochondrial ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Be	122	Total	C	N	O	S	0	0
			972	628	168	173	3		

- Molecule 38 is a protein called Mitochondrial ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bf	108	Total	C	N	O	S	0	0
			827	519	154	150	4		

- Molecule 39 is a protein called Mitochondrial ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Bg	148	Total	C	N	O	S	0	0
			1167	727	225	212	3		

- Molecule 40 is a protein called Mitochondrial ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Bh	289	Total	C	N	O	S	0	0
			2319	1486	399	426	8		

- Molecule 41 is a protein called Mitochondrial ribosomal protein L45.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Bi	260	Total	C	N	O	S	0	0
			2138	1370	379	379	10		

- Molecule 42 is a protein called Mitochondrial ribosomal protein L46.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Bj	217	Total	C	N	O	S	0	0
			1775	1137	311	321	6		

- Molecule 43 is a protein called Mitochondrial ribosomal protein L48.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Bk	136	Total	C	N	O	S	0	0
			1087	692	185	205	5		

- Molecule 44 is a protein called Mrpl34.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Bl	133	Total	C	N	O	S	0	0
			1097	709	192	194	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bl	59	ARG	LYS	conflict	UNP A0A0R4J8D6

- Molecule 45 is a protein called Mitochondrial ribosomal protein L50.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Bm	109	Total	C	N	O	S	0	0
			893	568	160	162	3		

- Molecule 46 is a protein called Mitochondrial ribosomal protein L51.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Bn	97	Total	C	N	O	S	0	0
			837	539	166	128	4		

- Molecule 47 is a protein called Mitochondrial ribosomal protein L52.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Bo	97	Total	C	N	O	S	0	0
			772	481	148	141	2		

- Molecule 48 is a protein called mL53, MRPL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Bp	97	Total	C	N	O	S	0	0
			742	459	143	134	6		

- Molecule 49 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Bq	68	Total	C	N	O	S	0	0
			542	344	102	95	1		

- Molecule 50 is a protein called Mitochondrial ribosomal protein L57.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Bt	94	Total	C	N	O	S	0	0
			780	485	168	126	1		

- Molecule 51 is a protein called Mitochondrial ribosomal protein L58.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Bu	151	Total	C	N	O	S	0	0
			1198	738	233	222	5		

- Molecule 52 is a protein called 'Mitochondrial ribosomal protein L59.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Bv	135	Total	C	N	O	S	0	0
			1131	692	223	211	5		

- Molecule 53 is a protein called mL65, MRPS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Bw	387	Total	C	N	O	S	0	0
			3126	2011	548	555	12		

- Molecule 54 is a protein called Mitochondrial ribosomal protein S18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Bx	162	Total	C	N	O	S	0	0
			1325	845	249	224	7		

- Molecule 55 is a protein called unassigned secondary structure elements.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	Bz	82	Total	C	N	O	0	0
			410	246	82	82		

- Molecule 56 is a RNA chain called P-site fMet-tRNA^{Met}, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AV	71	Total	C	N	O	P	0	0
			1498	673	264	491	70		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AV	69	C	-	insertion	GB 1208989970
AV	70	C	-	insertion	GB 1208989970
AV	71	A	-	insertion	GB 1208989970

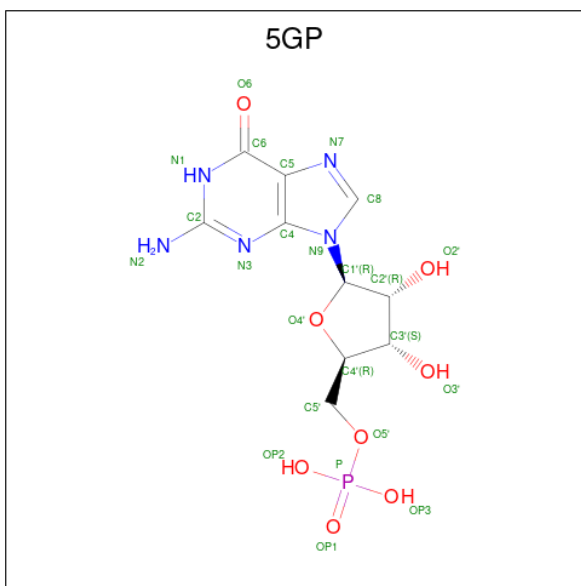
- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	B3	1	Total	Mg	0
			1	1	
57	BA	203	Total	Mg	0
			203	203	
57	BB	1	Total	Mg	0
			1	1	
57	BC	1	Total	Mg	0
			1	1	
57	BD	3	Total	Mg	0
			3	3	
57	BP	2	Total	Mg	0
			2	2	
57	BQ	1	Total	Mg	0
			1	1	
57	Be	2	Total	Mg	0
			2	2	
57	Bl	1	Total	Mg	0
			1	1	
57	Bt	1	Total	Mg	0
			1	1	

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

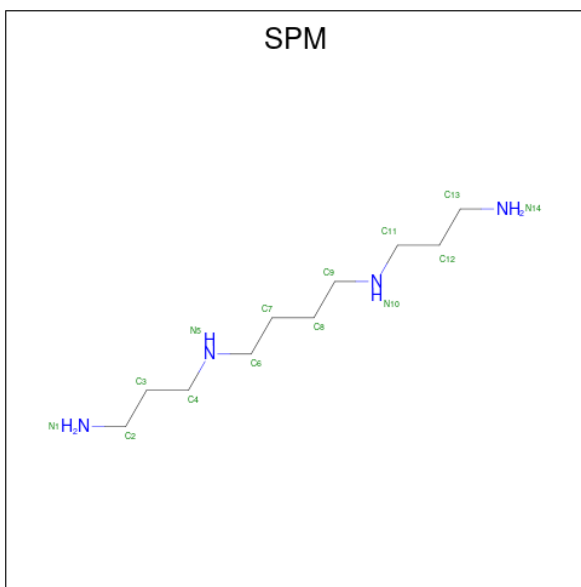
Mol	Chain	Residues	Atoms		AltConf
58	B5	1	Total	Zn	0
			1	1	
58	B9	1	Total	Zn	0
			1	1	
58	BJ	1	Total	Zn	0
			1	1	

- Molecule 59 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula: $C_{10}H_{14}N_5O_8P$).



Mol	Chain	Residues	Atoms					AltConf
59	BA	1	Total	C	N	O	P	0
			24	10	5	8	1	
59	BA	1	Total	C	N	O	P	0
			24	10	5	8	1	

- Molecule 60 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



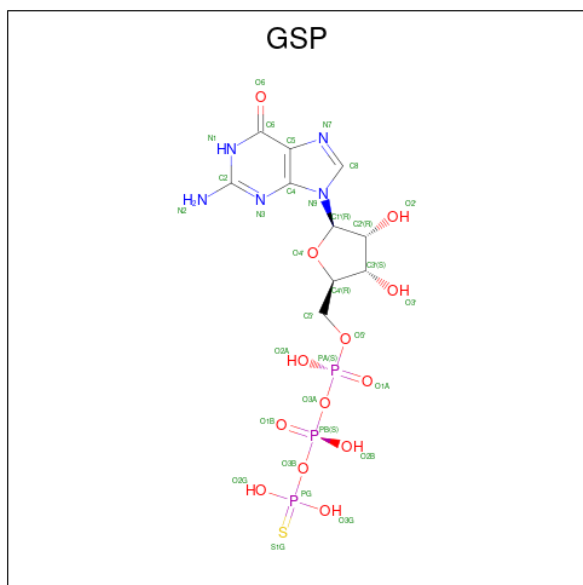
Mol	Chain	Residues	Atoms				AltConf
60	BA	1	Total	C	N		0
			14	10	4		

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Mol	Chain	Residues	Atoms			AltConf
60	BR	1	Total	C	N	0
			14	10	4	

- Molecule 61 is 5'-GUANOSINE-DIPHOSPHATE-MONOTHIOPHOSPHATE (CCD ID: GSP) (formula: $C_{10}H_{16}N_5O_{13}P_3S$) (labeled as "Ligand of Interest" by depositor).

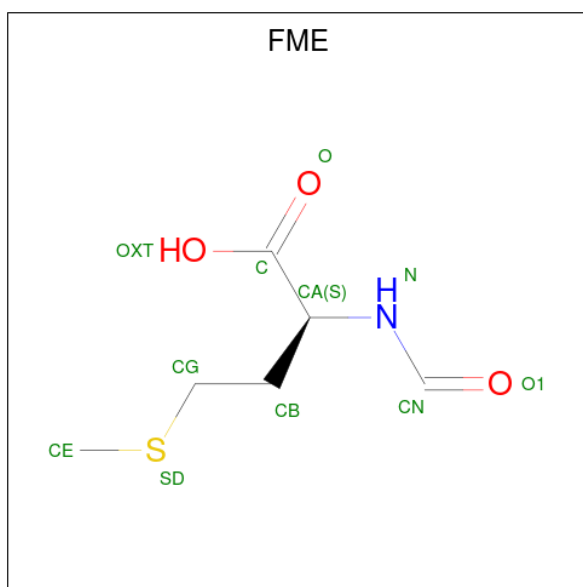


Mol	Chain	Residues	Atoms						AltConf
61	BC	1	Total	C	N	O	P	S	0
			32	10	5	13	3	1	

- Molecule 62 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
62	BC	1	Total	Na	0
			1	1	

- Molecule 63 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: $C_6H_{11}NO_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
63	AV	1	Total	C	N	O	S	0
			10	6	1	2	1	

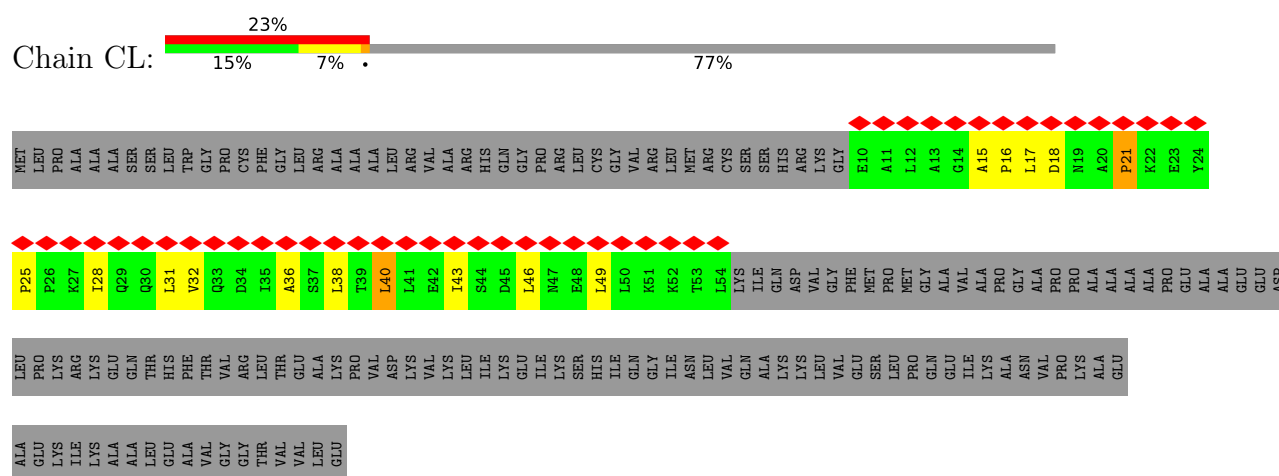
- Molecule 64 is water.

Mol	Chain	Residues	Atoms		AltConf
64	BC	2	Total	O	0
			2	2	

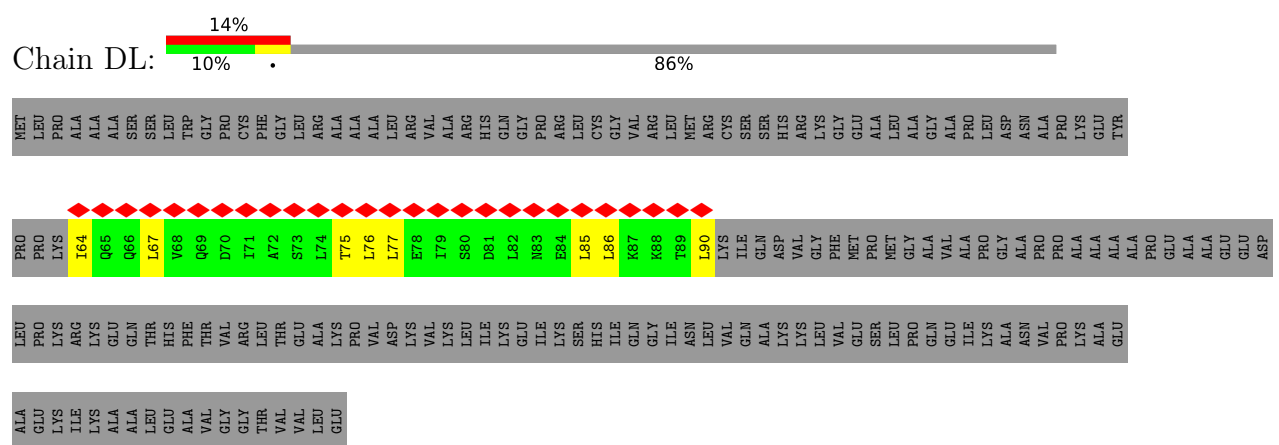
3 Residue-property plots [i](#)

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.

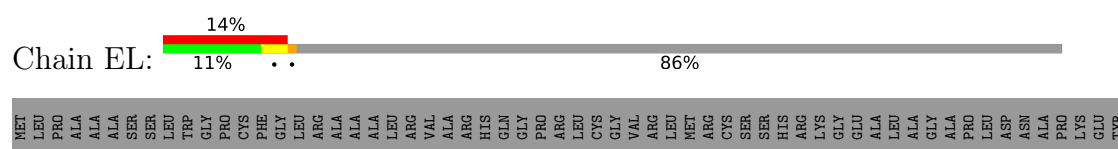
• Molecule 1: Mitochondrial ribosomal protein L12

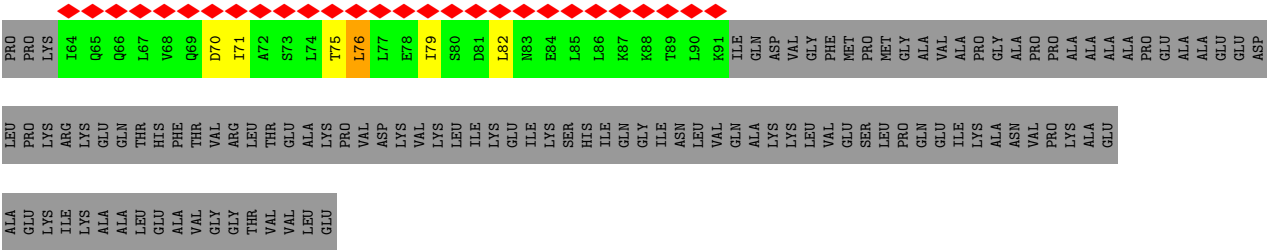


• Molecule 1: Mitochondrial ribosomal protein L12

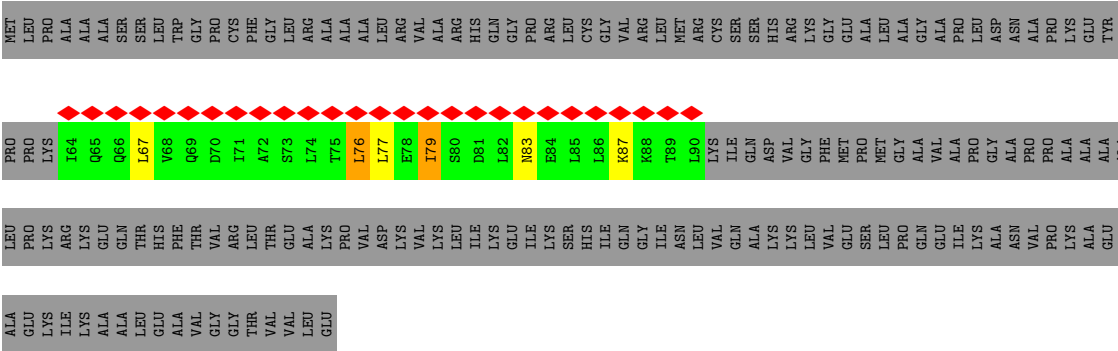


• Molecule 1: Mitochondrial ribosomal protein L12

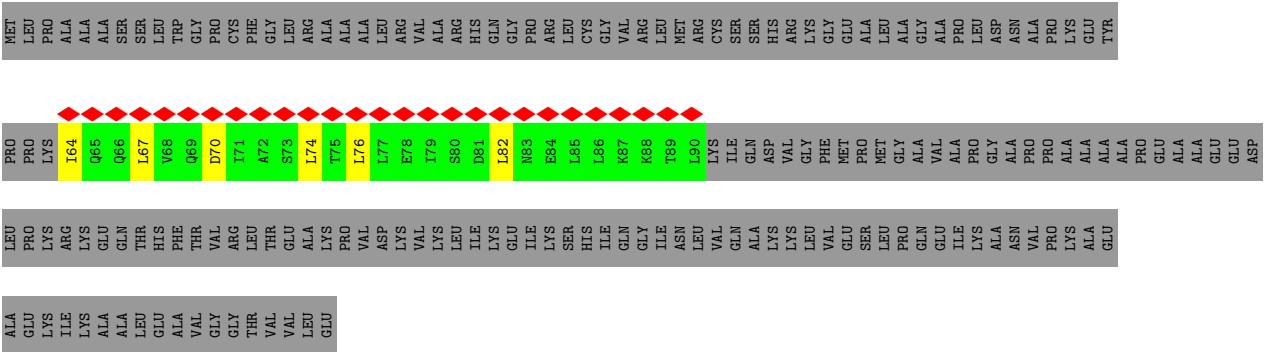




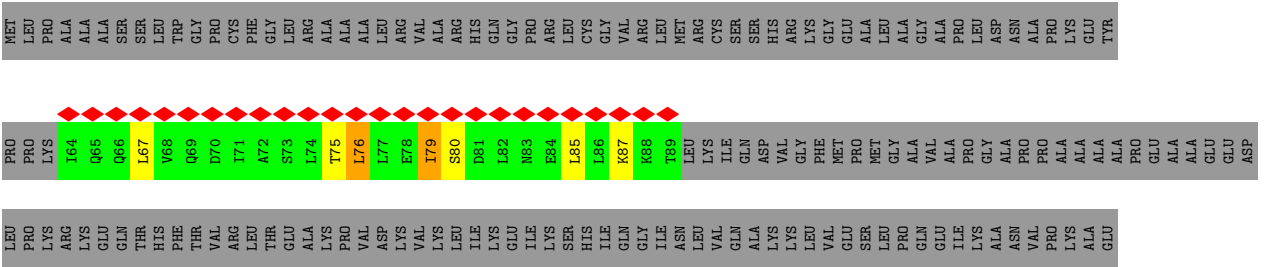
• Molecule 1: Mitochondrial ribosomal protein L12



• Molecule 1: Mitochondrial ribosomal protein L12



• Molecule 1: Mitochondrial ribosomal protein L12



ALA
GLU
LYS
ILE
LYS
ALA
ALA
LEU
GLU
ALA
VAL
GLY
GLY
THR
VAL
VAL
LEU
GLU

• Molecule 1: Mitochondrial ribosomal protein L12

Chain BL: 35%
28% 7% 65%

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

PRO
PRO
ILE
ILE
GLN
LEU
VAL
GLN
ASP
ASP
ILE
GLY
THR
SER
SER
LEU
THR
GLY
LEU
LEU
ARG
ALA
ALA
ILE
SER
ASP
P139
VAL
GLU
D141
K142
V143
K144
L145
I146
K147
E148
I149
K150
K151
H152
I153
Q154
G155
I156
N157
L158
V159
Q160
A161
K162
K163
L164
V165
E166
S167
L168
P169
Q170
E171
I172
K173
A174
N175
V176
P177
K178
A179
E180

A181
E182
K183
I184
K185
A187
L188
E189
A190
V191
G192
T194
V195
V196
L197
E198

• Molecule 2: Mitochondrial ribosomal protein L27

Chain B0: 50% 22% 26%

MET
ALA
LEU
ALA
VAL
LEU
ALA
LEU
ARG
ARG
ALA
ALA
VAL
THR
ALA
VAL
THR
ALA
LEU
LEU
SER
PRO
PRO
GLN
ALA
ALA
LEU
ALA
VAL
VAL
ARG
TYR
ALA
SER
LYS
LYS
THR
GLY
SER
S39
K40
K49
R50
I53
K54
K55
M56
E57
V61
H62
N65
I66
L67
T69
R74

H75
H76
C88
L89
Y90
T100
E102
V117
T118
R119
P121
Q122
G123
A124
V125
L126
Y127
K128
T129
F130
V131
H132
V133
V134
P135
T141
M147
L148

• Molecule 3: Mitochondrial ribosomal protein L28

Chain B1: 21% 66% 25% 5%

MET
P2
K5
V6
K12
Q13
L14
R15
L16
W17
E18
G19
I20
R23
L24
P25
R26
H27
Y28
L29
R30
S31
L32
E33
A34
A35
R36
H42
Y43
R44
P45
H46
G47
A48
K49
F50
K51
R55
E60
R61
V62
E63
D64
V69
S75
Q76
L77
G78
L79
W80
E83

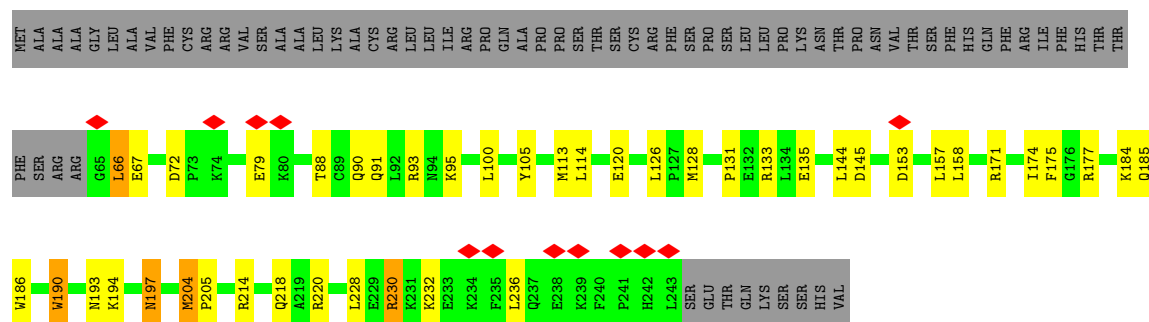
G84
W85
V86
L87
V92
R93
K96
L97
S98
R99
R100
V101
R102
K103
V104
P107
Q108
L109
R112
E117
I118
L119
D120
T126
V127
T128
M129
D133
D136
C139
Y144
I145
L146
K147
T148
E151
D152
L153
C154
S155
K156
M159
D160
L161
K162
R163
G164
M165

L166
L167
R168
L169
Q172
D173
F174
Q175
L176
H177
F178
D179
D180
R184
D189
R190
Y191
K192
I196
P197
E198
A199
E200
E202
W203
V204
Q205
E220
K221
D222
F223
I224
P225
L226
E232
E233
L234
L235
Q236
Q237
L238
Q239
Q240
Q241
A242
L243
S244
E245
PRO
ALA
VAL
VAL
GLN

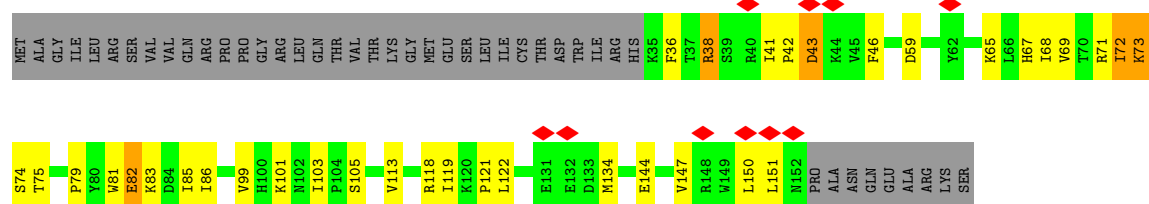
THR
ARG
ALA
SER
ARG
LYS

• Molecule 4: Mitochondrial ribosomal protein L47

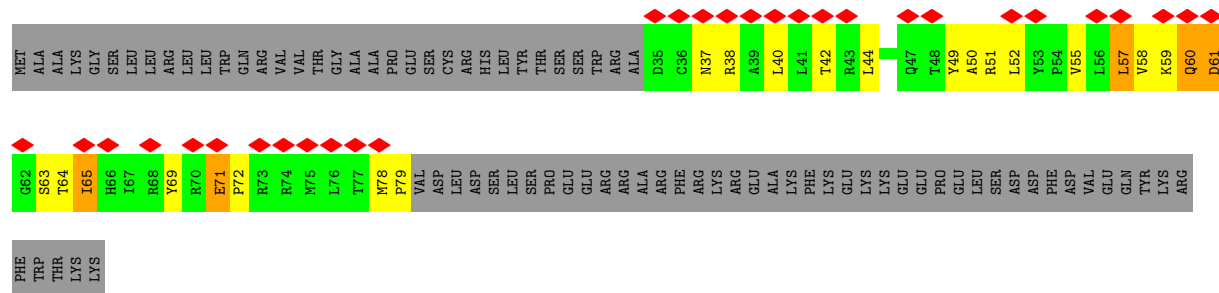
Chain B2: 5% 54% 15% 29%



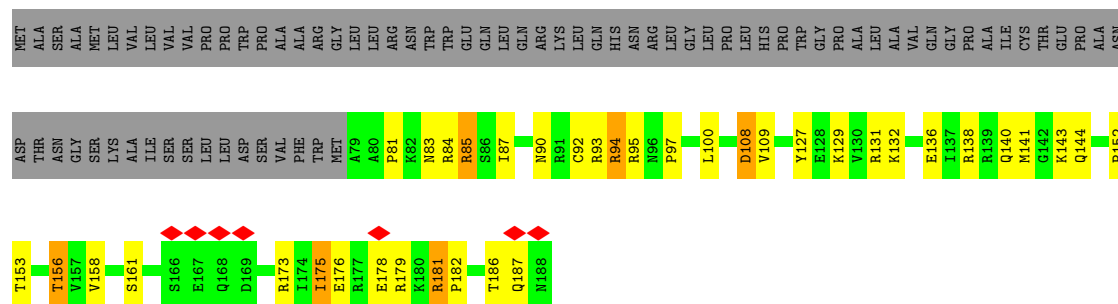
• Molecule 5: 'Mitochondrial ribosomal protein L30



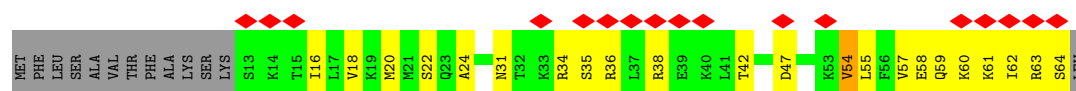
• Molecule 6: 'Mitochondrial ribosomal protein L55



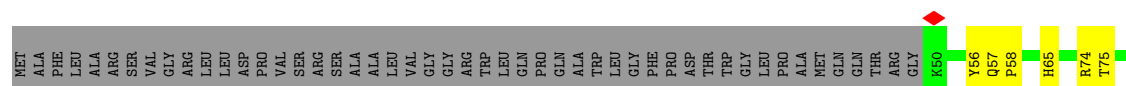
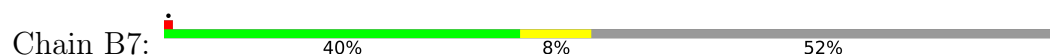
• Molecule 7: Mitochondrial ribosomal protein L32



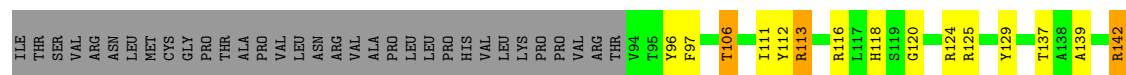
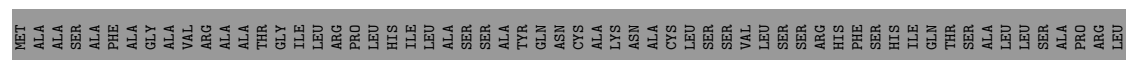
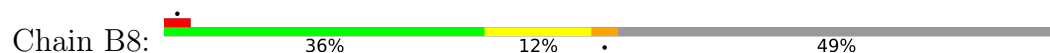
• Molecule 8: Mitochondrial ribosomal protein L33



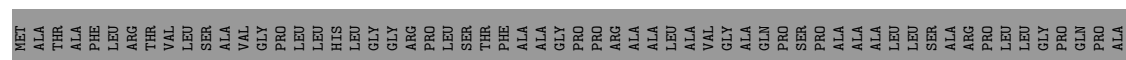
• Molecule 9: Mitochondrial ribosomal protein L34



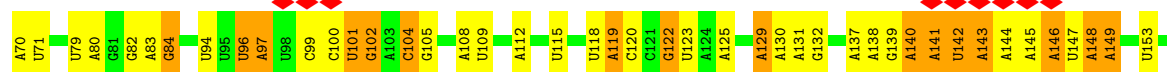
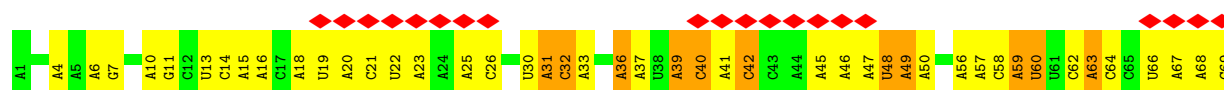
• Molecule 10: Mitochondrial ribosomal protein L35

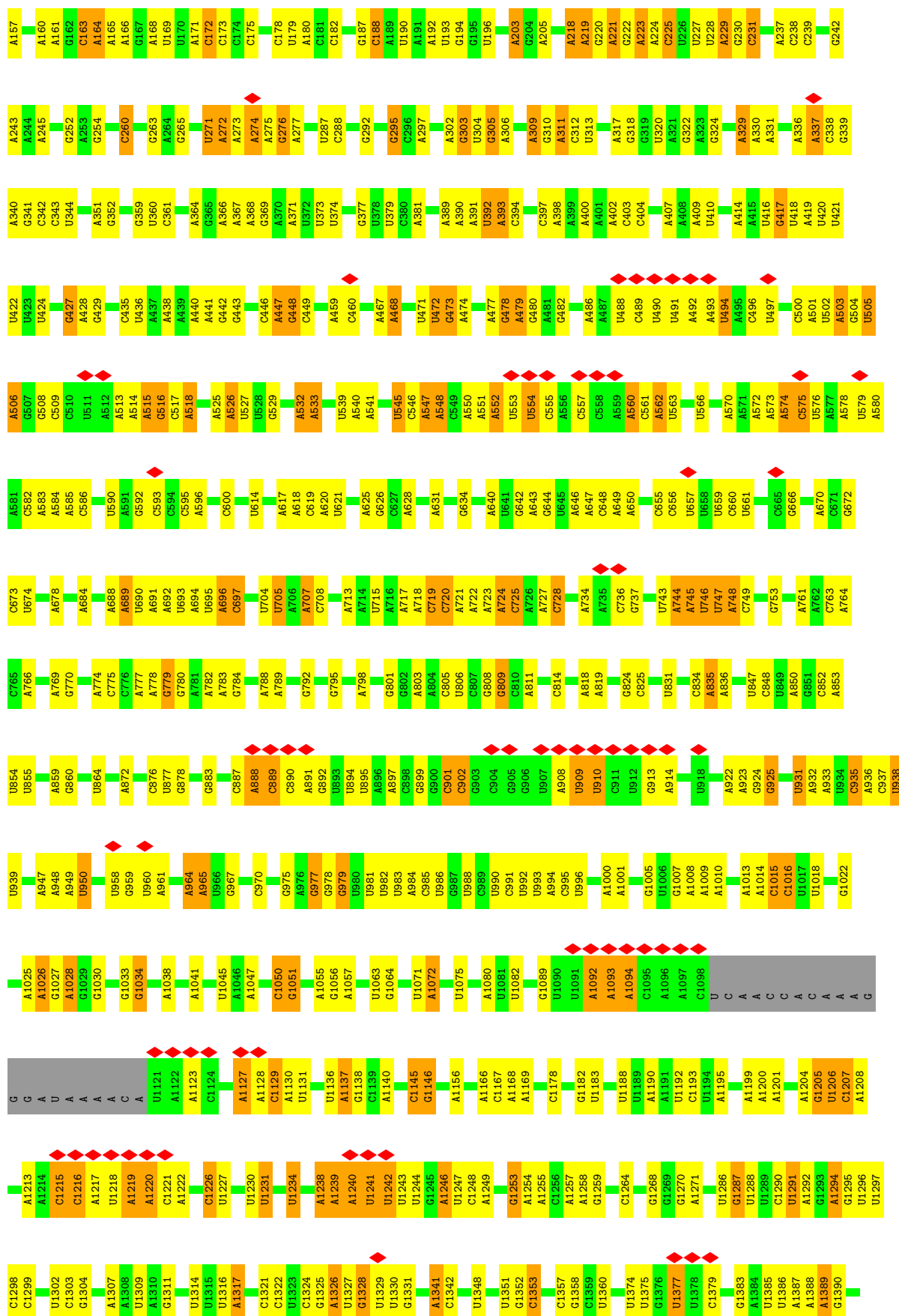


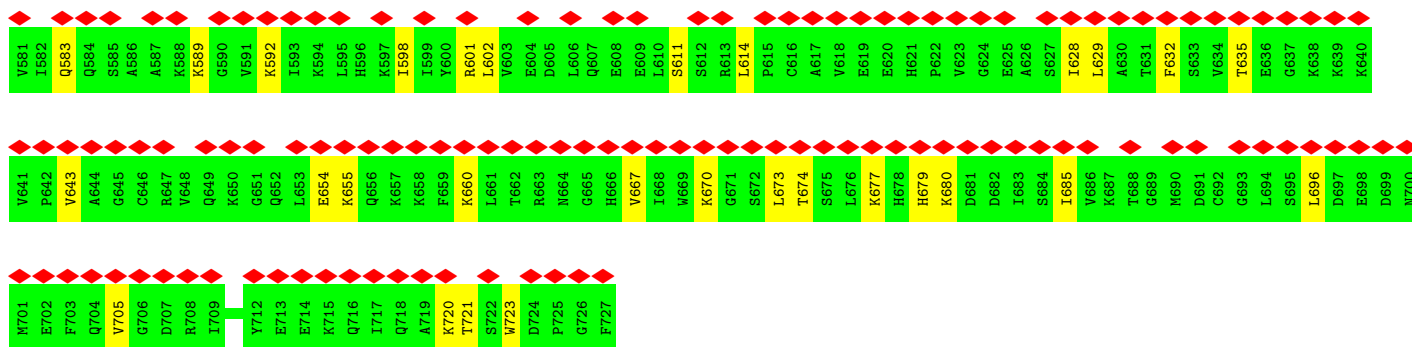
• Molecule 11: Ribosomal protein



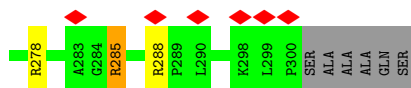
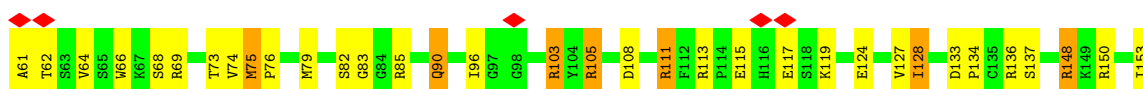
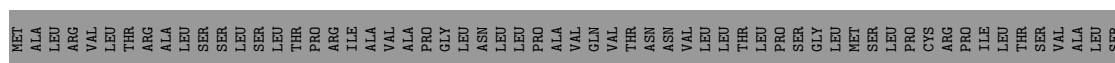
• Molecule 12: 16S ribosomal RNA, mitochondrial



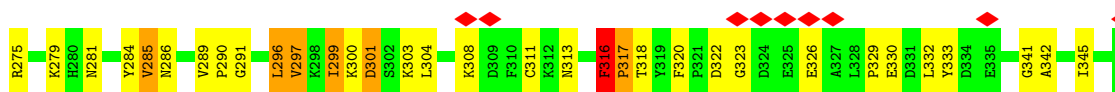
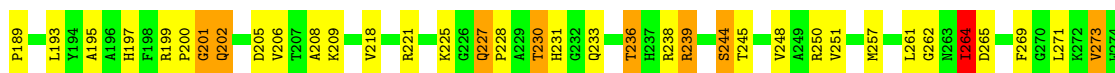
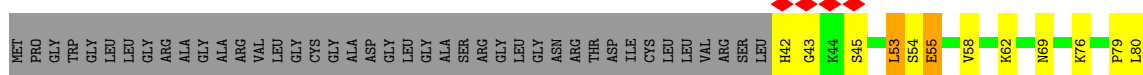




• Molecule 15: Mitochondrial ribosomal protein L2

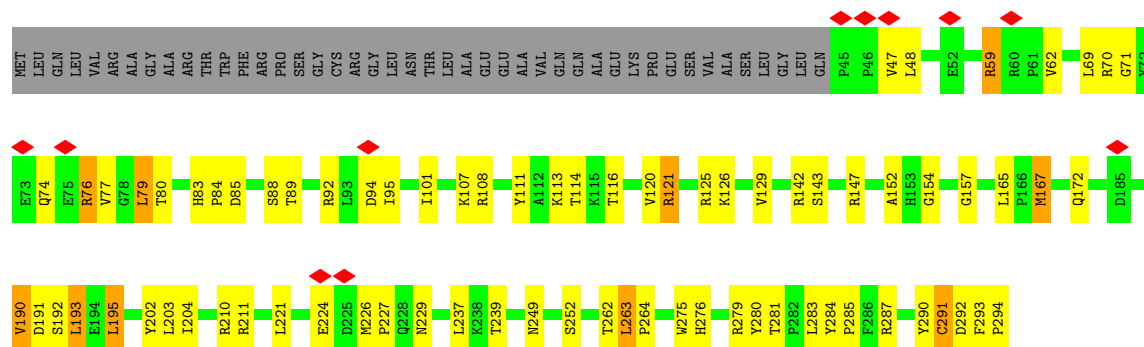


• Molecule 16: ICT1

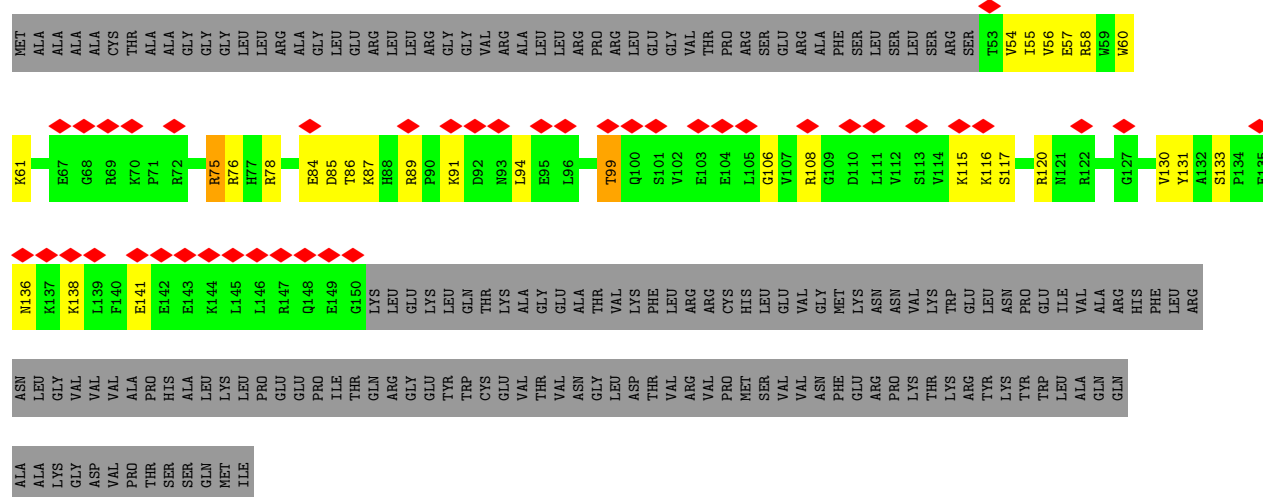


• Molecule 17: Mitochondrial ribosomal protein L4

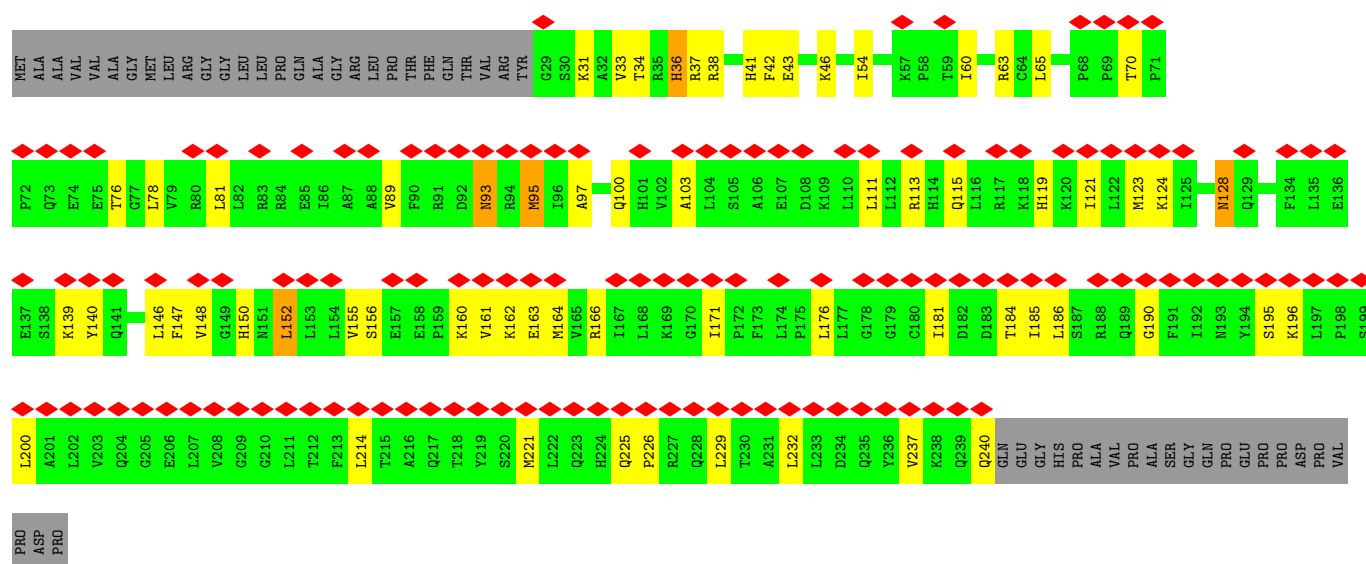




• Molecule 18: Mitochondrial ribosomal protein L9

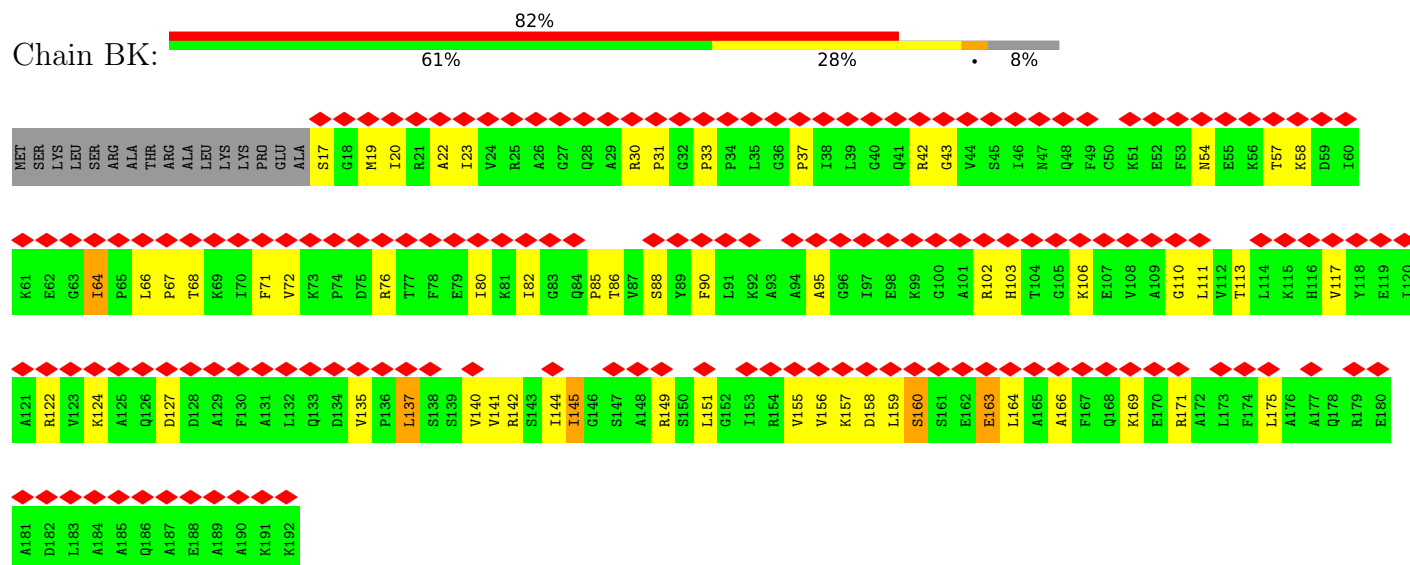


• Molecule 19: Mitochondrial ribosomal protein L10



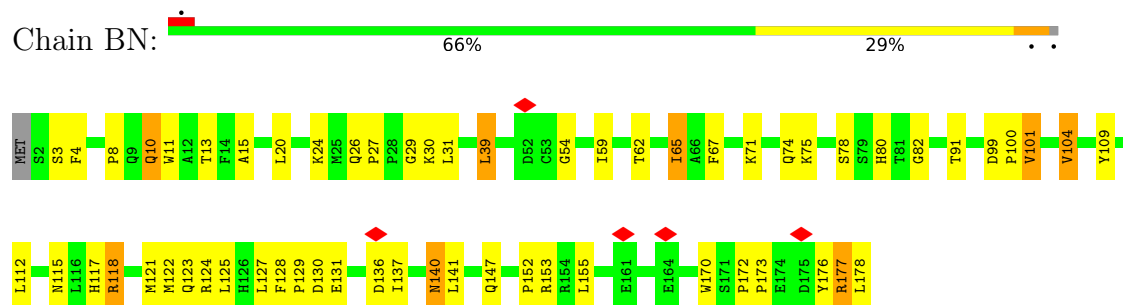
- Molecule 20: Mitochondrial ribosomal protein L11

Chain BK:



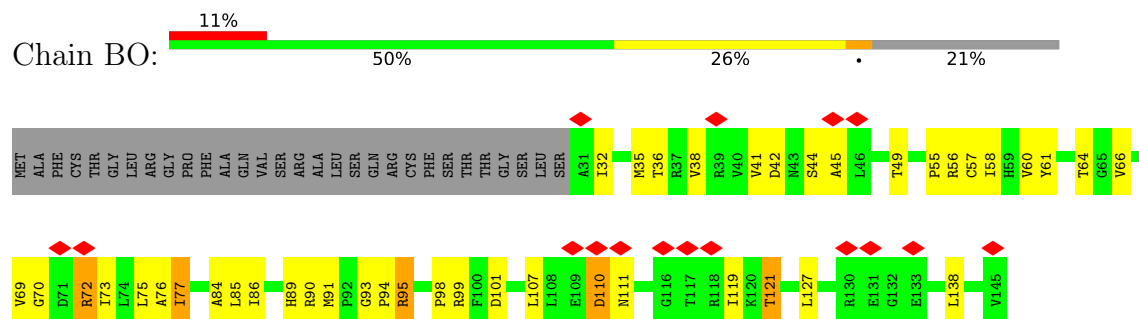
- Molecule 21: Mitochondrial ribosomal protein L13

Chain BN:



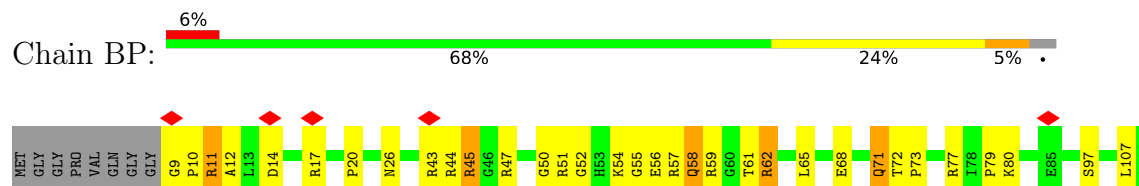
- Molecule 22: Mitochondrial ribosomal protein L14

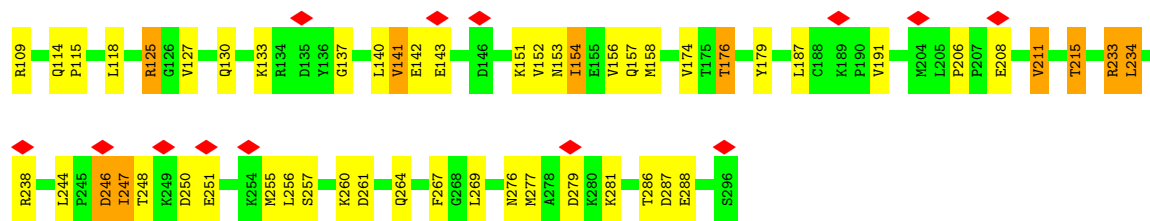
Chain BO:



- Molecule 23: Mitochondrial ribosomal protein L15

Chain BP:





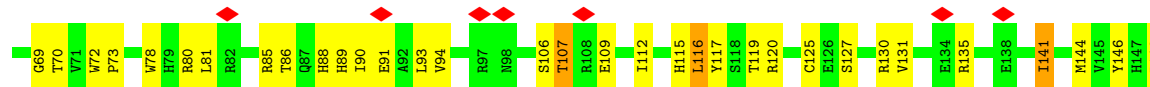
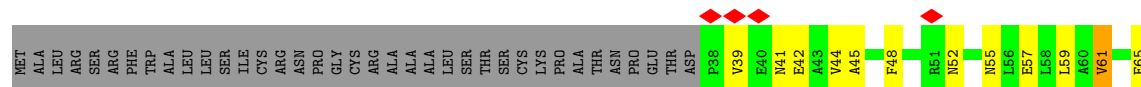
• Molecule 24: Mitochondrial ribosomal protein L16



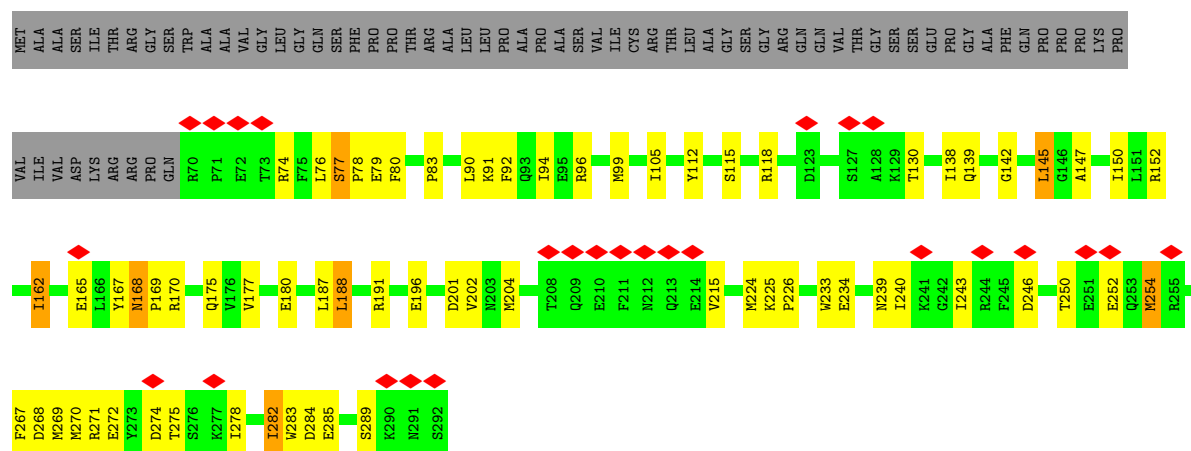
• Molecule 25: Mitochondrial ribosomal protein L17



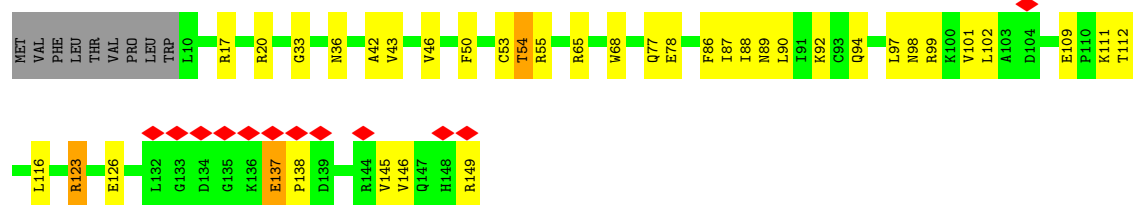
• Molecule 26: Mitochondrial ribosomal protein L18



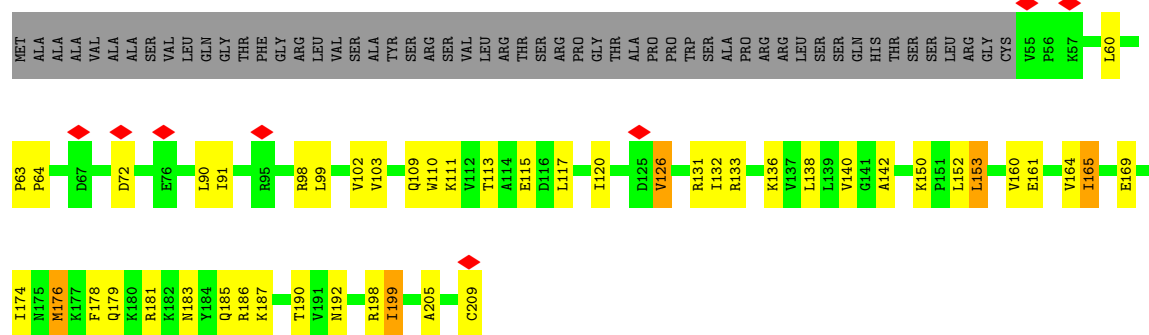
• Molecule 27: Mitochondrial ribosomal protein L19



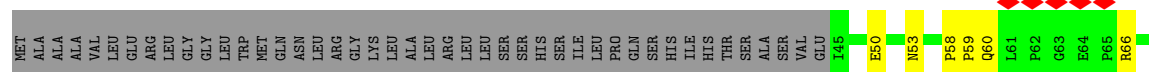
• Molecule 28: Mitochondrial ribosomal protein L20

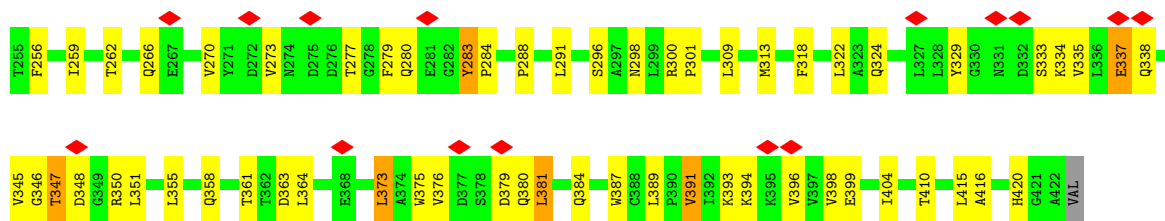


• Molecule 29: Mitochondrial ribosomal protein L21

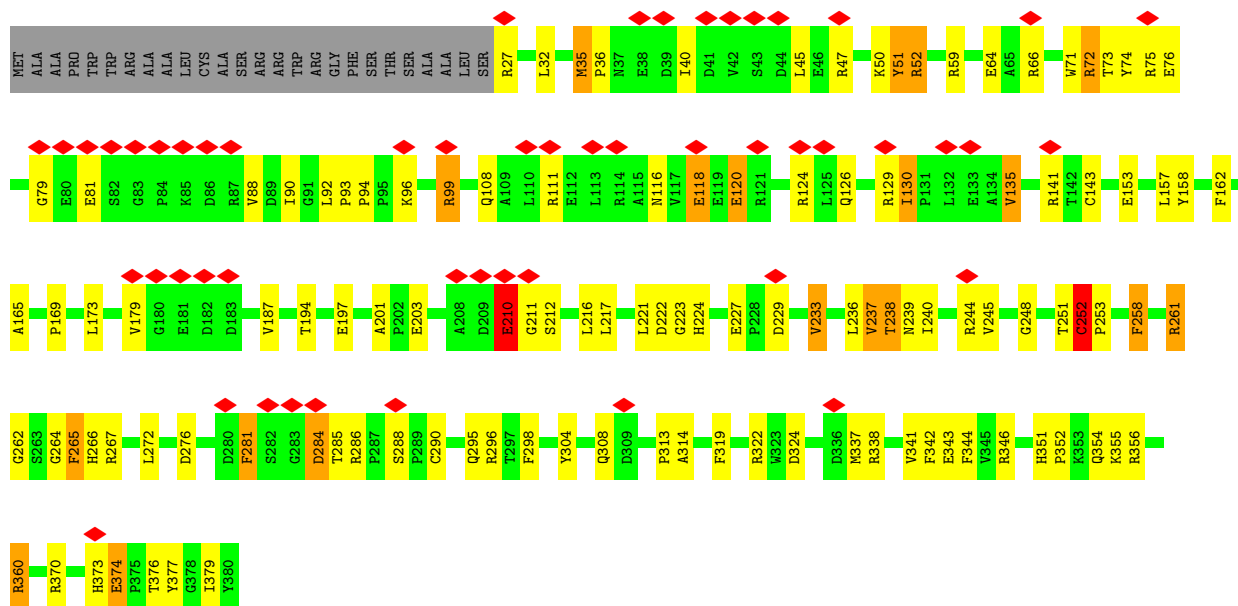


• Molecule 30: Mitochondrial ribosomal protein L22

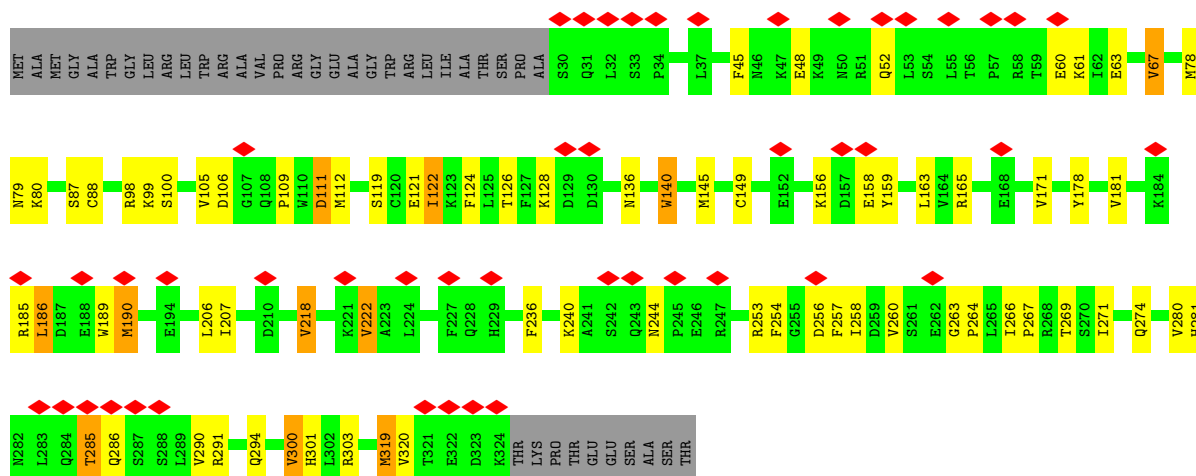




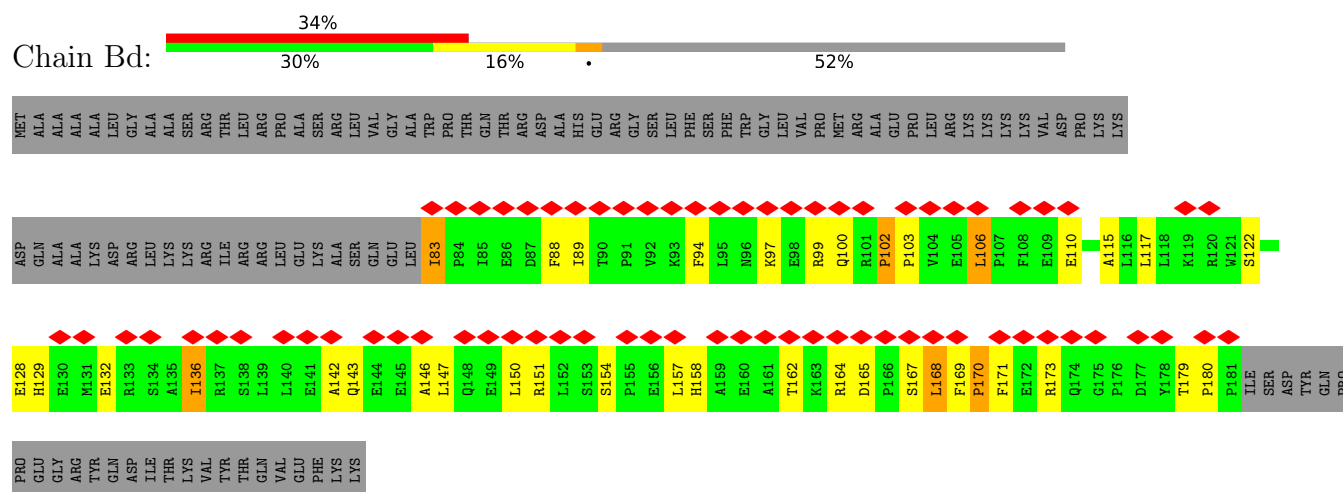
• Molecule 34: Mitochondrial ribosomal protein L38



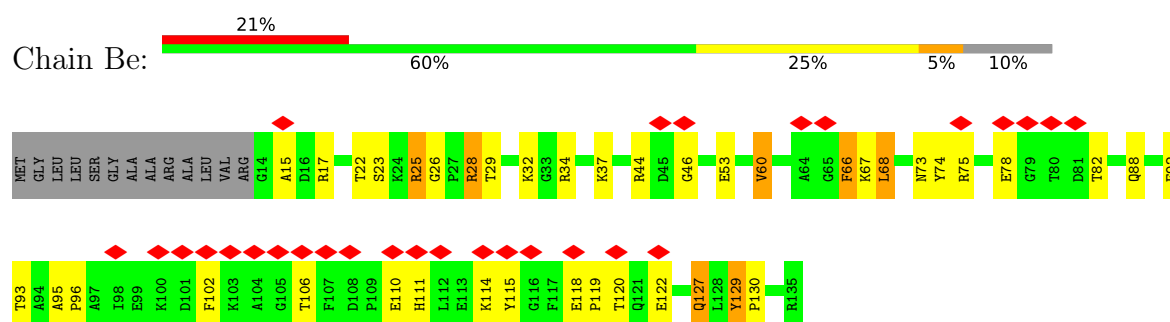
• Molecule 35: Mitochondrial ribosomal protein L39



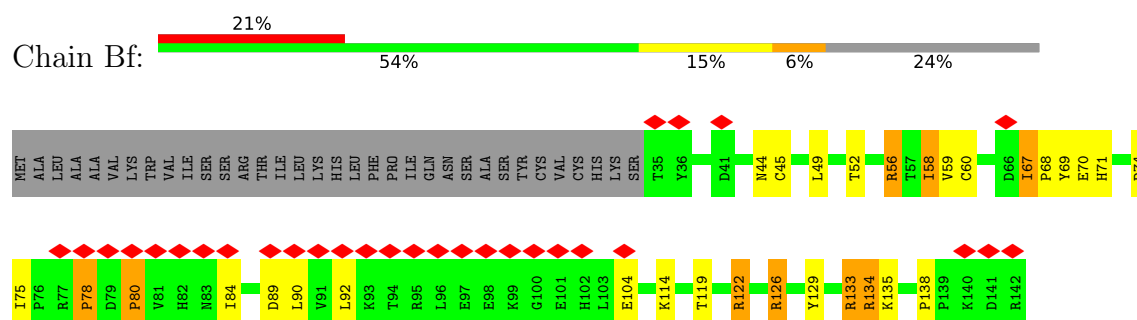
• Molecule 36: Mitochondrial ribosomal protein L40



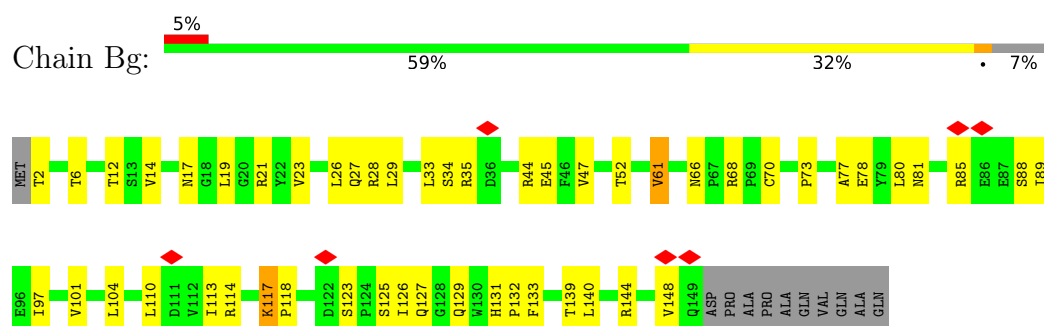
• Molecule 37: Mitochondrial ribosomal protein L41



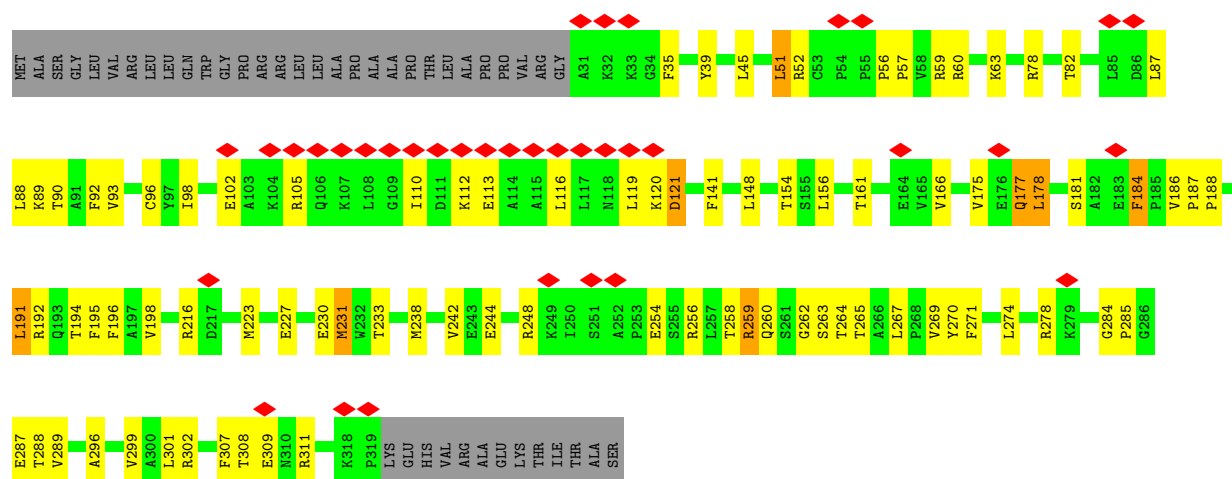
• Molecule 38: Mitochondrial ribosomal protein L42



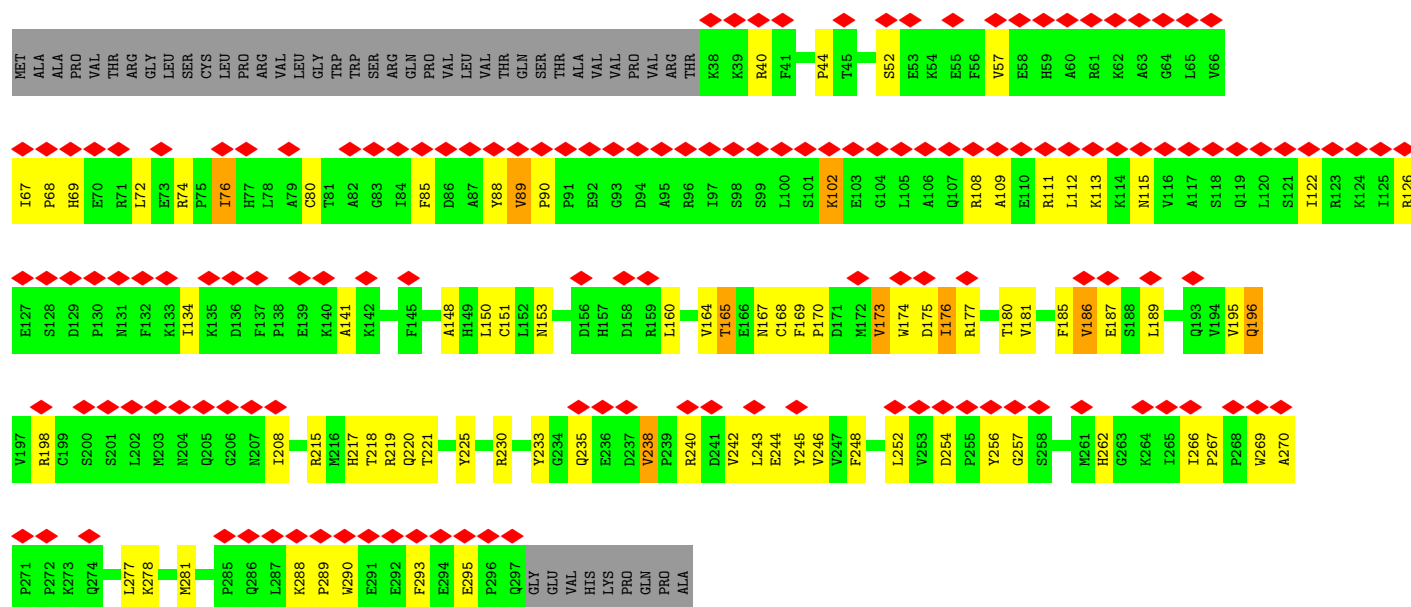
• Molecule 39: Mitochondrial ribosomal protein L43



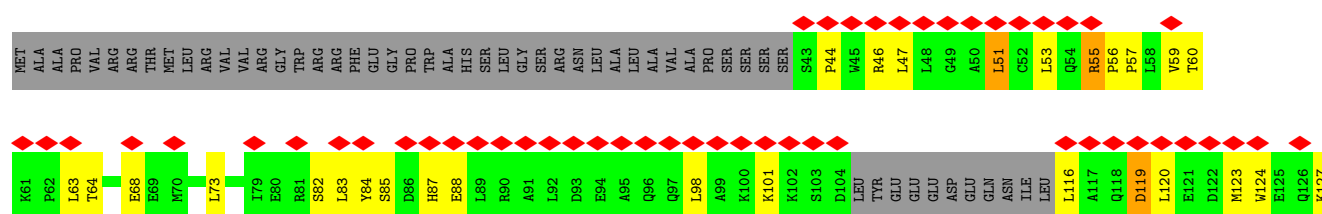
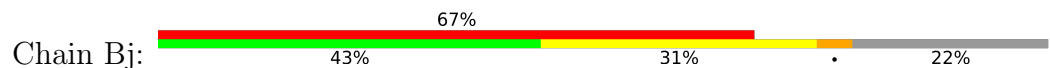
• Molecule 40: Mitochondrial ribosomal protein L44

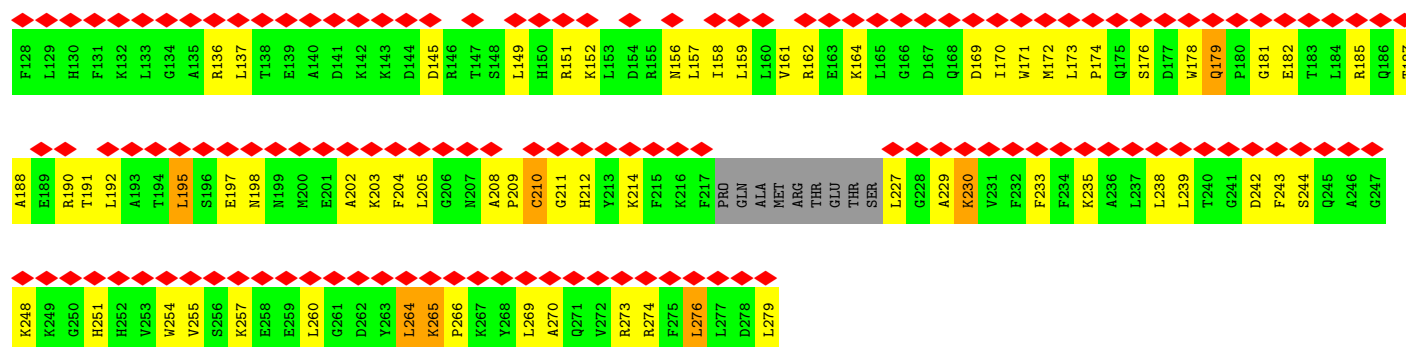


• Molecule 41: Mitochondrial ribosomal protein L45

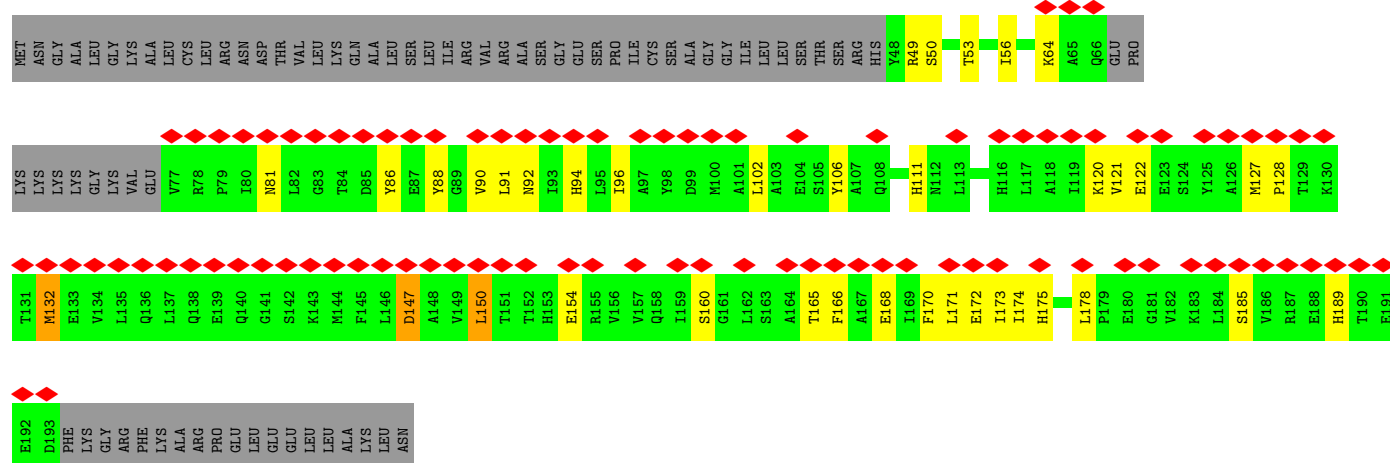


• Molecule 42: Mitochondrial ribosomal protein L46

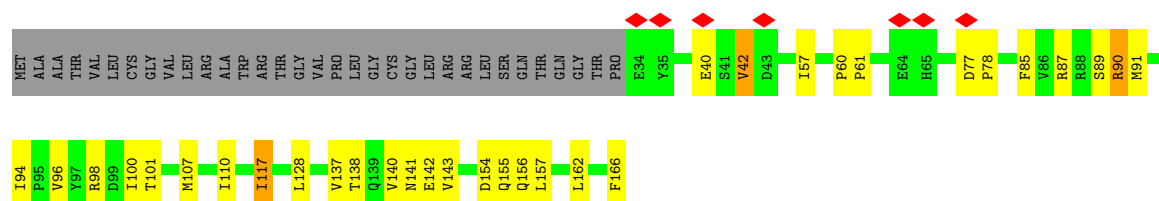




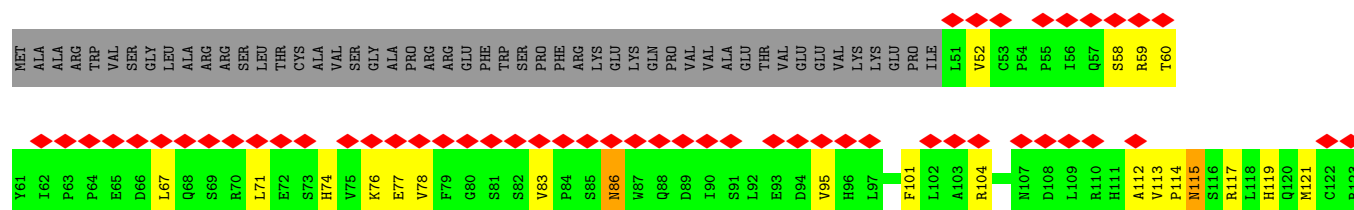
• Molecule 43: Mitochondrial ribosomal protein L48



• Molecule 44: Mrpl34

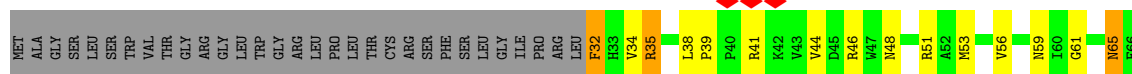


• Molecule 45: Mitochondrial ribosomal protein L50





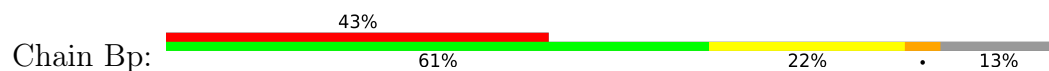
- Molecule 46: Mitochondrial ribosomal protein L51



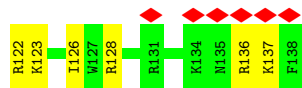
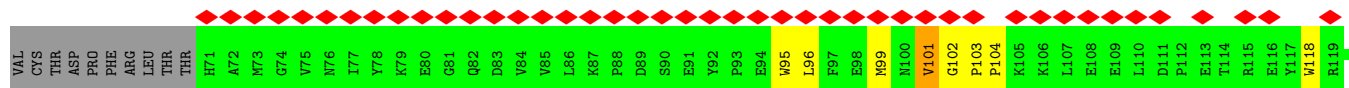
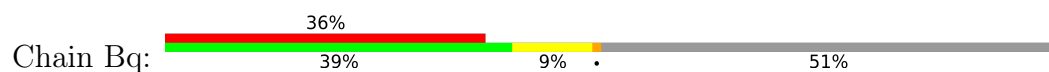
- Molecule 47: Mitochondrial ribosomal protein L52



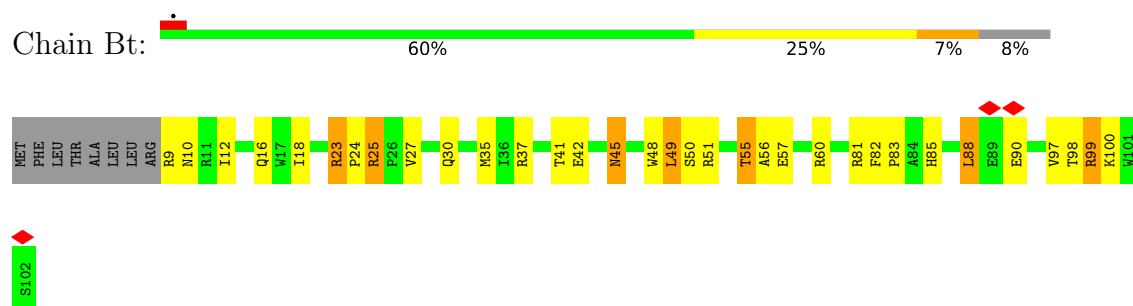
- Molecule 48: mL53, MRPL53



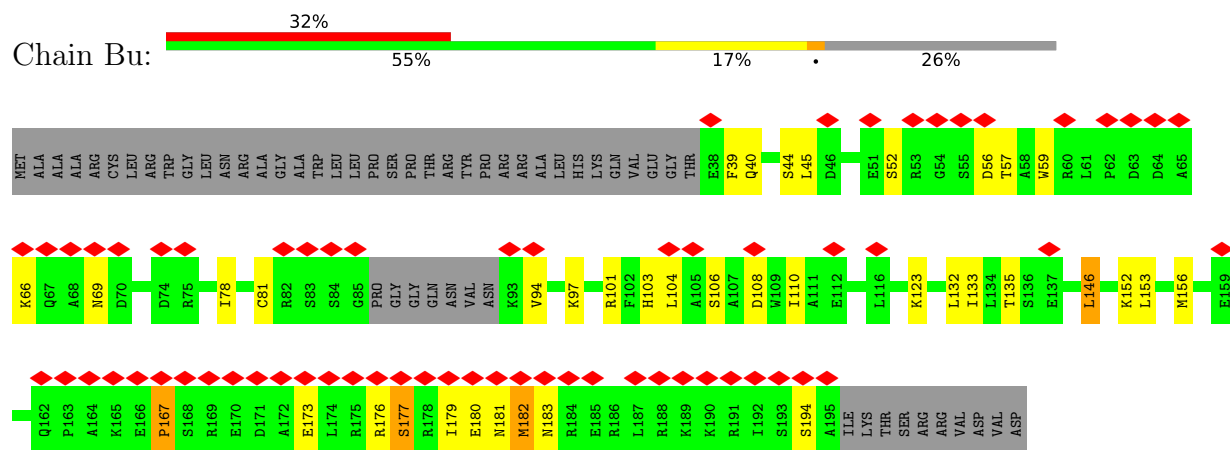
- Molecule 49: Uncharacterized protein



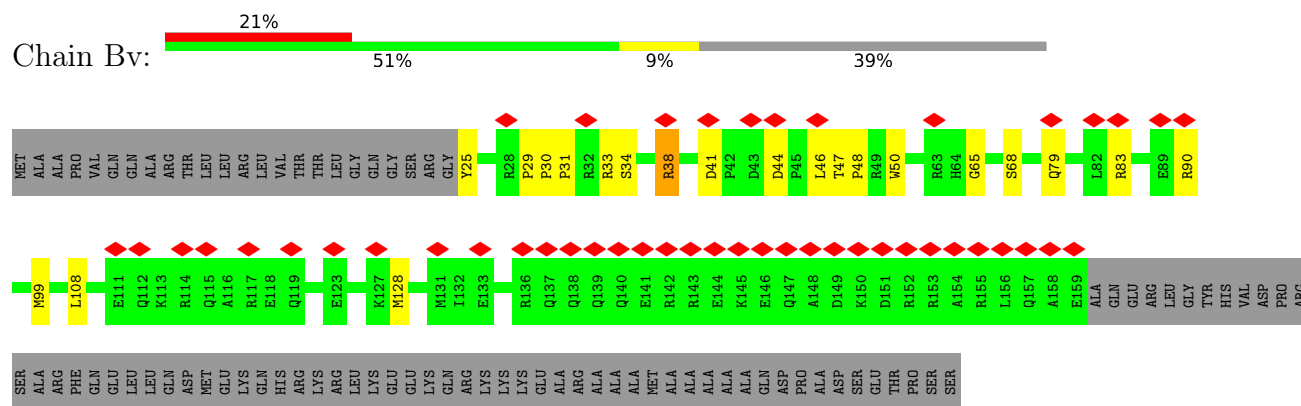
- Molecule 50: Mitochondrial ribosomal protein L57



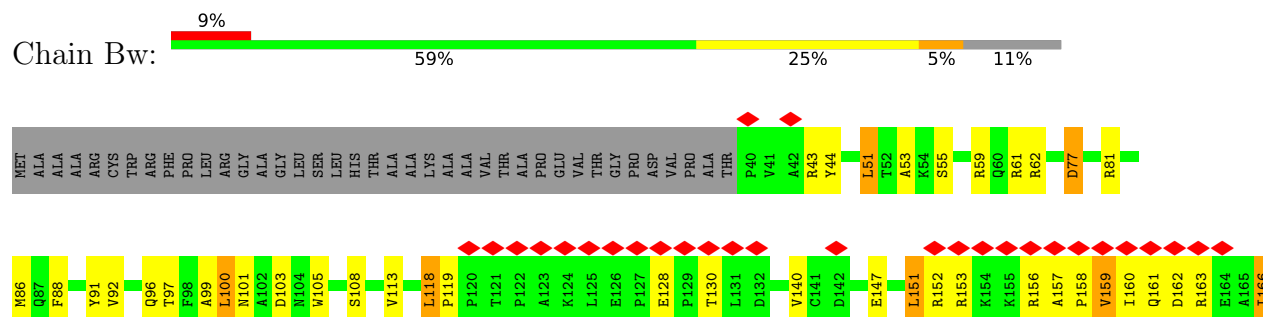
- Molecule 51: Mitochondrial ribosomal protein L58

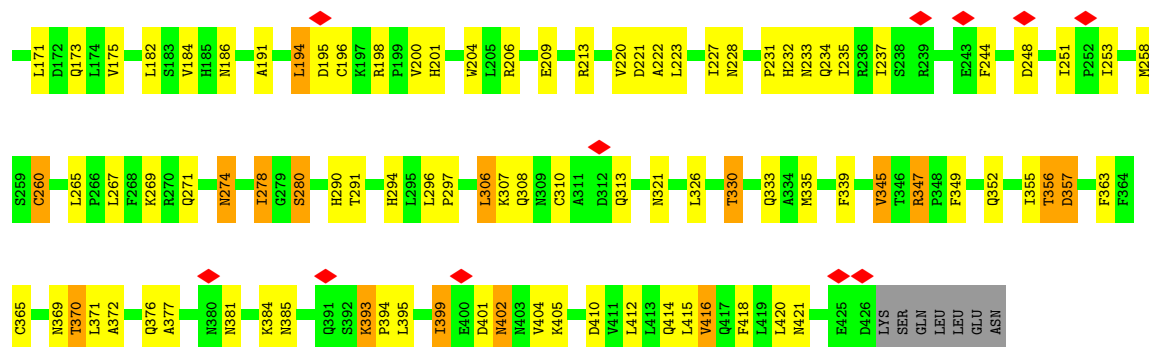


- Molecule 52: 'Mitochondrial ribosomal protein L59

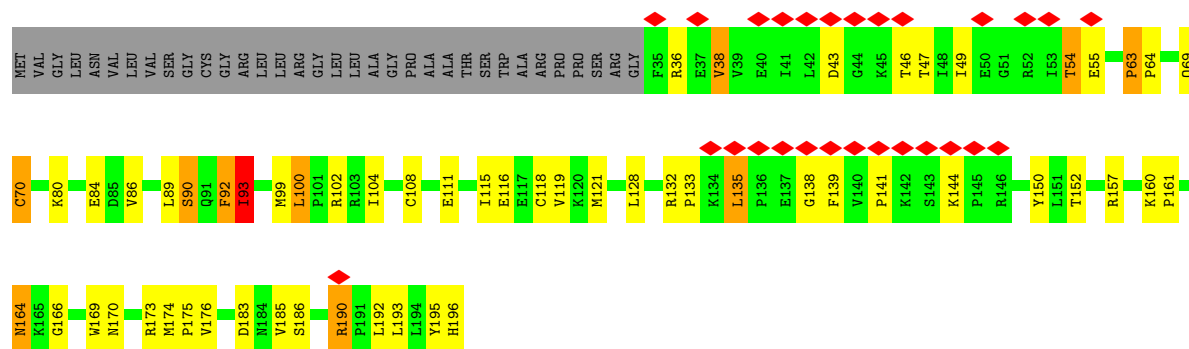


- Molecule 53: mL65, MRPS30





• Molecule 54: Mitochondrial ribosomal protein S18A



• Molecule 55: unassigned secondary structure elements



• Molecule 56: P-site fMet-tRNA^{Met}, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75666	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.658	Depositor
Minimum map value	-0.328	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	390.59, 390.59, 390.59	wwPDB
Map dimensions	281, 281, 281	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, GSP, MG, 5GP, FME, ZN, SPM

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	BL	0.53	0/542	0.83	0/729
1	CL	0.70	0/319	1.17	4/435 (0.9%)
1	DL	0.54	0/212	0.70	0/286
1	EL	0.63	0/221	0.83	0/297
1	FL	0.59	0/212	0.74	0/286
1	GL	0.63	0/212	0.67	0/286
1	HL	0.68	0/204	0.72	0/275
2	B0	0.56	0/880	0.87	1/1189 (0.1%)
3	B1	0.42	0/2093	0.82	0/2835
4	B2	0.45	0/1586	0.84	1/2123 (0.0%)
5	B3	0.49	0/993	0.99	3/1341 (0.2%)
6	B4	0.35	0/388	0.97	2/523 (0.4%)
7	B5	0.43	0/917	0.88	2/1227 (0.2%)
8	B6	0.42	0/430	0.91	2/570 (0.4%)
9	B7	0.60	0/395	0.82	0/524
10	B8	0.51	0/853	0.89	0/1136
11	B9	0.50	0/342	0.78	0/450
12	BA	0.31	0/36903	0.46	0/57455
13	BB	0.23	0/1595	0.35	0/2475
14	BC	0.43	0/4432	0.83	4/5989 (0.1%)
15	BD	0.45	0/1898	0.93	3/2555 (0.1%)
16	BE	0.50	0/2493	1.02	14/3387 (0.4%)
17	BF	0.53	0/2069	0.95	5/2816 (0.2%)
18	BI	0.43	0/819	0.87	1/1101 (0.1%)
19	BJ	0.47	0/1742	0.87	5/2358 (0.2%)
20	BK	0.46	0/1323	0.87	1/1785 (0.1%)
21	BN	0.52	0/1487	0.89	3/2017 (0.1%)
22	BO	0.45	0/912	0.87	0/1231
23	BP	0.50	0/2368	0.89	5/3198 (0.2%)
24	BQ	0.46	0/1850	0.85	1/2491 (0.0%)
25	BR	0.47	0/1262	0.84	0/1700
26	BS	0.46	0/1197	0.90	2/1624 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	BT	0.42	0/1888	0.86	3/2548 (0.1%)
28	BU	0.57	0/1179	0.89	2/1578 (0.1%)
29	BV	0.55	0/1256	0.97	5/1706 (0.3%)
30	BW	0.51	0/1407	0.88	2/1891 (0.1%)
31	BX	0.48	0/1211	0.94	2/1646 (0.1%)
32	BY	0.40	0/1719	0.89	2/2329 (0.1%)
33	Ba	0.43	0/3267	0.88	4/4455 (0.1%)
34	Bb	0.44	0/3047	0.93	8/4139 (0.2%)
35	Bc	0.39	0/2464	0.87	4/3330 (0.1%)
36	Bd	0.44	0/853	0.92	3/1153 (0.3%)
37	Be	0.44	0/1000	0.98	8/1345 (0.6%)
38	Bf	0.45	0/851	0.94	5/1159 (0.4%)
39	Bg	0.48	0/1191	0.98	6/1614 (0.4%)
40	Bh	0.47	0/2372	0.95	9/3211 (0.3%)
41	Bi	0.44	0/2199	0.95	9/2980 (0.3%)
42	Bj	0.40	0/1811	0.83	0/2436
43	Bk	0.39	0/1108	0.82	0/1499
44	Bl	0.48	0/1135	0.84	0/1549
45	Bm	0.40	0/917	0.80	0/1248
46	Bn	0.50	0/860	0.93	0/1150
47	Bo	0.43	0/787	0.81	3/1056 (0.3%)
48	Bp	0.43	0/752	0.90	3/1013 (0.3%)
49	Bq	0.46	0/558	0.85	2/756 (0.3%)
50	Bt	0.50	0/798	1.03	4/1073 (0.4%)
51	Bu	0.37	0/1214	0.79	1/1630 (0.1%)
52	Bv	0.37	0/1157	0.71	0/1560
53	Bw	0.47	0/3206	0.92	9/4354 (0.2%)
54	Bx	0.51	0/1364	0.97	5/1849 (0.3%)
55	Bz	0.51	0/404	0.67	0/556
56	AV	0.24	0/1673	0.37	0/2602
All	All	0.42	0/116797	0.76	158/166109 (0.1%)

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
6	B4	0	1
16	BE	0	1
26	BS	0	1
34	Bb	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
46	Bn	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 158 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	Bh	284	GLY	CA-C-N	12.91	132.96	120.31
40	Bh	284	GLY	C-N-CA	12.91	132.96	120.31
41	Bi	89	VAL	CA-C-N	9.45	130.11	120.38
41	Bi	89	VAL	C-N-CA	9.45	130.11	120.38
6	B4	71	GLU	CA-C-N	8.92	128.56	119.82

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	B4	61	ASP	Peptide
16	BE	316	PHE	Peptide
26	BS	69	GLY	Peptide
34	Bb	210	GLU	Peptide
46	Bn	65	ASN	Peptide

5.2 Too-close contacts ⓘ

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	BL	537	0	591	12	0
1	CL	317	0	309	12	0
1	DL	213	0	234	7	0
1	EL	222	0	247	6	0
1	FL	213	0	234	7	0
1	GL	213	0	234	5	0
1	HL	205	0	223	9	0
2	B0	857	0	878	20	0
3	B1	2036	0	2058	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B2	1548	0	1583	27	0
5	B3	968	0	1018	26	0
6	B4	381	0	400	19	0
7	B5	902	0	916	33	0
8	B6	425	0	471	16	0
9	B7	387	0	413	7	0
10	B8	833	0	883	21	0
11	B9	335	0	359	11	0
12	BA	32950	0	16673	363	0
13	BB	1427	0	726	14	0
14	BC	4364	0	4371	82	0
15	BD	1860	0	1923	40	0
16	BE	2420	0	2418	75	0
17	BF	2011	0	2049	62	0
18	BI	805	0	845	26	0
19	BJ	1705	0	1804	46	0
20	BK	1303	0	1343	39	0
21	BN	1444	0	1437	49	0
22	BO	896	0	946	34	0
23	BP	2312	0	2373	61	0
24	BQ	1803	0	1841	32	0
25	BR	1240	0	1260	27	0
26	BS	1168	0	1159	49	0
27	BT	1845	0	1856	42	0
28	BU	1159	0	1228	23	0
29	BV	1231	0	1278	28	0
30	BW	1374	0	1405	28	0
31	BX	1181	0	1139	31	0
32	BY	1678	0	1683	44	0
33	Ba	3173	0	3153	88	0
34	Bb	2952	0	2840	91	0
35	Bc	2408	0	2415	53	0
36	Bd	832	0	828	41	0
37	Be	972	0	971	33	0
38	Bf	827	0	736	30	0
39	Bg	1167	0	1173	37	0
40	Bh	2319	0	2332	64	0
41	Bi	2138	0	2139	61	0
42	Bj	1775	0	1797	74	0
43	Bk	1087	0	1080	34	0
44	Bl	1097	0	1080	13	0
45	Bm	893	0	878	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	Bn	837	0	860	31	0
47	Bo	772	0	773	19	0
48	Bp	742	0	749	20	0
49	Bq	542	0	485	14	0
50	Bt	780	0	792	22	0
51	Bu	1198	0	1192	23	0
52	Bv	1131	0	1093	15	0
53	Bw	3126	0	3153	91	0
54	Bx	1325	0	1354	53	0
55	Bz	410	0	404	5	0
56	AV	1498	0	765	9	0
57	B3	1	0	0	0	0
57	BA	203	0	0	0	0
57	BB	1	0	0	0	0
57	BC	1	0	0	0	0
57	BD	3	0	0	0	0
57	BP	2	0	0	0	0
57	BQ	1	0	0	0	0
57	Be	2	0	0	0	0
57	Bl	1	0	0	0	0
57	Bt	1	0	0	0	0
58	B5	1	0	0	0	0
58	B9	1	0	0	0	0
58	BJ	1	0	0	0	0
59	BA	48	0	24	0	0
60	BA	14	0	26	2	0
60	BR	14	0	26	0	0
61	BC	32	0	12	1	0
62	BC	1	0	0	0	0
63	AV	10	0	10	0	0
64	BC	2	0	0	0	0
All	All	111109	0	93948	1934	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 9.

The worst 5 of 1934 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)
26:BS:85:ARG:HB3	26:BS:120:ARG:HH12	1.20	1.04
37:Be:44:ARG:HH12	53:Bw:157:ALA:HB3	1.20	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Be:25:ARG:HG2	37:Be:25:ARG:HH11	1.26	0.99
35:Bc:186:LEU:HG	35:Bc:189:TRP:HE1	1.29	0.98
35:Bc:294:GLN:HE22	35:Bc:320:VAL:H	1.13	0.94

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BL	68/198 (34%)	65 (96%)	3 (4%)	0	100	100
1	CL	43/198 (22%)	41 (95%)	1 (2%)	1 (2%)	5	29
1	DL	25/198 (13%)	25 (100%)	0	0	100	100
1	EL	26/198 (13%)	25 (96%)	1 (4%)	0	100	100
1	FL	25/198 (13%)	25 (100%)	0	0	100	100
1	GL	25/198 (13%)	25 (100%)	0	0	100	100
1	HL	24/198 (12%)	24 (100%)	0	0	100	100
2	B0	108/148 (73%)	105 (97%)	3 (3%)	0	100	100
3	B1	242/256 (94%)	238 (98%)	4 (2%)	0	100	100
4	B2	177/252 (70%)	171 (97%)	6 (3%)	0	100	100
5	B3	116/161 (72%)	114 (98%)	2 (2%)	0	100	100
6	B4	43/126 (34%)	40 (93%)	3 (7%)	0	100	100
7	B5	108/188 (57%)	107 (99%)	1 (1%)	0	100	100
8	B6	50/65 (77%)	49 (98%)	1 (2%)	0	100	100
9	B7	44/95 (46%)	43 (98%)	1 (2%)	0	100	100
10	B8	93/188 (50%)	91 (98%)	2 (2%)	0	100	100
11	B9	36/100 (36%)	36 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	BC	569/657 (87%)	545 (96%)	23 (4%)	1 (0%)	43	73
15	BD	238/306 (78%)	225 (94%)	13 (6%)	0	100	100
16	BE	305/348 (88%)	282 (92%)	20 (7%)	3 (1%)	12	45
17	BF	248/294 (84%)	237 (96%)	11 (4%)	0	100	100
18	BI	96/268 (36%)	91 (95%)	5 (5%)	0	100	100
19	BJ	210/262 (80%)	203 (97%)	7 (3%)	0	100	100
20	BK	174/192 (91%)	164 (94%)	9 (5%)	1 (1%)	21	56
21	BN	175/178 (98%)	172 (98%)	3 (2%)	0	100	100
22	BO	113/145 (78%)	108 (96%)	5 (4%)	0	100	100
23	BP	286/296 (97%)	276 (96%)	10 (4%)	0	100	100
24	BQ	220/251 (88%)	218 (99%)	2 (1%)	0	100	100
25	BR	151/169 (89%)	146 (97%)	5 (3%)	0	100	100
26	BS	141/180 (78%)	128 (91%)	12 (8%)	1 (1%)	18	52
27	BT	221/292 (76%)	214 (97%)	7 (3%)	0	100	100
28	BU	138/149 (93%)	134 (97%)	4 (3%)	0	100	100
29	BV	153/209 (73%)	147 (96%)	6 (4%)	0	100	100
30	BW	164/210 (78%)	159 (97%)	5 (3%)	0	100	100
31	BX	147/150 (98%)	146 (99%)	1 (1%)	0	100	100
32	BY	204/216 (94%)	192 (94%)	12 (6%)	0	100	100
33	Ba	391/423 (92%)	375 (96%)	16 (4%)	0	100	100
34	Bb	352/380 (93%)	330 (94%)	22 (6%)	0	100	100
35	Bc	293/334 (88%)	279 (95%)	14 (5%)	0	100	100
36	Bd	97/206 (47%)	89 (92%)	7 (7%)	1 (1%)	12	45
37	Be	120/135 (89%)	114 (95%)	6 (5%)	0	100	100
38	Bf	106/142 (75%)	102 (96%)	2 (2%)	2 (2%)	6	33
39	Bg	146/159 (92%)	137 (94%)	9 (6%)	0	100	100
40	Bh	287/332 (86%)	274 (96%)	13 (4%)	0	100	100
41	Bi	258/306 (84%)	250 (97%)	8 (3%)	0	100	100
42	Bj	211/279 (76%)	200 (95%)	10 (5%)	1 (0%)	24	59
43	Bk	132/212 (62%)	126 (96%)	6 (4%)	0	100	100
44	Bl	131/166 (79%)	127 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	Bm	107/159 (67%)	103 (96%)	4 (4%)	0	100	100
46	Bn	95/128 (74%)	89 (94%)	6 (6%)	0	100	100
47	Bo	95/124 (77%)	91 (96%)	4 (4%)	0	100	100
48	Bp	95/112 (85%)	89 (94%)	6 (6%)	0	100	100
49	Bq	66/138 (48%)	64 (97%)	1 (2%)	1 (2%)	8	37
50	Bt	92/102 (90%)	86 (94%)	6 (6%)	0	100	100
51	Bu	147/205 (72%)	137 (93%)	9 (6%)	1 (1%)	18	52
52	Bv	133/222 (60%)	132 (99%)	1 (1%)	0	100	100
53	Bw	385/433 (89%)	364 (94%)	20 (5%)	1 (0%)	36	68
54	Bx	160/196 (82%)	156 (98%)	3 (2%)	1 (1%)	21	56
55	Bz	70/82 (85%)	70 (100%)	0	0	100	100
All	All	9175/12712 (72%)	8795 (96%)	365 (4%)	15 (0%)	44	73

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	CL	21	PRO
38	Bf	78	PRO
38	Bf	80	PRO
51	Bu	167	PRO
16	BE	202	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BL	59/157 (38%)	59 (100%)	0	100	100
1	CL	30/157 (19%)	29 (97%)	1 (3%)	33	65
1	DL	26/157 (17%)	24 (92%)	2 (8%)	12	41
1	EL	27/157 (17%)	25 (93%)	2 (7%)	13	43
1	FL	26/157 (17%)	24 (92%)	2 (8%)	12	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	GL	26/157 (17%)	25 (96%)	1 (4%)	29	62
1	HL	25/157 (16%)	23 (92%)	2 (8%)	11	40
2	B0	90/115 (78%)	77 (86%)	13 (14%)	3	16
3	B1	219/229 (96%)	189 (86%)	30 (14%)	3	18
4	B2	164/228 (72%)	146 (89%)	18 (11%)	6	26
5	B3	110/147 (75%)	99 (90%)	11 (10%)	7	30
6	B4	42/114 (37%)	34 (81%)	8 (19%)	1	9
7	B5	99/163 (61%)	87 (88%)	12 (12%)	5	22
8	B6	49/60 (82%)	47 (96%)	2 (4%)	27	60
9	B7	41/78 (53%)	38 (93%)	3 (7%)	13	43
10	B8	87/162 (54%)	77 (88%)	10 (12%)	5	24
11	B9	36/77 (47%)	30 (83%)	6 (17%)	2	11
14	BC	464/556 (84%)	445 (96%)	19 (4%)	27	60
15	BD	193/248 (78%)	169 (88%)	24 (12%)	4	21
16	BE	263/290 (91%)	234 (89%)	29 (11%)	6	26
17	BF	217/251 (86%)	192 (88%)	25 (12%)	5	24
18	BI	88/228 (39%)	85 (97%)	3 (3%)	32	64
19	BJ	192/230 (84%)	179 (93%)	13 (7%)	14	46
20	BK	129/151 (85%)	119 (92%)	10 (8%)	11	41
21	BN	156/157 (99%)	137 (88%)	19 (12%)	5	22
22	BO	99/123 (80%)	88 (89%)	11 (11%)	6	25
23	BP	245/249 (98%)	216 (88%)	29 (12%)	5	23
24	BQ	190/210 (90%)	176 (93%)	14 (7%)	13	43
25	BR	132/143 (92%)	118 (89%)	14 (11%)	6	27
26	BS	123/153 (80%)	113 (92%)	10 (8%)	11	39
27	BT	204/258 (79%)	179 (88%)	25 (12%)	4	22
28	BU	118/127 (93%)	109 (92%)	9 (8%)	12	42
29	BV	136/178 (76%)	119 (88%)	17 (12%)	4	21
30	BW	144/180 (80%)	130 (90%)	14 (10%)	8	32
31	BX	116/134 (87%)	103 (89%)	13 (11%)	6	25
32	BY	185/192 (96%)	160 (86%)	25 (14%)	4	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Ba	348/365 (95%)	305 (88%)	43 (12%)	4	21
34	Bb	310/328 (94%)	272 (88%)	38 (12%)	4	22
35	Bc	271/299 (91%)	254 (94%)	17 (6%)	16	48
36	Bd	92/181 (51%)	86 (94%)	6 (6%)	15	47
37	Be	100/108 (93%)	86 (86%)	14 (14%)	3	17
38	Bf	80/133 (60%)	66 (82%)	14 (18%)	2	10
39	Bg	128/136 (94%)	112 (88%)	16 (12%)	4	21
40	Bh	251/284 (88%)	223 (89%)	28 (11%)	6	25
41	Bi	236/275 (86%)	219 (93%)	17 (7%)	13	44
42	Bj	190/242 (78%)	172 (90%)	18 (10%)	8	32
43	Bk	119/181 (66%)	112 (94%)	7 (6%)	18	50
44	Bl	122/147 (83%)	106 (87%)	16 (13%)	4	19
45	Bm	103/145 (71%)	94 (91%)	9 (9%)	9	36
46	Bn	88/113 (78%)	77 (88%)	11 (12%)	4	21
47	Bo	77/97 (79%)	68 (88%)	9 (12%)	5	23
48	Bp	79/88 (90%)	72 (91%)	7 (9%)	9	34
49	Bq	50/114 (44%)	47 (94%)	3 (6%)	17	50
50	Bt	75/82 (92%)	56 (75%)	19 (25%)	0	3
51	Bu	126/177 (71%)	116 (92%)	10 (8%)	11	40
52	Bv	115/183 (63%)	111 (96%)	4 (4%)	32	64
53	Bw	340/373 (91%)	298 (88%)	42 (12%)	4	21
54	Bx	149/173 (86%)	133 (89%)	16 (11%)	6	27
All	All	7999/10754 (74%)	7189 (90%)	810 (10%)	9	30

5 of 810 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	Ba	193	LEU
38	Bf	114	LYS
54	Bx	93	ILE
33	Ba	277	THR
33	Ba	189	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 191 such sidechains are listed below:

Mol	Chain	Res	Type
34	Bb	354	GLN
42	Bj	87	HIS
35	Bc	274	GLN
39	Bg	127	GLN
43	Bk	138	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	BA	1547/1571 (98%)	509 (32%)	10 (0%)
13	BB	65/73 (89%)	25 (38%)	1 (1%)
56	AV	70/71 (98%)	31 (44%)	0
All	All	1682/1715 (98%)	565 (33%)	11 (0%)

5 of 565 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	BA	4	A
12	BA	6	A
12	BA	7	G
12	BA	11	G
12	BA	15	A

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	BA	1220	A
12	BA	1240	A
13	BB	20	U
12	BA	1241	U
12	BA	1093	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 226 ligands modelled in this entry, 220 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
61	GSP	BC	901	57,62	30,34,34	1.92	2 (6%)	41,54,54	1.76	9 (21%)
63	FME	AV	101	56	8,9,10	0.96	0	7,9,11	0.67	0
60	SPM	BA	3205	-	13,13,13	0.37	0	12,12,12	0.81	0
59	5GP	BA	3204	-	26,26,26	0.85	1 (3%)	40,40,40	1.74	9 (22%)
60	SPM	BR	201	-	13,13,13	0.48	0	12,12,12	0.77	0
59	5GP	BA	3203	-	26,26,26	0.96	1 (3%)	40,40,40	2.09	9 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
61	GSP	BC	901	57,62	-	0/21/38/38	0/3/3/3
63	FME	AV	101	56	-	4/7/9/11	-
60	SPM	BA	3205	-	-	6/11/11/11	-
59	5GP	BA	3204	-	-	5/10/26/26	0/3/3/3
60	SPM	BR	201	-	-	7/11/11/11	-
59	5GP	BA	3203	-	-	6/10/26/26	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	BC	901	GSP	PG-S1G	-9.35	1.70	1.90
59	BA	3203	5GP	C6-N1	-2.71	1.33	1.38
61	BC	901	GSP	C2-N3	2.40	1.38	1.33
59	BA	3204	5GP	C6-N1	-2.12	1.34	1.38

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	BA	3203	5GP	C5-C4-N3	-7.46	116.36	128.46
59	BA	3204	5GP	C5-C4-N3	-5.92	118.86	128.46
59	BA	3203	5GP	C2-N3-C4	5.45	122.01	112.30
61	BC	901	GSP	C5-C4-N3	-4.97	120.40	128.46
59	BA	3203	5GP	N9-C4-N3	4.69	135.37	125.94

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

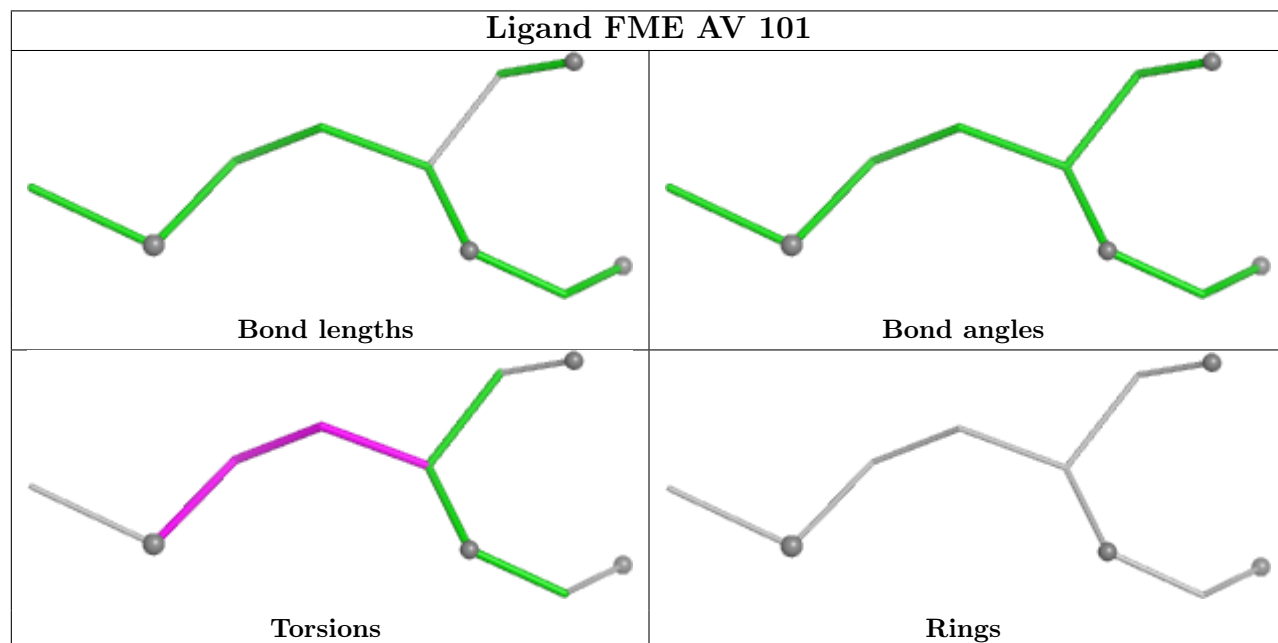
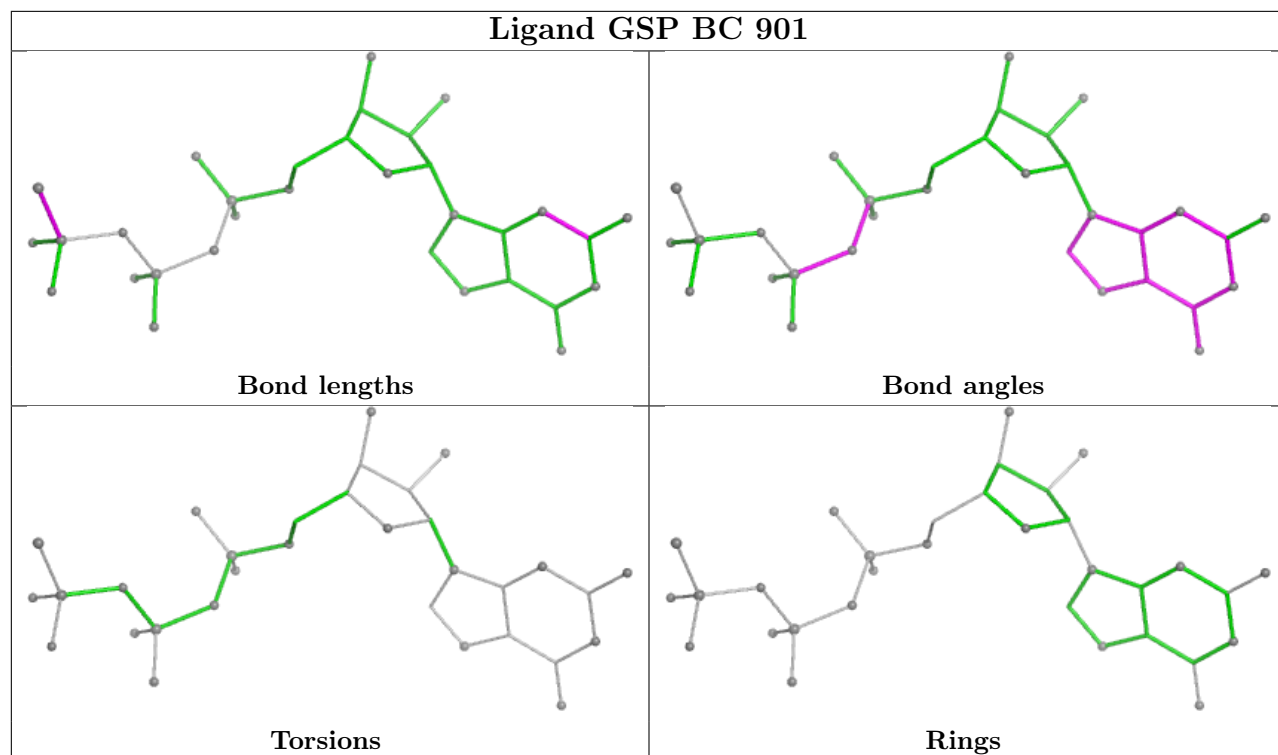
Mol	Chain	Res	Type	Atoms
59	BA	3203	5GP	C5'-O5'-P-OP1
59	BA	3203	5GP	C5'-O5'-P-OP3
59	BA	3203	5GP	C5'-O5'-P-OP2
59	BA	3204	5GP	C5'-O5'-P-OP1
59	BA	3204	5GP	C5'-O5'-P-OP3

There are no ring outliers.

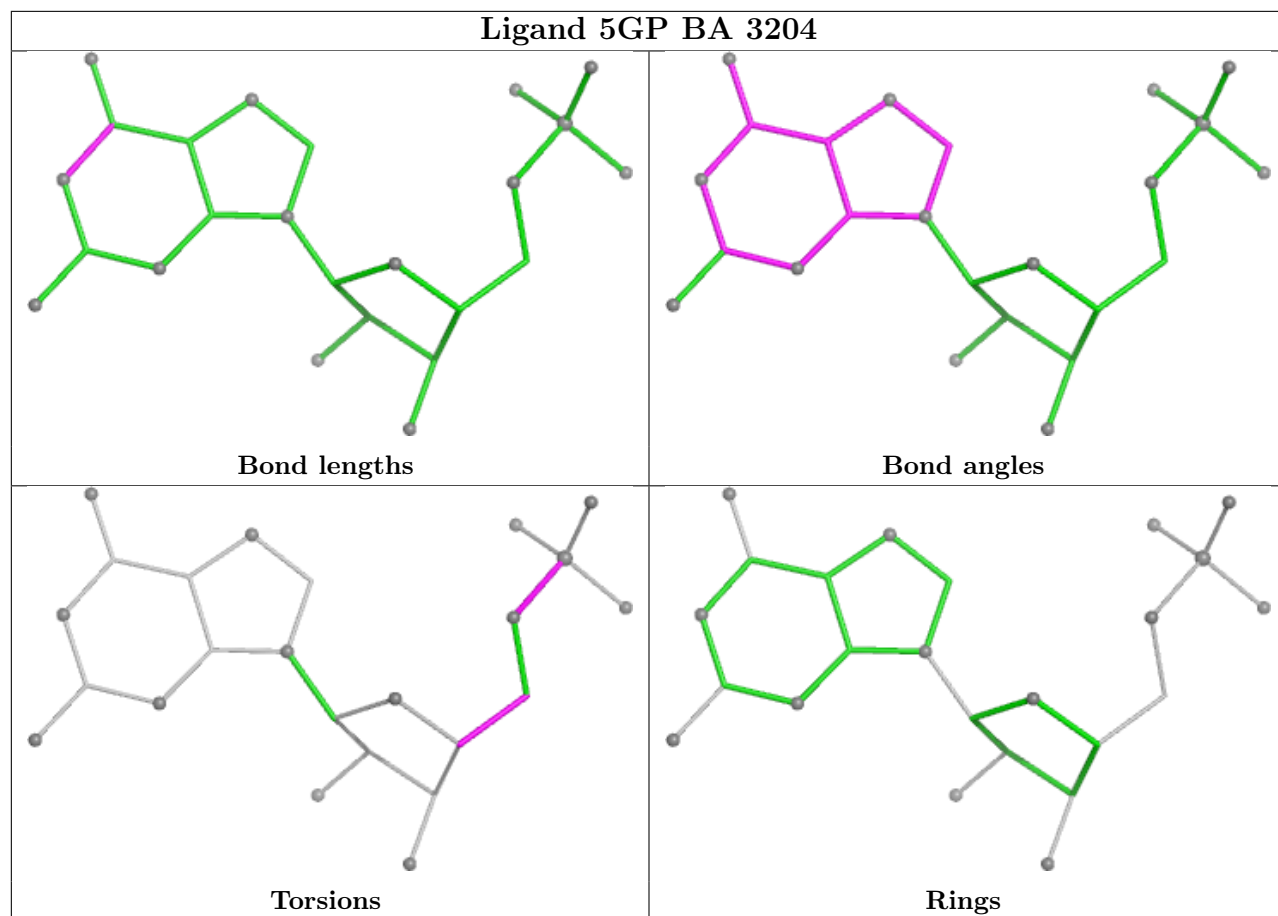
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
61	BC	901	GSP	1	0
60	BA	3205	SPM	2	0

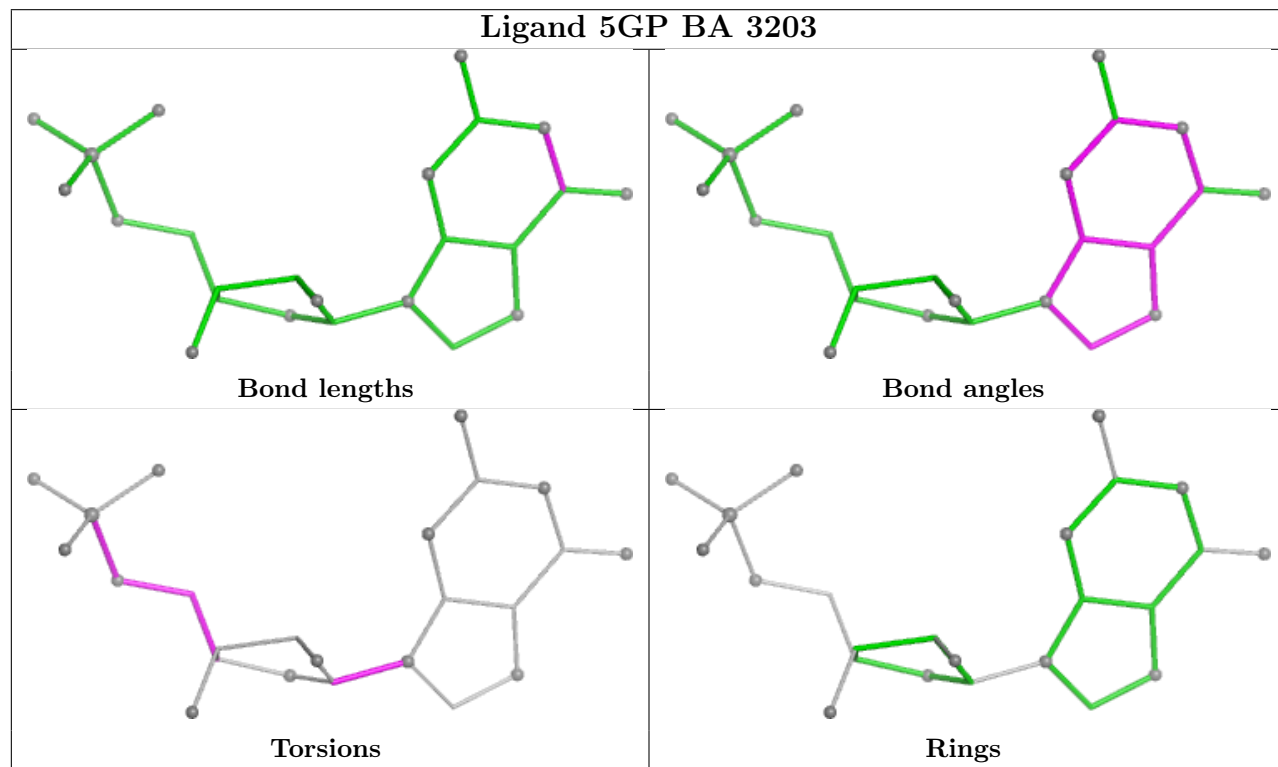
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



Ligand 5GP BA 3204



Ligand 5GP BA 3203



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
55	Bz	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Bz	710:ALA	C	1001:ALA	N	60.04
1	Bz	415:ALA	C	601:ALA	N	51.34
1	Bz	106:ALA	C	301:ALA	N	30.40
1	Bz	615:ALA	C	700:ALA	N	17.65
1	Bz	315:ALA	C	399:ALA	N	16.53

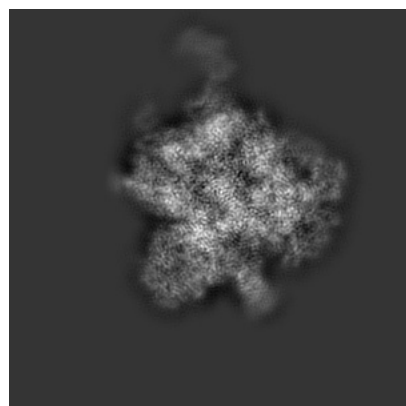
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4370. These allow visual inspection of the internal detail of the map and identification of artifacts.

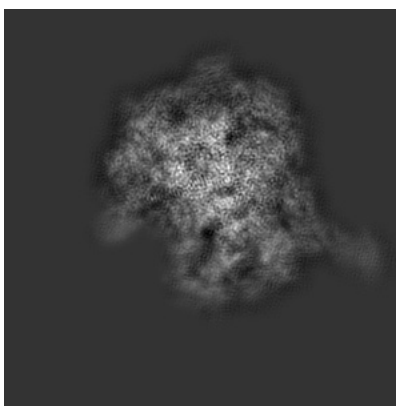
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

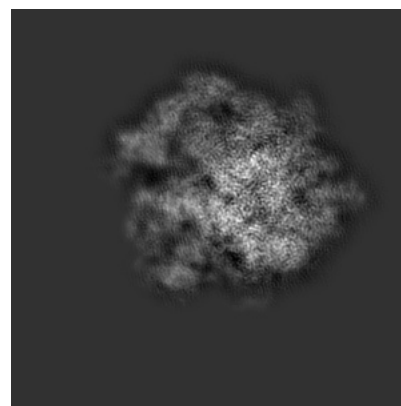
6.1.1 Primary map



X

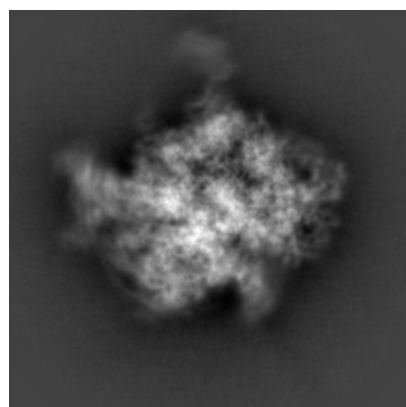


Y

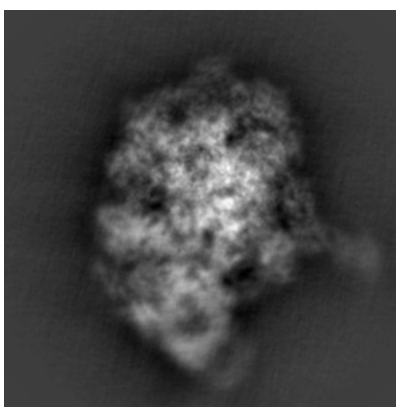


Z

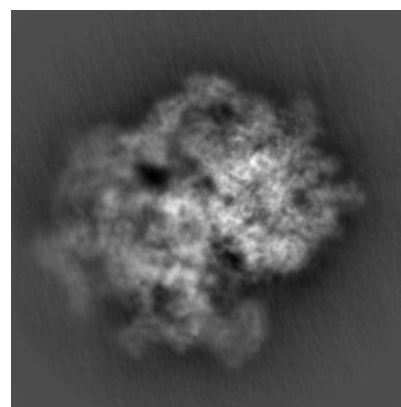
6.1.2 Raw map



X



Y

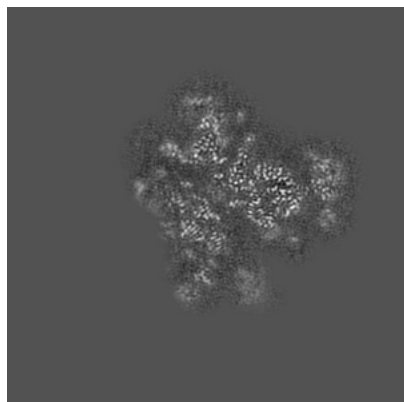


Z

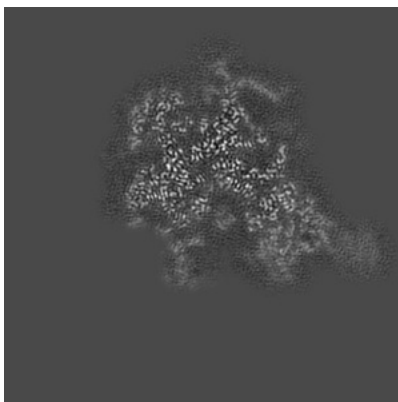
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

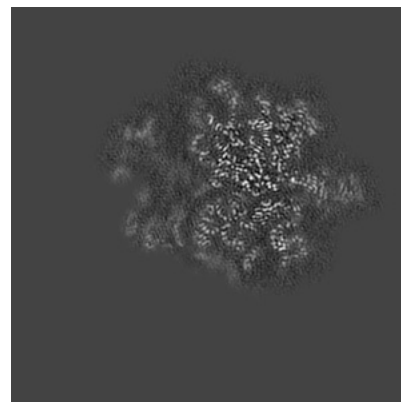
6.2.1 Primary map



X Index: 140

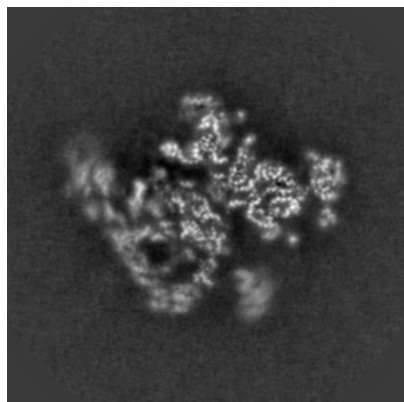


Y Index: 140

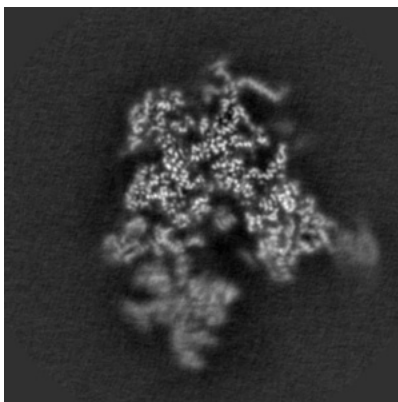


Z Index: 140

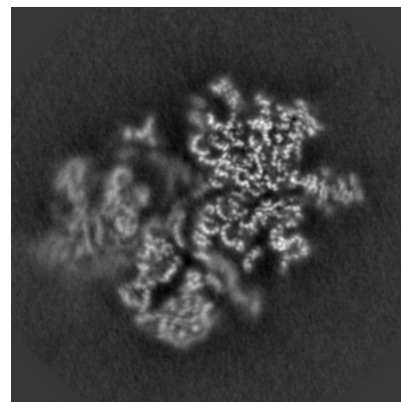
6.2.2 Raw map



X Index: 140



Y Index: 140

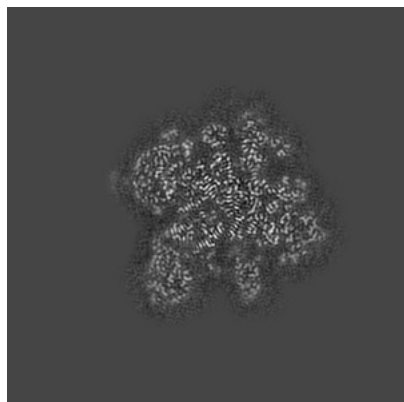


Z Index: 140

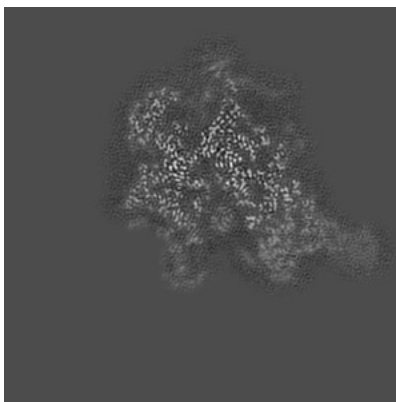
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

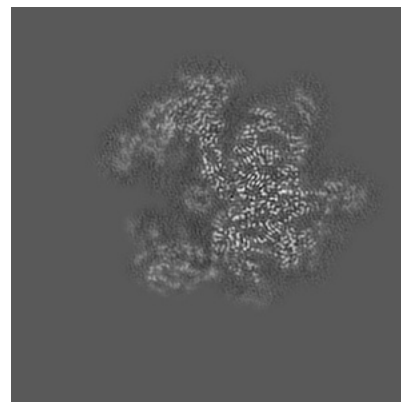
6.3.1 Primary map



X Index: 169

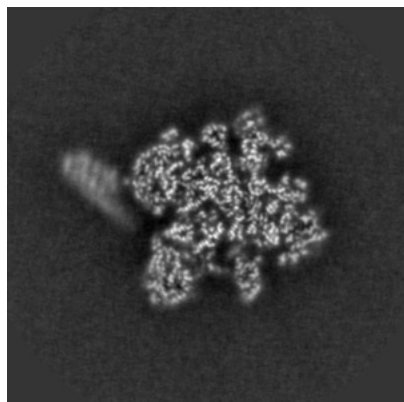


Y Index: 142

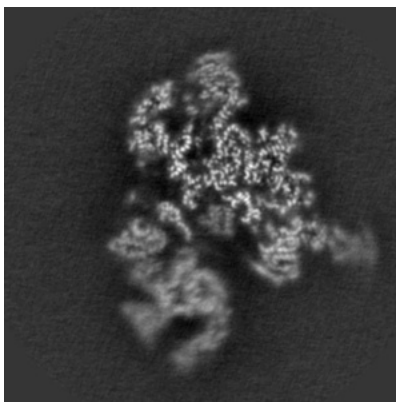


Z Index: 153

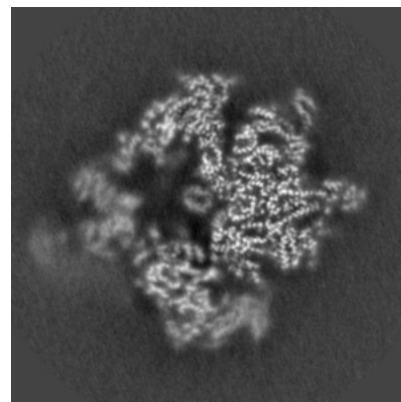
6.3.2 Raw map



X Index: 169



Y Index: 148

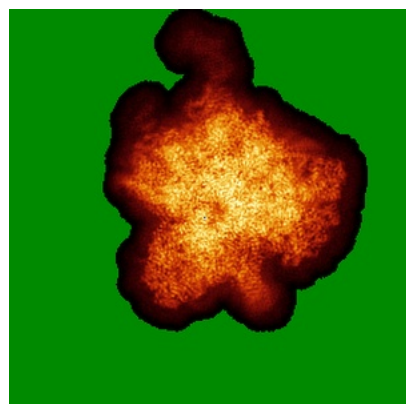


Z Index: 153

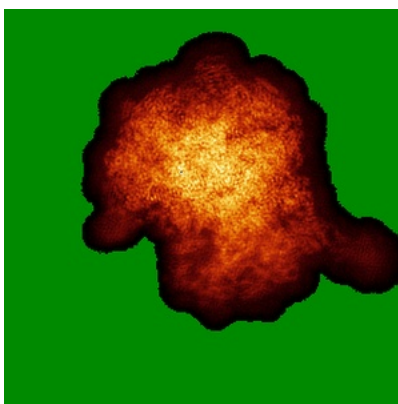
The images above show the largest variance slices of the map in three orthogonal directions.

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

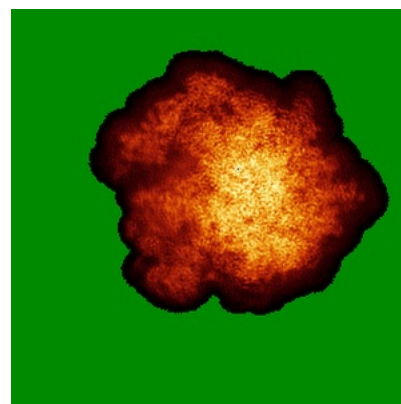
6.4.1 Primary map



X

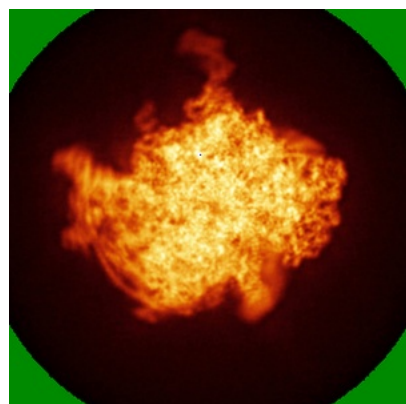


Y

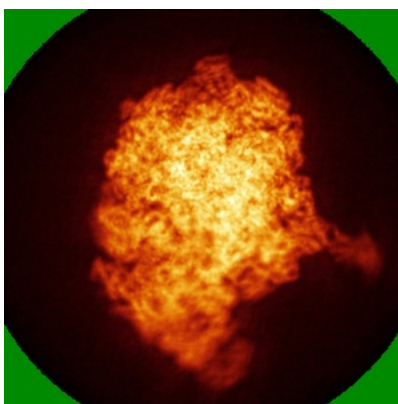


Z

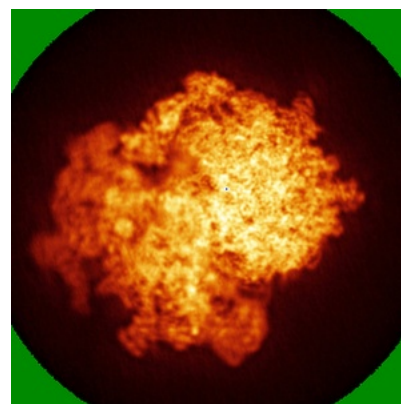
6.4.2 Raw map



X



Y



Z

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

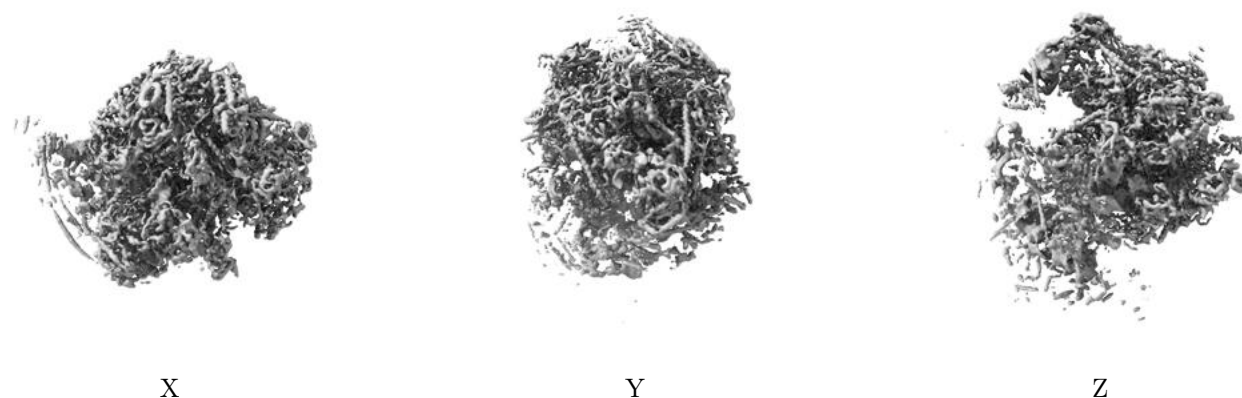
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

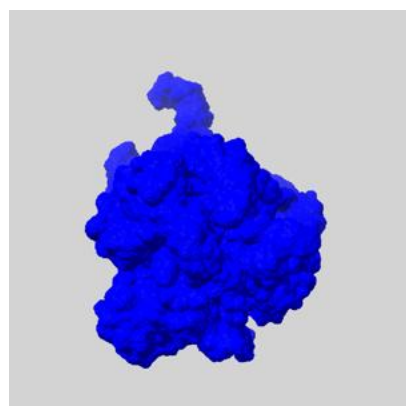
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

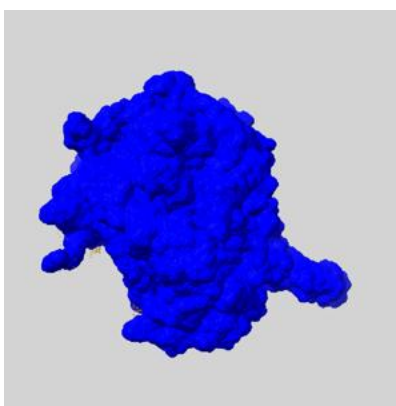
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

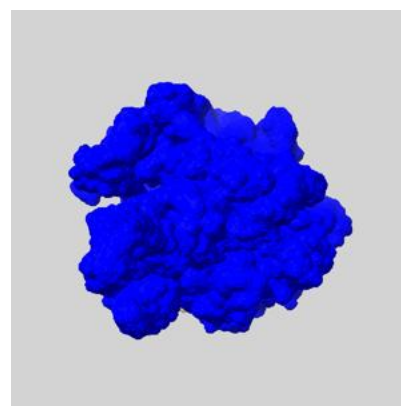
6.6.1 emd_4370_msk_1.map [i](#)



X



Y

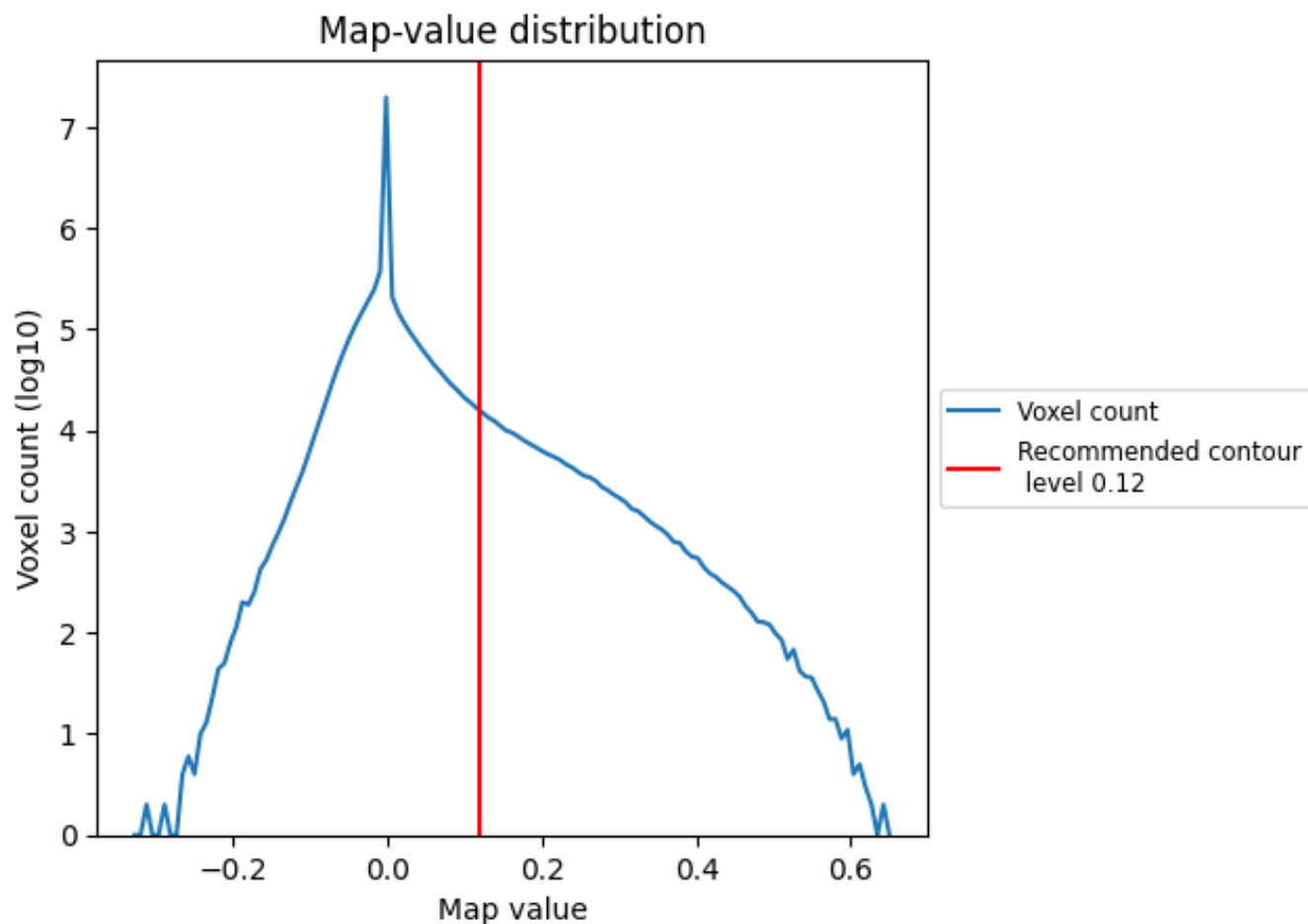


Z

7 Map analysis [i](#)

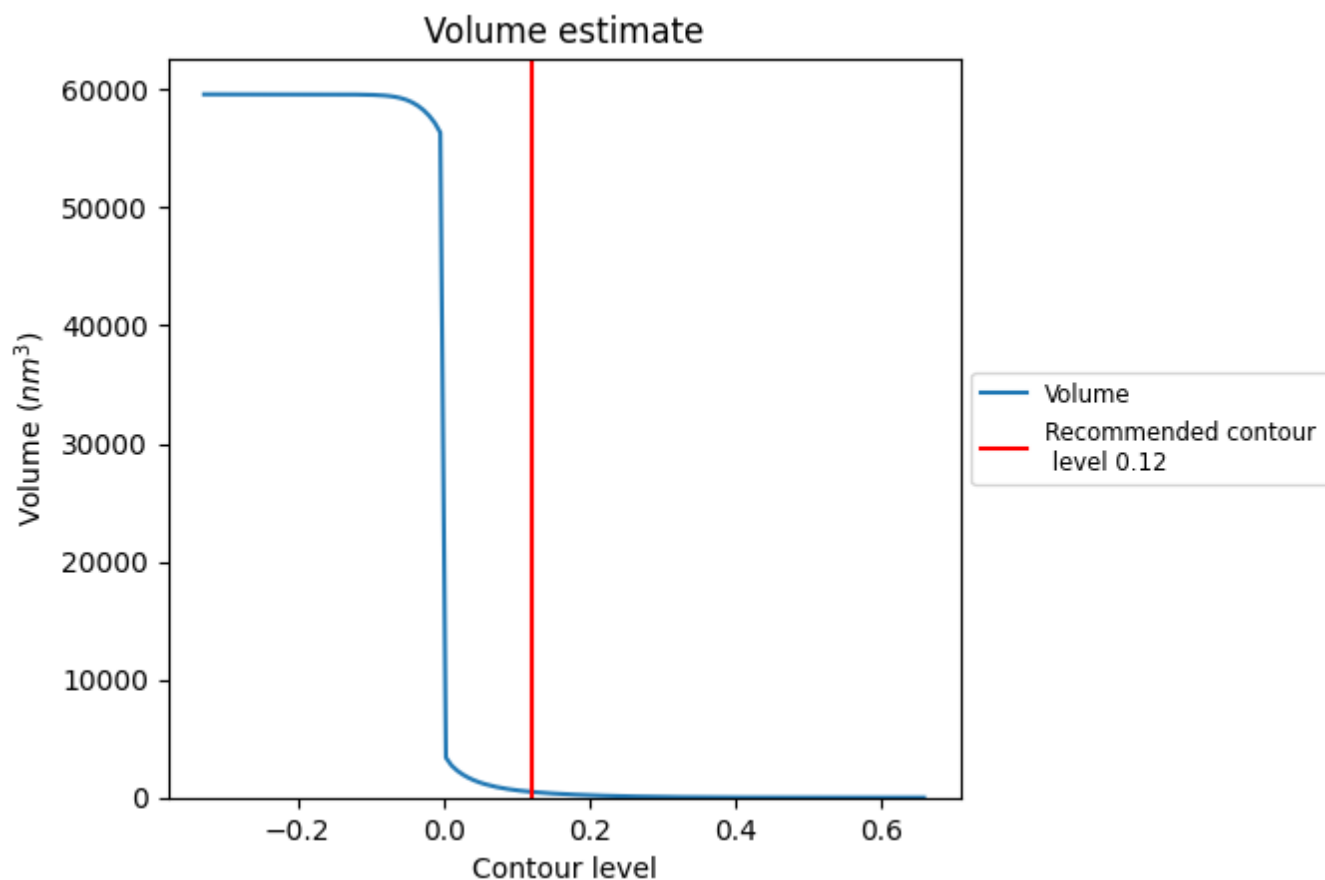
This section contains the results of statistical analysis of the map.

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.

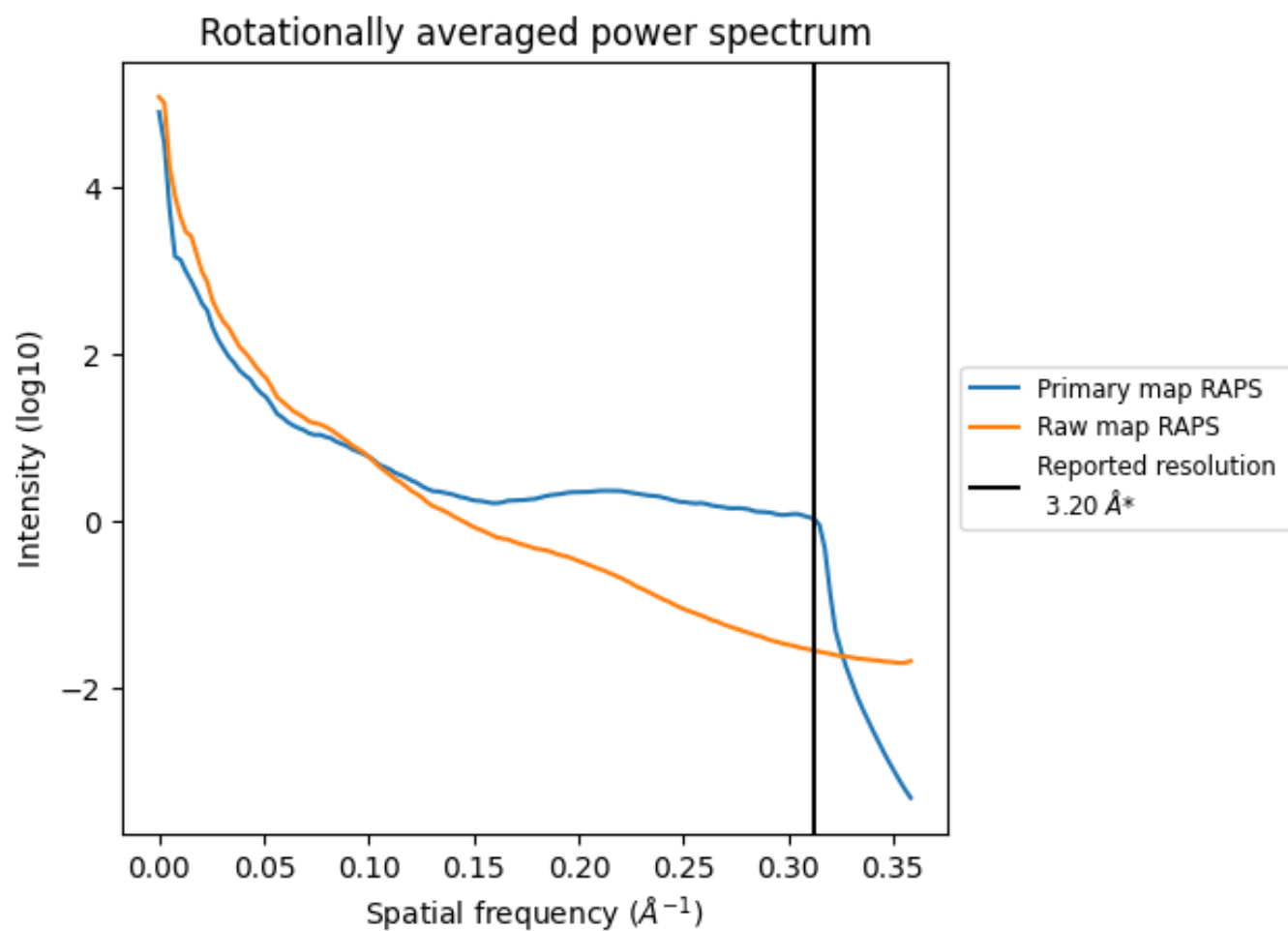
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 485 nm^3 ; this corresponds to an approximate mass of 438 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](#)

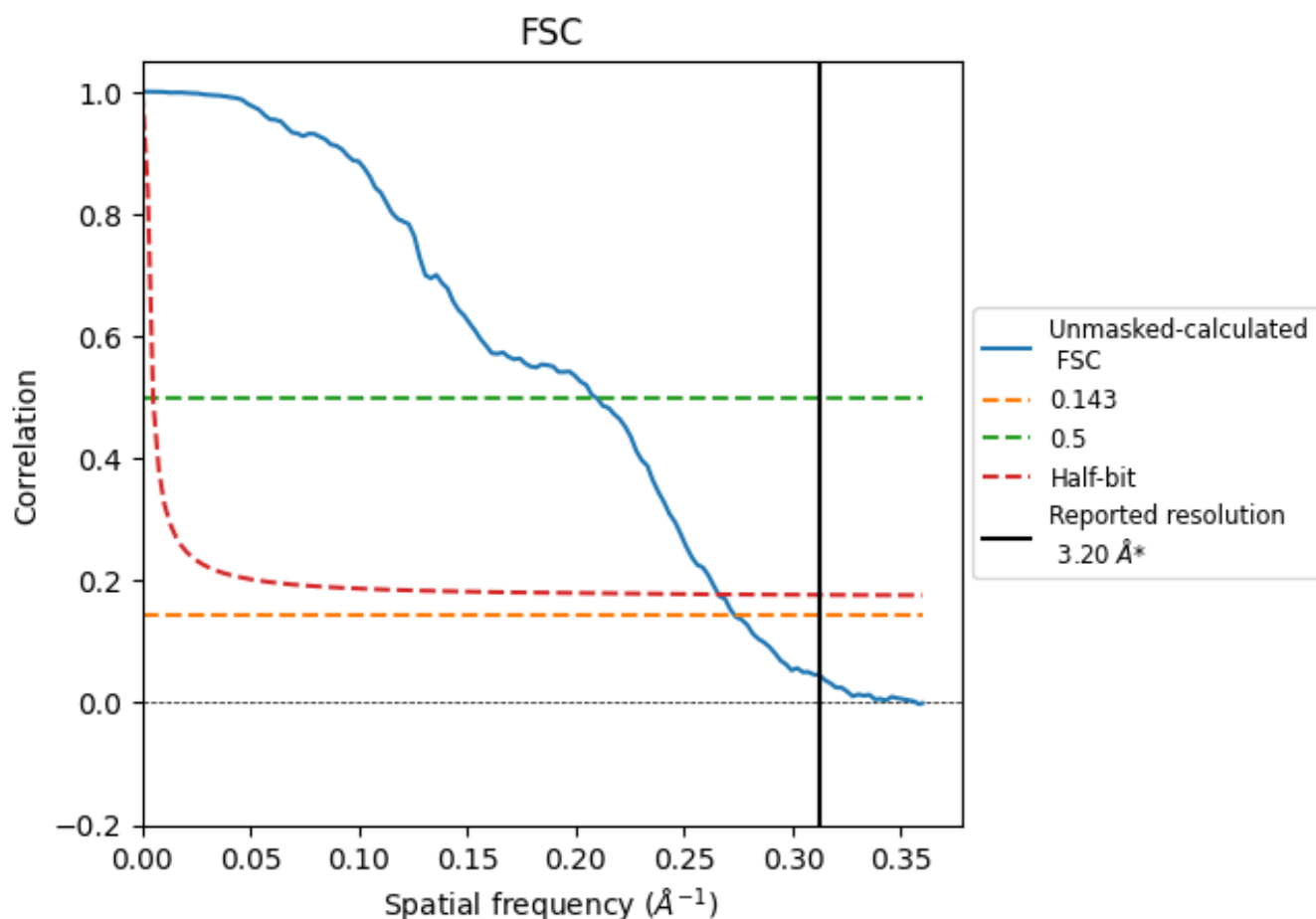


*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

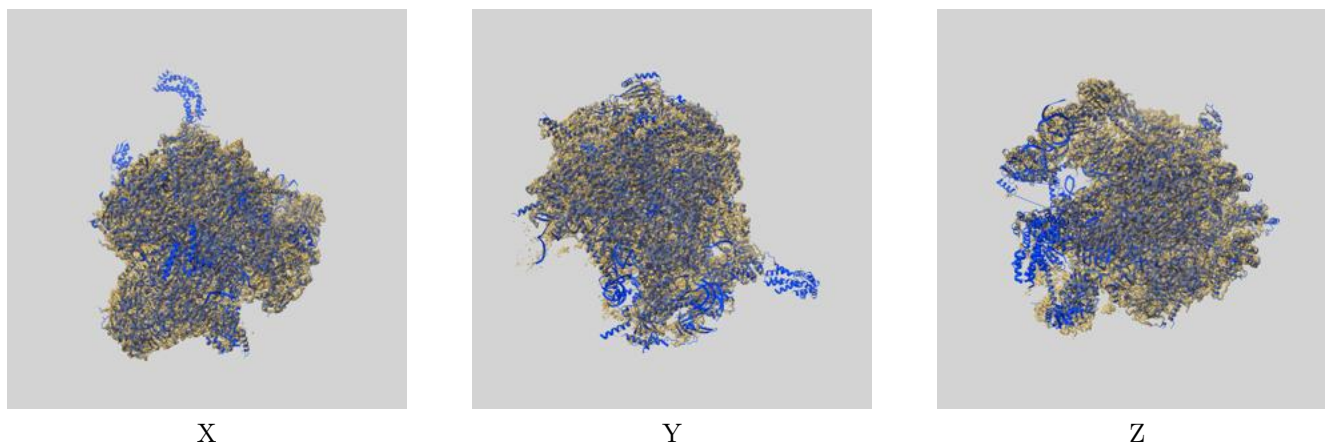
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.66	4.78	3.76

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.66 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

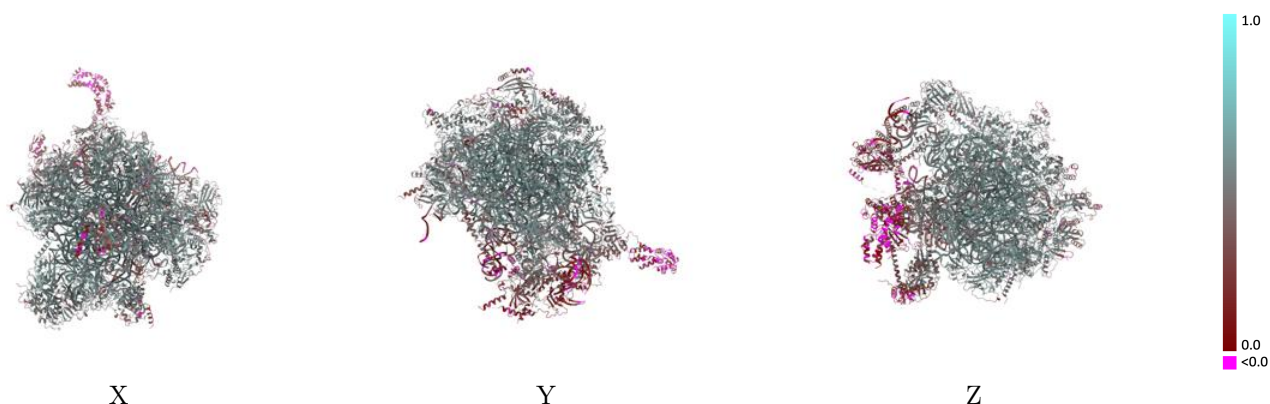
This section contains information regarding the fit between EMDB map EMD-4370 and PDB model 6GB2. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

9.1 Map-model overlay [i](#)



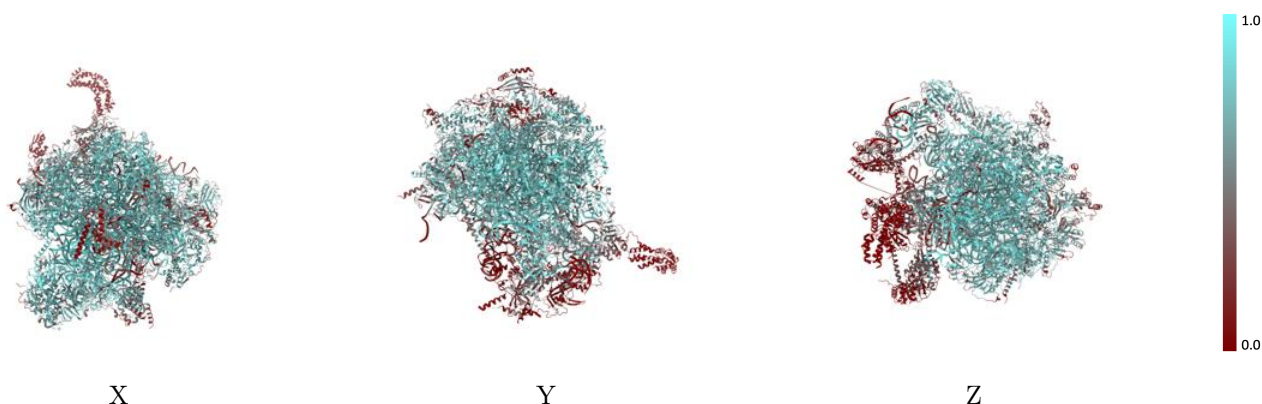
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



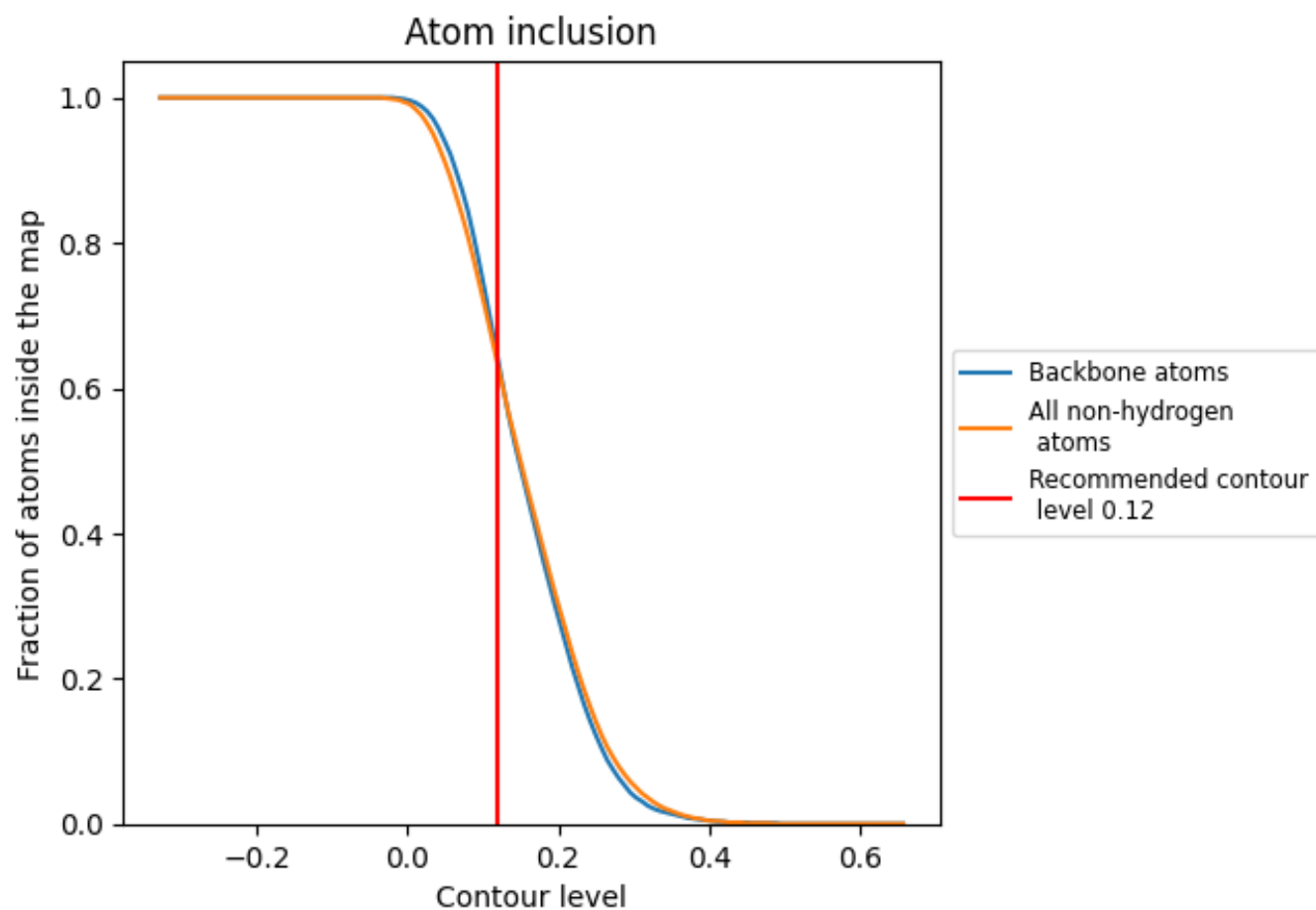
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).

9.4 Atom inclusion ⓘ



At the recommended contour level, 64% of all backbone atoms, 63% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6310	 0.4810
AV	 0.0440	 0.1900
B0	 0.7590	 0.5630
B1	 0.6000	 0.4850
B2	 0.7180	 0.5260
B3	 0.7270	 0.5410
B4	 0.3340	 0.2940
B5	 0.6980	 0.5220
B6	 0.4810	 0.4760
B7	 0.8020	 0.5900
B8	 0.7720	 0.5710
B9	 0.7820	 0.5530
BA	 0.8420	 0.5520
BB	 0.4940	 0.2870
BC	 0.2590	 0.3620
BD	 0.6690	 0.5360
BE	 0.7180	 0.5320
BF	 0.7370	 0.5480
BI	 0.4800	 0.4340
BJ	 0.3390	 0.3300
BK	 0.1670	 0.2330
BL	 0.0040	 0.1550
BN	 0.7750	 0.5590
BO	 0.6180	 0.5250
BP	 0.7330	 0.5470
BQ	 0.6820	 0.5310
BR	 0.7360	 0.5470
BS	 0.6810	 0.5090
BT	 0.6410	 0.5130
BU	 0.7540	 0.5500
BV	 0.7220	 0.5330
BW	 0.7250	 0.5520
BX	 0.6800	 0.5080
BY	 0.4290	 0.4340
Ba	 0.6580	 0.4990



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bb	 0.6590	 0.4740
Bc	 0.6020	 0.4660
Bd	 0.2790	 0.2660
Be	 0.5850	 0.4820
Bf	 0.6390	 0.4810
Bg	 0.7220	 0.5470
Bh	 0.6650	 0.4940
Bi	 0.3580	 0.3980
Bj	 0.1740	 0.1960
Bk	 0.3150	 0.3150
Bl	 0.7220	 0.5250
Bm	 0.2810	 0.3950
Bn	 0.7640	 0.5620
Bo	 0.6580	 0.5030
Bp	 0.3790	 0.3700
Bq	 0.3300	 0.3570
Bt	 0.7460	 0.5540
Bu	 0.4530	 0.3870
Bv	 0.4930	 0.4090
Bw	 0.6910	 0.5090
Bx	 0.6750	 0.5040
Bz	 0.0150	 0.0900
CL	 0.0090	 0.1490
DL	 0.0050	 0.1210
EL	 0.0000	 0.0300
FL	 0.0050	 0.0730
GL	 0.0000	 0.0360
HL	 0.0000	 0.0780