



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 08:07 PM UTC

PDB ID : 7O9M / pdb_00007o9m
EMDB ID : EMD-12764
Title : Human mitochondrial ribosome large subunit assembly intermediate with MTERF4-NSUN4, MRM2, MTG1 and the MALSU module
Authors : Valentin Gese, G.; Hallberg, B.M.
Deposited on : 2021-04-16
Resolution : 2.60 Å(reported)
Based on initial model : 5OOL

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:

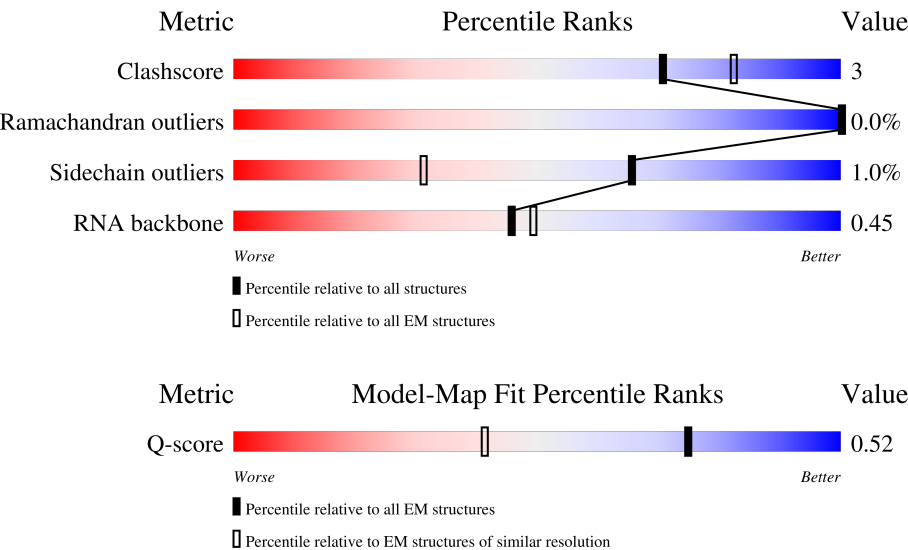
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.60 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.



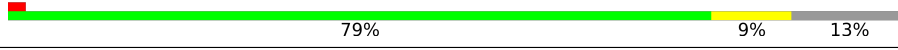
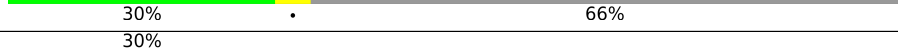
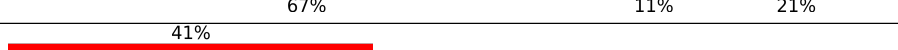
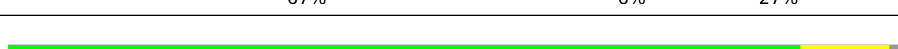
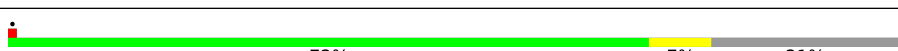
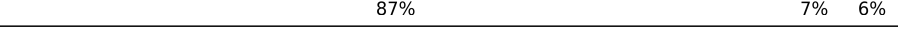
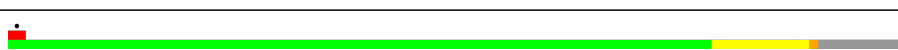
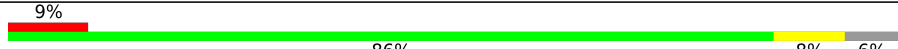
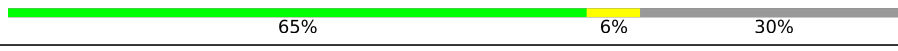
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	A	1559	
2	B	69	
3	C	333	

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Mol	Chain	Length	Quality of chain
4	D	305	
5	E	348	
6	F	311	
7	H	267	
8	I	261	
9	J	192	
10	K	178	
11	L	145	
12	M	296	
13	N	251	
14	O	175	
15	P	179	
16	Q	292	
17	R	149	
18	S	205	
19	T	212	
20	U	153	
21	V	216	
22	W	148	
23	X	256	
24	Y	250	
25	Z	161	
26	a	142	
27	0	188	
28	1	65	

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Mol	Chain	Length	Quality of chain
29	2	92	
30	3	188	
31	4	103	
32	5	423	
33	6	380	
34	7	338	
35	8	206	
36	9	137	
37	b	215	
38	c	332	
39	d	302	
40	e	279	
41	f	212	
42	g	166	
43	h	158	
44	i	128	
45	j	123	
46	k	112	
47	l	138	
48	m	128	
49	o	102	
50	p	205	
51	q	222	
52	r	196	
53	s	439	

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Mol	Chain	Length	Quality of chain
54	n	246	
55	A1	384	
56	A2	381	
57	v	70	
58	u	234	
59	t1	198	
59	t2	198	
59	t3	198	
59	t4	198	
59	t5	198	
59	t6	198	
60	w	156	
61	UNK	26	

2 Entry composition

There are 66 unique types of molecules in this entry. The entry contains 110030 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1441	Total	C	N	O	P	0	2
			30552	13711	5512	9889	1440		

- Molecule 2 is a RNA chain called MT-TRNAVAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	60	Total	C	N	O	P	0	0
			1275	572	230	413	60		

- Molecule 3 is a protein called Mitochondrial ribosome-associated GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	240	Total	C	N	O	S	0	0
			1878	1195	330	342	11		

- Molecule 4 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	238	Total	C	N	O	S	0	0
			1859	1157	376	317	9		

- Molecule 5 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	304	Total	C	N	O	S	0	0
			2396	1539	416	430	11		

- Molecule 6 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	250	Total	C	N	O	S	0	0
			2013	1294	365	348	6		

- Molecule 7 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	H	90	Total	C	N	O	0	0
			749	477	146	126		

- Molecule 8 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	205	Total	C	N	O	S	0	0
			1646	1059	293	283	11		

- Molecule 9 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	140	Total	C	N	O	S	0	0
			1061	680	192	187	2		

- Molecule 10 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 11 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 12 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 13 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	206	Total	C	N	O	S	0	0
			1676	1076	302	289	9		

- Molecule 14 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 15 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	141	Total	C	N	O	S	0	0
			1148	719	221	203	5		

- Molecule 16 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	217	Total	C	N	O	S	0	0
			1805	1159	317	320	9		

- Molecule 17 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	140	Total	C	N	O	S	0	0
			1153	732	231	186	4		

- Molecule 18 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 19 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	166	Total	C	N	O	S	0	0
			1368	875	254	232	7		

- Molecule 20 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	139	Total	C	N	O	S	0	0
			1154	734	220	197	3		

- Molecule 21 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	202	Total	C	N	O	S	0	0
			1652	1053	294	297	8		

- Molecule 22 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	101	Total	C	N	O	S	0	0
			805	520	151	131	3		

- Molecule 23 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	243	Total	C	N	O	S	0	0
			2035	1317	351	362	5		

- Molecule 24 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 25 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	120	Total	C	N	O	S	0	0
			978	626	183	166	3		

- Molecule 26 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	82	Total	C	N	O	S	0	0
			686	434	124	123	5		

- Molecule 27 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 28 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 29 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	2	45	Total	C	N	O	S	0	0
			367	227	81	58	1		

- Molecule 30 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 31 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 32 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	5	392	Total	C	N	O	S	0	0
			3199	2067	558	563	11		

- Molecule 33 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	6	324	Total	C	N	O	S	0	0
			2723	1743	488	484	8		

- Molecule 34 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	7	287	Total	C	N	O	S	0	0
			2334	1495	397	425	17		

- Molecule 35 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	8	85	Total	C	N	O	S	0	0
			719	454	129	134	2		

- Molecule 36 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	9	123	Total	C	N	O	S	0	0
			992	642	169	179	2		

- Molecule 37 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 38 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	c	286	Total	C	N	O	S	0	0
			2300	1469	396	426	9		

- Molecule 39 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	d	220	Total	C	N	O	S	0	0
			1819	1170	310	327	12		

- Molecule 40 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	e	217	Total	C	N	O	S	0	0
			1762	1124	310	323	5		

- Molecule 41 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	f	130	Total	C	N	O	S	0	0
			1044	669	172	200	3		

- Molecule 42 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	g	131	Total	C	N	O	S	0	0
			1085	701	190	192	2		

- Molecule 43 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	h	105	Total	C	N	O	S	0	0
			862	548	151	160	3		

- Molecule 44 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 45 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	j	85	Total	C	N	O	S	0	0
			684	423	133	126	2		

- Molecule 46 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	k	95	Total	C	N	O	S	0	0
			732	456	139	132	5		

- Molecule 47 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	l	44	Total	C	N	O	S	0	0
			395	251	76	67	1		

- Molecule 48 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	m	42	Total	C	N	O	S	0	0
			345	216	70	57	2		

- Molecule 49 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	o	80	Total	C	N	O	S	0	0
			670	423	131	113	3		

- Molecule 50 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	127	Total	C	N	O	S	0	0
			1058	661	201	192	4		

- Molecule 51 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	q	135	Total	C	N	O	S	0	0
			1134	705	222	202	5		

- Molecule 52 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	r	157	Total	C	N	O	S	0	0
			1283	817	245	213	8		

- Molecule 53 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	372	Total	C	N	O	S	0	0
			3052	1956	544	538	14		

- Molecule 54 is a protein called rRNA methyltransferase 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	n	215	Total	C	N	O	S	0	0
			1667	1055	303	303	6		

- Molecule 55 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A1	335	Total	C	N	O	S	0	0
			2652	1690	463	482	17		

- Molecule 56 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	A2	238	Total	C	N	O	S	0	0
			1942	1244	336	350	12		

- Molecule 57 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	v	69	Total	C	N	O		0	0
			589	372	116	101			

- Molecule 58 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	u	129	Total	C	N	O	S	0	0
			1064	685	175	194	10		

- Molecule 59 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	t1	46	Total	C	N	O		0	0
			354	228	56	70			
59	t2	30	Total	C	N	O		0	0
			238	154	38	46			
59	t3	30	Total	C	N	O		0	0
			238	154	38	46			
59	t4	29	Total	C	N	O		0	0
			229	148	36	45			
59	t6	27	Total	C	N	O		0	0
			214	137	34	43			
59	t5	29	Total	C	N	O		0	0
			229	148	36	45			

- Molecule 60 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	w	87	Total	C	N	O	S	0	0
			705	452	103	144	6		

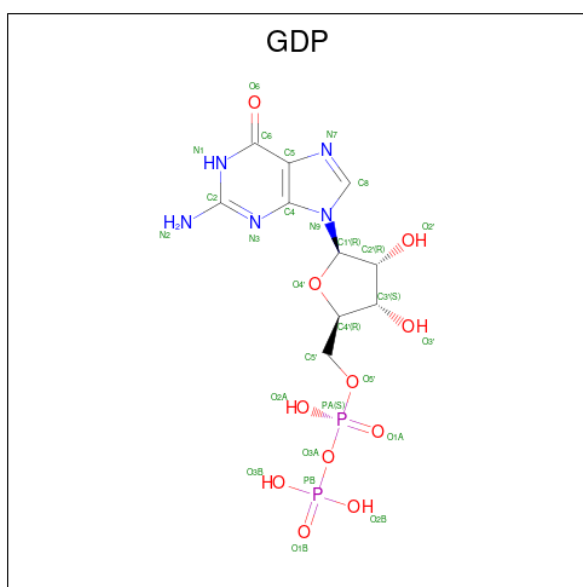
- Molecule 61 is a protein called Unknown residues.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	UNK	26	Total	C	N	O		0	0
			130	78	26	26			

- Molecule 62 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
62	A	101	Total	Mg	0
			101	101	
62	D	1	Total	Mg	0
			1	1	
62	F	1	Total	Mg	0
			1	1	
62	n	1	Total	Mg	0
			1	1	

- Molecule 63 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

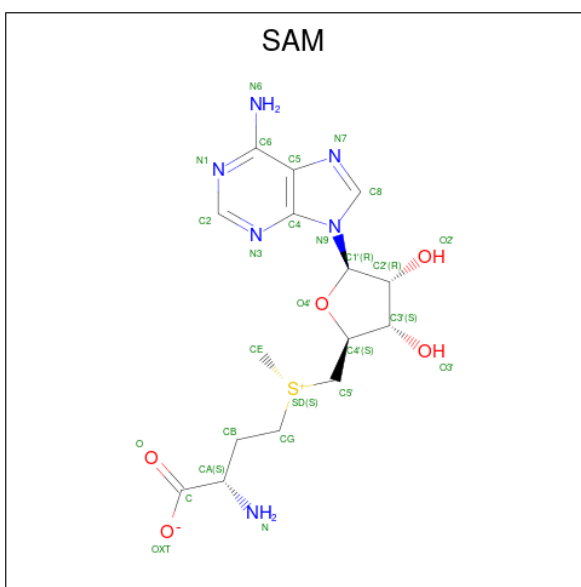


Mol	Chain	Residues	Atoms					AltConf
63	C	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 64 is ZINC ION (CCD ID: ZN) (formula: Zn).

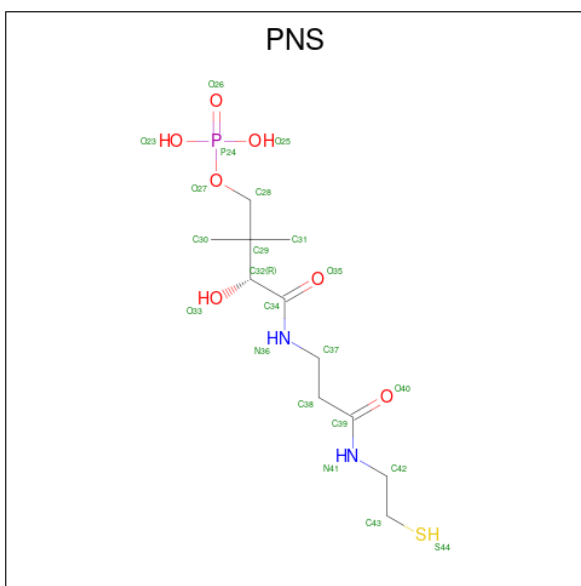
Mol	Chain	Residues	Atoms		AltConf
64	0	1	Total	Zn	0
			1	1	
64	4	1	Total	Zn	0
			1	1	

- Molecule 65 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: C₁₅H₂₂N₆O₅S).



Mol	Chain	Residues	Atoms					AltConf
65	A1	1	Total	C	N	O	S	0
			27	15	6	5	1	

- Molecule 66 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: $C_{11}H_{23}N_2O_7PS$).

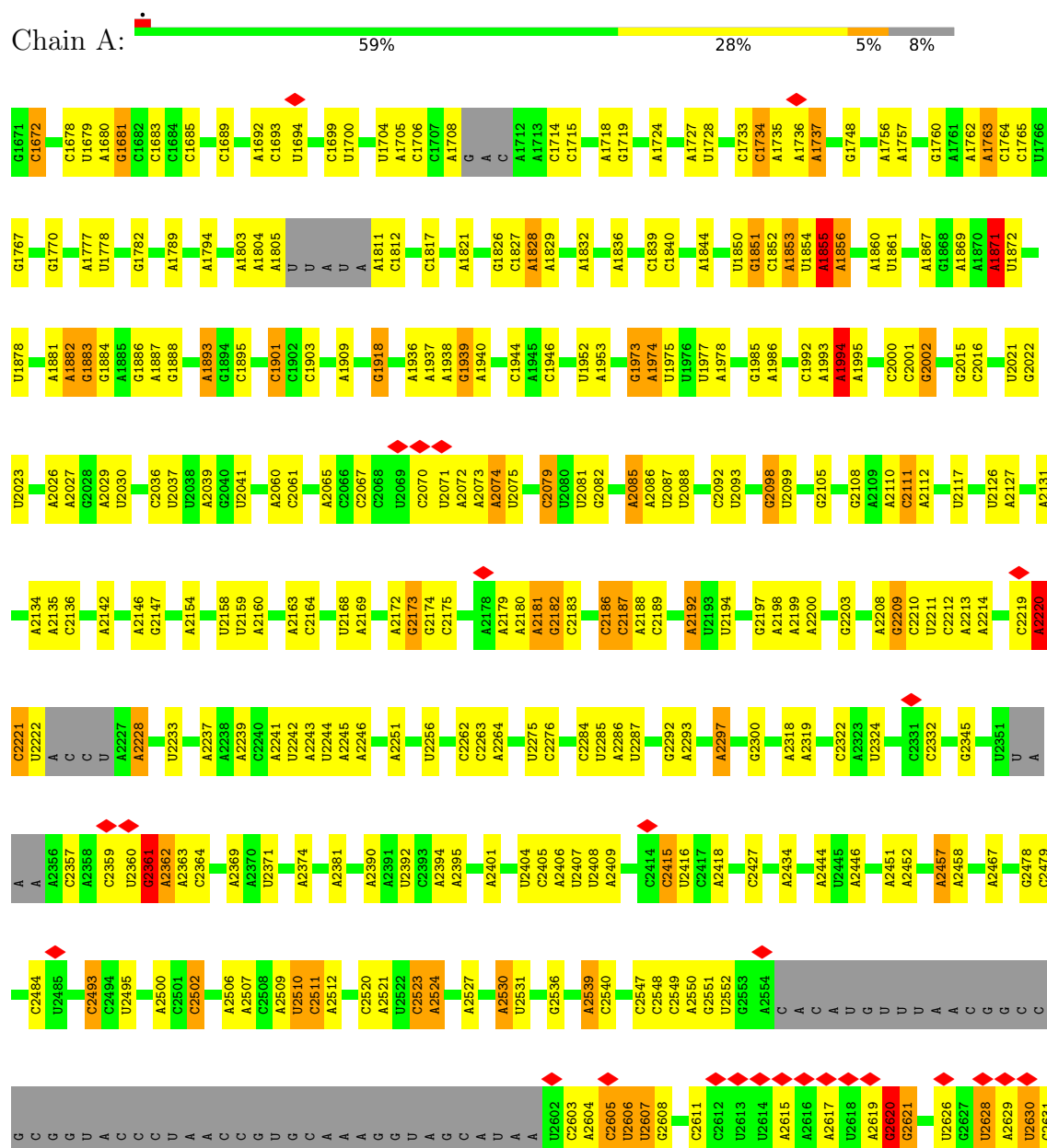


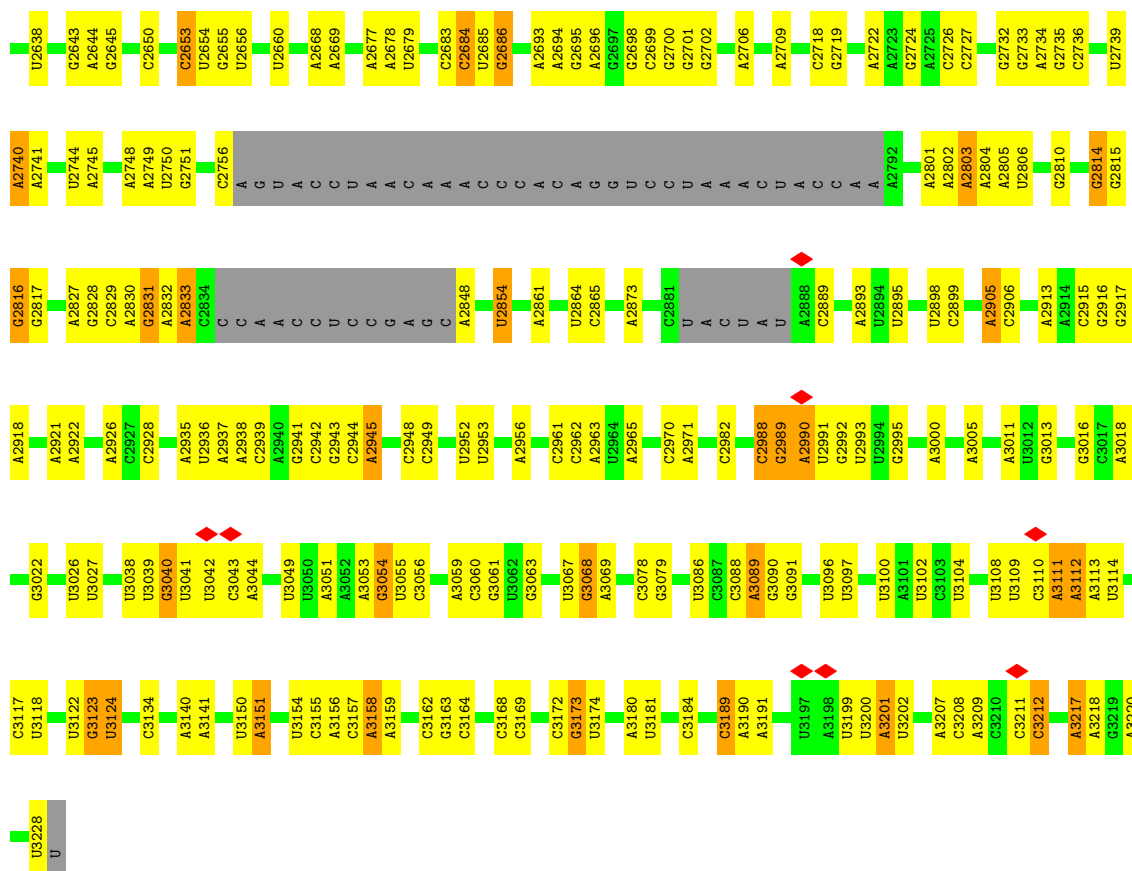
Mol	Chain	Residues	Atoms						AltConf
66	w	1	Total	C	N	O	P	S	0
			21	11	2	6	1	1	

3 Residue-property plots

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: 16S rRNA

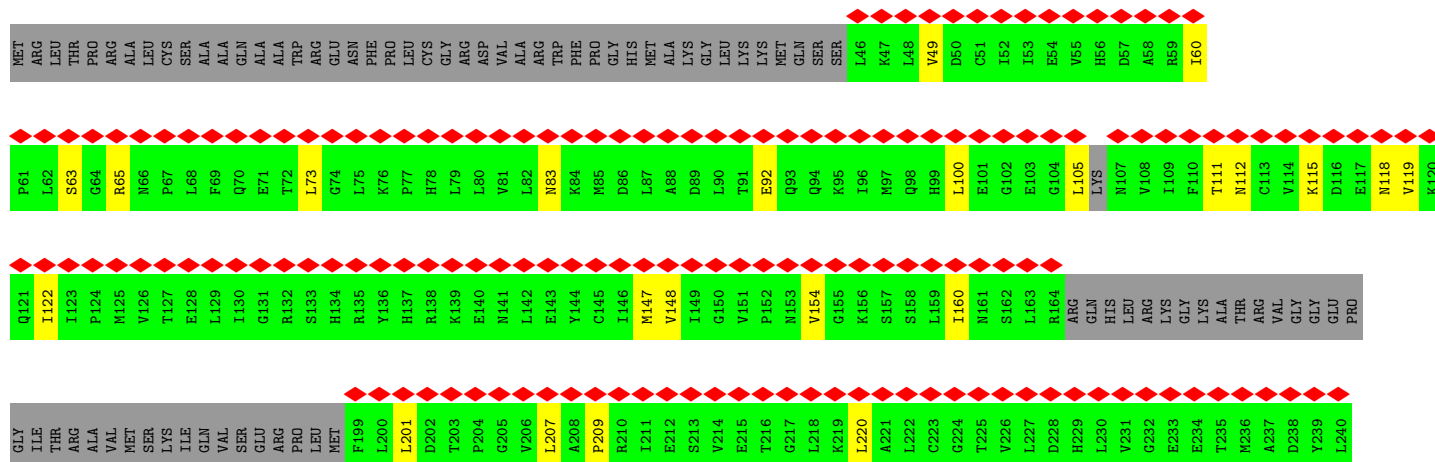




• Molecule 2: MT-TRNAVAL



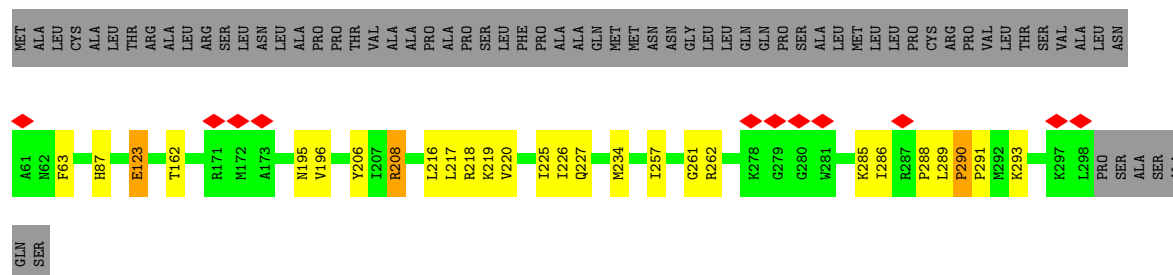
• Molecule 3: Mitochondrial ribosome-associated GTPase 1





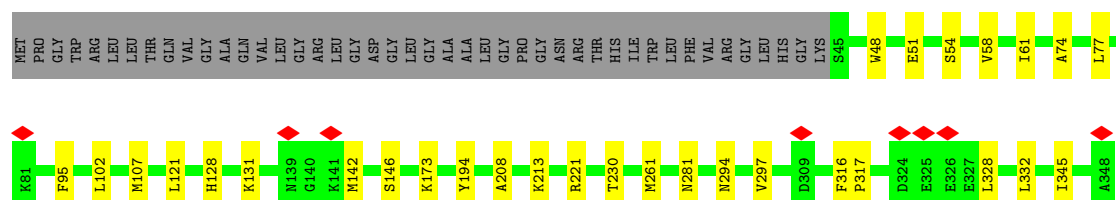
- Molecule 4: 39S ribosomal protein L2, mitochondrial

Chain D: 69% 8% 22%



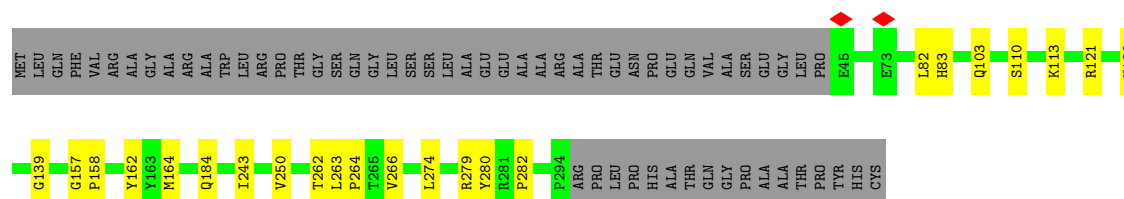
- Molecule 5: 39S ribosomal protein L3, mitochondrial

Chain E: 79% 9% 13%



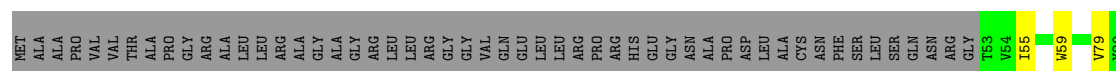
- Molecule 6: 39S ribosomal protein L4, mitochondrial

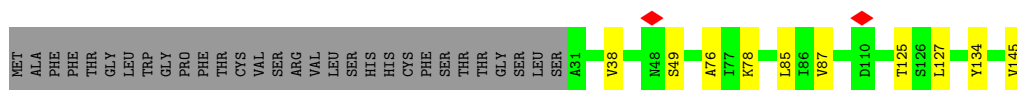
Chain F: 73% 7% 20%



- Molecule 7: 39S ribosomal protein L9, mitochondrial

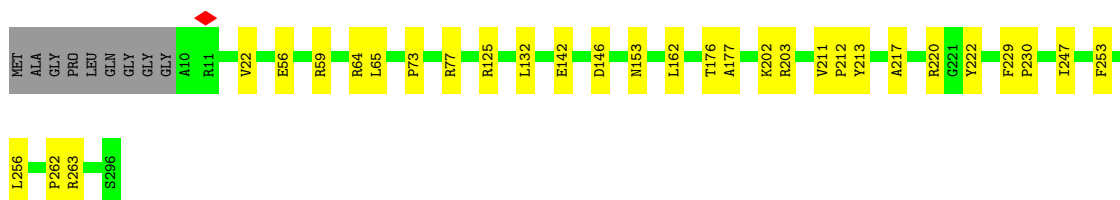
Chain H: 30% 66%





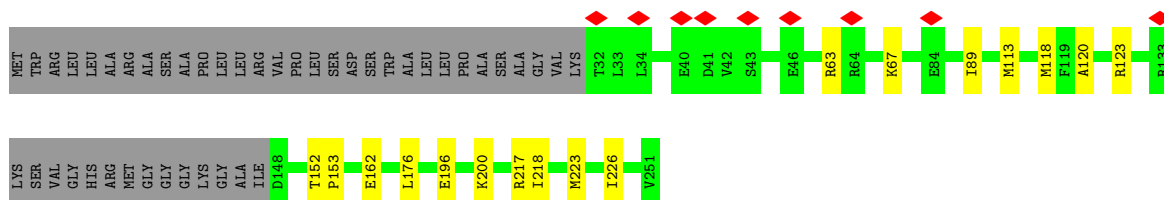
- Molecule 12: 39S ribosomal protein L15, mitochondrial

Chain M: 87% 10% .



- Molecule 13: 39S ribosomal protein L16, mitochondrial

Chain N: 75% 7% 18%



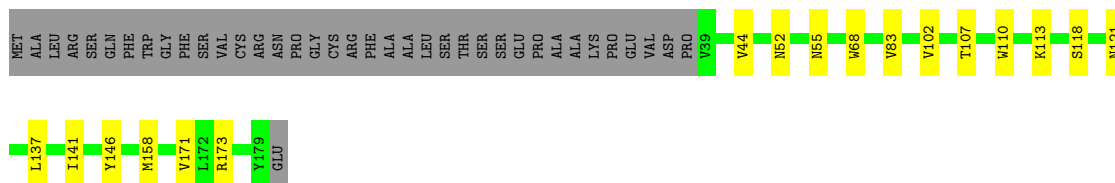
- Molecule 14: 39S ribosomal protein L17, mitochondrial

Chain O: 78% 9% 13%



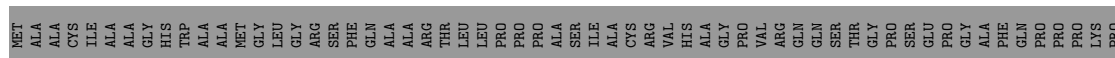
- Molecule 15: Mitochondrial ribosomal protein L18, isoform CRA_b

Chain P: 69% 9% 21%



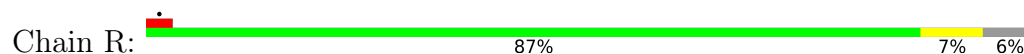
- Molecule 16: 39S ribosomal protein L19, mitochondrial

Chain Q: 68% 6% 26%

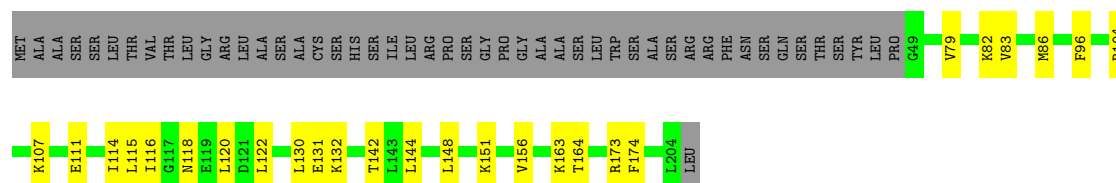




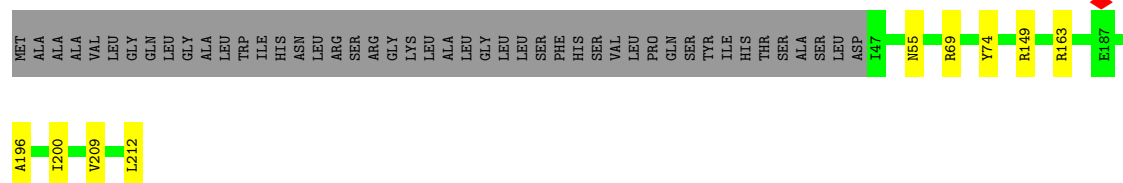
- Molecule 17: 39S ribosomal protein L20, mitochondrial



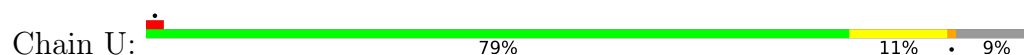
- Molecule 18: 39S ribosomal protein L21, mitochondrial



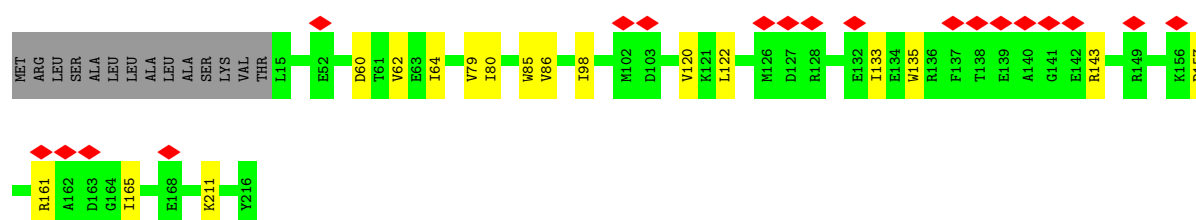
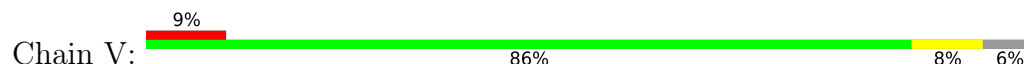
- Molecule 19: 39S ribosomal protein L22, mitochondrial



- Molecule 20: 39S ribosomal protein L23, mitochondrial

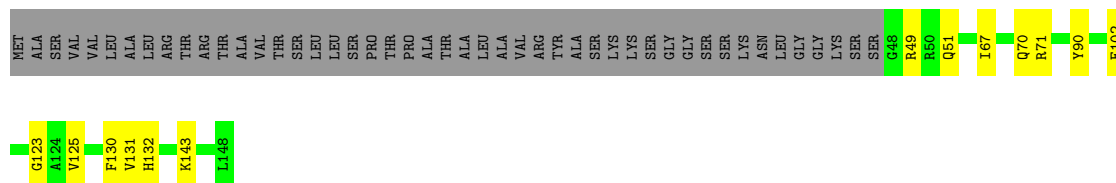


- Molecule 21: 39S ribosomal protein L24, mitochondrial



- Molecule 22: 39S ribosomal protein L27, mitochondrial

Chain W:  59% 9% 32%



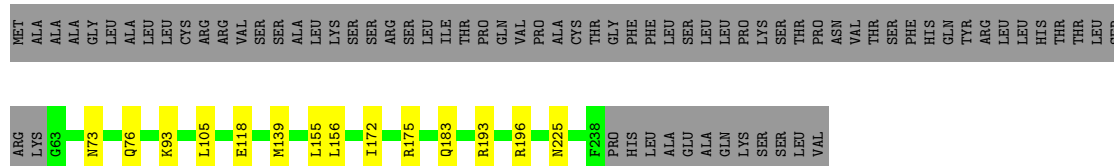
- Molecule 23: 39S ribosomal protein L28, mitochondrial

Chain X:  85% 10% 5%



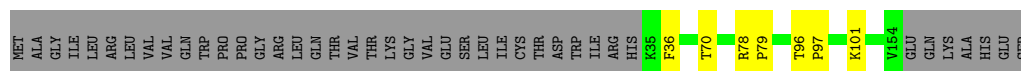
- Molecule 24: 39S ribosomal protein L47, mitochondrial

Chain Y:  65% 6% 30%



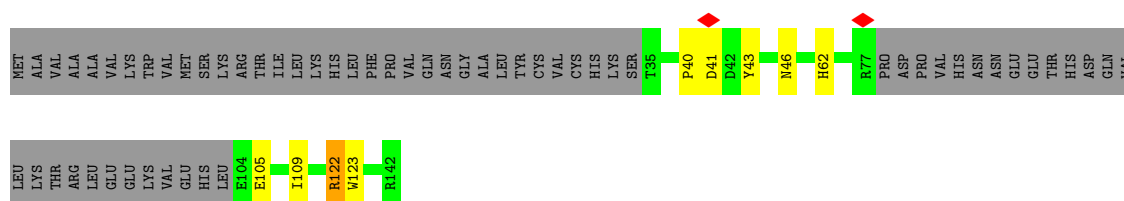
- Molecule 25: 39S ribosomal protein L30, mitochondrial

Chain Z:  70% 25%

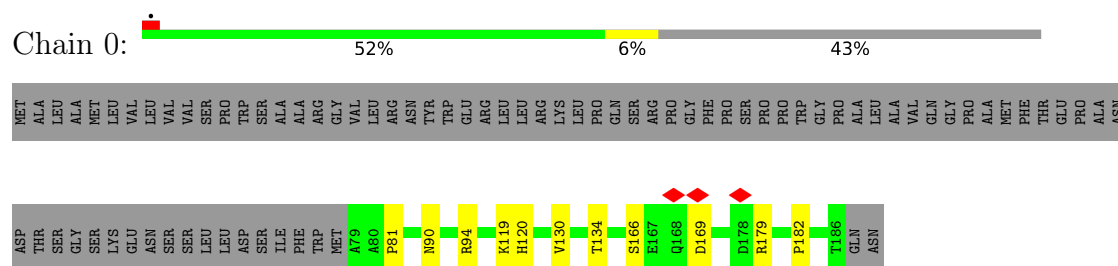


- Molecule 26: 39S ribosomal protein L42, mitochondrial

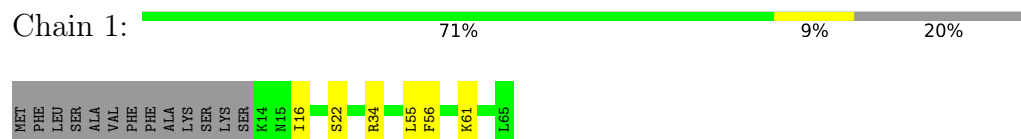
Chain a:  51% 6% 42%



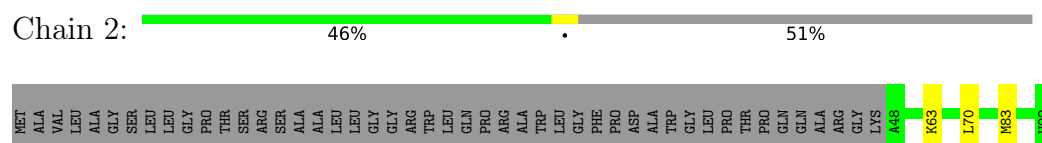
- Molecule 27: 39S ribosomal protein L32, mitochondrial



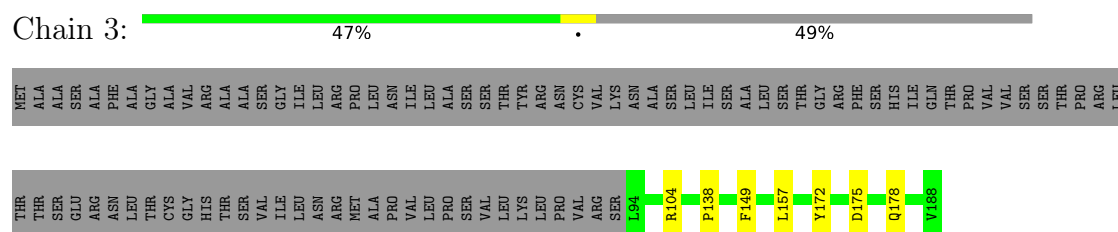
- Molecule 28: 39S ribosomal protein L33, mitochondrial



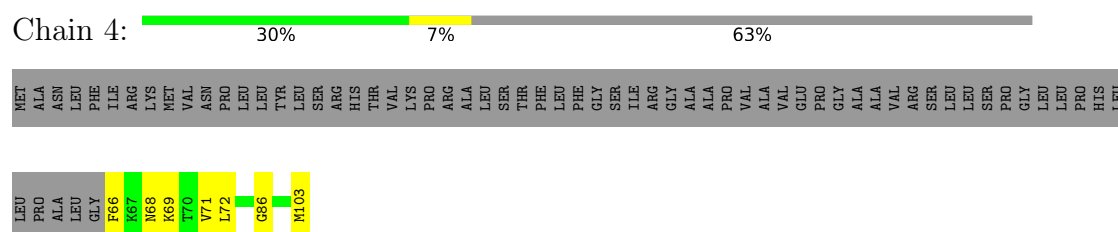
- Molecule 29: 39S ribosomal protein L34, mitochondrial



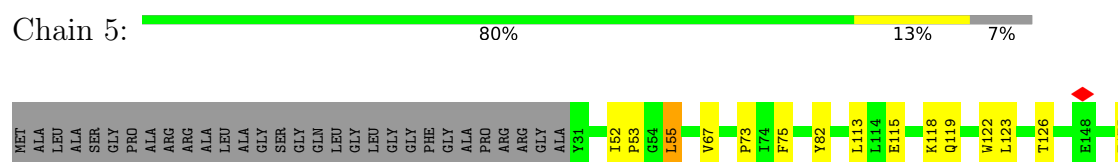
- Molecule 30: 39S ribosomal protein L35, mitochondrial

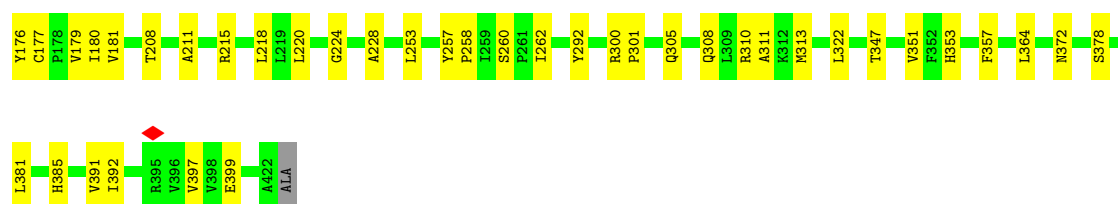


- Molecule 31: 39S ribosomal protein L36, mitochondrial

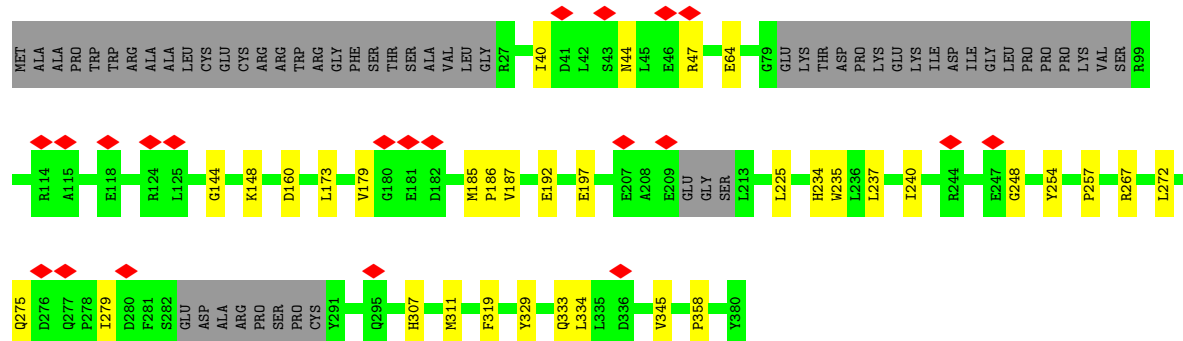
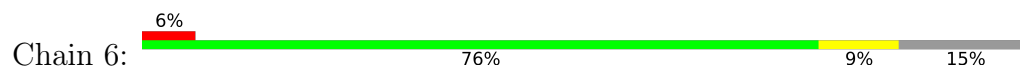


- Molecule 32: 39S ribosomal protein L37, mitochondrial

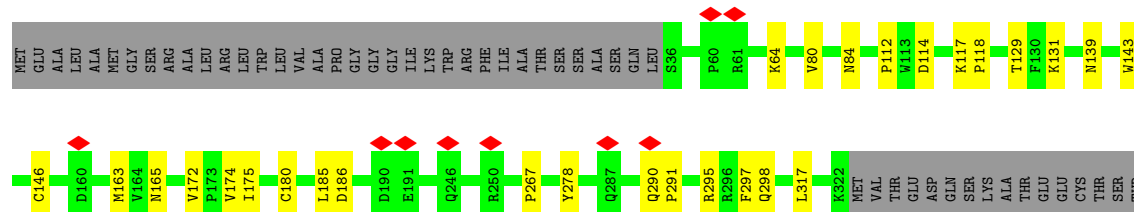
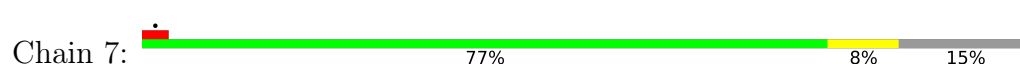




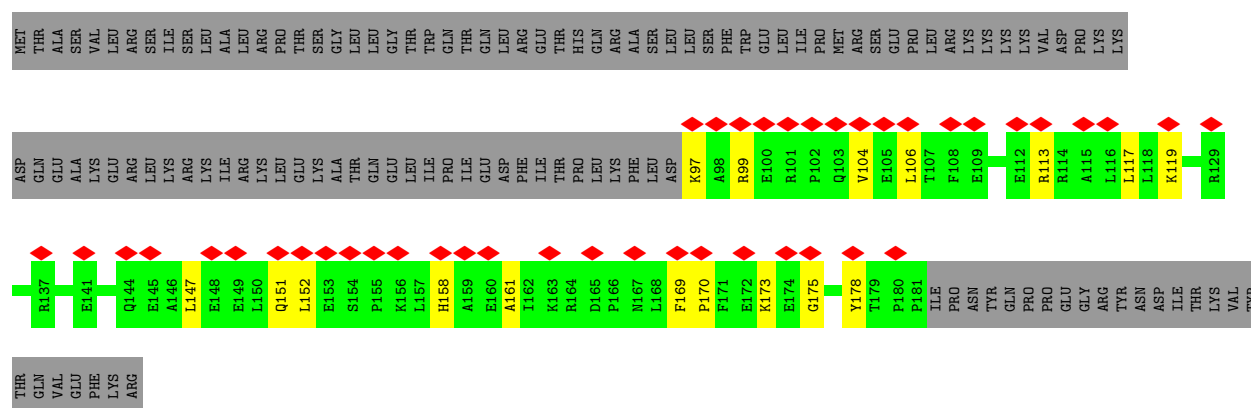
- Molecule 33: 39S ribosomal protein L38, mitochondrial



- Molecule 34: 39S ribosomal protein L39, mitochondrial

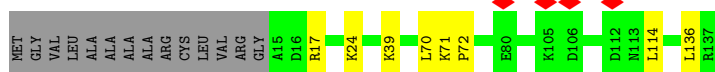


- Molecule 35: 39S ribosomal protein L40, mitochondrial



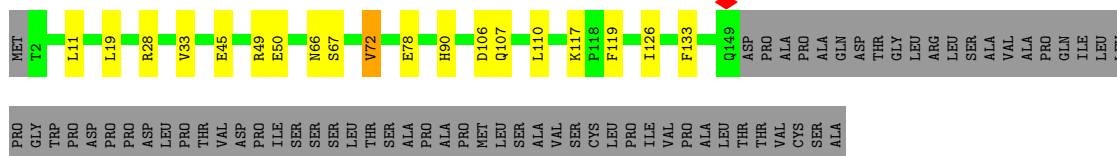
- Molecule 36: 39S ribosomal protein L41, mitochondrial

Chain 9: 



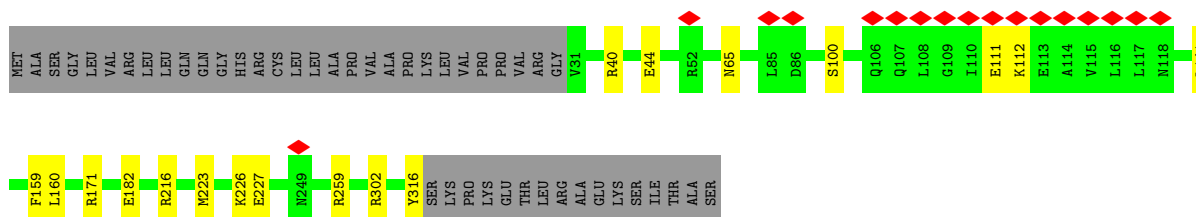
- Molecule 37: 39S ribosomal protein L43, mitochondrial

Chain b: 



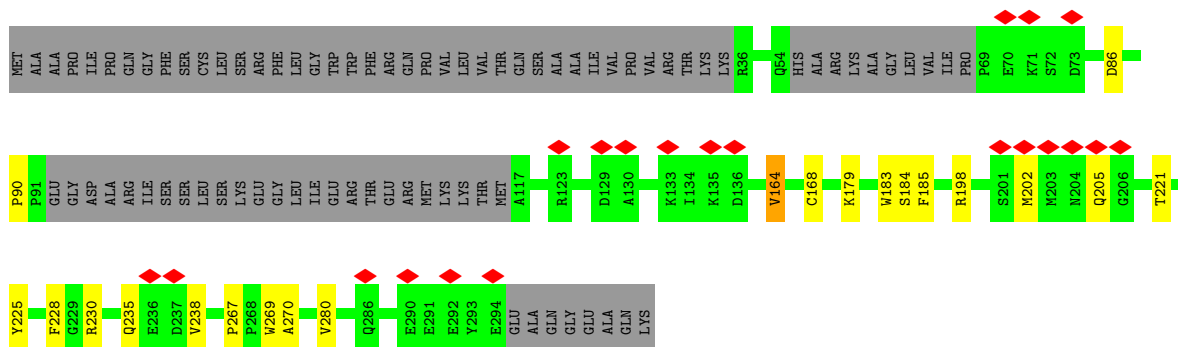
- Molecule 38: 39S ribosomal protein L44, mitochondrial

Chain c: 



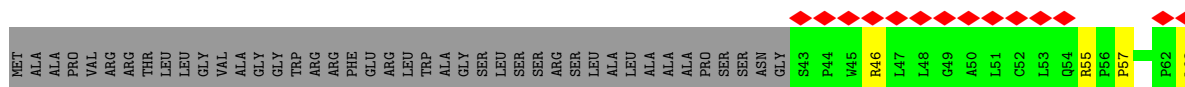
- Molecule 39: 39S ribosomal protein L45, mitochondrial

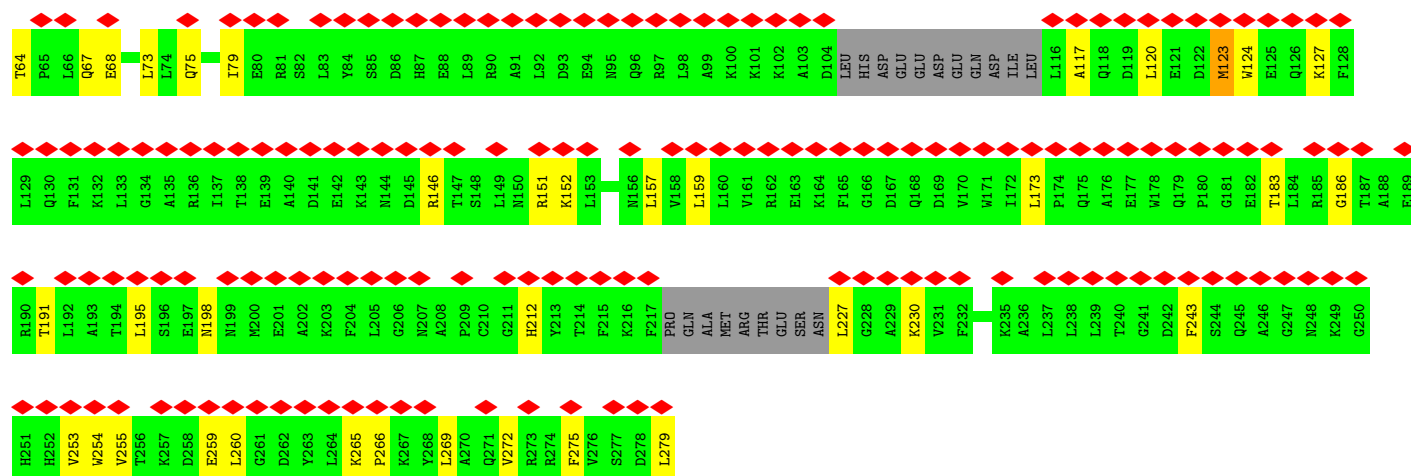
Chain d: 



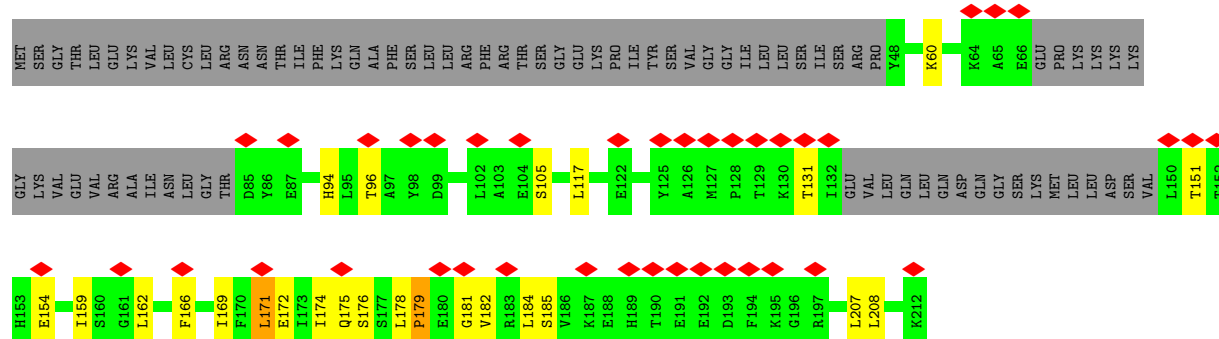
- Molecule 40: 39S ribosomal protein L46, mitochondrial

Chain e: 

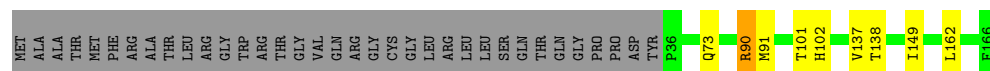




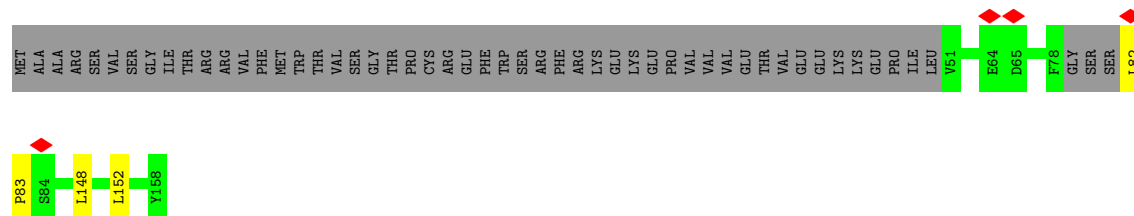
- Molecule 41: 39S ribosomal protein L48, mitochondrial



- Molecule 42: 39S ribosomal protein L49, mitochondrial

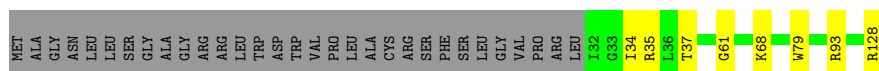


- Molecule 43: 39S ribosomal protein L50, mitochondrial



- Molecule 44: 39S ribosomal protein L51, mitochondrial

Chain i: 



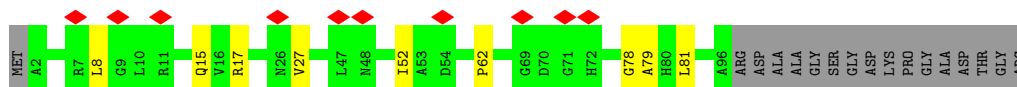
- Molecule 45: 39S ribosomal protein L52, mitochondrial

Chain j: 



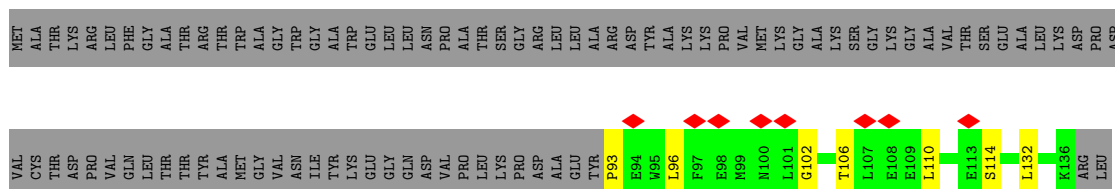
- Molecule 46: 39S ribosomal protein L53, mitochondrial

Chain k: 



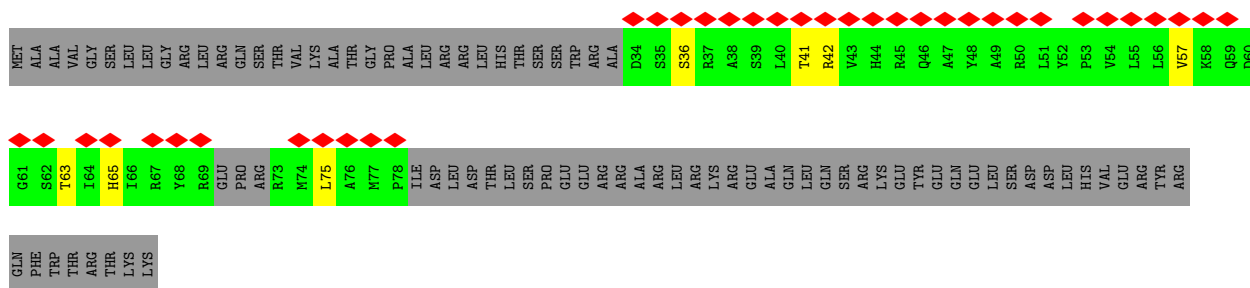
- Molecule 47: 39S ribosomal protein L54, mitochondrial

Chain l: 



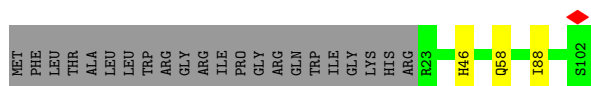
- Molecule 48: 39S ribosomal protein L55, mitochondrial

Chain m: 

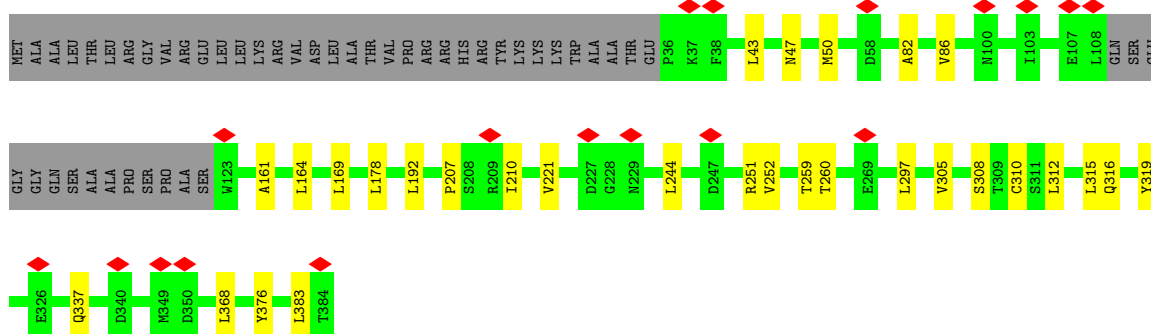
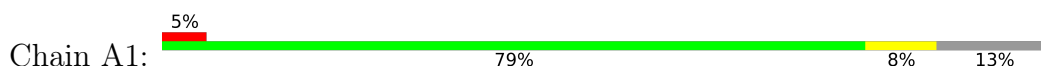


- Molecule 49: Ribosomal protein 63, mitochondrial

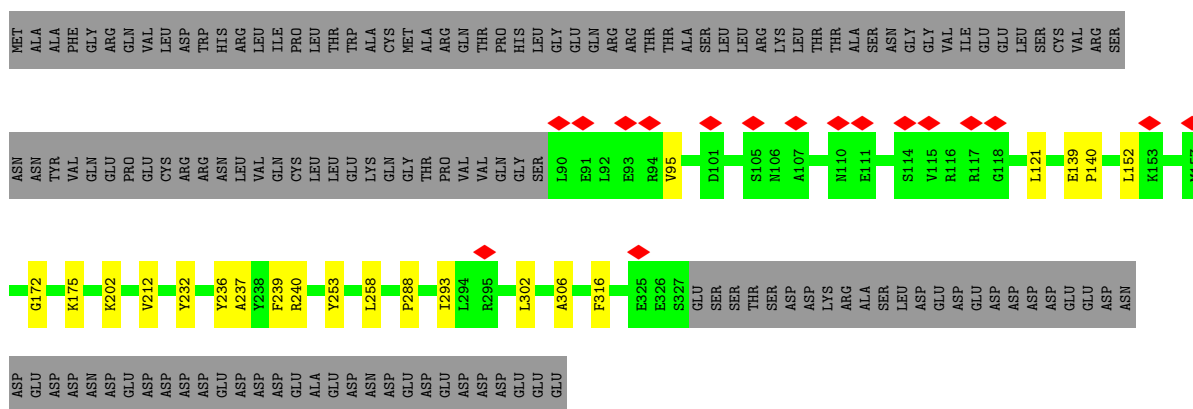
Chain o: 



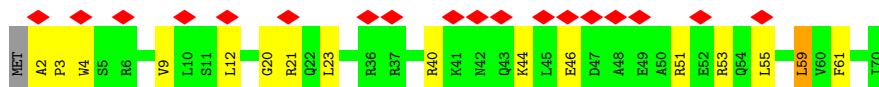
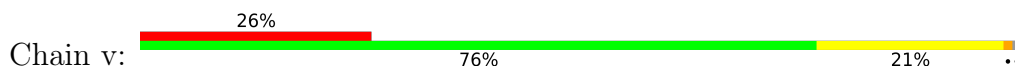
- Molecule 55: 5-methylcytosine rRNA methyltransferase NSUN4



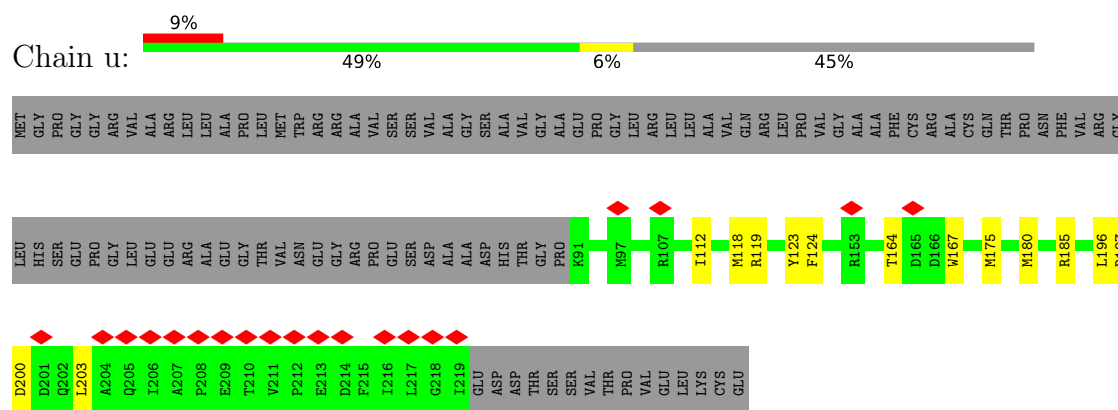
- Molecule 56: Transcription termination factor 4, mitochondrial



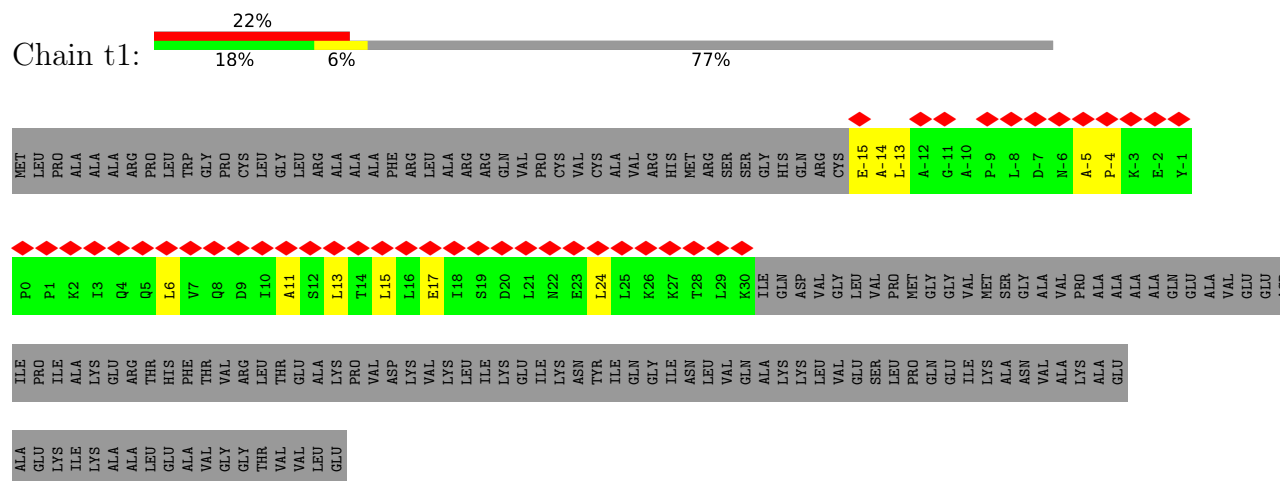
- Molecule 57: MIEF1 upstream open reading frame protein



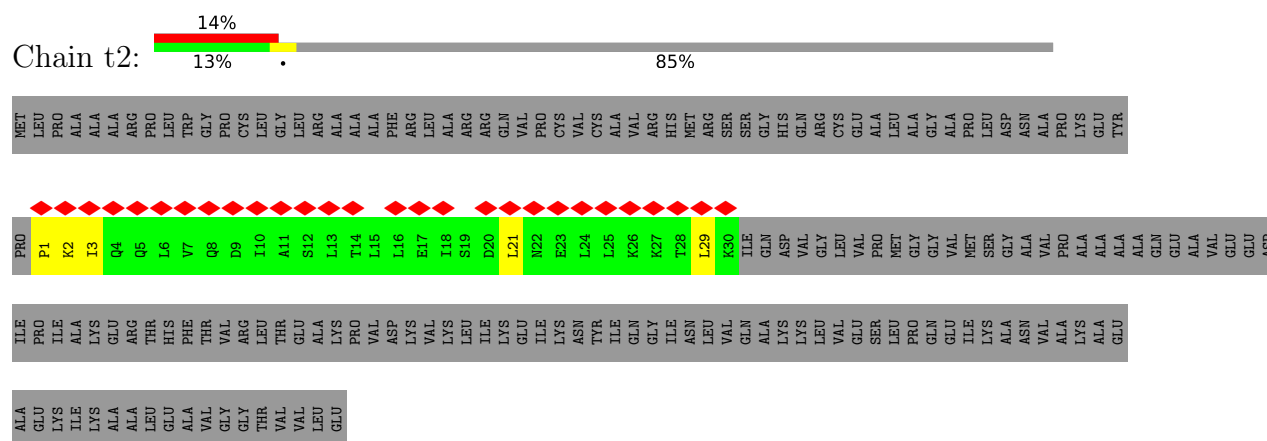
- Molecule 58: Mitochondrial assembly of ribosomal large subunit protein 1



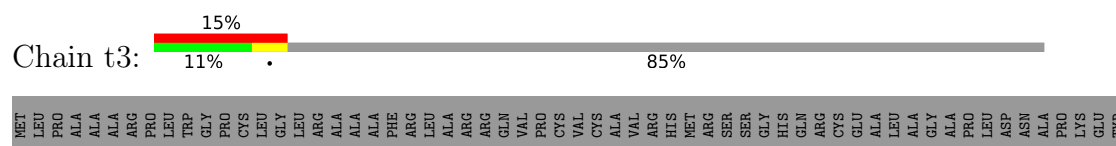
- Molecule 59: 39S ribosomal protein L12, mitochondrial

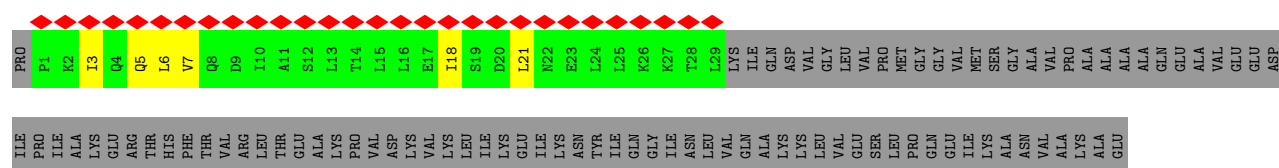


- Molecule 59: 39S ribosomal protein L12, mitochondrial



- Molecule 59: 39S ribosomal protein L12, mitochondrial





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

● Molecule 60: Acyl carrier protein, mitochondrial



MET
ALA
SER
ARG
VAL
LEU
SER
ALA
TYR
VAL
SER
ARG
LEU
PRO
ALA
ALA
PHE
ALA
PRO
LEU
PRO
VAL
ARG
VAL
ARG
MET
LEU
ALA
VAL
ALA
ARG
PRO
LEU
SER
THR
ALA
CYS
SER
GLY
THR
GLN
PRO
ALA
VAL
LEU
LEU
ALA
GLN
VAL
PRO
GLY
ARG

VAL
THR
GLN
LEU
CYS
ARG
GLN
TYR
SER
D70
M71
P72
P73
L74
T76
L76
E77
G78
I79
Q80
D81
R82
W83
L84
W85
V86
L87
K88
L89
Y90
D91
K92
I93
D94
P95
E96
K97
L98
S99
V100
M101
S102
H103
F104
M105
K106
D107
L108
G109
L110
D111
S112
L113
E117
M120
A121
M122
E123

D124
E125
F126
G127
F128
E129
I130
P131
D132
I133
D134
A135
E136
K137
L138
M139
Q142
E143
I144
V145
D146
Y147
I148
A149
D150
K151
K152
D153
V154
Y155
E156

● Molecule 61: Unknown residues



X1
X2
X3
X4
X5
X6
X7
X8
X9
X10
X11
X12
X13
X14
X15
X16
X17
X18
X19
X20
X21
X22
X23
X24
X25
X26

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48646	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.254	Depositor
Minimum map value	-0.513	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.081	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	215.22, 279.47998, 250.92	wwPDB
Map dimensions	246, 274, 211	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.02, 1.02, 1.02	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, MG, SAM, ZN, OMG, PNS

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.46	0/34198	0.71	21/53222 (0.0%)
2	B	0.50	0/1423	0.71	1/2206 (0.0%)
3	C	0.37	1/1905 (0.1%)	0.87	3/2573 (0.1%)
4	D	0.46	0/1896	0.93	1/2549 (0.0%)
5	E	0.45	0/2465	0.95	0/3344
6	F	0.45	0/2071	1.00	0/2817
7	H	0.44	0/762	1.06	0/1022
8	I	0.46	1/1682 (0.1%)	0.98	0/2280
9	J	0.49	0/1077	1.17	1/1452 (0.1%)
10	K	0.46	0/1495	1.01	0/2029
11	L	0.46	0/904	0.97	0/1218
12	M	0.45	0/2359	1.05	0/3185
13	N	0.46	0/1721	1.04	0/2322
14	O	0.44	0/1269	1.05	0/1708
15	P	0.43	0/1173	0.98	0/1588
16	Q	0.42	0/1846	0.99	0/2487
17	R	0.43	0/1174	1.12	0/1572
18	S	0.44	0/1276	0.95	0/1729
19	T	0.47	0/1402	1.00	0/1886
20	U	0.44	0/1183	0.97	0/1600
21	V	0.46	0/1697	0.98	0/2302
22	W	0.48	0/827	0.92	0/1118
23	X	0.43	0/2090	1.04	0/2825
24	Y	0.41	0/1552	1.08	0/2079
25	Z	0.46	0/1003	0.98	1/1354 (0.1%)
26	a	0.50	0/709	0.99	0/963
27	0	0.44	0/895	1.06	0/1201
28	1	0.40	0/438	0.87	0/583
29	2	0.44	0/373	1.03	0/496
30	3	0.40	0/852	0.93	0/1136
31	4	0.41	0/350	0.82	0/461
32	5	0.46	0/3294	0.98	1/4488 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	6	0.47	0/2809	1.03	0/3818
34	7	0.44	0/2391	1.06	0/3234
35	8	0.46	0/734	1.17	0/986
36	9	0.45	0/1020	1.01	0/1374
37	b	0.47	0/1202	0.98	0/1626
38	c	0.45	0/2348	1.14	0/3174
39	d	0.46	0/1872	0.99	0/2536
40	e	0.44	0/1797	1.05	1/2422 (0.0%)
41	f	0.45	0/1063	1.04	0/1430
42	g	0.46	0/1121	0.96	0/1528
43	h	0.49	0/884	1.07	0/1203
44	i	0.43	0/849	0.97	0/1135
45	j	0.45	0/698	1.16	0/940
46	k	0.46	0/743	1.08	0/1003
47	l	0.41	0/407	1.11	0/547
48	m	0.48	0/350	0.90	0/469
49	o	0.45	0/687	1.07	0/924
50	p	0.44	0/1071	1.07	0/1433
51	q	0.46	0/1165	1.16	0/1575
52	r	0.47	0/1322	1.00	0/1793
53	s	0.44	0/3130	0.99	0/4247
54	n	0.46	0/1703	1.08	0/2314
55	A1	0.45	0/2713	1.02	0/3681
56	A2	0.43	0/1973	1.16	0/2651
57	v	0.41	0/598	1.11	0/796
58	u	0.44	0/1089	1.02	0/1474
59	t1	0.14	0/358	0.25	0/486
59	t2	0.09	0/238	0.25	0/319
59	t3	0.09	0/238	0.22	0/319
59	t4	0.09	0/229	0.19	0/308
59	t5	0.10	0/229	0.33	0/308
59	t6	0.07	0/213	0.21	0/286
60	w	0.43	0/717	1.14	0/967
All	All	0.45	2/115322 (0.0%)	0.92	30/163101 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	209	PRO	C-N	7.23	1.44	1.33
8	I	196	LYS	C-N	-6.30	1.24	1.33

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	209	PRO	CA-C-N	-11.35	105.42	123.23
3	C	209	PRO	C-N-CA	-11.35	105.42	123.23
1	A	2457	A	C2'-C3'-O3'	10.04	124.55	109.50
1	A	2182	G	C2'-C3'-O3'	8.65	122.48	109.50
1	A	1994	A	C4'-C3'-O3'	8.64	122.36	109.40
1	A	1855	A	C2'-C3'-O3'	8.03	125.74	113.70
9	J	33	PRO	N-CA-C	7.57	119.93	110.70
4	D	290	PRO	N-CA-C	7.36	119.68	110.70
1	A	1973	G	C2'-C3'-O3'	7.16	124.44	113.70
1	A	2530	A	C4'-C3'-O3'	6.98	119.87	109.40
3	C	209	PRO	O-C-N	6.81	131.15	122.91
1	A	2220	A	C4'-C3'-O3'	6.71	119.47	109.40
1	A	2209	G	C2'-C3'-O3'	6.67	123.70	113.70
1	A	2905	A	C2'-C3'-O3'	6.63	123.65	113.70
1	A	2653	C	C4'-C3'-O3'	6.46	122.68	113.00
1	A	3217	A	C4'-C3'-O3'	-6.42	103.37	113.00
2	B	1607	U	C2'-C3'-O3'	6.34	123.21	113.70
1	A	1871	A	C2'-C3'-O3'	6.27	123.11	113.70
25	Z	96	THR	CB-CA-C	6.01	116.56	109.47
1	A	2628	U	C2'-C3'-O3'	6.00	118.50	109.50
1	A	2361	G	C2'-C3'-O3'	5.76	118.14	109.50
1	A	2620	G	C2'-C3'-O3'	5.68	122.22	113.70
1	A	2628	U	C4'-C3'-O3'	5.54	117.70	109.40
1	A	2361	G	C4'-C3'-O3'	5.34	117.41	109.40
40	e	64	THR	CB-CA-C	5.24	116.40	108.86
1	A	2182	G	C4'-C3'-O3'	5.24	117.25	109.40
1	A	2605	C	C4'-C3'-O3'	5.23	117.25	109.40
1	A	2510	U	C2'-C3'-O3'	-5.23	105.86	113.70
1	A	2530	A	C2'-C3'-O3'	5.06	117.09	109.50
32	5	175	THR	CB-CA-C	5.01	117.15	109.03

There are no chirality outliers.

There are no planarity outliers.

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	A	30552	0	15539	170	0
2	B	1275	0	650	8	0
3	C	1878	0	1949	19	0
4	D	1859	0	1920	19	0
5	E	2396	0	2402	17	0
6	F	2013	0	2043	16	0
7	H	749	0	798	6	0
8	I	1646	0	1731	21	0
9	J	1061	0	1141	5	0
10	K	1451	0	1448	12	0
11	L	889	0	941	6	0
12	M	2305	0	2378	18	0
13	N	1676	0	1694	12	0
14	O	1245	0	1283	10	0
15	P	1148	0	1148	11	0
16	Q	1805	0	1841	11	0
17	R	1153	0	1214	8	0
18	S	1251	0	1322	17	0
19	T	1368	0	1410	7	0
20	U	1154	0	1154	14	0
21	V	1652	0	1658	11	0
22	W	805	0	829	10	0
23	X	2035	0	2054	16	0
24	Y	1517	0	1561	10	0
25	Z	978	0	1030	4	0
26	a	686	0	658	6	0
27	0	880	0	902	7	0
28	1	433	0	475	5	0
29	2	367	0	393	3	0
30	3	831	0	883	5	0
31	4	342	0	361	7	0
32	5	3199	0	3196	34	0
33	6	2723	0	2615	22	0
34	7	2334	0	2343	13	0
35	8	719	0	723	9	0
36	9	992	0	984	6	0
37	b	1178	0	1180	15	0
38	c	2300	0	2313	12	0
39	d	1819	0	1793	12	0
40	e	1762	0	1767	25	0
41	f	1044	0	1046	16	0
42	g	1085	0	1077	5	0
43	h	862	0	845	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	i	827	0	857	6	0
45	j	684	0	673	2	0
46	k	732	0	745	5	0
47	l	395	0	391	2	0
48	m	345	0	360	4	0
49	o	670	0	665	3	0
50	p	1058	0	1083	8	0
51	q	1134	0	1110	8	0
52	r	1283	0	1310	14	0
53	s	3052	0	3037	25	0
54	n	1667	0	1673	14	0
55	A1	2652	0	2632	15	0
56	A2	1942	0	2035	11	0
57	v	589	0	604	8	0
58	u	1064	0	1060	8	0
59	t1	354	0	380	12	0
59	t2	238	0	270	4	0
59	t3	238	0	270	8	0
59	t4	229	0	257	8	0
59	t5	229	0	257	4	0
59	t6	214	0	236	8	0
60	w	705	0	691	3	0
61	UNK	130	0	28	0	0
62	A	101	0	0	0	0
62	D	1	0	0	0	0
62	F	1	0	0	0	0
62	n	1	0	0	0	0
63	C	28	0	12	0	0
64	0	1	0	0	0	0
64	4	1	0	0	0	0
65	A1	27	0	22	0	0
66	w	21	0	21	2	0
All	All	110030	0	95371	704	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 3.

All (704) 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)
8:I:139:LYS:HG3	59:t1:-15:GLU:O	1.46	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5:126:THR:HG22	32:5:372:ASN:HB2	1.46	0.95
20:U:24:PHE:HB2	20:U:45:PRO:HG3	1.60	0.84
32:5:313:MET:HE1	32:5:353:HIS:HB2	1.60	0.82
52:r:99:MET:HE3	52:r:116:GLU:HA	1.62	0.80
24:Y:93:LYS:HD2	36:9:70:LEU:HD21	1.65	0.79
27:0:179:ARG:HH12	27:0:182:PRO:HG3	1.48	0.79
8:I:221:LEU:HA	8:I:224:HIS:HD2	1.52	0.75
6:F:262:THR:HG22	6:F:264:PRO:HD2	1.68	0.74
33:6:237:LEU:HB3	33:6:240:ILE:HD11	1.69	0.74
53:s:212:ARG:HD3	53:s:379:LEU:HD12	1.70	0.74
32:5:310:ARG:HA	32:5:313:MET:HE3	1.70	0.73
41:f:96:THR:HB	41:f:154:GLU:OE1	1.89	0.73
4:D:285:LYS:HD2	4:D:293:LYS:HE3	1.71	0.72
46:k:15:GLN:HE21	46:k:52:ILE:HD12	1.57	0.70
34:7:114:ASP:HB2	34:7:117:LYS:HB2	1.73	0.69
32:5:181:VAL:HG21	32:5:347:THR:HG21	1.75	0.69
1:A:1826:G:H4'	1:A:1828:A:C2	2.29	0.68
37:b:49:ARG:HG3	37:b:50:GLU:HG2	1.76	0.67
27:0:90:ASN:O	27:0:94:ARG:HG2	1.93	0.67
4:D:217:LEU:HD13	4:D:227:GLN:HB2	1.76	0.67
1:A:1826:G:H4'	1:A:1828:A:H2	1.60	0.67
18:S:164:THR:HG22	37:b:107:GLN:HG2	1.76	0.67
41:f:159:ILE:HG22	41:f:162:LEU:HD11	1.77	0.67
1:A:2607:U:H2'	1:A:2608:G:H8	1.61	0.66
55:A1:207:PRO:HA	55:A1:210:ILE:HG22	1.77	0.66
16:Q:96:ARG:HA	16:Q:99:MET:HE3	1.77	0.66
3:C:65:ARG:HH12	3:C:105:LEU:HD13	1.61	0.66
32:5:122:TRP:HA	32:5:253:LEU:HD23	1.77	0.65
37:b:72:VAL:HG23	37:b:90:HIS:HB2	1.79	0.65
5:E:95:PHE:HD2	5:E:142:MET:HE1	1.62	0.65
53:s:214:GLU:HB3	53:s:226:ILE:HD11	1.78	0.65
1:A:2086:A:H2'	1:A:2087:U:C6	2.32	0.65
1:A:1994:A:H61	1:A:2736:C:H4'	1.61	0.65
1:A:2187:C:H2'	1:A:2188:A:C8	2.31	0.64
3:C:60:ILE:HB	3:C:63:SER:HB2	1.79	0.64
18:S:131:GLU:HG2	18:S:151:LYS:HE3	1.78	0.64
39:d:267:PRO:HG2	39:d:270:ALA:HB2	1.79	0.63
52:r:70:CYS:HB2	52:r:73:CYS:H	1.62	0.63
1:A:1706:C:OP1	24:Y:193:ARG:NH2	2.32	0.63
6:F:184:GLN:HE22	12:M:22:VAL:H	1.47	0.62
1:A:2186:C:H2'	1:A:2187:C:C6	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:86:THR:HG23	7:H:89:ARG:HE	1.64	0.62
41:f:94:HIS:HB2	41:f:185:SER:HB3	1.80	0.62
39:d:90:PRO:HB2	39:d:269:TRP:HE1	1.62	0.62
18:S:111:GLU:HG2	37:b:19:LEU:HD11	1.82	0.62
53:s:405:ILE:HG12	53:s:410:VAL:HG12	1.82	0.61
22:W:67:ILE:HG21	22:W:131:VAL:HG11	1.82	0.61
30:3:149:PHE:HB2	33:6:358:PRO:O	1.99	0.61
51:q:40:PRO:HG3	51:q:51:GLN:HB3	1.81	0.61
4:D:217:LEU:CD1	4:D:227:GLN:HB2	2.31	0.61
1:A:3123:G:HO2'	1:A:3124:U:H6	1.47	0.61
34:7:143:TRP:HE1	34:7:172:VAL:HG13	1.66	0.61
12:M:142:GLU:HB2	12:M:162:LEU:HD23	1.83	0.61
12:M:222:TYR:HE2	12:M:262:PRO:HB3	1.65	0.60
1:A:1977:U:H2'	1:A:1978:A:H8	1.66	0.60
34:7:112:PRO:HB2	34:7:267:PRO:HG2	1.83	0.60
40:e:63:LEU:HD13	40:e:68:GLU:HB3	1.83	0.60
4:D:290:PRO:HA	4:D:293:LYS:HE2	1.83	0.60
41:f:171:LEU:HA	41:f:174:ILE:HG12	1.83	0.60
52:r:117:GLU:HG2	52:r:180:LEU:HD12	1.83	0.60
1:A:2292:G:C8	17:R:11:ARG:HB3	2.35	0.60
1:A:2816:G:H2'	1:A:2817:G:H8	1.65	0.60
1:A:3013:G:HO2'	31:4:66:PHE:N	1.98	0.60
1:A:1871:A:N3	30:3:104:ARG:NH2	2.50	0.60
4:D:286:ILE:O	4:D:290:PRO:HD3	2.02	0.60
1:A:1855:A:H5''	1:A:2695:G:H22	1.66	0.60
16:Q:278:ILE:O	16:Q:282:ILE:HG12	2.02	0.60
1:A:1839:C:H2'	1:A:1840:C:C6	2.37	0.59
32:5:115:GLU:HB2	32:5:119:GLN:HB2	1.84	0.59
59:t3:21:LEU:HD23	59:t4:3:ILE:HG23	1.83	0.59
37:b:133:PHE:HB3	38:c:259:ARG:HD3	1.85	0.59
15:P:102:VAL:HG11	15:P:141:ILE:HD11	1.83	0.59
40:e:157:LEU:HD23	40:e:254:TRP:HB3	1.83	0.59
1:A:2523:C:H4'	1:A:2524:A:OP1	2.03	0.59
5:E:107:MET:HG2	5:E:121:LEU:HD11	1.85	0.59
53:s:239:ASN:HB2	53:s:299:PHE:HB2	1.85	0.59
13:N:196:GLU:HG3	13:N:200:LYS:HE2	1.85	0.59
33:6:187:VAL:HG13	33:6:319:PHE:HB3	1.84	0.59
40:e:183:THR:HG23	40:e:186:GLY:H	1.68	0.59
57:v:2:ALA:N	57:v:51:ARG:HD2	2.18	0.59
1:A:2016:C:OP2	12:M:59:ARG:NH1	2.36	0.58
1:A:2067:C:H5''	41:f:60:LYS:HG2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:t3:20:ASP:HB2	59:t4:3:ILE:HD13	1.85	0.58
1:A:2953:U:H5''	31:4:71:VAL:HG22	1.84	0.58
4:D:286:ILE:HG23	4:D:288:PRO:HD2	1.85	0.58
32:5:215:ARG:O	32:5:218:LEU:HB2	2.02	0.58
9:J:145:ILE:HD11	9:J:155:VAL:HG21	1.86	0.58
59:t6:17:GLU:HG2	59:t5:3:ILE:HD11	1.85	0.58
40:e:152:LYS:HB2	40:e:157:LEU:HD11	1.85	0.57
52:r:35:PHE:N	52:r:56:THR:HG1	2.01	0.57
13:N:218:ILE:HG23	13:N:223:MET:HB2	1.85	0.57
1:A:1778:U:C5	6:F:121:ARG:HD2	2.39	0.57
1:A:2275:U:H1'	17:R:12:ASN:OD1	2.05	0.57
1:A:2816:G:H2'	1:A:2817:G:C8	2.39	0.57
32:5:392:ILE:HG12	32:5:397:VAL:HG22	1.86	0.57
40:e:124:TRP:HA	40:e:127:LYS:HE2	1.86	0.57
1:A:2467:A:O2'	1:A:3154:U:H4'	2.05	0.57
21:V:135:TRP:HB3	21:V:143:ARG:HH21	1.69	0.57
3:C:49:VAL:HG11	3:C:147:MET:HG2	1.86	0.57
12:M:64:ARG:HA	44:i:128:ARG:HD3	1.87	0.56
1:A:2192:A:H4'	9:J:139:SER:HB3	1.86	0.56
33:6:307:HIS:O	33:6:311:MET:HB3	2.06	0.56
56:A2:202:LYS:HG3	56:A2:212:VAL:HG21	1.88	0.56
58:u:200:ASP:HB3	58:u:203:LEU:HD23	1.86	0.56
37:b:66:ASN:HD21	38:c:65:ASN:HD21	1.53	0.56
44:i:68:LYS:HE2	51:q:31:PRO:HB2	1.87	0.56
53:s:152:GLN:HA	53:s:156:TYR:HB2	1.87	0.56
5:E:208:ALA:HB2	5:E:297:VAL:HG12	1.87	0.56
20:U:110:LEU:HD12	24:Y:118:GLU:HG2	1.86	0.56
23:X:202:GLU:HB3	23:X:214:LYS:HZ1	1.71	0.56
53:s:92:MET:HE1	53:s:276:ARG:HH11	1.71	0.56
1:A:3189:C:H5''	31:4:86:GLY:H	1.70	0.56
18:S:107:LYS:HD3	19:T:212:LEU:HD22	1.87	0.55
22:W:51:GLN:HE22	22:W:71:ARG:HB2	1.70	0.55
1:A:1672:C:O2'	19:T:149:ARG:O	2.25	0.55
33:6:240:ILE:HD13	33:6:248:GLY:HA3	1.88	0.55
53:s:271:LEU:O	53:s:273:LEU:N	2.40	0.55
6:F:113:LYS:HG3	6:F:157:GLY:H	1.70	0.55
59:t1:6:LEU:HD11	59:t2:21:LEU:HD11	1.88	0.55
25:Z:36:PHE:HE2	25:Z:79:PRO:HG3	1.71	0.55
40:e:266:PRO:HG2	40:e:269:LEU:HB2	1.87	0.55
53:s:174:LEU:HB3	53:s:175:PRO:HD3	1.89	0.55
1:A:2187:C:H2'	1:A:2188:A:H8	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2523:C:C2'	1:A:2523:C:O2	2.54	0.55
2:B:1628:C:H2'	2:B:1629:A:H8	1.72	0.55
1:A:1939:G:H1'	1:A:1974:A:OP1	2.06	0.54
58:u:112:ILE:HG13	58:u:124:PHE:HB3	1.88	0.54
53:s:228:ASP:OD1	53:s:230:ARG:NH1	2.41	0.54
12:M:202:LYS:HD2	12:M:263:ARG:HD3	1.88	0.54
21:V:60:ASP:HB2	21:V:157:PRO:HG3	1.88	0.54
8:I:97:ALA:HB3	8:I:154:LEU:HB2	1.89	0.54
23:X:202:GLU:HB3	23:X:214:LYS:NZ	2.22	0.54
40:e:198:ASN:HB3	40:e:243:PHE:HD1	1.72	0.54
40:e:265:LYS:N	40:e:266:PRO:HD2	2.23	0.54
1:A:2606:U:O2'	1:A:2607:U:O2	2.26	0.54
37:b:66:ASN:HD21	38:c:65:ASN:ND2	2.06	0.54
18:S:163:LYS:HB2	37:b:106:ASP:HB3	1.88	0.54
3:C:148:VAL:HG21	3:C:160:ILE:HD11	1.90	0.54
8:I:214:LEU:HD12	59:t:15:LEU:HD22	1.90	0.54
23:X:118:ILE:HD11	23:X:191:TYR:CD2	2.43	0.53
5:E:128:HIS:HB2	5:E:173:LYS:HE3	1.91	0.53
12:M:177:ALA:HA	12:M:222:TYR:CD1	2.43	0.53
3:C:278:LYS:HE2	3:C:278:LYS:HA	1.90	0.53
12:M:162:LEU:HD11	50:p:144:PHE:HB3	1.91	0.53
22:W:49:ARG:HD3	22:W:49:ARG:H	1.73	0.53
4:D:226:ILE:HD11	4:D:234:MET:HE2	1.91	0.53
18:S:83:VAL:HA	18:S:86:MET:HE3	1.90	0.53
18:S:132:LYS:HA	18:S:148:LEU:HD22	1.91	0.53
17:R:10:LEU:HB3	17:R:13:ARG:HD2	1.91	0.53
41:f:178:LEU:HD11	41:f:182:VAL:HB	1.89	0.53
40:e:120:LEU:HA	40:e:123:MET:SD	2.48	0.53
1:A:2511:C:H3'	1:A:2512:A:H8	1.73	0.53
53:s:92:MET:HE1	53:s:276:ARG:HD3	1.89	0.53
57:v:20:GLY:HA2	57:v:23:LEU:HD23	1.90	0.53
16:Q:182:ARG:HG3	16:Q:187:LEU:HD11	1.91	0.53
21:V:161:ARG:HD2	21:V:165:ILE:HG12	1.91	0.53
35:8:147:LEU:O	35:8:151:GLN:HG2	2.08	0.53
46:k:27:VAL:HG12	46:k:62:PRO:HG3	1.91	0.53
53:s:90:LYS:HD2	53:s:232:GLN:HB2	1.91	0.53
1:A:3134:C:O4'	1:A:3134:C:O2	2.26	0.52
1:A:2685:U:O2'	1:A:3104:U:H5'	2.09	0.52
13:N:113:MET:HG3	13:N:118:MET:HG3	1.92	0.52
1:A:3067:U:H2'	1:A:3068:G:H5''	1.91	0.52
53:s:118:LEU:HD11	53:s:420:GLN:HE21	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2220:A:H4'	1:A:2221:C:OP1	2.09	0.52
20:U:8:PRO:HA	24:Y:183:GLN:HE22	1.75	0.52
19:T:212:LEU:HA	37:b:119:PHE:CE2	2.44	0.52
1:A:1782:G:O6	6:F:121:ARG:HD3	2.09	0.52
1:A:2275:U:H2'	1:A:2276:C:C6	2.45	0.52
1:A:3212:C:O2	1:A:3212:C:O4'	2.28	0.52
8:I:139:LYS:CG	59:t1:-15:GLU:O	2.38	0.52
1:A:1886:G:H1	44:i:61:GLY:HA3	1.74	0.52
1:A:2361:G:H4'	1:A:2362:A:OP1	2.10	0.52
59:t1:11:ALA:HA	59:t4:15:LEU:HD12	1.92	0.52
1:A:1737:A:H61	1:A:1760:G:H1'	1.74	0.52
3:C:112:ASN:HB3	3:C:115:LYS:HB3	1.91	0.52
15:P:118:SER:OG	15:P:121:ASN:ND2	2.43	0.52
21:V:79:VAL:HG22	21:V:86:VAL:HG12	1.92	0.52
1:A:2523:C:O2	1:A:2523:C:H2'	2.10	0.52
3:C:119:VAL:HA	3:C:122:ILE:HD12	1.92	0.52
4:D:293:LYS:HD2	56:A2:239:PHE:CD1	2.44	0.51
13:N:123:ARG:NH1	13:N:162:GLU:OE2	2.43	0.51
23:X:125:VAL:HG11	23:X:157:PHE:HE2	1.76	0.51
32:5:126:THR:HG21	32:5:357:PHE:HE1	1.75	0.51
59:t4:19:SER:HA	59:t4:22:ASN:HD21	1.74	0.51
1:A:2079:C:O4'	1:A:2079:C:O2	2.28	0.51
1:A:3054:G:H2'	1:A:3055:U:C6	2.46	0.51
1:A:3123:G:O2'	1:A:3124:U:H6	1.93	0.51
8:I:214:LEU:HD11	59:t2:29:LEU:HD22	1.92	0.51
20:U:88:LYS:NZ	20:U:91:ASP:OD1	2.42	0.51
3:C:100:LEU:HD12	3:C:105:LEU:HD22	1.92	0.51
53:s:92:MET:HE3	53:s:276:ARG:HB2	1.91	0.51
4:D:257:ILE:HG23	4:D:262:ARG:HB2	1.91	0.51
54:n:150:VAL:HG23	54:n:190:THR:HB	1.91	0.51
32:5:391:VAL:HB	32:5:399:GLU:HB2	1.91	0.51
1:A:2952:U:H5'	31:4:103:MET:HE1	1.91	0.51
4:D:289:LEU:N	4:D:290:PRO:CD	2.73	0.51
19:T:55:ASN:ND2	19:T:74:TYR:O	2.39	0.51
33:6:235:TRP:HB3	33:6:254:TYR:HA	1.93	0.51
1:A:2502:C:H1'	1:A:3096:U:H5'	1.91	0.51
1:A:2961:C:H2'	1:A:2961:C:O2	2.09	0.51
34:7:185:LEU:HD13	34:7:295:ARG:HD3	1.93	0.51
37:b:28:ARG:HH12	37:b:78:GLU:CD	2.19	0.51
54:n:58:PHE:HA	54:n:61:LEU:HD12	1.92	0.51
3:C:285:LEU:HD23	3:C:290:ASN:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M:229:PHE:N	12:M:230:PRO:HD2	2.27	0.51
15:P:44:VAL:HG12	33:6:225:LEU:HB3	1.93	0.51
1:A:2213:A:H2'	1:A:2214:A:H5'	1.93	0.50
3:C:73:LEU:HD21	3:C:105:LEU:HD12	1.94	0.50
55:A1:260:THR:HA	55:A1:310:CYS:SG	2.51	0.50
56:A2:302:LEU:HA	56:A2:306:ALA:HB3	1.93	0.50
1:A:2740:A:H2'	1:A:2741:A:C8	2.46	0.50
13:N:63:ARG:HB2	13:N:67:LYS:HZ3	1.75	0.50
34:7:290:GLN:HB2	34:7:291:PRO:HD3	1.92	0.50
8:I:184:THR:HA	59:t1:-13:LEU:HD13	1.94	0.50
26:a:105:GLU:O	26:a:109:ILE:HG12	2.12	0.50
32:5:113:LEU:HD12	32:5:311:ALA:HB1	1.93	0.50
53:s:215:GLU:HB2	53:s:229:LEU:HD11	1.91	0.50
1:A:2085:A:H2'	1:A:2086:A:C8	2.47	0.50
10:K:80:HIS:CD2	10:K:81:THR:O	2.65	0.50
24:Y:73:ASN:HA	24:Y:76:GLN:HG3	1.93	0.50
19:T:196:ALA:O	19:T:200:ILE:HG12	2.12	0.50
1:A:1952:U:H2'	1:A:1953:A:C8	2.46	0.49
5:E:74:ALA:HA	5:E:77:LEU:HD23	1.94	0.49
5:E:221:ARG:HG3	5:E:261:MET:HB3	1.94	0.49
10:K:7:ALA:HB3	10:K:8:PRO:HD3	1.94	0.49
23:X:36:ARG:NH2	23:X:151:GLU:HB2	2.27	0.49
30:3:172:TYR:HB2	30:3:175:ASP:HB2	1.94	0.49
1:A:2169:A:H1'	1:A:2192:A:C2	2.47	0.49
1:A:2740:A:N3	1:A:2921:A:O2'	2.38	0.49
3:C:147:MET:HE1	3:C:201:LEU:HD11	1.94	0.49
27:0:119:LYS:O	27:0:120:HIS:ND1	2.45	0.49
32:5:260:SER:OG	32:5:262:ILE:HG12	2.12	0.49
1:A:2256:U:O2'	18:S:118:ASN:ND2	2.45	0.49
10:K:178:LEU:HD12	52:r:100:LEU:HD21	1.95	0.49
24:Y:172:ILE:CD1	29:2:70:LEU:HD13	2.42	0.49
4:D:257:ILE:O	4:D:262:ARG:HG3	2.12	0.49
8:I:47:LEU:HD22	13:N:226:ILE:HG12	1.95	0.49
11:L:145:VAL:HG11	16:Q:160:VAL:HG11	1.94	0.49
37:b:45:GLU:HG2	37:b:49:ARG:HE	1.77	0.49
58:u:118:MET:HE3	58:u:197:ARG:HG3	1.94	0.49
1:A:3078:C:H2'	1:A:3079:G:C8	2.47	0.49
7:H:94:LEU:HD22	7:H:116:LYS:HA	1.95	0.49
40:e:255:VAL:HG13	40:e:259:GLU:HB2	1.94	0.49
1:A:3039:U:H2'	1:A:3040:OMG:C8	2.48	0.49
9:J:25:ARG:HA	9:J:65:PRO:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M:247:ILE:HG22	12:M:253:PHE:HD1	1.78	0.49
44:i:79:TRP:HB2	44:i:93:ARG:HG2	1.94	0.49
55:A1:161:ALA:HA	55:A1:164:LEU:HD23	1.94	0.49
8:I:98:VAL:HG11	8:I:146:LEU:HB3	1.94	0.49
52:r:79:HIS:HB3	52:r:184:ASN:HA	1.95	0.49
60:w:75:THR:HG23	60:w:78:GLY:H	1.77	0.49
23:X:41:VAL:HG11	23:X:83:GLU:HB3	1.95	0.49
19:T:69:ARG:HD2	39:d:228:PHE:HB3	1.95	0.48
26:a:122:ARG:CG	26:a:122:ARG:HH11	2.26	0.48
1:A:3158:A:H2'	1:A:3159:A:C8	2.48	0.48
10:K:70:ASN:HD21	52:r:154:TRP:H	1.60	0.48
18:S:96:PHE:HB3	37:b:126:ILE:HD13	1.94	0.48
23:X:208:LEU:O	23:X:212:ILE:HG12	2.13	0.48
55:A1:169:LEU:HG	55:A1:251:ARG:HD3	1.96	0.48
59:t3:11:ALA:O	59:t6:14:THR:OG1	2.32	0.48
9:J:140:VAL:O	9:J:144:ILE:HG12	2.13	0.48
43:h:82:LEU:HB3	43:h:83:PRO:HD3	1.95	0.48
1:A:2127:A:H4'	1:A:2251:A:C5	2.49	0.48
3:C:92:GLU:HB3	3:C:318:MET:SD	2.53	0.48
18:S:79:VAL:HA	18:S:82:LYS:HE3	1.95	0.48
23:X:119:LEU:HD22	32:5:53:PRO:HD2	1.95	0.48
18:S:120:LEU:HB3	18:S:122:LEU:HD12	1.96	0.48
20:U:11:ARG:HG3	21:V:211:LYS:HB3	1.94	0.48
38:c:141:LEU:HD11	38:c:223:MET:HE1	1.96	0.48
56:A2:95:VAL:HG21	56:A2:121:LEU:HB3	1.95	0.48
59:t6:9:ASP:O	59:t6:13:LEU:HG	2.13	0.48
59:t5:18:ILE:HA	59:t5:21:LEU:HD12	1.96	0.48
1:A:2702:G:H5'	10:K:114:LYS:HE2	1.96	0.48
32:5:126:THR:HG21	32:5:357:PHE:CE1	2.48	0.48
33:6:160:ASP:OD2	33:6:267:ARG:NH2	2.47	0.48
14:O:130:LEU:HD22	27:0:134:THR:HG23	1.96	0.48
20:U:64:PRO:HB2	20:U:100:ALA:HB3	1.96	0.48
41:f:169:ILE:O	41:f:172:GLU:HG3	2.14	0.48
46:k:78:GLY:HA2	46:k:81:LEU:HB2	1.94	0.48
57:v:40:ARG:O	57:v:44:LYS:HB2	2.14	0.48
59:t1:13:LEU:HD13	59:t1:17:GLU:HG2	1.95	0.48
59:t6:22:ASN:OD1	59:t6:23:GLU:N	2.46	0.48
8:I:144:LEU:N	8:I:145:PRO:HD2	2.29	0.48
24:Y:175:ARG:NH2	29:2:83:MET:SD	2.84	0.48
1:A:1683:C:N4	24:Y:225:ASN:HD21	2.12	0.47
2:B:1620:A:H2'	2:B:1621:A:H4'	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:233:LEU:O	8:I:237:ILE:HG13	2.13	0.47
1:A:2686:G:H5'	1:A:3104:U:H4'	1.96	0.47
32:5:123:LEU:HD22	32:5:220:LEU:HD21	1.95	0.47
7:H:59:TRP:NE1	7:H:81:LYS:HG2	2.28	0.47
32:5:176:TYR:HA	32:5:179:VAL:HG12	1.96	0.47
40:e:67:GLN:HE22	48:m:36:SER:HB2	1.78	0.47
52:r:102:ARG:HD2	52:r:109:GLN:HA	1.96	0.47
1:A:1852:C:H2'	1:A:1853:A:C4	2.49	0.47
1:A:2075:U:O2'	1:A:2833:A:N7	2.41	0.47
33:6:44:ASN:HD22	33:6:47:ARG:HB2	1.79	0.47
55:A1:178:LEU:HB3	55:A1:252:VAL:HG22	1.96	0.47
1:A:3201:A:H2'	1:A:3202:U:C6	2.50	0.47
24:Y:193:ARG:HA	24:Y:196:ARG:HE	1.80	0.47
35:8:175:GLY:HA3	41:f:181:GLY:HA2	1.96	0.47
1:A:2275:U:H2'	1:A:2276:C:H6	1.80	0.47
37:b:33:VAL:O	37:b:67:SER:HA	2.15	0.47
1:A:2620:G:H2'	1:A:2621:G:C8	2.49	0.47
1:A:3011:A:O2'	1:A:3173:G:N2	2.47	0.47
2:B:1642:G:H4'	35:8:119:LYS:HG3	1.96	0.47
15:P:83:VAL:HG21	15:P:158:MET:HE1	1.97	0.47
16:Q:148:THR:HG22	16:Q:165:GLU:HG2	1.97	0.47
22:W:123:GLY:HA3	33:6:40:ILE:HG21	1.96	0.47
23:X:42:HIS:CG	23:X:86:ILE:HD11	2.50	0.47
25:Z:101:LYS:HE3	45:j:80:LEU:HD22	1.95	0.47
33:6:173:LEU:HD13	33:6:272:LEU:HD22	1.97	0.47
41:f:208:LEU:HG	55:A1:244:LEU:HD21	1.96	0.47
50:p:176:HIS:O	50:p:180:ILE:HG12	2.14	0.47
1:A:1705:A:C8	36:9:39:LYS:HD3	2.50	0.47
22:W:125:VAL:HG21	33:6:64:GLU:HG3	1.96	0.47
59:t3:13:LEU:HB3	59:t3:17:GLU:HB2	1.97	0.47
66:w:201:PNS:H371	66:w:201:PNS:H32	1.66	0.47
13:N:223:MET:HE2	49:o:46:HIS:HE1	1.80	0.47
28:1:22:SER:HB3	28:1:56:PHE:CZ	2.49	0.47
32:5:181:VAL:CG2	32:5:347:THR:HG21	2.44	0.47
38:c:216:ARG:HD3	38:c:316:TYR:CD1	2.49	0.47
47:l:93:PRO:HB2	47:l:96:LEU:HG	1.97	0.47
6:F:279:ARG:HH12	6:F:282:PRO:HD3	1.80	0.46
38:c:40:ARG:O	38:c:44:GLU:HG2	2.15	0.46
59:t3:18:ILE:HA	59:t3:21:LEU:HD12	1.97	0.46
1:A:1680:A:H5'	1:A:1681:G:OP2	2.15	0.46
14:O:141:HIS:O	14:O:147:GLN:NE2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:Q:113:VAL:O	16:Q:137:CYS:O	2.33	0.46
40:e:279:LEU:HD13	41:f:176:SER:HB2	1.96	0.46
52:r:71:PRO:HD2	52:r:107:LEU:HD23	1.97	0.46
53:s:201:ASP:HB2	53:s:240:GLN:HB3	1.97	0.46
3:C:256:TYR:HA	3:C:275:LYS:HD3	1.96	0.46
5:E:131:LYS:HB3	5:E:146:SER:HB2	1.98	0.46
18:S:130:LEU:HB2	18:S:156:VAL:HG23	1.96	0.46
40:e:212:HIS:HE1	40:e:230:LYS:HB2	1.79	0.46
55:A1:252:VAL:HB	55:A1:305:VAL:HG12	1.97	0.46
59:t6:14:THR:HG23	59:t6:17:GLU:H	1.79	0.46
1:A:2607:U:H2'	1:A:2608:G:C8	2.47	0.46
13:N:217:ARG:HE	13:N:223:MET:HE1	1.81	0.46
1:A:2898:U:H2'	1:A:2899:C:O4'	2.15	0.46
1:A:3151:A:N1	1:A:3163:G:O2'	2.41	0.46
33:6:186:PRO:HB3	50:p:191:LYS:HZ2	1.81	0.46
53:s:215:GLU:HB2	53:s:229:LEU:CD1	2.45	0.46
1:A:2081:U:H2'	1:A:2082:G:C8	2.50	0.46
1:A:2873:A:H4'	22:W:90:TYR:CZ	2.50	0.46
4:D:196:VAL:HG22	4:D:206:TYR:HB2	1.97	0.46
18:S:130:LEU:HB2	18:S:156:VAL:CG2	2.46	0.46
56:A2:172:GLY:H	56:A2:175:LYS:HB2	1.81	0.46
6:F:280:TYR:CD1	12:M:125:ARG:HD2	2.51	0.46
40:e:146:ARG:HH21	40:e:151:ARG:HE	1.64	0.46
42:g:73:GLN:HB3	42:g:162:LEU:HD11	1.97	0.46
66:w:201:PNS:H382	66:w:201:PNS:H421	1.72	0.46
1:A:1839:C:H2'	1:A:1840:C:H6	1.79	0.46
32:5:300:ARG:N	32:5:301:PRO:HD2	2.30	0.46
55:A1:315:LEU:HA	55:A1:319:TYR:HD2	1.81	0.46
59:t5:5:GLN:NE2	59:t5:6:LEU:HD22	2.30	0.46
1:A:2297:A:H5'	17:R:40:ARG:HH22	1.80	0.46
1:A:2484:C:O2	1:A:2484:C:O4'	2.33	0.46
1:A:3078:C:H2'	1:A:3079:G:H8	1.81	0.46
14:O:30:ARG:HD2	14:O:78:PHE:O	2.16	0.46
40:e:117:ALA:HA	40:e:120:LEU:HD12	1.96	0.46
46:k:15:GLN:HE22	46:k:17:ARG:HB2	1.81	0.46
59:t6:18:ILE:HD13	59:t6:21:LEU:HD12	1.99	0.46
1:A:3027:U:H4'	1:A:3173:G:H5'	1.98	0.45
6:F:110:SER:O	6:F:158:PRO:HA	2.16	0.45
18:S:115:LEU:HB2	37:b:11:LEU:HD11	1.97	0.45
20:U:48:MET:HE2	20:U:53:LEU:HA	1.97	0.45
26:a:40:PRO:HG2	26:a:43:TYR:HE2	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:e:146:ARG:NH2	40:e:151:ARG:HE	2.14	0.45
8:I:231:THR:O	8:I:235:GLN:HG2	2.16	0.45
13:N:113:MET:HE1	13:N:120:ALA:HB2	1.98	0.45
60:w:138:LEU:HD12	60:w:144:ILE:HG13	1.97	0.45
1:A:2827:A:H2'	1:A:2828:G:C8	2.51	0.45
1:A:3026:U:H5'	31:4:68:ASN:OD1	2.16	0.45
28:1:16:ILE:HD11	28:1:34:ARG:NH2	2.32	0.45
32:5:73:PRO:HG2	32:5:75:PHE:CZ	2.51	0.45
55:A1:192:LEU:HD13	55:A1:221:VAL:HG21	1.98	0.45
1:A:1733:C:O2'	1:A:1734:C:H5'	2.17	0.45
2:B:1660:G:H2'	2:B:1661:A:C8	2.51	0.45
8:I:119:HIS:HB3	8:I:163:GLU:HG3	1.98	0.45
15:P:52:ASN:HB3	15:P:55:ASN:HB2	1.99	0.45
38:c:159:PHE:CZ	38:c:226:LYS:HE2	2.52	0.45
1:A:1993:A:N3	1:A:1993:A:H2'	2.31	0.45
32:5:305:GLN:HB2	32:5:308:GLN:HG3	1.97	0.45
35:8:97:LYS:HB3	35:8:99:ARG:HH11	1.82	0.45
38:c:216:ARG:HD3	38:c:316:TYR:HD1	1.82	0.45
18:S:114:ILE:HD12	18:S:116:ILE:HD11	1.99	0.45
20:U:19:VAL:HB	36:9:136:LEU:HD23	1.98	0.45
35:8:169:PHE:HB2	35:8:170:PRO:HD3	1.99	0.45
39:d:86:ASP:HB2	39:d:198:ARG:HG3	1.99	0.45
41:f:178:LEU:HA	41:f:179:PRO:HD3	1.89	0.45
53:s:208:PHE:HE1	53:s:341:MET:HG3	1.80	0.45
1:A:2073:A:C5	1:A:2074:A:H1'	2.51	0.45
1:A:2180:A:H4'	1:A:2181:A:H8	1.81	0.45
1:A:3111:A:O2'	1:A:3112:A:H5''	2.16	0.45
1:A:3181:U:H5'	52:r:99:MET:O	2.17	0.45
5:E:328:LEU:HD13	5:E:332:LEU:HD11	1.99	0.45
1:A:1952:U:H2'	1:A:1953:A:H8	1.82	0.45
11:L:76:ALA:HB1	54:n:165:LEU:HD13	1.99	0.45
22:W:102:GLU:HB2	22:W:130:PHE:CD1	2.51	0.45
1:A:3173:G:H2'	1:A:3174:U:O4'	2.17	0.45
3:C:60:ILE:HD12	3:C:220:LEU:HD23	1.98	0.45
26:a:109:ILE:HG23	26:a:123:TRP:HB2	1.98	0.45
39:d:184:SER:HB3	39:d:221:THR:OG1	2.17	0.45
58:u:123:TYR:HB2	58:u:175:MET:HG2	1.99	0.45
1:A:2854:U:H4'	30:3:138:PRO:HG2	1.98	0.45
2:B:1622:A:H2'	2:B:1623:G:C8	2.52	0.45
22:W:70:GLN:O	22:W:71:ARG:HB3	2.17	0.45
56:A2:139:GLU:HB2	56:A2:140:PRO:HD3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:t1:15:LEU:HB2	59:t4:11:ALA:HA	1.99	0.45
1:A:1871:A:N7	1:A:1901:C:N4	2.65	0.44
1:A:2408:U:H2'	1:A:2409:A:C8	2.52	0.44
20:U:11:ARG:HH21	32:5:82:TYR:HE1	1.64	0.44
23:X:183:ARG:O	23:X:187:ILE:HG12	2.17	0.44
25:Z:70:THR:HG22	25:Z:97:PRO:HA	1.99	0.44
2:B:1607:U:H2'	2:B:1608:G:C8	2.52	0.44
2:B:1626:C:H2'	2:B:1627:C:C6	2.52	0.44
3:C:60:ILE:O	3:C:60:ILE:HG13	2.18	0.44
12:M:73:PRO:O	12:M:77:ARG:HG3	2.18	0.44
13:N:223:MET:HE2	49:o:46:HIS:CE1	2.53	0.44
20:U:143:ARG:HA	39:d:280:VAL:HG21	2.00	0.44
42:g:101:THR:HG22	42:g:102:HIS:ND1	2.32	0.44
55:A1:259:THR:HG23	55:A1:316:GLN:HE22	1.82	0.44
1:A:1860:A:H2'	1:A:1861:U:C6	2.53	0.44
1:A:1918:G:O5'	29:2:63:LYS:NZ	2.49	0.44
1:A:2087:U:H2'	1:A:2088:U:C6	2.52	0.44
1:A:2802:A:H2'	1:A:2803:A:C8	2.53	0.44
1:A:3088:C:H4'	1:A:3089:A:C5	2.52	0.44
5:E:316:PHE:HB3	5:E:317:PRO:HD3	2.00	0.44
15:P:110:TRP:HA	15:P:113:LYS:HB2	1.99	0.44
41:f:131:THR:HA	41:f:151:THR:HG22	1.98	0.44
1:A:1756:A:H2'	1:A:1757:A:H8	1.83	0.44
6:F:103:GLN:HE22	6:F:250:VAL:H	1.65	0.44
8:I:219:HIS:O	8:I:223:GLN:HG2	2.17	0.44
40:e:55:ARG:HH21	40:e:57:PRO:HA	1.82	0.44
1:A:2286:A:H2'	1:A:2287:U:C6	2.53	0.44
3:C:83:ASN:ND2	3:C:154:VAL:O	2.43	0.44
21:V:62:VAL:HG12	21:V:122:LEU:HD23	1.98	0.44
1:A:2989:G:H5''	1:A:2990:A:C2	2.52	0.44
28:1:16:ILE:HD12	28:1:61:LYS:HG3	1.99	0.44
40:e:146:ARG:HB3	40:e:253:VAL:HG13	2.00	0.44
55:A1:82:ALA:O	55:A1:86:VAL:HG23	2.17	0.44
1:A:1884:G:H1'	1:A:1895:C:H1'	1.99	0.44
1:A:2668:A:H2'	1:A:2669:A:C8	2.53	0.44
54:n:91:VAL:HG11	54:n:122:ALA:HB2	1.99	0.44
1:A:2684:C:N3	17:R:32:ARG:HD3	2.33	0.44
4:D:63:PHE:HB3	4:D:87:HIS:HA	1.99	0.44
5:E:194:TYR:HD1	5:E:281:ASN:HD21	1.63	0.44
13:N:89:ILE:HD11	13:N:176:LEU:HB3	2.00	0.44
14:O:16:ARG:HB2	14:O:18:MET:HE3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:c:111:GLU:HG2	38:c:112:LYS:HD2	2.00	0.44
44:i:35:ARG:HH21	44:i:37:THR:HG23	1.83	0.44
54:n:212:PHE:CG	54:n:234:ALA:HB1	2.53	0.44
1:A:1718:A:H2'	1:A:1719:G:O4'	2.18	0.44
15:P:146:TYR:OH	15:P:158:MET:HE2	2.17	0.44
56:A2:237:ALA:HB2	56:A2:253:TYR:CZ	2.53	0.44
57:v:3:PRO:O	57:v:4:TRP:C	2.61	0.44
59:t3:11:ALA:HA	59:t6:15:LEU:HB2	1.99	0.44
1:A:1994:A:H2'	1:A:2002:G:N7	2.32	0.43
1:A:2173:G:H2'	1:A:2174:G:H8	1.83	0.43
1:A:2805:A:H2'	1:A:2806:U:C6	2.53	0.43
1:A:2970:C:H2'	1:A:2971:A:O4'	2.18	0.43
3:C:111:THR:HA	3:C:122:ILE:HD11	2.00	0.43
28:1:55:LEU:H	51:q:128:MET:HE1	1.82	0.43
33:6:144:GLY:O	33:6:148:LYS:HG2	2.17	0.43
1:A:2041:U:H5'	12:M:56:GLU:HB3	1.98	0.43
3:C:207:LEU:H	3:C:207:LEU:HD23	1.83	0.43
10:K:91:THR:HG22	52:r:161:PRO:HB3	2.00	0.43
23:X:89:GLN:HE21	23:X:100:ARG:HG2	1.83	0.43
33:6:192:GLU:OE1	50:p:185:ARG:HD2	2.19	0.43
33:6:333:GLN:HG2	33:6:334:LEU:HD12	2.00	0.43
40:e:73:LEU:HD23	48:m:42:ARG:HH22	1.83	0.43
1:A:2750:U:H2'	1:A:2751:G:C8	2.53	0.43
1:A:2898:U:O2	1:A:2898:U:O4'	2.34	0.43
3:C:118:ASN:O	3:C:122:ILE:HG13	2.18	0.43
33:6:234:HIS:HE1	33:6:257:PRO:HA	1.83	0.43
36:9:71:LYS:HB3	36:9:72:PRO:HD2	2.00	0.43
1:A:2679:U:O2'	27:0:81:PRO:O	2.35	0.43
39:d:164:VAL:HG13	39:d:168:CYS:HB3	1.99	0.43
59:t1:-5:ALA:HA	59:t1:-4:PRO:HD3	1.87	0.43
59:t6:25:LEU:HG	59:t5:7:VAL:HG22	2.00	0.43
1:A:2395:A:H1'	32:5:385:HIS:HB2	2.00	0.43
6:F:113:LYS:HD2	6:F:157:GLY:HA2	1.99	0.43
22:W:143:LYS:HE2	33:6:345:VAL:HG11	2.00	0.43
31:4:69:LYS:HB2	31:4:72:LEU:HD23	1.99	0.43
34:7:64:LYS:HD2	34:7:80:VAL:HG12	2.01	0.43
1:A:1789:A:H5''	36:9:17:ARG:HH21	1.82	0.43
1:A:2677:A:H2'	1:A:2678:A:C8	2.53	0.43
21:V:80:ILE:HB	21:V:85:TRP:HB2	2.00	0.43
41:f:105:SER:HB2	48:m:41:THR:HG21	2.01	0.43
54:n:57:ALA:HB2	54:n:85:ALA:HB1	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2392:U:H2'	1:A:2394:A:H62	1.84	0.43
33:6:185:MET:HE2	50:p:189:ARG:HD3	2.01	0.43
42:g:138:THR:HG22	42:g:149:ILE:HG13	2.01	0.43
58:u:164:THR:OG1	58:u:167:TRP:O	2.36	0.43
1:A:1881:A:OP1	42:g:90:ARG:HG3	2.18	0.43
1:A:1882:A:N6	1:A:1893:A:O4'	2.51	0.43
1:A:2098:G:H2'	1:A:2099:U:C6	2.54	0.43
1:A:2801:A:H2'	1:A:2802:A:C8	2.54	0.43
4:D:123:GLU:HG2	4:D:162:THR:HG22	2.01	0.43
5:E:54:SER:O	5:E:58:VAL:HG23	2.19	0.43
8:I:163:GLU:O	8:I:166:ARG:HG2	2.18	0.43
8:I:183:ASP:O	59:t1:-13:LEU:HD21	2.19	0.43
12:M:211:VAL:N	12:M:212:PRO:HD2	2.34	0.43
21:V:122:LEU:HD12	21:V:133:ILE:HG13	1.99	0.43
26:a:41:ASP:HB2	26:a:46:ASN:HA	2.00	0.43
1:A:3091:G:H4'	54:n:42:PRO:HG3	2.00	0.43
11:L:49:SER:OG	11:L:78:LYS:HD2	2.19	0.43
23:X:163:ARG:HE	32:5:55:LEU:HD13	1.83	0.43
32:5:310:ARG:HD3	32:5:378:SER:HB3	2.00	0.43
33:6:329:TYR:HB3	33:6:333:GLN:HE22	1.84	0.43
40:e:255:VAL:HG11	40:e:260:LEU:HB3	1.99	0.43
1:A:1851:G:C2	1:A:2099:U:H4'	2.54	0.43
1:A:2111:C:C4	1:A:2945:A:H5'	2.54	0.43
1:A:2607:U:C2	1:A:2608:G:N7	2.87	0.43
21:V:86:VAL:HG21	21:V:120:VAL:HG21	2.01	0.43
53:s:66:TRP:O	53:s:69:THR:OG1	2.35	0.43
53:s:85:LYS:HE3	53:s:86:MET:HE2	2.01	0.43
1:A:2493:C:O4'	1:A:2493:C:O2	2.37	0.42
1:A:2510:U:C5	1:A:2539:A:C6	3.07	0.42
6:F:243:ILE:HG22	51:q:27:ALA:HB2	2.01	0.42
6:F:263:LEU:HA	6:F:266:VAL:HG12	2.01	0.42
12:M:217:ALA:O	12:M:220:ARG:HD2	2.19	0.42
20:U:74:HIS:HB2	36:9:24:LYS:HE3	2.00	0.42
40:e:191:THR:HG23	40:e:195:LEU:HD21	2.01	0.42
53:s:92:MET:CE	53:s:276:ARG:HD3	2.49	0.42
59:t3:27:LYS:HA	59:t3:27:LYS:HD2	1.85	0.42
34:7:180:CYS:HA	34:7:297:PHE:O	2.20	0.42
38:c:160:LEU:HD11	38:c:223:MET:HE3	2.01	0.42
1:A:1839:C:H5''	10:K:115:ASN:HB2	2.00	0.42
1:A:2212:C:H2'	1:A:2213:A:H8	1.84	0.42
1:A:2700:G:H2'	1:A:2701:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:U:36:PRO:HD3	53:s:270:LYS:HB3	2.01	0.42
39:d:183:TRP:CH2	39:d:185:PHE:HB2	2.54	0.42
40:e:46:ARG:HE	40:e:227:LEU:HG	1.84	0.42
53:s:92:MET:CE	53:s:276:ARG:HH11	2.33	0.42
59:t4:19:SER:HA	59:t4:22:ASN:ND2	2.34	0.42
1:A:2479:C:O2	5:E:230:THR:HB	2.19	0.42
14:O:52:MET:HE2	14:O:52:MET:HB3	1.95	0.42
18:S:142:THR:HG23	26:a:62:HIS:NE2	2.34	0.42
51:q:141:GLU:O	51:q:145:LYS:HG2	2.19	0.42
1:A:1763:A:OP2	44:i:68:LYS:NZ	2.52	0.42
1:A:1977:U:H2'	1:A:1978:A:C8	2.52	0.42
1:A:2495:U:O4	1:A:2509:A:H2	2.02	0.42
33:6:275:GLN:HE21	33:6:279:ILE:HG22	1.85	0.42
34:7:146:CYS:O	34:7:278:TYR:OH	2.36	0.42
1:A:2186:C:H2'	1:A:2187:C:H6	1.81	0.42
11:L:125:THR:HG21	58:u:119:ARG:HD2	2.00	0.42
32:5:123:LEU:HD22	32:5:220:LEU:CD2	2.50	0.42
35:8:113:ARG:O	35:8:117:LEU:HG	2.20	0.42
55:A1:308:SER:HA	55:A1:376:TYR:O	2.20	0.42
57:v:61:PHE:HB2	58:u:196:LEU:HD11	2.02	0.42
59:t1:24:LEU:HD12	59:t2:3:ILE:HG22	2.01	0.42
1:A:2293:A:H5'	17:R:12:ASN:HB2	2.01	0.42
1:A:2814:G:H1	1:A:2988:C:H42	1.67	0.42
5:E:102:LEU:HD21	5:E:294:ASN:HA	2.02	0.42
6:F:83:HIS:CG	6:F:274:LEU:HD11	2.54	0.42
7:H:55:ILE:HG21	23:X:44:ARG:HG2	2.01	0.42
9:J:118:TYR:CD1	47:l:96:LEU:HD21	2.55	0.42
32:5:351:VAL:HG22	32:5:381:LEU:HB3	2.02	0.42
38:c:100:SER:HB3	38:c:182:GLU:HG2	2.01	0.42
45:j:91:TRP:CD2	49:o:58:GLN:HG2	2.55	0.42
19:T:69:ARG:O	39:d:230:ARG:HD3	2.20	0.42
32:5:208:THR:HA	32:5:224:GLY:O	2.20	0.42
1:A:1851:G:H21	1:A:2134:A:N6	2.17	0.42
1:A:2415:C:H3'	53:s:165:ARG:HH21	1.85	0.42
7:H:95:GLU:HB3	7:H:111:LEU:HD11	2.01	0.42
11:L:87:VAL:HG12	11:L:127:LEU:HD11	2.02	0.42
13:N:152:THR:HA	13:N:153:PRO:HD3	1.90	0.42
41:f:178:LEU:HD13	41:f:184:LEU:HD11	2.01	0.42
46:k:62:PRO:HD2	46:k:79:ALA:HB2	2.01	0.42
55:A1:368:LEU:HD21	56:A2:316:PHE:HB2	2.02	0.42
1:A:3181:U:OP1	52:r:101:PRO:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:K:27:PRO:HG2	10:K:30:LYS:HB2	2.02	0.42
28:1:55:LEU:H	51:q:128:MET:CE	2.32	0.42
40:e:75:GLN:O	40:e:79:ILE:HG12	2.19	0.42
40:e:269:LEU:O	40:e:272:VAL:HG23	2.20	0.42
54:n:53:ARG:HB2	54:n:85:ALA:HB2	2.00	0.42
12:M:153:ASN:HB2	12:M:256:LEU:HD23	2.02	0.41
16:Q:165:GLU:HB2	16:Q:168:ASN:HB2	2.00	0.41
25:Z:36:PHE:CE2	25:Z:79:PRO:HG3	2.53	0.41
30:3:175:ASP:HB3	30:3:178:GLN:HB2	2.01	0.41
38:c:227:GLU:OE2	38:c:302:ARG:NH1	2.52	0.41
5:E:213:LYS:HG3	5:E:261:MET:HE2	2.01	0.41
8:I:132:LYS:HB3	8:I:133:PRO:HD3	2.01	0.41
10:K:60:MET:HB3	10:K:133:ILE:HD11	2.02	0.41
12:M:176:THR:HG21	12:M:213:TYR:HE1	1.84	0.41
15:P:137:LEU:HB3	50:p:188:LEU:HD21	2.03	0.41
1:A:2026:A:H2'	1:A:2027:A:C8	2.55	0.41
6:F:162:TYR:CE1	6:F:164:MET:HE3	2.55	0.41
11:L:85:LEU:HD11	11:L:134:TYR:HE1	1.84	0.41
14:O:62:TYR:CD2	14:O:75:MET:HG2	2.55	0.41
20:U:46:MET:HE1	20:U:72:VAL:HG13	2.01	0.41
54:n:188:GLY:HA2	54:n:236:GLN:HA	2.02	0.41
1:A:2072:A:H2'	1:A:2073:A:C8	2.55	0.41
1:A:2173:G:H2'	1:A:2174:G:C8	2.55	0.41
4:D:216:LEU:HD21	4:D:219:LYS:HD2	2.02	0.41
5:E:61:ILE:HD11	14:O:149:LEU:HD22	2.02	0.41
14:O:134:PRO:HD3	27:O:130:VAL:HG21	2.01	0.41
41:f:117:LEU:HB3	41:f:166:PHE:HZ	1.85	0.41
55:A1:337:GLN:HB2	55:A1:383:LEU:HD11	2.02	0.41
56:A2:288:PRO:HG2	56:A2:293:ILE:HD11	2.03	0.41
1:A:3191:A:H4'	52:r:123:HIS:HB3	2.03	0.41
5:E:48:TRP:CZ2	5:E:51:GLU:HG3	2.56	0.41
8:I:139:LYS:O	59:t1:-14:ALA:HA	2.21	0.41
8:I:221:LEU:HA	8:I:224:HIS:CD2	2.43	0.41
14:O:106:ARG:HD3	14:O:135:LEU:HD21	2.03	0.41
15:P:68:TRP:CH2	22:W:132:HIS:HE1	2.39	0.41
16:Q:240:ILE:HG21	16:Q:243:ILE:HD12	2.03	0.41
32:5:228:ALA:HB1	32:5:292:TYR:HB2	2.02	0.41
32:5:313:MET:HE1	32:5:353:HIS:CB	2.39	0.41
50:p:77:THR:HB	50:p:102:ARG:HG3	2.01	0.41
12:M:177:ALA:HB1	12:M:203:ARG:HH22	1.85	0.41
16:Q:80:PHE:HB3	16:Q:282:ILE:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:7:139:ASN:HB3	34:7:174:VAL:HG21	2.02	0.41
1:A:1756:A:H2'	1:A:1757:A:C8	2.56	0.41
5:E:345:ILE:HG12	16:Q:169:PRO:HB2	2.03	0.41
34:7:84:ASN:O	34:7:118:PRO:HB3	2.21	0.41
39:d:235:GLN:HG3	39:d:238:VAL:HB	2.03	0.41
43:h:148:LEU:HD22	43:h:152:LEU:HD23	2.02	0.41
59:t1:13:LEU:HD22	59:t1:17:GLU:HG2	2.03	0.41
1:A:2318:A:H2'	1:A:2319:A:C8	2.56	0.41
1:A:2650:C:H4'	54:n:199:SER:HB3	2.03	0.41
1:A:2748:A:H2'	1:A:2749:A:C8	2.56	0.41
1:A:3117:C:H2'	1:A:3118:U:C6	2.56	0.41
10:K:172:PRO:HG2	52:r:56:THR:HG22	2.03	0.41
14:O:18:MET:HG3	14:O:25:ARG:HG3	2.02	0.41
15:P:107:THR:O	15:P:113:LYS:HG3	2.21	0.41
34:7:163:MET:HB3	34:7:186:ASP:HB3	2.02	0.41
54:n:135:THR:HA	54:n:138:ARG:HD3	2.02	0.41
55:A1:47:ASN:HA	55:A1:50:MET:HE2	2.03	0.41
57:v:12:LEU:HD13	57:v:59:LEU:HD12	2.01	0.41
1:A:1851:G:H2'	1:A:1852:C:C6	2.55	0.41
1:A:1883:G:OP1	42:g:91:MET:HG2	2.20	0.41
1:A:1974:A:H5'	4:D:261:GLY:HA2	2.02	0.41
1:A:2146:A:N6	37:b:117:LYS:HG2	2.35	0.41
1:A:2630:U:H2'	1:A:2631:G:C4	2.56	0.41
1:A:2726:C:H2'	1:A:2727:C:C6	2.56	0.41
1:A:2734:A:H2'	1:A:2735:G:H8	1.86	0.41
4:D:218:ARG:HG2	4:D:225:ILE:HB	2.02	0.41
10:K:138:LEU:HD23	10:K:138:LEU:HA	1.97	0.41
15:P:171:VAL:HG12	15:P:173:ARG:H	1.86	0.41
21:V:64:ILE:HG13	21:V:120:VAL:HG12	2.02	0.41
24:Y:105:LEU:HD13	24:Y:139:MET:HG2	2.03	0.41
27:O:166:SER:H	27:O:169:ASP:HB2	1.85	0.41
33:6:179:VAL:HG11	33:6:197:GLU:HG2	2.02	0.41
34:7:129:THR:HG23	34:7:131:LYS:H	1.86	0.41
35:8:173:LYS:HG3	41:f:175:GLN:HB2	2.03	0.41
39:d:202:MET:HE3	39:d:205:GLN:HA	2.03	0.41
53:s:369:PHE:HB3	53:s:424:PHE:CE2	2.56	0.41
54:n:25:LYS:HG2	54:n:27:ARG:HG3	2.02	0.41
56:A2:236:TYR:CE2	56:A2:240:ARG:HD3	2.56	0.41
59:t2:1:PRO:HB2	59:t2:2:LYS:H	1.62	0.41
59:t3:24:LEU:HD12	59:t4:3:ILE:HG22	2.02	0.41
1:A:2203:G:H21	1:A:2208:A:H62	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2228:A:C2	31:4:103:MET:HE3	2.56	0.41
1:A:2726:C:H2'	1:A:2727:C:H6	1.86	0.41
17:R:17:ARG:O	17:R:21:ILE:HG12	2.21	0.41
32:5:177:CYS:O	32:5:180:ILE:HG22	2.20	0.41
32:5:257:TYR:CD1	32:5:258:PRO:HA	2.56	0.41
1:A:2072:A:N6	1:A:2831:G:H5'	2.36	0.40
1:A:2948:C:H2'	1:A:2949:C:C6	2.56	0.40
1:A:3155:C:H2'	1:A:3156:A:C8	2.56	0.40
35:8:178:TYR:HE2	48:m:65:HIS:HB2	1.86	0.40
50:p:113:GLU:HA	50:p:116:ARG:HE	1.85	0.40
51:q:124:CYS:O	51:q:128:MET:HG2	2.22	0.40
58:u:180:MET:HE2	58:u:185:ARG:HA	2.03	0.40
4:D:195:ASN:ND2	4:D:208:ARG:HB3	2.36	0.40
4:D:290:PRO:N	4:D:291:PRO:HD2	2.37	0.40
6:F:82:LEU:HD22	6:F:266:VAL:HG21	2.04	0.40
10:K:25:MET:HB2	10:K:151:ILE:HG12	2.03	0.40
20:U:130:LEU:HD11	21:V:98:ILE:HD11	2.02	0.40
53:s:237:PRO:HB3	53:s:300:HIS:CE1	2.56	0.40
1:A:1855:A:H2'	1:A:1856:A:C8	2.56	0.40
1:A:3117:C:H2'	1:A:3118:U:H6	1.87	0.40
2:B:1659:U:H2'	2:B:1660:G:C8	2.56	0.40
8:I:200:LEU:N	8:I:201:PRO:HD2	2.36	0.40
32:5:52:ILE:HA	32:5:53:PRO:HD3	1.86	0.40
32:5:115:GLU:HB3	32:5:118:LYS:HB2	2.03	0.40
39:d:179:LYS:HB2	39:d:225:TYR:O	2.22	0.40
40:e:272:VAL:HA	40:e:275:PHE:CE2	2.57	0.40
56:A2:232:TYR:HD2	56:A2:258:LEU:HD11	1.86	0.40
57:v:21:ARG:HH21	60:w:120:MET:HB3	1.86	0.40
57:v:46:GLU:HG3	57:v:51:ARG:HG3	2.03	0.40
1:A:3163:G:H2'	1:A:3164:C:C6	2.56	0.40
7:H:79:VAL:HG22	23:X:89:GLN:HB2	2.04	0.40
17:R:51:VAL:HG21	18:S:174:PHE:HB3	2.03	0.40
23:X:143:PHE:HE2	23:X:190:LYS:HE2	1.87	0.40
34:7:180:CYS:HB3	34:7:298:GLN:HG2	2.03	0.40
35:8:158:HIS:HA	35:8:161:ALA:HB3	2.04	0.40
54:n:109:LEU:HD13	54:n:143:LEU:HG	2.03	0.40
54:n:170:LEU:HD23	54:n:196:TRP:H	1.85	0.40
6:F:126:LYS:HG3	6:F:139:GLY:HA2	2.04	0.40
8:I:224:HIS:O	8:I:228:GLN:N	2.51	0.40
16:Q:138:ILE:HA	16:Q:187:LEU:HB2	2.04	0.40
23:X:174:PRO:HA	23:X:184:ARG:NE	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:5:211:ALA:HB1	32:5:322:LEU:HD23	2.04	0.40
51:q:29:PRO:HA	51:q:30:PRO:HD3	1.97	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	C	234/333 (70%)	231 (99%)	3 (1%)	0	100	100
4	D	236/305 (77%)	229 (97%)	6 (2%)	1 (0%)	30	51
5	E	302/348 (87%)	290 (96%)	12 (4%)	0	100	100
6	F	248/311 (80%)	243 (98%)	5 (2%)	0	100	100
7	H	86/267 (32%)	85 (99%)	1 (1%)	0	100	100
8	I	203/261 (78%)	196 (97%)	7 (3%)	0	100	100
9	J	138/192 (72%)	134 (97%)	4 (3%)	0	100	100
10	K	175/178 (98%)	172 (98%)	3 (2%)	0	100	100
11	L	113/145 (78%)	109 (96%)	4 (4%)	0	100	100
12	M	285/296 (96%)	280 (98%)	5 (2%)	0	100	100
13	N	202/251 (80%)	201 (100%)	1 (0%)	0	100	100
14	O	150/175 (86%)	150 (100%)	0	0	100	100
15	P	139/179 (78%)	135 (97%)	4 (3%)	0	100	100
16	Q	215/292 (74%)	210 (98%)	5 (2%)	0	100	100
17	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
18	S	154/205 (75%)	151 (98%)	3 (2%)	0	100	100
19	T	164/212 (77%)	160 (98%)	4 (2%)	0	100	100
20	U	135/153 (88%)	132 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	V	200/216 (93%)	196 (98%)	4 (2%)	0	100	100
22	W	99/148 (67%)	94 (95%)	5 (5%)	0	100	100
23	X	241/256 (94%)	235 (98%)	6 (2%)	0	100	100
24	Y	174/250 (70%)	171 (98%)	3 (2%)	0	100	100
25	Z	118/161 (73%)	114 (97%)	4 (3%)	0	100	100
26	a	78/142 (55%)	76 (97%)	2 (3%)	0	100	100
27	0	106/188 (56%)	102 (96%)	4 (4%)	0	100	100
28	1	50/65 (77%)	50 (100%)	0	0	100	100
29	2	43/92 (47%)	42 (98%)	1 (2%)	0	100	100
30	3	93/188 (50%)	91 (98%)	2 (2%)	0	100	100
31	4	36/103 (35%)	36 (100%)	0	0	100	100
32	5	390/423 (92%)	381 (98%)	9 (2%)	0	100	100
33	6	316/380 (83%)	310 (98%)	6 (2%)	0	100	100
34	7	285/338 (84%)	268 (94%)	17 (6%)	0	100	100
35	8	83/206 (40%)	80 (96%)	3 (4%)	0	100	100
36	9	121/137 (88%)	120 (99%)	1 (1%)	0	100	100
37	b	146/215 (68%)	139 (95%)	7 (5%)	0	100	100
38	c	284/332 (86%)	279 (98%)	5 (2%)	0	100	100
39	d	214/302 (71%)	208 (97%)	6 (3%)	0	100	100
40	e	211/279 (76%)	200 (95%)	11 (5%)	0	100	100
41	f	124/212 (58%)	121 (98%)	2 (2%)	1 (1%)	16	34
42	g	129/166 (78%)	125 (97%)	4 (3%)	0	100	100
43	h	101/158 (64%)	100 (99%)	1 (1%)	0	100	100
44	i	95/128 (74%)	91 (96%)	4 (4%)	0	100	100
45	j	83/123 (68%)	83 (100%)	0	0	100	100
46	k	93/112 (83%)	90 (97%)	3 (3%)	0	100	100
47	l	42/138 (30%)	41 (98%)	0	1 (2%)	4	9
48	m	38/128 (30%)	35 (92%)	3 (8%)	0	100	100
49	o	78/102 (76%)	78 (100%)	0	0	100	100
50	p	119/205 (58%)	115 (97%)	4 (3%)	0	100	100
51	q	133/222 (60%)	132 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	r	153/196 (78%)	152 (99%)	1 (1%)	0	100	100
53	s	368/439 (84%)	359 (98%)	8 (2%)	1 (0%)	36	58
54	n	213/246 (87%)	211 (99%)	2 (1%)	0	100	100
55	A1	331/384 (86%)	328 (99%)	3 (1%)	0	100	100
56	A2	236/381 (62%)	233 (99%)	3 (1%)	0	100	100
57	v	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
58	u	127/234 (54%)	125 (98%)	2 (2%)	0	100	100
59	t1	44/198 (22%)	43 (98%)	1 (2%)	0	100	100
59	t2	28/198 (14%)	28 (100%)	0	0	100	100
59	t3	28/198 (14%)	28 (100%)	0	0	100	100
59	t4	27/198 (14%)	27 (100%)	0	0	100	100
59	t5	27/198 (14%)	27 (100%)	0	0	100	100
59	t6	25/198 (13%)	25 (100%)	0	0	100	100
60	w	85/156 (54%)	82 (96%)	3 (4%)	0	100	100
All	All	9399/13661 (69%)	9179 (98%)	216 (2%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
47	l	102	GLY
53	s	272	PRO
4	D	220	VAL
41	f	179	PRO

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	
3	C	211/286 (74%)	207 (98%)	4 (2%)	50	75
4	D	192/245 (78%)	190 (99%)	2 (1%)	68	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	259/290 (89%)	259 (100%)	0	100	100
6	F	217/262 (83%)	217 (100%)	0	100	100
7	H	82/228 (36%)	82 (100%)	0	100	100
8	I	189/232 (82%)	188 (100%)	1 (0%)	81	92
9	J	113/150 (75%)	111 (98%)	2 (2%)	51	76
10	K	155/156 (99%)	154 (99%)	1 (1%)	78	91
11	L	98/124 (79%)	97 (99%)	1 (1%)	68	86
12	M	245/249 (98%)	242 (99%)	3 (1%)	63	83
13	N	179/211 (85%)	179 (100%)	0	100	100
14	O	133/150 (89%)	133 (100%)	0	100	100
15	P	123/154 (80%)	123 (100%)	0	100	100
16	Q	199/256 (78%)	198 (100%)	1 (0%)	81	92
17	R	118/126 (94%)	116 (98%)	2 (2%)	53	78
18	S	141/180 (78%)	138 (98%)	3 (2%)	47	73
19	T	146/182 (80%)	144 (99%)	2 (1%)	59	81
20	U	124/135 (92%)	123 (99%)	1 (1%)	73	88
21	V	180/191 (94%)	180 (100%)	0	100	100
22	W	83/119 (70%)	83 (100%)	0	100	100
23	X	219/229 (96%)	218 (100%)	1 (0%)	81	92
24	Y	159/223 (71%)	157 (99%)	2 (1%)	61	82
25	Z	111/147 (76%)	110 (99%)	1 (1%)	70	87
26	a	78/133 (59%)	77 (99%)	1 (1%)	61	82
27	0	97/164 (59%)	97 (100%)	0	100	100
28	1	49/60 (82%)	49 (100%)	0	100	100
29	2	39/72 (54%)	39 (100%)	0	100	100
30	3	88/166 (53%)	87 (99%)	1 (1%)	65	84
31	4	37/89 (42%)	37 (100%)	0	100	100
32	5	353/368 (96%)	350 (99%)	3 (1%)	73	88
33	6	286/332 (86%)	286 (100%)	0	100	100
34	7	263/303 (87%)	260 (99%)	3 (1%)	65	84
35	8	77/190 (40%)	74 (96%)	3 (4%)	28	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	9	104/112 (93%)	103 (99%)	1 (1%)	68	86
37	b	130/186 (70%)	128 (98%)	2 (2%)	57	80
38	c	250/288 (87%)	249 (100%)	1 (0%)	84	93
39	d	204/271 (75%)	203 (100%)	1 (0%)	81	92
40	e	188/236 (80%)	185 (98%)	3 (2%)	55	79
41	f	114/188 (61%)	112 (98%)	2 (2%)	51	76
42	g	121/148 (82%)	119 (98%)	2 (2%)	53	78
43	h	100/148 (68%)	100 (100%)	0	100	100
44	i	86/110 (78%)	85 (99%)	1 (1%)	63	83
45	j	68/97 (70%)	66 (97%)	2 (3%)	37	65
46	k	80/90 (89%)	79 (99%)	1 (1%)	61	82
47	l	43/116 (37%)	39 (91%)	4 (9%)	8	18
48	m	37/113 (33%)	34 (92%)	3 (8%)	11	24
49	o	68/87 (78%)	67 (98%)	1 (2%)	57	80
50	p	117/180 (65%)	117 (100%)	0	100	100
51	q	115/178 (65%)	114 (99%)	1 (1%)	70	87
52	r	143/169 (85%)	137 (96%)	6 (4%)	26	52
53	s	328/381 (86%)	326 (99%)	2 (1%)	78	91
54	n	179/209 (86%)	178 (99%)	1 (1%)	78	91
55	A1	290/328 (88%)	287 (99%)	3 (1%)	68	86
56	A2	221/350 (63%)	220 (100%)	1 (0%)	81	92
57	v	59/60 (98%)	55 (93%)	4 (7%)	14	32
58	u	120/200 (60%)	120 (100%)	0	100	100
59	t1	40/158 (25%)	40 (100%)	0	100	100
59	t2	29/158 (18%)	29 (100%)	0	100	100
59	t3	29/158 (18%)	29 (100%)	0	100	100
59	t4	28/158 (18%)	28 (100%)	0	100	100
59	t5	28/158 (18%)	28 (100%)	0	100	100
59	t6	26/158 (16%)	26 (100%)	0	100	100
60	w	81/136 (60%)	80 (99%)	1 (1%)	63	83
All	All	8469/11731 (72%)	8388 (99%)	81 (1%)	65	86

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	276	LEU
3	C	278	LYS
3	C	288	THR
3	C	290	ASN
4	D	123	GLU
4	D	208	ARG
8	I	82	LEU
9	J	35	LEU
9	J	114	LEU
10	K	2	SER
11	L	38	VAL
12	M	65	LEU
12	M	132	LEU
12	M	146	ASP
16	Q	101	GLU
17	R	95	VAL
17	R	101	VAL
18	S	104	ARG
18	S	144	LEU
18	S	173	ARG
19	T	163	ARG
19	T	209	VAL
20	U	130	LEU
23	X	109	LEU
24	Y	155	LEU
24	Y	156	LEU
25	Z	78	ARG
26	a	122	ARG
30	3	157	LEU
32	5	55	LEU
32	5	67	VAL
32	5	364	LEU
34	7	165	ASN
34	7	175	ILE
34	7	317	LEU
35	8	104	VAL
35	8	106	LEU
35	8	152	LEU
36	9	114	LEU
37	b	72	VAL
37	b	110	LEU
38	c	171	ARG

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Mol	Chain	Res	Type
39	d	164	VAL
40	e	123	MET
40	e	159	LEU
40	e	173	LEU
41	f	171	LEU
41	f	207	LEU
42	g	90	ARG
42	g	137	VAL
44	i	34	ILE
45	j	88	LEU
45	j	93	LEU
46	k	8	LEU
47	l	106	THR
47	l	110	LEU
47	l	114	SER
47	l	132	LEU
48	m	57	VAL
48	m	63	THR
48	m	75	LEU
49	o	88	ILE
51	q	125	MET
52	r	39	VAL
52	r	56	THR
52	r	70	CYS
52	r	135	LEU
52	r	140	VAL
52	r	159	VAL
53	s	66	TRP
53	s	271	LEU
54	n	235	THR
55	A1	43	LEU
55	A1	297	LEU
55	A1	312	LEU
56	A2	152	LEU
57	v	9	VAL
57	v	53	ARG
57	v	55	LEU
57	v	59	LEU
60	w	144	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (145) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	107	ASN
4	D	252	HIS
4	D	276	HIS
5	E	63	GLN
5	E	125	GLN
5	E	139	ASN
5	E	227	GLN
5	E	237	HIS
5	E	277	ASN
5	E	280	HIS
5	E	281	ASN
5	E	286	ASN
6	F	103	GLN
6	F	105	ASN
6	F	184	GLN
6	F	249	ASN
7	H	126	GLN
7	H	136	ASN
8	I	204	GLN
9	J	48	GLN
9	J	116	HIS
9	J	126	GLN
9	J	133	GLN
10	K	70	ASN
10	K	80	HIS
10	K	94	GLN
10	K	117	HIS
11	L	103	ASN
11	L	143	ASN
12	M	26	ASN
12	M	84	ASN
12	M	99	ASN
12	M	114	GLN
12	M	130	GLN
12	M	170	ASN
12	M	219	ASN
13	N	173	GLN
13	N	202	GLN
14	O	141	HIS
14	O	147	GLN
14	O	150	GLN
14	O	154	GLN
15	P	89	HIS

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Mol	Chain	Res	Type
15	P	147	GLN
15	P	162	GLN
16	Q	139	GLN
16	Q	172	GLN
16	Q	218	ASN
16	Q	258	GLN
16	Q	261	ASN
16	Q	262	GLN
17	R	36	ASN
17	R	89	ASN
17	R	98	ASN
18	S	118	ASN
19	T	62	GLN
19	T	109	ASN
20	U	16	GLN
20	U	55	ASN
20	U	62	ASN
20	U	74	HIS
21	V	84	ASN
22	W	51	GLN
23	X	4	HIS
23	X	89	GLN
23	X	177	HIS
23	X	215	GLN
24	Y	92	ASN
24	Y	99	HIS
24	Y	183	GLN
24	Y	225	ASN
25	Z	67	HIS
25	Z	148	GLN
27	0	140	GLN
28	1	15	ASN
28	1	35	ASN
32	5	119	GLN
32	5	160	HIS
32	5	183	ASN
32	5	195	HIS
32	5	305	GLN
32	5	324	GLN
32	5	358	GLN
32	5	384	GLN
33	6	243	ASN

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Mol	Chain	Res	Type
33	6	275	GLN
33	6	332	HIS
33	6	354	GLN
34	7	247	ASN
34	7	298	GLN
35	8	143	GLN
36	9	90	GLN
37	b	16	HIS
37	b	27	GLN
37	b	90	HIS
37	b	123	ASN
37	b	129	GLN
38	c	42	GLN
38	c	65	ASN
38	c	69	HIS
38	c	128	GLN
38	c	139	GLN
38	c	155	ASN
38	c	172	ASN
38	c	193	GLN
38	c	204	GLN
38	c	236	ASN
38	c	315	ASN
39	d	149	HIS
39	d	154	ASN
40	e	67	GLN
40	e	87	HIS
41	f	153	HIS
43	h	87	GLN
44	i	59	ASN
45	j	31	GLN
46	k	15	GLN
47	l	125	ASN
49	o	96	ASN
51	q	60	GLN
51	q	120	HIS
51	q	157	GLN
52	r	131	HIS
52	r	148	ASN
52	r	184	ASN
53	s	67	GLN
53	s	107	GLN

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Mol	Chain	Res	Type
53	s	179	GLN
53	s	382	GLN
53	s	386	ASN
53	s	420	GLN
53	s	427	ASN
55	A1	55	GLN
55	A1	85	HIS
55	A1	230	GLN
55	A1	263	HIS
55	A1	290	GLN
55	A1	316	GLN
55	A1	317	ASN
55	A1	343	HIS
56	A2	158	GLN
56	A2	192	GLN
56	A2	217	HIS
59	t2	8	GLN
59	t5	5	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1434/1559 (91%)	362 (25%)	47 (3%)
2	B	56/69 (81%)	13 (23%)	2 (3%)
All	All	1490/1628 (91%)	375 (25%)	49 (3%)

All (375) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1672	C
1	A	1678	C
1	A	1679	U
1	A	1681	G
1	A	1685	C
1	A	1689	C
1	A	1692	A
1	A	1693	C
1	A	1694	U
1	A	1699	C
1	A	1700	U
1	A	1704	U

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Mol	Chain	Res	Type
1	A	1708	A
1	A	1714	C
1	A	1715	C
1	A	1724	A
1	A	1727	A
1	A	1728	U
1	A	1734	C
1	A	1735	A
1	A	1736	A
1	A	1737	A
1	A	1748	G
1	A	1762	A
1	A	1763	A
1	A	1764	C
1	A	1765	C
1	A	1767	G
1	A	1770	G
1	A	1777	A
1	A	1794	A
1	A	1803	A
1	A	1804	A
1	A	1805	A
1	A	1812	C
1	A	1817	C
1	A	1821	A
1	A	1827	C
1	A	1828	A
1	A	1829	A
1	A	1832	A
1	A	1836	A
1	A	1844	A
1	A	1850	U
1	A	1851	G
1	A	1853	A
1	A	1854	U
1	A	1855	A
1	A	1856	A
1	A	1867	A
1	A	1869	A
1	A	1871	A
1	A	1872	U
1	A	1878	U

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Mol	Chain	Res	Type
1	A	1882	A
1	A	1883	G
1	A	1887	A
1	A	1888	G
1	A	1893	A
1	A	1901	C
1	A	1903	C
1	A	1909	A
1	A	1918	G
1	A	1936	A
1	A	1937	A
1	A	1938	A
1	A	1939	G
1	A	1940	A
1	A	1944	C
1	A	1946	C
1	A	1974	A
1	A	1975	U
1	A	1985	G
1	A	1986	A
1	A	1992	C
1	A	1994	A
1	A	1995	A
1	A	2000	C
1	A	2001	C
1	A	2002	G
1	A	2015	G
1	A	2021	U
1	A	2022	G
1	A	2023	U
1	A	2029	A
1	A	2030	U
1	A	2036	C
1	A	2037	U
1	A	2039	A
1	A	2060	A
1	A	2061	C
1	A	2065	A
1	A	2070	C
1	A	2071	U
1	A	2074	A
1	A	2079	C

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Mol	Chain	Res	Type
1	A	2085	A
1	A	2092	C
1	A	2093	U
1	A	2098	G
1	A	2108	G
1	A	2110	A
1	A	2111	C
1	A	2112	A
1	A	2126	U
1	A	2131	A
1	A	2135	A
1	A	2136	C
1	A	2142	A
1	A	2147	G
1	A	2154	A
1	A	2158	U
1	A	2159	U
1	A	2163	A
1	A	2164	C
1	A	2168	U
1	A	2172	A
1	A	2173	G
1	A	2175	C
1	A	2179	A
1	A	2181	A
1	A	2182	G
1	A	2183	C
1	A	2187	C
1	A	2189	C
1	A	2192	A
1	A	2194	U
1	A	2197	G
1	A	2198	A
1	A	2199	A
1	A	2200	A
1	A	2210	C
1	A	2211	U
1	A	2220	A
1	A	2221	C
1	A	2222	U
1	A	2228	A
1	A	2233	U

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Mol	Chain	Res	Type
1	A	2237	A
1	A	2239	A
1	A	2241	A
1	A	2242	U
1	A	2243	A
1	A	2244	U
1	A	2245	A
1	A	2246	A
1	A	2262	C
1	A	2263	C
1	A	2264	A
1	A	2284	C
1	A	2285	U
1	A	2297	A
1	A	2300	G
1	A	2322	C
1	A	2324	U
1	A	2332	C
1	A	2345	G
1	A	2357	C
1	A	2359	C
1	A	2360	U
1	A	2361	G
1	A	2362	A
1	A	2363	A
1	A	2364	C
1	A	2369	A
1	A	2371	U
1	A	2374	A
1	A	2381	A
1	A	2390	A
1	A	2401	A
1	A	2404	U
1	A	2405	C
1	A	2406	A
1	A	2407	U
1	A	2415	C
1	A	2416	U
1	A	2418	A
1	A	2427	C
1	A	2434	A
1	A	2444	A

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Mol	Chain	Res	Type
1	A	2446	A
1	A	2451	A
1	A	2452	A
1	A	2457	A
1	A	2458	A
1	A	2478	G
1	A	2493	C
1	A	2500	A
1	A	2502	C
1	A	2507	A
1	A	2511	C
1	A	2520	C
1	A	2521	A
1	A	2523	C
1	A	2524	A
1	A	2527	A
1	A	2530	A
1	A	2531	U
1	A	2536	G
1	A	2539	A
1	A	2540	C
1	A	2547	C
1	A	2548	C
1	A	2549	C
1	A	2550	A
1	A	2551	G
1	A	2552	U
1	A	2603	C
1	A	2604	A
1	A	2605	C
1	A	2606	U
1	A	2607	U
1	A	2611	C
1	A	2615	A
1	A	2617	A
1	A	2619	A
1	A	2621	G
1	A	2626	U
1	A	2628	U
1	A	2629	A
1	A	2630	U
1	A	2633	A

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Mol	Chain	Res	Type
1	A	2634	U
1	A	2638	U
1	A	2643	G
1	A	2644	A
1	A	2645	G
1	A	2654	U
1	A	2655	G
1	A	2656	U
1	A	2660	U
1	A	2683	C
1	A	2684	C
1	A	2686	G
1	A	2693	A
1	A	2694	A
1	A	2696	A
1	A	2698	G
1	A	2699	C
1	A	2706	A
1	A	2709	A
1	A	2718	C
1	A	2719	G
1	A	2722	A
1	A	2724	G
1	A	2732	G
1	A	2733	G
1	A	2739	U
1	A	2740	A
1	A	2744	U
1	A	2745	A
1	A	2756	C
1	A	2803	A
1	A	2804	A
1	A	2810	G
1	A	2814	G
1	A	2815	G
1	A	2816	G
1	A	2829	C
1	A	2831	G
1	A	2832	A
1	A	2833	A
1	A	2854	U
1	A	2861	A

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Mol	Chain	Res	Type
1	A	2864	U
1	A	2865	C
1	A	2889	C
1	A	2893	A
1	A	2895	U
1	A	2906	C
1	A	2913	A
1	A	2915	C
1	A	2916	G
1	A	2917	G
1	A	2918	A
1	A	2922	A
1	A	2926	A
1	A	2928	C
1	A	2935	A
1	A	2936	U
1	A	2937	A
1	A	2938	A
1	A	2939	C
1	A	2941	G
1	A	2942	C
1	A	2943	G
1	A	2944	C
1	A	2945	A
1	A	2956	A
1	A	2962	C
1	A	2963	A
1	A	2965	A
1	A	2982	C
1	A	2989	G
1	A	2990	A
1	A	2991	U
1	A	2992	G
1	A	2993	U
1	A	2995	G
1	A	3000	A
1	A	3005	A
1	A	3016	G
1	A	3018	A
1	A	3022	G
1	A	3038	U
1	A	3042	U

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Mol	Chain	Res	Type
1	A	3043	C
1	A	3044	A
1	A	3049	U
1	A	3051	A
1	A	3053	A
1	A	3054	G
1	A	3056	C
1	A	3059	A
1	A	3060	C
1	A	3061	G
1	A	3063	G
1	A	3068	G
1	A	3069	A
1	A	3086	U
1	A	3089	A
1	A	3090	G
1	A	3097	U
1	A	3100	U
1	A	3102	U
1	A	3108	U
1	A	3109	U
1	A	3110	C
1	A	3111	A
1	A	3112	A
1	A	3113	A
1	A	3114	U
1	A	3122	U
1	A	3123	G
1	A	3124	U
1	A	3140	A
1	A	3141	A
1	A	3150	U
1	A	3151	A
1	A	3157	C
1	A	3158	A
1	A	3162	C
1	A	3168	C
1	A	3169	C
1	A	3172	C
1	A	3173	G
1	A	3180	A
1	A	3184	C

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Mol	Chain	Res	Type
1	A	3189	C
1	A	3190	A
1	A	3199	U
1	A	3200	U
1	A	3201	A
1	A	3207	A
1	A	3208	C
1	A	3209	A
1	A	3211	C
1	A	3212	C
1	A	3217	A
1	A	3218	A
1	A	3220	A
1	A	3228	U
2	B	1608	G
2	B	1609	U
2	B	1610	A
2	B	1611	G
2	B	1615	A
2	B	1617	C
2	B	1620	A
2	B	1621	A
2	B	1634	A
2	B	1644	G
2	B	1645	A
2	B	1651	A
2	B	1669	G

All (49) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1736	A
1	A	1811	A
1	A	1853	A
1	A	1855	A
1	A	1871	A
1	A	1888	G
1	A	1936	A
1	A	1973	G
1	A	1974	A
1	A	1994	A
1	A	2021	U

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Mol	Chain	Res	Type
1	A	2029	A
1	A	2065	A
1	A	2135	A
1	A	2160	A
1	A	2182	G
1	A	2186	C
1	A	2209	G
1	A	2219	C
1	A	2220	A
1	A	2245	A
1	A	2359	C
1	A	2361	G
1	A	2363	A
1	A	2457	A
1	A	2506	A
1	A	2530	A
1	A	2548	C
1	A	2605	C
1	A	2620	G
1	A	2628	U
1	A	2643	G
1	A	2653	C
1	A	2660	U
1	A	2698	G
1	A	2744	U
1	A	2815	G
1	A	2905	A
1	A	2938	A
1	A	2943	G
1	A	2988	C
1	A	2989	G
1	A	2991	U
1	A	2992	G
1	A	3041	U
1	A	3059	A
1	A	3123	G
2	B	1607	U
2	B	1620	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	$\# Z > 2$
1	OMG	A	3040	1	23,26,27	1.23	3 (13%)	32,38,41	2.12	8 (25%)

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
1	OMG	A	3040	1	-	1/9/27/28	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	3040	OMG	C5-C4	3.38	1.48	1.38
1	A	3040	OMG	C6-N1	-2.15	1.34	1.38
1	A	3040	OMG	C5-N7	-2.07	1.34	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3040	OMG	C5-C4-N3	-6.39	118.22	128.39
1	A	3040	OMG	C2-N3-C4	5.33	121.48	112.30
1	A	3040	OMG	N9-C4-N3	4.71	135.36	125.95
1	A	3040	OMG	C6-C5-N7	3.25	136.20	130.29
1	A	3040	OMG	C4-C5-N7	-2.56	106.62	110.67
1	A	3040	OMG	O2'-C2'-C1'	2.27	113.30	108.99
1	A	3040	OMG	C2'-C1'-N9	-2.10	110.25	114.24
1	A	3040	OMG	O6-C6-C5	-2.10	120.99	126.53

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	3040	OMG	C1'-C2'-O2'-CM2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	3040	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 109 ligands modelled in this entry, 106 are monoatomic - leaving 3 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	$\# Z > 2$
63	GDP	C	401	-	29,30,30	1.14	3 (10%)	45,47,47	1.79	5 (11%)
65	SAM	A1	401	-	27,29,29	0.49	1 (3%)	34,42,42	0.71	1 (2%)
66	PNS	w	201	60	14,20,21	0.35	0	18,26,29	0.78	0

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
63	GDP	C	401	-	-	3/16/32/32	0/3/3/3
65	SAM	A1	401	-	-	5/17/33/33	0/3/3/3
66	PNS	w	201	60	-	12/24/26/27	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
63	C	401	GDP	C5-C4	3.13	1.47	1.38
63	C	401	GDP	C6-N1	-2.40	1.34	1.38
65	A1	401	SAM	OXT-C	-2.18	1.23	1.30
63	C	401	GDP	C5-N7	-2.05	1.35	1.39

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
63	C	401	GDP	C5-C4-N3	-6.08	118.71	128.39
63	C	401	GDP	C2-N3-C4	5.01	120.92	112.30
63	C	401	GDP	N9-C4-N3	4.40	134.75	125.95
63	C	401	GDP	C6-C5-N7	3.40	136.49	130.29
65	A1	401	SAM	OXT-C-O	-2.88	117.55	124.08
63	C	401	GDP	C4-C5-N7	-2.82	106.19	110.67

There are no chirality outliers.

All (20) torsion outliers are listed below:

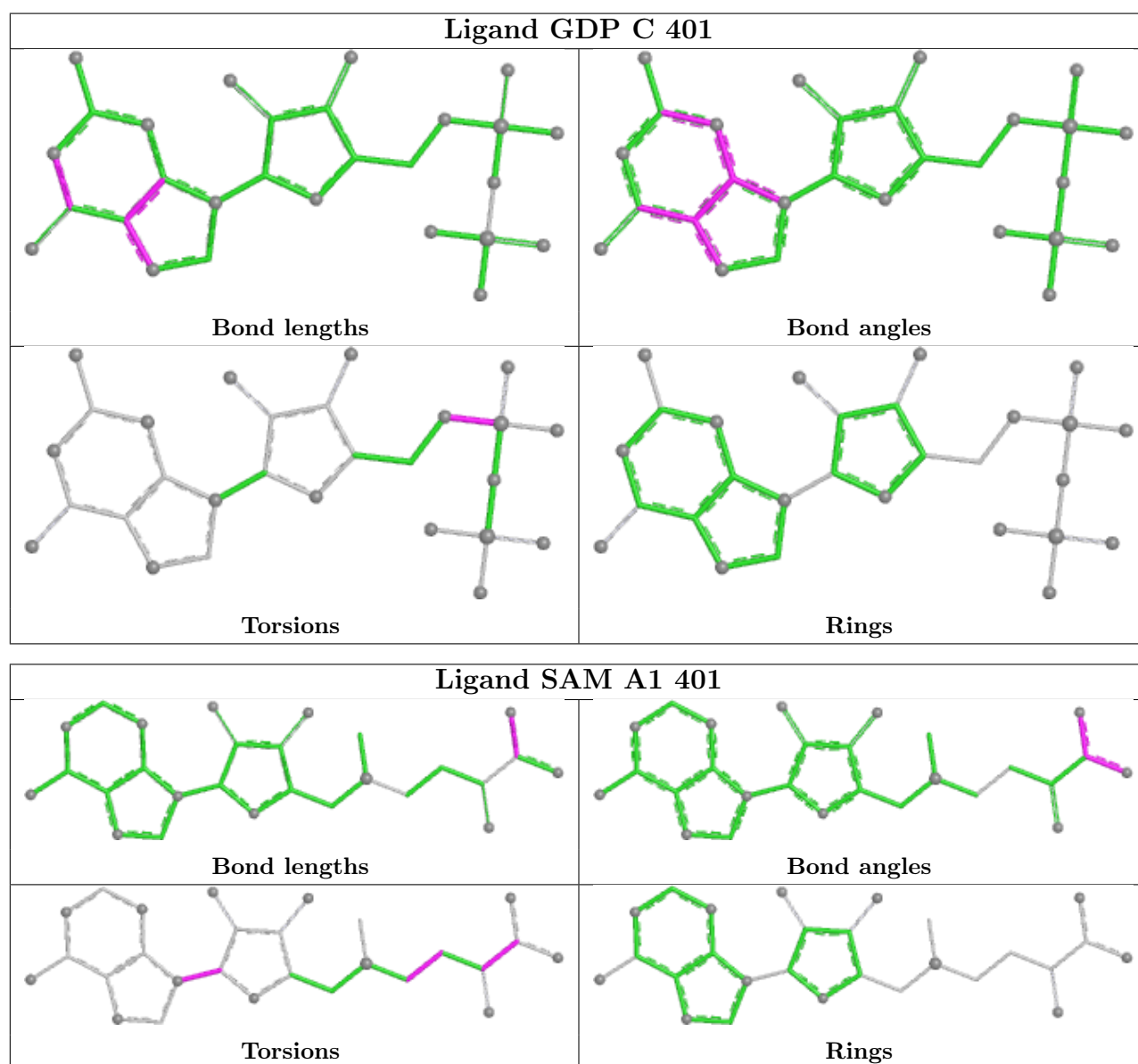
Mol	Chain	Res	Type	Atoms
63	C	401	GDP	C5'-O5'-PA-O3A
63	C	401	GDP	C5'-O5'-PA-O1A
63	C	401	GDP	C5'-O5'-PA-O2A
66	w	201	PNS	C28-C29-C32-O33
66	w	201	PNS	C28-C29-C32-C34
66	w	201	PNS	C30-C29-C32-C34
66	w	201	PNS	C31-C29-C32-O33
66	w	201	PNS	C31-C29-C32-C34
66	w	201	PNS	O33-C32-C34-O35
66	w	201	PNS	C32-C34-N36-C37
66	w	201	PNS	C38-C39-N41-C42
66	w	201	PNS	O35-C34-N36-C37
66	w	201	PNS	O40-C39-N41-C42
65	A1	401	SAM	C2'-C1'-N9-C8
65	A1	401	SAM	CA-CB-CG-SD
65	A1	401	SAM	O4'-C1'-N9-C8
66	w	201	PNS	C30-C29-C32-O33
65	A1	401	SAM	C2'-C1'-N9-C4
66	w	201	PNS	O33-C32-C34-N36
65	A1	401	SAM	OXT-C-CA-N

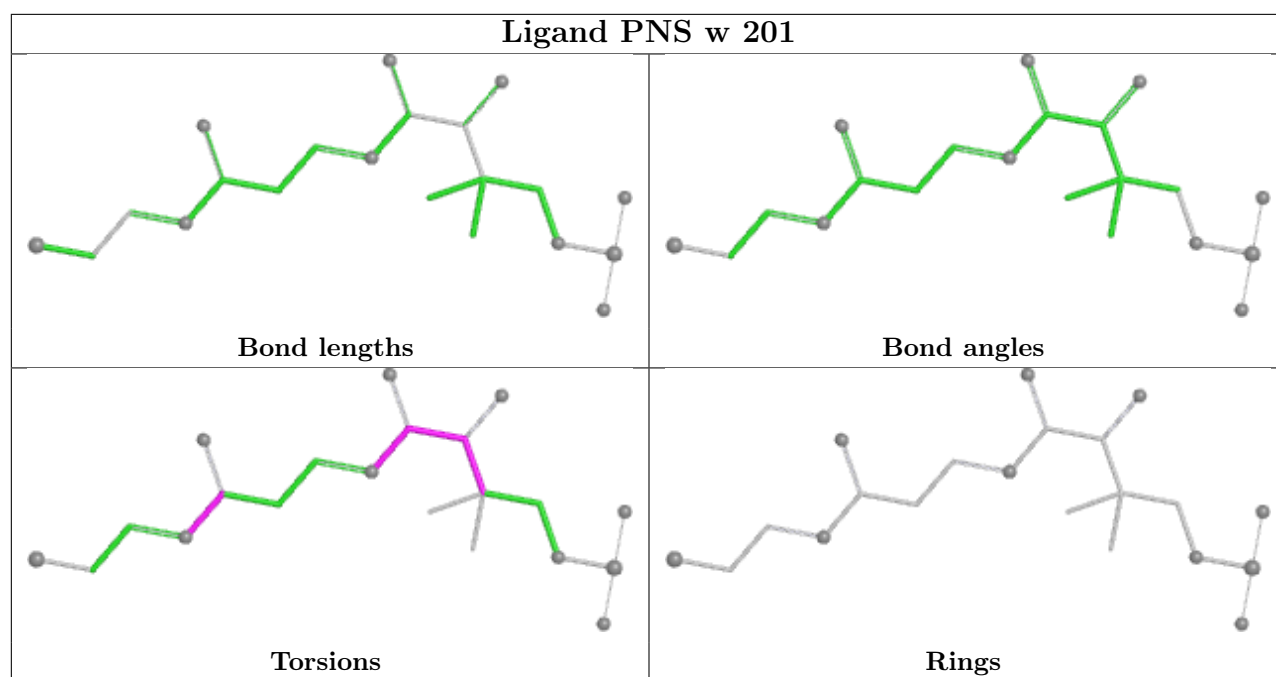
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	w	201	PNS	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.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

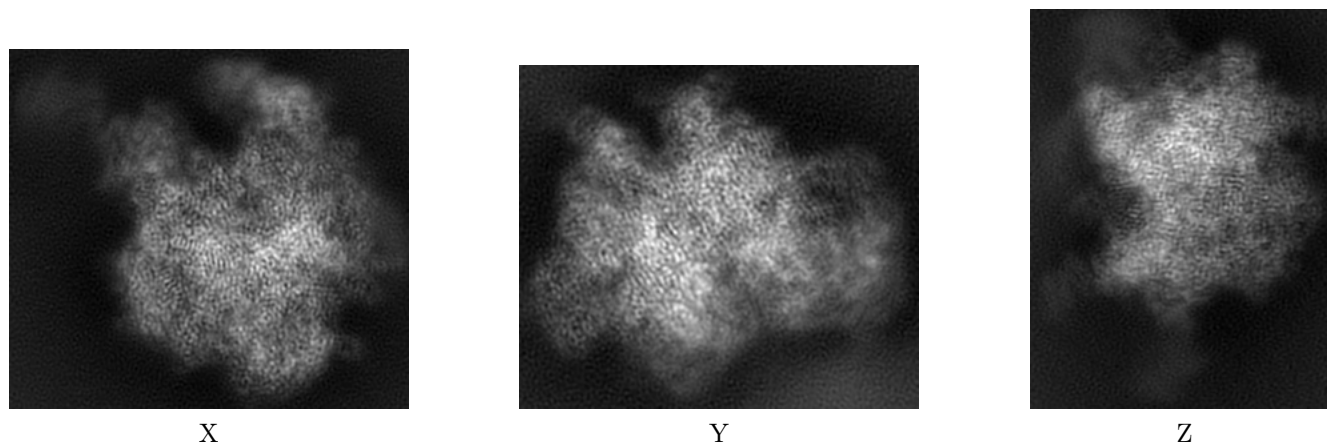
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12764. These allow visual inspection of the internal detail of the map and identification of artifacts.

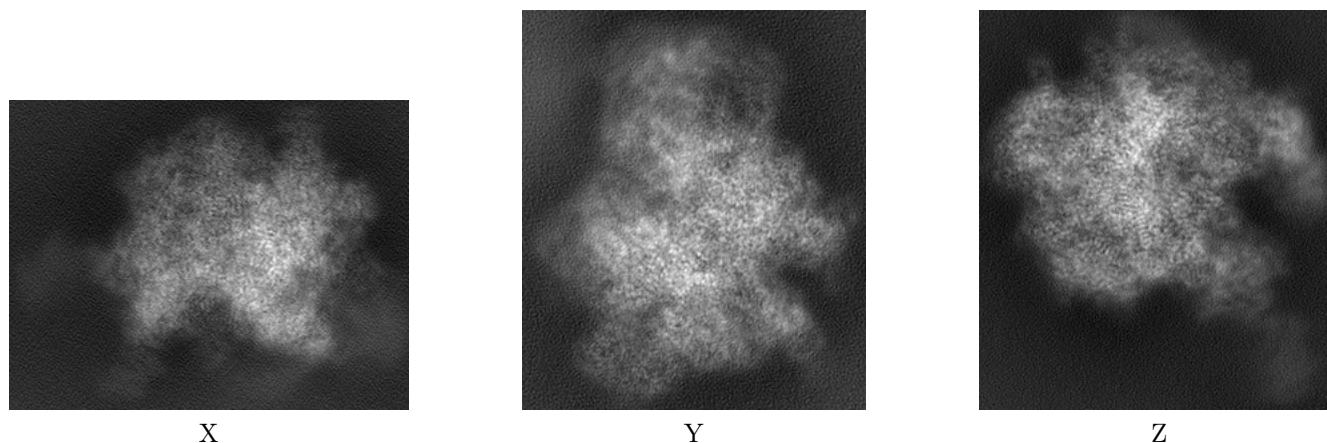
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



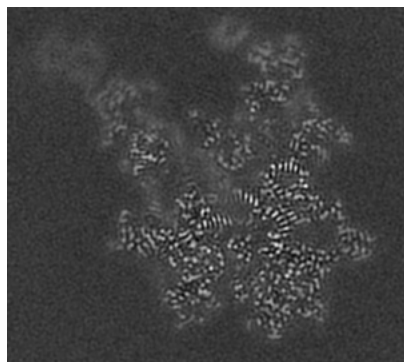
6.1.2 Raw map



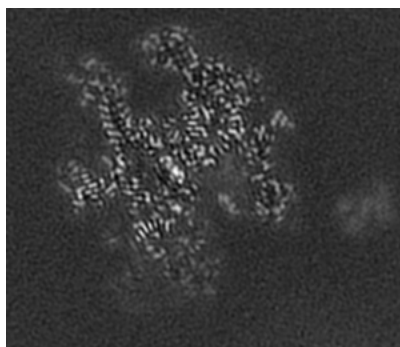
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

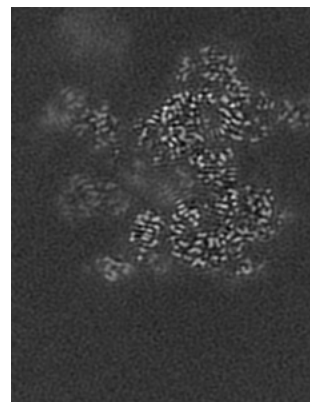
6.2.1 Primary map



X Index: 105

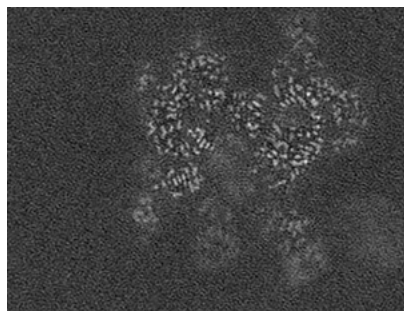


Y Index: 137

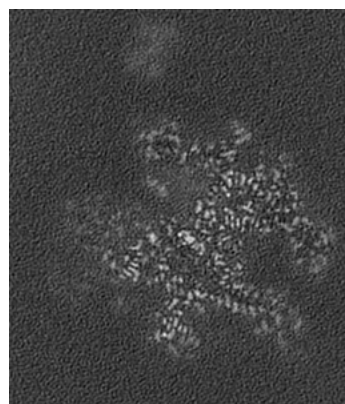


Z Index: 123

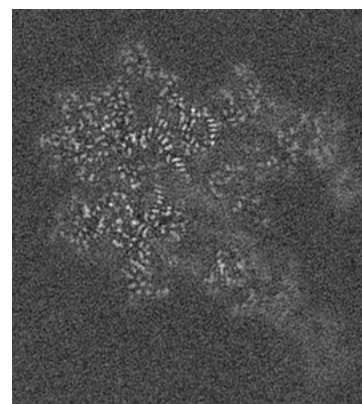
6.2.2 Raw map



X Index: 123



Y Index: 137

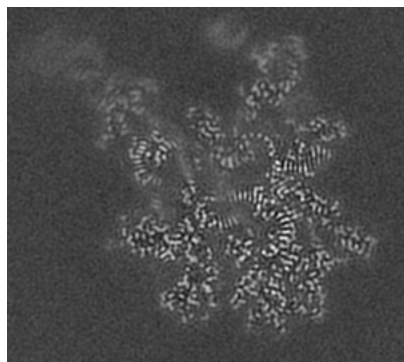


Z Index: 105

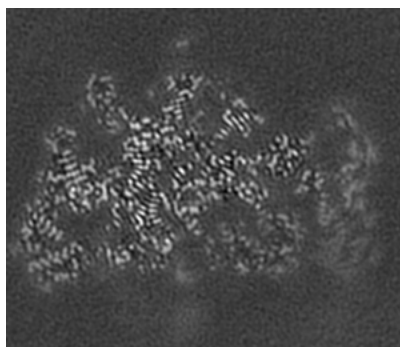
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

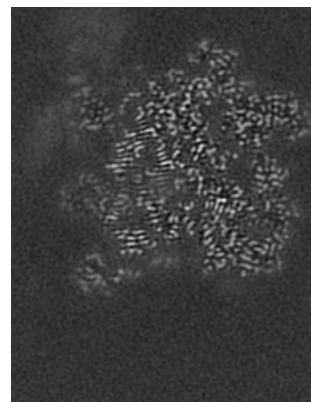
6.3.1 Primary map



X Index: 102

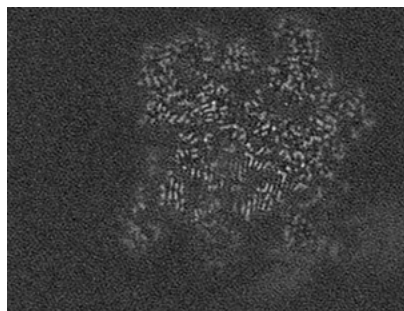


Y Index: 181

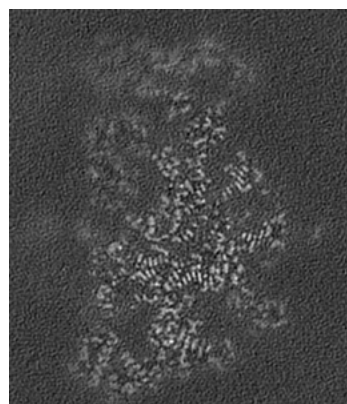


Z Index: 114

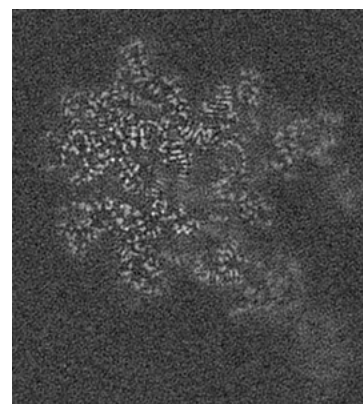
6.3.2 Raw map



X Index: 114



Y Index: 181

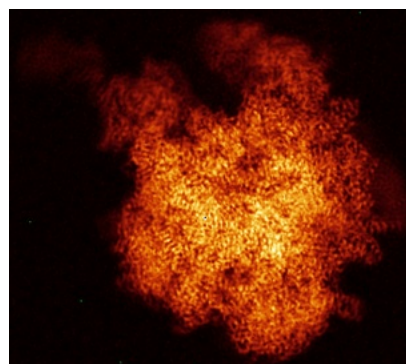


Z Index: 101

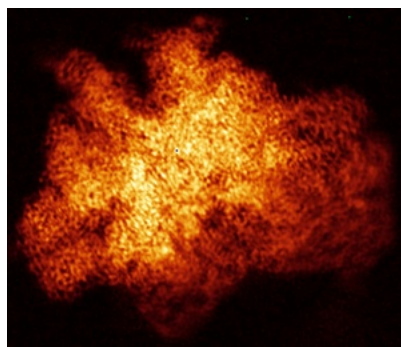
The images above show the largest variance slices of the map in three orthogonal directions.

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

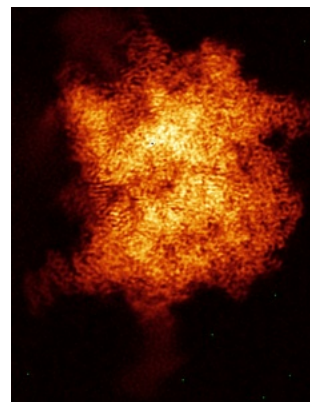
6.4.1 Primary map



X

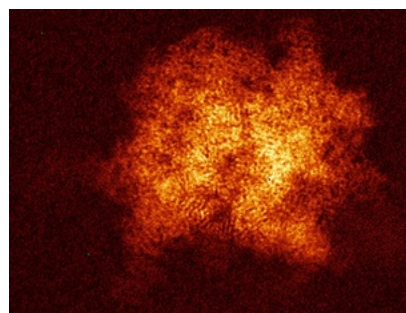


Y

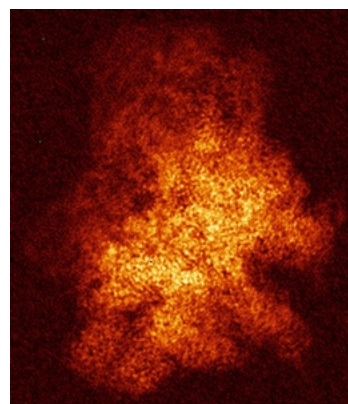


Z

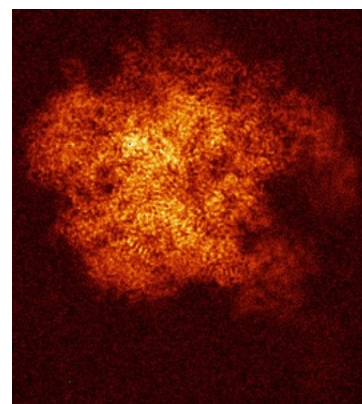
6.4.2 Raw map



X



Y

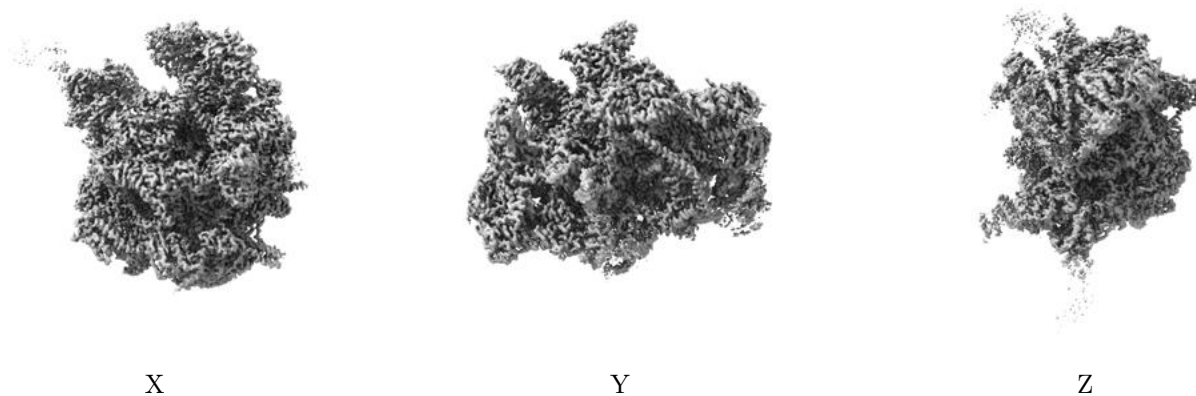


Z

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

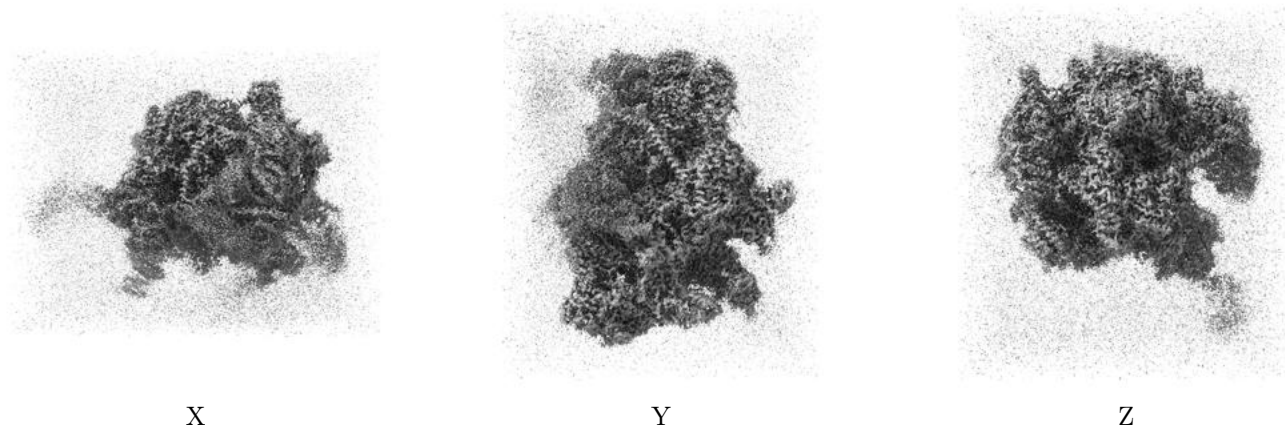
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

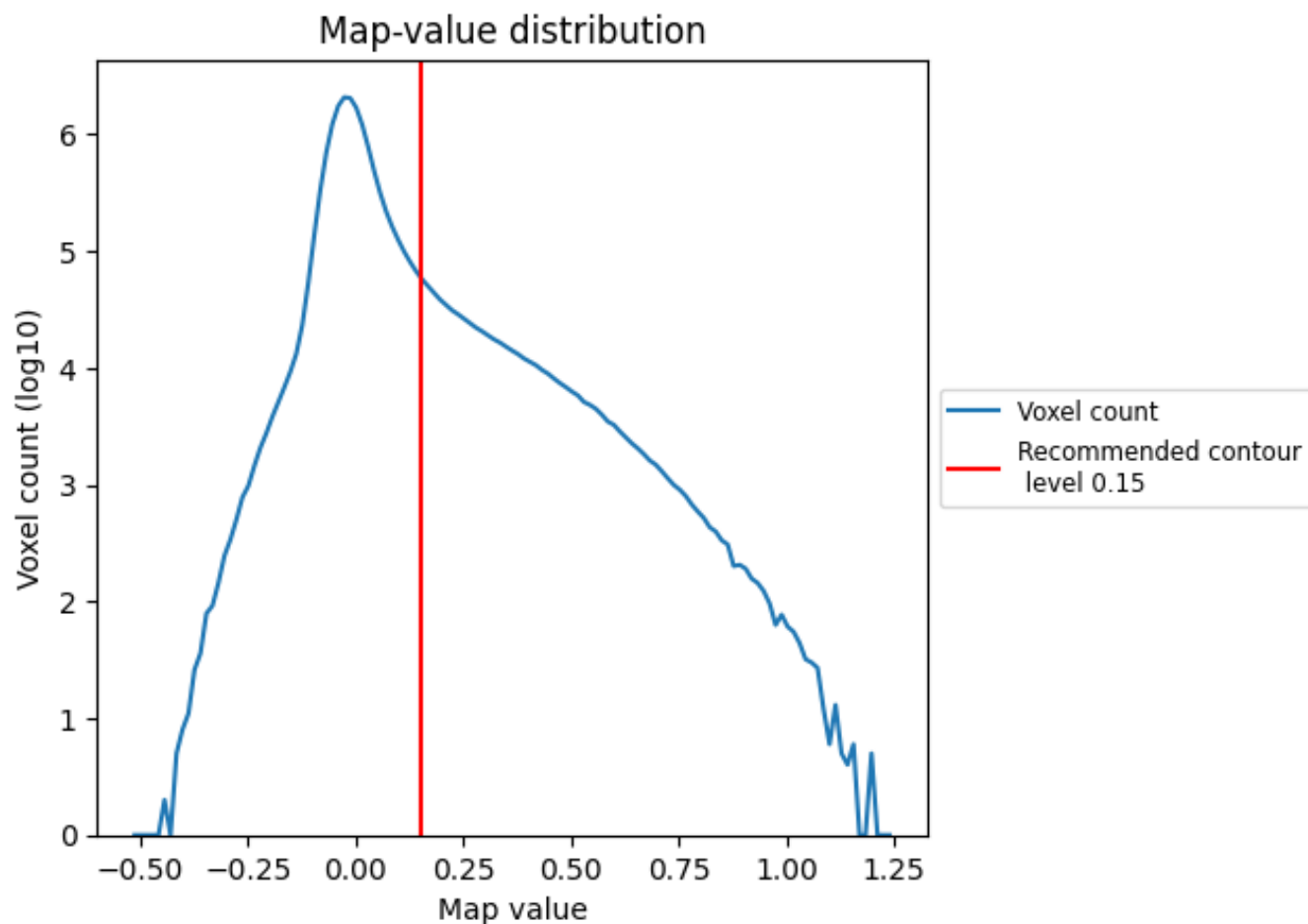
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

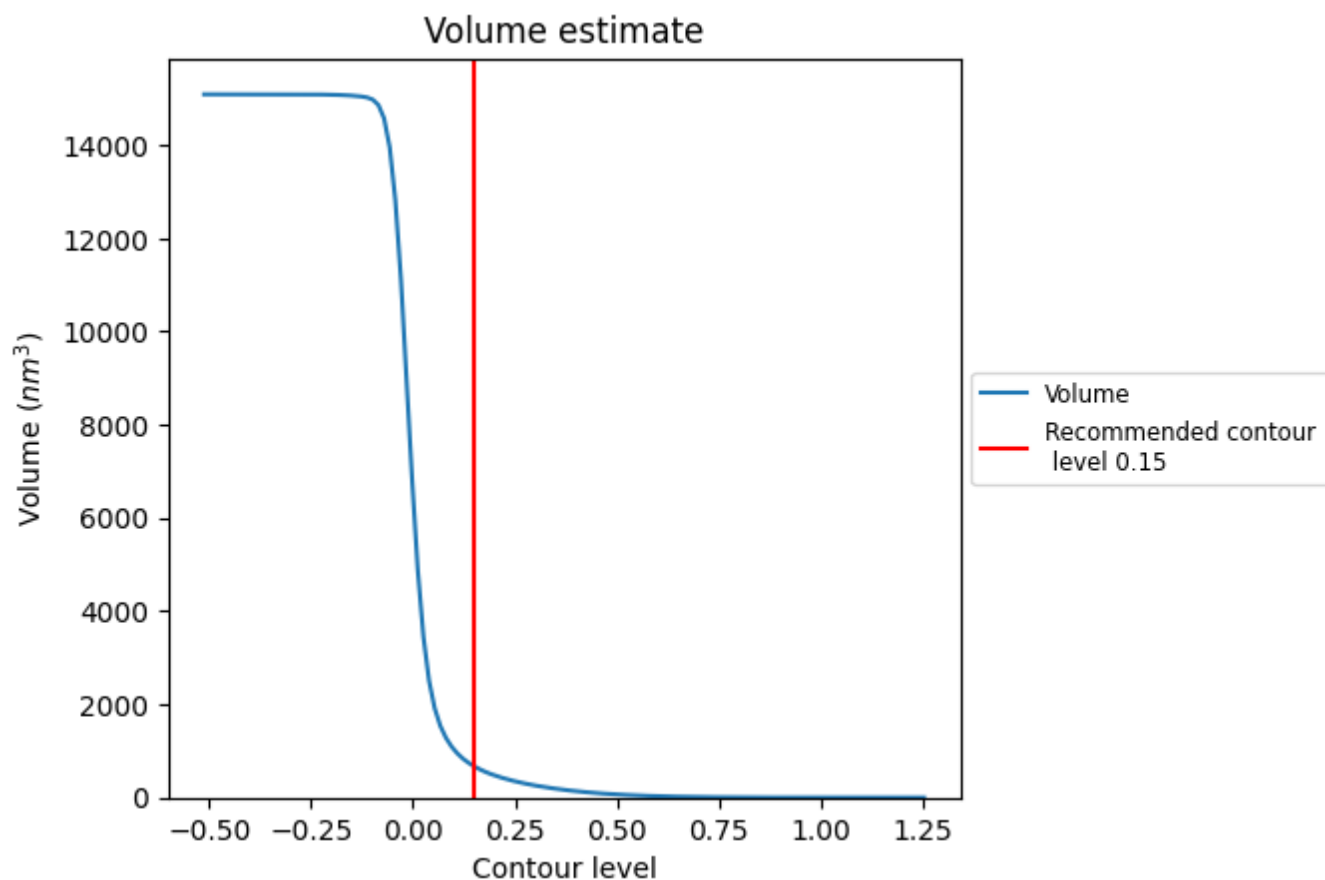
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

7.2 Volume estimate [i](#)



The volume at the recommended contour level is 671 nm³; this corresponds to an approximate mass of 606 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)

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

8 Fourier-Shell correlation ⓘ

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

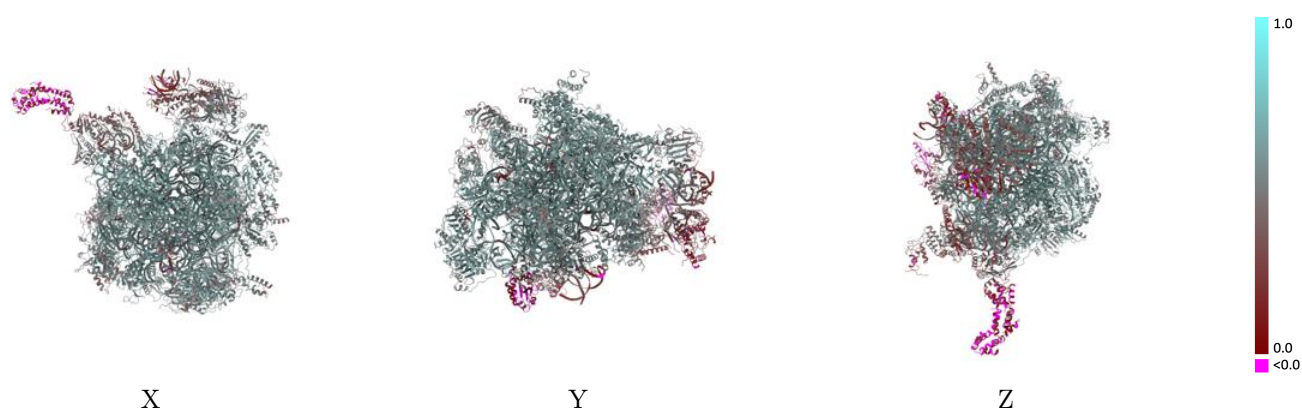
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12764 and PDB model 7O9M. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)

This section was not generated.

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

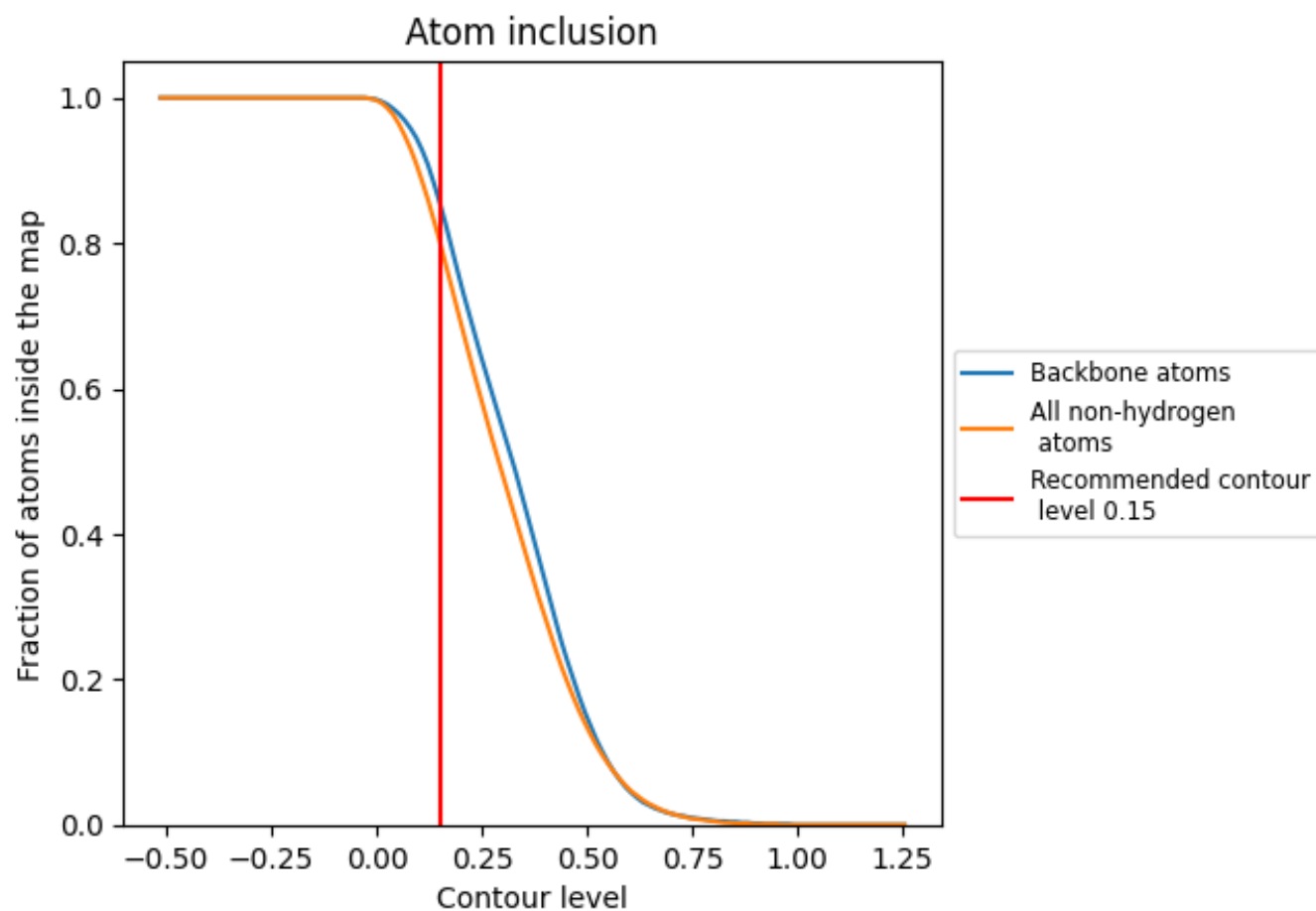


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8030	 0.5200
0	 0.8640	 0.5660
1	 0.8210	 0.5560
2	 0.9740	 0.6290
3	 0.9540	 0.6120
4	 0.9170	 0.6030
5	 0.8650	 0.5590
6	 0.7810	 0.4920
7	 0.7830	 0.5180
8	 0.3910	 0.2560
9	 0.8300	 0.5560
A	 0.9370	 0.5640
A1	 0.7350	 0.5280
A2	 0.7040	 0.4950
B	 0.7660	 0.3510
C	 0.0400	 0.1520
D	 0.8710	 0.5690
E	 0.8980	 0.5820
F	 0.9070	 0.5880
H	 0.7750	 0.5140
I	 0.4740	 0.3300
J	 0.3600	 0.2510
K	 0.9290	 0.5980
L	 0.8710	 0.5710
M	 0.9090	 0.5830
N	 0.8090	 0.5500
O	 0.8990	 0.5900
P	 0.8350	 0.5340
Q	 0.8560	 0.5670
R	 0.9190	 0.5940
S	 0.9010	 0.5880
T	 0.9180	 0.5960
U	 0.8880	 0.5780
UNK	 0.2850	 0.2430
V	 0.7450	 0.5060



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Chain	Atom inclusion	Q-score
W	 0.9250	 0.5930
X	 0.8400	 0.5550
Y	 0.8720	 0.5770
Z	 0.9010	 0.5930
a	 0.8860	 0.5800
b	 0.9200	 0.5940
c	 0.8110	 0.5460
d	 0.7490	 0.5080
e	 0.1970	 0.1870
f	 0.5390	 0.3900
g	 0.8990	 0.5760
h	 0.7840	 0.5250
i	 0.9360	 0.6050
j	 0.8290	 0.5630
k	 0.6640	 0.4360
l	 0.6410	 0.4200
m	 0.1800	 0.2060
n	 0.4930	 0.4950
o	 0.9010	 0.5850
p	 0.7490	 0.5070
q	 0.7550	 0.5150
r	 0.8740	 0.5600
s	 0.8910	 0.5790
t1	 0.0680	 0.0990
t2	 0.0500	 0.1070
t3	 0.0000	 0.0380
t4	 0.0000	 0.0660
t5	 0.0000	 0.0150
t6	 0.0000	 0.0170
u	 0.6970	 0.5090
v	 0.5950	 0.4160
w	 0.1510	 0.2180