



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 04:47 PM UTC

PDB ID : 7O9K / pdb_00007o9k
EMDB ID : EMD-12763
Title : Human mitochondrial ribosome large subunit assembly intermediate with MTERF4-NSUN4, MRM2, MTG1, the MALSU module, GTPBP5 and mtEF-Tu
Authors : Valentin Gese, G.; Hallberg, B.M.
Deposited on : 2021-04-16
Resolution : 3.10 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:

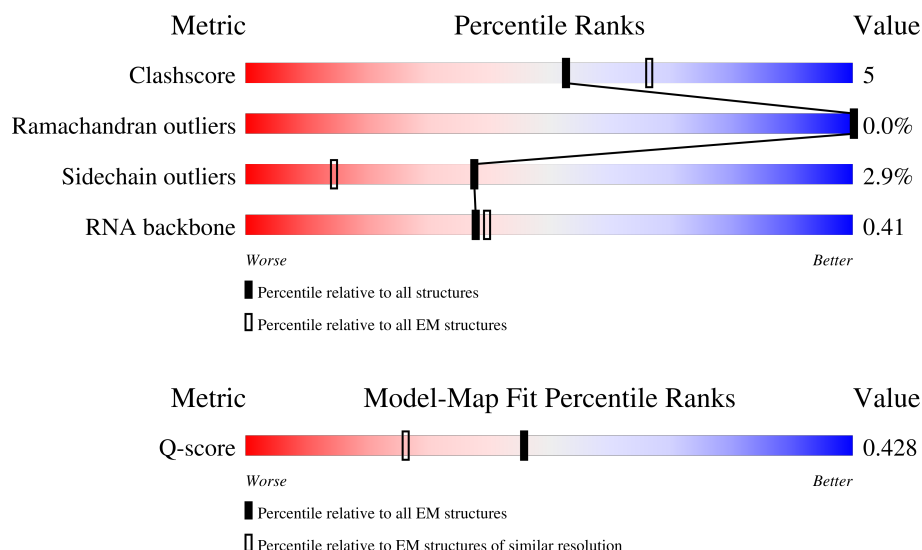
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	0	188	
2	a	142	

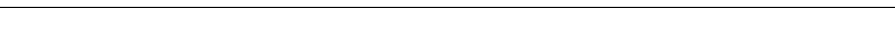
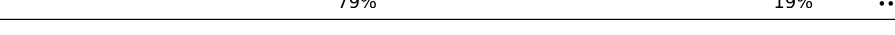
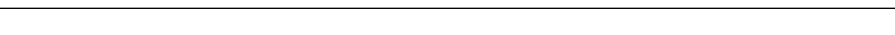
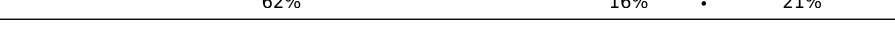
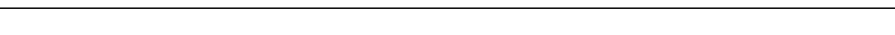
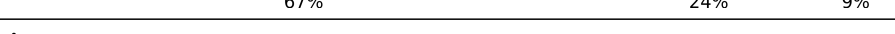
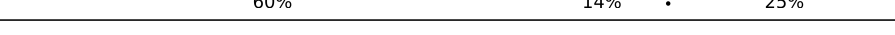
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Mol	Chain	Length	Quality of chain
3	1	65	
4	2	92	
5	3	188	
6	4	103	
7	5	423	
8	6	380	
9	7	338	
10	8	206	
11	9	137	
12	A	1559	
13	A1	384	
14	B	69	
15	A2	381	
16	C	334	
17	D	305	
18	E	348	
19	F	311	
20	FF	198	
20	t1	198	
20	t2	198	
20	t3	198	
20	t4	198	
20	t5	198	
20	t6	198	
21	G	414	

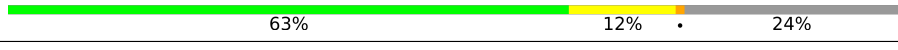
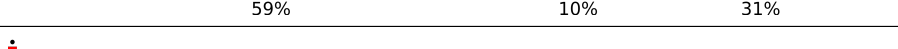
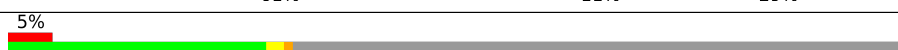
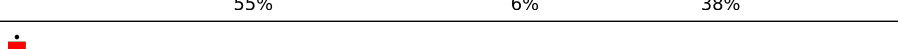
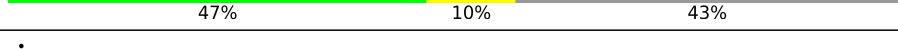
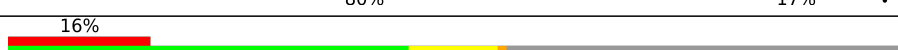
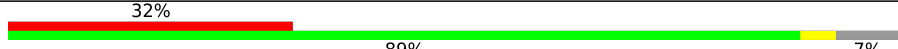
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Mol	Chain	Length	Quality of chain
22	H	267	
23	I	261	
24	J	192	
25	K	178	
26	L	145	
27	M	296	
28	N	251	
29	O	175	
30	P	179	
31	Q	292	
32	R	149	
33	S	205	
34	T	212	
35	U	153	
36	V	216	
37	W	148	
38	X	256	
39	Y	250	
40	Z	161	
41	b	215	
42	c	332	
43	d	306	
44	e	279	
45	f	212	
46	g	166	

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Mol	Chain	Length	Quality of chain
47	h	158	
48	i	128	
49	j	123	
50	k	112	
51	l	138	
52	m	128	
53	n	246	
54	o	102	
55	p	206	
56	q	222	
57	r	196	
58	s	439	
59	t	452	
60	u	234	
61	v	70	
62	w	156	
63	UNK	28	

2 Entry composition

There are 70 unique types of molecules in this entry. The entry contains 115679 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 2 is a protein called 39S ribosomal protein L42, mitochondrial.

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

- Molecule 3 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 4 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	2	45	Total	C	N	O	S	0	0
			367	227	81	58	1		

- Molecule 5 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 6 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 7 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	5	392	Total	C	N	O	S	0	0
			3199	2067	558	563	11		

- Molecule 8 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	6	331	Total	C	N	O	S	0	0
			2692	1723	480	480	9		

- Molecule 9 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	7	290	Total	C	N	O	S	0	0
			2356	1509	400	429	18		

- Molecule 10 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	8	85	Total	C	N	O	S	0	0
			719	454	129	134	2		

- Molecule 11 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	9	123	Total	C	N	O	S	0	0
			992	642	169	179	2		

- Molecule 12 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	A	1436	Total	C	N	O	P	0	0
			30486	13680	5498	9872	1436		

- Molecule 13 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A1	344	Total	C	N	O	S	0	0
			2731	1743	476	495	17		

- Molecule 14 is a RNA chain called MT-TRNAVAL.

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

- Molecule 15 is a protein called Transcription termination factor 4, mitochondrial.

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

- Molecule 16 is a protein called Mitochondrial ribosome-associated GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	C	255	Total	C	N	O	S	0	0
			1990	1267	349	360	14		

- Molecule 17 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D	237	Total	C	N	O	S	0	0
			1851	1151	375	316	9		

- Molecule 18 is a protein called 39S ribosomal protein L3, mitochondrial.

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

- Molecule 19 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 20 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	FF	70	Total	C	N	O	0	0
			540	348	92	100		
20	t1	46	Total	C	N	O	0	0
			354	228	56	70		
20	t2	30	Total	C	N	O	0	0
			238	154	38	46		

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Mol	Chain	Residues	Atoms				AltConf	Trace
20	t3	30	Total	C	N	O	0	0
			238	154	38	46		
20	t4	29	Total	C	N	O	0	0
			229	148	36	45		
20	t5	29	Total	C	N	O	0	0
			229	148	36	45		
20	t6	27	Total	C	N	O	0	0
			214	137	34	43		

- Molecule 21 is a protein called Mitochondrial ribosome-associated GTPase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	G	337	Total	C	N	O	S	0	0
			2549	1608	466	467	8		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	407	ASP	-	expression tag	UNP Q9H4K7
G	408	TYR	-	expression tag	UNP Q9H4K7
G	409	LYS	-	expression tag	UNP Q9H4K7
G	410	ASP	-	expression tag	UNP Q9H4K7
G	411	ASP	-	expression tag	UNP Q9H4K7
G	412	ASP	-	expression tag	UNP Q9H4K7
G	413	ASP	-	expression tag	UNP Q9H4K7
G	414	LYS	-	expression tag	UNP Q9H4K7

- Molecule 22 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	H	95	Total	C	N	O	0	0
			784	498	152	134		

- Molecule 23 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	I	212	Total	C	N	O	S	0	0
			1695	1088	304	292	11		

- Molecule 24 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	J	138	Total	C	N	O	S	0	0
			1050	673	190	185	2		

- Molecule 25 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 26 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 27 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 28 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	N	179	Total	C	N	O	S	0	0
			1457	930	267	251	9		

- Molecule 29 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 30 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

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

- Molecule 31 is a protein called 39S ribosomal protein L19, mitochondrial.

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

- Molecule 32 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 33 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 34 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 35 is a protein called 39S ribosomal protein L23, mitochondrial.

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

- Molecule 36 is a protein called 39S ribosomal protein L24, mitochondrial.

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

- Molecule 37 is a protein called 39S ribosomal protein L27, mitochondrial.

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

- Molecule 38 is a protein called 39S ribosomal protein L28, mitochondrial.

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

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

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

- Molecule 40 is a protein called 39S ribosomal protein L30, mitochondrial.

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

- Molecule 41 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 42 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	c	275	Total	C	N	O	S	0	0
			2217	1415	383	410	9		

- Molecule 43 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	d	223	Total	C	N	O	S	0	0
			1847	1187	317	330	13		

- Molecule 44 is a protein called 39S ribosomal protein L46, mitochondrial.

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

- Molecule 45 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	f	123	Total	C	N	O	S	0	0
			979	625	164	187	3		

- Molecule 46 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	g	129	Total	C	N	O	S	0	0
			1067	690	185	190	2		

- Molecule 47 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	h	107	Total	C	N	O	S	0	0
			871	551	153	164	3		

- Molecule 48 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 49 is a protein called 39S ribosomal protein L52, mitochondrial.

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

- Molecule 50 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	k	80	Total	C	N	O	S	0	0
			627	392	116	114	5		

- Molecule 51 is a protein called 39S ribosomal protein L54, mitochondrial.

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

- Molecule 52 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	m	35	Total	C	N	O	0	0
			287	180	57	50		

- Molecule 53 is a protein called rRNA methyltransferase 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	n	189	Total	C	N	O	S	0	0
			1450	917	259	268	6		

- Molecule 54 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	o	91	Total	C	N	O	S	0	0
			771	487	156	125	3		

- Molecule 55 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

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

- Molecule 56 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

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

- Molecule 57 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	r	155	Total	C	N	O	S	0	0
			1268	806	243	211	8		

- Molecule 58 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	s	370	Total	C	N	O	S	0	0
			3036	1946	542	534	14		

- Molecule 59 is a protein called Elongation factor Tu, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	t	381	Total	C	N	O	S	0	0
			2939	1860	519	545	15		

- Molecule 60 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	u	133	Total	C	N	O	S	0	0
			1092	702	181	199	10		

- Molecule 61 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	v	68	Total	C	N	O		0	0
			584	369	115	100			

- Molecule 62 is a protein called Acyl carrier protein, mitochondrial.

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

- Molecule 63 is a protein called UNK.

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

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

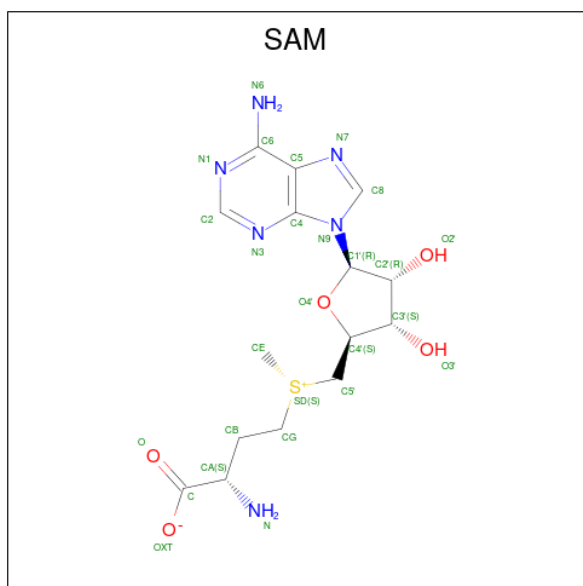
Mol	Chain	Residues	Atoms		AltConf
65	A	85	Total	Mg	0
			85	85	
65	D	1	Total	Mg	0
			1	1	

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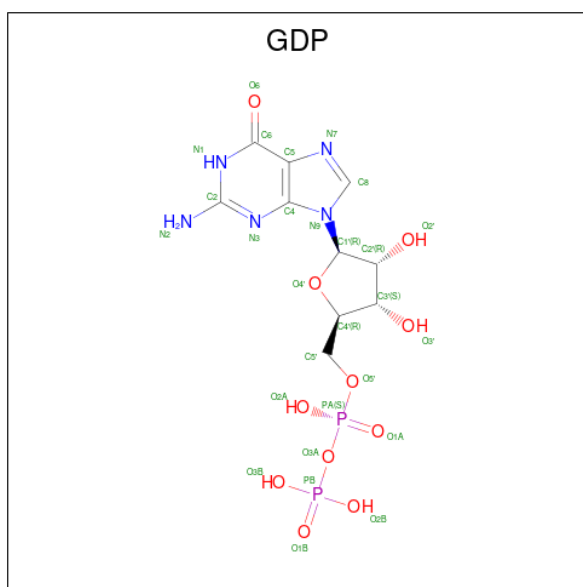
Mol	Chain	Residues	Atoms		AltConf
65	E	1	Total	Mg	0
			1	1	
65	G	2	Total	Mg	0
			2	2	
65	M	1	Total	Mg	0
			1	1	
65	W	1	Total	Mg	0
			1	1	
65	g	1	Total	Mg	0
			1	1	
65	t	1	Total	Mg	0
			1	1	

- Molecule 66 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



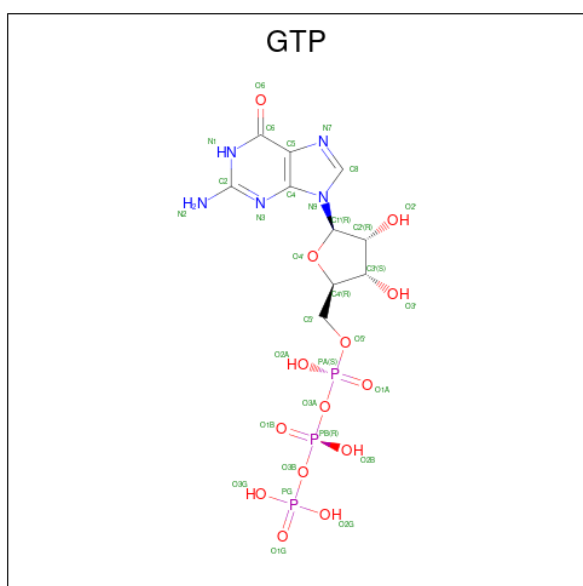
Mol	Chain	Residues	Atoms					AltConf
66	A1	1	Total	C	N	O	S	0
			27	15	6	5	1	

- Molecule 67 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



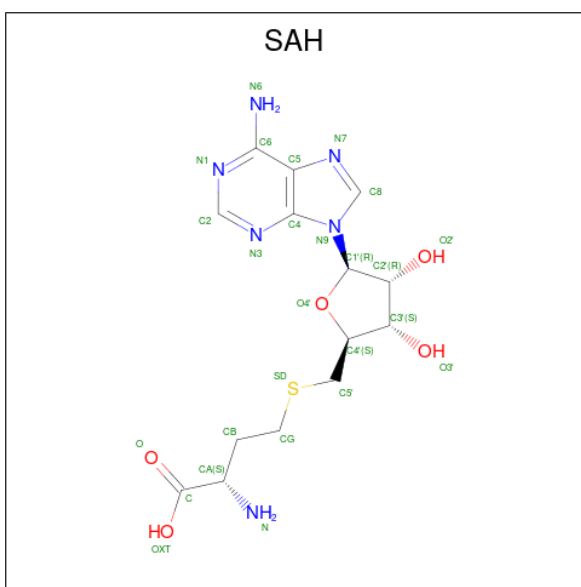
Mol	Chain	Residues	Atoms					AltConf
67	C	1	Total 28	C 10	N 5	O 11	P 2	0
67	t	1	Total 28	C 10	N 5	O 11	P 2	0

- Molecule 68 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



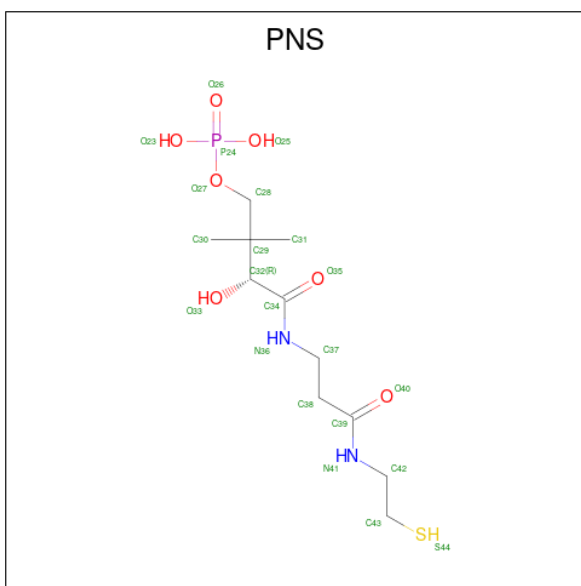
Mol	Chain	Residues	Atoms					AltConf
68	G	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 69 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms					AltConf
69	n	1	Total	C	N	O	S	0
			26	14	6	5	1	

- Molecule 70 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: $C_{11}H_{23}N_2O_7PS$).

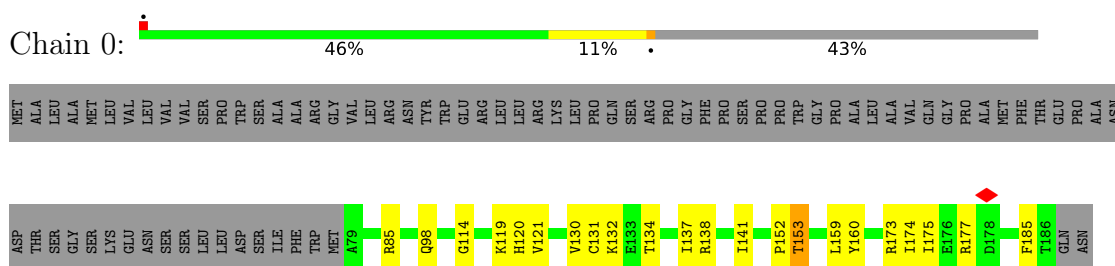


Mol	Chain	Residues	Atoms						AltConf
70	w	1	Total	C	N	O	P	S	0
			21	11	2	6	1	1	

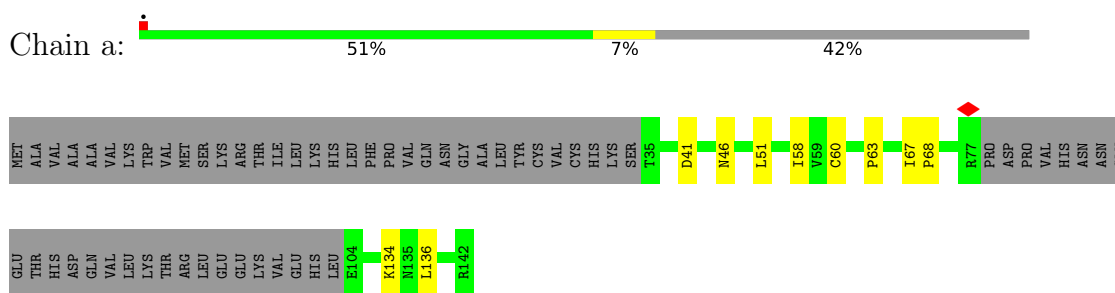
3 Residue-property plots

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.

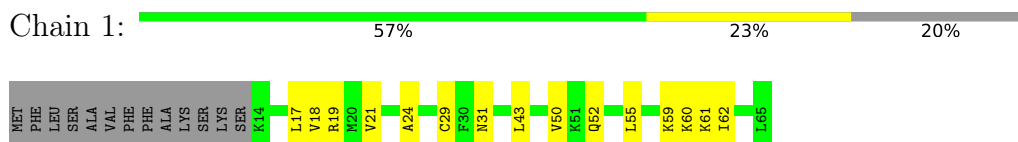
- Molecule 1: 39S ribosomal protein L32, mitochondrial



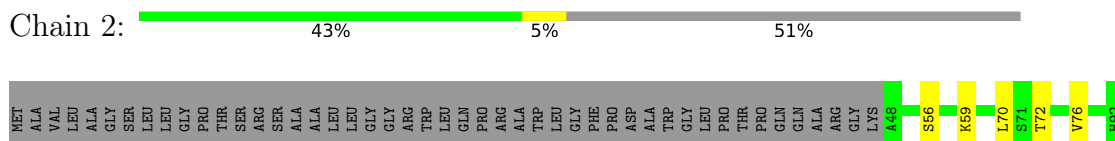
- Molecule 2: 39S ribosomal protein L42, mitochondrial



- Molecule 3: 39S ribosomal protein L33, mitochondrial

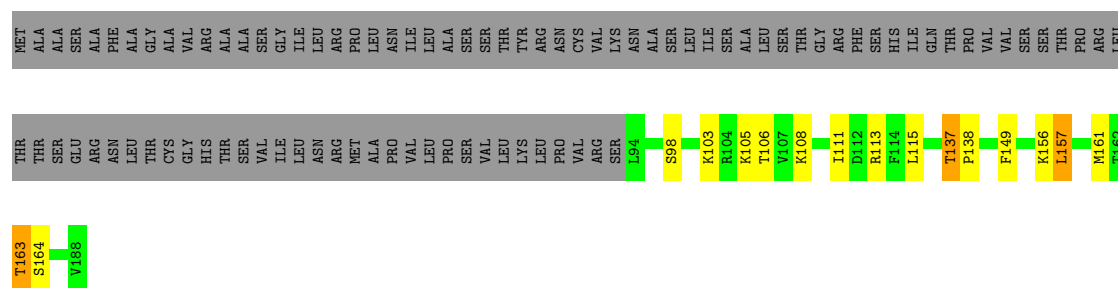


- Molecule 4: 39S ribosomal protein L34, mitochondrial



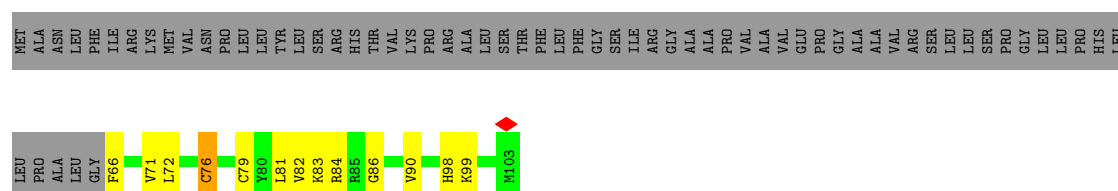
- Molecule 5: 39S ribosomal protein L35, mitochondrial

Chain 3: 



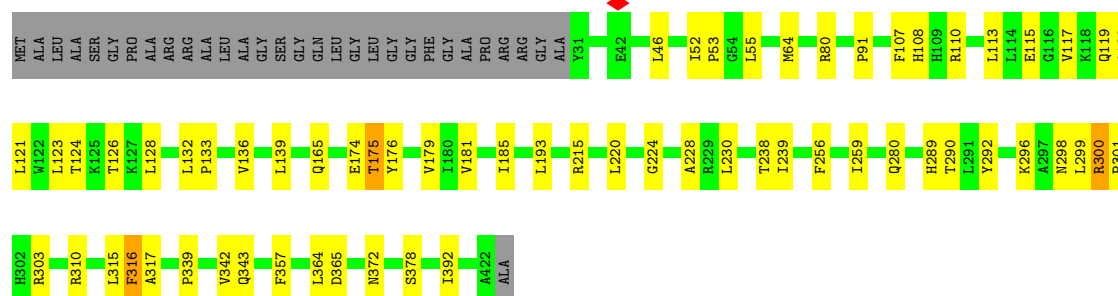
- Molecule 6: 39S ribosomal protein L36, mitochondrial

Chain 4: 



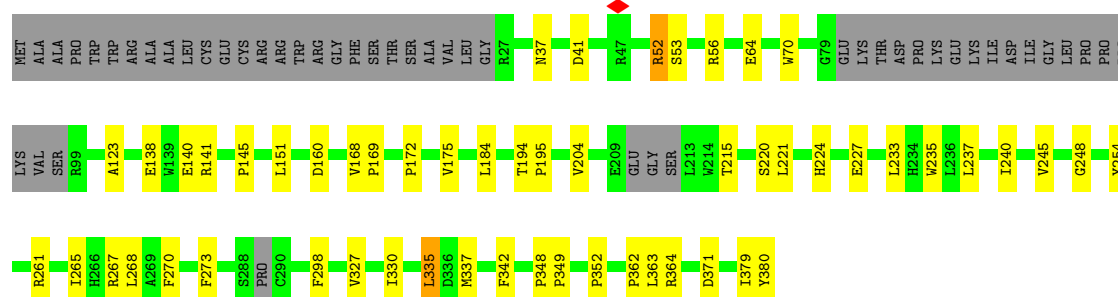
- Molecule 7: 39S ribosomal protein L37, mitochondrial

Chain 5: 



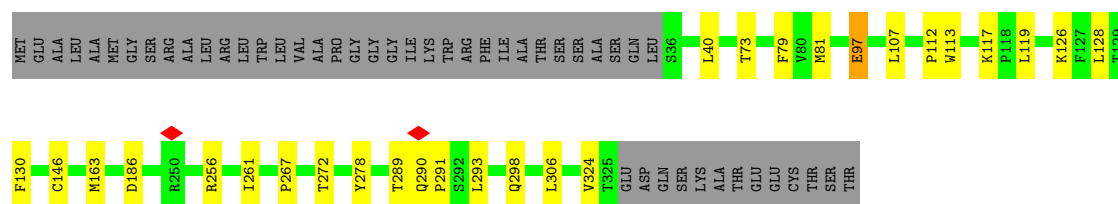
- Molecule 8: 39S ribosomal protein L38, mitochondrial

Chain 6: 



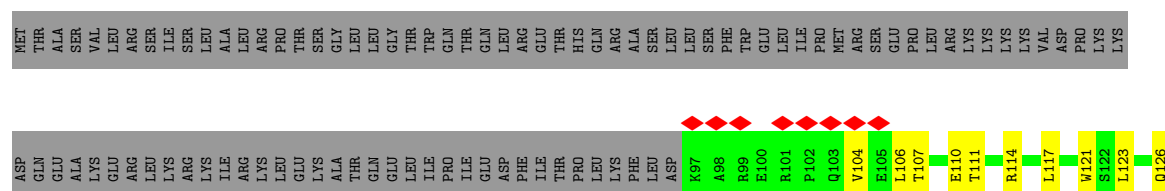
- Molecule 9: 39S ribosomal protein L39, mitochondrial

Chain 7:  78% 8% 14%



- Molecule 10: 39S ribosomal protein L40, mitochondrial

Chain 8:  7% 33% 8% 59%



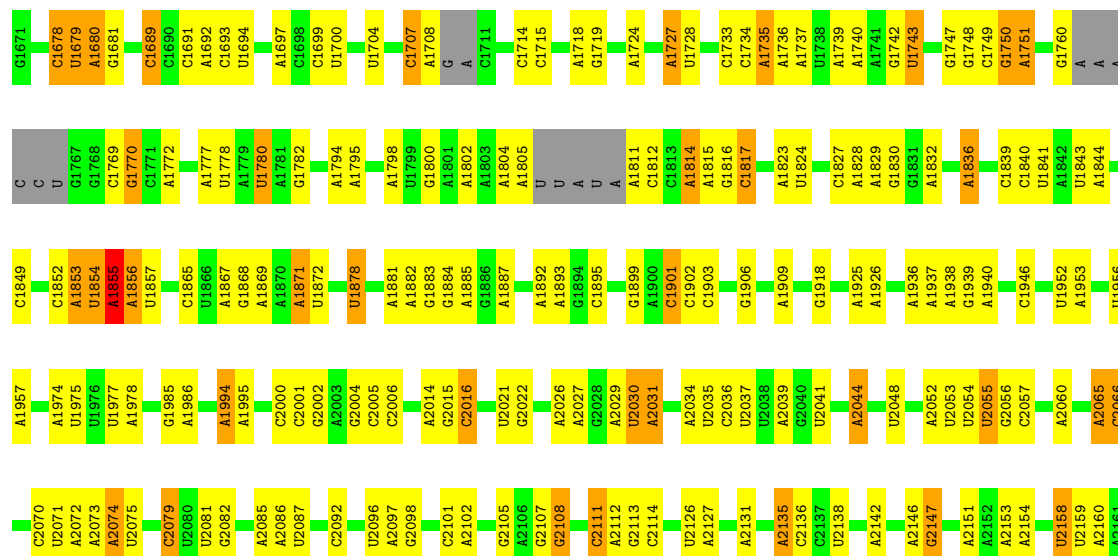
- Molecule 11: 39S ribosomal protein L41, mitochondrial

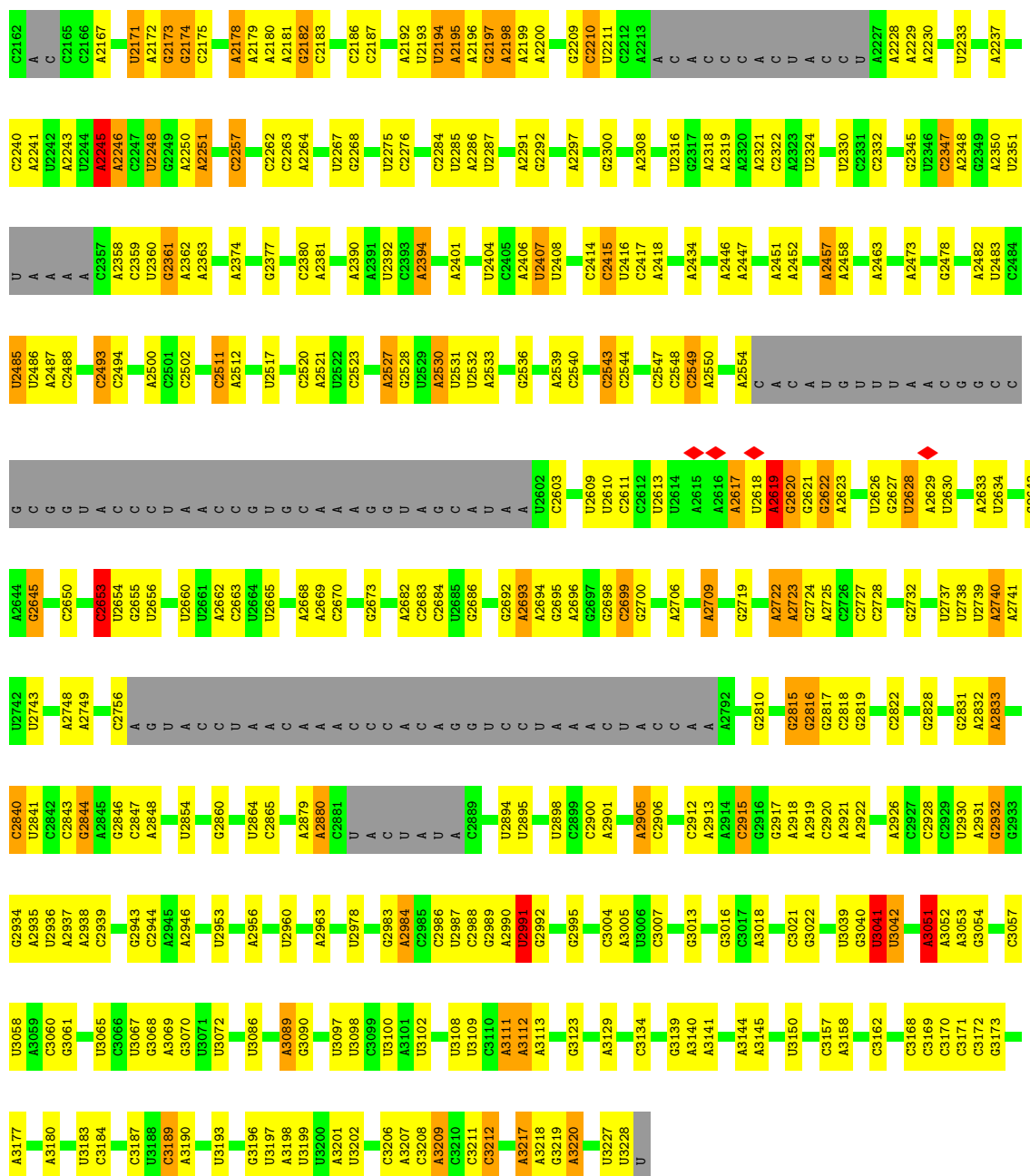
Chain 9:  77% 12% 10%



- Molecule 12: 16S rRNA

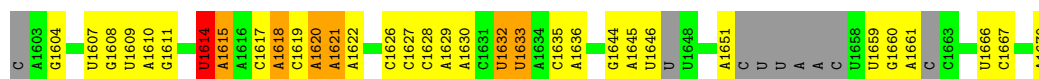
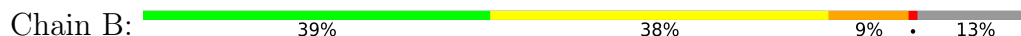
Chain A:  57% 28% 6% 8%



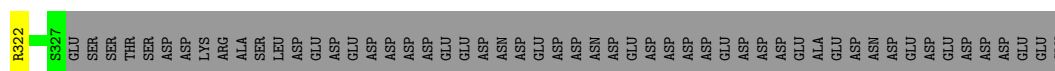
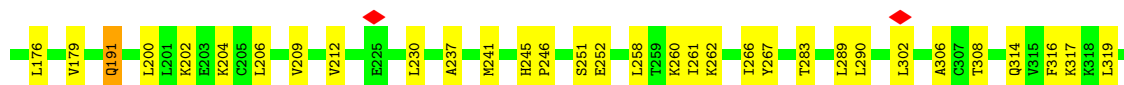
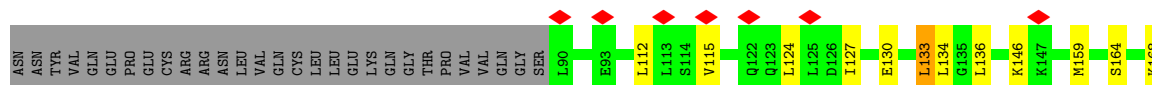
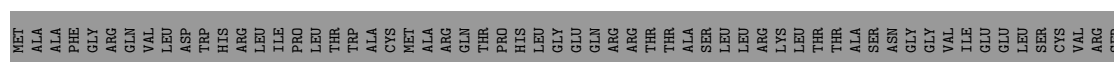




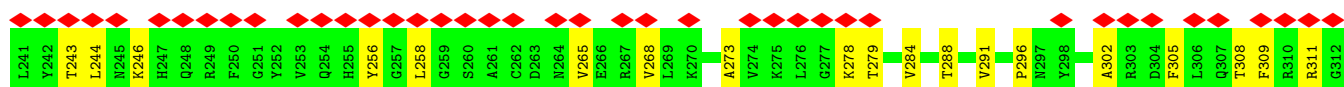
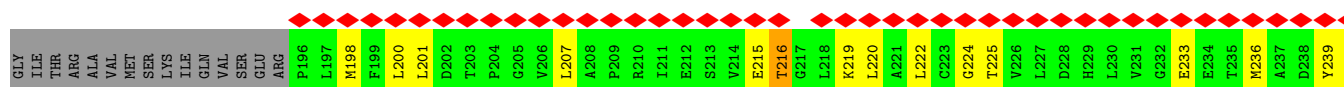
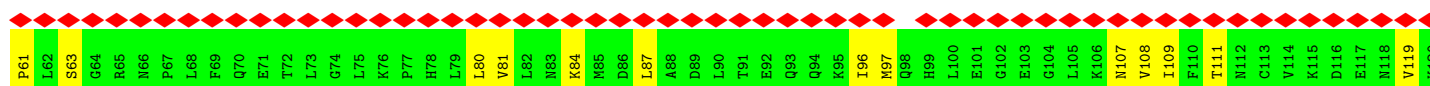
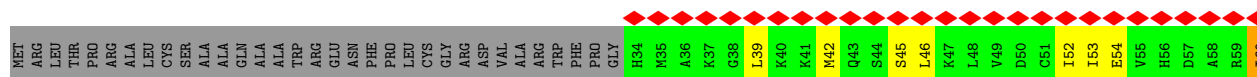
• Molecule 14: MT-TRNAVAL

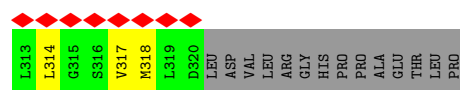


• Molecule 15: Transcription termination factor 4, mitochondrial

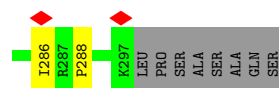
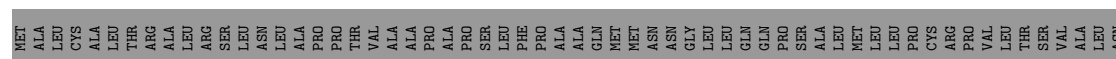


• Molecule 16: Mitochondrial ribosome-associated GTPase 1

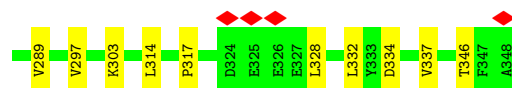
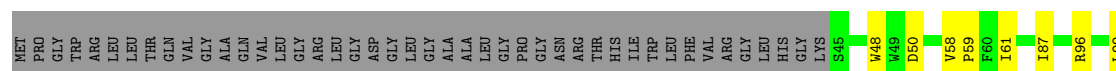




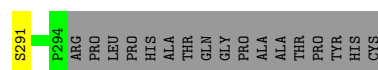
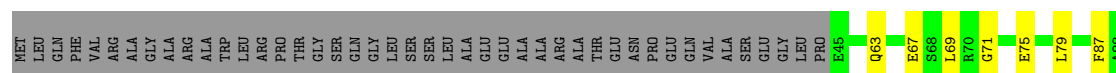
- Molecule 17: 39S ribosomal protein L2, mitochondrial



- Molecule 18: 39S ribosomal protein L3, mitochondrial



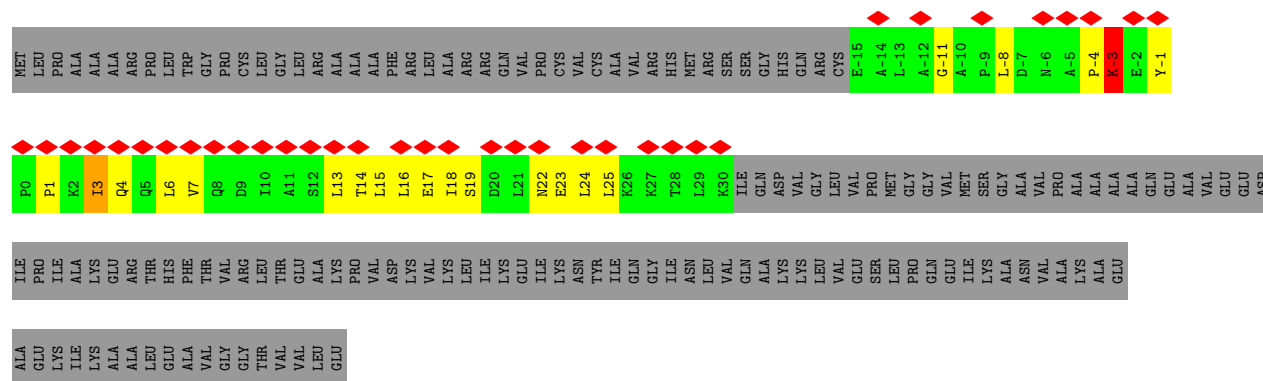
- Molecule 19: 39S ribosomal protein L4, mitochondrial



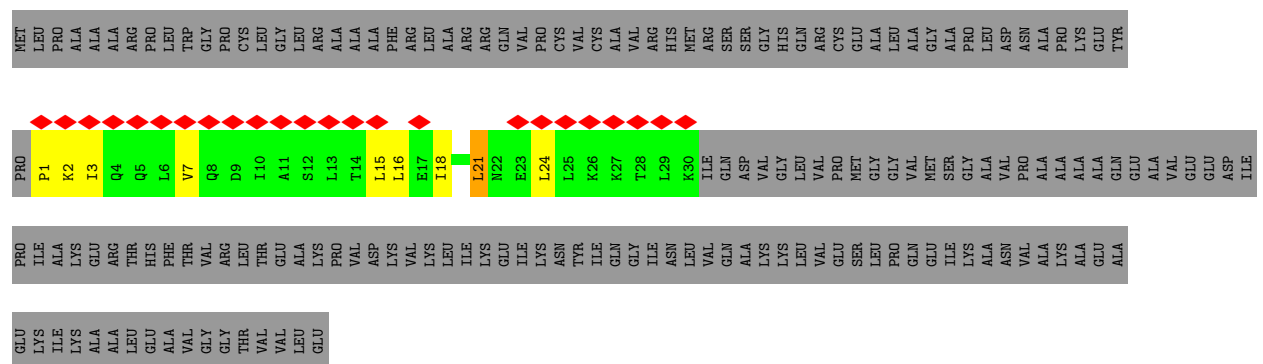
- Molecule 20: 39S ribosomal protein L12, mitochondrial



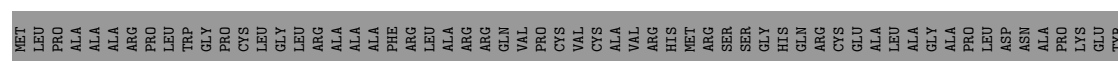
- Molecule 20: 39S ribosomal protein L12, mitochondrial



- Molecule 20: 39S ribosomal protein L12, mitochondrial



- Molecule 20: 39S ribosomal protein L12, mitochondrial



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

• Molecule 21: Mitochondrial ribosome-associated GTPase 2

Chain G:  66% 14% 19%

MET
ALA
PRO
LYS
ALA
ARG
CYS
PHE
SER
ALA
ARG
LEU
VAL
ARG
THR
VAL
PHE
GLN
GLY
VAL
GLY
HIS
TRP
ALA
LEU
SER
THR
TRP
ALA
GLY
LEU
LYS
PRO
SER
ARG
LEU
PRO
GLN
ARG
ALA
SER
LEU
ALA
LYS
HIS
GLN
GLU
LEU
PRO
G59

L62
L63
L68
V73
R76
Q86
A87
S90
G102
G105
G108
Q121
V128
V157
P158
K164
E165
R168
V169
H192
R193
F194
F195
P203
V204
T205
C206
T207
P208
A227
G228
M229
A235
L241
R242
P249
A250
V251
F256
T257

P261
I265
L272
V276
I282
I283
H284
G285
A286
H287
G291
L292
L297
H298
H299
I300
D311
L312
D323
S336
A341
K346
I347
R360
D361
H362
L363
G364
Q365
E366
V367
V369
L370
H384
L385
K386
V387
L388
Y389
D390
A391
Y392
A393
E394
A395

GLU
LEU
GLY
GLN
GLY
ARG
GLN
PRO
LEU
TRP
TRP
ASP
TYR
LYS
ASP
ASP
ASP
LYS

• Molecule 22: 39S ribosomal protein L9, mitochondrial

Chain H:  34% 64%

MET
ALA
ALA
PRO
VAL
VAL
THR
ALA
PRO
GLY
ARG
ALA
LEU
LEU
ARG
GLY
ALA
GLY
ARG
GLY
VAL
GLN
GLU
LEU
LEU
ARG
GLY
PRO
ARG
HIS
GLY
ASN
ASN
ALA
PRO
ASP
GLU
LEU
LEU
ASN
CYS
PHE
SER
SER
GLN
ASN
ARG
GLY
T53
V54
I55
V107
R108
Y131

L145
L146
R147
GLN
GLU
GLY
LYS
GLU
ILE
THR
LYS
GLY
ALA
GLY
GLY
ALA
THR
VAL
LYS
PHE
GLY
LEU
SER
CYS
ARG
THR
VAL
VAL
PRO
MET
SER
VAL
PHE
GLU
LYS
PRO
GLU
LEU
ASN
LYS
PRO
GLU
ILE
VAL
ALA
ARG
HIS
PHE
PHE
LYS
ASN
ALA
LYS
GLY
VAL
VAL
VAL
PRO

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

SER
PRO
GLN
ILE

• Molecule 23: 39S ribosomal protein L10, mitochondrial

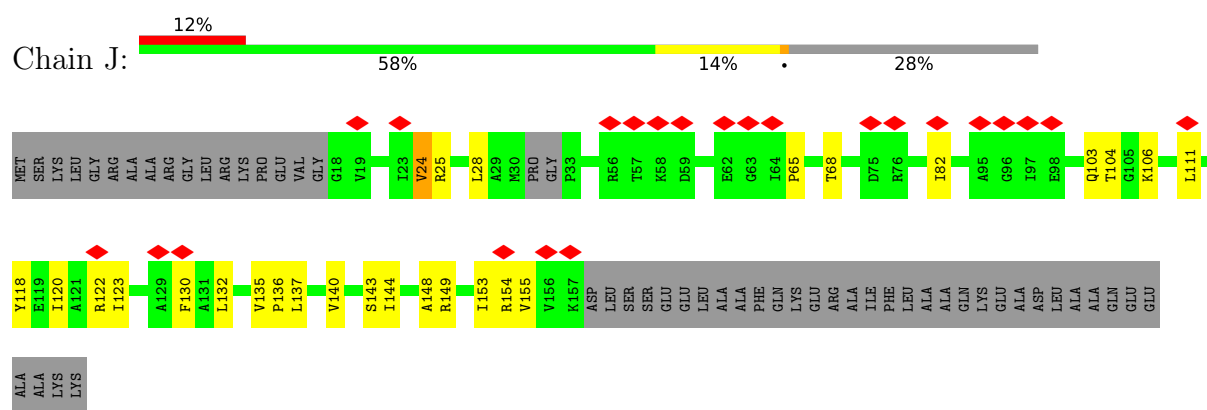
Chain I:  21% 65% 16% 19%

MET
ALA
ALA
VAL
ALA
GLY
MET
LEU
ARG
GLY
LEU
LEU
PRO
GLN
ALA
GLY
ARG
LEU
PRO
THR
LEU
GLN
THR
VAL
ARG
TYR
G29
V39
L47
V50
P69
S70
P71
P72
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G77
L78
R83
A97
M101
E107
L116
I121
L144

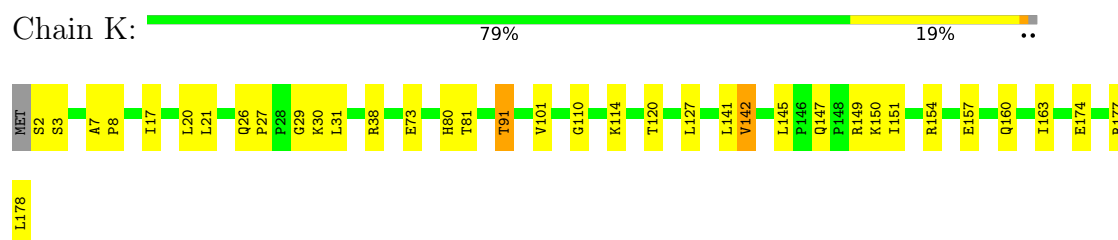
P145
L146
L154
L176
L177
G178
D182
I185
L186
S187
R188
Y194
S195
K196
L197
P198
S199
L200
P201
L202
V203
Q204
G205
E206
V208
G209
G210
L211
T212
C213
L214
T215
A216
Q217
T218
H219
S220
L221
L222
Q223
H224
Q225
P226
L227
Q228
L229
T230
T231
L232
L233
D234
Q235
V236
I237

R238
E239
Q240
ARG
GLU
LYS
ASP
SER
VAL
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LYS
PRO
ASP
PRO
ASP
THR
VAL
PRO
ASP
SER

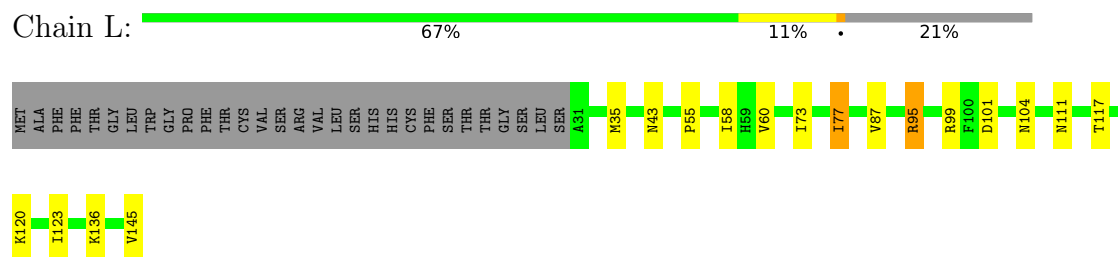
• Molecule 24: 39S ribosomal protein L11, mitochondrial



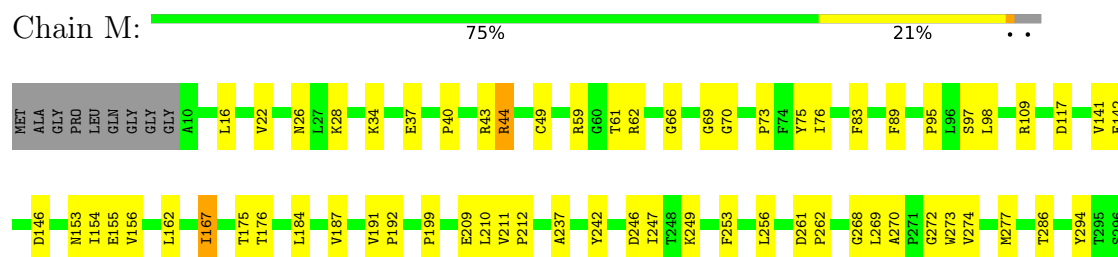
- Molecule 25: 39S ribosomal protein L13, mitochondrial



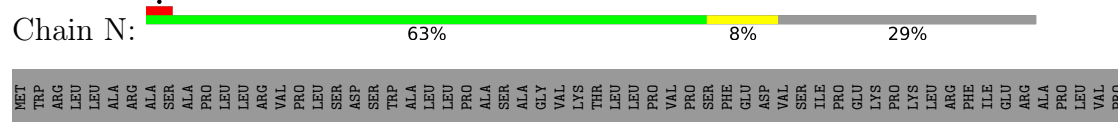
- Molecule 26: 39S ribosomal protein L14, mitochondrial

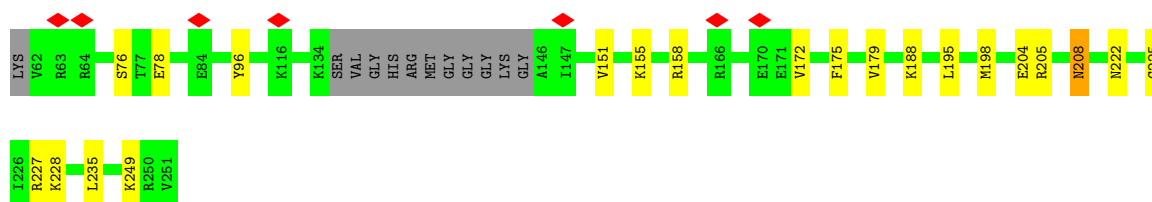


- Molecule 27: 39S ribosomal protein L15, mitochondrial



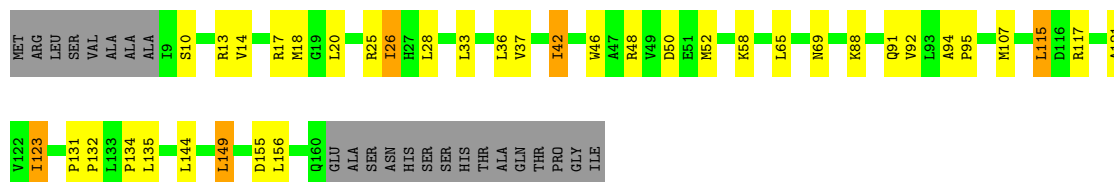
- Molecule 28: 39S ribosomal protein L16, mitochondrial





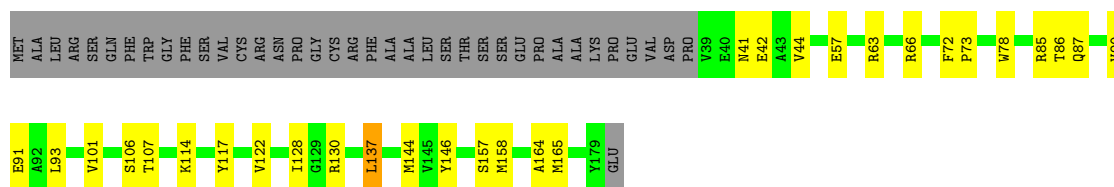
- Molecule 29: 39S ribosomal protein L17, mitochondrial

Chain O: 65% 19% 13%



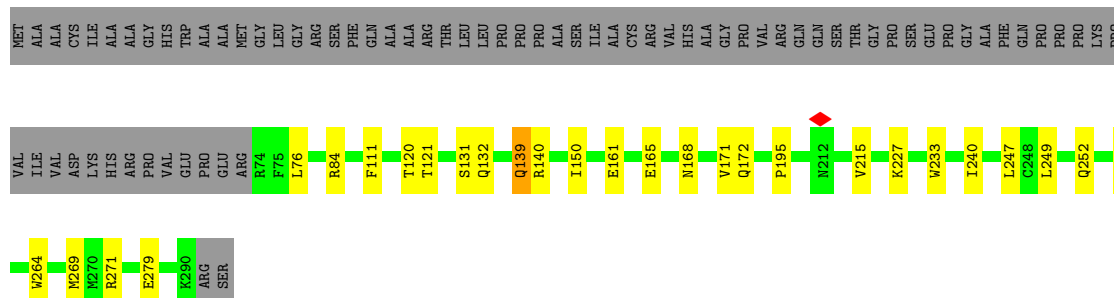
- Molecule 30: Mitochondrial ribosomal protein L18, isoform CRA_b

Chain P: 62% 16% 21%



- Molecule 31: 39S ribosomal protein L19, mitochondrial

Chain Q: 65% 9% 26%



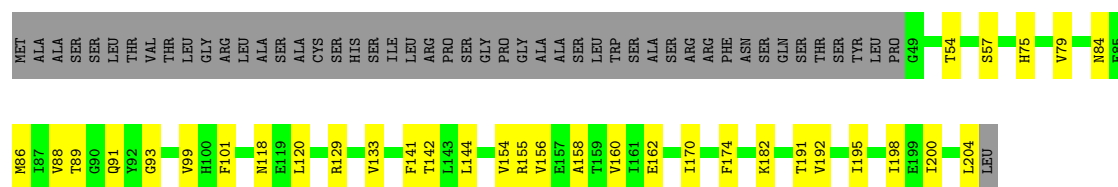
- Molecule 32: 39S ribosomal protein L20, mitochondrial

Chain R: 81% 11% 6%



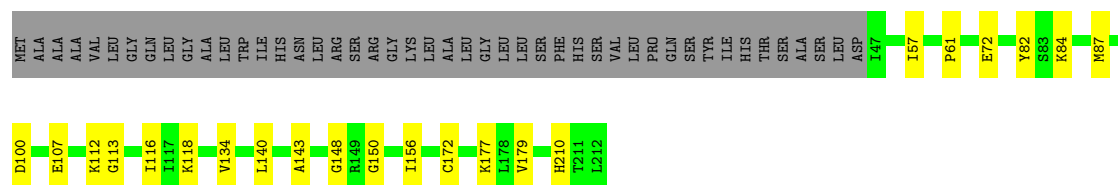
- Molecule 33: 39S ribosomal protein L21, mitochondrial

Chain S:  60% 17% 24%



- Molecule 34: 39S ribosomal protein L22, mitochondrial

Chain T:  68% 10% 22%



- Molecule 35: 39S ribosomal protein L23, mitochondrial

Chain U:  67% 24% 9%



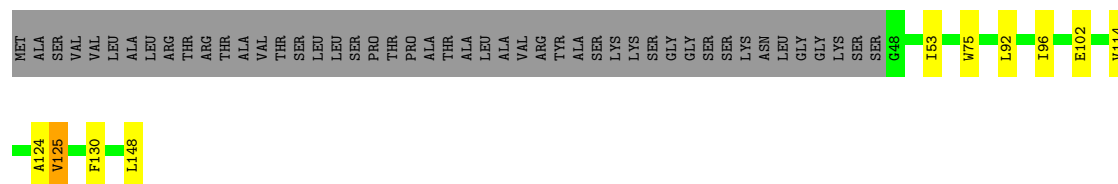
- Molecule 36: 39S ribosomal protein L24, mitochondrial

Chain V:  81% 11% 6%

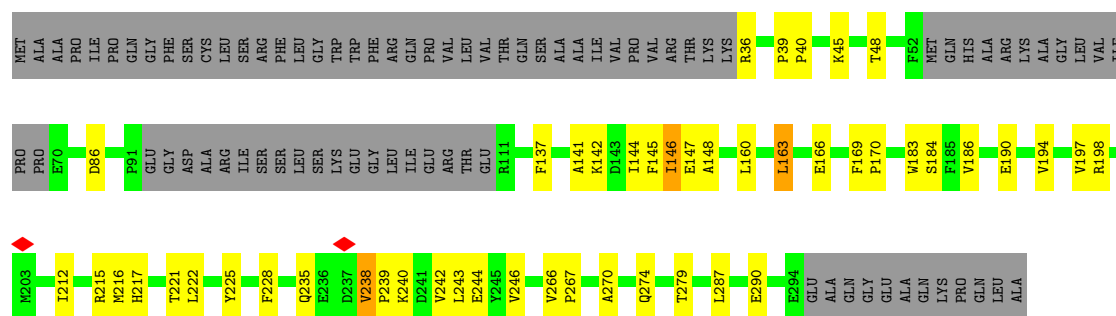


- Molecule 37: 39S ribosomal protein L27, mitochondrial

Chain W:  61% 6% 32%



Chain d:  57% 15% 27%



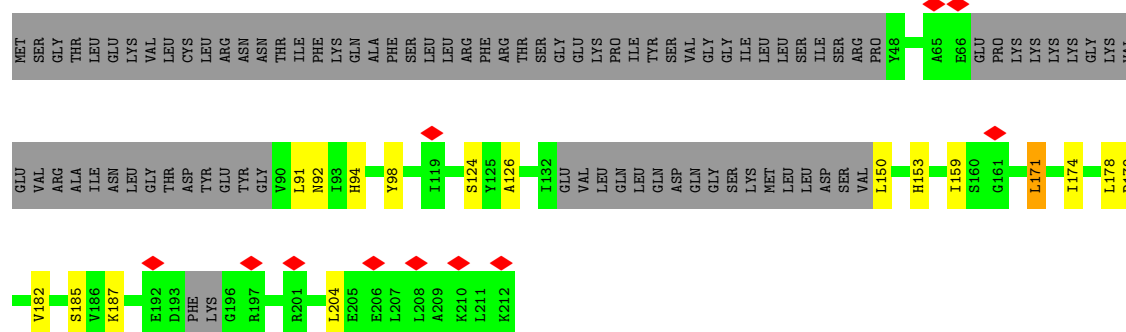
- Molecule 44: 39S ribosomal protein L46, mitochondrial

Chain e:  23% 65% 13% 22%



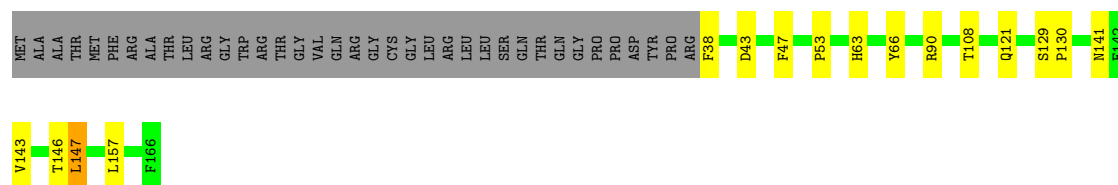
- Molecule 45: 39S ribosomal protein L48, mitochondrial

Chain f:  5% 50% 8% 42%

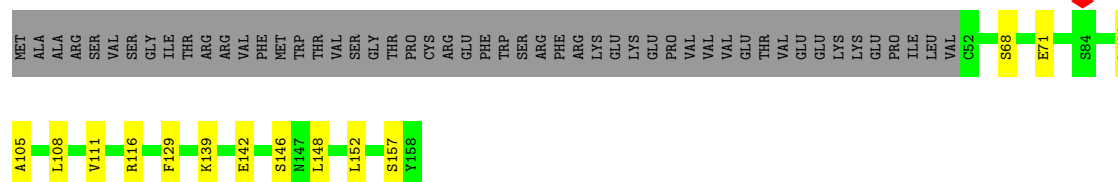


- Molecule 46: 39S ribosomal protein L49, mitochondrial

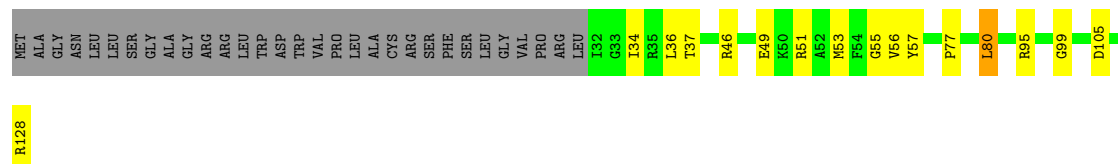
Chain g:  68% 9% 22%



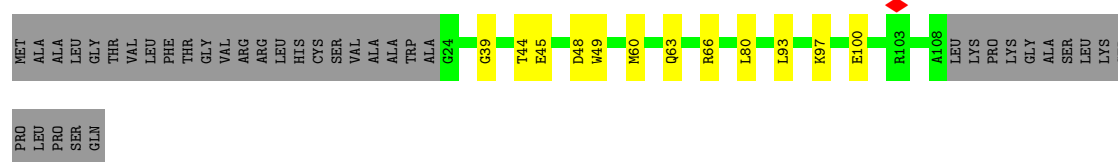
- Molecule 47: 39S ribosomal protein L50, mitochondrial



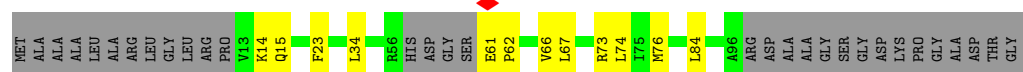
- Molecule 48: 39S ribosomal protein L51, mitochondrial



- Molecule 49: 39S ribosomal protein L52, mitochondrial

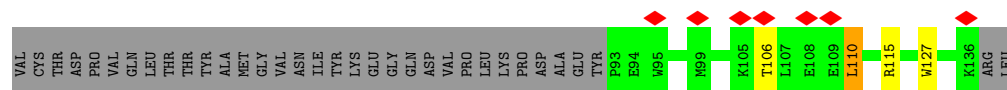


- Molecule 50: 39S ribosomal protein L53, mitochondrial

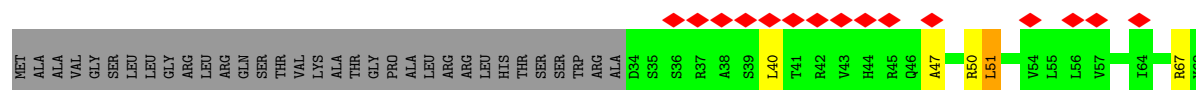


- Molecule 51: 39S ribosomal protein L54, mitochondrial

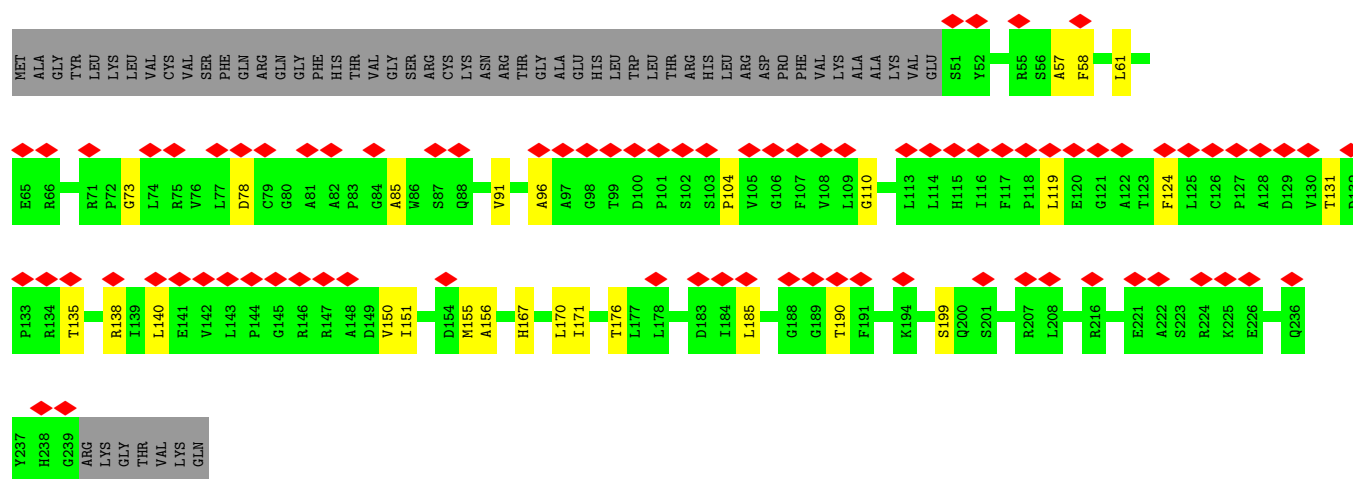




- Molecule 52: 39S ribosomal protein L55, mitochondrial



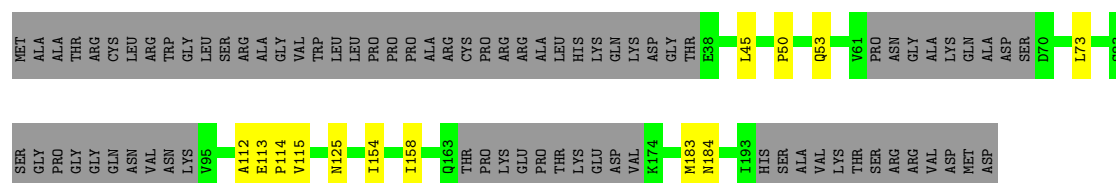
- Molecule 53: rRNA methyltransferase 2, mitochondrial



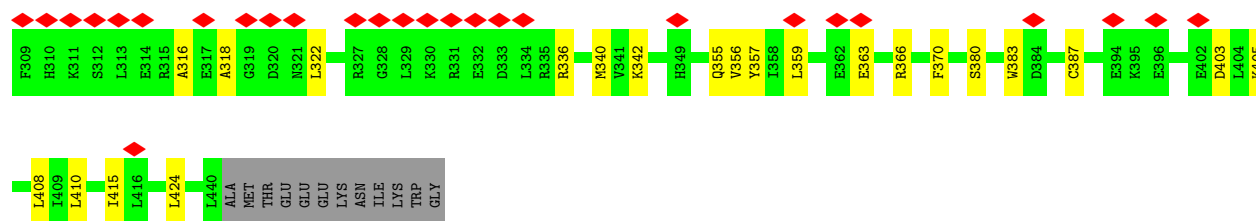
- Molecule 54: Ribosomal protein 63, mitochondrial



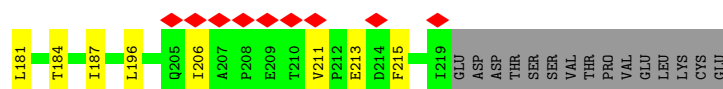
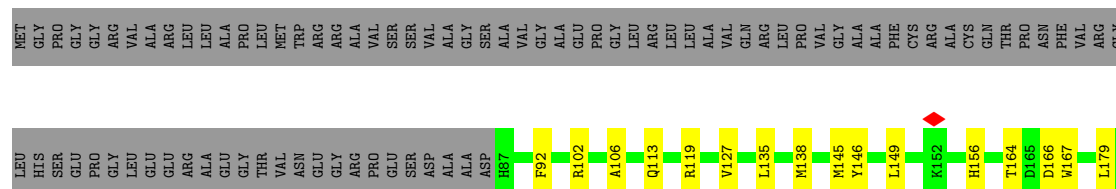
- Molecule 55: Peptidyl-tRNA hydrolase ICT1, mitochondrial



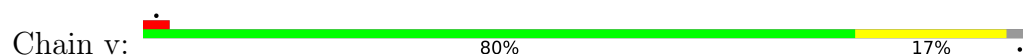
- Molecule 56: Growth arrest and DNA damage-inducible proteins-interacting protein 1



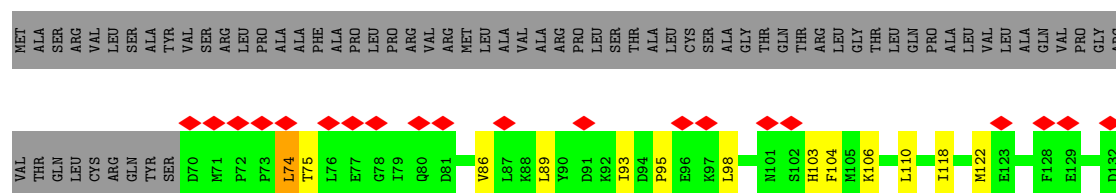
- Molecule 60: Mitochondrial assembly of ribosomal large subunit protein 1



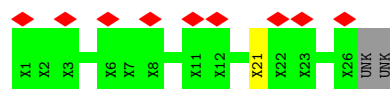
- Molecule 61: MIEF1 upstream open reading frame protein



- Molecule 62: Acyl carrier protein, mitochondrial



- Molecule 63: UNK



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39495	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 ($e^-/\text{\AA}^2$)	49.2	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	0.935	Depositor
Minimum map value	-0.278	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.082	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	221.34, 280.5, 250.92	wwPDB
Map dimensions	246, 275, 217	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: GTP, ZN, MG, SAM, OMG, PNS, SAH, GDP

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	0	0.44	0/895	1.05	0/1201
2	a	0.49	0/709	1.00	0/963
3	1	0.40	0/438	0.95	0/583
4	2	0.48	0/373	1.11	0/496
5	3	0.41	0/852	0.95	2/1136 (0.2%)
6	4	0.42	0/350	0.98	0/461
7	5	0.46	0/3294	0.99	1/4488 (0.0%)
8	6	0.47	0/2779	1.01	0/3787
9	7	0.43	0/2413	1.04	0/3264
10	8	0.45	0/734	1.14	0/986
11	9	0.45	0/1020	1.04	0/1374
12	A	0.50	0/34076	0.78	31/53028 (0.1%)
13	A1	0.45	0/2795	1.04	0/3792
14	B	0.50	0/1423	0.73	1/2206 (0.0%)
15	A2	0.42	0/1973	1.16	0/2651
16	C	0.43	0/2020	0.66	0/2724
17	D	0.47	0/1888	1.00	1/2538 (0.0%)
18	E	0.45	0/2465	0.99	0/3344
19	F	0.46	0/2071	1.00	0/2817
20	FF	0.44	0/544	1.17	0/730
20	t1	0.66	0/358	0.77	0/486
20	t2	0.10	0/238	0.22	0/319
20	t3	0.09	0/238	0.22	0/319
20	t4	0.10	0/229	0.20	0/308
20	t5	0.10	0/229	0.27	0/308
20	t6	0.10	0/213	0.27	0/286
21	G	0.47	0/2600	1.03	0/3513
22	H	0.44	0/798	1.07	0/1073
23	I	0.46	0/1731	1.02	0/2345
24	J	0.46	0/1064	1.13	0/1431
25	K	0.47	0/1495	1.02	1/2029 (0.0%)
26	L	0.46	0/904	1.00	0/1218

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
27	M	0.44	0/2359	1.04	0/3185
28	N	0.45	0/1494	1.05	0/2010
29	O	0.46	0/1269	1.09	0/1708
30	P	0.43	0/1173	1.05	0/1588
31	Q	0.42	0/1846	1.01	0/2487
32	R	0.45	0/1174	1.06	0/1572
33	S	0.46	0/1276	1.00	0/1729
34	T	0.47	0/1402	0.99	0/1886
35	U	0.45	0/1183	1.00	0/1600
36	V	0.46	0/1697	0.99	0/2302
37	W	0.48	0/827	0.96	0/1118
38	X	0.43	0/2090	1.02	1/2825 (0.0%)
39	Y	0.42	0/1552	1.08	0/2079
40	Z	0.48	0/1003	1.03	0/1354
41	b	0.48	0/1202	1.00	0/1626
42	c	0.44	0/2264	1.11	0/3059
43	d	0.46	0/1899	1.00	0/2569
44	e	0.44	0/1797	1.10	0/2422
45	f	0.45	0/994	1.05	0/1336
46	g	0.47	0/1102	0.96	0/1503
47	h	0.50	0/894	1.06	0/1217
48	i	0.45	0/849	1.00	0/1135
49	j	0.47	0/698	1.17	0/940
50	k	0.47	0/635	1.05	0/855
51	l	0.43	0/407	1.14	0/547
52	m	0.48	0/292	0.93	0/394
53	n	0.46	0/1480	1.05	0/2013
54	o	0.44	0/792	1.05	0/1064
55	p	0.45	0/1071	1.04	0/1433
56	q	0.47	0/1165	1.17	1/1575 (0.1%)
57	r	0.49	0/1305	1.06	1/1767 (0.1%)
58	s	0.44	0/3114	0.97	0/4225
59	t	0.47	0/2992	1.02	0/4047
60	u	0.43	0/1119	1.02	0/1516
61	v	0.39	0/593	1.17	0/788
62	w	0.43	0/717	1.16	0/967
All	All	0.47	0/120935	0.95	40/170645 (0.0%)

There are no bond length outliers.

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	A	2457	A	C2'-C3'-O3'	9.87	124.31	109.50
12	A	2653	C	C4'-C3'-O3'	8.50	125.75	113.00
12	A	1855	A	C2'-C3'-O3'	8.45	126.38	113.70
12	A	3217	A	C4'-C3'-O3'	-8.44	100.34	113.00
12	A	2182	G	C2'-C3'-O3'	8.18	125.97	113.70
12	A	3041	U	C4'-C3'-O3'	7.68	120.92	109.40
12	A	2628	U	C2'-C3'-O3'	7.53	120.80	109.50
12	A	2158	U	C4'-C3'-O3'	7.49	120.64	109.40
12	A	1871	A	C2'-C3'-O3'	7.42	124.82	113.70
12	A	2030	U	C4'-C3'-O3'	6.96	119.84	109.40
12	A	2905	A	C2'-C3'-O3'	6.91	124.07	113.70
14	B	1614	U	C4'-C3'-O3'	6.91	119.76	109.40
12	A	1994	A	C4'-C3'-O3'	6.65	119.37	109.40
12	A	2530	A	C2'-C3'-O3'	6.62	119.43	109.50
12	A	2530	A	C4'-C3'-O3'	6.62	119.33	109.40
12	A	1678	C	C2'-C3'-O3'	6.55	119.33	109.50
12	A	2361	G	C4'-C3'-O3'	6.43	119.04	109.40
12	A	2620	G	C2'-C3'-O3'	6.29	123.14	113.70
12	A	2619	A	C4'-C3'-O3'	6.22	118.72	109.40
12	A	2543	C	C2'-C3'-O3'	6.14	122.91	113.70
12	A	2347	C	C2'-C3'-O3'	6.10	122.85	113.70
12	A	2493	C	C4'-C3'-O3'	6.05	122.08	113.00
12	A	2915	C	C4'-C3'-O3'	-6.00	104.00	113.00
12	A	1678	C	C4'-C3'-O3'	-5.94	100.49	109.40
7	5	91	PRO	CB-CA-C	-5.82	105.92	111.39
38	X	124	THR	CB-CA-C	5.69	119.60	110.16
12	A	2245	A	C4'-C3'-O3'	5.46	117.59	109.40
12	A	3051	A	C4'-C3'-O3'	5.44	117.56	109.40
12	A	1814	A	C3'-C2'-O2'	5.37	118.76	110.70
25	K	120	THR	CB-CA-C	5.36	119.96	110.85
12	A	1878	U	C3'-C2'-O2'	5.31	118.67	110.70
57	r	175	PRO	CB-CA-C	-5.25	104.51	111.23
12	A	2991	U	C2'-C3'-O3'	5.19	117.28	109.50
17	D	206	TYR	CB-CA-C	5.17	118.09	109.56
12	A	2248	U	C3'-C2'-O2'	5.16	118.44	110.70
5	3	163	THR	CA-C-N	5.14	127.67	120.28
5	3	163	THR	C-N-CA	5.14	127.67	120.28
12	A	2180	A	C2'-C3'-O3'	-5.10	106.05	113.70
56	q	30	PRO	N-CA-C	5.10	115.36	110.47
12	A	1770	G	C4'-C3'-C2'	-5.01	97.59	102.60

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	0	880	0	902	20	0
2	a	686	0	658	9	0
3	1	433	0	475	11	0
4	2	367	0	393	3	0
5	3	831	0	883	13	0
6	4	342	0	361	11	0
7	5	3199	0	3196	33	0
8	6	2692	0	2509	33	0
9	7	2356	0	2368	19	0
10	8	719	0	723	11	0
11	9	992	0	984	14	0
12	A	30486	0	15484	198	0
13	A1	2731	0	2712	32	0
14	B	1275	0	650	13	0
15	A2	1942	0	2035	26	0
16	C	1990	0	2079	50	0
17	D	1851	0	1908	19	0
18	E	2396	0	2402	34	0
19	F	2013	0	2044	37	0
20	FF	540	0	592	12	0
20	t1	354	0	380	24	0
20	t2	238	0	270	25	0
20	t3	238	0	270	10	0
20	t4	229	0	257	8	0
20	t5	229	0	257	7	0
20	t6	214	0	236	8	0
21	G	2549	0	2551	39	0
22	H	784	0	832	5	0
23	I	1695	0	1786	48	0
24	J	1050	0	1131	18	0
25	K	1451	0	1448	21	0
26	L	889	0	941	9	0
27	M	2305	0	2378	41	0
28	N	1457	0	1461	13	0
29	O	1245	0	1283	24	0
30	P	1148	0	1148	20	0
31	Q	1805	0	1841	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	R	1153	0	1214	20	0
33	S	1251	0	1322	21	0
34	T	1368	0	1410	16	0
35	U	1154	0	1154	28	0
36	V	1652	0	1658	17	0
37	W	805	0	828	5	0
38	X	2035	0	2054	17	0
39	Y	1517	0	1561	18	0
40	Z	978	0	1030	15	0
41	b	1178	0	1180	17	0
42	c	2217	0	2220	21	0
43	d	1847	0	1832	35	0
44	e	1762	0	1767	25	0
45	f	979	0	992	9	0
46	g	1067	0	1056	9	0
47	h	871	0	850	9	0
48	i	827	0	857	8	0
49	j	684	0	673	8	0
50	k	627	0	636	8	0
51	l	395	0	391	3	0
52	m	287	0	294	3	0
53	n	1450	0	1450	13	0
54	o	771	0	775	22	0
55	p	1058	0	1083	6	0
56	q	1134	0	1110	10	0
57	r	1268	0	1291	14	0
58	s	3036	0	3022	24	0
59	t	2939	0	3007	34	0
60	u	1092	0	1084	16	0
61	v	584	0	600	7	0
62	w	705	0	691	9	0
63	UNK	130	0	28	1	0
64	0	1	0	0	0	0
64	4	1	0	0	0	0
65	A	85	0	0	0	0
65	D	1	0	0	0	0
65	E	1	0	0	0	0
65	G	2	0	0	0	0
65	M	1	0	0	0	0
65	W	1	0	0	0	0
65	g	1	0	0	0	0
65	t	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
66	A1	27	0	22	1	0
67	C	28	0	12	0	0
67	t	28	0	12	0	0
68	G	32	0	12	1	0
69	n	26	0	19	0	0
70	w	21	0	21	0	0
All	All	115679	0	101046	1143	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 5.

All (1143) 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)
23:I:194:TYR:CD1	20:t:2:16:LEU:HD21	1.38	1.55
23:I:194:TYR:CD1	20:t:2:16:LEU:CD2	2.20	1.24
23:I:194:TYR:CE1	20:t:2:16:LEU:HG	1.76	1.19
25:K:21:LEU:HD21	25:K:31:LEU:HD22	1.27	1.10
24:J:25:ARG:HA	24:J:65:PRO:HA	1.28	1.09
20:t:1:6:LEU:HD11	20:t:2:21:LEU:HD11	1.25	1.09
23:I:194:TYR:CE1	20:t:2:16:LEU:CG	2.35	1.08
16:C:153:ASN:HB2	16:C:225:THR:HA	1.43	0.98
12:A:2485:U:H3	12:A:2650:C:H42	1.06	0.96
23:I:194:TYR:HE1	20:t:2:16:LEU:HG	1.29	0.95
25:K:26:GLN:HE22	25:K:149:ARG:H	1.15	0.94
12:A:2292:G:C8	32:R:11:ARG:HB2	2.07	0.90
3:1:50:VAL:HG21	56:q:125:MET:HE3	1.55	0.88
43:d:235:GLN:HG3	43:d:238:VAL:HG23	1.55	0.88
6:4:84:ARG:HH21	12:A:3187:C:H3'	1.39	0.87
40:Z:104:PRO:HD2	54:o:59:GLU:OE1	1.77	0.85
23:I:194:TYR:HD1	20:t:2:16:LEU:HD21	1.02	0.84
59:t:260:LEU:HB2	59:t:340:MET:HB3	1.60	0.83
35:U:26:ILE:HD12	35:U:44:ILE:HD13	1.61	0.82
57:r:92:PHE:HE2	57:r:107:LEU:HD21	1.44	0.81
21:G:90:SER:HB2	21:G:205:THR:HB	1.62	0.81
6:4:66:PHE:N	12:A:3013:G:HO2'	1.79	0.80
20:t:1:7:VAL:HG21	20:t:2:24:LEU:HD23	1.62	0.79
43:d:267:PRO:HG2	43:d:270:ALA:HB2	1.65	0.79
25:K:21:LEU:HD21	25:K:31:LEU:CD2	2.12	0.78
20:t:1:15:LEU:HB2	20:t:4:11:ALA:HA	1.65	0.78
21:G:347:ILE:HG21	21:G:369:VAL:HG22	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:V:194:LEU:HA	39:Y:95:ASN:OD1	1.84	0.77
12:A:1737:A:H61	12:A:1760:G:H1'	1.50	0.77
12:A:2668:A:H2'	12:A:2669:A:C8	2.20	0.76
23:I:194:TYR:CE1	20:t2:16:LEU:CD2	2.68	0.76
57:r:92:PHE:CE2	57:r:107:LEU:HD21	2.21	0.76
34:T:113:GLY:HA2	34:T:116:ILE:HD12	1.69	0.74
8:6:235:TRP:HB3	8:6:254:TYR:HA	1.68	0.74
27:M:26:ASN:HD21	54:o:98:THR:HB	1.51	0.74
12:A:2610:U:H3	12:A:2622:G:H1	1.33	0.74
18:E:216:GLN:HG3	18:E:261:MET:HE2	1.69	0.74
23:I:194:TYR:CE1	20:t2:16:LEU:CD1	2.69	0.74
53:n:91:VAL:HG23	53:n:96:ALA:HB3	1.70	0.73
12:A:2198:A:H2	24:J:149:ARG:HH22	1.36	0.73
57:r:105:THR:HG23	57:r:107:LEU:HD23	1.71	0.73
33:S:93:GLY:O	42:c:312:ARG:HD2	1.90	0.72
16:C:152:PRO:O	16:C:225:THR:HB	1.89	0.72
23:I:225:GLN:HE22	20:t3:15:LEU:HD22	1.54	0.72
33:S:89:THR:HG23	33:S:91:GLN:HG2	1.72	0.72
20:t1:6:LEU:HD11	20:t2:21:LEU:CD1	2.14	0.72
20:t1:19:SER:HB3	20:t3:29:LEU:HD23	1.72	0.72
7:5:120:ALA:O	7:5:124:THR:HG22	1.89	0.72
25:K:38:ARG:HE	25:K:145:LEU:HD21	1.55	0.71
15:A2:258:LEU:HD23	15:A2:261:ILE:HD11	1.72	0.71
12:A:2171:U:C2	12:A:2173:G:H4'	2.25	0.71
25:K:7:ALA:HB3	25:K:8:PRO:HD3	1.73	0.71
12:A:1854:U:H1'	12:A:1855:A:H5'	1.73	0.71
35:U:26:ILE:HD12	35:U:44:ILE:CD1	2.20	0.71
16:C:119:VAL:HA	16:C:122:ILE:HD12	1.73	0.70
29:O:18:MET:HE3	29:O:48:ARG:HG2	1.70	0.70
14:B:1618:A:H62	14:B:1620:A:H1'	1.55	0.70
12:A:2240:C:H5'	25:K:29:GLY:HA3	1.73	0.70
13:A1:256:VAL:HG21	13:A1:288:GLN:HA	1.74	0.70
7:5:238:THR:HG21	7:5:339:PRO:HD2	1.74	0.70
12:A:2960:U:H3	21:G:73:VAL:HG13	1.56	0.70
32:R:13:ARG:HE	42:c:32:LYS:HZ3	1.40	0.70
12:A:2392:U:H2'	12:A:2394:A:H62	1.57	0.70
23:I:194:TYR:CE1	20:t2:16:LEU:HD11	2.27	0.69
12:A:2549:C:H2'	12:A:2549:C:O2	1.92	0.69
35:U:8:PRO:HA	39:Y:183:GLN:HE22	1.56	0.69
8:6:237:LEU:HB3	8:6:240:ILE:HD11	1.75	0.69
5:3:163:THR:HG21	12:A:1742:G:H5'	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:I:39:VAL:HG21	54:o:22:ARG:HD2	1.72	0.69
12:A:2416:U:H2'	12:A:2416:U:O2	1.91	0.69
23:I:224:HIS:O	23:I:228:GLN:N	2.26	0.69
16:C:215:GLU:HG3	16:C:219:LYS:HE3	1.74	0.69
13:A1:169:LEU:HD22	13:A1:251:ARG:HD2	1.75	0.69
59:t:366:ARG:HH12	59:t:370:PHE:HB3	1.58	0.68
20:t1:15:LEU:HB3	20:t3:29:LEU:HD21	1.72	0.68
12:A:1881:A:OP1	46:g:90:ARG:HG3	1.93	0.68
9:7:81:MET:HE2	43:d:279:THR:HB	1.75	0.68
59:t:359:LEU:HD12	59:t:363:GLU:HG2	1.75	0.68
7:5:107:PHE:CE1	7:5:113:LEU:HD21	2.29	0.68
16:C:97:MET:HE1	16:C:108:VAL:H	1.58	0.67
31:Q:131:SER:HB3	60:u:119:ARG:HD3	1.75	0.67
12:A:1737:A:N6	12:A:1760:G:H1'	2.09	0.67
7:5:165:GLN:HE22	7:5:175:THR:HG22	1.59	0.67
56:q:40:PRO:HG3	56:q:51:GLN:HB3	1.75	0.67
19:F:69:LEU:HG	19:F:190:MET:HE2	1.77	0.67
50:k:76:MET:HE3	57:r:49:ILE:HD11	1.77	0.67
12:A:1778:U:C5	19:F:121:ARG:HD2	2.29	0.67
48:i:53:MET:HE2	56:q:25:TYR:HB2	1.77	0.67
7:5:126:THR:HG22	7:5:372:ASN:HB2	1.75	0.66
27:M:209:GLU:HG2	27:M:210:LEU:HD12	1.75	0.66
12:A:2044:A:H61	12:A:2096:U:H3	1.42	0.66
27:M:286:THR:HG1	46:g:38:PHE:N	1.94	0.66
20:t1:24:LEU:HD12	20:t2:3:ILE:HG22	1.76	0.66
23:I:194:TYR:HD1	20:t2:16:LEU:CD2	1.78	0.66
26:L:43:ASN:HD21	26:L:117:THR:HB	1.60	0.65
27:M:156:VAL:O	27:M:176:THR:HA	1.96	0.65
39:Y:201:ALA:HB1	39:Y:205:VAL:HG11	1.76	0.65
12:A:2485:U:H3	12:A:2650:C:N4	1.88	0.65
6:4:71:VAL:HG12	12:A:2953:U:H5''	1.77	0.65
59:t:279:LEU:HD23	59:t:322:LEU:HD23	1.78	0.65
20:t5:18:ILE:HA	20:t5:21:LEU:HD12	1.79	0.65
7:5:310:ARG:HD3	7:5:378:SER:HB3	1.79	0.65
15:A2:302:LEU:HA	15:A2:306:ALA:HB3	1.77	0.65
2:a:51:LEU:HD12	32:R:141:ILE:HG22	1.78	0.64
4:2:56:SER:OG	4:2:59:LYS:HB2	1.98	0.64
12:A:2065:A:H1'	12:A:2066:C:C6	2.32	0.64
1:0:131:CYS:HA	1:0:134:THR:HG22	1.78	0.64
16:C:222:LEU:HD12	16:C:236:MET:HB2	1.79	0.64
48:i:77:PRO:HB2	48:i:80:LEU:HB2	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:A:1865:C:OP1	32:R:13:ARG:HD2	1.98	0.64
20:t1:23:GLU:OE2	20:t3:30:LYS:NZ	2.26	0.64
12:A:2086:A:H2'	12:A:2087:U:C6	2.32	0.64
35:U:22:THR:N	39:Y:102:TRP:CH2	2.64	0.64
25:K:160:GLN:HA	25:K:163:ILE:HG12	1.79	0.64
50:k:66:VAL:HB	50:k:74:LEU:HB3	1.79	0.64
8:6:64:GLU:HG3	37:W:125:VAL:HG11	1.80	0.63
25:K:26:GLN:NE2	25:K:149:ARG:H	1.92	0.63
54:o:16:GLN:HB2	54:o:23:ARG:HG2	1.80	0.63
18:E:236:THR:HG22	18:E:239:ARG:HE	1.62	0.63
21:G:165:GLU:HB3	21:G:168:ARG:HH12	1.63	0.63
42:c:160:LEU:HD21	42:c:223:MET:HG3	1.79	0.63
12:A:3227:U:H2'	18:E:156:ARG:HH21	1.64	0.63
21:G:256:PHE:HE1	21:G:283:ILE:HD11	1.63	0.63
25:K:101:VAL:HG13	25:K:127:LEU:HD23	1.79	0.63
3:1:24:ALA:HB1	56:q:125:MET:HE2	1.81	0.62
40:Z:126:GLN:HE21	40:Z:147:VAL:H	1.47	0.62
17:D:257:ILE:HG23	17:D:262:ARG:HB2	1.82	0.62
49:j:63:GLN:NE2	49:j:66:ARG:HH12	1.97	0.62
23:I:194:TYR:CZ	20:t2:16:LEU:HD11	2.35	0.62
58:s:188:LEU:HD21	58:s:422:VAL:HG13	1.80	0.62
8:6:240:ILE:HD13	8:6:248:GLY:HA3	1.81	0.62
16:C:153:ASN:CB	16:C:225:THR:HA	2.22	0.62
16:C:284:VAL:HG23	16:C:291:VAL:HG23	1.80	0.62
23:I:194:TYR:CD1	20:t2:16:LEU:CG	2.68	0.62
20:FF:132:VAL:HG13	20:FF:195:VAL:HG11	1.82	0.62
16:C:198:MET:HE3	16:C:200:LEU:HD11	1.81	0.62
20:FF:164:LEU:HD22	20:FF:170:GLN:HG3	1.80	0.62
1:0:114:GLY:HA3	9:7:73:THR:CG2	2.30	0.62
23:I:221:LEU:HA	23:I:224:HIS:HD2	1.62	0.62
12:A:2848:A:H4'	13:A1:215:LYS:HE3	1.82	0.61
20:t1:3:ILE:HG23	20:t1:4:GLN:HG2	1.82	0.61
56:q:128:MET:HB3	56:q:129:PRO:HD3	1.82	0.61
18:E:196:ALA:O	18:E:199:ARG:NH1	2.33	0.61
40:Z:101:LYS:HE3	49:j:80:LEU:HD22	1.80	0.61
12:A:2549:C:O2	12:A:2549:C:C2'	2.48	0.61
44:e:205:LEU:H	44:e:205:LEU:HD23	1.65	0.61
12:A:3051:A:O2'	12:A:3052:A:C8	2.51	0.61
34:T:134:VAL:HG11	34:T:140:LEU:HD11	1.83	0.61
13:A1:207:PRO:HA	13:A1:210:ILE:HG22	1.83	0.61
42:c:258:THR:HG22	42:c:259:ARG:HG3	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:v:20:GLY:HA2	61:v:23:LEU:HD13	1.83	0.61
46:g:141:ASN:HB3	46:g:146:THR:HG22	1.83	0.61
1:0:114:GLY:HA3	9:7:73:THR:HG21	1.83	0.61
20:t6:2:LYS:HD3	20:t6:5:GLN:HB2	1.82	0.60
30:P:91:GLU:HG2	30:P:106:SER:HB3	1.83	0.60
32:R:13:ARG:HE	42:c:32:LYS:NZ	1.97	0.60
23:I:47:LEU:HA	54:o:35:MET:HE1	1.82	0.60
12:A:2034:A:H2'	12:A:2035:U:O4'	2.02	0.60
16:C:153:ASN:HB2	16:C:225:THR:CA	2.27	0.60
20:t1:-1:TYR:HB3	20:t1:4:GLN:HG3	1.82	0.60
20:t6:2:LYS:HE2	20:t6:4:GLN:HB3	1.83	0.60
12:A:1735:A:H2'	12:A:1735:A:N3	2.17	0.60
12:A:1782:G:O6	19:F:121:ARG:HD3	2.02	0.60
24:J:130:PHE:HB3	24:J:132:LEU:HD23	1.83	0.60
16:C:256:TYR:HE2	16:C:268:VAL:HB	1.66	0.60
19:F:89:THR:HG22	19:F:179:THR:HG21	1.83	0.60
15:A2:176:LEU:HA	15:A2:179:VAL:HG12	1.83	0.60
17:D:187:LEU:HD21	17:D:244:VAL:HG22	1.83	0.59
58:s:237:PRO:HB3	58:s:300:HIS:NE2	2.17	0.59
20:t1:15:LEU:HD13	20:t3:29:LEU:HD11	1.84	0.59
34:T:72:GLU:OE2	34:T:177:LYS:HE2	2.01	0.59
7:5:123:LEU:HD22	7:5:220:LEU:HD21	1.84	0.59
16:C:45:SER:HB3	16:C:147:MET:HE1	1.83	0.59
30:P:144:MET:HE1	30:P:165:MET:HE2	1.83	0.59
42:c:72:ILE:HG23	42:c:88:LEU:HD22	1.84	0.59
15:A2:133:LEU:HD23	17:D:225:ILE:HD11	1.84	0.59
23:I:211:LEU:HD23	20:t1:22:ASN:OD1	2.03	0.59
44:e:171:TRP:HB3	44:e:263:TYR:CZ	2.37	0.59
36:V:125:PRO:HA	36:V:128:ARG:HH21	1.67	0.59
20:t1:16:LEU:HG	20:t4:11:ALA:HB1	1.84	0.59
18:E:87:ILE:HG23	18:E:317:PRO:HG3	1.84	0.59
19:F:243:ILE:HG22	56:q:27:ALA:HB2	1.85	0.59
21:G:298:ARG:NH1	21:G:299:HIS:HB3	2.17	0.59
20:t4:24:LEU:HD23	20:t4:27:LYS:HZ1	1.66	0.59
57:r:35:PHE:N	57:r:56:THR:HG1	2.01	0.59
25:K:110:GLY:O	25:K:114:LYS:NZ	2.35	0.59
12:A:2668:A:H2'	12:A:2669:A:H8	1.66	0.58
12:A:1750:G:O2'	12:A:1751:A:C8	2.56	0.58
25:K:174:GLU:HA	57:r:56:THR:HG21	1.83	0.58
34:T:143:ALA:HB2	34:T:179:VAL:HG23	1.85	0.58
35:U:24:PHE:CD2	35:U:48:MET:HE3	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:e:157:LEU:HD23	44:e:254:TRP:HB3	1.85	0.58
7:5:136:VAL:HA	7:5:139:LEU:HD12	1.85	0.58
12:A:1901:C:OP1	27:M:37:GLU:HB2	2.03	0.58
28:N:205:ARG:HH22	28:N:249:LYS:HA	1.66	0.58
2:a:67:ILE:HD13	42:c:258:THR:HG23	1.84	0.58
14:B:1618:A:H2'	14:B:1619:C:H6	1.67	0.58
40:Z:123:LYS:HG3	40:Z:144:GLU:HB3	1.85	0.58
44:e:162:ARG:HH22	44:e:169:ASP:HB3	1.69	0.58
24:J:137:LEU:HD23	24:J:137:LEU:H	1.68	0.58
41:b:74:ARG:HG2	41:b:88:SER:HA	1.85	0.58
44:e:265:LYS:N	44:e:266:PRO:HD2	2.19	0.58
36:V:78:GLN:HB3	36:V:87:VAL:HB	1.85	0.58
43:d:190:GLU:HB3	43:d:217:HIS:HB3	1.85	0.58
18:E:198:PHE:HD1	18:E:202:GLN:HE22	1.51	0.58
34:T:72:GLU:HB3	43:d:228:PHE:CE1	2.38	0.58
43:d:137:PHE:CZ	43:d:212:ILE:HD11	2.39	0.58
43:d:160:LEU:HD22	43:d:169:PHE:HD1	1.69	0.58
59:t:356:VAL:HG11	59:t:424:LEU:HD12	1.85	0.58
6:4:90:VAL:O	6:4:99:LYS:HA	2.03	0.58
21:G:105:GLY:HA3	21:G:192:ASN:H	1.68	0.58
30:P:137:LEU:HD11	55:p:184:ASN:HB3	1.86	0.58
62:w:103:HIS:CE1	62:w:106:LYS:HB3	2.39	0.58
14:B:1626:C:H2'	14:B:1627:C:C6	2.39	0.58
14:B:1620:A:H2'	14:B:1621:A:H4'	1.85	0.57
3:1:19:ARG:HH21	3:1:60:LYS:HE2	1.68	0.57
28:N:222:ASN:HB2	28:N:227:ARG:HE	1.69	0.57
42:c:32:LYS:HE3	42:c:32:LYS:HA	1.85	0.57
29:O:42:ILE:HG23	29:O:123:ILE:HG23	1.86	0.57
12:A:2523:C:O2	12:A:2523:C:H2'	2.02	0.57
17:D:111:ARG:HH21	17:D:163:ILE:HG21	1.68	0.57
3:1:55:LEU:H	56:q:128:MET:CE	2.18	0.57
7:5:115:GLU:HB2	7:5:119:GLN:HB2	1.85	0.57
60:u:127:VAL:HG23	60:u:179:LEU:HD13	1.85	0.57
8:6:233:LEU:HB2	8:6:298:PHE:CE1	2.39	0.57
21:G:241:LEU:HD23	21:G:249:PRO:HG3	1.86	0.57
23:I:207:LEU:HD11	20:t2:18:ILE:HD12	1.86	0.57
36:V:97:TYR:HE1	43:d:170:PRO:HB3	1.69	0.57
43:d:147:GLU:HG3	43:d:163:LEU:HD11	1.86	0.57
11:9:22:THR:HG22	11:9:24:LYS:H	1.70	0.57
17:D:217:LEU:HD11	17:D:227:GLN:HB3	1.87	0.57
29:O:58:LYS:HG2	31:Q:269:MET:HB3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:G:235:ALA:HA	21:G:311:ASP:HB2	1.86	0.56
12:A:2197:G:H4'	51:l:127:TRP:HE1	1.69	0.56
42:c:149:PRO:HD3	42:c:305:TYR:CE1	2.40	0.56
58:s:165:ARG:HH12	58:s:307:ARG:HH22	1.51	0.56
5:3:98:SER:HB3	5:3:105:LYS:HE3	1.87	0.56
5:3:137:THR:HG22	5:3:138:PRO:HD2	1.87	0.56
55:p:50:PRO:O	55:p:53:GLN:HG2	2.05	0.56
12:A:1952:U:H2'	12:A:1953:A:C8	2.41	0.56
18:E:248:ILE:CG2	18:E:250:ARG:HG2	2.35	0.56
43:d:160:LEU:HD22	43:d:169:PHE:CD1	2.40	0.56
12:A:2723:A:H5'	19:F:131:LYS:HB3	1.87	0.56
15:A2:130:GLU:HB3	15:A2:159:MET:HE3	1.86	0.56
1:0:130:VAL:HG21	29:O:134:PRO:HD3	1.88	0.56
16:C:53:ILE:HB	16:C:148:VAL:HG12	1.88	0.56
24:J:120:ILE:HA	24:J:123:ILE:HG12	1.87	0.56
28:N:76:SER:HA	28:N:155:LYS:HE2	1.88	0.56
47:h:139:LYS:HB3	54:o:101:TRP:NE1	2.21	0.56
12:A:2416:U:O2	12:A:2416:U:C2'	2.54	0.56
32:R:94:GLN:HE22	32:R:146:VAL:HB	1.71	0.56
33:S:84:ASN:O	33:S:88:VAL:HG23	2.06	0.56
40:Z:113:VAL:O	40:Z:117:ILE:HG12	2.06	0.56
12:A:1853:A:H62	12:A:2692:G:H1'	1.70	0.56
27:M:155:GLU:OE1	27:M:175:THR:HG23	2.06	0.56
53:n:73:GLY:HA3	53:n:104:PRO:HB2	1.87	0.56
4:2:70:LEU:HD13	39:Y:172:ILE:HD11	1.87	0.55
9:7:79:PHE:HB3	9:7:81:MET:HE3	1.88	0.55
12:A:1839:C:H2'	12:A:1840:C:C6	2.40	0.55
47:h:105:ALA:HB1	47:h:111:VAL:HG22	1.87	0.55
12:A:2081:U:H2'	12:A:2082:G:C8	2.41	0.55
13:A1:86:VAL:HG21	13:A1:154:GLU:HB2	1.87	0.55
9:7:163:MET:H	9:7:186:ASP:HB2	1.71	0.55
44:e:83:LEU:HG	44:e:84:TYR:H	1.72	0.55
12:A:2192:A:H5'	24:J:143:SER:HB2	1.89	0.55
21:G:242:ARG:HH11	21:G:251:VAL:HG12	1.72	0.55
20:t1:14:THR:HB	20:t4:11:ALA:O	2.07	0.55
61:v:20:GLY:HA3	61:v:32:PHE:HE1	1.71	0.55
12:A:2722:A:H61	12:A:2991:U:H5'	1.72	0.55
53:n:58:PHE:HA	53:n:61:LEU:HD12	1.88	0.55
59:t:221:LEU:HB3	59:t:227:ARG:HH21	1.71	0.55
10:8:121:TRP:HZ2	44:e:70:MET:HB2	1.72	0.55
12:A:1739:A:O2'	12:A:1740:A:H5'	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:5:165:GLN:NE2	7:5:175:THR:HG22	2.21	0.55
16:C:222:LEU:HD11	16:C:240:LEU:HD12	1.89	0.55
23:I:207:LEU:HD11	20:t2:18:ILE:HG23	1.88	0.55
31:Q:233:TRP:HB3	31:Q:240:ILE:HD12	1.88	0.55
12:A:2248:U:OP1	32:R:99:ARG:NH2	2.33	0.55
12:A:2995:G:O2'	12:A:3042:U:OP1	2.25	0.55
21:G:194:PHE:O	21:G:195:PHE:HB2	2.07	0.55
23:I:97:ALA:HB3	23:I:154:LEU:HB2	1.88	0.55
19:F:63:GLN:HG2	19:F:79:LEU:HD21	1.88	0.54
35:U:101:HIS:HB2	35:U:103:GLN:HE22	1.71	0.54
36:V:194:LEU:HD11	39:Y:99:HIS:HB2	1.88	0.54
12:A:2286:A:H2'	12:A:2287:U:C6	2.41	0.54
58:s:104:ARG:HE	58:s:262:PRO:HB3	1.73	0.54
1:0:173:ARG:HH11	1:0:175:ILE:HD11	1.72	0.54
12:A:2844:G:H4'	13:A1:207:PRO:HG2	1.89	0.54
33:S:99:VAL:HG12	33:S:133:VAL:HG22	1.89	0.54
6:4:84:ARG:HE	12:A:3187:C:H2'	1.73	0.54
12:A:2415:C:H3'	58:s:165:ARG:HH21	1.72	0.54
13:A1:76:LEU:HD13	13:A1:163:LEU:HD11	1.90	0.54
23:I:226:PRO:HB3	20:t5:29:LEU:HD13	1.90	0.54
2:a:67:ILE:HD12	41:b:138:THR:HG21	1.89	0.54
13:A1:244:LEU:HD23	13:A1:245:GLU:HG3	1.90	0.54
16:C:240:LEU:HD23	16:C:244:LEU:HD23	1.90	0.54
11:9:71:LYS:HB3	11:9:72:PRO:HD2	1.90	0.54
12:A:2054:U:C5	54:o:75:LYS:HG2	2.43	0.54
20:FF:132:VAL:HB	20:FF:173:LYS:HB2	1.90	0.54
31:Q:168:ASN:O	31:Q:171:VAL:HG12	2.07	0.54
43:d:235:GLN:HG3	43:d:238:VAL:CG2	2.35	0.54
47:h:116:ARG:HD3	47:h:129:PHE:HE1	1.73	0.54
16:C:256:TYR:CE2	16:C:268:VAL:HB	2.42	0.54
19:F:103:GLN:HE22	19:F:249:ASN:HD22	1.56	0.54
34:T:72:GLU:HB3	43:d:228:PHE:HE1	1.73	0.53
9:7:107:LEU:HB2	9:7:126:LYS:HG2	1.90	0.53
30:P:130:ARG:HG3	30:P:164:ALA:HB1	1.90	0.53
40:Z:69:VAL:HG22	40:Z:119:ILE:HG23	1.89	0.53
41:b:49:ARG:HG3	41:b:50:GLU:OE1	2.08	0.53
10:8:104:VAL:HG11	44:e:80:GLU:HB2	1.90	0.53
12:A:1868:G:H2'	27:M:40:PRO:HG3	1.90	0.53
12:A:2840:C:O2	12:A:2840:C:O4'	2.26	0.53
12:A:3129:A:H4'	21:G:265:ILE:HD11	1.90	0.53
16:C:288:THR:HG21	31:Q:195:PRO:HG3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:M:153:ASN:HB2	27:M:256:LEU:HD23	1.91	0.53
33:S:154:VAL:HG12	33:S:200:ILE:HG22	1.91	0.53
36:V:108:MET:HE2	43:d:166:GLU:HA	1.91	0.53
58:s:332:LEU:HD13	58:s:372:TYR:HB2	1.91	0.53
17:D:286:ILE:HB	17:D:288:PRO:HD2	1.89	0.53
50:k:61:GLU:N	50:k:62:PRO:CD	2.72	0.53
1:O:137:ILE:HG12	1:O:177:ARG:NH2	2.24	0.53
6:4:86:GLY:H	12:A:3189:C:H5''	1.73	0.53
12:A:2740:A:H2'	12:A:2741:A:C8	2.43	0.53
18:E:207:THR:HB	18:E:267:THR:HG23	1.91	0.53
24:J:135:VAL:N	24:J:136:PRO:HD2	2.23	0.53
12:A:2275:U:H2'	12:A:2276:C:C6	2.44	0.53
44:e:83:LEU:HD22	52:m:47:ALA:HB1	1.90	0.53
12:A:2153:A:H2'	54:o:30:ARG:NH2	2.24	0.53
16:C:84:LYS:HZ3	16:C:154:VAL:HA	1.74	0.53
36:V:135:TRP:HB3	36:V:143:ARG:HH21	1.74	0.53
45:f:171:LEU:HA	45:f:174:ILE:HG12	1.91	0.53
12:A:2267:U:H2'	12:A:2268:G:H8	1.74	0.53
12:A:2673:G:H5''	34:T:112:LYS:HB2	1.91	0.53
40:Z:56:TYR:CE1	54:o:44:GLU:HG2	2.44	0.53
49:j:48:ASP:H	49:j:60:MET:HE3	1.73	0.53
20:t4:18:ILE:HA	20:t4:21:LEU:HD12	1.89	0.53
7:5:108:HIS:HD2	7:5:110:ARG:H	1.57	0.52
12:A:1816:G:H2'	12:A:1817:C:O4'	2.09	0.52
12:A:2257:C:H4'	33:S:118:ASN:OD1	2.09	0.52
12:A:2682:A:H5''	32:R:34:ARG:NH2	2.24	0.52
13:A1:292:LEU:HD21	13:A1:380:MET:HE1	1.91	0.52
25:K:20:LEU:HB2	25:K:141:LEU:HD13	1.91	0.52
57:r:70:CYS:HB2	57:r:73:CYS:H	1.73	0.52
6:4:76:CYS:HB2	6:4:79:CYS:H	1.74	0.52
16:C:111:THR:HA	16:C:122:ILE:HD11	1.91	0.52
3:1:50:VAL:HG13	3:1:52:GLN:HB2	1.91	0.52
11:9:136:LEU:HD21	35:U:7:TYR:HA	1.90	0.52
13:A1:139:ILE:C	15:A2:322:ARG:HH22	2.18	0.52
12:A:2075:U:O2'	12:A:2833:A:N7	2.38	0.52
19:F:69:LEU:HG	19:F:190:MET:CE	2.38	0.52
58:s:210:TRP:HZ3	58:s:233:ILE:HG22	1.73	0.52
33:S:54:THR:HG22	33:S:57:SER:HB3	1.92	0.52
35:U:37:GLU:HB2	35:U:104:THR:HG23	1.90	0.52
61:v:3:PRO:HA	61:v:51:ARG:HB3	1.92	0.52
5:3:106:THR:HG22	5:3:163:THR:H	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:A:2473:A:H2'	12:A:2473:A:N3	2.25	0.52
44:e:265:LYS:N	44:e:266:PRO:CD	2.73	0.52
21:G:227:ALA:HB3	21:G:276:VAL:HG12	1.92	0.52
34:T:150:GLY:H	34:T:172:CYS:HA	1.74	0.52
43:d:169:PHE:N	43:d:170:PRO:HD2	2.25	0.52
58:s:332:LEU:HD21	58:s:359:ALA:HB2	1.91	0.52
12:A:1840:C:H2'	12:A:1841:U:C6	2.45	0.52
12:A:1854:U:H1'	12:A:1855:A:C5'	2.40	0.52
27:M:211:VAL:N	27:M:212:PRO:HD2	2.25	0.52
38:X:168:ARG:HG3	38:X:173:ASP:HB2	1.91	0.52
7:5:290:THR:HA	7:5:343:GLN:O	2.10	0.52
12:A:1843:U:C2	12:A:1853:A:H2'	2.45	0.51
16:C:46:LEU:HD22	16:C:52:ILE:HG12	1.91	0.51
20:FF:158:LEU:HD13	59:t:198:GLU:HG2	1.93	0.51
31:Q:120:THR:HG22	31:Q:132:GLN:HG2	1.92	0.51
12:A:2072:A:H2'	12:A:2073:A:C8	2.45	0.51
44:e:142:GLU:HG3	44:e:145:ASP:HB2	1.92	0.51
47:h:142:GLU:O	47:h:146:SER:HB3	2.10	0.51
7:5:181:VAL:O	7:5:185:ILE:HG12	2.10	0.51
27:M:154:ILE:HG21	27:M:167:ILE:HD13	1.92	0.51
20:t1:-4:PRO:O	20:t1:-3:LYS:C	2.53	0.51
33:S:162:GLU:HB3	33:S:192:VAL:HB	1.92	0.51
20:t1:-1:TYR:HB3	20:t1:4:GLN:CB	2.41	0.51
12:A:2650:C:H4'	53:n:199:SER:HB3	1.92	0.51
33:S:156:VAL:HG22	33:S:198:ILE:HG12	1.91	0.51
20:t3:5:GLN:HG2	20:t3:8:GLN:HE21	1.76	0.51
16:C:233:GLU:HG2	16:C:302:ALA:HB1	1.93	0.51
23:I:225:GLN:NE2	20:t3:15:LEU:HD22	2.24	0.51
27:M:142:GLU:HB3	27:M:162:LEU:HD23	1.92	0.51
35:U:127:TYR:HA	35:U:130:LEU:HD12	1.92	0.51
37:W:53:ILE:HD11	37:W:75:TRP:CE2	2.46	0.51
59:t:260:LEU:HD21	59:t:279:LEU:HD22	1.93	0.51
12:A:1814:A:H2'	12:A:1815:A:C8	2.46	0.51
23:I:83:ARG:NE	23:I:83:ARG:HA	2.25	0.51
27:M:16:LEU:HD11	54:o:92:LEU:HD22	1.93	0.51
62:w:74:LEU:HD22	62:w:152:LYS:HB3	1.93	0.51
12:A:2127:A:H4'	12:A:2251:A:C5	2.46	0.51
35:U:68:VAL:HG22	35:U:97:VAL:HG22	1.93	0.51
35:U:153:LEU:HB3	43:d:240:LYS:HE2	1.91	0.51
49:j:45:GLU:HA	49:j:63:GLN:NE2	2.25	0.51
53:n:135:THR:HG22	53:n:138:ARG:HH21	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:r:79:HIS:HB3	57:r:184:ASN:HA	1.91	0.51
59:t:256:LYS:HB3	59:t:281:ARG:HH11	1.75	0.51
60:u:106:ALA:HA	60:u:138:MET:HE1	1.93	0.51
9:7:112:PRO:HB2	9:7:267:PRO:HG2	1.93	0.51
1:0:159:LEU:HD13	1:0:174:ILE:HG23	1.93	0.50
12:A:2276:C:HI1'	32:R:11:ARG:HH22	1.77	0.50
17:D:257:ILE:HG23	17:D:262:ARG:CB	2.41	0.50
23:I:225:GLN:HG3	23:I:226:PRO:HD3	1.92	0.50
28:N:175:PHE:O	28:N:179:VAL:HG23	2.11	0.50
29:O:18:MET:HB2	29:O:25:ARG:HG3	1.92	0.50
30:P:86:THR:HG22	30:P:87:GLN:H	1.75	0.50
35:U:67:ALA:HB3	35:U:98:GLN:HB2	1.94	0.50
43:d:184:SER:HB3	43:d:221:THR:OG1	2.12	0.50
60:u:166:ASP:HA	60:u:181:LEU:HD23	1.93	0.50
12:A:2027:A:O2'	12:A:2048:U:H5''	2.12	0.50
13:A1:153:MET:HE1	13:A1:219:SER:HB3	1.92	0.50
41:b:6:THR:HB	41:b:7:PRO:HD2	1.92	0.50
41:b:131:HIS:HB2	41:b:132:PRO:HD2	1.93	0.50
8:6:145:PRO:HB2	8:6:168:VAL:HG12	1.94	0.50
44:e:50:ALA:HB1	44:e:173:LEU:HD23	1.92	0.50
8:6:140:GLU:HG3	8:6:172:PRO:HB3	1.92	0.50
16:C:107:ASN:O	16:C:109:ILE:HG12	2.12	0.50
23:I:194:TYR:CD1	20:t2:16:LEU:HD11	2.46	0.50
27:M:89:PHE:HE2	38:X:56:ASN:HB2	1.76	0.50
30:P:66:ARG:HB2	37:W:92:LEU:HD13	1.93	0.50
59:t:168:ALA:HA	59:t:171:ILE:HG12	1.93	0.50
20:t1:25:LEU:HD23	20:t2:7:VAL:HG13	1.94	0.50
3:1:55:LEU:HB2	56:q:128:MET:HE1	1.94	0.50
9:7:107:LEU:HG	9:7:128:LEU:HD11	1.94	0.50
39:Y:116:GLU:HG2	39:Y:126:MET:SD	2.51	0.50
8:6:53:SER:HB3	8:6:56:ARG:HG3	1.94	0.50
12:A:1777:A:N6	12:A:1780:U:OP2	2.45	0.50
12:A:3212:C:O2	12:A:3212:C:O4'	2.30	0.50
13:A1:181:CYS:HB3	66:A1:401:SAM:H5'2	1.94	0.50
13:A1:247:ASP:OD1	13:A1:382:ARG:NH2	2.44	0.50
15:A2:261:ILE:HG13	15:A2:262:LYS:N	2.27	0.50
32:R:112:THR:HG23	33:S:142:THR:HG21	1.94	0.50
18:E:219:MET:HE2	18:E:226:GLY:HA3	1.94	0.50
19:F:69:LEU:HD12	19:F:193:LEU:HA	1.94	0.50
23:I:194:TYR:CG	20:t2:16:LEU:HD21	2.25	0.50
9:7:113:TRP:CZ2	9:7:117:LYS:HE3	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:8:106:LEU:HG	10:8:107:THR:H	1.76	0.50
12:A:2073:A:C5	12:A:2074:A:H1'	2.47	0.50
12:A:3065:U:H4'	18:E:239:ARG:NH2	2.26	0.50
12:A:3134:C:O4'	12:A:3134:C:O2	2.29	0.50
23:I:225:GLN:HA	23:I:228:GLN:HB2	1.94	0.50
27:M:22:VAL:HG22	54:o:95:LEU:HD21	1.94	0.50
28:N:222:ASN:OD1	28:N:225:GLY:HA2	2.12	0.50
29:O:94:ALA:HB3	29:O:95:PRO:HD3	1.93	0.50
42:c:228:LEU:HD23	42:c:229:PHE:CE1	2.46	0.50
49:j:97:LYS:O	49:j:100:GLU:HG3	2.12	0.50
12:A:1925:A:H2'	12:A:1926:A:C8	2.47	0.49
12:A:2052:A:H2'	12:A:2053:U:O4'	2.11	0.49
29:O:36:LEU:HD13	29:O:42:ILE:HG22	1.94	0.49
12:A:2079:C:O4'	12:A:2079:C:O2	2.30	0.49
13:A1:187:LYS:HD2	13:A1:255:ASP:OD2	2.11	0.49
21:G:312:LEU:HD12	21:G:347:ILE:HG22	1.94	0.49
50:k:23:PHE:HE1	20:t1:-8:LEU:HA	1.77	0.49
60:u:92:PHE:CE2	60:u:146:TYR:HA	2.47	0.49
1:0:137:ILE:HA	1:0:177:ARG:HH22	1.77	0.49
2:a:67:ILE:HD12	41:b:138:THR:CG2	2.42	0.49
7:5:107:PHE:HE1	7:5:113:LEU:HD21	1.73	0.49
10:8:121:TRP:CZ2	44:e:70:MET:HB2	2.47	0.49
12:A:2016:C:OP2	27:M:59:ARG:NH1	2.27	0.49
12:A:3039:U:C2	12:A:3041:U:H5'	2.47	0.49
23:I:200:LEU:HA	20:t2:15:LEU:HD13	1.94	0.49
26:L:87:VAL:HG11	26:L:123:ILE:HG22	1.93	0.49
59:t:60:VAL:O	59:t:124:HIS:HA	2.12	0.49
29:O:65:LEU:HB3	29:O:69:ASN:HD22	1.77	0.49
31:Q:121:THR:HG22	31:Q:171:VAL:HA	1.94	0.49
38:X:87:LEU:HD23	38:X:104:VAL:HG13	1.95	0.49
9:7:256:ARG:HG2	9:7:261:ILE:HG12	1.95	0.49
12:A:1856:A:H2'	12:A:1857:U:C6	2.48	0.49
12:A:2900:C:H2'	12:A:2901:A:H8	1.78	0.49
13:A1:202:ALA:HB3	13:A1:233:VAL:HG12	1.95	0.49
16:C:123:ILE:O	16:C:127:THR:OG1	2.27	0.49
16:C:152:PRO:HB2	16:C:225:THR:O	2.12	0.49
20:FF:146:ILE:HG22	20:FF:158:LEU:HD23	1.95	0.49
23:I:194:TYR:CZ	20:t2:16:LEU:CD1	2.95	0.49
30:P:93:LEU:HD21	30:P:101:VAL:HG22	1.94	0.49
32:R:13:ARG:HE	42:c:32:LYS:CE	2.25	0.49
37:W:102:GLU:HB2	37:W:130:PHE:CD1	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:h:148:LEU:HD22	47:h:152:LEU:HD23	1.94	0.49
12:A:2101:C:H2'	12:A:2102:A:H8	1.78	0.49
58:s:142:LEU:HD11	58:s:188:LEU:HD11	1.95	0.49
10:8:132:GLU:O	10:8:136:ILE:HG12	2.12	0.49
13:A1:222:PRO:HD2	13:A1:225:ILE:HD12	1.95	0.49
36:V:36:PRO:HG2	36:V:39:ILE:HG23	1.95	0.49
43:d:215:ARG:HE	43:d:243:LEU:HD11	1.78	0.49
1:0:152:PRO:HG3	1:0:173:ARG:HE	1.78	0.49
11:9:60:PHE:CD1	35:U:22:THR:HG21	2.48	0.49
12:A:1884:G:H1'	12:A:1895:C:H1'	1.95	0.49
12:A:2609:U:OP1	15:A2:260:LYS:HE2	2.13	0.49
13:A1:244:LEU:HD21	45:f:204:LEU:HD22	1.94	0.49
16:C:243:THR:HA	16:C:246:LYS:HD2	1.95	0.49
2:a:58:ILE:HD13	32:R:119:LEU:HD11	1.94	0.49
12:A:2486:U:H2'	12:A:2487:A:C8	2.47	0.49
12:A:2511:C:H3'	12:A:2512:A:H8	1.77	0.49
12:A:2740:A:N3	12:A:2921:A:O2'	2.42	0.49
20:t3:25:LEU:HG	20:t4:7:VAL:HG22	1.93	0.49
12:A:3220:A:OP1	18:E:215:PHE:HB2	2.13	0.48
19:F:67:GLU:HG2	19:F:190:MET:SD	2.52	0.48
29:O:10:SER:HB2	29:O:13:ARG:HG3	1.95	0.48
58:s:174:LEU:HB3	58:s:175:PRO:HD3	1.94	0.48
59:t:387:CYS:HB3	59:t:410:LEU:HD13	1.95	0.48
19:F:93:LEU:HD21	54:o:95:LEU:CD1	2.43	0.48
19:F:280:TYR:OH	27:M:109:ARG:HG2	2.13	0.48
26:L:111:ASN:HB3	60:u:164:THR:HG22	1.96	0.48
49:j:39:GLY:O	49:j:44:THR:HG21	2.13	0.48
58:s:345:PHE:CD1	58:s:351:VAL:HA	2.47	0.48
20:t1:13:LEU:HD13	20:t1:17:GLU:HG2	1.95	0.48
7:5:107:PHE:HE1	7:5:113:LEU:CD2	2.26	0.48
12:A:2318:A:H2'	12:A:2319:A:C8	2.48	0.48
15:A2:200:LEU:HD12	15:A2:204:LYS:HG3	1.94	0.48
26:L:95:ARG:HA	26:L:95:ARG:NE	2.27	0.48
40:Z:117:ILE:O	54:o:45:ASN:ND2	2.46	0.48
23:I:223:GLN:O	23:I:226:PRO:HD2	2.13	0.48
29:O:26:ILE:HD12	31:Q:264:TRP:HB2	1.95	0.48
41:b:7:PRO:HG2	41:b:113:ILE:HG21	1.94	0.48
7:5:174:GLU:HA	7:5:296:LYS:HB2	1.95	0.48
12:A:2816:G:H5'	12:A:2817:G:H5'	1.94	0.48
35:U:22:THR:H	39:Y:102:TRP:HH2	1.58	0.48
11:9:55:GLU:HG2	35:U:16:GLN:HA	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:A:2482:A:H2	12:A:2653:C:O2	1.96	0.48
27:M:117:ASP:HA	27:M:155:GLU:HB3	1.95	0.48
8:6:337:MET:HB2	30:P:42:GLU:HG3	1.94	0.48
13:A1:48:PHE:CD1	13:A1:52:TYR:HE2	2.30	0.48
20:FF:146:ILE:HD11	20:FF:165:VAL:HG11	1.94	0.48
20:FF:168:LEU:H	20:FF:169:PRO:HD3	1.79	0.48
23:I:234:ASP:O	23:I:238:ARG:HG3	2.14	0.48
24:J:148:ALA:HB1	24:J:153:ILE:HD11	1.96	0.48
12:A:1856:A:H2'	12:A:1857:U:H6	1.79	0.48
16:C:273:ALA:HA	16:C:278:LYS:HE3	1.96	0.48
27:M:62:ARG:HH21	48:i:128:ARG:HB2	1.78	0.48
29:O:33:LEU:O	29:O:37:VAL:HG23	2.14	0.48
43:d:235:GLN:HE22	43:d:240:LYS:HD3	1.79	0.48
59:t:284:LEU:H	59:t:316:ALA:HB3	1.79	0.48
62:w:103:HIS:HE1	62:w:106:LYS:HB3	1.79	0.48
18:E:334:ASP:HB3	18:E:337:VAL:HG23	1.96	0.48
21:G:346:LYS:HG2	68:G:502:GTP:C5	2.48	0.48
24:J:154:ARG:HE	24:J:155:VAL:H	1.60	0.48
30:P:146:TYR:OH	30:P:158:MET:HE2	2.13	0.48
55:p:112:ALA:HB3	55:p:115:VAL:HG22	1.95	0.48
59:t:380:SER:HB2	59:t:383:TRP:CZ2	2.49	0.48
11:9:61:VAL:HG11	35:U:20:PHE:CE2	2.49	0.48
12:A:2035:U:O2'	27:M:70:GLY:HA3	2.14	0.48
44:e:142:GLU:HG2	44:e:143:LYS:N	2.28	0.48
1:0:185:PHE:HD1	29:O:132:PRO:HD3	1.79	0.47
8:6:215:THR:HB	8:6:273:PHE:HB2	1.96	0.47
12:A:2665:U:OP2	29:O:17:ARG:HD2	2.14	0.47
33:S:158:ALA:HB2	33:S:195:ILE:HD13	1.96	0.47
7:5:256:PHE:HD2	7:5:259:ILE:HB	1.78	0.47
18:E:257:MET:HB2	18:E:258:PRO:CD	2.43	0.47
12:A:1718:A:H2'	12:A:1719:G:O4'	2.13	0.47
43:d:183:TRP:HD1	43:d:222:LEU:HD12	1.80	0.47
44:e:160:LEU:HD12	44:e:255:VAL:HB	1.96	0.47
9:7:290:GLN:N	9:7:291:PRO:HD2	2.30	0.47
14:B:1651:A:C2	14:B:1659:U:C2	3.03	0.47
19:F:71:GLY:O	19:F:210:ARG:NH2	2.47	0.47
19:F:253:MET:HG2	19:F:259:LEU:HD13	1.96	0.47
23:I:230:THR:HG21	20:t5:26:LYS:HE2	1.95	0.47
20:t1:-1:TYR:HB3	20:t1:4:GLN:CG	2.44	0.47
8:6:224:HIS:CD2	8:6:227:GLU:H	2.32	0.47
18:E:109:LEU:HD21	18:E:337:VAL:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:G:256:PHE:CE1	21:G:283:ILE:HD11	2.48	0.47
27:M:28:LYS:HD3	54:o:94:HIS:CE1	2.50	0.47
27:M:97:SER:HA	27:M:141:VAL:HG22	1.96	0.47
43:d:197:VAL:HB	43:d:212:ILE:HG22	1.96	0.47
12:A:2178:A:C8	21:G:291:GLY:HA2	2.50	0.47
12:A:2822:C:O2'	12:A:2915:C:OP2	2.30	0.47
24:J:140:VAL:O	24:J:144:ILE:HG12	2.15	0.47
33:S:86:MET:HE3	33:S:141:PHE:CD1	2.50	0.47
35:U:66:ALA:HB2	35:U:100:ALA:HB2	1.96	0.47
5:3:108:LYS:HZ1	12:A:1743:U:P	2.37	0.47
12:A:2330:U:H3	12:A:2447:A:H61	1.61	0.47
12:A:2960:U:H5''	21:G:76:ARG:HH12	1.79	0.47
12:A:3183:U:H3	25:K:177:ARG:HB3	1.79	0.47
16:C:54:GLU:O	16:C:81:VAL:N	2.48	0.47
16:C:60:ILE:HB	16:C:63:SER:OG	2.15	0.47
16:C:279:THR:HB	16:C:296:PRO:HB3	1.96	0.47
17:D:111:ARG:NH2	17:D:179:GLY:O	2.47	0.47
25:K:80:HIS:ND1	25:K:81:THR:O	2.44	0.47
25:K:154:ARG:HB2	25:K:157:GLU:HG3	1.96	0.47
32:R:51:VAL:HG21	33:S:174:PHE:HB3	1.96	0.47
44:e:179:GLN:HB2	44:e:182:GLU:HG2	1.96	0.47
58:s:239:ASN:HB2	58:s:299:PHE:HB2	1.96	0.47
59:t:279:LEU:HB3	59:t:318:ALA:HA	1.95	0.47
59:t:357:TYR:HE2	59:t:359:LEU:HD13	1.80	0.47
20:t1:24:LEU:HD12	20:t2:3:ILE:CG2	2.45	0.47
21:G:389:TYR:O	21:G:393:ALA:HB3	2.14	0.47
16:C:80:LEU:HG	16:C:107:ASN:HD22	1.80	0.47
19:F:263:LEU:N	19:F:264:PRO:HD2	2.29	0.47
30:P:57:GLU:HG3	30:P:78:TRP:CD2	2.50	0.47
30:P:72:PHE:CD1	30:P:73:PRO:HA	2.49	0.47
44:e:83:LEU:HG	44:e:84:TYR:N	2.29	0.47
58:s:406:GLU:HB2	58:s:411:LYS:NZ	2.30	0.47
7:5:133:PRO:HB3	7:5:239:ILE:HG21	1.97	0.47
7:5:174:GLU:OE1	7:5:298:ASN:ND2	2.48	0.47
13:A1:336:VAL:HA	13:A1:382:ARG:HA	1.96	0.47
16:C:60:ILE:HG13	16:C:220:LEU:HD23	1.97	0.47
21:G:256:PHE:HD1	21:G:292:LEU:HD12	1.80	0.47
12:A:1840:C:H2'	12:A:1841:U:H6	1.80	0.46
12:A:2894:U:H5''	12:A:2895:U:O4'	2.14	0.46
19:F:113:LYS:HG3	19:F:157:GLY:H	1.79	0.46
21:G:384:HIS:HA	21:G:387:VAL:HG12	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:M:268:GLY:HA3	46:g:47:PHE:CG	2.50	0.46
34:T:156:ILE:HB	43:d:48:THR:HG21	1.97	0.46
45:f:126:ALA:HB1	45:f:153:HIS:HE1	1.80	0.46
47:h:104:LEU:O	47:h:108:LEU:HB2	2.16	0.46
60:u:135:LEU:HD22	60:u:179:LEU:HB3	1.96	0.46
2:a:46:ASN:O	2:a:63:PRO:HD2	2.15	0.46
19:F:263:LEU:O	19:F:266:VAL:HG12	2.14	0.46
19:F:276:GLN:O	19:F:279:ARG:HG2	2.16	0.46
25:K:17:ILE:HG23	25:K:142:VAL:CG1	2.46	0.46
52:m:51:LEU:HB3	52:m:67:ARG:HB3	1.97	0.46
8:6:220:SER:HA	8:6:268:LEU:HG	1.97	0.46
12:A:2193:U:H5''	51:l:115:ARG:HH12	1.81	0.46
15:A2:164:SER:O	15:A2:168:LYS:HG2	2.14	0.46
15:A2:202:LYS:HZ2	15:A2:209:VAL:HA	1.80	0.46
16:C:122:ILE:O	16:C:125:MET:HG3	2.16	0.46
17:D:197:GLU:HG3	17:D:240:CYS:HB3	1.96	0.46
30:P:85:ARG:HG3	30:P:90:VAL:HG22	1.97	0.46
41:b:136:LYS:O	42:c:259:ARG:NH2	2.49	0.46
3:1:18:VAL:HG12	3:1:61:LYS:HA	1.96	0.46
12:A:2617:A:H62	12:A:2619:A:H62	1.63	0.46
31:Q:165:GLU:HB2	31:Q:168:ASN:HB2	1.97	0.46
35:U:144:ARG:HB3	35:U:147:VAL:HG12	1.98	0.46
36:V:63:GLU:OE2	36:V:73:GLN:HG3	2.16	0.46
58:s:212:ARG:HD2	58:s:379:LEU:HD12	1.97	0.46
8:6:335:LEU:HD12	30:P:41:ASN:HD21	1.80	0.46
12:A:1885:A:N6	19:F:281:ARG:NH1	2.63	0.46
35:U:20:PHE:HZ	36:V:199:MET:HG3	1.81	0.46
53:n:167:HIS:O	53:n:171:ILE:HG12	2.16	0.46
62:w:134:ASP:O	62:w:137:LYS:HG3	2.15	0.46
7:5:126:THR:HG21	7:5:357:PHE:HE1	1.81	0.46
12:A:1899:G:H4'	27:M:34:LYS:HD3	1.98	0.46
21:G:87:ALA:HB2	21:G:108:GLY:HA3	1.97	0.46
21:G:283:ILE:HD13	21:G:291:GLY:HA3	1.97	0.46
60:u:145:MET:HE3	60:u:149:LEU:HD11	1.96	0.46
12:A:2174:G:H21	24:J:104:THR:HG21	1.80	0.46
21:G:157:VAL:HG22	21:G:158:PRO:HD2	1.97	0.46
21:G:204:VAL:HG12	21:G:206:CYS:H	1.80	0.46
21:G:285:GLY:C	21:G:287:HIS:H	2.24	0.46
40:Z:77:ARG:HH11	40:Z:77:ARG:HB2	1.80	0.46
9:7:289:THR:HB	9:7:293:LEU:HA	1.97	0.46
12:A:3193:U:H5''	57:r:141:PRO:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:C:207:LEU:H	16:C:207:LEU:HD23	1.81	0.46
43:d:142:LYS:O	43:d:146:ILE:HD12	2.16	0.46
62:w:95:PRO:HA	62:w:98:LEU:HB3	1.98	0.46
12:A:1691:C:H2'	12:A:1692:A:O4'	2.16	0.46
15:A2:245:HIS:N	15:A2:246:PRO:HD2	2.32	0.46
33:S:86:MET:HE3	33:S:141:PHE:HD1	1.81	0.46
59:t:203:LEU:HD13	59:t:213:THR:HG21	1.98	0.46
20:t3:11:ALA:HA	20:t6:15:LEU:HB2	1.98	0.46
6:4:82:VAL:HG21	6:4:84:ARG:NH1	2.31	0.45
9:7:256:ARG:CG	9:7:261:ILE:HG12	2.46	0.45
11:9:97:ALA:N	11:9:98:PRO:HD2	2.31	0.45
12:A:3089:A:H1'	21:G:102:GLY:HA2	1.98	0.45
15:A2:191:GLN:HE21	15:A2:191:GLN:HA	1.81	0.45
42:c:83:PHE:CG	42:c:88:LEU:HD12	2.51	0.45
7:5:117:VAL:O	7:5:121:LEU:HG	2.15	0.45
7:5:123:LEU:HD22	7:5:220:LEU:CD2	2.45	0.45
16:C:239:TYR:O	16:C:243:THR:HG23	2.16	0.45
36:V:117:HIS:CE1	36:V:118:ARG:HH11	2.34	0.45
44:e:51:LEU:HD13	44:e:188:ALA:HB1	1.97	0.45
58:s:51:MET:HE1	58:s:65:ARG:HB2	1.99	0.45
58:s:374:LEU:HD21	58:s:377:LEU:HD11	1.99	0.45
7:5:224:GLY:HA2	7:5:316:PHE:CE1	2.51	0.45
8:6:327:VAL:HA	8:6:330:ILE:HD12	1.97	0.45
12:A:3057:C:H2'	12:A:3058:U:O4'	2.17	0.45
14:B:1632:U:N3	14:B:1635:C:OP2	2.45	0.45
11:9:114:LEU:HD23	11:9:114:LEU:H	1.81	0.45
16:C:311:ARG:HD3	16:C:311:ARG:HA	1.81	0.45
33:S:129:ARG:HH11	33:S:155:ARG:HH11	1.64	0.45
44:e:94:GLU:HA	44:e:97:ARG:HG2	1.97	0.45
50:k:61:GLU:N	50:k:62:PRO:HD3	2.31	0.45
59:t:268:VAL:HG11	61:v:21:ARG:HH21	1.81	0.45
12:A:1953:A:O2'	12:A:2463:A:OP1	2.35	0.45
18:E:100:ILE:HD13	18:E:175:THR:HG23	1.98	0.45
23:I:144:LEU:N	23:I:145:PRO:HD2	2.31	0.45
60:u:164:THR:OG1	60:u:167:TRP:O	2.34	0.45
15:A2:266:ILE:HG22	15:A2:316:PHE:HZ	1.81	0.45
18:E:61:ILE:HD11	29:O:149:LEU:CD1	2.47	0.45
35:U:41:GLN:HE21	35:U:96:TYR:HE2	1.65	0.45
43:d:145:PHE:CG	43:d:216:MET:HE1	2.52	0.45
8:6:138:GLU:HB3	8:6:141:ARG:HH21	1.81	0.45
8:6:337:MET:HE3	30:P:42:GLU:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:A2:200:LEU:HD23	15:A2:230:LEU:HD23	1.98	0.45
18:E:99:LEU:HD12	18:E:198:PHE:CE2	2.51	0.45
20:t2:1:PRO:HB2	20:t2:2:LYS:H	1.57	0.45
5:3:98:SER:CB	5:3:105:LYS:HE3	2.47	0.45
9:7:130:PHE:HB3	9:7:306:LEU:HD11	1.98	0.45
12:A:2407:U:H2'	12:A:2408:U:C6	2.52	0.45
18:E:198:PHE:HD1	18:E:202:GLN:NE2	2.14	0.45
19:F:103:GLN:NE2	19:F:249:ASN:HD22	2.15	0.45
46:g:129:SER:N	46:g:130:PRO:HD2	2.32	0.45
62:w:104:PHE:HB3	62:w:110:LEU:HD12	1.98	0.45
7:5:230:LEU:HD23	7:5:289:HIS:ND1	2.32	0.45
10:8:123:LEU:O	10:8:126:GLN:HB3	2.16	0.45
11:9:128:PHE:HD2	36:V:196:GLU:HG3	1.82	0.45
12:A:2983:G:H2'	12:A:2984:A:H8	1.80	0.45
13:A1:272:ILE:HA	13:A1:277:ARG:HH12	1.82	0.45
23:I:146:LEU:HD12	23:I:177:LEU:HB3	1.97	0.45
59:t:216:ILE:HG12	59:t:238:LYS:HB3	1.99	0.45
12:A:2692:G:H3'	12:A:2693:A:C5'	2.47	0.45
12:A:3219:G:H2'	12:A:3220:A:H5''	1.98	0.45
13:A1:288:GLN:OE1	13:A1:316:GLN:HB2	2.16	0.45
23:I:231:THR:O	23:I:235:GLN:HG2	2.16	0.45
36:V:186:THR:HG23	39:Y:94:SER:H	1.82	0.45
57:r:169:TRP:CE3	57:r:170:ASN:HB2	2.52	0.45
20:t6:24:LEU:HD23	20:t6:27:LYS:HD2	1.99	0.45
17:D:183:PRO:HA	17:D:241:VAL:HA	1.98	0.44
27:M:89:PHE:CE2	38:X:56:ASN:HB2	2.53	0.44
42:c:193:GLN:HE21	42:c:193:GLN:HB3	1.63	0.44
50:k:14:LYS:HB3	50:k:67:LEU:O	2.17	0.44
55:p:113:GLU:N	55:p:114:PRO:HD2	2.31	0.44
1:0:132:LYS:HG3	43:d:290:GLU:OE2	2.17	0.44
12:A:1853:A:H5''	12:A:1854:U:H6	1.81	0.44
21:G:86:GLY:O	21:G:208:PRO:HA	2.17	0.44
23:I:214:LEU:O	23:I:218:THR:HG23	2.18	0.44
24:J:132:LEU:HD12	24:J:140:VAL:HG22	1.98	0.44
31:Q:111:PHE:CE2	31:Q:140:ARG:HD2	2.52	0.44
34:T:107:GLU:HG2	34:T:118:LYS:HE3	1.99	0.44
49:j:44:THR:HG23	49:j:45:GLU:HG3	1.99	0.44
5:3:157:LEU:HG	5:3:161:MET:HE2	1.99	0.44
8:6:261:ARG:HH22	55:p:125:ASN:HB3	1.81	0.44
12:A:2316:U:H3	29:O:115:LEU:HD21	1.82	0.44
12:A:2727:C:H2'	12:A:2728:C:C6	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:H:55:ILE:HG21	38:X:44:ARG:HG2	1.98	0.44
30:P:107:THR:HG23	30:P:128:ILE:HD11	1.98	0.44
32:R:83:TYR:N	32:R:84:PRO:HD2	2.32	0.44
39:Y:109:ARG:HD3	39:Y:139:MET:HE1	2.00	0.44
61:v:48:ALA:HA	61:v:51:ARG:HD2	1.99	0.44
1:O:185:PHE:CD1	29:O:131:PRO:HA	2.52	0.44
14:B:1633:U:H3	45:f:124:SER:HB2	1.82	0.44
18:E:219:MET:HE3	18:E:238:ARG:HA	1.99	0.44
19:F:87:PHE:C	19:F:179:THR:HG22	2.42	0.44
25:K:17:ILE:HG23	25:K:142:VAL:HG11	2.00	0.44
31:Q:131:SER:HB3	60:u:119:ARG:CD	2.46	0.44
34:T:148:GLY:O	34:T:172:CYS:HB2	2.17	0.44
38:X:42:HIS:CG	38:X:86:ILE:HD11	2.52	0.44
46:g:121:GLN:HA	46:g:147:LEU:HD11	1.98	0.44
59:t:169:ARG:HD2	59:t:206:PHE:HB3	1.97	0.44
12:A:1977:U:H2'	12:A:1978:A:H8	1.83	0.44
12:A:3061:G:H1'	18:E:245:THR:HG23	2.00	0.44
22:H:131:TYR:HE1	38:X:136:ASP:HA	1.81	0.44
26:L:87:VAL:O	26:L:104:ASN:HB2	2.18	0.44
26:L:99:ARG:HH11	31:Q:161:GLU:HG3	1.82	0.44
41:b:68:ARG:HB3	47:h:157:SER:HB3	1.99	0.44
43:d:240:LYS:HE3	43:d:274:GLN:CD	2.43	0.44
48:i:57:TYR:CE1	56:q:30:PRO:HB3	2.53	0.44
57:r:71:PRO:HD3	57:r:106:GLY:O	2.17	0.44
59:t:342:LYS:HA	59:t:342:LYS:HE2	1.99	0.44
7:5:300:ARG:N	7:5:301:PRO:HD2	2.32	0.44
10:8:143:GLN:HG3	44:e:210:CYS:HA	2.00	0.44
24:J:24:VAL:HG23	24:J:28:LEU:HD23	1.99	0.44
38:X:92:ALA:HB3	38:X:98:SER:HB3	2.00	0.44
48:i:95:ARG:O	48:i:99:GLY:HA3	2.18	0.44
12:A:2146:A:N1	34:T:210:HIS:HA	2.33	0.44
14:B:1660:G:H2'	14:B:1661:A:C8	2.53	0.44
23:I:176:LEU:HD23	23:I:188:ARG:HG2	1.99	0.44
45:f:94:HIS:HB2	45:f:185:SER:HB2	2.00	0.44
47:h:116:ARG:HD3	47:h:129:PHE:CE1	2.53	0.44
59:t:196:GLU:HA	59:t:199:ILE:HD12	1.99	0.44
3:1:17:LEU:HD11	3:1:31:ASN:HB3	2.00	0.44
7:5:317:ALA:O	7:5:342:VAL:HG11	2.18	0.44
12:A:2748:A:H2'	12:A:2749:A:C8	2.52	0.44
12:A:3089:A:N7	13:A1:28:LYS:HE2	2.32	0.44
15:A2:202:LYS:CG	15:A2:212:VAL:HG21	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:C:258:LEU:HD21	16:C:268:VAL:HG12	1.99	0.44
19:F:156:ARG:HD2	19:F:156:ARG:HA	1.83	0.44
27:M:184:LEU:HA	27:M:187:VAL:HG12	2.00	0.44
33:S:75:HIS:O	33:S:79:VAL:HG23	2.18	0.44
5:3:137:THR:HG22	5:3:138:PRO:CD	2.47	0.44
10:8:169:PHE:HB3	10:8:170:PRO:HD3	1.99	0.44
11:9:39:LYS:HE2	35:U:7:TYR:CD1	2.53	0.44
12:A:2147:G:H4'	32:R:98:ASN:ND2	2.33	0.44
15:A2:127:ILE:HA	15:A2:159:MET:HE1	1.99	0.44
18:E:328:LEU:HD12	18:E:332:LEU:HD11	1.98	0.44
20:FF:143:VAL:O	20:FF:147:LYS:HG2	2.18	0.44
21:G:272:LEU:HD11	21:G:386:LYS:HE2	2.00	0.44
23:I:211:LEU:HD21	20:t1:18:ILE:HG23	2.00	0.44
27:M:66:GLY:O	27:M:73:PRO:HB3	2.18	0.44
28:N:172:VAL:HA	28:N:175:PHE:CE2	2.52	0.44
20:t5:24:LEU:HD21	20:t6:7:VAL:HG21	1.99	0.44
12:A:2517:U:OP1	15:A2:209:VAL:HG23	2.18	0.43
16:C:63:SER:HB3	16:C:216:THR:OG1	2.17	0.43
20:FF:146:ILE:HA	20:FF:150:LYS:HE3	2.00	0.43
29:O:46:TRP:CD1	29:O:121:ALA:HB2	2.52	0.43
43:d:137:PHE:CE2	43:d:212:ILE:HD11	2.53	0.43
57:r:155:ALA:O	57:r:158:SER:HB3	2.17	0.43
60:u:184:THR:HA	60:u:187:ILE:HG12	2.00	0.43
9:7:298:GLN:HE22	9:7:324:VAL:H	1.66	0.43
12:A:1906:G:H2'	12:A:2014:A:H61	1.83	0.43
13:A1:284:LEU:N	13:A1:285:PRO:HD2	2.32	0.43
17:D:141:LEU:HB2	17:D:150:TRP:CZ3	2.53	0.43
21:G:261:PRO:HG3	21:G:298:ARG:HH22	1.83	0.43
21:G:347:ILE:HG21	21:G:369:VAL:CG2	2.43	0.43
25:K:73:GLU:HA	25:K:91:THR:HG23	2.00	0.43
28:N:228:LYS:HD2	40:Z:78:ARG:HH21	1.84	0.43
38:X:99:LYS:HA	38:X:99:LYS:HD3	1.88	0.43
39:Y:63:GLY:O	39:Y:66:GLU:HG2	2.17	0.43
50:k:14:LYS:HD2	50:k:15:GLN:HB2	2.00	0.43
2:a:67:ILE:HA	2:a:68:PRO:HD3	1.86	0.43
8:6:335:LEU:HB3	8:6:337:MET:HG2	2.00	0.43
12:A:2135:A:N3	12:A:2135:A:H2'	2.33	0.43
12:A:2209:G:H3'	12:A:2210:C:H5''	1.99	0.43
16:C:61:PRO:HG2	16:C:96:ILE:HG21	2.00	0.43
23:I:237:ILE:HG23	20:t5:15:LEU:HG	2.01	0.43
31:Q:252:GLN:HA	31:Q:255:LYS:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:S:101:PHE:HE1	49:j:49:TRP:HB3	1.84	0.43
36:V:135:TRP:CZ3	36:V:143:ARG:HB3	2.54	0.43
42:c:63:LYS:HG2	42:c:64:PRO:HD2	2.00	0.43
58:s:84:THR:HB	58:s:280:ASN:HB2	2.00	0.43
58:s:90:LYS:O	58:s:275:LYS:HA	2.18	0.43
59:t:229:PRO:HA	59:t:233:LEU:HB2	2.00	0.43
59:t:408:LEU:H	59:t:408:LEU:HD23	1.82	0.43
20:t6:13:LEU:HD23	20:t6:14:THR:O	2.17	0.43
6:4:72:LEU:HD23	6:4:90:VAL:HG23	1.99	0.43
9:7:97:GLU:HG2	34:T:100:ASP:HB2	2.01	0.43
12:A:2026:A:H2'	12:A:2027:A:C8	2.54	0.43
12:A:2245:A:H4'	12:A:2246:A:OP1	2.19	0.43
14:B:1629:A:H2'	14:B:1630:A:H8	1.83	0.43
16:C:125:MET:HA	16:C:128:GLU:OE1	2.19	0.43
19:F:190:MET:O	19:F:262:THR:HA	2.17	0.43
21:G:229:MET:HE1	21:G:241:LEU:HB2	2.00	0.43
54:o:12:ILE:HG21	54:o:16:GLN:HA	2.00	0.43
1:0:85:ARG:HH11	12:A:2308:A:H5''	1.83	0.43
5:3:106:THR:HG22	5:3:163:THR:N	2.32	0.43
12:A:2056:G:H2'	12:A:2057:C:C6	2.54	0.43
12:A:2275:U:H1'	32:R:12:ASN:OD1	2.19	0.43
12:A:2898:U:O2	12:A:2898:U:O4'	2.35	0.43
23:I:233:LEU:HD22	20:t5:18:ILE:HG23	2.00	0.43
50:k:23:PHE:CE1	20:t1:-8:LEU:HA	2.54	0.43
55:p:154:ILE:O	55:p:158:ILE:HG12	2.19	0.43
13:A1:77:VAL:HG12	13:A1:130:ARG:HB2	1.99	0.43
13:A1:189:LEU:O	13:A1:193:GLN:HG2	2.17	0.43
15:A2:237:ALA:HA	15:A2:241:MET:HE3	2.00	0.43
17:D:173:ALA:HB1	17:D:188:PRO:HG3	1.99	0.43
18:E:99:LEU:CD2	18:E:193:LEU:HB3	2.49	0.43
21:G:164:LYS:HG2	21:G:169:VAL:HG12	2.01	0.43
23:I:199:SER:O	23:I:203:VAL:HG23	2.17	0.43
24:J:68:THR:HG22	24:J:82:ILE:HA	2.01	0.43
28:N:195:LEU:O	28:N:198:MET:HG3	2.19	0.43
35:U:137:ARG:HH22	36:V:103:ASP:HB2	1.83	0.43
41:b:39:SER:HA	41:b:91:CYS:SG	2.59	0.43
44:e:142:GLU:HG2	44:e:143:LYS:H	1.82	0.43
45:f:92:ASN:HB2	45:f:187:LYS:HB2	2.00	0.43
7:5:176:TYR:HA	7:5:179:VAL:HG12	2.00	0.43
12:A:1727:A:C8	12:A:2920:C:N4	2.87	0.43
12:A:1750:G:H5''	27:M:76:ILE:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:A:2748:A:H2'	12:A:2749:A:H8	1.82	0.43
13:A1:51:THR:O	13:A1:54:VAL:HG12	2.18	0.43
18:E:158:ALA:HB3	18:E:161:ILE:HD12	2.01	0.43
28:N:78:GLU:HB2	28:N:158:ARG:HH21	1.84	0.43
29:O:88:LYS:O	29:O:92:VAL:HB	2.19	0.43
38:X:12:LYS:HA	38:X:15:GLN:HE21	1.83	0.43
58:s:319:GLN:O	58:s:323:VAL:HG23	2.18	0.43
60:u:113:GLN:HB2	61:v:70:ILE:HD12	2.01	0.43
62:w:74:LEU:HB2	62:w:152:LYS:HD2	2.01	0.43
8:6:70:TRP:CD1	8:6:70:TRP:H	2.35	0.43
10:8:110:GLU:O	10:8:114:ARG:HG2	2.19	0.43
11:9:70:LEU:HD22	39:Y:85:TRP:HH2	1.83	0.43
12:A:2275:U:H2'	12:A:2276:C:H6	1.83	0.43
12:A:2392:U:H2'	12:A:2394:A:N6	2.27	0.43
15:A2:115:VAL:HG21	15:A2:146:LYS:HA	2.00	0.43
16:C:153:ASN:HB2	16:C:224:GLY:O	2.18	0.43
19:F:67:GLU:HB2	19:F:75:GLU:HA	2.00	0.43
19:F:222:THR:O	19:F:226:MET:HG3	2.18	0.43
23:I:178:GLY:HA3	23:I:187:SER:HA	2.00	0.43
25:K:3:SER:O	42:c:302:ARG:NH1	2.52	0.43
36:V:216:TYR:CZ	39:Y:188:TRP:HA	2.53	0.43
38:X:141:LEU:O	38:X:145:ILE:HG12	2.18	0.43
43:d:186:VAL:HG21	43:d:239:PRO:HB3	2.01	0.43
46:g:63:HIS:HB2	46:g:66:TYR:CE1	2.54	0.43
58:s:151:LEU:HD23	58:s:405:ILE:HD11	2.01	0.43
1:0:138:ARG:HA	1:0:141:ILE:HD12	2.01	0.43
12:A:1800:G:N2	12:A:1802:A:H3'	2.34	0.43
18:E:145:LEU:HD23	18:E:145:LEU:HA	1.88	0.43
21:G:297:LEU:O	21:G:300:ILE:HG22	2.19	0.43
31:Q:76:LEU:HD23	31:Q:279:GLU:HG2	2.01	0.43
38:X:80:TRP:CD1	38:X:80:TRP:N	2.85	0.43
57:r:89:LEU:HD22	57:r:119:VAL:HG23	2.00	0.43
1:0:119:LYS:O	1:0:120:HIS:ND1	2.51	0.43
14:B:1629:A:H2'	14:B:1630:A:C8	2.53	0.43
33:S:120:LEU:HD12	33:S:191:THR:HG21	2.01	0.43
53:n:119:LEU:HD12	53:n:124:PHE:HZ	1.83	0.43
59:t:336:ARG:NH1	60:u:102:ARG:HB3	2.33	0.43
7:5:300:ARG:HG2	7:5:303:ARG:NH2	2.34	0.42
8:6:380:TYR:HB3	27:M:95:PRO:HG2	2.01	0.42
12:A:2527:A:C5	17:D:67:LYS:HB3	2.54	0.42
51:l:106:THR:O	51:l:110:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:1:21:VAL:HG12	3:1:29:CYS:HB3	2.01	0.42
8:6:352:PRO:HD3	12:A:2860:G:H5''	2.01	0.42
12:A:3058:U:O2'	18:E:247:ASP:CG	2.62	0.42
35:U:3:ARG:HB3	35:U:24:PHE:CE1	2.54	0.42
43:d:148:ALA:HB2	43:d:163:LEU:HD22	2.00	0.42
59:t:80:ILE:HG21	59:t:236:VAL:HG21	2.01	0.42
7:5:215:ARG:HD2	7:5:364:LEU:O	2.20	0.42
8:6:145:PRO:HB3	8:6:169:PRO:O	2.19	0.42
12:A:2415:C:H3'	58:s:165:ARG:NH2	2.34	0.42
12:A:2931:A:H2'	12:A:2932:G:O4'	2.20	0.42
12:A:3144:A:H2'	12:A:3145:A:C8	2.54	0.42
18:E:58:VAL:N	18:E:59:PRO:HD2	2.34	0.42
19:F:290:TYR:CE1	46:g:53:PRO:HG2	2.54	0.42
22:H:55:ILE:HA	38:X:42:HIS:O	2.19	0.42
26:L:120:LYS:HE3	60:u:206:ILE:HD12	2.00	0.42
44:e:159:LEU:HD11	44:e:252:HIS:HB2	2.00	0.42
62:w:86:VAL:HG11	62:w:122:MET:HE3	2.01	0.42
1:0:185:PHE:CE1	29:O:131:PRO:HA	2.54	0.42
8:6:160:ASP:OD2	8:6:267:ARG:NH2	2.53	0.42
18:E:248:ILE:HG22	18:E:250:ARG:H	1.83	0.42
19:F:67:GLU:O	19:F:190:MET:HA	2.19	0.42
21:G:76:ARG:HG2	21:G:128:VAL:HG23	2.02	0.42
24:J:111:LEU:HD22	63:UNK:21:UNK:HA	2.01	0.42
41:b:35:ARG:HD2	54:o:102:SER:HB2	1.99	0.42
5:3:113:ARG:HD3	27:M:75:TYR:O	2.18	0.42
5:3:149:PHE:CZ	8:6:363:LEU:HD12	2.55	0.42
9:7:290:GLN:N	9:7:291:PRO:CD	2.82	0.42
12:A:2943:G:H2'	12:A:2944:C:H6	1.85	0.42
23:I:214:LEU:HD12	20:t4:15:LEU:HD22	2.01	0.42
35:U:22:THR:O	39:Y:102:TRP:HH2	2.02	0.42
40:Z:36:PHE:HE2	40:Z:79:PRO:HG3	1.84	0.42
6:4:76:CYS:SG	6:4:98:HIS:ND1	2.88	0.42
7:5:52:ILE:HA	7:5:53:PRO:HD3	1.85	0.42
15:A2:202:LYS:HG3	15:A2:212:VAL:HG21	2.00	0.42
15:A2:252:GLU:O	15:A2:252:GLU:HG3	2.20	0.42
16:C:308:THR:O	16:C:314:LEU:HD22	2.20	0.42
35:U:3:ARG:O	35:U:23:ASN:ND2	2.53	0.42
36:V:56:LEU:HD11	36:V:62:VAL:HG11	2.00	0.42
40:Z:36:PHE:CE2	40:Z:79:PRO:HG3	2.55	0.42
41:b:80:LEU:HD13	41:b:80:LEU:HA	1.92	0.42
59:t:355:GLN:HA	59:t:405:LYS:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:t3:7:VAL:HG21	20:t4:24:LEU:HB2	2.02	0.42
61:v:3:PRO:N	61:v:51:ARG:HD3	2.35	0.42
12:A:2682:A:OP1	32:R:34:ARG:NH2	2.47	0.42
13:A1:203:ASN:HA	13:A1:234:THR:O	2.19	0.42
14:B:1614:U:H4'	14:B:1615:A:OP1	2.19	0.42
14:B:1666:U:H2'	14:B:1667:C:C6	2.55	0.42
19:F:160:SER:HB2	48:i:80:LEU:HD13	2.02	0.42
19:F:249:ASN:ND2	48:i:55:GLY:O	2.53	0.42
39:Y:174:GLY:HA2	39:Y:201:ALA:HB2	2.00	0.42
40:Z:75:THR:HB	40:Z:83:LYS:HG2	2.01	0.42
43:d:242:VAL:HG22	43:d:244:GLU:HG2	2.00	0.42
12:A:1689:C:O2	12:A:1689:C:O4'	2.37	0.42
12:A:1939:G:C6	17:D:259:LYS:HB2	2.55	0.42
12:A:2031:A:N6	12:A:2044:A:O2'	2.53	0.42
12:A:2723:A:H5'	19:F:131:LYS:HE3	2.02	0.42
16:C:147:MET:HG2	16:C:201:LEU:HG	2.01	0.42
57:r:111:GLU:O	57:r:115:ILE:HD12	2.20	0.42
60:u:213:GLU:C	60:u:215:PHE:H	2.28	0.42
1:0:119:LYS:C	1:0:121:VAL:H	2.28	0.42
1:0:153:THR:HG22	29:O:91:GLN:HB2	2.00	0.42
12:A:1830:G:H5''	41:b:2:THR:HG21	2.01	0.42
12:A:1939:G:C5	17:D:259:LYS:HB2	2.54	0.42
12:A:2055:U:C2	54:o:71:PHE:CZ	3.08	0.42
16:C:39:LEU:HA	16:C:42:MET:HE2	2.01	0.42
18:E:200:PRO:HA	18:E:273:VAL:O	2.20	0.42
20:FF:139:PRO:HA	20:FF:142:LYS:HB2	2.01	0.42
23:I:221:LEU:HA	23:I:224:HIS:CD2	2.50	0.42
27:M:246:ASP:OD2	27:M:249:LYS:HG2	2.20	0.42
27:M:247:ILE:HG22	27:M:253:PHE:HD1	1.84	0.42
38:X:111:GLU:CD	38:X:111:GLU:H	2.28	0.42
40:Z:78:ARG:HD3	40:Z:82:GLU:OE1	2.20	0.42
44:e:85:SER:HB2	52:m:50:ARG:H	1.85	0.42
45:f:91:LEU:HB2	45:f:159:ILE:HG13	2.02	0.42
59:t:169:ARG:HB2	59:t:170:GLN:NE2	2.35	0.42
4:2:72:THR:O	4:2:76:VAL:HG23	2.20	0.42
8:6:37:ASN:OD1	37:W:124:ALA:HA	2.20	0.42
11:9:36:ARG:HG3	35:U:46:MET:CE	2.50	0.42
12:A:2005:C:H2'	12:A:2006:C:C6	2.55	0.42
12:A:2194:U:O2'	12:A:2195:A:H8	2.03	0.42
12:A:2643:G:O2'	12:A:2645:G:OP2	2.33	0.42
12:A:3209:A:H1'	18:E:158:ALA:HA	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:J:135:VAL:N	24:J:136:PRO:CD	2.83	0.42
28:N:204:GLU:O	28:N:208:ASN:HB3	2.19	0.42
31:Q:120:THR:OG1	31:Q:172:GLN:HB2	2.20	0.42
41:b:143:LEU:HG	41:b:147:GLU:HG2	2.01	0.42
8:6:123:ALA:HB2	30:P:117:TYR:CD2	2.55	0.41
12:A:2879:A:H2'	12:A:2880:A:C8	2.55	0.41
22:H:131:TYR:CE1	38:X:136:ASP:HA	2.54	0.41
25:K:27:PRO:HG2	25:K:30:LYS:HB2	2.02	0.41
28:N:227:ARG:HH12	28:N:235:LEU:HD11	1.85	0.41
29:O:50:ASP:HB2	29:O:107:MET:HE1	2.01	0.41
31:Q:139:GLN:HG2	31:Q:150:ILE:HG22	2.02	0.41
34:T:61:PRO:HB3	43:d:225:TYR:CD2	2.55	0.41
34:T:82:TYR:HD2	34:T:87:MET:HE2	1.85	0.41
44:e:170:VAL:HG23	44:e:265:LYS:HE3	2.00	0.41
46:g:108:THR:HG21	46:g:157:LEU:HD12	2.02	0.41
58:s:49:ALA:O	58:s:61:ARG:HD3	2.19	0.41
59:t:355:GLN:HB2	59:t:405:LYS:HG2	2.02	0.41
7:5:228:ALA:HB1	7:5:292:TYR:HB2	2.02	0.41
8:6:348:PRO:HA	8:6:349:PRO:HD3	1.94	0.41
11:9:36:ARG:HG3	35:U:46:MET:HE3	2.02	0.41
12:A:2699:C:H2'	12:A:2700:G:H8	1.85	0.41
17:D:228:LEU:HB3	17:D:229:PRO:CD	2.50	0.41
18:E:96:ARG:HH21	18:E:314:LEU:HD13	1.85	0.41
18:E:208:ALA:HB2	18:E:297:VAL:HG12	2.02	0.41
19:F:89:THR:H	19:F:179:THR:HG21	1.85	0.41
26:L:60:VAL:HG22	26:L:73:ILE:HG22	2.01	0.41
27:M:261:ASP:HB2	27:M:262:PRO:HD2	2.01	0.41
27:M:272:GLY:HA3	27:M:294:TYR:CD2	2.55	0.41
28:N:96:TYR:HB3	28:N:151:VAL:HB	2.02	0.41
32:R:13:ARG:NH2	42:c:32:LYS:HD3	2.34	0.41
33:S:120:LEU:HD23	33:S:120:LEU:HA	1.89	0.41
47:h:68:SER:O	47:h:71:GLU:HB2	2.20	0.41
12:A:2055:U:H2'	12:A:2056:G:H8	1.85	0.41
12:A:2532:U:H2'	12:A:2533:A:C8	2.55	0.41
12:A:2662:A:H2'	12:A:2663:C:C6	2.55	0.41
12:A:3111:A:H4'	12:A:3112:A:OP1	2.19	0.41
15:A2:251:SER:HB2	15:A2:290:LEU:HD22	2.02	0.41
23:I:116:LEU:HD22	23:I:121:ILE:HB	2.02	0.41
26:L:55:PRO:HB3	26:L:77:ILE:HG12	2.01	0.41
41:b:40:SER:HA	41:b:73:PRO:HG3	2.03	0.41
45:f:98:TYR:HH	45:f:150:LEU:N	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:t:252:ARG:HH22	59:t:254:LEU:HD21	1.85	0.41
5:3:115:LEU:HD12	27:M:83:PHE:HB3	2.00	0.41
12:A:2692:G:OP1	54:o:15:ARG:HA	2.20	0.41
18:E:99:LEU:HD12	18:E:198:PHE:HE2	1.84	0.41
22:H:107:VAL:HG22	22:H:108:ARG:H	1.85	0.41
23:I:212:THR:O	23:I:212:THR:HG22	2.20	0.41
24:J:118:TYR:O	24:J:122:ARG:HG2	2.21	0.41
27:M:270:ALA:HB3	27:M:273:TRP:CE2	2.55	0.41
34:T:150:GLY:N	34:T:172:CYS:HA	2.35	0.41
58:s:66:TRP:O	58:s:69:THR:OG1	2.37	0.41
60:u:135:LEU:HD11	60:u:181:LEU:HD22	2.02	0.41
8:6:175:VAL:HG11	8:6:270:PHE:CE2	2.56	0.41
8:6:194:THR:HA	8:6:195:PRO:HD3	1.97	0.41
8:6:362:PRO:HB2	8:6:364:ARG:HG2	2.02	0.41
10:8:126:GLN:O	10:8:129:ARG:HG3	2.21	0.41
12:A:2737:U:H2'	12:A:2738:U:C6	2.56	0.41
12:A:2841:U:O2	12:A:2841:U:O4'	2.39	0.41
13:A1:308:SER:HA	13:A1:376:TYR:O	2.20	0.41
16:C:87:LEU:HD11	16:C:309:PHE:O	2.20	0.41
19:F:93:LEU:HD21	54:o:95:LEU:HD13	2.03	0.41
30:P:114:LYS:HA	30:P:114:LYS:HD3	1.90	0.41
53:n:156:ALA:HA	53:n:170:LEU:HD13	2.03	0.41
7:5:80:ARG:NH2	12:A:1707:C:O2	2.53	0.41
12:A:3139:G:H2'	12:A:3140:A:C8	2.55	0.41
13:A1:272:ILE:HA	13:A1:277:ARG:NH1	2.36	0.41
15:A2:314:GLN:HA	15:A2:317:LYS:NZ	2.36	0.41
27:M:191:VAL:N	27:M:192:PRO:HD2	2.34	0.41
29:O:42:ILE:CG2	29:O:123:ILE:HG23	2.50	0.41
42:c:54:PRO:HA	42:c:55:PRO:HD3	1.95	0.41
43:d:141:ALA:O	43:d:144:ILE:HG22	2.21	0.41
20:t6:13:LEU:HD21	20:t6:17:GLU:HB2	2.02	0.41
2:a:41:ASP:OD1	2:a:46:ASN:HA	2.19	0.41
11:9:32:GLY:HA3	12:A:2377:G:O2'	2.20	0.41
12:A:2900:C:H2'	12:A:2901:A:C8	2.55	0.41
19:F:127:PRO:HG3	19:F:141:ILE:HG23	2.03	0.41
20:FF:185:LYS:HD3	20:FF:188:LEU:HD11	2.01	0.41
21:G:68:LEU:HD22	21:G:68:LEU:HA	1.89	0.41
32:R:82:LYS:HB3	32:R:84:PRO:HD2	2.03	0.41
54:o:12:ILE:HA	54:o:13:PRO:HD3	1.95	0.41
8:6:52:ARG:HD3	14:B:1636:A:H4'	2.03	0.41
8:6:342:PHE:HZ	30:P:44:VAL:HG11	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:A:1679:U:O2'	12:A:1680:A:H8	2.04	0.41
12:A:1697:A:P	39:Y:164:ARG:HH22	2.43	0.41
16:C:123:ILE:HB	16:C:124:PRO:HD3	2.03	0.41
17:D:109:PHE:HB3	17:D:204:ALA:HB3	2.03	0.41
21:G:192:ASN:OD1	21:G:203:PRO:HA	2.20	0.41
41:b:30:SER:O	41:b:75:VAL:HA	2.21	0.41
53:n:150:VAL:HG13	53:n:190:THR:HG23	2.02	0.41
10:8:110:GLU:HG3	10:8:111:THR:N	2.36	0.41
12:A:2267:U:C5	27:M:44:ARG:NH2	2.89	0.41
12:A:2815:G:H22	12:A:2938:A:H5'	1.85	0.41
16:C:46:LEU:HD13	16:C:52:ILE:HG12	2.01	0.41
17:D:129:VAL:HG21	17:D:157:MET:O	2.21	0.41
25:K:147:GLN:HE22	25:K:151:ILE:HD11	1.85	0.41
27:M:26:ASN:O	54:o:94:HIS:HD2	2.04	0.41
27:M:199:PRO:HB3	27:M:274:VAL:HG22	2.03	0.41
28:N:188:LYS:HD2	28:N:188:LYS:HA	1.93	0.41
42:c:83:PHE:CD1	42:c:88:LEU:HD12	2.56	0.41
42:c:275:TYR:HA	42:c:280:LEU:HA	2.03	0.41
43:d:86:ASP:HB3	43:d:198:ARG:HG3	2.03	0.41
59:t:191:MET:HA	59:t:194:LEU:HD12	2.01	0.41
59:t:258:PHE:CZ	59:t:342:LYS:HE3	2.56	0.41
59:t:306:ILE:HG22	59:t:322:LEU:HD12	2.01	0.41
62:w:93:ILE:HG23	62:w:110:LEU:HD21	2.02	0.41
1:0:98:GLN:NE2	12:A:2709:A:N3	2.69	0.41
5:3:163:THR:CG2	5:3:164:SER:N	2.83	0.41
12:A:1747:G:N2	12:A:1750:G:O2'	2.54	0.41
12:A:2930:U:H2'	12:A:2931:A:C8	2.56	0.41
16:C:240:LEU:HD22	16:C:305:PHE:CZ	2.55	0.41
18:E:48:TRP:CD1	18:E:50:ASP:HB2	2.56	0.41
27:M:237:ALA:HA	27:M:242:TYR:CE1	2.55	0.41
35:U:40:VAL:HG12	35:U:105:PHE:HD2	1.86	0.41
42:c:213:LEU:HD13	42:c:213:LEU:HA	1.97	0.41
43:d:39:PRO:HA	43:d:40:PRO:HD3	1.95	0.41
43:d:216:MET:HE2	43:d:246:VAL:HG21	2.03	0.41
58:s:51:MET:HG2	58:s:61:ARG:NH1	2.35	0.41
20:t5:3:ILE:HG23	20:t6:21:LEU:HD23	2.03	0.41
3:l:55:LEU:H	56:q:128:MET:HE1	1.85	0.40
16:C:42:MET:O	16:C:46:LEU:HG	2.21	0.40
20:FF:180:GLU:HA	20:FF:183:LYS:HE2	2.02	0.40
24:J:122:ARG:HD2	24:J:137:LEU:HD12	2.04	0.40
39:Y:202:LEU:HD12	39:Y:203:PRO:HD3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:5:126:THR:HG21	7:5:357:PHE:CE1	2.54	0.40
9:7:81:MET:CE	43:d:279:THR:HB	2.47	0.40
9:7:146:CYS:O	9:7:278:TYR:OH	2.38	0.40
16:C:46:LEU:HD21	16:C:149:ILE:HG13	2.03	0.40
19:F:67:GLU:CB	19:F:75:GLU:HA	2.51	0.40
23:I:185:ILE:HD11	20:t1:-11:GLY:H	1.87	0.40
29:O:117:ARG:HD3	29:O:117:ARG:HA	1.83	0.40
33:S:84:ASN:HD22	33:S:204:LEU:HB2	1.85	0.40
33:S:129:ARG:HH11	33:S:155:ARG:NH1	2.20	0.40
44:e:264:LEU:HB2	44:e:266:PRO:HD2	2.03	0.40
48:i:46:ARG:HA	48:i:51:ARG:HD2	2.02	0.40
53:n:151:ILE:HG12	53:n:185:LEU:HD13	2.02	0.40
1:0:160:TYR:HA	1:0:177:ARG:HB3	2.03	0.40
3:1:59:LYS:HA	3:1:59:LYS:HD3	1.95	0.40
6:4:83:LYS:HG2	12:A:3189:C:H5'	2.03	0.40
8:6:204:VAL:HG13	8:6:245:VAL:HG21	2.04	0.40
12:A:2075:U:OP1	40:Z:38:ARG:HD2	2.22	0.40
12:A:2138:U:O2'	12:A:2151:A:N3	2.48	0.40
13:A1:171:LEU:HD23	13:A1:251:ARG:HG3	2.02	0.40
15:A2:267:TYR:HE2	15:A2:308:THR:HG21	1.86	0.40
29:O:52:MET:HE3	29:O:52:MET:HB3	1.97	0.40
39:Y:71:PRO:HA	39:Y:74:TRP:CD2	2.56	0.40
45:f:178:LEU:HD21	45:f:182:VAL:H	1.86	0.40
53:n:78:ASP:O	53:n:110:GLY:HA2	2.21	0.40
59:t:357:TYR:HD1	59:t:403:ASP:HB3	1.87	0.40
2:a:134:LYS:HG3	12:A:1836:A:C8	2.57	0.40
12:A:2004:G:H2'	12:A:2005:C:C6	2.56	0.40
12:A:2041:U:O2	27:M:69:GLY:HA3	2.21	0.40
12:A:2108:G:H4'	12:A:2111:C:H42	1.86	0.40
12:A:2727:C:H2'	12:A:2728:C:H6	1.85	0.40
17:D:111:ARG:HH21	17:D:163:ILE:CG2	2.31	0.40
19:F:89:THR:HG22	19:F:179:THR:CG2	2.51	0.40
19:F:96:LEU:HD23	19:F:96:LEU:HA	1.93	0.40
21:G:157:VAL:CG2	21:G:158:PRO:HD2	2.51	0.40
32:R:111:LYS:HB2	41:b:127:GLN:OE1	2.21	0.40
12:A:2511:C:H3'	12:A:2512:A:C8	2.56	0.40
12:A:2938:A:H2'	12:A:2939:C:C6	2.56	0.40
13:A1:161:ALA:HB2	13:A1:372:PHE:HB3	2.04	0.40
13:A1:178:LEU:HB3	13:A1:252:VAL:HG22	2.03	0.40
15:A2:112:LEU:HD21	15:A2:124:LEU:HD21	2.03	0.40
16:C:265:VAL:O	16:C:268:VAL:HG22	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:E:129:VAL:HG23	18:E:193:LEU:HD11	2.02	0.40
21:G:363:LEU:HB3	21:G:367:VAL:HG21	2.04	0.40
30:P:122:VAL:HG13	30:P:157:SER:HA	2.03	0.40
30:P:137:LEU:HD13	30:P:137:LEU:HA	1.94	0.40
38:X:80:TRP:C	38:X:82:GLY:H	2.29	0.40
38:X:147:LYS:HE3	38:X:194:PHE:HZ	1.85	0.40
53:n:57:ALA:HB2	53:n:85:ALA:HB1	2.03	0.40
53:n:131:THR:HA	53:n:176:THR:HG21	2.03	0.40
54:o:23:ARG:HA	54:o:24: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	
1	0	106/188 (56%)	103 (97%)	3 (3%)	0	100	100
2	a	78/142 (55%)	75 (96%)	3 (4%)	0	100	100
3	1	50/65 (77%)	50 (100%)	0	0	100	100
4	2	43/92 (47%)	42 (98%)	1 (2%)	0	100	100
5	3	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
6	4	36/103 (35%)	36 (100%)	0	0	100	100
7	5	390/423 (92%)	376 (96%)	14 (4%)	0	100	100
8	6	323/380 (85%)	310 (96%)	13 (4%)	0	100	100
9	7	288/338 (85%)	274 (95%)	14 (5%)	0	100	100
10	8	83/206 (40%)	75 (90%)	8 (10%)	0	100	100
11	9	121/137 (88%)	117 (97%)	4 (3%)	0	100	100
13	A1	340/384 (88%)	330 (97%)	10 (3%)	0	100	100
15	A2	236/381 (62%)	233 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	C	251/334 (75%)	245 (98%)	6 (2%)	0	100	100
17	D	235/305 (77%)	225 (96%)	10 (4%)	0	100	100
18	E	302/348 (87%)	288 (95%)	14 (5%)	0	100	100
19	F	248/311 (80%)	243 (98%)	5 (2%)	0	100	100
20	FF	68/198 (34%)	65 (96%)	3 (4%)	0	100	100
20	t1	44/198 (22%)	38 (86%)	4 (9%)	2 (4%)	2	12
20	t2	28/198 (14%)	28 (100%)	0	0	100	100
20	t3	28/198 (14%)	28 (100%)	0	0	100	100
20	t4	27/198 (14%)	27 (100%)	0	0	100	100
20	t5	27/198 (14%)	27 (100%)	0	0	100	100
20	t6	25/198 (13%)	24 (96%)	1 (4%)	0	100	100
21	G	335/414 (81%)	316 (94%)	19 (6%)	0	100	100
22	H	93/267 (35%)	91 (98%)	2 (2%)	0	100	100
23	I	210/261 (80%)	207 (99%)	3 (1%)	0	100	100
24	J	134/192 (70%)	127 (95%)	7 (5%)	0	100	100
25	K	175/178 (98%)	173 (99%)	2 (1%)	0	100	100
26	L	113/145 (78%)	107 (95%)	6 (5%)	0	100	100
27	M	285/296 (96%)	279 (98%)	6 (2%)	0	100	100
28	N	175/251 (70%)	170 (97%)	5 (3%)	0	100	100
29	O	150/175 (86%)	144 (96%)	6 (4%)	0	100	100
30	P	139/179 (78%)	137 (99%)	2 (1%)	0	100	100
31	Q	215/292 (74%)	209 (97%)	6 (3%)	0	100	100
32	R	138/149 (93%)	137 (99%)	1 (1%)	0	100	100
33	S	154/205 (75%)	149 (97%)	5 (3%)	0	100	100
34	T	164/212 (77%)	161 (98%)	3 (2%)	0	100	100
35	U	135/153 (88%)	131 (97%)	4 (3%)	0	100	100
36	V	200/216 (93%)	196 (98%)	4 (2%)	0	100	100
37	W	99/148 (67%)	99 (100%)	0	0	100	100
38	X	241/256 (94%)	239 (99%)	2 (1%)	0	100	100
39	Y	174/250 (70%)	170 (98%)	4 (2%)	0	100	100
40	Z	118/161 (73%)	113 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	b	146/215 (68%)	138 (94%)	8 (6%)	0	100	100
42	c	271/332 (82%)	267 (98%)	4 (2%)	0	100	100
43	d	217/306 (71%)	207 (95%)	10 (5%)	0	100	100
44	e	211/279 (76%)	202 (96%)	9 (4%)	0	100	100
45	f	115/212 (54%)	107 (93%)	7 (6%)	1 (1%)	14	44
46	g	127/166 (76%)	125 (98%)	2 (2%)	0	100	100
47	h	105/158 (66%)	101 (96%)	4 (4%)	0	100	100
48	i	95/128 (74%)	92 (97%)	3 (3%)	0	100	100
49	j	83/123 (68%)	82 (99%)	1 (1%)	0	100	100
50	k	76/112 (68%)	73 (96%)	3 (4%)	0	100	100
51	l	42/138 (30%)	42 (100%)	0	0	100	100
52	m	33/128 (26%)	31 (94%)	2 (6%)	0	100	100
53	n	187/246 (76%)	186 (100%)	1 (0%)	0	100	100
54	o	89/102 (87%)	84 (94%)	5 (6%)	0	100	100
55	p	119/206 (58%)	115 (97%)	4 (3%)	0	100	100
56	q	133/222 (60%)	132 (99%)	1 (1%)	0	100	100
57	r	149/196 (76%)	143 (96%)	6 (4%)	0	100	100
58	s	366/439 (83%)	353 (96%)	13 (4%)	0	100	100
59	t	377/452 (83%)	368 (98%)	9 (2%)	0	100	100
60	u	131/234 (56%)	124 (95%)	7 (5%)	0	100	100
61	v	66/70 (94%)	61 (92%)	5 (8%)	0	100	100
62	w	85/156 (54%)	83 (98%)	2 (2%)	0	100	100
All	All	10140/14731 (69%)	9819 (97%)	318 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	t1	-3	LYS
45	f	179	PRO
20	t1	1	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	
1	0	97/164 (59%)	96 (99%)	1 (1%)	68	79
2	a	78/133 (59%)	76 (97%)	2 (3%)	40	68
3	1	49/60 (82%)	47 (96%)	2 (4%)	27	59
4	2	39/72 (54%)	39 (100%)	0	100	100
5	3	88/166 (53%)	83 (94%)	5 (6%)	18	49
6	4	37/89 (42%)	35 (95%)	2 (5%)	20	50
7	5	353/368 (96%)	339 (96%)	14 (4%)	28	60
8	6	271/332 (82%)	262 (97%)	9 (3%)	33	63
9	7	266/303 (88%)	262 (98%)	4 (2%)	57	75
10	8	77/190 (40%)	75 (97%)	2 (3%)	40	68
11	9	104/112 (93%)	101 (97%)	3 (3%)	37	66
13	A1	297/328 (90%)	292 (98%)	5 (2%)	53	74
15	A2	221/350 (63%)	213 (96%)	8 (4%)	31	62
16	C	224/287 (78%)	220 (98%)	4 (2%)	51	73
17	D	191/245 (78%)	188 (98%)	3 (2%)	55	75
18	E	259/290 (89%)	254 (98%)	5 (2%)	50	73
19	F	217/262 (83%)	211 (97%)	6 (3%)	38	66
20	FF	58/158 (37%)	58 (100%)	0	100	100
20	t1	40/158 (25%)	38 (95%)	2 (5%)	22	53
20	t2	29/158 (18%)	28 (97%)	1 (3%)	32	63
20	t3	29/158 (18%)	29 (100%)	0	100	100
20	t4	28/158 (18%)	27 (96%)	1 (4%)	31	62
20	t5	28/158 (18%)	28 (100%)	0	100	100
20	t6	26/158 (16%)	26 (100%)	0	100	100
21	G	264/328 (80%)	253 (96%)	11 (4%)	26	58
22	H	86/228 (38%)	85 (99%)	1 (1%)	63	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	I	194/232 (84%)	190 (98%)	4 (2%)	47	71
24	J	112/150 (75%)	109 (97%)	3 (3%)	39	67
25	K	155/156 (99%)	150 (97%)	5 (3%)	34	64
26	L	98/124 (79%)	91 (93%)	7 (7%)	13	41
27	M	245/249 (98%)	236 (96%)	9 (4%)	30	61
28	N	152/211 (72%)	151 (99%)	1 (1%)	76	82
29	O	133/150 (89%)	121 (91%)	12 (9%)	9	33
30	P	123/154 (80%)	121 (98%)	2 (2%)	55	75
31	Q	199/256 (78%)	192 (96%)	7 (4%)	32	62
32	R	118/126 (94%)	113 (96%)	5 (4%)	26	58
33	S	141/180 (78%)	137 (97%)	4 (3%)	38	66
34	T	146/182 (80%)	144 (99%)	2 (1%)	59	76
35	U	124/135 (92%)	120 (97%)	4 (3%)	34	64
36	V	180/191 (94%)	172 (96%)	8 (4%)	25	56
37	W	83/119 (70%)	79 (95%)	4 (5%)	23	54
38	X	219/229 (96%)	216 (99%)	3 (1%)	59	76
39	Y	159/223 (71%)	156 (98%)	3 (2%)	50	73
40	Z	111/147 (76%)	105 (95%)	6 (5%)	20	50
41	b	130/186 (70%)	122 (94%)	8 (6%)	16	46
42	c	241/288 (84%)	233 (97%)	8 (3%)	33	63
43	d	207/274 (76%)	199 (96%)	8 (4%)	28	60
44	e	188/236 (80%)	184 (98%)	4 (2%)	47	71
45	f	108/188 (57%)	107 (99%)	1 (1%)	70	80
46	g	119/148 (80%)	116 (98%)	3 (2%)	42	69
47	h	101/148 (68%)	101 (100%)	0	100	100
48	i	86/110 (78%)	79 (92%)	7 (8%)	11	36
49	j	68/97 (70%)	67 (98%)	1 (2%)	57	75
50	k	71/90 (79%)	68 (96%)	3 (4%)	26	58
51	l	43/116 (37%)	42 (98%)	1 (2%)	44	70
52	m	31/113 (27%)	29 (94%)	2 (6%)	15	44
53	n	157/209 (75%)	155 (99%)	2 (1%)	61	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	o	78/87 (90%)	74 (95%)	4 (5%)	21	52
55	p	117/181 (65%)	114 (97%)	3 (3%)	40	68
56	q	115/178 (65%)	113 (98%)	2 (2%)	53	74
57	r	141/169 (83%)	135 (96%)	6 (4%)	26	57
58	s	326/381 (86%)	319 (98%)	7 (2%)	47	71
59	t	317/371 (85%)	313 (99%)	4 (1%)	61	77
60	u	123/200 (62%)	120 (98%)	3 (2%)	43	69
61	v	59/60 (98%)	55 (93%)	4 (7%)	14	42
62	w	81/136 (60%)	76 (94%)	5 (6%)	16	46
All	All	9055/12593 (72%)	8789 (97%)	266 (3%)	38	66

All (266) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	153	THR
2	a	60	CYS
2	a	136	LEU
3	1	43	LEU
3	1	62	ILE
5	3	103	LYS
5	3	111	ILE
5	3	137	THR
5	3	156	LYS
5	3	157	LEU
6	4	76	CYS
6	4	81	LEU
7	5	46	LEU
7	5	55	LEU
7	5	64	MET
7	5	128	LEU
7	5	132	LEU
7	5	175	THR
7	5	193	LEU
7	5	280	GLN
7	5	299	LEU
7	5	300	ARG
7	5	315	LEU
7	5	316	PHE
7	5	365	ASP

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Mol	Chain	Res	Type
7	5	392	ILE
8	6	41	ASP
8	6	52	ARG
8	6	151	LEU
8	6	184	LEU
8	6	221	LEU
8	6	265	ILE
8	6	335	LEU
8	6	371	ASP
8	6	379	ILE
9	7	40	LEU
9	7	97	GLU
9	7	119	LEU
9	7	272	THR
10	8	117	LEU
10	8	168	LEU
11	9	55	GLU
11	9	69	LYS
11	9	86	LEU
13	A1	59	LEU
13	A1	163	LEU
13	A1	189	LEU
13	A1	200	LEU
13	A1	258	CYS
15	A2	133	LEU
15	A2	134	LEU
15	A2	136	LEU
15	A2	191	GLN
15	A2	206	LEU
15	A2	283	THR
15	A2	289	LEU
15	A2	319	LEU
16	C	60	ILE
16	C	216	THR
16	C	317	VAL
16	C	318	MET
17	D	187	LEU
17	D	207	ILE
17	D	281	TRP
18	E	152	VAL
18	E	245	THR
18	E	289	VAL

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Mol	Chain	Res	Type
18	E	303	LYS
18	E	346	THR
19	F	93	LEU
19	F	130	GLN
19	F	131	LYS
19	F	250	VAL
19	F	263	LEU
19	F	291	SER
21	G	63	LEU
21	G	68	LEU
21	G	121	GLN
21	G	257	THR
21	G	265	ILE
21	G	282	ILE
21	G	297	LEU
21	G	298	ARG
21	G	300	ILE
21	G	370	LEU
21	G	385	LEU
22	H	145	LEU
23	I	50	VAL
23	I	78	LEU
23	I	101	ASN
23	I	197	LEU
24	J	24	VAL
24	J	103	GLN
24	J	106	LYS
25	K	2	SER
25	K	91	THR
25	K	142	VAL
25	K	150	LYS
25	K	178	LEU
26	L	35	MET
26	L	58	ILE
26	L	77	ILE
26	L	95	ARG
26	L	101	ASP
26	L	136	LYS
26	L	145	VAL
27	M	43	ARG
27	M	44	ARG
27	M	49	CYS

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Mol	Chain	Res	Type
27	M	61	THR
27	M	98	LEU
27	M	146	ASP
27	M	167	ILE
27	M	269	LEU
27	M	277	MET
28	N	208	ASN
29	O	14	VAL
29	O	20	LEU
29	O	26	ILE
29	O	28	LEU
29	O	42	ILE
29	O	115	LEU
29	O	123	ILE
29	O	135	LEU
29	O	144	LEU
29	O	149	LEU
29	O	155	ASP
29	O	156	LEU
30	P	63	ARG
30	P	137	LEU
31	Q	84	ARG
31	Q	139	GLN
31	Q	215	VAL
31	Q	227	LYS
31	Q	247	LEU
31	Q	249	LEU
31	Q	271	ARG
32	R	11	ARG
32	R	32	ARG
32	R	82	LYS
32	R	87	ILE
32	R	104	ASP
33	S	144	LEU
33	S	160	VAL
33	S	170	ILE
33	S	182	LYS
34	T	57	ILE
34	T	84	LYS
35	U	11	ARG
35	U	12	LEU
35	U	27	GLN

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Mol	Chain	Res	Type
35	U	126	LEU
36	V	56	LEU
36	V	65	LEU
36	V	91	LEU
36	V	186	THR
36	V	194	LEU
36	V	195	GLN
36	V	202	MET
36	V	213	VAL
37	W	96	ILE
37	W	114	VAL
37	W	125	VAL
37	W	148	LEU
38	X	87	LEU
38	X	99	LYS
38	X	161	LEU
39	Y	202	LEU
39	Y	226	LEU
39	Y	237	LYS
40	Z	41	ILE
40	Z	73	LYS
40	Z	109	LYS
40	Z	119	ILE
40	Z	141	SER
40	Z	154	VAL
41	b	36	ASP
41	b	80	LEU
41	b	86	GLU
41	b	94	VAL
41	b	100	LEU
41	b	115	ILE
41	b	122	ASP
41	b	123	ASN
42	c	68	TYR
42	c	86	ASP
42	c	173	LEU
42	c	193	GLN
42	c	213	LEU
42	c	235	ILE
42	c	280	LEU
42	c	287	GLU
43	d	36	ARG

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Mol	Chain	Res	Type
43	d	45	LYS
43	d	146	ILE
43	d	163	LEU
43	d	194	VAL
43	d	238	VAL
43	d	266	VAL
43	d	287	LEU
44	e	48	LEU
44	e	126	GLN
44	e	243	PHE
44	e	269	LEU
45	f	171	LEU
46	g	43	ASP
46	g	143	VAL
46	g	147	LEU
48	i	34	ILE
48	i	36	LEU
48	i	37	THR
48	i	49	GLU
48	i	56	VAL
48	i	80	LEU
48	i	105	ASP
49	j	93	LEU
50	k	34	LEU
50	k	73	ARG
50	k	84	LEU
51	l	110	LEU
52	m	40	LEU
52	m	51	LEU
53	n	140	LEU
53	n	155	MET
54	o	42	GLU
54	o	58	GLN
54	o	91	GLN
54	o	98	THR
55	p	45	LEU
55	p	73	LEU
55	p	183	MET
56	q	96	LEU
56	q	133	VAL
57	r	70	CYS
57	r	99	MET

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Mol	Chain	Res	Type
57	r	108	CYS
57	r	115	ILE
57	r	119	VAL
57	r	159	VAL
58	s	52	THR
58	s	150	LEU
58	s	243	ILE
58	s	264	ILE
58	s	279	GLU
58	s	379	LEU
58	s	419	LEU
59	t	80	ILE
59	t	221	LEU
59	t	279	LEU
59	t	415	ILE
20	t1	-3	LYS
20	t1	3	ILE
20	t2	21	LEU
20	t4	15	LEU
60	u	156	HIS
60	u	196	LEU
60	u	211	VAL
61	v	16	LEU
61	v	45	LEU
61	v	47	ASP
61	v	69	ILE
62	w	74	LEU
62	w	75	THR
62	w	89	LEU
62	w	118	ILE
62	w	154	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (140) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	83	ASN
5	3	181	HIS
7	5	96	HIS
7	5	149	ASN
7	5	165	GLN
7	5	214	ASN
7	5	280	GLN

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Mol	Chain	Res	Type
7	5	385	HIS
8	6	66	GLN
8	6	69	HIS
8	6	292	GLN
8	6	307	HIS
8	6	354	GLN
9	7	49	ASN
9	7	84	ASN
9	7	111	GLN
9	7	298	GLN
10	8	143	GLN
11	9	90	GLN
13	A1	55	GLN
13	A1	317	ASN
13	A1	331	GLN
15	A2	191	GLN
15	A2	245	HIS
16	C	93	GLN
16	C	121	GLN
16	C	229	HIS
16	C	247	HIS
16	C	295	GLN
16	C	297	ASN
17	D	128	GLN
17	D	165	ASN
17	D	194	ASN
17	D	195	ASN
17	D	252	HIS
18	E	72	GLN
18	E	139	ASN
18	E	202	GLN
18	E	294	ASN
19	F	103	GLN
21	G	121	GLN
21	G	214	GLN
21	G	287	HIS
21	G	288	GLN
21	G	299	HIS
23	I	93	ASN
23	I	223	GLN
23	I	225	GLN
24	J	48	GLN

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Mol	Chain	Res	Type
24	J	54	ASN
24	J	116	HIS
25	K	26	GLN
25	K	126	HIS
25	K	147	GLN
26	L	59	HIS
26	L	103	ASN
26	L	143	ASN
27	M	26	ASN
27	M	30	ASN
27	M	92	GLN
28	N	86	ASN
28	N	210	GLN
29	O	69	ASN
29	O	147	GLN
30	P	97	GLN
30	P	142	ASN
30	P	162	GLN
31	Q	107	HIS
31	Q	218	ASN
32	R	22	GLN
32	R	79	HIS
32	R	94	GLN
33	S	84	ASN
34	T	132	HIS
34	T	133	ASN
34	T	151	GLN
35	U	74	HIS
35	U	103	GLN
35	U	138	GLN
37	W	72	HIS
37	W	80	HIS
37	W	110	ASN
38	X	4	HIS
38	X	15	GLN
38	X	94	ASN
39	Y	73	ASN
39	Y	88	GLN
39	Y	89	GLN
39	Y	92	ASN
39	Y	99	HIS
39	Y	117	GLN

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Mol	Chain	Res	Type
39	Y	147	GLN
39	Y	183	GLN
40	Z	98	GLN
40	Z	100	HIS
41	b	16	HIS
41	b	120	HIS
42	c	42	GLN
42	c	107	GLN
42	c	122	ASN
42	c	172	ASN
42	c	193	GLN
43	d	149	HIS
43	d	157	HIS
43	d	161	HIS
43	d	204	ASN
44	e	54	GLN
44	e	67	GLN
44	e	175	GLN
44	e	252	HIS
44	e	271	GLN
45	f	111	HIS
45	f	153	HIS
45	f	189	HIS
47	h	67	GLN
49	j	63	GLN
49	j	82	GLN
49	j	92	GLN
53	n	200	GLN
53	n	214	ASN
54	o	21	HIS
54	o	33	GLN
54	o	94	HIS
55	p	96	ASN
57	r	65	ASN
57	r	112	HIS
58	s	87	GLN
58	s	101	ASN
58	s	107	GLN
58	s	179	GLN
58	s	240	GLN
59	t	310	HIS
59	t	349	HIS

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Mol	Chain	Res	Type
59	t	355	GLN
20	t3	8	GLN
60	u	148	HIS
60	u	156	HIS
61	v	54	GLN
62	w	103	HIS
62	w	115	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	A	1427/1559 (91%)	361 (25%)	54 (3%)
14	B	56/69 (81%)	19 (33%)	2 (3%)
All	All	1483/1628 (91%)	380 (25%)	56 (3%)

All (380) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	A	1678	C
12	A	1679	U
12	A	1680	A
12	A	1681	G
12	A	1689	C
12	A	1693	C
12	A	1694	U
12	A	1699	C
12	A	1700	U
12	A	1704	U
12	A	1707	C
12	A	1708	A
12	A	1714	C
12	A	1715	C
12	A	1724	A
12	A	1728	U
12	A	1733	C
12	A	1734	C
12	A	1735	A
12	A	1736	A
12	A	1743	U
12	A	1748	G
12	A	1749	C

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Mol	Chain	Res	Type
12	A	1750	G
12	A	1751	A
12	A	1769	C
12	A	1770	G
12	A	1780	U
12	A	1794	A
12	A	1795	A
12	A	1798	A
12	A	1804	A
12	A	1805	A
12	A	1812	C
12	A	1817	C
12	A	1824	U
12	A	1827	C
12	A	1828	A
12	A	1829	A
12	A	1832	A
12	A	1836	A
12	A	1844	A
12	A	1849	C
12	A	1852	C
12	A	1853	A
12	A	1854	U
12	A	1855	A
12	A	1856	A
12	A	1867	A
12	A	1869	A
12	A	1872	U
12	A	1878	U
12	A	1882	A
12	A	1883	G
12	A	1887	A
12	A	1892	A
12	A	1893	A
12	A	1901	C
12	A	1902	C
12	A	1903	C
12	A	1909	A
12	A	1918	G
12	A	1936	A
12	A	1937	A
12	A	1938	A

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Mol	Chain	Res	Type
12	A	1940	A
12	A	1946	C
12	A	1956	U
12	A	1957	A
12	A	1974	A
12	A	1975	U
12	A	1985	G
12	A	1986	A
12	A	1994	A
12	A	1995	A
12	A	2000	C
12	A	2001	C
12	A	2002	G
12	A	2015	G
12	A	2016	C
12	A	2021	U
12	A	2022	G
12	A	2029	A
12	A	2030	U
12	A	2031	A
12	A	2036	C
12	A	2037	U
12	A	2039	A
12	A	2044	A
12	A	2055	U
12	A	2060	A
12	A	2065	A
12	A	2066	C
12	A	2070	C
12	A	2071	U
12	A	2074	A
12	A	2079	C
12	A	2085	A
12	A	2092	C
12	A	2097	A
12	A	2098	G
12	A	2105	G
12	A	2107	G
12	A	2108	G
12	A	2111	C
12	A	2112	A
12	A	2113	G

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Mol	Chain	Res	Type
12	A	2114	C
12	A	2126	U
12	A	2131	A
12	A	2135	A
12	A	2136	C
12	A	2142	A
12	A	2147	G
12	A	2154	A
12	A	2158	U
12	A	2159	U
12	A	2160	A
12	A	2167	A
12	A	2171	U
12	A	2172	A
12	A	2173	G
12	A	2174	G
12	A	2175	C
12	A	2178	A
12	A	2179	A
12	A	2181	A
12	A	2182	G
12	A	2183	C
12	A	2187	C
12	A	2194	U
12	A	2195	A
12	A	2196	A
12	A	2197	G
12	A	2198	A
12	A	2199	A
12	A	2200	A
12	A	2210	C
12	A	2211	U
12	A	2228	A
12	A	2229	A
12	A	2230	A
12	A	2233	U
12	A	2237	A
12	A	2241	A
12	A	2243	A
12	A	2245	A
12	A	2246	A
12	A	2250	A

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Mol	Chain	Res	Type
12	A	2251	A
12	A	2257	C
12	A	2262	C
12	A	2263	C
12	A	2264	A
12	A	2284	C
12	A	2285	U
12	A	2297	A
12	A	2300	G
12	A	2321	A
12	A	2322	C
12	A	2324	U
12	A	2332	C
12	A	2345	G
12	A	2348	A
12	A	2350	A
12	A	2351	U
12	A	2358	A
12	A	2359	C
12	A	2360	U
12	A	2361	G
12	A	2362	A
12	A	2363	A
12	A	2374	A
12	A	2381	A
12	A	2390	A
12	A	2394	A
12	A	2401	A
12	A	2404	U
12	A	2406	A
12	A	2407	U
12	A	2414	C
12	A	2415	C
12	A	2417	C
12	A	2418	A
12	A	2434	A
12	A	2446	A
12	A	2451	A
12	A	2452	A
12	A	2457	A
12	A	2458	A
12	A	2478	G

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Mol	Chain	Res	Type
12	A	2483	U
12	A	2485	U
12	A	2488	C
12	A	2493	C
12	A	2494	C
12	A	2500	A
12	A	2502	C
12	A	2511	C
12	A	2520	C
12	A	2521	A
12	A	2527	A
12	A	2528	G
12	A	2530	A
12	A	2531	U
12	A	2536	G
12	A	2539	A
12	A	2540	C
12	A	2544	C
12	A	2547	C
12	A	2548	C
12	A	2549	C
12	A	2550	A
12	A	2554	A
12	A	2603	C
12	A	2611	C
12	A	2613	U
12	A	2617	A
12	A	2618	U
12	A	2619	A
12	A	2620	G
12	A	2621	G
12	A	2622	G
12	A	2623	A
12	A	2626	U
12	A	2627	G
12	A	2628	U
12	A	2629	A
12	A	2630	U
12	A	2633	A
12	A	2634	U
12	A	2645	G
12	A	2654	U

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Mol	Chain	Res	Type
12	A	2655	G
12	A	2656	U
12	A	2660	U
12	A	2670	C
12	A	2683	C
12	A	2684	C
12	A	2686	G
12	A	2693	A
12	A	2694	A
12	A	2695	G
12	A	2696	A
12	A	2698	G
12	A	2699	C
12	A	2706	A
12	A	2709	A
12	A	2719	G
12	A	2722	A
12	A	2723	A
12	A	2724	G
12	A	2725	A
12	A	2732	G
12	A	2739	U
12	A	2740	A
12	A	2743	U
12	A	2756	C
12	A	2810	G
12	A	2815	G
12	A	2816	G
12	A	2819	G
12	A	2828	G
12	A	2831	G
12	A	2832	A
12	A	2833	A
12	A	2840	C
12	A	2843	C
12	A	2844	G
12	A	2847	C
12	A	2854	U
12	A	2864	U
12	A	2865	C
12	A	2880	A
12	A	2906	C

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Mol	Chain	Res	Type
12	A	2912	C
12	A	2913	A
12	A	2917	G
12	A	2918	A
12	A	2919	A
12	A	2922	A
12	A	2926	A
12	A	2928	C
12	A	2932	G
12	A	2934	G
12	A	2935	A
12	A	2936	U
12	A	2937	A
12	A	2946	A
12	A	2956	A
12	A	2963	A
12	A	2978	U
12	A	2984	A
12	A	2986	C
12	A	2987	U
12	A	2988	C
12	A	2989	G
12	A	2990	A
12	A	2991	U
12	A	2992	G
12	A	3005	A
12	A	3007	C
12	A	3016	G
12	A	3018	A
12	A	3021	C
12	A	3022	G
12	A	3041	U
12	A	3042	U
12	A	3051	A
12	A	3053	A
12	A	3054	G
12	A	3060	C
12	A	3067	U
12	A	3068	G
12	A	3069	A
12	A	3070	G
12	A	3072	U

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Mol	Chain	Res	Type
12	A	3086	U
12	A	3089	A
12	A	3090	G
12	A	3097	U
12	A	3098	U
12	A	3100	U
12	A	3102	U
12	A	3108	U
12	A	3109	U
12	A	3111	A
12	A	3112	A
12	A	3113	A
12	A	3123	G
12	A	3141	A
12	A	3150	U
12	A	3157	C
12	A	3158	A
12	A	3162	C
12	A	3168	C
12	A	3169	C
12	A	3170	C
12	A	3171	C
12	A	3172	C
12	A	3173	G
12	A	3177	A
12	A	3180	A
12	A	3184	C
12	A	3189	C
12	A	3190	A
12	A	3196	G
12	A	3197	U
12	A	3198	A
12	A	3199	U
12	A	3201	A
12	A	3202	U
12	A	3207	A
12	A	3208	C
12	A	3209	A
12	A	3211	C
12	A	3212	C
12	A	3217	A
12	A	3218	A

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Mol	Chain	Res	Type
12	A	3220	A
12	A	3228	U
14	B	1604	G
14	B	1608	G
14	B	1609	U
14	B	1610	A
14	B	1611	G
14	B	1614	U
14	B	1615	A
14	B	1617	C
14	B	1618	A
14	B	1620	A
14	B	1621	A
14	B	1622	A
14	B	1628	C
14	B	1632	U
14	B	1633	U
14	B	1644	G
14	B	1645	A
14	B	1646	U
14	B	1670	A

All (56) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	A	1727	A
12	A	1749	C
12	A	1772	A
12	A	1811	A
12	A	1823	A
12	A	1824	U
12	A	1853	A
12	A	1854	U
12	A	1855	A
12	A	1871	A
12	A	1936	A
12	A	1956	U
12	A	1974	A
12	A	1994	A
12	A	2001	C
12	A	2015	G
12	A	2021	U

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Mol	Chain	Res	Type
12	A	2030	U
12	A	2065	A
12	A	2097	A
12	A	2135	A
12	A	2158	U
12	A	2182	G
12	A	2186	C
12	A	2245	A
12	A	2291	A
12	A	2347	C
12	A	2361	G
12	A	2380	C
12	A	2417	C
12	A	2457	A
12	A	2527	A
12	A	2530	A
12	A	2543	C
12	A	2619	A
12	A	2620	G
12	A	2628	U
12	A	2629	A
12	A	2630	U
12	A	2653	C
12	A	2723	A
12	A	2724	G
12	A	2739	U
12	A	2818	C
12	A	2832	A
12	A	2846	G
12	A	2905	A
12	A	2926	A
12	A	2935	A
12	A	2991	U
12	A	3004	C
12	A	3041	U
12	A	3068	G
12	A	3206	C
14	B	1607	U
14	B	1614	U

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
12	OMG	A	3040	12	23,26,27	1.23	2 (8%)	32,38,41	2.00	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
12	OMG	A	3040	12	-	2/9/27/28	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	A	3040	OMG	C5-C4	3.61	1.48	1.38
12	A	3040	OMG	C5-N7	-2.08	1.34	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	A	3040	OMG	C5-C4-N3	-5.84	119.10	128.39
12	A	3040	OMG	C2-N3-C4	4.95	120.82	112.30
12	A	3040	OMG	N9-C4-N3	4.24	134.43	125.95
12	A	3040	OMG	C2'-C1'-N9	-3.41	107.77	114.24
12	A	3040	OMG	C6-C5-N7	3.01	135.77	130.29
12	A	3040	OMG	O4'-C1'-N9	2.30	113.57	108.36
12	A	3040	OMG	O6-C6-C5	-2.20	120.71	126.53
12	A	3040	OMG	C4-C5-N7	-2.19	107.19	110.67

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	A	3040	OMG	O4'-C1'-N9-C4
12	A	3040	OMG	O4'-C1'-N9-C8

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 101 ligands modelled in this entry, 95 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
70	PNS	w	201	62	14,20,21	0.35	0	18,26,29	0.74	0
69	SAH	n	301	-	27,28,28	0.49	1 (3%)	36,40,40	0.74	1 (2%)
66	SAM	A1	401	-	27,29,29	0.50	1 (3%)	34,42,42	0.76	1 (2%)
67	GDP	C	401	-	29,30,30	1.17	3 (10%)	45,47,47	1.77	7 (15%)
68	GTP	G	502	65	33,34,34	0.57	0	50,54,54	0.55	0
67	GDP	t	501	65	29,30,30	1.17	3 (10%)	45,47,47	1.84	8 (17%)

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
70	PNS	w	201	62	-	16/24/26/27	-
69	SAH	n	301	-	-	10/15/31/31	0/3/3/3
66	SAM	A1	401	-	-	6/17/33/33	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
67	GDP	C	401	-	-	0/16/32/32	0/3/3/3
68	GTP	G	502	65	-	2/22/38/38	0/3/3/3
67	GDP	t	501	65	-	0/16/32/32	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	t	501	GDP	C5-C4	3.38	1.48	1.38
67	C	401	GDP	C5-C4	3.17	1.47	1.38
67	C	401	GDP	C6-N1	-2.40	1.34	1.38
69	n	301	SAH	OXT-C	-2.20	1.23	1.30
66	A1	401	SAM	OXT-C	-2.13	1.23	1.30
67	t	501	GDP	C6-N1	-2.10	1.34	1.38
67	C	401	GDP	C5-N7	-2.06	1.34	1.39
67	t	501	GDP	C5-N7	-2.05	1.35	1.39

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	t	501	GDP	C5-C4-N3	-6.35	118.28	128.39
67	C	401	GDP	C5-C4-N3	-6.27	118.41	128.39
67	t	501	GDP	C2-N3-C4	5.36	121.52	112.30
67	C	401	GDP	C2-N3-C4	5.13	121.14	112.30
67	t	501	GDP	N9-C4-N3	4.72	135.38	125.95
67	C	401	GDP	N9-C4-N3	4.67	135.28	125.95
69	n	301	SAH	OXT-C-O	-3.60	115.90	124.08
67	t	501	GDP	C6-C5-N7	3.34	136.37	130.29
67	C	401	GDP	C6-C5-N7	3.11	135.94	130.29
66	A1	401	SAM	OXT-C-O	-3.07	117.12	124.08
67	t	501	GDP	C4-C5-N7	-2.57	106.60	110.67
67	C	401	GDP	C4-C5-N7	-2.52	106.67	110.67
67	C	401	GDP	C3'-C2'-C1'	2.25	105.73	101.46
67	t	501	GDP	O6-C6-C5	-2.11	120.95	126.53
67	C	401	GDP	O6-C6-C5	-2.05	121.11	126.53
67	t	501	GDP	C5-C6-N1	2.03	118.43	113.25
67	t	501	GDP	C3'-C2'-C1'	2.01	105.26	101.46

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
66	A1	401	SAM	N-CA-CB-CG
66	A1	401	SAM	CA-CB-CG-SD
66	A1	401	SAM	C4'-C5'-SD-CE
66	A1	401	SAM	C2'-C1'-N9-C8
69	n	301	SAH	O-C-CA-N
70	w	201	PNS	O27-C28-C29-C30
70	w	201	PNS	O27-C28-C29-C31
70	w	201	PNS	O27-C28-C29-C32
70	w	201	PNS	C28-C29-C32-C34
70	w	201	PNS	O33-C32-C34-N36
70	w	201	PNS	C32-C34-N36-C37
70	w	201	PNS	O35-C34-N36-C37
70	w	201	PNS	N36-C37-C38-C39
69	n	301	SAH	OXT-C-CA-N
66	A1	401	SAM	C2'-C1'-N9-C4
70	w	201	PNS	O40-C39-N41-C42
70	w	201	PNS	C38-C39-N41-C42
66	A1	401	SAM	C-CA-CB-CG
70	w	201	PNS	O33-C32-C34-O35
69	n	301	SAH	O-C-CA-CB
69	n	301	SAH	C2'-C1'-N9-C8
69	n	301	SAH	C-CA-CB-CG
70	w	201	PNS	C30-C29-C32-C34
70	w	201	PNS	C31-C29-C32-C34
69	n	301	SAH	OXT-C-CA-CB
69	n	301	SAH	N-CA-CB-CG
69	n	301	SAH	CB-CG-SD-C5'
70	w	201	PNS	N41-C42-C43-S44
69	n	301	SAH	C2'-C1'-N9-C4
69	n	301	SAH	O4'-C1'-N9-C8
70	w	201	PNS	C37-C38-C39-O40
68	G	502	GTP	PA-O3A-PB-O2B
70	w	201	PNS	C37-C38-C39-N41
68	G	502	GTP	PA-O3A-PB-O1B

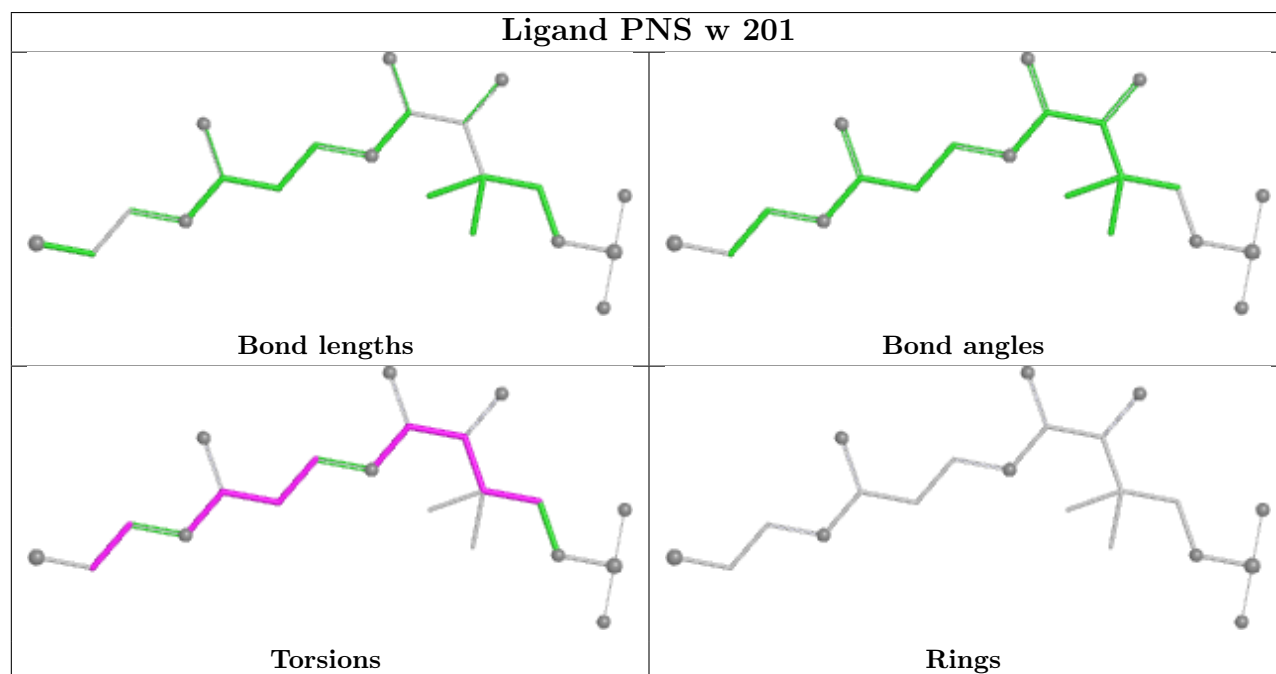
There are no ring outliers.

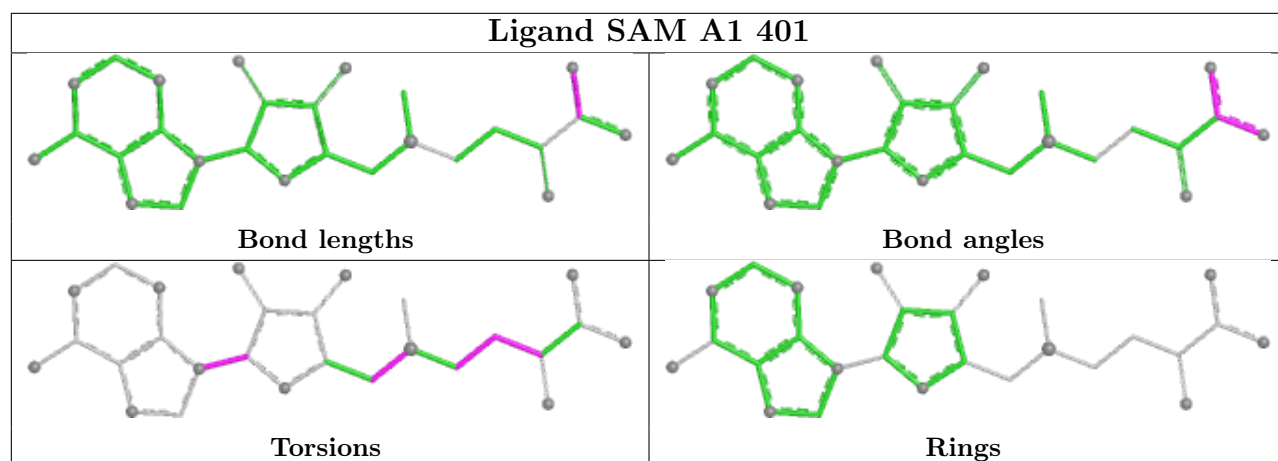
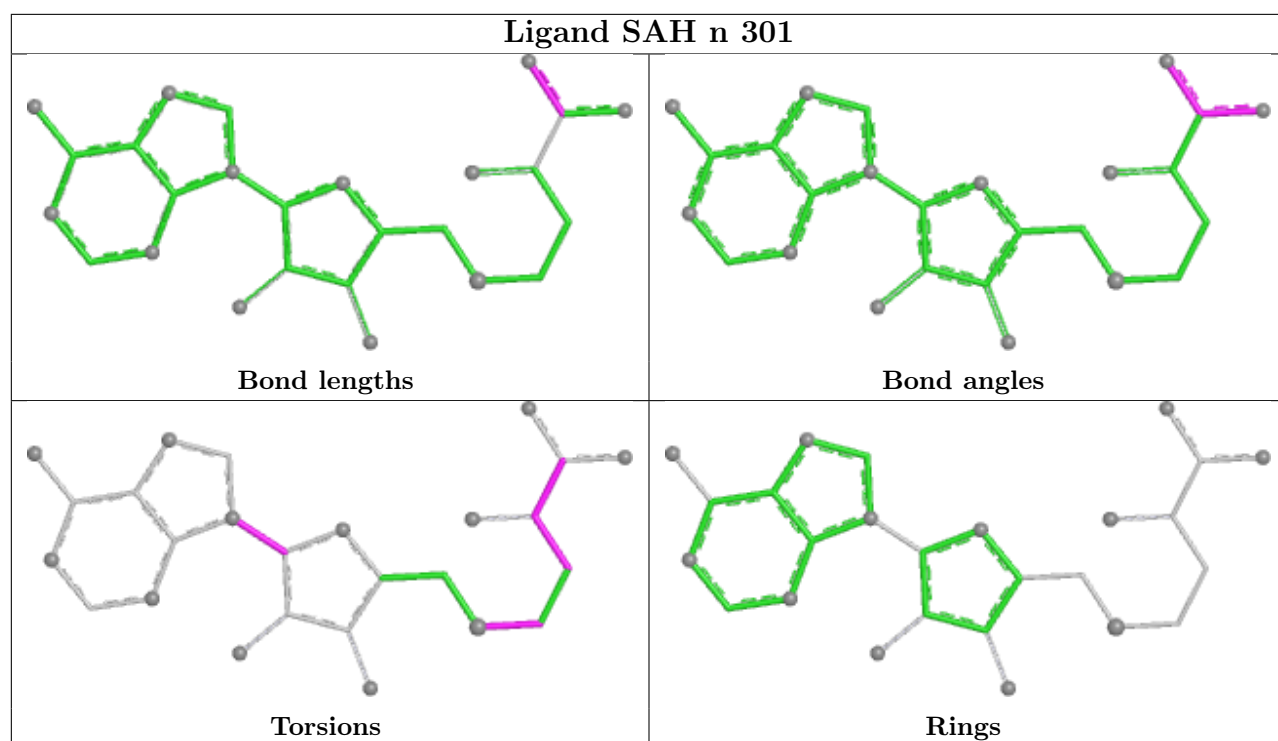
2 monomers are involved in 2 short contacts:

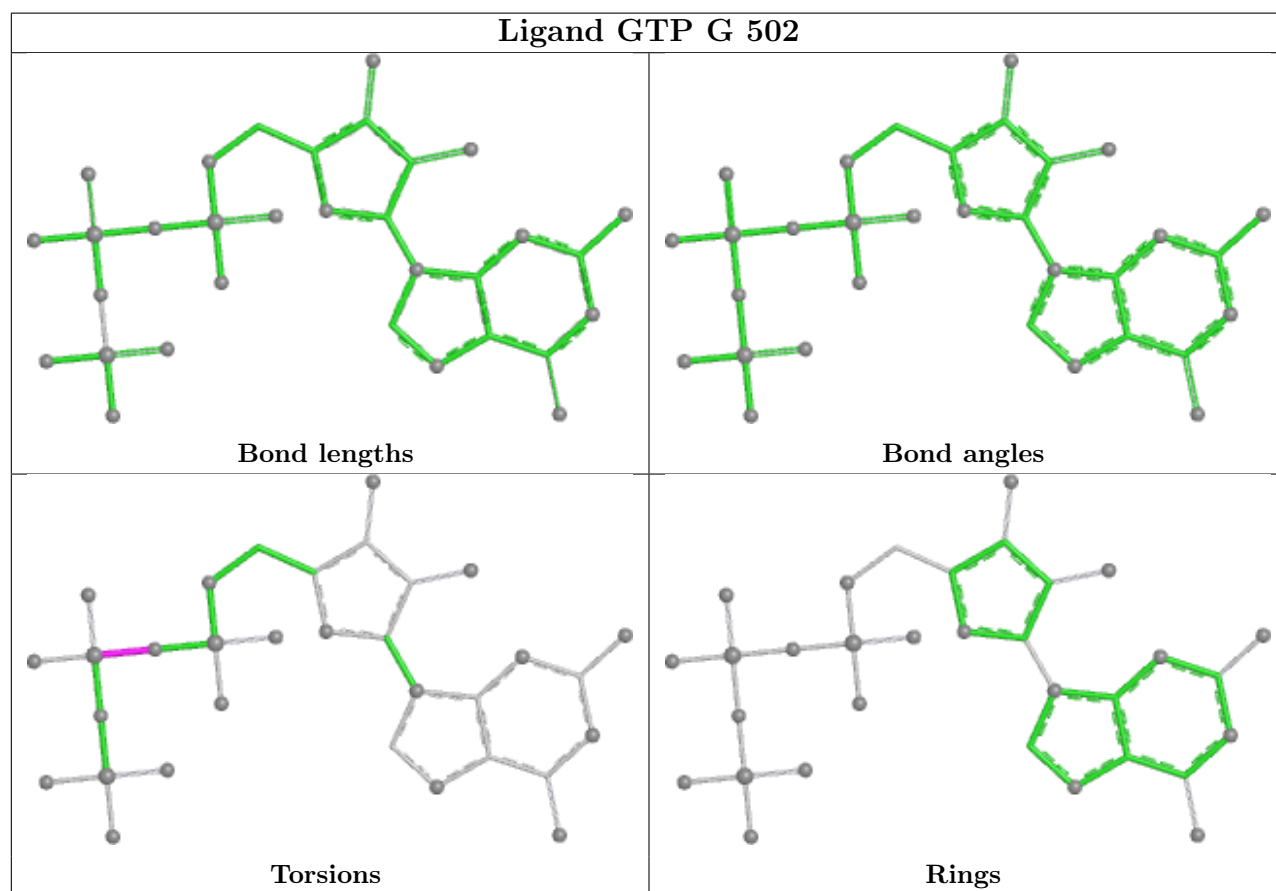
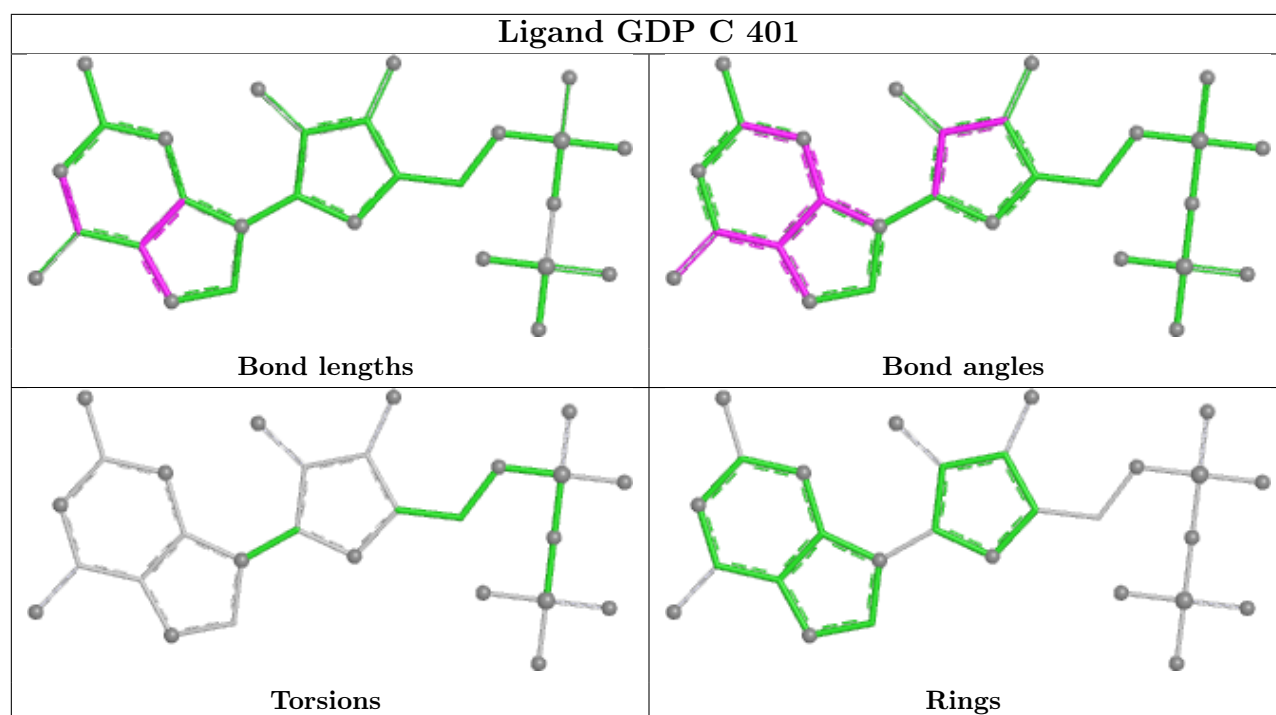
Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	A1	401	SAM	1	0
68	G	502	GTP	1	0

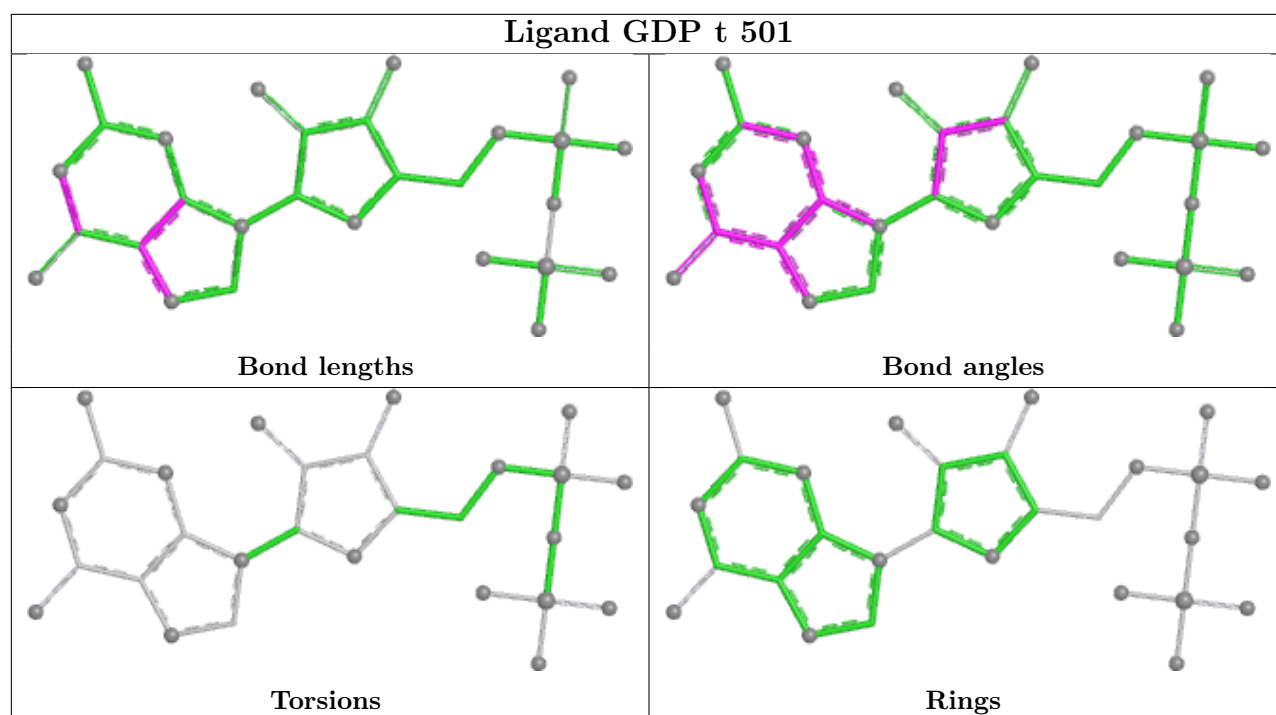
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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.

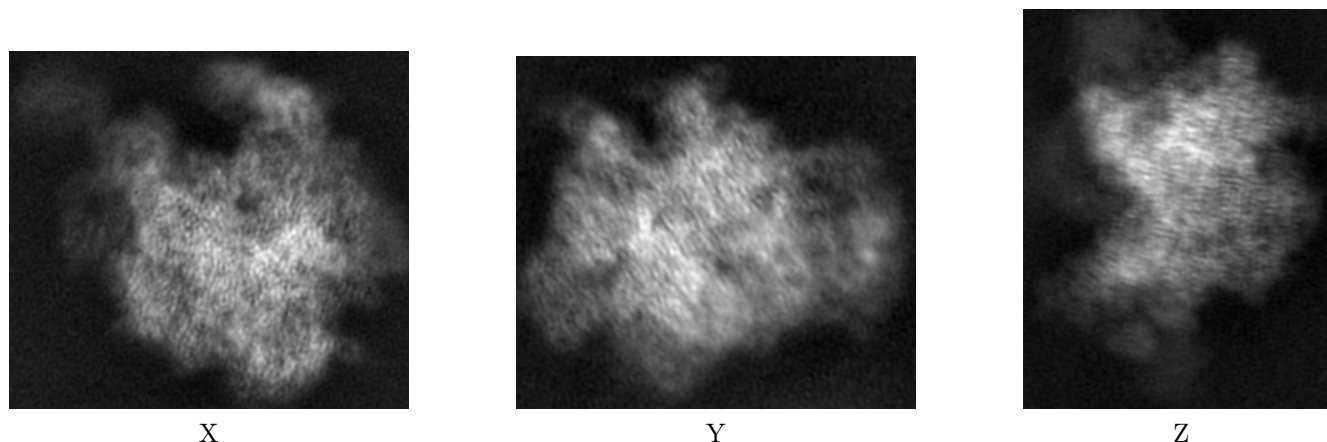
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12763. These allow visual inspection of the internal detail of the map and identification of artifacts.

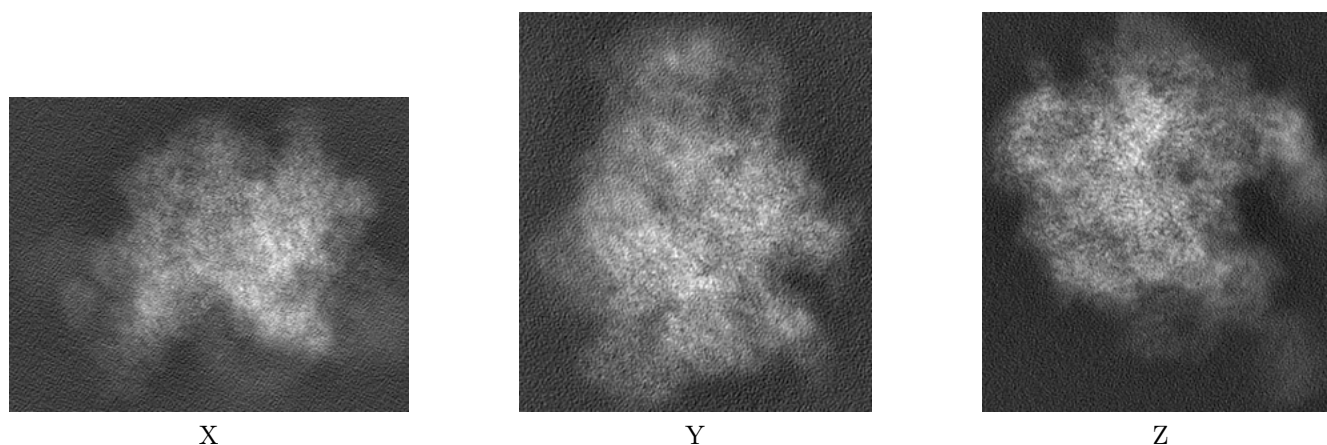
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



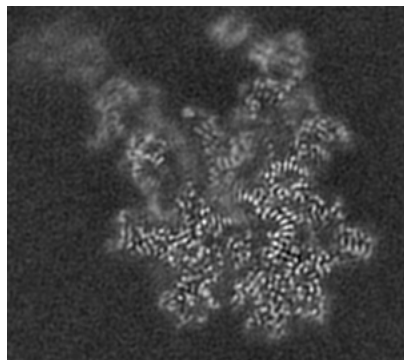
6.1.2 Raw map



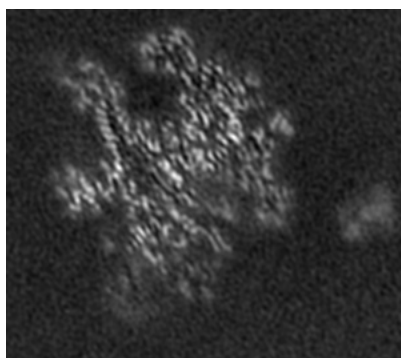
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

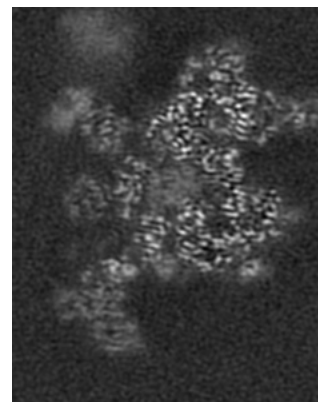
6.2.1 Primary map



X Index: 108

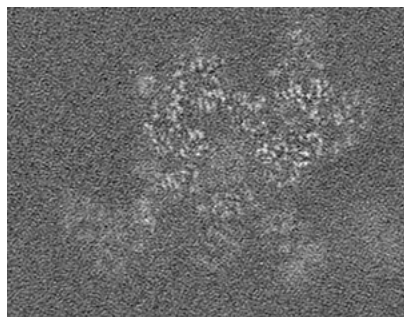


Y Index: 137

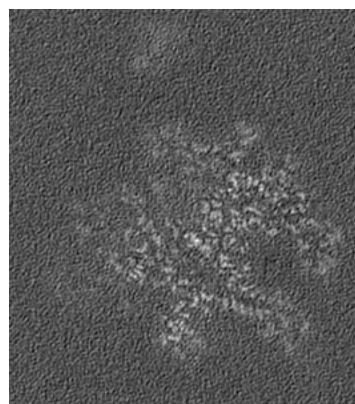


Z Index: 123

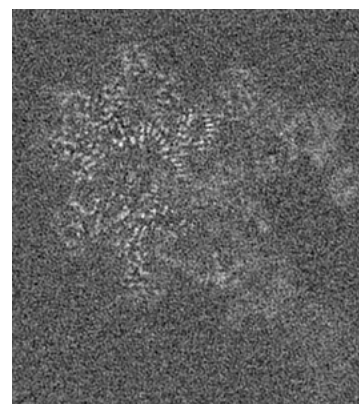
6.2.2 Raw map



X Index: 123



Y Index: 138

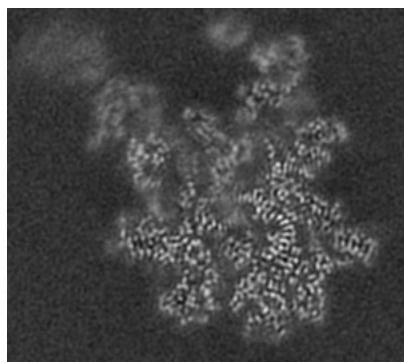


Z Index: 108

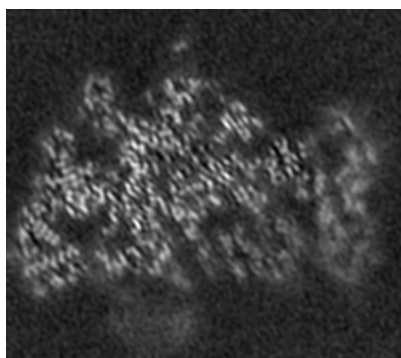
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

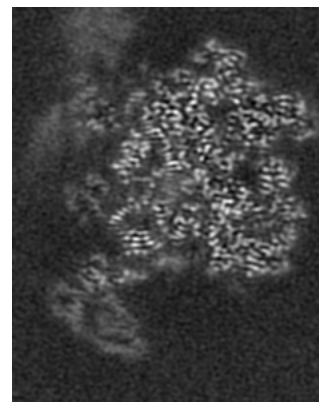
6.3.1 Primary map



X Index: 106

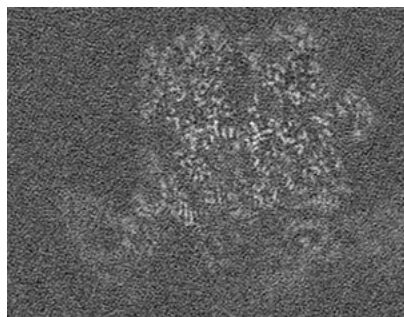


Y Index: 181

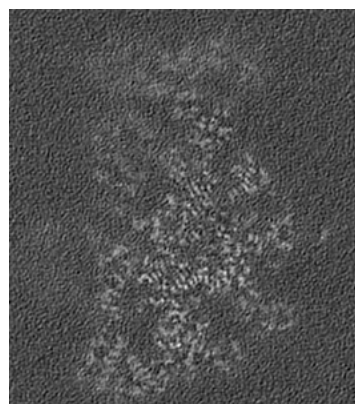


Z Index: 113

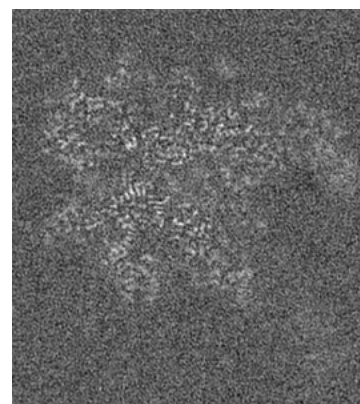
6.3.2 Raw map



X Index: 110



Y Index: 182

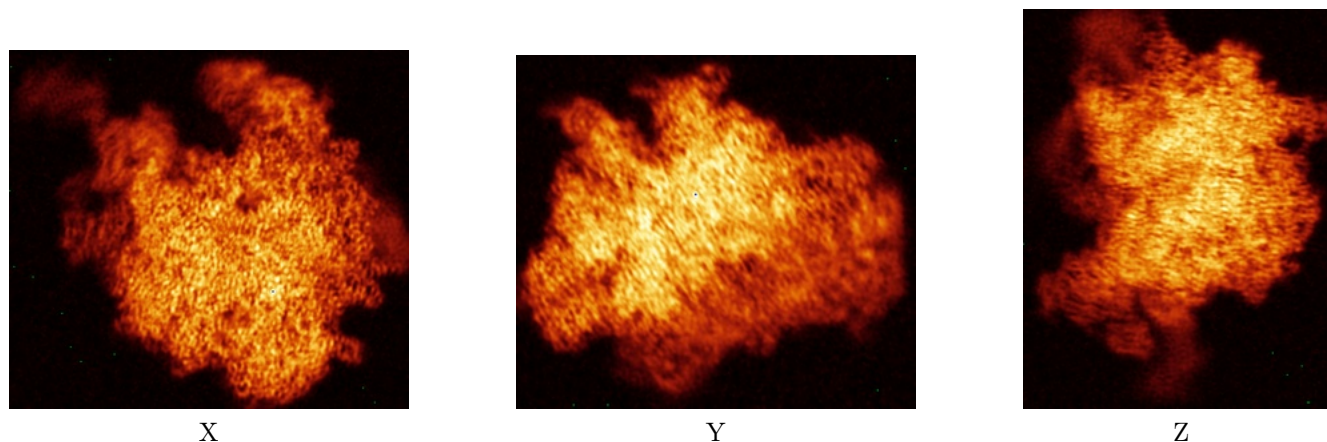


Z Index: 117

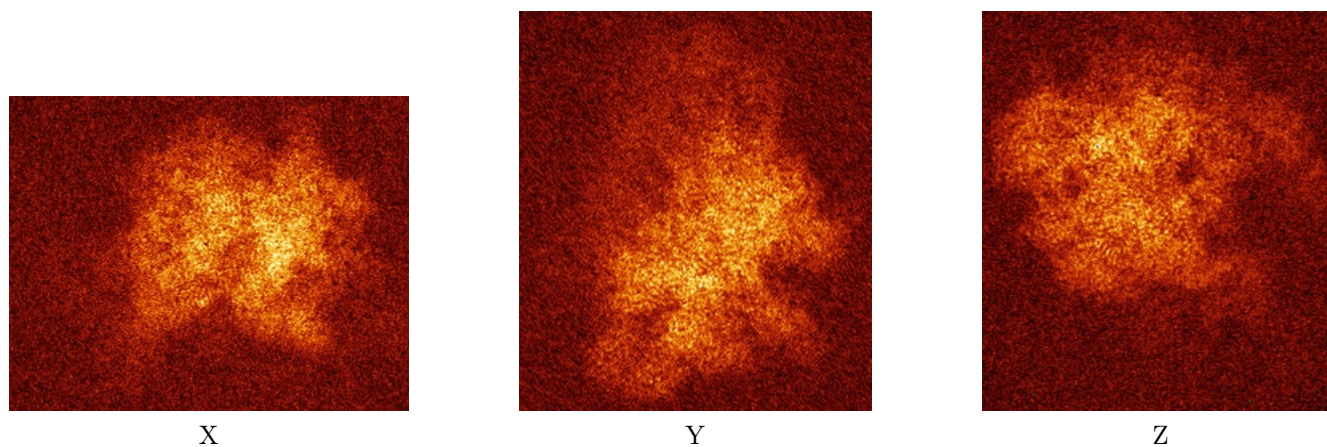
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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.

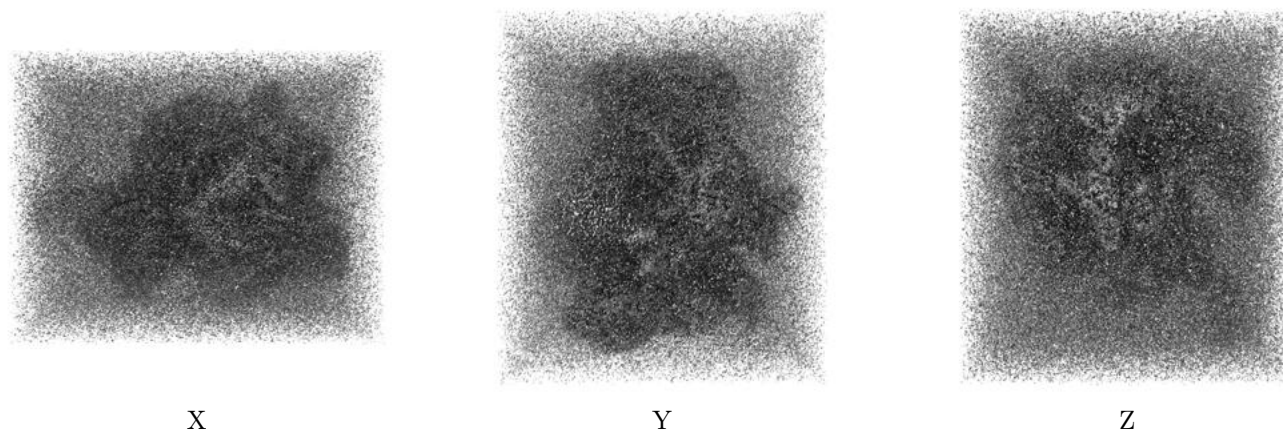
6.5 Orthogonal surface views [i](#)

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.

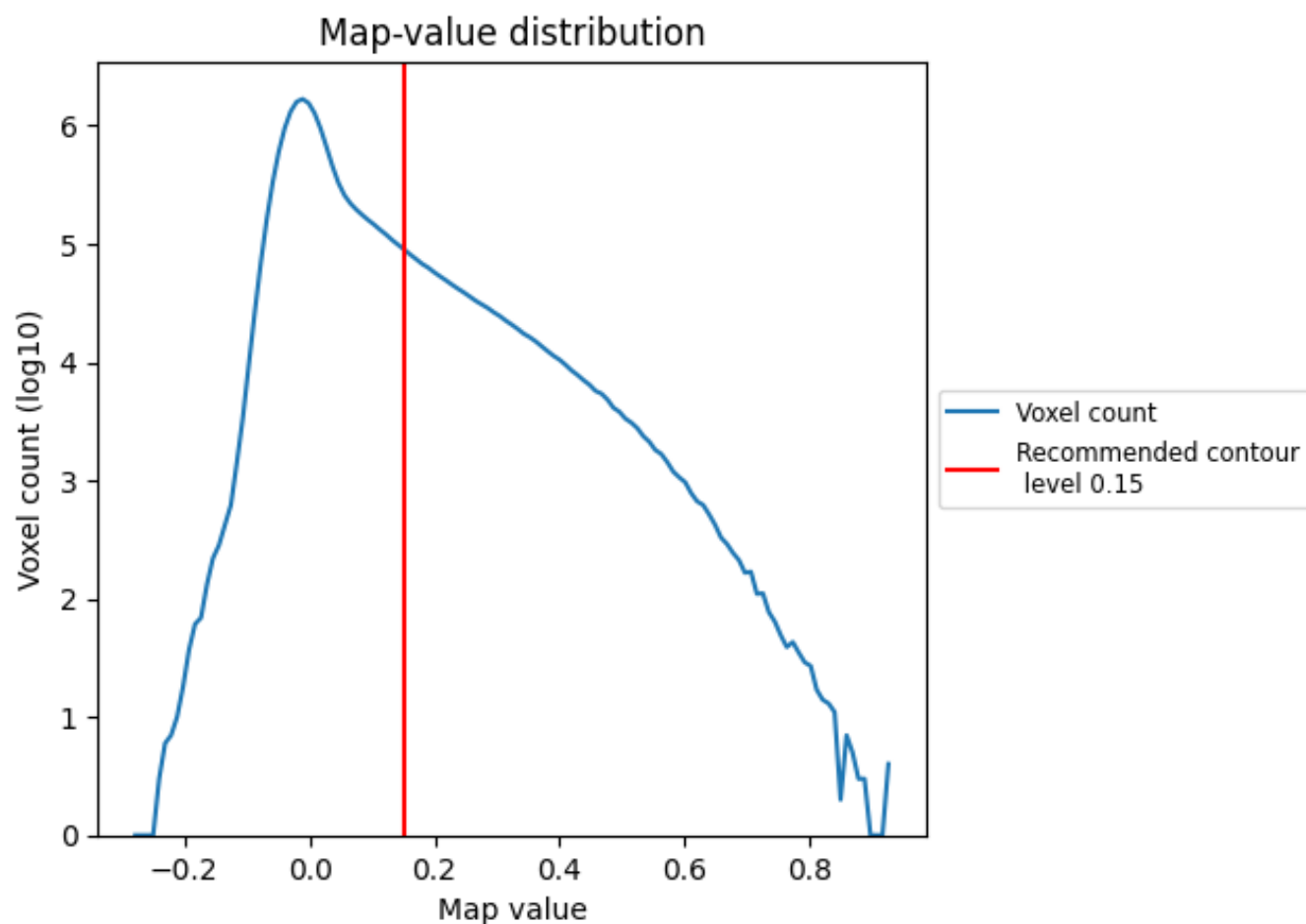
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

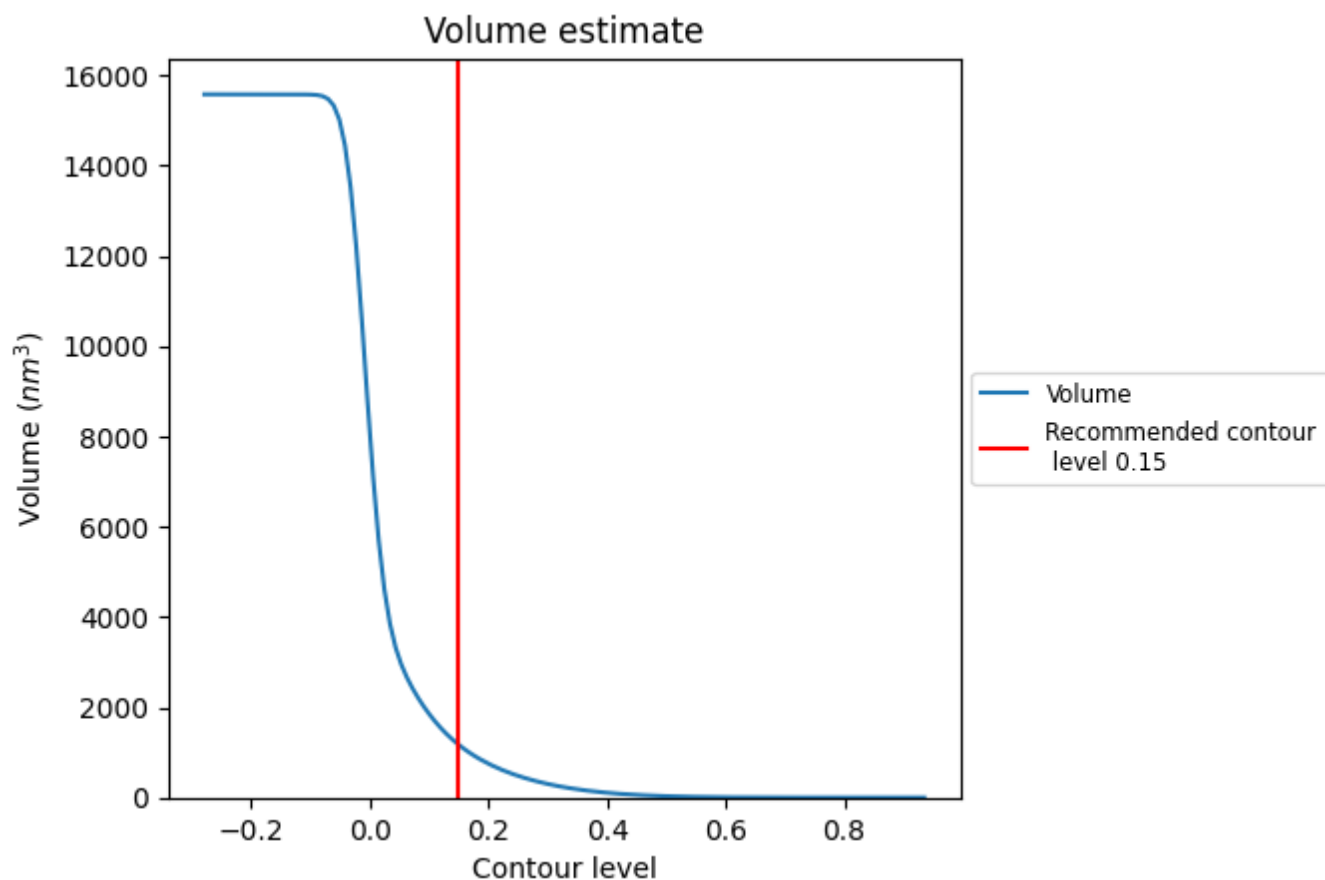
This section contains the results of statistical analysis of the map.

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 1174 nm³; this corresponds to an approximate mass of 1061 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.

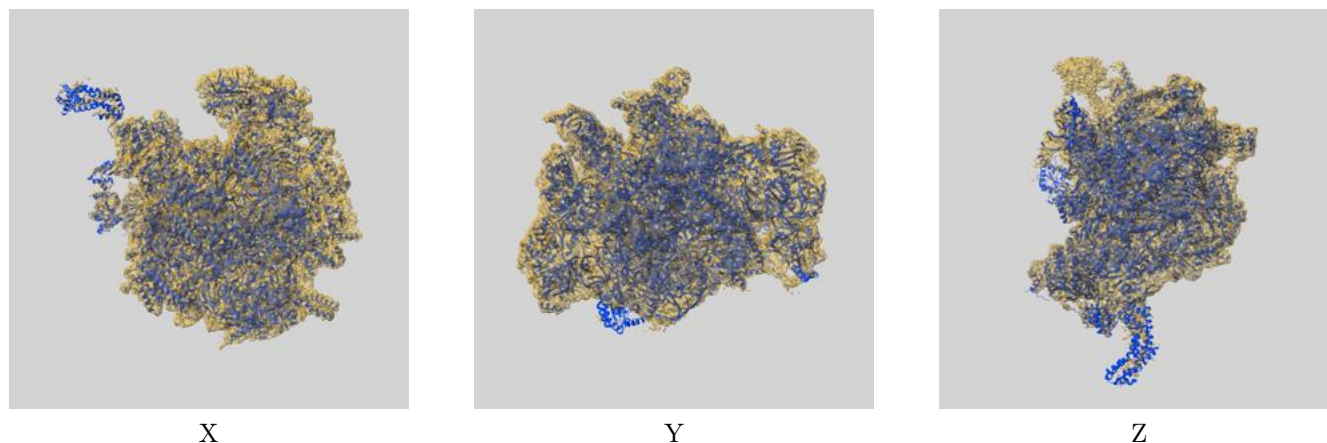
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

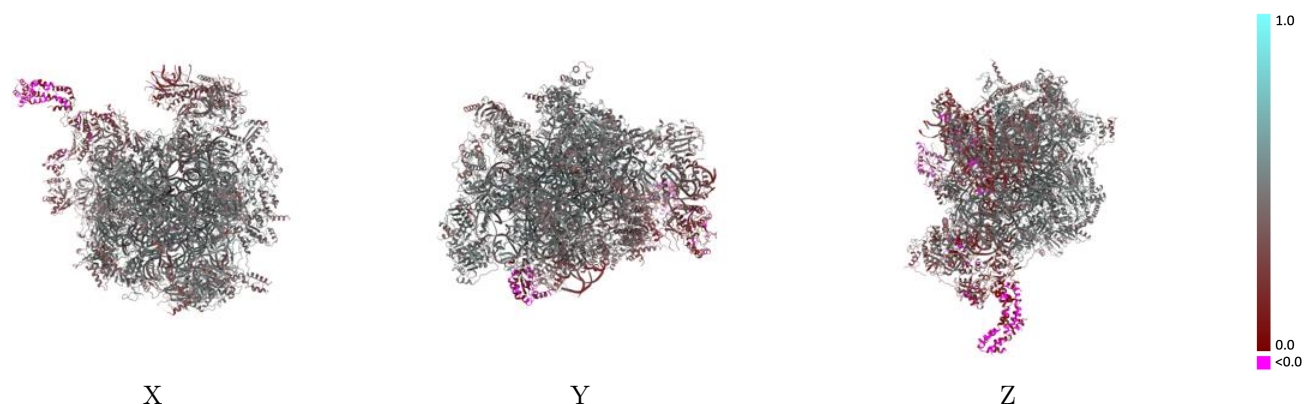
This section contains information regarding the fit between EMDB map EMD-12763 and PDB model 7O9K. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



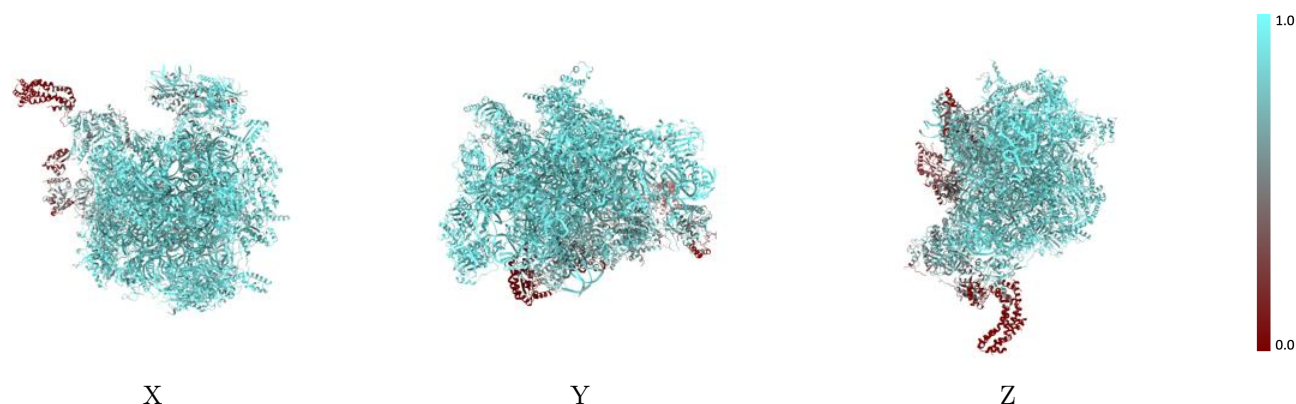
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



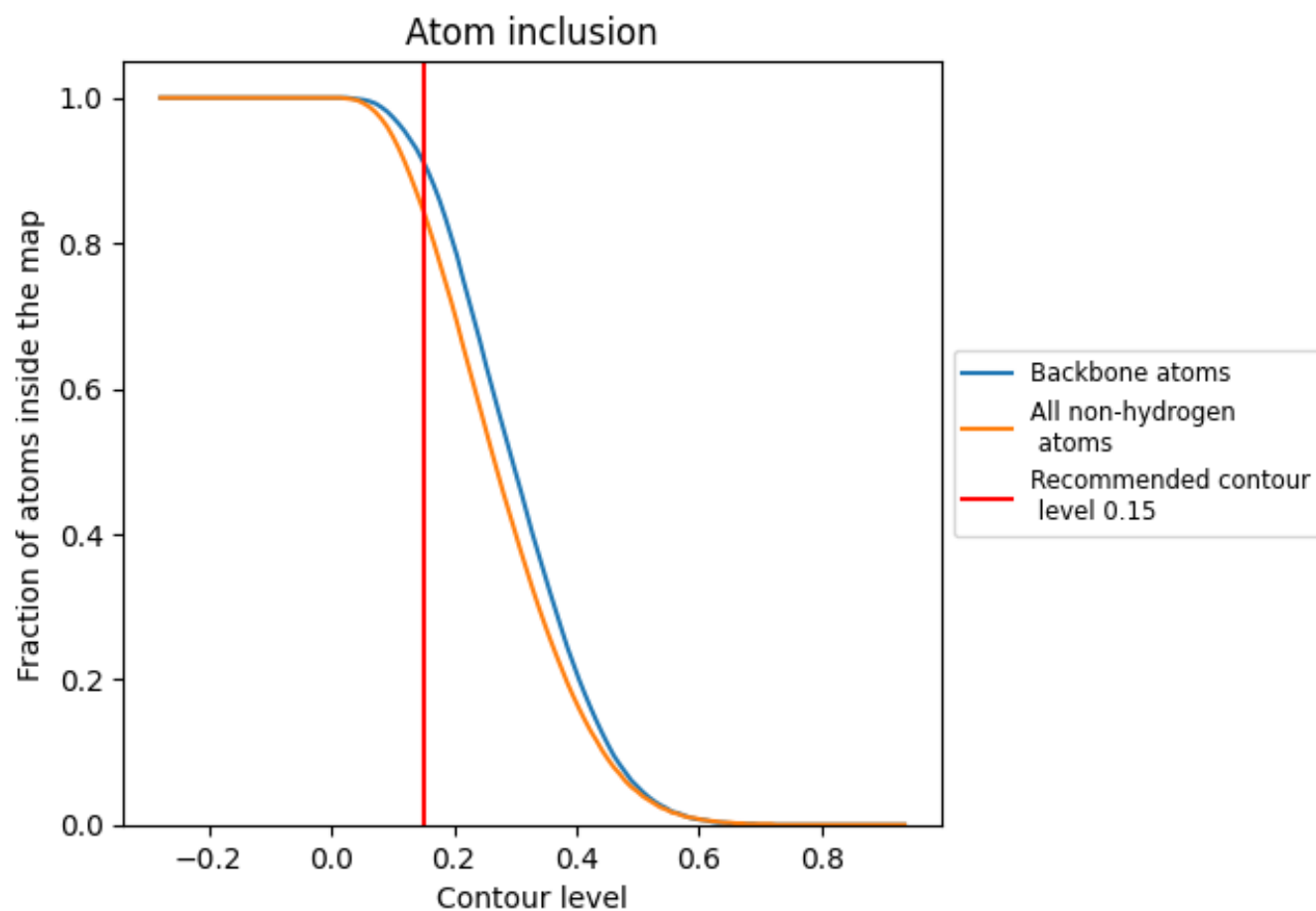
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 84% 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	 0.8450	 0.4280
0	 0.9100	 0.4650
1	 0.8620	 0.4650
2	 0.9540	 0.5310
3	 0.9510	 0.5170
4	 0.8870	 0.4770
5	 0.9150	 0.4760
6	 0.9120	 0.4280
7	 0.8580	 0.4310
8	 0.6190	 0.2450
9	 0.9060	 0.4700
A	 0.9740	 0.4660
A1	 0.7460	 0.4070
A2	 0.7390	 0.4000
B	 0.9570	 0.3150
C	 0.1210	 0.1320
D	 0.9000	 0.4820
E	 0.9110	 0.4810
F	 0.9200	 0.4910
FF	 0.1140	 0.1840
G	 0.7600	 0.4150
H	 0.8470	 0.4470
I	 0.5970	 0.2430
J	 0.6770	 0.1950
K	 0.9350	 0.4990
L	 0.8630	 0.4870
M	 0.9310	 0.4880
N	 0.8120	 0.3930
O	 0.9360	 0.4960
P	 0.9200	 0.4410
Q	 0.8980	 0.4750
R	 0.9350	 0.5020
S	 0.8990	 0.4880
T	 0.9120	 0.5010
U	 0.9310	 0.4860



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Chain	Atom inclusion	Q-score
UNK	 0.6080	 0.2820
V	 0.8450	 0.4210
W	 0.8990	 0.4920
X	 0.8850	 0.4680
Y	 0.9160	 0.4760
Z	 0.9120	 0.4900
a	 0.9140	 0.4930
b	 0.9200	 0.4970
c	 0.8740	 0.4610
d	 0.8420	 0.4170
e	 0.5650	 0.2060
f	 0.6870	 0.3080
g	 0.9360	 0.4810
h	 0.8560	 0.4230
i	 0.9420	 0.5120
j	 0.8910	 0.4660
k	 0.8240	 0.3110
l	 0.7390	 0.2770
m	 0.5150	 0.1920
n	 0.4320	 0.4110
o	 0.9070	 0.4640
p	 0.8880	 0.4230
q	 0.8270	 0.3940
r	 0.9100	 0.4670
s	 0.9390	 0.4910
t	 0.4820	 0.3220
t1	 0.2380	 0.1210
t2	 0.2230	 0.1260
t3	 0.0500	 0.0150
t4	 0.0220	 0.0060
t5	 0.0040	 0.0220
t6	 0.0050	 -0.0020
u	 0.7700	 0.4430
v	 0.7520	 0.4020
w	 0.5010	 0.2740