



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 07:11 AM UTC

PDB ID : 6NU3 / pdb_00006nu3
EMDB ID : EMD-0515
Title : Structural insights into unique features of the human mitochondrial ribosome recycling
Authors : Sharma, M.R.; Koripella, R.K.; Agrawal, R.K.
Deposited on : 2019-01-30
Resolution : 4.40 Å(reported)
Based on initial model : 3J9M

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:

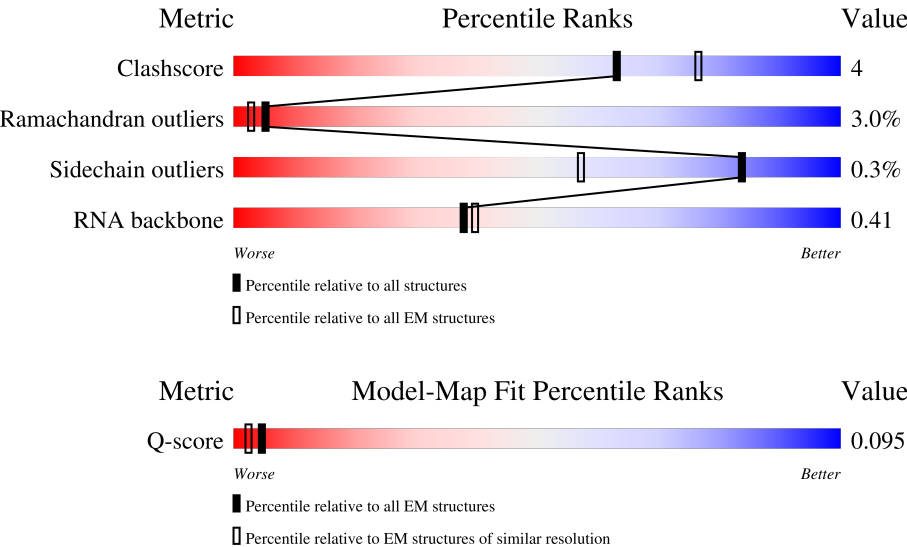
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.40 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	3132 (3.91 - 4.90)

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

Mol	Chain	Length	Quality of chain
1	A	1472	
2	B	56	
3	D	305	

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Mol	Chain	Length	Quality of chain
4	E	348	
5	F	311	
6	H	267	
7	I	261	
8	J	192	
9	K	178	
10	L	145	
11	M	296	
12	N	251	
13	O	175	
14	P	180	
15	Q	219	
16	R	149	
17	S	205	
18	T	206	
19	U	153	
20	V	216	
21	W	148	
22	X	243	
23	Y	250	
24	Z	161	
25	0	188	
26	1	65	
27	2	92	
28	3	188	

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Mol	Chain	Length	Quality of chain
29	4	103	
30	5	394	
31	6	380	
32	7	338	
33	8	206	
34	9	137	
35	a	142	
36	b	215	
37	c	332	
38	d	306	
39	e	279	
40	f	212	
41	g	166	
42	h	158	
43	i	128	
44	j	123	
45	k	112	
46	l	138	
47	m	128	
48	o	102	
49	p	206	
50	q	222	
51	r	196	
52	s	439	
53	t	28	

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Mol	Chain	Length	Quality of chain
54	u	2	
55	AA	923	
56	AB	296	
57	AC	167	
58	AD	430	
59	AE	125	
60	AF	242	
61	AG	396	
62	AH	201	
63	AI	194	
64	AJ	138	
65	AK	128	
66	AL	257	
67	AM	137	
68	AN	130	
69	AO	185	
70	AP	142	
71	AQ	86	
72	AR	360	
73	AS	190	
74	AT	173	
75	AU	205	
76	AV	414	
77	AW	187	
78	AX	398	

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Mol	Chain	Length	Quality of chain
79	AY	395	
80	AZ	106	
81	A0	225	
82	A1	323	
83	A2	118	
84	A3	199	
85	A4	474	

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 291640 atoms, of which 133281 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	1472	Total	C	H	N	O	P	0	0
			47126	14025	15865	5642	10122	1472		

- Molecule 2 is a RNA chain called mt-tRNAVal.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	56	Total	C	H	N	O	P	0	0
			1794	534	603	214	387	56		

- Molecule 3 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	D	236	Total	C	H	N	O	S	0	0
			3738	1145	1896	373	315	9		

- Molecule 4 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	E	300	Total	C	H	N	O	S	0	0
			4743	1523	2378	410	422	10		

- Molecule 5 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	F	250	Total	C	H	N	O	S	0	0
			4058	1294	2045	365	348	6		

- Molecule 6 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	H	95	Total	C	H	N	O		0	0
			1616	498	832	152	134			

- Molecule 7 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	I	158	Total	C	H	N	O	S	0	0
			2652	828	1369	235	210	10		

- Molecule 8 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	J	140	Total	C	H	N	O	S	0	0
			2202	680	1141	192	187	2		

- Molecule 9 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	K	177	Total	C	H	N	O	S	0	0
			2899	934	1448	259	251	7		

- Molecule 10 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	L	115	Total	C	H	N	O	S	0	0
			1830	559	941	171	154	5		

- Molecule 11 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	M	287	Total	C	H	N	O	S	0	0
			4683	1472	2378	425	402	6		

- Molecule 12 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	N	205	Total	C	H	N	O	S	0	0
			3335	1056	1681	308	280	10		

- Molecule 13 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	O	152	Total	C	H	N	O	S	0	0
			2528	784	1283	239	215	7		

- Molecule 14 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	P	133	Total	C	H	N	O	S	0	0
			2161	677	1081	209	189	5		

- Molecule 15 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	Q	219	Total	C	H	N	O	S	0	0
			3681	1168	1859	322	323	9		

- Molecule 16 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	R	140	Total	C	H	N	O	S	0	0
			2367	732	1214	231	186	4		

- Molecule 17 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	S	156	Total	C	H	N	O	S	0	0
			2573	806	1322	222	219	4		

- Molecule 18 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	T	166	Total	C	H	N	O	S	0	0
			2778	875	1410	254	232	7		

- Molecule 19 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	U	111	Total	C	H	N	O	S	0	0
			1857	591	935	176	153	2		

- Molecule 20 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	V	189	Total	C	H	N	O	S	0	0
			3109	987	1558	278	278	8		

- Molecule 21 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	W	111	Total	C	H	N	O	S	0	0
			1769	558	898	164	146	3		

- Molecule 22 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	X	243	Total	C	H	N	O	S	0	0
			4062	1317	2027	351	362	5		

- Molecule 23 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	Y	176	Total	C	H	N	O	S	0	0
			3078	970	1561	291	252	4		

- Molecule 24 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Z	120	Total	C	H	N	O	S	0	0
			2008	626	1030	183	166	3		

- Molecule 25 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	0	108	Total	C	H	N	O	S	0	0
			1784	545	904	172	157	6		

- Molecule 26 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	1	52	Total	C	H	N	O	S	0	0
			908	278	475	83	70	2		

- Molecule 27 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	2	46	Total	C	H	N	O	S	0	0
			782	233	406	83	59	1		

- Molecule 28 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	3	95	Total	C	H	N	O	S	0	0
			1714	539	883	162	127	3		

- Molecule 29 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	4	36	Total	C	H	N	O	S	0	0
			667	203	345	70	46	3		

- Molecule 30 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	5	376	Total	C	H	N	O	S	0	0
			6123	1987	3059	529	538	10		

- Molecule 31 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	6	325	Total	C	H	N	O	S	0	0
			5086	1692	2450	465	470	9		

- Molecule 32 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	7	266	Total	C	H	N	O	S	0	0
			4331	1383	2173	371	388	16		

- Molecule 33 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	8	99	Total	C	H	N	O	S	0	0
			1680	535	844	144	155	2		

- Molecule 34 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	9	109	Total	C	H	N	O	S	0	0
			1751	565	878	152	154	2		

- Molecule 35 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	a	82	Total	C	H	N	O	S	0	0
			1344	434	658	124	123	5		

- Molecule 36 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	b	148	Total	C	H	N	O	S	0	0
			2358	733	1180	229	213	3		

- Molecule 37 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	c	275	Total	C	H	N	O	S	0	0
			4437	1415	2220	383	410	9		

- Molecule 38 is a protein called cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	d	162	Total	C	H	N	O	S	0	0
			2690	870	1343	234	235	8		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
39	e	217	Total	C	H	N	O	S	0	0
			3529	1124	1767	310	323	5		

- Molecule 40 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	f	131	Total	C	H	N	O	S	0	0
			2083	663	1044	169	203	4		

- Molecule 41 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	g	129	Total	C	H	N	O	S	0	0
			2123	690	1056	185	190	2		

- Molecule 42 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	h	100	Total	C	H	N	O	S	0	0
			1633	524	806	146	155	2		

- Molecule 43 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	i	97	Total	C	H	N	O	S	0	0
			1684	532	857	165	126	4		

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	j	85	Total	C	H	N	O	S	0	0
			1357	423	673	133	126	2		

- Molecule 45 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	k	84	Total	C	H	N	O	S	0	0
			1311	407	656	122	121	5		

- Molecule 46 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	l	23	Total	C	H	N	O		
			448	137	227	52	32	0	0

- Molecule 47 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	m	45	Total	C	H	N	O	S	0	0
			759	232	387	76	62	2		

- Molecule 48 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	o	94	Total	C	H	N	O	S	0	0
			1601	501	804	165	128	3		

- Molecule 49 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	p	127	Total	C	H	N	O	S	0	0
			2141	661	1083	201	192	4		

- Molecule 50 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	q	128	Total	C	H	N	O	S	0	0
			2125	671	1049	208	192	5		

- Molecule 51 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	r	146	Total	C	H	N	O	S	0	0
			2424	764	1221	232	199	8		

- Molecule 52 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	s	370	Total	C	H	N	O	S	0	0
			6058	1946	3022	542	534	14		

- Molecule 53 is a protein called Unknown protein/protein extension.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	t	28	Total	C	H	N	O		
			170	84	30	28	28	0	0

- Molecule 54 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	u	2	Total	C	H	N	O	P	0	0
			65	19	23	8	13	2		

- Molecule 55 is a RNA chain called 12S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	AA	923	Total	C	H	N	O	P	0	0
			29558	8790	9952	3535	6358	923		

- Molecule 56 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	AB	217	Total	C	H	N	O	S	0	0
			3534	1131	1766	321	306	10		

- Molecule 57 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	AC	132	Total	C	H	N	O	S	0	0
			2170	699	1088	195	184	4		

- Molecule 58 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	AD	322	Total	C	H	N	O	S	0	0
			5153	1611	2596	476	457	13		

- Molecule 59 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	AE	122	Total	C	H	N	O	S	0	0
			1973	614	1001	177	177	4		

- Molecule 60 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	AF	201	Total	C	H	N	O	S	0	0
			3384	1069	1716	305	283	11		

- Molecule 61 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	AG	305	Total	C	H	N	O	S	0	0
			5019	1599	2503	448	455	14		

- Molecule 62 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	AH	122	Total	C	H	N	O	S	0	0
			2023	643	1024	168	185	3		

- Molecule 63 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	AI	136	Total	C	H	N	O	S	0	0
			2063	637	1052	192	178	4		

- Molecule 64 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	AJ	108	Total	C	H	N	O	S	0	0
			1725	521	887	169	142	6		

- Molecule 65 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	AK	101	Total	C	H	N	O	S	0	0
			1746	537	885	179	140	5		

- Molecule 66 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	AL	164	Total	C	H	N	O	S	0	0
			2854	883	1472	257	235	7		

- Molecule 67 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	AM	116	Total	C	H	N	O	S	0	0
			1871	582	951	182	150	6		

- Molecule 68 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	AN	107	Total	C	H	N	O	S	0	0
			1754	549	908	153	141	3		

- Molecule 69 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	AO	185	Total	C	H	N	O	S	0	0
			3016	970	1488	285	267	6		

- Molecule 70 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	AP	96	Total	C	H	N	O	S	0	0
			1578	498	804	133	135	8		

- Molecule 71 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	AQ	86	Total	C	H	N	O	S	0	0
			1476	455	741	147	124	9		

- Molecule 72 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	AR	242	Total	C	H	N	O	S	0	0
			4039	1285	2031	343	372	8		

- Molecule 73 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	AS	126	Total	C	H	N	O	S	0	0
			2079	673	1037	183	185	1		

- Molecule 74 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	AT	162	Total	C	H	N	O	S	0	0
			2674	850	1344	231	238	11		

- Molecule 75 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	AU	173	Total	C	H	N	O	S	0	0
			2932	900	1471	294	263	4		

- Molecule 76 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	AV	328	Total	C	H	N	O	S	0	0
			5392	1737	2690	452	502	11		

- Molecule 77 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	AW	97	Total	C	H	N	O	S	0	0
			1551	486	785	137	139	4		

- Molecule 78 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	AX	316	Total	C	H	N	O	S	0	0
			5051	1625	2520	440	455	11		

- Molecule 79 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
79	AY	108	Total	C	H	N	O	S	0	0
			1773	593	859	150	169	2		

- Molecule 80 is a protein called 28S ribosomal protein S33, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	AZ	87	Total	C	H	N	O	S	0	0
			1487	473	747	133	130	4		

- Molecule 81 is a protein called 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
81	A0	201	Total	C	H	N	O	S	0	0
			3369	1065	1685	322	292	5		

- Molecule 82 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
82	A1	256	Total	C	H	N	O	S	0	0
			4173	1321	2097	350	395	10		

- Molecule 83 is a protein called Coiled-coil-helix-coiled-coil-helix domain-containing protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
83	A2	116	Total	C	H	N	O	S	0	0
			1887	574	962	181	162	8		

- Molecule 84 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
84	A3	69	Total	C	H	N	O	S	0	0
			1292	393	682	130	86	1		

- Molecule 85 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial, mS39.

Mol	Chain	Residues	Atoms						AltConf	Trace
85	A4	414	Total	C	H	N	O	S	0	0
			5097	1805	2259	490	529	14		

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	A	97	Total	Mg	0
			97	97	
86	M	1	Total	Mg	0
			1	1	
86	g	1	Total	Mg	0
			1	1	
86	AA	28	Total	Mg	0
			28	28	

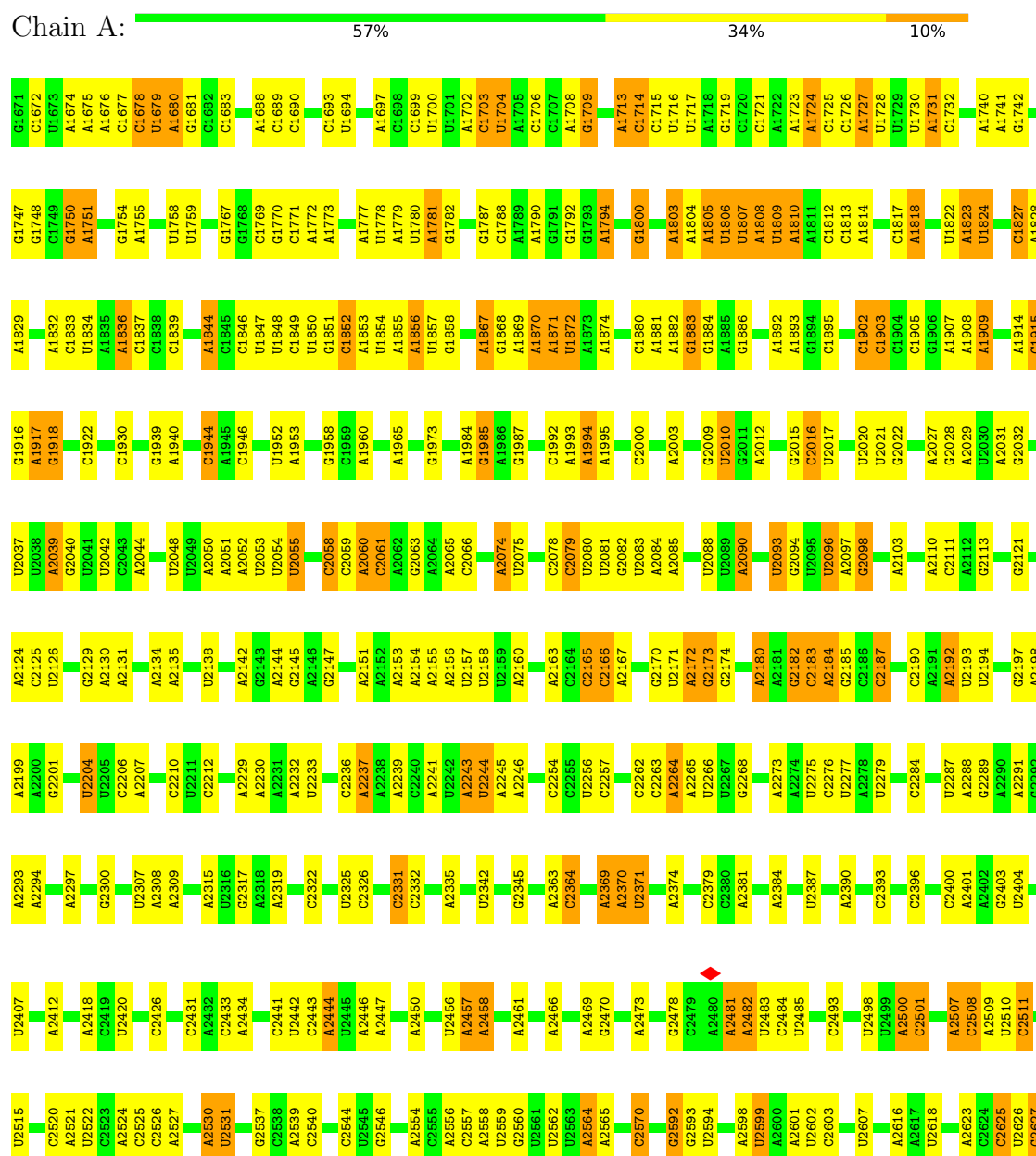
- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

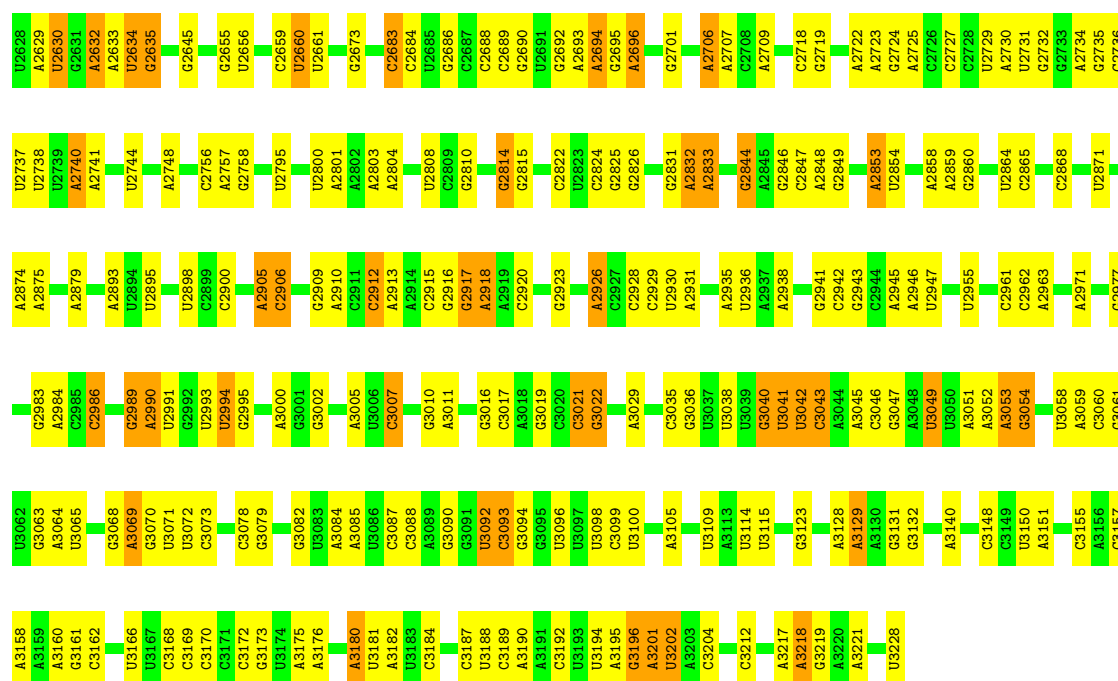
Mol	Chain	Residues	Atoms		AltConf
87	0	1	Total	Zn	0
			1	1	
87	4	1	Total	Zn	0
			1	1	
87	r	1	Total	Zn	0
			1	1	
87	AB	1	Total	Zn	0
			1	1	
87	AO	1	Total	Zn	0
			1	1	
87	AP	1	Total	Zn	0
			1	1	
87	AT	1	Total	Zn	0
			1	1	

3 Residue-property plots

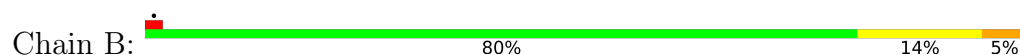
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S rRNA

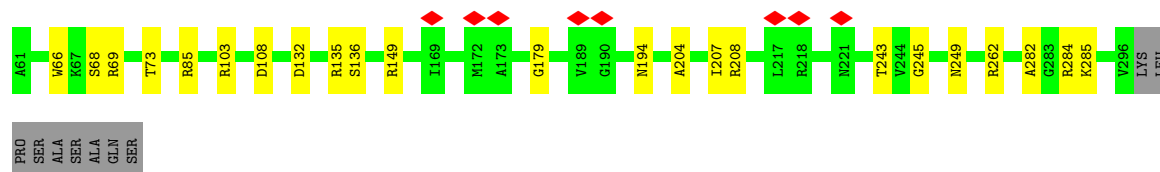
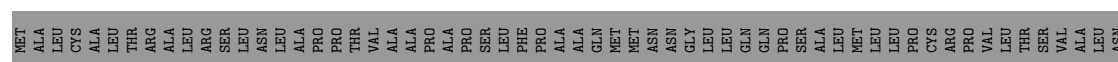




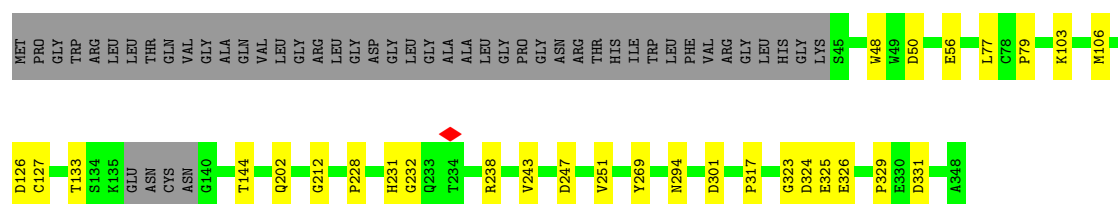
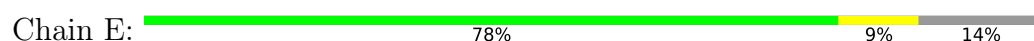
• Molecule 2: mt-tRNAVal



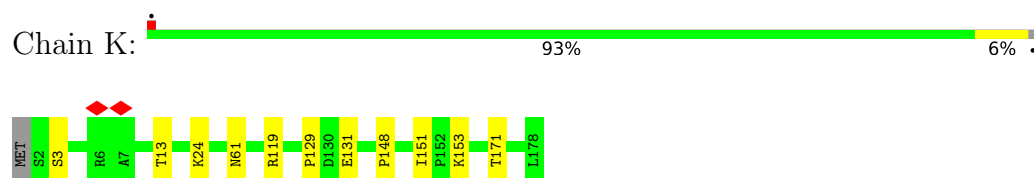
• Molecule 3: 39S ribosomal protein L2, mitochondrial



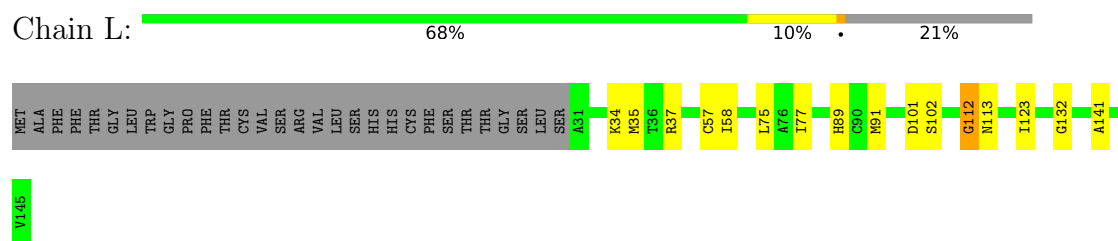
• Molecule 4: 39S ribosomal protein L3, mitochondrial



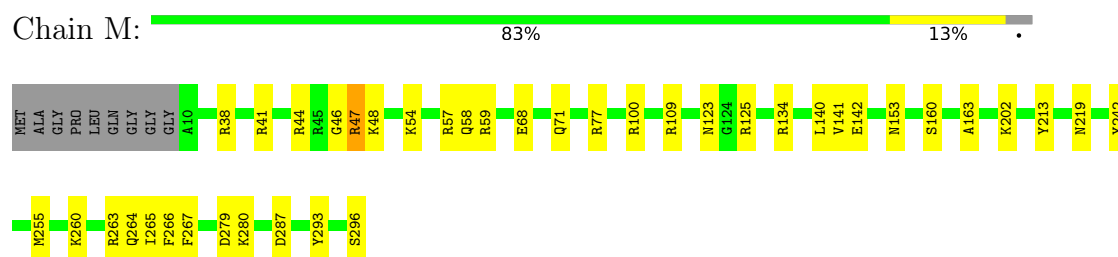
- Molecule 9: 39S ribosomal protein L13, mitochondrial



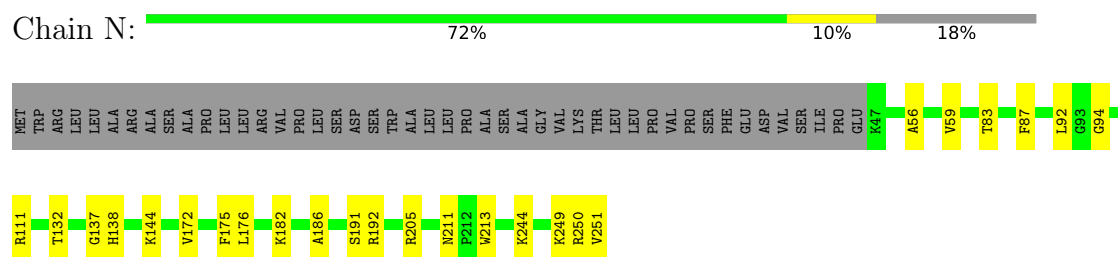
- Molecule 10: 39S ribosomal protein L14, mitochondrial



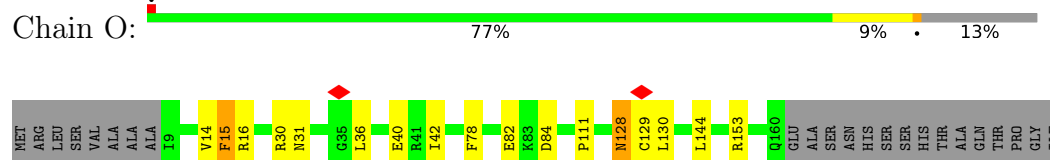
- Molecule 11: 39S ribosomal protein L15, mitochondrial



- Molecule 12: 39S ribosomal protein L16, mitochondrial

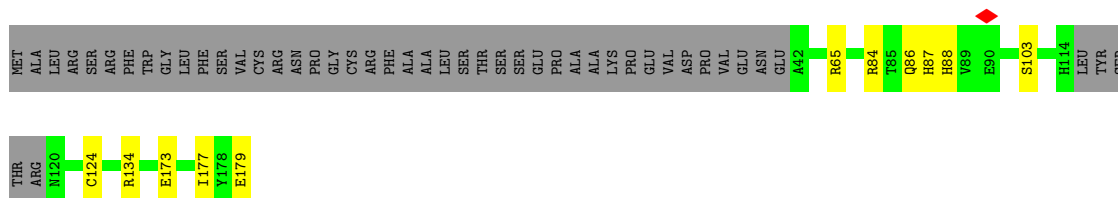


- Molecule 13: 39S ribosomal protein L17, mitochondrial



- Molecule 14: 39S ribosomal protein L18, mitochondrial





- Molecule 15: 39S ribosomal protein L19, mitochondrial

Chain Q: 95% 5%



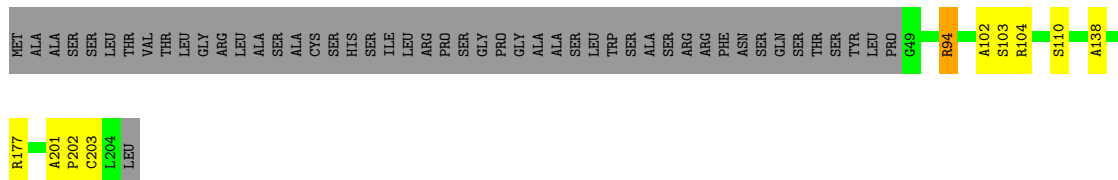
- Molecule 16: 39S ribosomal protein L20, mitochondrial

Chain R: 85% 8% 6%



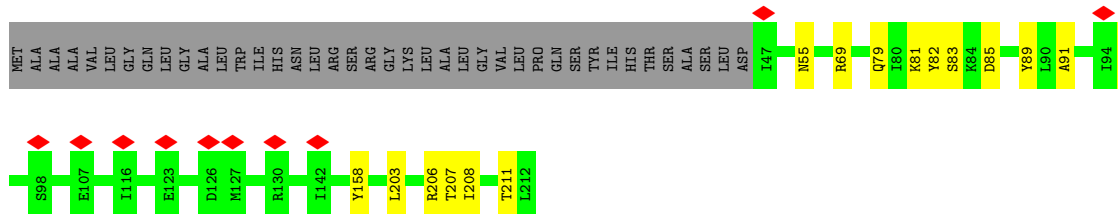
- Molecule 17: 39S ribosomal protein L21, mitochondrial

Chain S: 71% 24%



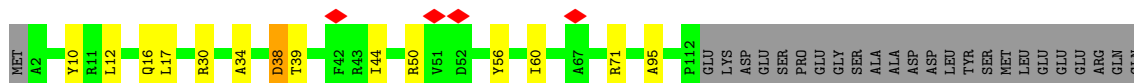
- Molecule 18: 39S ribosomal protein L22, mitochondrial

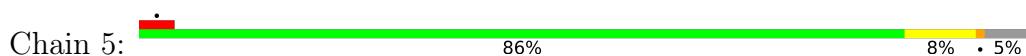
Chain T: 5% 73% 8% 19%

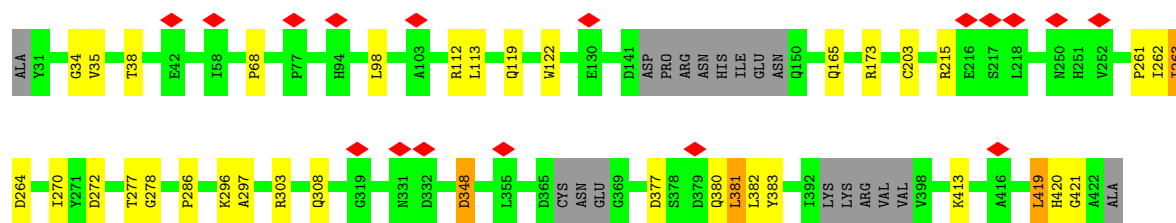


- Molecule 19: 39S ribosomal protein L23, mitochondrial

Chain U: 63% 8% 27%

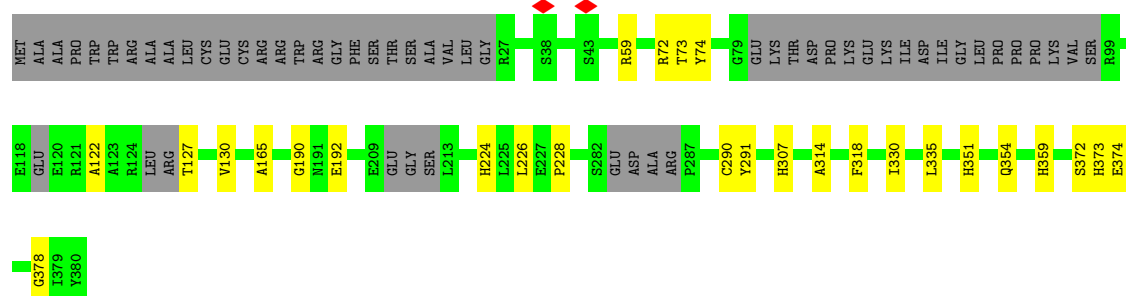






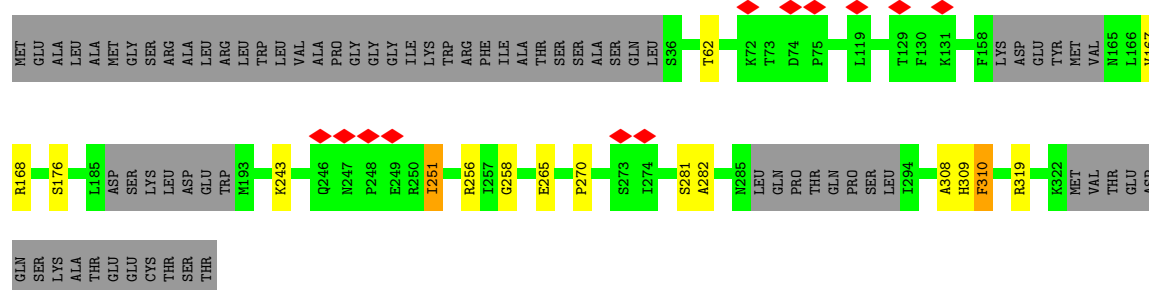
- Molecule 31: 39S ribosomal protein L38, mitochondrial

Chain 6:



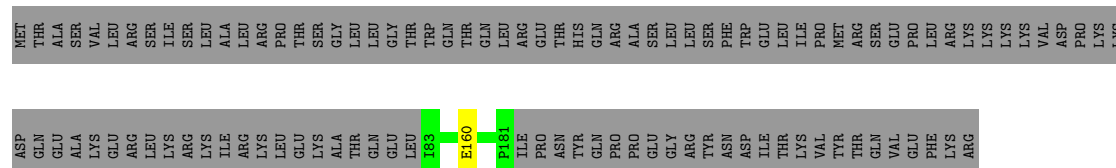
- Molecule 32: 39S ribosomal protein L39, mitochondrial

Chain 7:



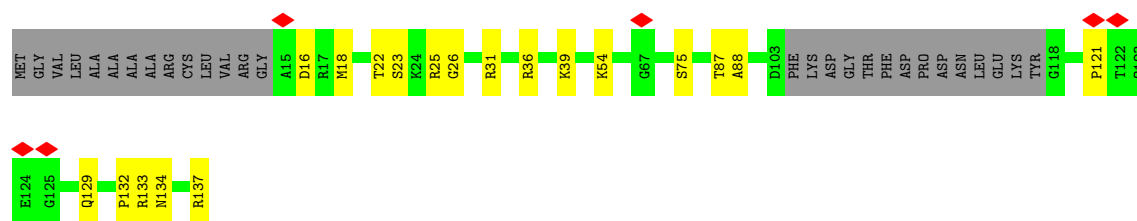
- Molecule 33: 39S ribosomal protein L40, mitochondrial

Chain 8:



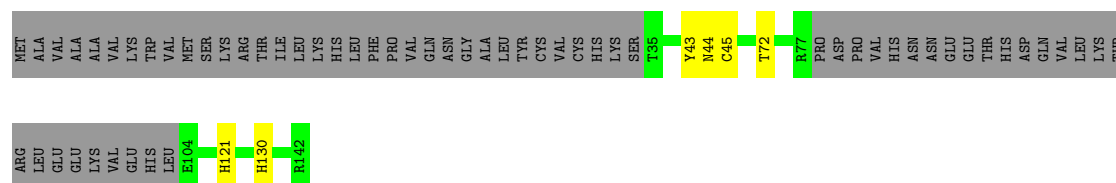
- Molecule 34: 39S ribosomal protein L41, mitochondrial

Chain 9:



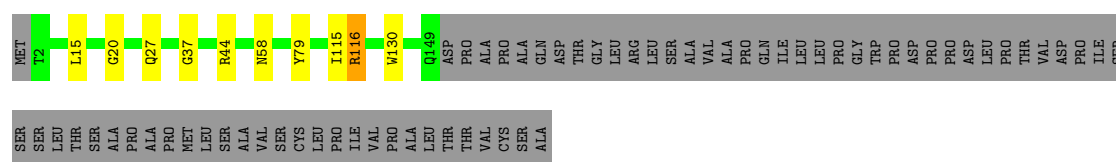
- Molecule 35: 39S ribosomal protein L42, mitochondrial

Chain a: 54% 42%



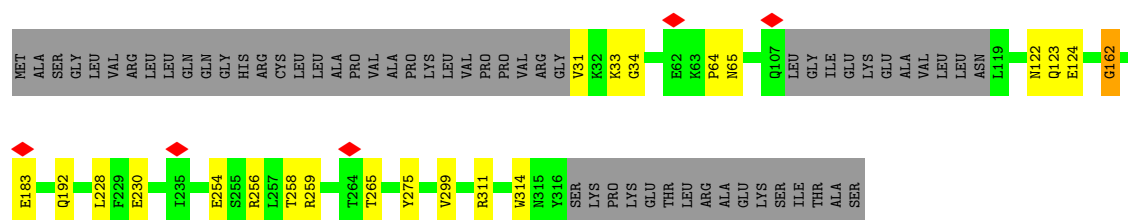
- Molecule 36: 39S ribosomal protein L43, mitochondrial

Chain b: 64% 31%



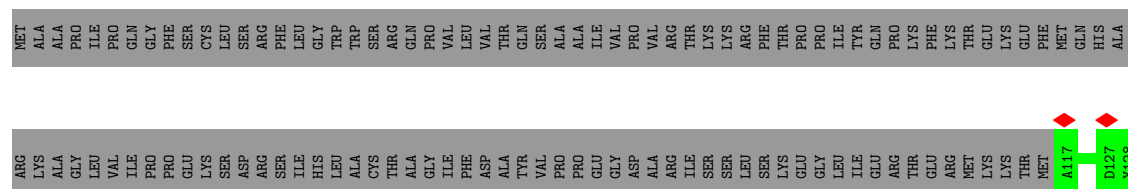
- Molecule 37: 39S ribosomal protein L44, mitochondrial

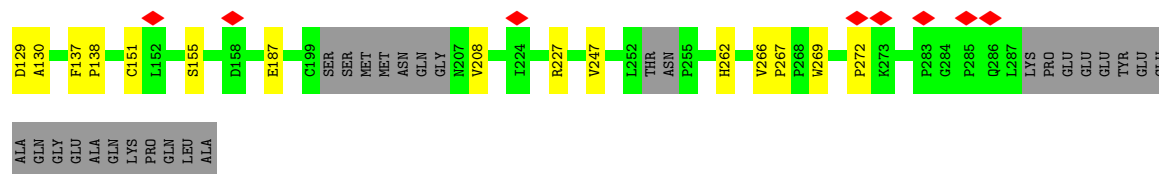
Chain c: 76% 6% 17%



- Molecule 38: cDNA FLJ61100, highly similar to 39S ribosomal protein L45, mitochondrial

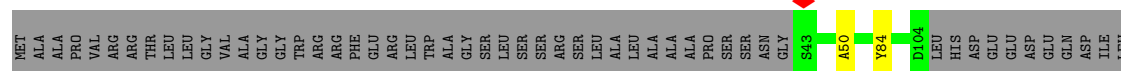
Chain d: 48% 5% 47%





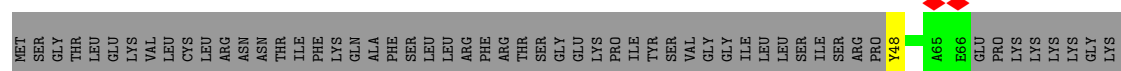
- Molecule 39: 39S ribosomal protein L46, mitochondrial

Chain e: 72% 5% 22%



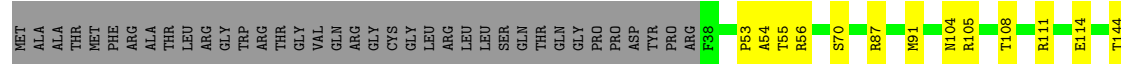
- Molecule 40: 39S ribosomal protein L48, mitochondrial

Chain f: 60% 0% 38%



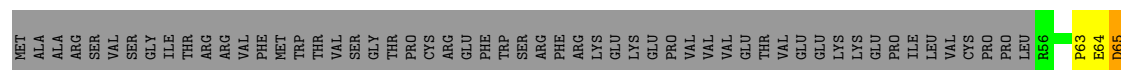
- Molecule 41: 39S ribosomal protein L49, mitochondrial

Chain g: 68% 10% 22%

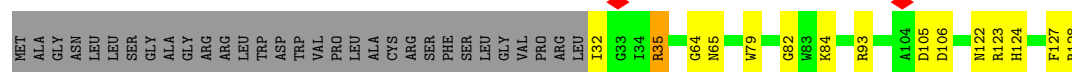


- Molecule 42: 39S ribosomal protein L50, mitochondrial

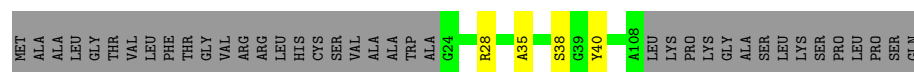
Chain h: 53% 9% 37%



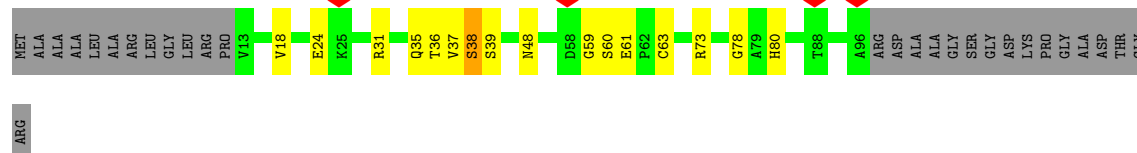
- Molecule 43: 39S ribosomal protein L51, mitochondrial



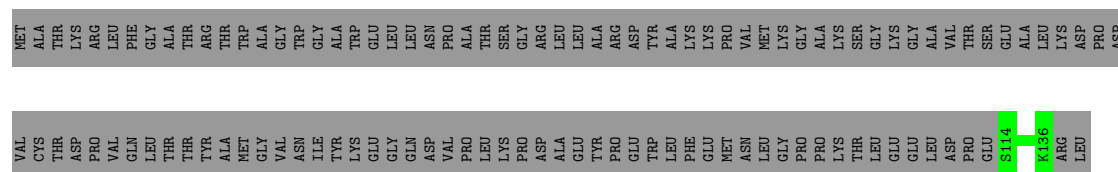
- Molecule 44: 39S ribosomal protein L52, mitochondrial



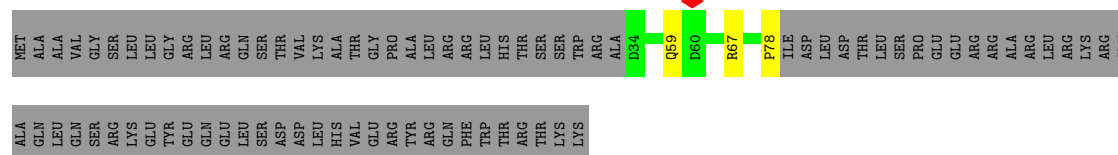
- Molecule 45: 39S ribosomal protein L53, mitochondrial



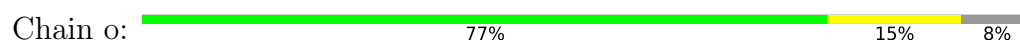
- Molecule 46: 39S ribosomal protein L54, mitochondrial



- Molecule 47: 39S ribosomal protein L55, mitochondrial

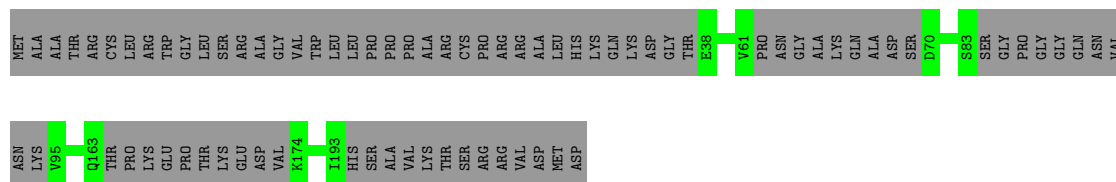


- Molecule 48: Ribosomal protein 63, mitochondrial



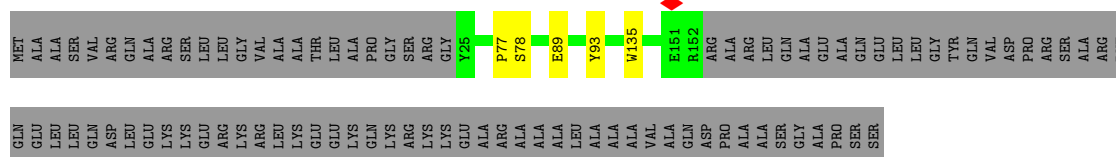
- Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p:  62% 38%



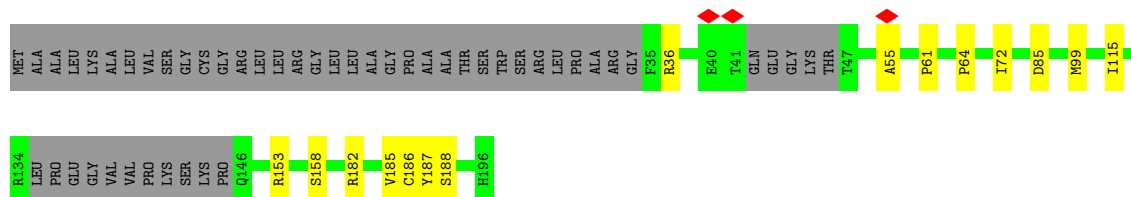
- Molecule 50: Growth arrest and DNA damage-inducible proteins-interacting protein 1

Chain q:  55% 42%



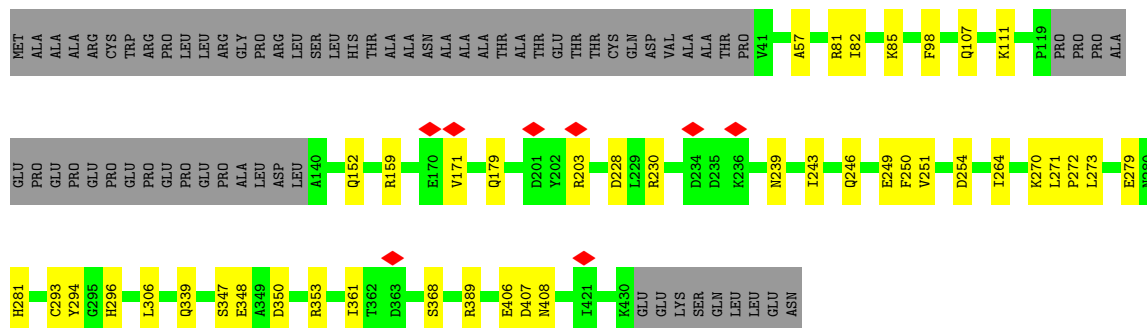
- Molecule 51: 39S ribosomal protein S18a, mitochondrial

Chain r:  67% 8% 26%



- Molecule 52: 39S ribosomal protein S30, mitochondrial

Chain s:  74% 10% 16%



- Molecule 53: Unknown protein/protein extension

Chain t:  100%

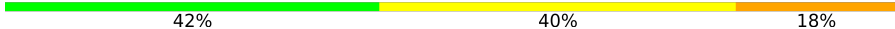
There are no outlier residues recorded for this chain.

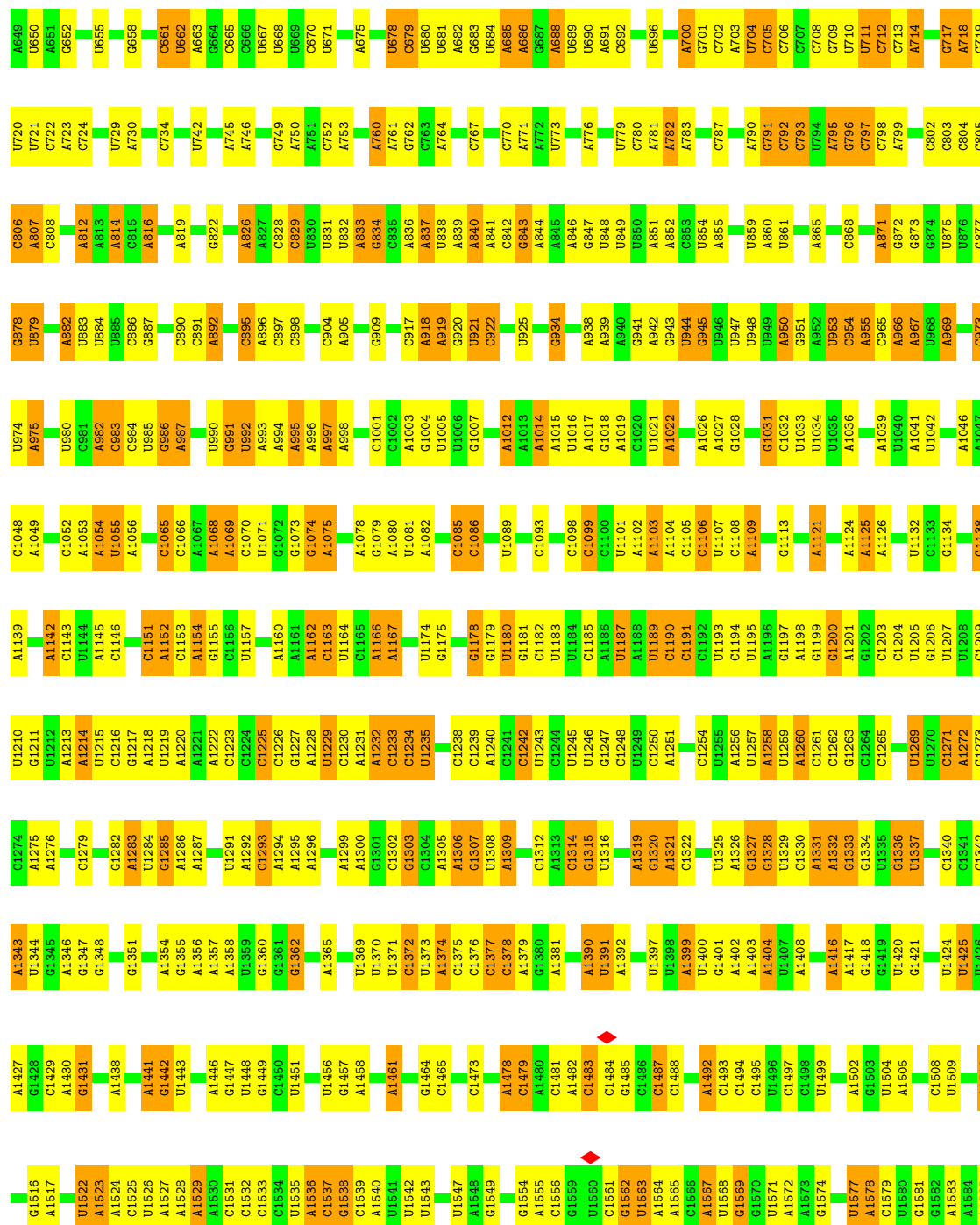
- Molecule 54: E-site tRNA

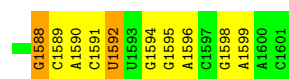
Chain u:  50% 50%

C1
A2

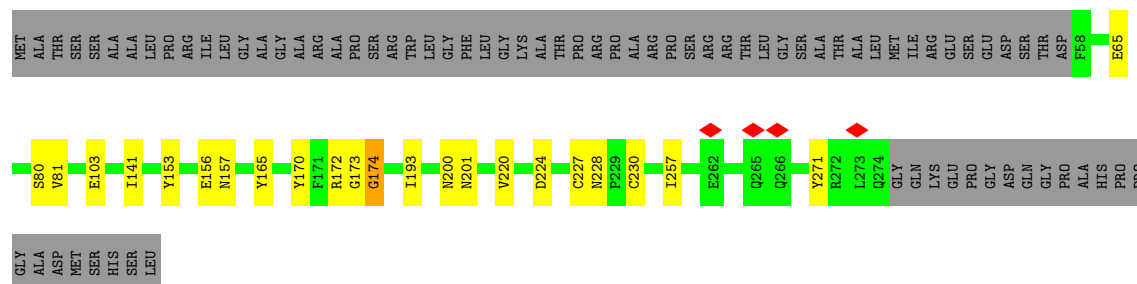
● Molecule 55: 12S rRNA

Chain AA:  42% 40% 18%

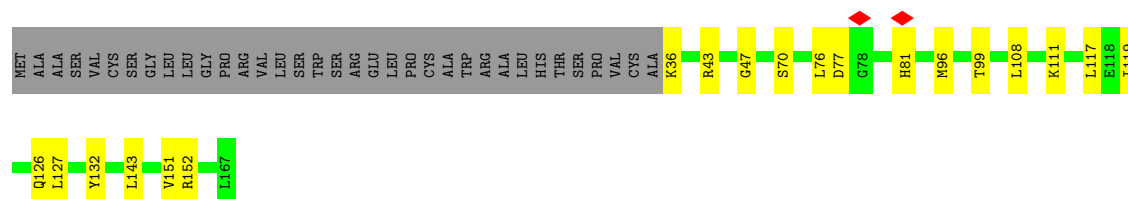




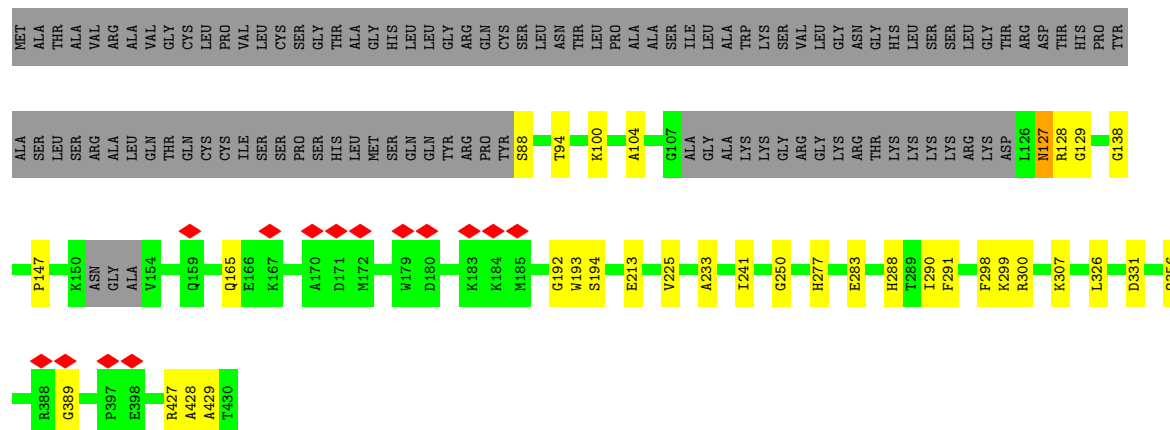
- Molecule 56: 28S ribosomal protein S2, mitochondrial



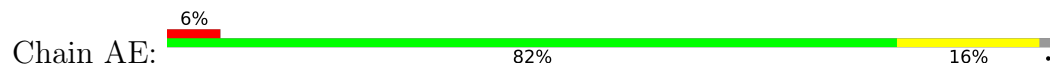
- Molecule 57: 28S ribosomal protein S24, mitochondrial



- Molecule 58: 28S ribosomal protein S5, mitochondrial

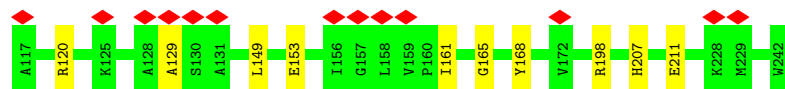
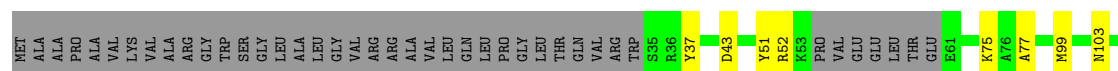
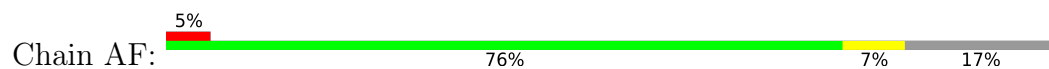


- Molecule 59: 28S ribosomal protein S6, mitochondrial

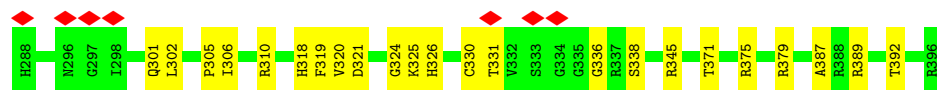
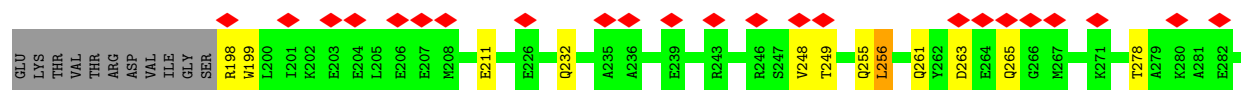
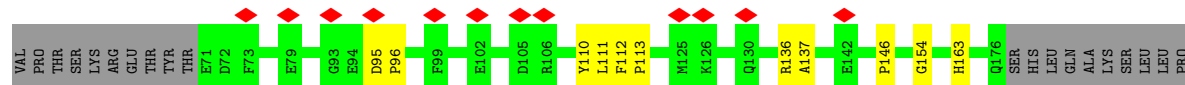




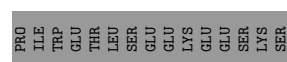
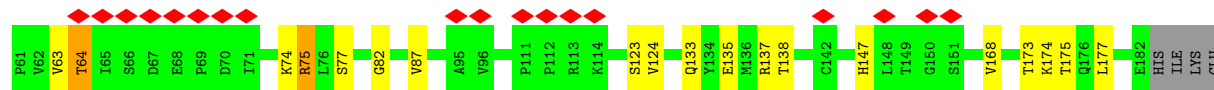
- Molecule 60: 28S ribosomal protein S7, mitochondrial



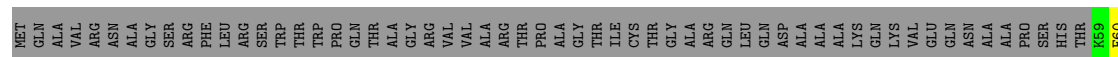
- Molecule 61: 28S ribosomal protein S9, mitochondrial

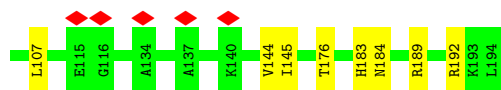


- Molecule 62: 28S ribosomal protein S10, mitochondrial

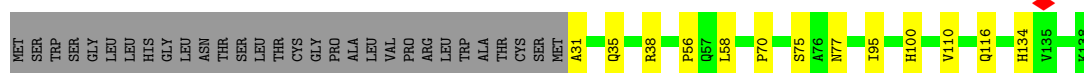


- Molecule 63: 28S ribosomal protein S11, mitochondrial





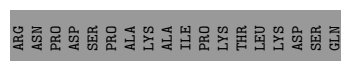
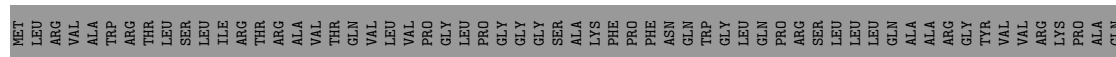
- Molecule 64: 28S ribosomal protein S12, mitochondrial



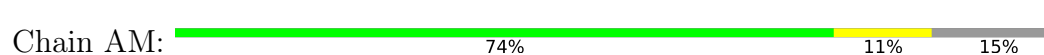
- Molecule 65: 28S ribosomal protein S14, mitochondrial



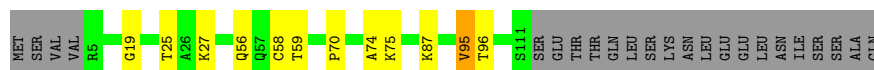
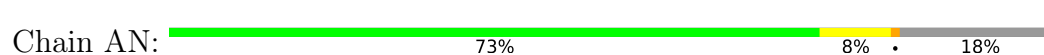
- Molecule 66: 28S ribosomal protein S15, mitochondrial



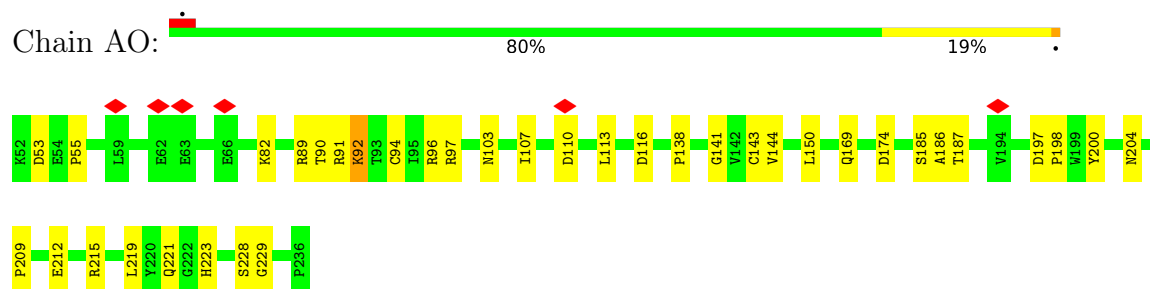
- Molecule 67: 28S ribosomal protein S16, mitochondrial



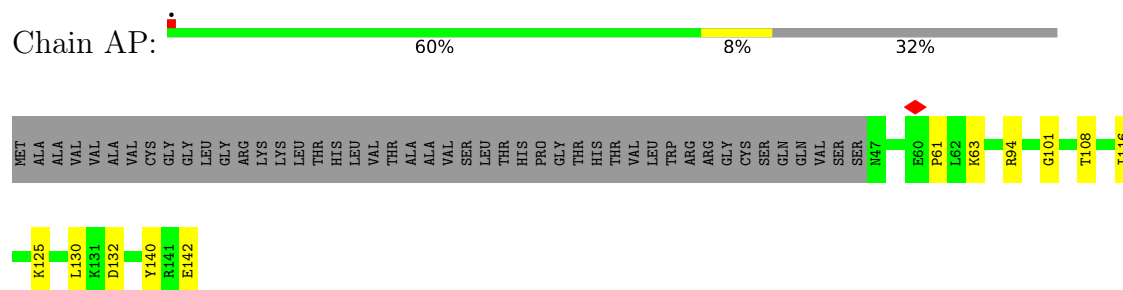
- Molecule 68: 28S ribosomal protein S17, mitochondrial



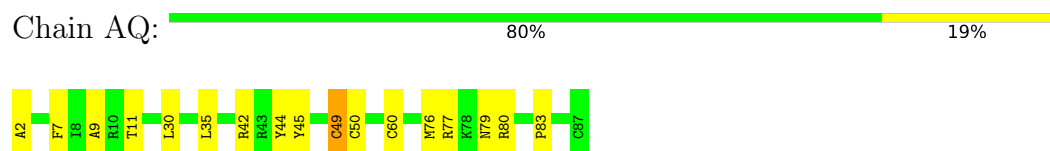
- Molecule 69: 28S ribosomal protein S18b, mitochondrial



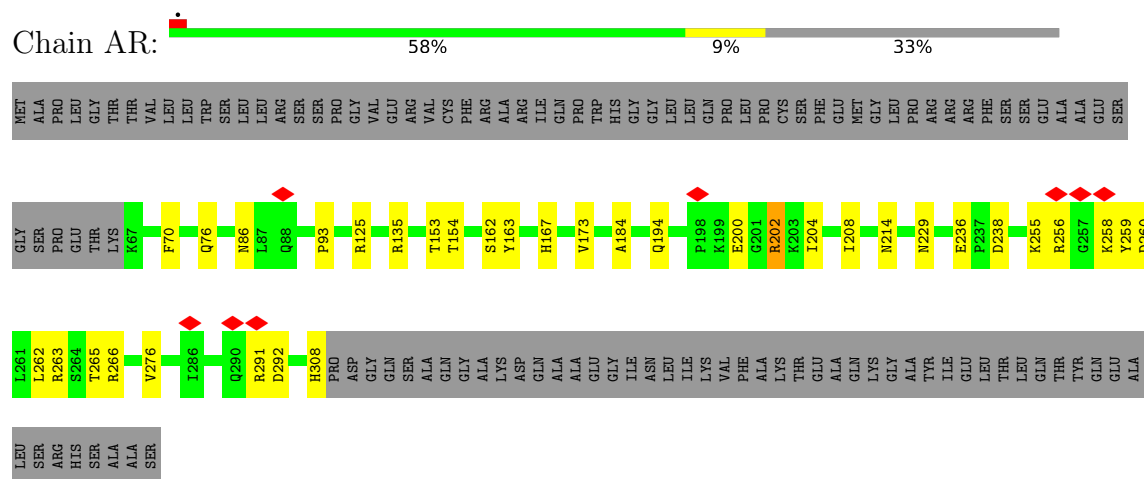
- Molecule 70: 28S ribosomal protein S18c, mitochondrial



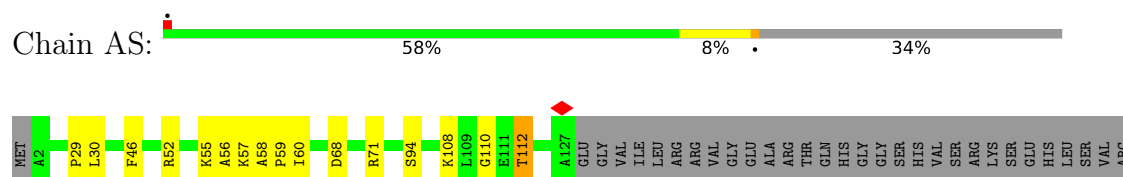
- Molecule 71: 28S ribosomal protein S21, mitochondrial



- Molecule 72: 28S ribosomal protein S22, mitochondrial



- Molecule 73: 28S ribosomal protein S23, mitochondrial



PRO GLN THR ALA LEU GLU ASN GLU THR GLN LYS GLU VAL PRO GLN ASP GLN HIS LEU GLU ALA PRO ASP GLN LYS SER GLY LEU LEU PRO PRO

- Molecule 74: 28S ribosomal protein S25, mitochondrial

Chain AT:



MET P2 Y15 N20 N33 F50 N51 I52 N59 T71 P74 N95 K96 E100 R103 K104 I105 G130 P131 R132 K133 L135 R137 E138 C139 I140 C141 E142 V143 E144 S151 E158 H159 R160 G161 K162 Y163 LYS ALA ALA LEU LYS ALA ASP ALA GLN ASP

- Molecule 75: 28S ribosomal protein S26, mitochondrial

Chain AU:



MET LEU ARG ALA LEU SER ARG LEU GLY ALA GLY THR PRO CYS ARG PRO ARG ALA PRO LEU VAL LEU PRO ALA ARG GLY R27 K28 T29 R30 R31 R32 P33 P34 S37 K38 T39 M43 M44 P45 L56 M57 E58 R59 L70 E73 E77 H117 I121 R134 R141 F167 A179 A180 S183 A190 I191 T192 R193 V198 R199 PRO GLN ARG ASP SER

- Molecule 76: 28S ribosomal protein S27, mitochondrial

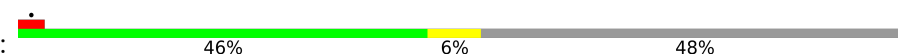
Chain AV:



MET ALA ALA SER ILE VAL ARG ARG GLY MET LEU LEU ALA ARG GLN VAL VAL LEU PRO GLN GLN SER PRO PRO ALA GLY LYS TYR LEU LEU SER SER ALA TYR D36 K64 S80 E84 W102 Y103 I152 D159 A160 V164 A172 F173 V174 V175 P176 S177 T178 Q179 L180 L181 D196 F196 S197 K214 Q215 K216 Y226 L230 E235 R241 A242 V243 I250 Y255 L256 D257 V262 M263 E264 K265 V266 S269 PRO GLU ASP ILE LYS LEU CYS ARG E278 T291 SER ALA ASP GLY ALA SER SER GLU GLN GLN SER GLN ASP

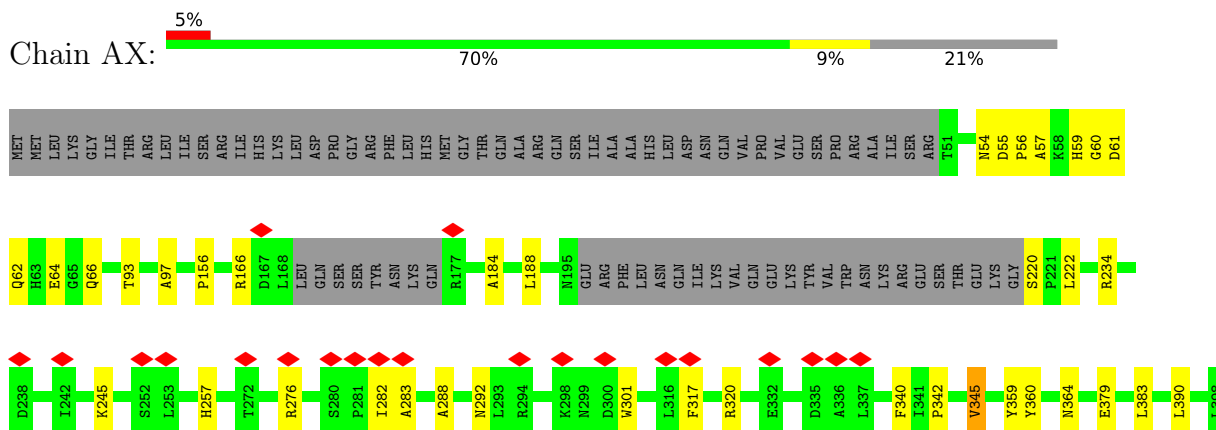
- Molecule 77: 28S ribosomal protein S28, mitochondrial

Chain AW:

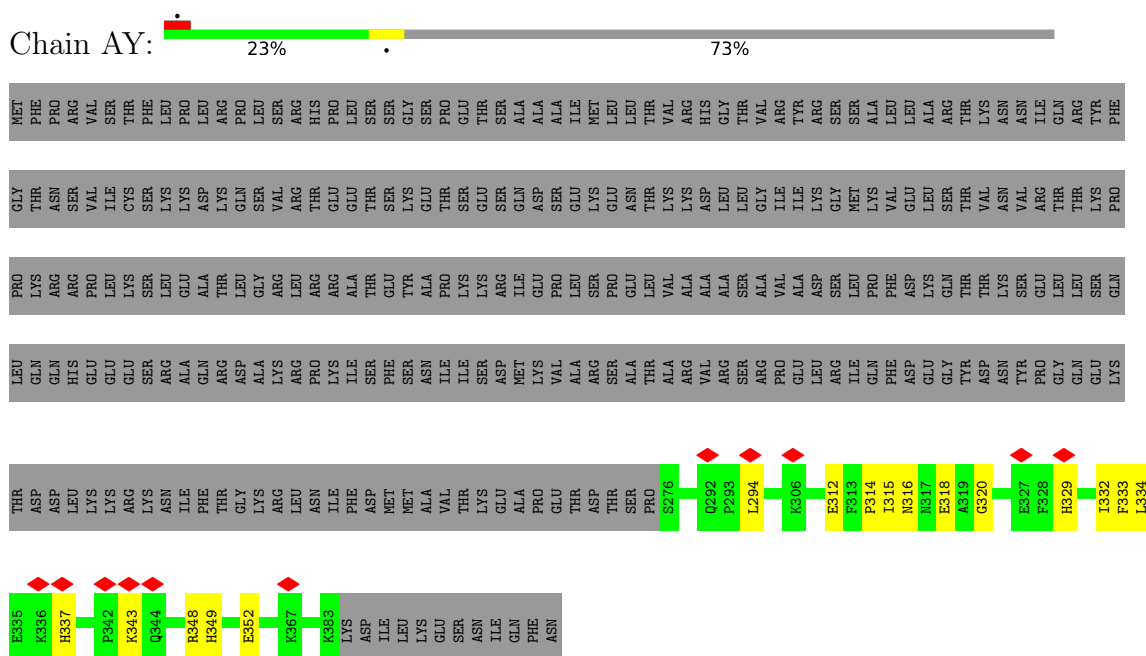


MET ALA ALA LEU LEU LYS VAL THR ARG VAL VAL VAL ALA ALA GLU SER HIS PHE LEU ARG VAL PHE LEU PHE PHE PRO PHE ARG GLY ARG GLY VAL GLY THR GLU SER GLY GLU L142 L143 L144 D146 F153 A156 M166 Q173 GLU SER LYS ASP SER ARG GLY PHE SER SER GLU HIS LEU ARG HIS LYS

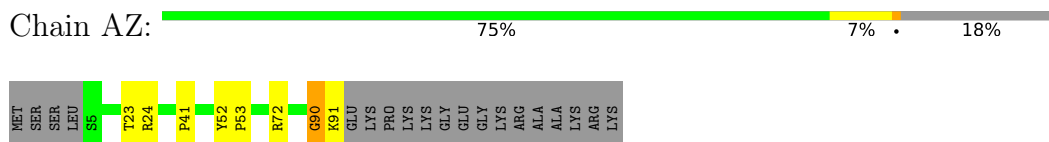
- Molecule 78: 28S ribosomal protein S29, mitochondrial



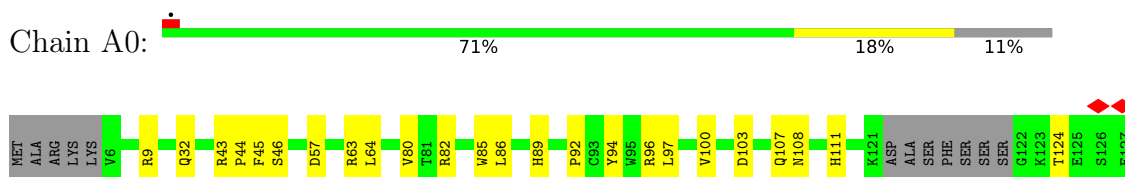
- Molecule 79: 28S ribosomal protein S31, mitochondrial

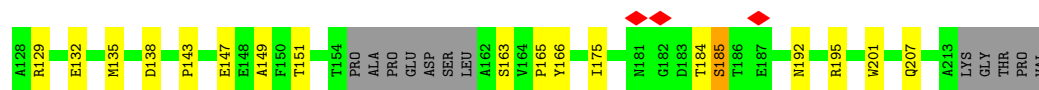


- Molecule 80: 28S ribosomal protein S33, mitochondrial

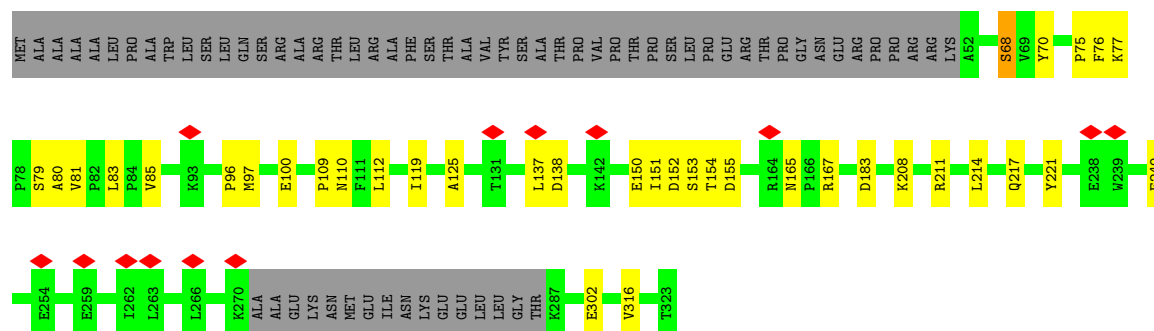


- Molecule 81: 28S ribosomal protein S34, mitochondrial

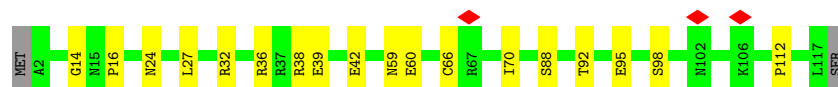
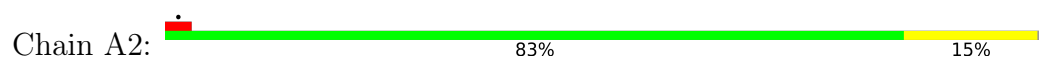




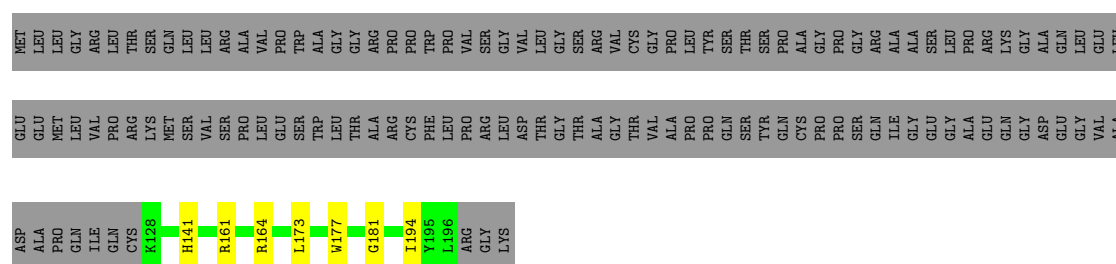
- Molecule 82: 28S ribosomal protein S35, mitochondrial



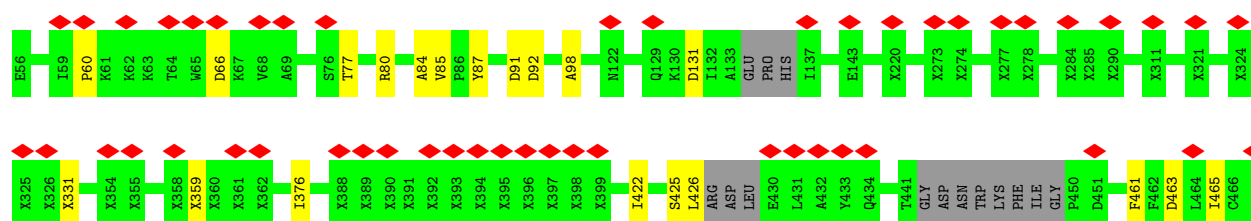
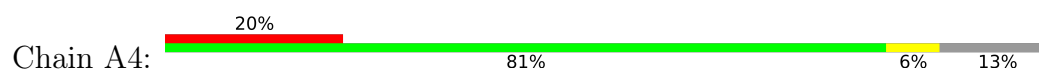
- Molecule 83: Coiled-coil-helix-coiled-coil-helix domain-containing protein 1

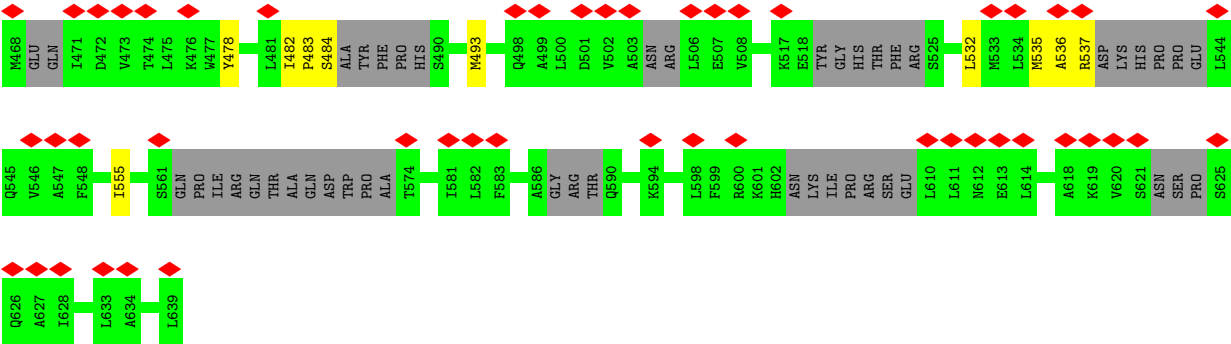


- Molecule 84: Aurora kinase A-interacting protein



- Molecule 85: Pentatricopeptide repeat domain-containing protein 3, mitochondrial, mS39





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26195	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.462	Depositor
Minimum map value	-0.346	Depositor
Average map value	0.022	Depositor
Map value standard deviation	0.095	Depositor
Recommended contour level	0.165	Depositor
Map size ($\text{\AA}$)	414.2, 414.2, 414.2	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.09, 1.09, 1.09	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.07	0/34967	0.19	0/54407
2	B	0.06	0/1328	0.17	0/2056
3	D	0.09	0/1879	0.24	0/2527
4	E	0.07	0/2433	0.21	0/3299
5	F	0.09	0/2071	0.23	0/2817
6	H	0.09	0/798	0.22	0/1073
7	I	0.08	0/1308	0.21	0/1761
8	J	0.09	0/1077	0.22	0/1452
9	K	0.08	0/1495	0.21	0/2029
10	L	0.08	0/904	0.23	0/1218
11	M	0.09	0/2359	0.24	0/3185
12	N	0.08	0/1697	0.21	0/2281
13	O	0.10	0/1269	0.25	0/1708
14	P	0.09	0/1103	0.24	0/1491
15	Q	0.08	0/1863	0.20	0/2509
16	R	0.09	0/1174	0.26	0/1572
17	S	0.07	0/1276	0.21	0/1729
18	T	0.08	0/1402	0.22	0/1886
19	U	0.09	0/946	0.24	0/1283
20	V	0.08	0/1590	0.22	0/2151
21	W	0.08	0/893	0.20	0/1204
22	X	0.08	0/2090	0.22	0/2825
23	Y	0.09	0/1552	0.22	0/2079
24	Z	0.07	0/1003	0.21	0/1354
25	0	0.11	0/895	0.23	0/1201
26	1	0.08	0/438	0.24	0/583
27	2	0.09	0/382	0.24	0/507
28	3	0.08	0/852	0.22	0/1136
29	4	0.09	0/329	0.21	0/435
30	5	0.08	0/3154	0.23	0/4295
31	6	0.08	0/2722	0.23	0/3709
32	7	0.08	0/2207	0.20	0/2978

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	8	0.08	0/855	0.20	0/1152
34	9	0.08	0/896	0.22	0/1205
35	a	0.07	0/709	0.22	0/963
36	b	0.09	0/1202	0.25	0/1626
37	c	0.08	0/2264	0.21	0/3059
38	d	0.09	0/1385	0.23	0/1877
39	e	0.07	0/1797	0.19	0/2422
40	f	0.06	0/1055	0.17	0/1427
41	g	0.09	0/1102	0.23	0/1503
42	h	0.10	0/847	0.31	0/1150
43	i	0.09	0/849	0.23	0/1135
44	j	0.08	0/698	0.25	0/940
45	k	0.08	0/665	0.22	0/897
46	l	0.10	0/226	0.29	0/299
47	m	0.11	0/379	0.24	0/510
48	o	0.10	0/818	0.24	0/1097
49	p	0.08	0/1071	0.20	0/1433
50	q	0.09	0/1107	0.24	0/1498
51	r	0.09	0/1238	0.24	0/1676
52	s	0.08	0/3114	0.23	0/4225
54	u	0.03	0/46	0.11	0/69
55	AA	0.08	0/21926	0.21	0/34121
56	AB	0.09	0/1811	0.23	0/2451
57	AC	0.08	0/1112	0.22	0/1505
58	AD	0.08	0/2607	0.21	0/3498
59	AE	0.10	0/989	0.28	0/1335
60	AF	0.08	0/1708	0.22	0/2291
61	AG	0.09	0/2570	0.23	0/3443
62	AH	0.08	0/1019	0.21	0/1379
63	AI	0.09	0/1031	0.24	0/1390
64	AJ	0.09	0/854	0.24	0/1148
65	AK	0.11	0/879	0.28	0/1182
66	AL	0.09	0/1406	0.23	0/1878
67	AM	0.09	0/941	0.26	0/1265
68	AN	0.08	0/864	0.21	0/1169
69	AO	0.11	0/1580	0.27	0/2150
70	AP	0.07	0/791	0.19	0/1062
71	AQ	0.10	0/747	0.26	0/995
72	AR	0.09	0/2050	0.23	0/2770
73	AS	0.09	0/1069	0.23	0/1441
74	AT	0.09	0/1361	0.23	0/1829
75	AU	0.11	0/1482	0.28	0/1987
76	AV	0.08	0/2758	0.20	0/3724

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	AW	0.09	0/778	0.21	0/1048
78	AX	0.07	0/2596	0.21	0/3519
79	AY	0.07	0/943	0.20	0/1274
80	AZ	0.09	0/757	0.24	0/1011
81	A0	0.10	0/1727	0.27	0/2338
82	A1	0.09	0/2121	0.23	0/2873
83	A2	0.11	0/939	0.27	0/1256
84	A3	0.10	0/621	0.25	0/820
85	A4	0.07	0/2137	0.20	0/2872
All	All	0.08	0/165953	0.22	0/235927

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	31261	15865	15878	363	0
2	B	1191	603	607	5	0
3	D	1842	1896	1896	15	0
4	E	2365	2378	2378	17	0
5	F	2013	2045	2044	27	0
6	H	784	832	832	6	0
7	I	1283	1369	1370	10	0
8	J	1061	1141	1141	3	0
9	K	1451	1448	1448	5	0
10	L	889	941	941	9	0
11	M	2305	2378	2378	26	0
12	N	1654	1681	1681	12	0
13	O	1245	1283	1283	10	0
14	P	1080	1081	1081	7	0
15	Q	1822	1859	1859	4	0
16	R	1153	1214	1214	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	S	1251	1322	1322	5	0
18	T	1368	1410	1410	10	0
19	U	922	935	935	8	0
20	V	1551	1558	1558	6	0
21	W	871	898	898	5	0
22	X	2035	2027	2054	8	0
23	Y	1517	1561	1561	14	0
24	Z	978	1030	1030	7	0
25	0	880	904	904	11	0
26	1	433	475	475	4	0
27	2	376	406	406	6	0
28	3	831	883	883	6	0
29	4	322	345	344	1	0
30	5	3064	3059	3059	15	0
31	6	2636	2450	2450	10	0
32	7	2158	2173	2173	6	0
33	8	836	844	844	2	0
34	9	873	878	878	13	0
35	a	686	658	658	5	0
36	b	1178	1180	1180	9	0
37	c	2217	2220	2220	11	0
38	d	1347	1343	1343	7	0
39	e	1762	1767	1767	8	0
40	f	1039	1044	1044	3	0
41	g	1067	1056	1056	11	0
42	h	827	806	806	10	0
43	i	827	857	857	8	0
44	j	684	673	673	2	0
45	k	655	656	656	7	0
46	l	221	227	227	0	0
47	m	372	387	387	2	0
48	o	797	804	804	9	0
49	p	1058	1083	1083	0	0
50	q	1076	1049	1049	3	0
51	r	1203	1221	1221	7	0
52	s	3036	3022	3022	25	0
53	t	140	30	30	0	0
54	u	42	23	23	1	0
55	AA	19606	9952	9960	272	0
56	AB	1768	1766	1765	13	0
57	AC	1082	1088	1088	15	0
58	AD	2557	2596	2596	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	AE	972	1001	1001	10	0
60	AF	1668	1716	1716	13	0
61	AG	2516	2503	2503	28	0
62	AH	999	1024	1024	15	0
63	AI	1011	1052	1052	6	0
64	AJ	838	887	887	9	0
65	AK	861	885	885	22	0
66	AL	1382	1472	1472	17	0
67	AM	920	951	951	11	0
68	AN	846	908	908	4	0
69	AO	1528	1488	1488	18	0
70	AP	774	804	804	5	0
71	AQ	735	741	746	12	0
72	AR	2008	2031	2031	13	0
73	AS	1042	1037	1037	5	0
74	AT	1330	1344	1344	12	0
75	AU	1461	1471	1471	23	0
76	AV	2702	2690	2690	17	0
77	AW	766	785	785	2	0
78	AX	2531	2520	2520	23	0
79	AY	914	859	859	6	0
80	AZ	740	747	747	8	0
81	A0	1684	1685	1685	21	0
82	A1	2076	2097	2097	24	0
83	A2	925	962	962	9	0
84	A3	610	682	682	7	0
85	A4	2838	2259	2274	18	0
86	A	97	0	0	0	0
86	AA	28	0	0	0	0
86	M	1	0	0	0	0
86	g	1	0	0	0	0
87	0	1	0	0	0	0
87	4	1	0	0	0	0
87	AB	1	0	0	0	0
87	AO	1	0	0	0	0
87	AP	1	0	0	0	0
87	AT	1	0	0	0	0
87	r	1	0	0	0	0
All	All	158359	133281	133351	1175	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 4.

All (1175) 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)
55:AA:1162:A:O2'	55:AA:1163:C:OP1	1.84	0.95
55:AA:1465:C:OP1	83:A2:38:ARG:NH2	2.02	0.93
55:AA:953:U:O2'	55:AA:954:C:OP2	1.88	0.92
55:AA:1372:C:O2'	55:AA:1373:U:O4'	1.87	0.91
55:AA:1027:A:O3'	55:AA:1054:A:O2'	1.90	0.89
55:AA:991:G:O2'	55:AA:992:U:O4'	1.92	0.87
55:AA:1017:A:OP2	55:AA:1018:G:O2'	1.92	0.87
55:AA:967:A:O2'	55:AA:1028:G:N2	2.07	0.87
1:A:3078:C:N4	1:A:3079:G:O6	2.07	0.87
67:AM:38:HIS:HD1	67:AM:41:CYS:HG	1.24	0.86
1:A:1907:A:N3	1:A:2930:U:O2'	2.08	0.85
1:A:2129:G:O2'	1:A:2153:A:O2'	1.93	0.84
55:AA:708:C:O2	55:AA:841:A:O2'	1.95	0.84
72:AR:255:LYS:O	72:AR:258:LYS:NZ	2.09	0.84
1:A:1769:C:O2	1:A:2289:G:N2	2.11	0.84
1:A:1851:G:O4'	1:A:2134:A:N6	2.09	0.84
1:A:2129:G:HO2'	1:A:2153:A:HO2'	1.21	0.84
55:AA:1190:C:O2'	55:AA:1191:C:O5'	1.96	0.84
55:AA:1021:U:O2'	55:AA:1022:A:OP2	1.96	0.84
55:AA:1085:C:OP1	63:AI:192:ARG:NH1	2.10	0.84
30:5:262:ILE:O	30:5:264:ASP:N	2.12	0.83
55:AA:1565:A:OP2	55:AA:1569:G:O2'	1.96	0.83
1:A:2173:G:O6	1:A:2187:C:N4	2.12	0.83
55:AA:997:A:O2'	55:AA:1085:C:O2	1.96	0.83
55:AA:1331:A:O2'	55:AA:1332:A:OP2	1.95	0.83
1:A:2655:G:O2'	1:A:2660:U:O4	1.96	0.83
1:A:1871:A:O2'	1:A:1872:U:OP1	1.97	0.82
55:AA:941:G:O2'	55:AA:1109:A:OP2	1.95	0.82
55:AA:795:A:O2'	55:AA:796:G:OP1	1.98	0.81
55:AA:1068:A:O2'	55:AA:1588:G:O4'	1.99	0.81
1:A:2994:U:O2	1:A:3040:G:N2	2.14	0.81
1:A:2822:C:O2'	1:A:2915:C:OP2	1.99	0.81
1:A:1703:C:O2'	1:A:1704:U:OP2	1.99	0.81
1:A:2737:U:O2'	1:A:3084:A:N3	2.14	0.80
55:AA:703:A:N3	55:AA:842:C:O2'	2.15	0.80
1:A:2482:A:O2'	1:A:2483:U:O4'	2.00	0.80
55:AA:1271:C:N4	55:AA:1321:A:OP2	2.13	0.80
1:A:2912:C:O2	1:A:2917:G:O2'	1.99	0.80
1:A:2971:A:O2'	12:N:182:LYS:O	2.00	0.80
55:AA:1018:G:N2	55:AA:1018:G:OP1	2.14	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AA:1104:A:OP1	55:AA:1591:C:O2'	2.01	0.79
2:B:1607:U:O2'	2:B:1608:G:OP1	2.00	0.79
1:A:2060:A:O2'	1:A:2061:C:O2	1.99	0.79
1:A:1730:U:O2'	1:A:1731:A:N7	2.16	0.79
55:AA:701:G:N2	55:AA:841:A:O2'	2.15	0.79
1:A:3082:G:N2	1:A:3085:A:OP2	2.15	0.79
1:A:2075:U:O2'	1:A:2833:A:N7	2.16	0.79
55:AA:1197:G:O6	55:AA:1425:U:O2	2.01	0.79
55:AA:1201:A:O2'	55:AA:1417:A:N3	2.16	0.78
1:A:1724:A:N6	1:A:2040:G:N2	2.31	0.78
55:AA:1370:U:O2'	55:AA:1390:A:OP2	2.01	0.78
1:A:3017:C:O2'	1:A:3019:G:OP2	2.01	0.78
1:A:1847:U:O2'	1:A:1848:U:O4'	2.01	0.78
1:A:2989:G:O2'	1:A:2990:A:OP2	2.01	0.77
55:AA:705:C:O2'	81:A0:43:ARG:NH2	2.17	0.77
1:A:1922:C:O2	3:D:85:ARG:NH2	2.18	0.77
68:AN:58:CYS:SG	68:AN:87:LYS:NZ	2.58	0.77
1:A:2943:G:OP1	48:o:11:ARG:NH2	2.17	0.77
1:A:2507:A:O2'	1:A:2508:C:OP1	2.01	0.77
1:A:2084:A:O2'	1:A:2085:A:N7	2.17	0.77
1:A:2625:C:O2'	1:A:2627:G:OP1	2.02	0.77
1:A:1917:A:OP1	1:A:1918:G:N2	2.17	0.77
1:A:1994:A:N1	1:A:2735:G:O2'	2.16	0.77
55:AA:1399:A:O2'	55:AA:1400:U:O4'	2.00	0.76
55:AA:1271:C:O2'	55:AA:1272:A:O5'	2.01	0.76
1:A:2059:C:OP2	1:A:2078:C:N4	2.18	0.76
55:AA:1362:G:N2	55:AA:1448:U:O2	2.19	0.76
1:A:3011:A:O2'	1:A:3173:G:N2	2.19	0.76
1:A:2138:U:O2'	1:A:2151:A:N3	2.19	0.76
1:A:1724:A:H61	1:A:2040:G:N2	1.83	0.76
1:A:2995:G:O2'	1:A:3042:U:OP1	2.03	0.76
18:T:89:TYR:OH	25:0:94:ARG:O	2.04	0.76
55:AA:665:C:O4'	55:AA:1166:A:N6	2.19	0.76
1:A:2814:G:O2'	1:A:2983:G:OP1	2.03	0.76
55:AA:1099:C:O2'	55:AA:1155:G:N2	2.19	0.76
60:AF:52:ARG:NH1	61:AG:321:ASP:OD2	2.19	0.75
72:AR:194:GLN:NE2	72:AR:202:ARG:O	2.18	0.75
78:AX:61:ASP:OD1	78:AX:66:GLN:NE2	2.19	0.75
1:A:2570:C:O5'	1:A:2592:G:O2'	2.04	0.75
32:7:176:SER:O	32:7:319:ARG:NH1	2.20	0.75
55:AA:670:C:OP1	69:AO:89:ARG:NH1	2.19	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
63:AI:192:ARG:NE	71:AQ:44:TYR:OH	2.19	0.75
1:A:2027:A:O2'	1:A:2048:U:OP1	2.04	0.75
61:AG:302:LEU:O	78:AX:320:ARG:NH2	2.20	0.75
55:AA:1209:C:O2'	55:AA:1210:U:O4'	2.02	0.75
55:AA:1487:C:O2	55:AA:1488:C:N4	2.20	0.74
55:AA:1362:G:O2'	55:AA:1449:G:OP1	2.05	0.74
1:A:2501:C:OP1	27:2:47:LYS:N	2.20	0.74
55:AA:717:G:N2	55:AA:719:G:O6	2.20	0.74
11:M:263:ARG:NH1	11:M:296:SER:O	2.20	0.74
37:c:34:GLY:O	43:i:35:ARG:NH2	2.20	0.74
55:AA:975:A:OP1	59:AE:90:ARG:NH1	2.20	0.74
74:AT:139:CYS:SG	74:AT:140:ILE:N	2.60	0.74
1:A:2598:A:N6	1:A:2625:C:O5'	2.20	0.74
66:AL:137:ARG:NH2	66:AL:141:GLU:OE1	2.21	0.74
1:A:1823:A:O2'	1:A:1824:U:OP2	2.04	0.74
1:A:2145:G:N1	1:A:2256:U:O4	2.21	0.74
55:AA:1279:C:OP1	58:AD:277:HIS:NE2	2.21	0.73
55:AA:1529:A:O2'	76:AV:64:LYS:O	2.06	0.73
1:A:2515:U:OP1	3:D:284:ARG:NH1	2.21	0.73
13:O:30:ARG:NH1	13:O:78:PHE:O	2.21	0.73
1:A:2232:A:O2'	1:A:3002:G:N3	2.21	0.73
55:AA:683:G:OP1	74:AT:162:LYS:NZ	2.21	0.73
59:AE:5:GLU:N	59:AE:94:VAL:O	2.21	0.73
1:A:2144:A:OP1	16:R:57:ARG:NH1	2.21	0.73
1:A:1867:A:O2'	1:A:1903:C:O2	2.04	0.73
1:A:1884:G:O2'	1:A:1895:C:O2	2.06	0.73
1:A:2145:G:N3	17:S:104:ARG:NH2	2.36	0.73
1:A:2420:U:O2'	34:9:23:SER:OG	2.06	0.73
1:A:2661:U:OP1	4:E:238:ARG:NH2	2.20	0.73
1:A:3068:G:OP2	1:A:3068:G:N2	2.14	0.73
1:A:3218:A:OP2	4:E:212:GLY:N	2.22	0.73
55:AA:986:G:O2'	55:AA:987:A:O5'	2.06	0.73
25:0:119:LYS:O	25:0:120:HIS:ND1	2.21	0.73
55:AA:782:A:N6	55:AA:950:A:OP1	2.21	0.73
1:A:1719:G:N2	1:A:2009:G:O2'	2.22	0.73
55:AA:1483:C:OP1	55:AA:1484:C:O2'	2.07	0.73
1:A:1787:G:N2	1:A:1790:A:OP2	2.21	0.73
1:A:2875:A:O2'	14:P:179:GLU:OE2	2.07	0.72
55:AA:688:A:N6	55:AA:822:G:O6	2.21	0.72
1:A:1769:C:N4	5:F:104:LYS:O	2.22	0.72
1:A:2511:C:N4	1:A:2539:A:O2'	2.21	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AA:1233:C:O2	65:AK:86:ARG:NH1	2.22	0.72
1:A:2457:A:O2'	1:A:2458:A:OP2	2.06	0.72
52:s:159:ARG:NH2	52:s:171:VAL:O	2.23	0.72
1:A:2165:C:O2'	1:A:2166:C:OP1	2.07	0.72
1:A:1930:C:O2'	1:A:1944:C:N4	2.22	0.71
1:A:2003:A:OP2	1:A:2734:A:O2'	2.07	0.71
11:M:142:GLU:OE2	11:M:160:SER:OG	2.08	0.71
1:A:3219:G:O2'	1:A:3221:A:OP2	2.07	0.71
52:s:293:CYS:O	52:s:339:GLN:NE2	2.23	0.71
55:AA:872:G:N2	55:AA:920:G:O2'	2.24	0.71
55:AA:969:A:O2'	66:AL:148:LYS:O	2.07	0.71
55:AA:996:A:H61	55:AA:1075:A:C4'	2.02	0.71
62:AH:137:ARG:NH2	65:AK:128:TRP:O	2.23	0.71
55:AA:1464:G:O2'	55:AA:1465:C:O4'	2.06	0.71
1:A:2926:A:O2'	1:A:3087:C:OP1	2.08	0.71
1:A:1800:G:N7	20:V:20:ARG:NH1	2.38	0.71
1:A:2182:G:O2'	1:A:2183:C:OP1	2.09	0.71
55:AA:878:G:O2'	55:AA:879:U:OP1	2.09	0.71
67:AM:41:CYS:SG	67:AM:46:ARG:NH2	2.64	0.71
1:A:2694:A:O2'	1:A:2941:G:N2	2.24	0.70
55:AA:1180:U:N3	55:AA:1181:G:O6	2.24	0.70
5:F:95:ILE:HD13	5:F:172:LEU:HD22	1.74	0.70
55:AA:917:C:O2'	55:AA:921:U:OP1	2.08	0.70
1:A:2853:A:OP2	26:1:45:HIS:ND1	2.24	0.70
55:AA:812:A:O2'	55:AA:814:A:N7	2.23	0.70
1:A:1880:C:OP2	41:g:111:ARG:NH1	2.24	0.70
7:I:148:VAL:O	45:k:31:ARG:NH2	2.23	0.70
7:I:182:ASP:OD1	7:I:184:THR:OG1	2.10	0.70
19:U:30:ARG:NH1	23:Y:118:GLU:OE2	2.24	0.70
55:AA:661:C:O2'	55:AA:662:U:OP1	2.08	0.70
55:AA:951:G:O2'	55:AA:1132:U:OP1	2.08	0.70
55:AA:1322:C:OP1	57:AC:36:LYS:NZ	2.25	0.70
1:A:1674:A:O2'	1:A:1814:A:N6	2.25	0.70
1:A:2265:A:OP1	11:M:47:ARG:NH2	2.25	0.70
72:AR:125:ARG:O	72:AR:266:ARG:NH2	2.24	0.70
1:A:1834:U:O4	18:T:207:THR:N	2.25	0.70
1:A:1881:A:OP2	41:g:111:ARG:NH2	2.25	0.70
1:A:1827:C:O2'	1:A:1844:A:OP1	2.02	0.69
71:AQ:76:MET:SD	71:AQ:79:ASN:ND2	2.65	0.69
83:A2:59:ASN:ND2	83:A2:66:CYS:SG	2.65	0.69
1:A:1834:U:OP2	36:b:116:ARG:NH2	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1884:G:N7	5:F:281:ARG:NH1	2.39	0.69
30:5:113:LEU:O	30:5:308:GLN:NE2	2.25	0.69
55:AA:833:A:O2'	55:AA:834:G:OP1	2.10	0.69
81:A0:132:GLU:OE1	81:A0:207:GLN:NE2	2.26	0.69
82:A1:211:ARG:NH1	82:A1:221:TYR:OH	2.25	0.69
1:A:2795:U:O2	6:H:87:LYS:NZ	2.25	0.69
26:1:42:THR:O	50:q:135:TRP:NE1	2.26	0.69
1:A:2294:A:OP2	11:M:41:ARG:NH1	2.26	0.69
28:3:96:TYR:N	43:i:122:ASN:OD1	2.26	0.69
30:5:122:TRP:O	30:5:215:ARG:NH1	2.25	0.69
32:7:243:LYS:NZ	32:7:265:GLU:OE1	2.26	0.69
55:AA:1442:G:N1	55:AA:1446:A:O2'	2.25	0.69
83:A2:88:SER:O	83:A2:92:THR:OG1	2.09	0.69
55:AA:658:G:N3	55:AA:1286:A:O2'	2.22	0.69
55:AA:709:G:O2'	55:AA:840:A:O2'	2.11	0.69
85:A4:98:ALA:O	85:A4:478:TYR:OH	2.10	0.69
55:AA:1183:U:O3'	83:A2:36:ARG:NH1	2.26	0.68
55:AA:1225:C:OP2	55:AA:1360:G:N2	2.26	0.68
55:AA:1502:A:OP1	84:A3:164:ARG:NH2	2.26	0.68
59:AE:90:ARG:NH2	70:AP:116:ILE:O	2.26	0.68
39:e:173:LEU:O	39:e:175:GLN:N	2.26	0.68
1:A:2080:U:O2'	48:o:59:GLU:O	2.12	0.68
1:A:2917:G:O6	11:M:77:ARG:NH2	2.27	0.68
55:AA:844:A:N6	81:A0:201:TRP:O	2.25	0.68
1:A:2369:A:O2'	1:A:2370:A:O4'	2.09	0.68
55:AA:997:A:O2'	55:AA:1073:G:N2	2.26	0.68
1:A:2093:U:O2	1:A:2266:U:O2'	2.11	0.68
55:AA:760:A:N6	55:AA:783:A:O4'	2.27	0.68
56:AB:65:GLU:OE1	56:AB:271:TYR:OH	2.08	0.68
61:AG:136:ARG:NH2	61:AG:211:GLU:OE2	2.27	0.68
1:A:1697:A:OP1	23:Y:164:ARG:NH2	2.27	0.68
1:A:1892:A:OP1	28:3:169:ARG:NH1	2.27	0.68
55:AA:982:A:O2'	55:AA:983:C:OP1	2.08	0.68
55:AA:1213:A:O2'	55:AA:1239:C:O2	2.12	0.67
72:AR:70:PHE:O	72:AR:76:GLN:NE2	2.26	0.67
82:A1:68:SER:OG	85:A4:80:ARG:O	2.10	0.67
1:A:1848:U:O2'	11:M:54:LYS:NZ	2.27	0.67
55:AA:1106:C:N4	83:A2:16:PRO:O	2.26	0.67
1:A:2277:U:O2	5:F:104:LYS:NZ	2.19	0.67
65:AK:58:ARG:NE	65:AK:72:ASP:OD1	2.27	0.67
1:A:2369:A:O2'	1:A:2370:A:O5'	2.11	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AA:985:U:O2'	63:AI:107:LEU:O	2.13	0.67
55:AA:1055:U:O2'	55:AA:1589:C:O2	2.12	0.67
55:AA:1285:G:O2'	55:AA:1286:A:O4'	2.10	0.67
43:i:79:TRP:O	43:i:93:ARG:NE	2.28	0.67
74:AT:15:TYR:OH	74:AT:50:PHE:O	2.13	0.67
55:AA:1151:C:O2	66:AL:201:ARG:NH2	2.28	0.67
1:A:1681:G:P	23:Y:226:LEU:HD11	2.35	0.67
34:9:129:GLN:OE1	34:9:134:ASN:ND2	2.28	0.67
1:A:2042:U:OP2	11:M:57:ARG:NH1	2.28	0.67
1:A:3064:A:O4'	1:A:3099:C:N4	2.28	0.66
55:AA:1295:A:OP1	56:AB:200:ASN:ND2	2.28	0.66
59:AE:3:ARG:NH2	59:AE:100:GLN:OE1	2.28	0.66
69:AO:221:GLN:NE2	76:AV:314:VAL:O	2.27	0.66
81:A0:85:TRP:O	81:A0:89:HIS:N	2.27	0.66
1:A:2288:A:O2'	5:F:101:MET:SD	2.48	0.66
31:6:122:ALA:O	31:6:127:THR:N	2.28	0.66
1:A:1688:A:OP2	22:X:5:LYS:NZ	2.28	0.66
1:A:2020:U:O4	11:M:58:GLN:NE2	2.28	0.66
1:A:2081:U:OP1	48:o:64:ALA:N	2.28	0.66
1:A:1706:C:OP1	23:Y:193:ARG:NH2	2.29	0.66
7:I:181:ILE:O	7:I:184:THR:OG1	2.12	0.66
55:AA:1362:G:OP1	61:AG:389:ARG:NH1	2.29	0.66
1:A:2103:A:N3	24:Z:35:LYS:N	2.44	0.66
1:A:2130:A:O2'	48:o:25:ARG:NH1	2.29	0.66
1:A:2054:U:O2'	1:A:2055:U:O4'	2.13	0.66
34:9:26:GLY:O	34:9:31:ARG:NH1	2.29	0.66
82:A1:70:TYR:OH	82:A1:80:ALA:O	2.14	0.66
1:A:2599:U:OP2	1:A:2625:C:N4	2.29	0.66
61:AG:255:GLN:OE1	61:AG:256:LEU:N	2.28	0.66
63:AI:189:ARG:O	71:AQ:45:TYR:N	2.29	0.65
1:A:2074:A:N1	1:A:2832:A:O2'	2.29	0.65
1:A:2832:A:HO2'	40:f:48:TYR:HH	1.38	0.65
34:9:22:THR:OG1	34:9:36:ARG:NH1	2.29	0.65
3:D:204:ALA:O	3:D:208:ARG:NH1	2.29	0.65
57:AC:126:GLN:N	57:AC:132:TYR:OH	2.29	0.65
78:AX:97:ALA:O	78:AX:359:TYR:OH	2.11	0.65
18:T:83:SER:OG	18:T:85:ASP:OD1	2.07	0.65
55:AA:704:U:N3	81:A0:57:ASP:OD2	2.29	0.65
30:5:173:ARG:NH1	30:5:348:ASP:OD1	2.30	0.65
82:A1:76:PHE:N	82:A1:110:ASN:OD1	2.28	0.65
85:A4:85:VAL:N	85:A4:91:ASP:OD1	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:AC:152:ARG:NH2	85:A4:87:TYR:OH	2.30	0.65
55:AA:661:C:HO2'	55:AA:662:U:P	2.18	0.65
55:AA:1374:A:O2'	78:AX:317:PHE:N	2.29	0.64
55:AA:1085:C:N3	55:AA:1086:C:N4	2.45	0.64
32:7:281:SER:OG	32:7:282:ALA:N	2.28	0.64
82:A1:79:SER:OG	85:A4:92:ASP:OD1	2.13	0.64
52:s:246:GLN:OE1	52:s:353:ARG:NH1	2.31	0.64
13:O:128:ASN:OD1	13:O:130:LEU:N	2.30	0.64
55:AA:1305:A:OP2	55:AA:1306:A:N6	2.30	0.64
52:s:271:LEU:O	52:s:273:LEU:N	2.30	0.64
55:AA:780:C:O2	66:AL:197:ARG:NH2	2.29	0.64
69:AO:169:GLN:NE2	72:AR:229:ASN:O	2.31	0.64
1:A:1846:C:N3	1:A:1857:U:O4	2.30	0.64
57:AC:96:MET:O	57:AC:99:THR:OG1	2.16	0.64
78:AX:288:ALA:O	78:AX:292:ASN:ND2	2.31	0.64
81:A0:107:GLN:O	81:A0:108:ASN:ND2	2.31	0.64
83:A2:95:GLU:OE1	83:A2:98:SER:OG	2.15	0.64
55:AA:718:A:N6	55:AA:799:A:O2'	2.31	0.63
39:e:50:ALA:N	39:e:232:PHE:O	2.31	0.63
56:AB:153:TYR:O	56:AB:157:ASN:ND2	2.31	0.63
1:A:1724:A:N6	1:A:2040:G:H21	1.96	0.63
55:AA:1562:G:O2'	55:AA:1563:U:O5'	2.12	0.63
1:A:2874:A:O3'	14:P:65:ARG:NH2	2.31	0.63
1:A:3181:U:OP2	1:A:3182:A:O2'	2.12	0.63
30:5:34:GLY:O	30:5:38:THR:OG1	2.17	0.63
55:AA:934:G:O6	64:AJ:31:ALA:N	2.32	0.63
1:A:2279:U:OP1	5:F:255:LYS:NZ	2.30	0.63
1:A:2858:A:O2'	1:A:2874:A:N6	2.30	0.63
55:AA:1333:G:OP1	65:AK:33:ARG:NH1	2.32	0.63
60:AF:161:ILE:O	60:AF:168:TYR:N	2.31	0.63
1:A:3058:U:O2'	4:E:247:ASP:OD1	2.16	0.62
1:A:2860:G:O2'	21:W:65:ASN:OD1	2.07	0.62
55:AA:1103:A:O2'	55:AA:1104:A:OP1	2.13	0.62
1:A:1792:G:O2'	5:F:125:ARG:NH2	2.32	0.62
1:A:2456:U:OP1	13:O:16:ARG:NH1	2.32	0.62
1:A:3063:G:N2	1:A:3063:G:OP1	2.32	0.62
23:Y:164:ARG:NH1	23:Y:181:PHE:O	2.31	0.62
1:A:1777:A:N6	1:A:1780:U:OP2	2.31	0.62
1:A:1675:A:N1	1:A:1813:C:N4	2.48	0.62
1:A:1680:A:O2'	20:V:40:ARG:NH1	2.32	0.62
3:D:132:ASP:OD2	3:D:135:ARG:NH1	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AA:1340:C:O2'	55:AA:1343:A:O4'	2.18	0.62
42:h:138:SER:OG	42:h:139:LYS:N	2.33	0.62
55:AA:1026:A:O2'	55:AA:1104:A:O2'	2.18	0.62
55:AA:1056:A:H4'	55:AA:1588:G:H22	1.65	0.62
1:A:1836:A:N3	35:a:130:HIS:ND1	2.47	0.62
31:6:190:GLY:N	31:6:318:PHE:O	2.32	0.62
51:r:72:ILE:HD11	51:r:115:ILE:HD11	1.81	0.62
55:AA:1377:C:OP1	78:AX:320:ARG:NH1	2.33	0.62
55:AA:1478:A:OP2	55:AA:1479:C:N4	2.32	0.62
55:AA:1522:U:O2'	55:AA:1523:A:OP1	2.18	0.62
58:AD:88:SER:N	65:AK:28:HIS:O	2.33	0.62
58:AD:138:GLY:O	58:AD:165:GLN:NE2	2.33	0.62
10:L:101:ASP:OD2	15:Q:152:ARG:NH2	2.32	0.62
1:A:1833:C:OP1	36:b:116:ARG:NE	2.33	0.61
3:D:136:SER:O	3:D:249:ASN:ND2	2.33	0.61
55:AA:1162:A:HO2'	55:AA:1163:C:P	2.22	0.61
62:AH:77:SER:O	62:AH:174:LYS:N	2.33	0.61
1:A:2500:A:OP2	1:A:2501:C:O2'	2.18	0.61
1:A:2050:A:N1	1:A:2090:A:N6	2.39	0.61
39:e:160:LEU:HD22	39:e:255:VAL:HG21	1.83	0.61
1:A:2602:U:O4'	1:A:3078:C:O2'	2.11	0.61
69:AO:91:ARG:NH1	69:AO:103:ASN:O	2.34	0.61
1:A:2110:A:OP1	7:I:35:ARG:NH2	2.33	0.61
62:AH:173:THR:O	82:A1:154:THR:OG1	2.17	0.61
70:AP:94:ARG:NH1	70:AP:101:GLY:O	2.33	0.61
1:A:1909:A:N1	1:A:2010:U:C4	2.69	0.61
39:e:146:ARG:NH1	39:e:259:GLU:OE2	2.34	0.61
55:AA:1142:A:OP1	55:AA:1160:A:N6	2.33	0.61
55:AA:1319:A:O2'	55:AA:1320:G:OP1	2.17	0.61
63:AI:184:ASN:OD1	71:AQ:42:ARG:NH1	2.33	0.61
1:A:2918:A:O2'	1:A:2920:C:OP2	2.13	0.60
42:h:69:ARG:NH2	42:h:107:ASP:OD1	2.34	0.60
55:AA:837:A:N6	55:AA:854:U:O4'	2.34	0.60
55:AA:1457:G:O2'	60:AF:99:MET:SD	2.58	0.60
61:AG:306:ILE:O	61:AG:310:ARG:NE	2.34	0.60
71:AQ:9:ALA:O	71:AQ:11:THR:HG23	2.01	0.60
1:A:1870:A:O2'	1:A:1871:A:OP1	2.20	0.60
5:F:291:SER:OG	41:g:53:PRO:O	2.13	0.60
55:AA:1200:G:O6	55:AA:1365:A:N1	2.35	0.60
55:AA:1447:G:OP2	55:AA:1447:G:N2	2.28	0.60
76:AV:175:VAL:O	76:AV:177:SER:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:102:SER:OG	15:Q:158:GLN:NE2	2.34	0.60
36:b:37:GLY:O	36:b:44:ARG:NH2	2.34	0.60
1:A:2052:A:OP1	41:g:150:LYS:NZ	2.22	0.60
1:A:2673:G:OP1	18:T:82:TYR:OH	2.18	0.60
5:F:114:THR:O	5:F:156:ARG:NH2	2.35	0.60
40:f:101:THR:OG1	47:m:67:ARG:NH1	2.34	0.60
65:AK:62:ILE:HG22	65:AK:63:LEU:H	1.65	0.60
61:AG:310:ARG:HH12	78:AX:390:LEU:HD22	1.66	0.60
76:AV:164:VAL:HG13	76:AV:181:LEU:HD11	1.83	0.60
1:A:1675:A:O2'	43:i:32:ILE:O	2.19	0.60
22:X:36:ARG:N	22:X:151:GLU:OE2	2.35	0.60
1:A:2740:A:N1	1:A:2741:A:N6	2.48	0.60
22:X:150:LYS:HG2	22:X:159:MET:HE1	1.84	0.60
36:b:15:LEU:O	36:b:15:LEU:HD23	2.02	0.60
1:A:1724:A:N6	1:A:2040:G:C2	2.70	0.59
1:A:1779:A:N3	1:A:1781:A:O2'	2.35	0.59
1:A:1908:A:H62	1:A:2012:A:H61	1.50	0.59
85:A4:461:PHE:CZ	85:A4:465:ILE:HD11	2.37	0.59
1:A:1856:A:OP2	1:A:2986:C:O2'	2.20	0.59
1:A:2461:A:OP1	4:E:238:ARG:N	2.35	0.59
1:A:3166:U:O2'	4:E:269:TYR:O	2.16	0.59
76:AV:80:SER:N	76:AV:84:GLU:OE1	2.35	0.59
30:5:119:GLN:NE2	30:5:261:PRO:O	2.35	0.59
85:A4:376:ILE:CG2	85:A4:422:ILE:HD13	2.33	0.59
37:c:254:GLU:N	37:c:275:TYR:O	2.35	0.59
55:AA:1401:G:N2	55:AA:1404:A:OP2	2.35	0.59
66:AL:213:VAL:HG21	84:A3:177:TRP:CD1	2.38	0.59
1:A:2273:A:N1	1:A:2293:A:O2'	2.34	0.59
78:AX:62:GLN:O	78:AX:66:GLN:NE2	2.35	0.59
7:I:174:LEU:O	7:I:188:ARG:NH2	2.35	0.59
17:S:94:ARG:NE	17:S:110:SER:OG	2.35	0.59
55:AA:1146:C:OP1	84:A3:161:ARG:NH1	2.36	0.59
60:AF:51:TYR:O	60:AF:52:ARG:NE	2.35	0.59
72:AR:262:LEU:O	72:AR:263:ARG:NH2	2.34	0.59
81:A0:82:ARG:NH1	81:A0:138:ASP:O	2.36	0.59
51:r:186:CYS:O	51:r:188:SER:N	2.36	0.59
55:AA:1378:C:N4	61:AG:301:GLN:OE1	2.36	0.59
55:AA:1402:A:OP2	65:AK:58:ARG:NH2	2.36	0.59
64:AJ:95:ILE:O	64:AJ:100:HIS:NE2	2.36	0.59
20:V:117:HIS:O	20:V:119:GLN:N	2.36	0.58
55:AA:1461:A:N6	60:AF:43:ASP:OD2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
65:AK:90:ARG:NH1	65:AK:95:SER:O	2.36	0.58
62:AH:82:GLY:O	62:AH:138:THR:OG1	2.11	0.58
1:A:2846:G:O2'	1:A:2895:U:O4	2.19	0.58
55:AA:1151:C:O2'	55:AA:1152:A:OP1	2.21	0.58
55:AA:1234:C:O2'	55:AA:1235:U:OP1	2.16	0.58
62:AH:74:LYS:NZ	82:A1:150:GLU:OE2	2.36	0.58
1:A:2706:A:OP2	35:a:121:HIS:NE2	2.37	0.58
65:AK:29:TYR:OH	80:AZ:53:PRO:O	2.19	0.58
1:A:2182:G:N2	1:A:2199:A:O2'	2.35	0.58
55:AA:1336:G:O2'	55:AA:1337:U:OP1	2.18	0.58
1:A:1846:C:N4	1:A:1858:G:O6	2.37	0.58
1:A:2627:G:O2'	1:A:2630:U:OP2	2.05	0.58
1:A:3059:A:OP1	1:A:3061:G:O2'	2.19	0.58
55:AA:663:A:O2'	55:AA:1167:A:N6	2.37	0.58
75:AU:192:THR:OG1	75:AU:193:ARG:N	2.37	0.58
1:A:1683:C:OP1	23:Y:222:ARG:NH2	2.36	0.58
56:AB:80:SER:OG	56:AB:81:VAL:N	2.36	0.58
57:AC:96:MET:HB2	57:AC:108:LEU:HD11	1.86	0.58
1:A:1680:A:OP2	23:Y:230:LYS:NZ	2.26	0.58
1:A:2370:A:OP2	19:U:71:ARG:NH1	2.37	0.58
55:AA:1447:G:N2	55:AA:1449:G:O6	2.37	0.58
1:A:3051:A:H61	1:A:3115:U:H4'	1.68	0.57
1:A:1874:A:O2'	1:A:2090:A:N3	2.37	0.57
1:A:2158:U:O2'	51:r:153:ARG:NH2	2.37	0.57
1:A:3035:C:O2	10:L:34:LYS:NZ	2.37	0.57
1:A:1794:A:OP1	5:F:142:ARG:NH2	2.38	0.57
1:A:2058:C:N3	24:Z:109:LYS:NZ	2.53	0.57
1:A:2993:U:O2'	1:A:2994:U:OP2	2.19	0.57
27:2:57:ASN:ND2	34:9:25:ARG:O	2.38	0.57
62:AH:77:SER:N	62:AH:174:LYS:O	2.38	0.57
62:AH:177:LEU:N	82:A1:151:ILE:O	2.36	0.57
72:AR:208:ILE:O	72:AR:214:ASN:ND2	2.37	0.57
1:A:2507:A:HO2'	1:A:2508:C:P	2.27	0.57
55:AA:1227:G:O3'	65:AK:96:ARG:NH2	2.36	0.57
37:c:228:LEU:O	37:c:230:GLU:N	2.37	0.57
1:A:2063:G:N2	21:W:56:MET:SD	2.78	0.57
55:AA:684:U:O2'	74:AT:151:SER:O	2.19	0.57
55:AA:1145:A:O2'	55:AA:1499:U:O2'	2.22	0.57
22:X:68:PRO:O	22:X:69:ILE:HG22	2.05	0.57
69:AO:187:THR:HG23	81:A0:175:ILE:HG21	1.86	0.57
72:AR:153:THR:O	72:AR:154:THR:OG1	2.13	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
74:AT:100:GLU:OE1	74:AT:103:ARG:NH1	2.38	0.56
77:AW:124:CYS:SG	77:AW:125:ARG:N	2.78	0.56
1:A:2088:U:O2	41:g:104:ASN:ND2	2.38	0.56
25:0:116:LEU:O	25:0:116:LEU:HD12	2.05	0.56
55:AA:855:A:OP2	67:AM:28:ASN:N	2.36	0.56
24:Z:133:ASN:O	24:Z:135:SER:N	2.38	0.56
37:c:162:GLY:O	37:c:192:GLN:NE2	2.37	0.56
50:q:77:PRO:O	50:q:78:SER:OG	2.20	0.56
71:AQ:49:CYS:SG	71:AQ:50:CYS:N	2.78	0.56
1:A:2824:C:O2	1:A:2893:A:O2'	2.21	0.56
1:A:2993:U:N3	1:A:3071:U:O2	2.37	0.56
11:M:264:GLN:NE2	11:M:267:PHE:O	2.38	0.56
1:A:2706:A:OP2	9:K:119:ARG:NH1	2.39	0.56
57:AC:96:MET:CB	57:AC:108:LEU:HD11	2.35	0.56
5:F:165:LEU:O	5:F:170:ARG:NH2	2.38	0.56
16:R:114:LYS:NZ	35:a:43:TYR:O	2.39	0.56
42:h:63:PRO:HA	42:h:64:GLU:HB2	1.86	0.56
74:AT:158:GLU:O	74:AT:160:ARG:NH2	2.39	0.56
1:A:1771:C:OP1	37:c:33:LYS:NZ	2.37	0.56
55:AA:918:A:O2'	55:AA:919:A:O5'	2.23	0.56
59:AE:5:GLU:O	59:AE:94:VAL:N	2.36	0.56
55:AA:717:G:O2'	55:AA:718:A:OP2	2.19	0.56
63:AI:176:THR:HA	71:AQ:11:THR:HG22	1.86	0.56
1:A:1709:G:N2	23:Y:189:HIS:O	2.39	0.56
1:A:2879:A:O2'	26:l:53:ARG:NH2	2.39	0.56
76:AV:195:ASP:O	76:AV:197:SER:N	2.39	0.56
55:AA:986:G:HO2'	55:AA:987:A:P	2.29	0.55
66:AL:209:LEU:O	66:AL:213:VAL:HG23	2.06	0.55
85:A4:535:MET:O	85:A4:537:ARG:N	2.38	0.55
1:A:1883:G:OP2	11:M:100:ARG:NH2	2.39	0.55
1:A:2291:A:N3	16:R:12:ASN:ND2	2.53	0.55
13:O:36:LEU:O	13:O:40:GLU:N	2.37	0.55
55:AA:685:A:O2'	55:AA:686:A:OP1	2.21	0.55
55:AA:843:G:O2'	55:AA:844:A:N7	2.35	0.55
1:A:2017:U:OP2	11:M:59:ARG:NH2	2.38	0.55
1:A:2938:A:OP1	1:A:2984:A:N6	2.39	0.55
55:AA:875:U:O2'	55:AA:882:A:N1	2.38	0.55
1:A:2172:A:C5	8:J:23:ILE:HG22	2.42	0.55
1:A:2442:U:OP1	52:s:81:ARG:NH1	2.40	0.55
55:AA:1187:U:O2	55:AA:1429:C:N4	2.39	0.55
1:A:2510:U:OP2	1:A:2539:A:N6	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AA:878:G:O2'	55:AA:879:U:P	2.63	0.55
55:AA:1190:C:HO2'	55:AA:1191:C:C5'	2.17	0.55
81:A0:94:TYR:OH	81:A0:96:ARG:NH1	2.39	0.55
21:W:72:HIS:O	21:W:74:ARG:N	2.40	0.55
33:8:160:GLU:O	39:e:207:ASN:ND2	2.40	0.55
69:AO:174:ASP:OD1	72:AR:167:HIS:N	2.40	0.55
31:6:372:SER:O	31:6:374:GLU:N	2.38	0.55
39:e:158:VAL:N	39:e:255:VAL:O	2.40	0.55
1:A:2039:A:N6	1:A:2729:U:O2	2.39	0.55
1:A:2554:A:N3	3:D:285:LYS:NZ	2.53	0.55
61:AG:330:CYS:SG	61:AG:331:THR:N	2.79	0.55
69:AO:212:GLU:OE2	69:AO:215:ARG:NH1	2.40	0.55
60:AF:207:HIS:NE2	60:AF:211:GLU:OE2	2.40	0.55
1:A:1758:U:C4	1:A:1759:U:O4	2.60	0.54
1:A:2180:A:O2'	1:A:2206:C:O3'	2.26	0.54
12:N:92:LEU:N	12:N:186:ALA:O	2.39	0.54
55:AA:679:C:OP1	55:AA:919:A:N6	2.38	0.54
23:Y:143:ASP:OD1	34:9:137:ARG:NH1	2.40	0.54
1:A:2470:G:O2'	10:L:35:MET:O	2.23	0.54
11:M:213:TYR:O	11:M:219:ASN:ND2	2.38	0.54
69:AO:197:ASP:OD1	69:AO:204:ASN:ND2	2.41	0.54
30:5:419:LEU:O	30:5:421:GLY:N	2.39	0.54
55:AA:804:C:OP2	55:AA:807:A:N6	2.39	0.54
55:AA:1473:C:O2'	83:A2:32:ARG:NH1	2.40	0.54
61:AG:324:GLY:O	61:AG:326:HIS:N	2.40	0.54
1:A:2082:G:N2	24:Z:88:MET:SD	2.81	0.54
29:4:67:LYS:O	29:4:101:ARG:N	2.41	0.54
43:i:124:HIS:O	43:i:128:ARG:NH2	2.40	0.54
55:AA:658:G:H21	55:AA:1286:A:H1'	1.72	0.54
55:AA:1441:A:N1	55:AA:1449:G:O6	2.40	0.54
1:A:2243:A:O2'	1:A:2244:U:P	2.66	0.54
11:M:46:GLY:O	11:M:48:LYS:N	2.41	0.54
69:AO:92:LYS:O	69:AO:144:VAL:N	2.33	0.54
1:A:1778:U:O4'	5:F:142:ARG:NH2	2.41	0.54
16:R:133:GLY:O	16:R:135:GLY:N	2.41	0.54
55:AA:1014:A:N6	55:AA:1031:G:O6	2.40	0.54
1:A:1726:C:HO2'	1:A:1727:A:C5'	2.20	0.53
1:A:3128:A:O2'	1:A:3129:A:O5'	2.25	0.53
12:N:172:VAL:HG13	12:N:175:PHE:CZ	2.43	0.53
67:AM:18:THR:N	67:AM:37:ALA:O	2.41	0.53
55:AA:1138:G:O2'	55:AA:1139:A:O5'	2.27	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
78:AX:59:HIS:O	78:AX:61:ASP:N	2.41	0.53
1:A:2331:C:OP2	1:A:2444:A:N6	2.41	0.53
11:M:109:ARG:NH1	41:g:91:MET:SD	2.82	0.53
55:AA:1162:A:N3	55:AA:1497:C:O2'	2.30	0.53
59:AE:50:ARG:NH1	59:AE:59:ASN:OD1	2.42	0.53
81:A0:44:PRO:O	81:A0:46:SER:N	2.41	0.53
55:AA:1307:G:N2	55:AA:1319:A:H62	2.06	0.53
1:A:1868:G:H21	1:A:1868:G:P	2.31	0.53
4:E:202:GLN:NE2	4:E:301:ASP:OD1	2.42	0.53
61:AG:95:ASP:N	61:AG:96:PRO:CD	2.72	0.53
66:AL:198:ARG:O	66:AL:200:HIS:N	2.41	0.53
1:A:1871:A:HO2'	1:A:1872:U:P	2.28	0.53
55:AA:1451:U:O3'	62:AH:133:GLN:NE2	2.38	0.53
1:A:1681:G:OP2	23:Y:226:LEU:HD11	2.09	0.53
1:A:2446:A:N6	52:s:82:ILE:O	2.42	0.53
55:AA:991:G:N1	55:AA:996:A:OP2	2.41	0.53
55:AA:1381:A:O2'	78:AX:166:ARG:NH2	2.42	0.53
74:AT:141:CYS:SG	74:AT:142:GLU:N	2.81	0.53
1:A:2155:A:O2'	1:A:2156:A:O4'	2.26	0.53
6:H:53:THR:OG1	6:H:54:VAL:N	2.42	0.53
64:AJ:58:LEU:N	64:AJ:110:VAL:O	2.42	0.53
4:E:56:GLU:OE2	13:O:153:ARG:NH2	2.41	0.53
7:I:176:LEU:O	7:I:188:ARG:NE	2.42	0.53
1:A:1678:C:O2'	1:A:1679:U:OP2	2.23	0.52
1:A:2083:U:OP2	48:o:66:ARG:NH1	2.41	0.52
1:A:2363:A:O2'	1:A:2364:C:OP1	2.27	0.52
42:h:65:ASP:O	42:h:67:GLN:N	2.42	0.52
55:AA:678:U:O2'	55:AA:679:C:OP1	2.26	0.52
1:A:2154:A:N7	48:o:30:ARG:NH2	2.56	0.52
1:A:2564:A:O2'	1:A:2565:A:OP1	2.19	0.52
41:g:144:THR:O	41:g:146:THR:N	2.42	0.52
48:o:100:LYS:O	48:o:102:SER:N	2.42	0.52
55:AA:991:G:O2'	55:AA:992:U:O5'	2.25	0.52
1:A:1809:U:O2'	1:A:1810:A:O5'	2.23	0.52
1:A:1908:A:O2'	1:A:2929:C:O2	2.27	0.52
1:A:2016:C:O2	1:A:2931:A:O2'	2.28	0.52
1:A:3041:U:O2'	1:A:3042:U:O5'	2.24	0.52
1:A:3180:A:O2'	51:r:99:MET:O	2.26	0.52
11:M:264:GLN:O	11:M:266:PHE:N	2.43	0.52
52:s:228:ASP:O	52:s:230:ARG:NH1	2.42	0.52
69:AO:223:HIS:NE2	75:AU:45:PRO:O	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1870:A:O2'	1:A:1871:A:P	2.68	0.52
55:AA:678:U:O2'	55:AA:919:A:N1	2.41	0.52
61:AG:110:TYR:CZ	82:A1:119:ILE:HD11	2.44	0.52
1:A:2060:A:N6	1:A:2078:C:O2'	2.42	0.52
1:A:2078:C:O2'	1:A:2079:C:O2	2.22	0.52
4:E:103:LYS:O	4:E:294:ASN:N	2.41	0.52
7:I:150:HIS:O	45:k:35:GLN:NE2	2.42	0.52
20:V:178:SER:O	34:9:75:SER:OG	2.23	0.52
55:AA:1302:C:O2'	57:AC:43:ARG:NH2	2.42	0.52
1:A:2403:G:OP1	3:D:103:ARG:N	2.42	0.52
1:A:3195:A:OP2	1:A:3196:G:O2'	2.24	0.52
7:I:120:LYS:O	7:I:156:SER:OG	2.27	0.52
55:AA:704:U:O2	55:AA:705:C:N4	2.42	0.52
1:A:2167:A:N6	1:A:2212:C:OP2	2.42	0.52
1:A:2832:A:O2'	40:f:48:TYR:OH	2.12	0.52
52:s:249:GLU:O	52:s:251:VAL:N	2.43	0.52
55:AA:996:A:H62	55:AA:1074:G:C2'	2.22	0.52
56:AB:156:GLU:OE1	61:AG:163:HIS:ND1	2.42	0.52
82:A1:79:SER:OG	85:A4:91:ASP:O	2.28	0.52
12:N:132:THR:OG1	12:N:144:LYS:NZ	2.40	0.52
55:AA:873:G:N2	55:AA:922:C:OP1	2.43	0.52
66:AL:154:ARG:NH1	66:AL:158:MET:SD	2.83	0.52
1:A:3176:A:N6	1:A:3194:U:O4	2.43	0.52
70:AP:140:TYR:O	70:AP:142:GLU:N	2.42	0.51
1:A:2204:U:N3	1:A:2207:A:OP2	2.38	0.51
1:A:3201:A:O2'	1:A:3202:U:O5'	2.21	0.51
1:A:1850:U:H1'	1:A:2098:G:H21	1.76	0.51
1:A:1958:G:N3	1:A:1960:A:N6	2.58	0.51
1:A:2507:A:O2'	1:A:2508:C:P	2.69	0.51
1:A:2616:A:O2'	1:A:3046:C:O2	2.21	0.51
1:A:2655:G:N2	1:A:2659:C:O2'	2.43	0.51
58:AD:192:GLY:O	58:AD:194:SER:N	2.43	0.51
58:AD:298:PHE:O	58:AD:300:ARG:N	2.43	0.51
62:AH:175:THR:OG1	82:A1:153:SER:O	2.27	0.51
82:A1:165:ASN:O	82:A1:167:ARG:N	2.43	0.51
52:s:361:ILE:HD11	52:s:368:SER:OG	2.11	0.51
55:AA:1178:G:N2	55:AA:1567:A:O2'	2.36	0.51
55:AA:1537:C:O2	55:AA:1538:G:N1	2.44	0.51
55:AA:1316:U:O2'	61:AG:379:ARG:NH1	2.41	0.51
60:AF:52:ARG:NH2	61:AG:319:PHE:O	2.43	0.51
75:AU:179:ALA:O	75:AU:183:SER:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:AC:127:LEU:N	57:AC:132:TYR:OH	2.43	0.51
1:A:1726:C:O2'	1:A:1727:A:O5'	2.28	0.51
1:A:2131:A:OP1	48:o:23:ARG:NH1	2.43	0.51
1:A:2308:A:OP1	25:0:85:ARG:NH1	2.43	0.51
82:A1:155:ASP:OD1	82:A1:155:ASP:N	2.41	0.51
1:A:1847:U:OP1	11:M:47:ARG:NE	2.44	0.51
32:7:256:ARG:NH1	32:7:258:GLY:O	2.44	0.51
55:AA:1233:C:O4'	55:AA:1402:A:N6	2.43	0.51
67:AM:38:HIS:ND1	67:AM:41:CYS:SG	2.67	0.51
1:A:1747:G:O2'	1:A:1751:A:N6	2.42	0.51
1:A:1871:A:O2'	1:A:1872:U:P	2.69	0.51
1:A:2243:A:O2'	1:A:2244:U:OP2	2.25	0.51
30:5:263:ILE:HG23	30:5:264:ASP:H	1.76	0.51
55:AA:1229:U:O2'	55:AA:1442:G:N2	2.44	0.51
55:AA:1562:G:HO2'	55:AA:1563:U:P	2.33	0.51
1:A:1800:G:N1	1:A:1803:A:OP2	2.39	0.51
55:AA:702:C:OP1	55:AA:848:U:O2'	2.25	0.51
55:AA:1256:A:OP1	55:AA:1331:A:N6	2.44	0.51
62:AH:87:VAL:HG11	62:AH:168:VAL:HG23	1.92	0.51
82:A1:152:ASP:OD1	82:A1:152:ASP:N	2.43	0.51
1:A:1713:A:O2'	1:A:1714:C:OP1	2.23	0.50
1:A:2060:A:N7	1:A:2078:C:O2'	2.44	0.50
1:A:2308:A:OP2	1:A:2309:A:O2'	2.14	0.50
1:A:3161:G:N2	1:A:3162:C:O2'	2.43	0.50
55:AA:767:C:OP1	68:AN:75:LYS:N	2.43	0.50
76:AV:226:TYR:CZ	76:AV:230:LEU:HD11	2.45	0.50
78:AX:245:LYS:NZ	78:AX:292:ASN:OD1	2.25	0.50
1:A:2165:C:O2'	1:A:2166:C:P	2.69	0.50
1:A:2727:C:O2'	1:A:2815:G:N2	2.43	0.50
1:A:2848:A:N6	1:A:2849:G:O6	2.44	0.50
1:A:1788:C:O2	27:2:64:HIS:NE2	2.40	0.50
1:A:1960:A:OP1	1:A:2431:C:N4	2.44	0.50
1:A:3092:U:O2'	1:A:3093:C:P	2.69	0.50
55:AA:1512:A:N7	55:AA:1536:A:O2'	2.39	0.50
3:D:108:ASP:OD2	3:D:149:ARG:NH1	2.43	0.50
11:M:140:LEU:HD22	11:M:163:ALA:HB1	1.92	0.50
55:AA:1197:G:O6	55:AA:1425:U:C2	2.63	0.50
76:AV:250:ILE:O	76:AV:255:TYR:OH	2.29	0.50
1:A:3049:U:H3	1:A:3053:A:H62	1.58	0.50
3:D:69:ARG:NH1	3:D:73:THR:OG1	2.44	0.50
3:D:194:ASN:ND2	3:D:245:GLY:O	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:91:ALA:O	18:T:95:ARG:N	2.44	0.50
55:AA:806:C:OP2	55:AA:807:A:N6	2.45	0.50
81:A0:135:MET:SD	81:A0:135:MET:N	2.84	0.50
1:A:3105:A:O2'	4:E:251:VAL:O	2.28	0.50
52:s:279:GLU:OE1	52:s:281:HIS:NE2	2.44	0.50
55:AA:996:A:N6	55:AA:1074:G:O2'	2.43	0.50
55:AA:1032:C:O2	55:AA:1033:U:C5	2.65	0.50
76:AV:173:PHE:HA	76:AV:178:THR:HG22	1.93	0.50
1:A:2905:A:O2'	1:A:2906:C:P	2.69	0.50
11:M:202:LYS:NZ	11:M:293:TYR:O	2.43	0.50
38:d:151:CYS:O	38:d:155:SER:N	2.44	0.50
55:AA:895:C:N3	55:AA:898:C:N4	2.60	0.50
69:AO:185:SER:OG	69:AO:186:ALA:N	2.45	0.50
55:AA:826:A:H62	64:AJ:56:PRO:HD2	1.76	0.50
55:AA:1456:U:OP1	61:AG:338:SER:N	2.45	0.50
59:AE:53:ALA:HA	59:AE:54:HIS:HB3	1.94	0.50
69:AO:110:ASP:OD2	69:AO:113:LEU:HD12	2.11	0.50
1:A:2874:A:O2'	14:P:65:ARG:NH2	2.44	0.50
42:h:91:LEU:O	42:h:93:ASP:N	2.43	0.50
55:AA:1069:A:N7	55:AA:1089:U:N3	2.59	0.50
55:AA:1456:U:O2'	60:AF:103:ASN:OD1	2.23	0.50
1:A:1852:C:O2'	1:A:1856:A:N6	2.44	0.49
1:A:2826:G:OP1	21:W:49:ARG:NE	2.45	0.49
14:P:84:ARG:NH1	14:P:124:CYS:SG	2.85	0.49
30:5:112:ARG:NH2	30:5:303:ARG:O	2.45	0.49
55:AA:1293:C:O2'	56:AB:201:ASN:OD1	2.29	0.49
61:AG:111:LEU:HD12	82:A1:112:LEU:HD13	1.94	0.49
12:N:205:ARG:NH1	12:N:249:LYS:O	2.45	0.49
1:A:1952:U:O4	1:A:1953:A:N6	2.45	0.49
55:AA:681:U:O4	55:AA:682:A:N6	2.46	0.49
55:AA:991:G:N2	55:AA:995:A:O5'	2.42	0.49
76:AV:214:LYS:O	76:AV:216:LYS:N	2.44	0.49
85:A4:84:ALA:O	85:A4:484:SER:N	2.44	0.49
19:U:38:ASP:OD1	19:U:39:THR:N	2.45	0.49
21:W:39:SER:O	21:W:39:SER:OG	2.26	0.49
31:6:330:ILE:HG22	31:6:335:LEU:HD13	1.94	0.49
55:AA:1021:U:O2'	55:AA:1022:A:P	2.70	0.49
57:AC:143:LEU:HD12	57:AC:151:VAL:HG11	1.94	0.49
1:A:1769:C:O2'	1:A:2276:C:O2	2.28	0.49
1:A:2515:U:O2'	3:D:282:ALA:O	2.30	0.49
55:AA:703:A:OP2	75:AU:43:ASN:ND2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
60:AF:77:ALA:O	61:AG:345:ARG:NH1	2.45	0.49
73:AS:68:ASP:OD1	73:AS:71:ARG:NH2	2.45	0.49
38:d:266:VAL:HG23	38:d:267:PRO:HD3	1.95	0.49
55:AA:849:U:O4'	75:AU:38:LYS:NZ	2.46	0.49
55:AA:1269:U:O2'	55:AA:1320:G:N2	2.37	0.49
56:AB:141:ILE:HG23	56:AB:165:TYR:CE2	2.48	0.49
75:AU:190:ALA:N	75:AU:198:VAL:O	2.41	0.49
25:0:113:CYS:SG	25:0:115:HIS:ND1	2.85	0.49
28:3:185:ASN:O	31:6:354:GLN:NE2	2.46	0.49
72:AR:276:VAL:O	72:AR:308:HIS:NE2	2.46	0.49
76:AV:324:GLN:O	76:AV:326:LYS:N	2.46	0.49
1:A:2683:C:P	25:0:86:THR:HG22	2.53	0.49
13:O:14:VAL:HG22	13:O:15:PHE:H	1.78	0.49
39:e:265:LYS:N	39:e:266:PRO:CD	2.75	0.49
55:AA:1106:C:O2'	55:AA:1108:C:OP2	2.28	0.49
74:AT:130:GLY:O	74:AT:132:ARG:N	2.46	0.49
1:A:2371:U:OP2	52:s:270:LYS:NZ	2.46	0.49
52:s:406:GLU:O	52:s:408:ASN:N	2.46	0.49
56:AB:228:ASN:O	56:AB:230:CYS:N	2.46	0.49
85:A4:493:MET:SD	85:A4:493:MET:N	2.85	0.49
4:E:331:ASP:N	4:E:331:ASP:OD1	2.44	0.49
34:9:16:ASP:O	34:9:25:ARG:NH1	2.44	0.49
60:AF:120:ARG:NE	78:AX:93:THR:OG1	2.45	0.49
41:g:54:ALA:O	41:g:56:ARG:N	2.45	0.48
75:AU:29:THR:O	75:AU:31:HIS:N	2.45	0.48
1:A:2050:A:O2'	1:A:2051:A:O5'	2.31	0.48
1:A:2418:A:OP2	19:U:50:ARG:NH1	2.46	0.48
5:F:83:HIS:HB3	5:F:86:VAL:HG12	1.95	0.48
5:F:190:MET:N	5:F:261:LEU:O	2.44	0.48
55:AA:973:C:N4	55:AA:974:U:O4	2.47	0.48
76:AV:152:ILE:HD13	76:AV:180:LEU:HD22	1.95	0.48
85:A4:376:ILE:HG21	85:A4:422:ILE:HD13	1.95	0.48
1:A:1905:C:OP1	5:F:117:ARG:NH1	2.42	0.48
12:N:83:THR:HG23	12:N:83:THR:O	2.13	0.48
22:X:144:TYR:O	22:X:148:THR:HG23	2.13	0.48
55:AA:1232:A:O2'	55:AA:1403:A:N7	2.45	0.48
60:AF:43:ASP:OD1	60:AF:75:LYS:NZ	2.46	0.48
79:AY:348:ARG:NH1	79:AY:352:GLU:OE2	2.47	0.48
55:AA:802:C:O3'	55:AA:816:A:N6	2.46	0.48
71:AQ:7:PHE:C	71:AQ:11:THR:HG21	2.38	0.48
1:A:1868:G:OP1	11:M:41:ARG:NH2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2028:G:O2'	1:A:2265:A:N6	2.45	0.48
1:A:2537:G:O2'	1:A:2634:U:OP2	2.24	0.48
30:5:263:ILE:HG23	30:5:264:ASP:N	2.28	0.48
55:AA:1121:A:OP2	55:AA:1283:A:N6	2.46	0.48
65:AK:46:GLU:O	65:AK:48:ALA:N	2.46	0.48
1:A:2381:A:N6	1:A:2412:A:N1	2.62	0.48
1:A:2729:U:O4	1:A:2730:A:N6	2.46	0.48
1:A:1871:A:N3	28:3:104:ARG:NH2	2.61	0.48
1:A:2165:C:HO2'	1:A:2166:C:P	2.36	0.48
19:U:16:GLN:NE2	34:9:54:LYS:O	2.45	0.48
55:AA:871:A:N1	55:AA:918:A:O2'	2.38	0.48
67:AM:74:ARG:NH2	75:AU:77:GLU:OE1	2.46	0.48
85:A4:131:ASP:OD1	85:A4:131:ASP:N	2.47	0.48
1:A:2028:G:N2	1:A:2264:A:OP2	2.44	0.48
1:A:3041:U:O2'	1:A:3042:U:P	2.71	0.48
55:AA:1189:U:O2'	55:AA:1190:C:OP2	2.23	0.48
58:AD:356:GLN:OE1	58:AD:356:GLN:N	2.47	0.48
1:A:2466:A:OP1	15:Q:235:ARG:NH2	2.47	0.48
36:b:27:GLN:NE2	36:b:79:TYR:O	2.47	0.48
42:h:63:PRO:HA	42:h:64:GLU:CB	2.44	0.48
55:AA:1242:C:N3	55:AA:1348:G:N1	2.61	0.48
62:AH:63:VAL:O	62:AH:64:THR:OG1	2.29	0.48
67:AM:20:ARG:NH2	67:AM:41:CYS:O	2.47	0.48
1:A:1809:U:O2'	1:A:1810:A:P	2.71	0.48
14:P:86:GLN:O	14:P:88:HIS:N	2.46	0.48
45:k:36:THR:OG1	45:k:37:VAL:N	2.47	0.48
50:q:89:GLU:O	50:q:93:TYR:N	2.47	0.48
55:AA:711:U:OP1	75:AU:30:ARG:NH1	2.47	0.48
73:AS:58:ALA:O	73:AS:60:ILE:N	2.47	0.48
74:AT:33:ASN:OD1	74:AT:33:ASN:N	2.47	0.48
1:A:1723:A:H61	1:A:1726:C:H3'	1.79	0.47
1:A:2325:U:OP1	52:s:57:ALA:N	2.42	0.47
5:F:86:VAL:HG23	5:F:175:LYS:HG2	1.95	0.47
55:AA:1258:A:O2'	55:AA:1328:G:OP1	2.32	0.47
11:M:68:GLU:OE1	11:M:71:GLN:NE2	2.45	0.47
31:6:290:CYS:SG	31:6:291:TYR:N	2.86	0.47
61:AG:318:HIS:ND1	78:AX:379:GLU:OE2	2.46	0.47
69:AO:116:ASP:N	69:AO:116:ASP:OD1	2.47	0.47
35:a:72:THR:OG1	37:c:256:ARG:NH1	2.47	0.47
37:c:258:THR:OG1	37:c:259:ARG:N	2.47	0.47
58:AD:127:ASN:OD1	80:AZ:72:ARG:NH2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:AU:117:HIS:NE2	75:AU:121:ILE:HD11	2.29	0.47
1:A:1773:A:OP1	37:c:31:VAL:N	2.48	0.47
1:A:1807:U:O2'	1:A:1808:A:O5'	2.22	0.47
55:AA:1005:U:OP1	71:AQ:2:ALA:N	2.46	0.47
55:AA:1581:G:O6	84:A3:141:HIS:NE2	2.43	0.47
66:AL:79:VAL:O	66:AL:79:VAL:HG23	2.15	0.47
66:AL:85:VAL:HG22	66:AL:86:ASP:H	1.79	0.47
1:A:1909:A:N1	1:A:2010:U:O4	2.47	0.47
1:A:1914:A:H4'	27:2:74:ALA:HB1	1.96	0.47
1:A:1993:A:O4'	1:A:2498:U:O2'	2.27	0.47
34:9:132:PRO:O	34:9:134:ASN:N	2.48	0.47
69:AO:90:THR:HG21	69:AO:141:GLY:HA2	1.95	0.47
78:AX:340:PHE:HD1	82:A1:316:VAL:HG11	1.79	0.47
82:A1:183:ASP:OD1	82:A1:183:ASP:N	2.48	0.47
1:A:1772:A:OP1	16:R:10:LEU:N	2.48	0.47
1:A:2287:U:O4	1:A:2288:A:N6	2.47	0.47
42:h:146:SER:O	42:h:148:LEU:N	2.48	0.47
55:AA:717:G:O2'	55:AA:791:G:O4'	2.33	0.47
81:A0:103:ASP:OD1	81:A0:103:ASP:N	2.46	0.47
1:A:1868:G:OP2	1:A:1868:G:N2	2.44	0.47
1:A:2096:U:H2'	1:A:2096:U:O2	2.14	0.47
1:A:2868:C:O2'	11:M:77:ARG:NH1	2.45	0.47
1:A:3188:U:O2'	1:A:3192:C:N4	2.47	0.47
4:E:48:TRP:NE1	4:E:50:ASP:O	2.47	0.47
20:V:178:SER:OG	20:V:179:VAL:N	2.47	0.47
30:5:165:GLN:OE1	30:5:165:GLN:N	2.48	0.47
55:AA:878:G:HO2'	55:AA:879:U:P	2.33	0.47
71:AQ:77:ARG:O	71:AQ:80:ARG:NH1	2.48	0.47
78:AX:220:SER:O	78:AX:222:LEU:N	2.44	0.47
80:AZ:90:GLY:HA3	80:AZ:91:LYS:C	2.40	0.47
8:J:23:ILE:HG23	8:J:23:ILE:O	2.14	0.47
35:a:43:TYR:O	35:a:45:CYS:N	2.47	0.47
38:d:129:ASP:N	38:d:130:ALA:HA	2.29	0.47
55:AA:1327:G:N1	55:AA:1328:G:O6	2.48	0.47
1:A:1909:A:N6	1:A:2012:A:H62	2.13	0.47
41:g:87:ARG:NH1	41:g:114:GLU:OE1	2.47	0.47
45:k:24:GLU:N	45:k:61:GLU:OE2	2.44	0.47
55:AA:919:A:OP2	69:AO:96:ARG:NH2	2.48	0.47
55:AA:1033:U:C2	55:AA:1034:U:C5	3.03	0.47
57:AC:76:LEU:O	65:AK:103:ARG:NH2	2.48	0.47
1:A:1699:C:O2	27:2:66:TRP:NE1	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:AA:826:A:H62	64:AJ:56:PRO:CD	2.27	0.47
59:AE:119:SER:O	59:AE:123:ARG:NH1	2.48	0.46
61:AG:198:ARG:NH1	61:AG:199:TRP:O	2.49	0.46
1:A:2307:U:H2'	1:A:2308:A:O4'	2.15	0.46
58:AD:225:VAL:HG13	58:AD:241:ILE:HG23	1.96	0.46
65:AK:34:MET:HE3	80:AZ:52:TYR:CD1	2.50	0.46
66:AL:85:VAL:HG21	66:AL:89:VAL:HG11	1.97	0.46
73:AS:55:LYS:O	73:AS:57:LYS:N	2.49	0.46
1:A:1822:U:O2'	1:A:2707:A:O2'	2.27	0.46
1:A:2695:G:OP2	1:A:2941:G:O2'	2.14	0.46
1:A:2800:U:C2	1:A:2801:A:C8	3.04	0.46
1:A:3148:C:O2'	4:E:106:MET:SD	2.72	0.46
1:A:3151:A:O2'	15:Q:165:GLU:OE1	2.25	0.46
9:K:61:ASN:ND2	9:K:131:GLU:OE2	2.47	0.46
37:c:122:ASN:O	37:c:124:GLU:N	2.48	0.46
42:h:64:GLU:O	42:h:65:ASP:CB	2.63	0.46
76:AV:241:ARG:O	76:AV:243:VAL:N	2.48	0.46
79:AY:332:ILE:O	79:AY:334:LEU:N	2.48	0.46
55:AA:717:G:H1'	55:AA:718:A:OP2	2.15	0.46
55:AA:1211:G:N2	55:AA:1214:A:N7	2.63	0.46
1:A:2431:C:OP2	1:A:2433:C:N4	2.47	0.46
5:F:85:ASP:OD1	41:g:87:ARG:NH2	2.48	0.46
5:F:278:SER:O	5:F:278:SER:OG	2.29	0.46
60:AF:75:LYS:O	61:AG:371:THR:OG1	2.34	0.46
66:AL:213:VAL:HG21	84:A3:177:TRP:HD1	1.80	0.46
1:A:2275:U:O2	16:R:11:ARG:NH1	2.48	0.46
1:A:3038:U:O4	1:A:3045:A:N6	2.49	0.46
23:Y:205:VAL:HG12	23:Y:205:VAL:O	2.15	0.46
55:AA:678:U:O2	55:AA:920:G:C6	2.68	0.46
55:AA:1314:C:O2'	55:AA:1315:G:OP1	2.30	0.46
55:AA:1390:A:O2'	55:AA:1416:A:OP2	2.30	0.46
55:AA:1596:A:OP2	83:A2:24:ASN:ND2	2.48	0.46
1:A:1907:A:OP1	5:F:130:GLN:NE2	2.48	0.46
1:A:1985:G:N2	1:A:2003:A:O3'	2.49	0.46
55:AA:705:C:HO2'	81:A0:43:ARG:NH2	2.11	0.46
2:B:1607:U:HO2'	2:B:1608:G:P	2.39	0.46
12:N:172:VAL:HG12	12:N:176:LEU:HG	1.97	0.46
60:AF:149:LEU:O	60:AF:153:GLU:N	2.44	0.46
62:AH:75:ARG:NH2	62:AH:77:SER:OG	2.49	0.46
1:A:3007:C:N4	1:A:3054:G:N7	2.64	0.46
1:A:3201:A:N3	1:A:3201:A:H2'	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:250:ARG:NH1	12:N:251:VAL:O	2.48	0.46
67:AM:108:GLU:OE2	75:AU:59:ARG:NH2	2.49	0.46
1:A:1693:C:O2	1:A:1693:C:H2'	2.16	0.46
1:A:2192:A:O3'	8:J:139:SER:OG	2.33	0.46
1:A:2945:A:O2'	1:A:2947:U:O4	2.33	0.46
47:m:59:GLN:NE2	47:m:78:PRO:O	2.49	0.46
55:AA:762:G:N1	55:AA:779:U:O4	2.49	0.46
55:AA:1504:U:O4	55:AA:1505:A:N6	2.49	0.46
85:A4:425:SER:OG	85:A4:426:LEU:N	2.48	0.46
26:1:62:ILE:HG23	26:1:62:ILE:O	2.16	0.45
55:AA:1232:A:H62	65:AK:85:VAL:HG11	1.81	0.45
55:AA:1374:A:N3	55:AA:1374:A:H2'	2.31	0.45
57:AC:111:LYS:NZ	82:A1:110:ASN:OD1	2.49	0.45
1:A:2236:C:N4	1:A:2688:C:O2	2.48	0.45
31:6:224:HIS:O	31:6:226:LEU:N	2.49	0.45
58:AD:427:ARG:O	58:AD:429:ALA:N	2.49	0.45
66:AL:209:LEU:HD13	84:A3:173:LEU:HD22	1.98	0.45
1:A:1846:C:OP2	17:S:177:ARG:N	2.50	0.45
1:A:2909:G:N7	28:3:131:LYS:NZ	2.54	0.45
5:F:86:VAL:HG11	5:F:270:GLU:HG2	1.98	0.45
10:L:57:CYS:SG	10:L:58:ILE:N	2.90	0.45
55:AA:678:U:OP1	64:AJ:134:HIS:NE2	2.47	0.45
55:AA:1307:G:H21	55:AA:1319:A:H62	1.63	0.45
56:AB:193:ILE:O	56:AB:220:VAL:N	2.46	0.45
77:AW:141:ARG:C	77:AW:142:LEU:HD22	2.40	0.45
1:A:1747:G:N2	1:A:1750:G:O2'	2.49	0.45
2:B:1624:C:OP1	31:6:59:ARG:NH1	2.49	0.45
55:AA:859:U:H3'	55:AA:860:A:H5'	1.97	0.45
55:AA:1242:C:N4	55:AA:1348:G:O6	2.49	0.45
55:AA:1275:A:O2'	55:AA:1276:A:O5'	2.30	0.45
76:AV:341:LEU:O	76:AV:345:GLY:N	2.50	0.45
1:A:2121:G:OP1	24:Z:80:TYR:N	2.50	0.45
38:d:247:VAL:O	38:d:262:HIS:N	2.46	0.45
55:AA:1163:C:H2'	55:AA:1164:U:C6	2.52	0.45
65:AK:81:ASP:O	65:AK:82:SER:OG	2.31	0.45
74:AT:59:ASN:OD1	74:AT:59:ASN:N	2.49	0.45
78:AX:345:VAL:HG23	78:AX:345:VAL:O	2.16	0.45
1:A:1713:A:HO2'	1:A:1714:C:P	2.38	0.45
1:A:2032:G:O6	1:A:2044:A:N6	2.50	0.45
11:M:123:ASN:O	11:M:125:ARG:NH1	2.46	0.45
12:N:94:GLY:N	12:N:244:LYS:O	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:s:350:ASP:OD2	52:s:389:ARG:NH1	2.49	0.45
66:AL:143:LEU:O	66:AL:147:ARG:NH1	2.50	0.45
78:AX:55:ASP:O	78:AX:57:ALA:N	2.50	0.45
1:A:3021:C:H3'	1:A:3022:G:H5''	1.99	0.45
1:A:3088:C:HO2'	1:A:3090:G:H8	1.64	0.45
1:A:3204:C:O2	1:A:3204:C:O4'	2.34	0.45
2:B:1607:U:O2'	2:B:1608:G:P	2.75	0.45
18:T:207:THR:HG22	18:T:208:ILE:H	1.82	0.45
38:d:266:VAL:N	38:d:267:PRO:HD2	2.32	0.45
52:s:107:GLN:O	52:s:111:LYS:N	2.45	0.45
55:AA:944:U:H2'	55:AA:945:G:C8	2.52	0.45
55:AA:1036:A:O2'	66:AL:142:HIS:ND1	2.48	0.45
56:AB:172:ARG:O	56:AB:174:GLY:N	2.50	0.45
57:AC:108:LEU:HD13	57:AC:119:ILE:HG23	1.99	0.45
61:AG:320:VAL:HG12	61:AG:320:VAL:O	2.16	0.45
1:A:2689:C:N4	1:A:2690:G:O6	2.50	0.45
31:6:73:THR:OG1	31:6:74:TYR:N	2.50	0.45
55:AA:752:C:O2'	55:AA:793:C:N3	2.47	0.45
55:AA:791:G:O2'	55:AA:792:C:OP1	2.29	0.45
55:AA:1400:U:O2'	55:AA:1401:G:O4'	2.23	0.45
78:AX:383:LEU:HD12	78:AX:383:LEU:O	2.17	0.45
34:9:22:THR:OG1	34:9:23:SER:N	2.48	0.45
55:AA:953:U:HO2'	55:AA:954:C:P	2.26	0.45
55:AA:1308:U:C5	55:AA:1309:A:N7	2.85	0.45
58:AD:291:PHE:O	58:AD:307:LYS:NZ	2.49	0.45
1:A:2061:C:O2	1:A:2061:C:O4'	2.35	0.45
1:A:2268:G:N7	11:M:44:ARG:NH1	2.59	0.45
1:A:2401:A:OP2	3:D:262:ARG:NH1	2.50	0.45
19:U:56:TYR:CE2	19:U:60:ILE:HD12	2.52	0.45
25:0:112:GLU:O	25:0:114:GLY:N	2.50	0.45
33:8:160:GLU:OE1	39:e:207:ASN:ND2	2.48	0.45
55:AA:1263:G:O6	55:AA:1329:U:C4	2.70	0.45
78:AX:360:TYR:O	78:AX:364:ASN:N	2.50	0.45
7:I:179:GLY:O	7:I:186:LEU:N	2.49	0.44
19:U:44:ILE:HD12	19:U:95:ALA:HB2	1.99	0.44
32:7:167:VAL:HG13	32:7:168:ARG:N	2.32	0.44
55:AA:1014:A:O2'	55:AA:1031:G:O5'	2.34	0.44
71:AQ:60:CYS:SG	83:A2:27:LEU:HD21	2.58	0.44
75:AU:57:MET:HE3	75:AU:57:MET:HA	1.98	0.44
82:A1:214:LEU:HD12	82:A1:217:GLN:NE2	2.32	0.44
1:A:2050:A:O2'	41:g:105:ARG:NH2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1626:C:N4	14:P:86:GLN:OE1	2.50	0.44
55:AA:965:C:O2'	55:AA:966:A:OP1	2.31	0.44
55:AA:974:U:N3	55:AA:1031:G:C6	2.86	0.44
55:AA:1134:G:N7	64:AJ:35:GLN:NE2	2.65	0.44
55:AA:1296:A:O5'	56:AB:170:TYR:OH	2.25	0.44
55:AA:1431:G:N2	55:AA:1458:A:OP2	2.46	0.44
55:AA:1492:A:N6	55:AA:1556:C:OP2	2.50	0.44
1:A:1902:C:HO2'	1:A:1903:C:P	2.41	0.44
61:AG:263:ASP:O	61:AG:265:GLN:N	2.50	0.44
75:AU:33:PRO:O	75:AU:34:LEU:O	2.35	0.44
9:K:171:THR:O	9:K:171:THR:OG1	2.33	0.44
55:AA:1032:C:O2	55:AA:1032:C:H2'	2.17	0.44
62:AH:135:GLU:OE2	65:AK:128:TRP:N	2.39	0.44
74:AT:95:ASN:OD1	74:AT:96:LYS:N	2.48	0.44
13:O:129:CYS:SG	25:O:156:THR:OG1	2.61	0.44
55:AA:1181:G:H2'	55:AA:1182:C:O4'	2.17	0.44
1:A:2184:A:C2	1:A:2185:G:N7	2.86	0.44
1:A:2370:A:HO2'	1:A:2371:U:H6	1.64	0.44
16:R:41:LEU:O	16:R:45:THR:OG1	2.33	0.44
52:s:243:ILE:HD12	52:s:296:HIS:CD2	2.52	0.44
65:AK:56:SER:O	65:AK:60:ASN:ND2	2.51	0.44
72:AR:258:LYS:O	72:AR:260:ASP:N	2.51	0.44
85:A4:532:LEU:HD11	85:A4:555:ILE:HG21	1.99	0.44
1:A:2080:U:O2	1:A:2080:U:O4'	2.36	0.44
10:L:112:GLY:HA2	10:L:113:ASN:C	2.43	0.44
45:k:37:VAL:O	45:k:38:SER:OG	2.27	0.44
55:AA:1203:C:C2	55:AA:1204:C:C5	3.06	0.44
55:AA:1214:A:O5'	55:AA:1351:G:N2	2.51	0.44
55:AA:1577:U:O4	55:AA:1578:A:N6	2.46	0.44
61:AG:278:THR:O	61:AG:278:THR:OG1	2.34	0.44
55:AA:790:A:O2'	55:AA:791:G:O3'	2.34	0.44
55:AA:955:A:N3	55:AA:955:A:H2'	2.33	0.44
78:AX:184:ALA:O	78:AX:188:LEU:HD23	2.18	0.44
1:A:1755:A:O2'	6:H:64:LEU:O	2.36	0.44
4:E:323:GLY:HA2	4:E:324:ASP:HB2	1.99	0.44
5:F:192:SER:O	5:F:194:GLU:N	2.51	0.44
36:b:58:ASN:OD1	36:b:58:ASN:N	2.51	0.44
55:AA:795:A:H3'	55:AA:796:G:C4'	2.47	0.44
55:AA:1162:A:O2'	55:AA:1163:C:P	2.73	0.44
55:AA:1257:U:O4	55:AA:1260:A:N6	2.51	0.44
55:AA:1303:G:HO2'	55:AA:1320:G:HO2'	1.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:AU:73:GLU:OE1	81:A0:166:TYR:OH	2.26	0.44
76:AV:159:ASP:OD1	76:AV:160:ALA:N	2.51	0.44
1:A:2060:A:O4'	1:A:2079:C:N4	2.51	0.43
9:K:3:SER:HB2	37:c:299:VAL:HG13	2.00	0.43
52:s:361:ILE:C	52:s:361:ILE:HD12	2.44	0.43
55:AA:1265:C:OP1	65:AK:112:ARG:NH1	2.49	0.43
69:AO:107:ILE:CD1	69:AO:150:LEU:HD11	2.48	0.43
85:A4:482:ILE:HB	85:A4:483:PRO:HD3	1.99	0.43
1:A:2632:A:O2'	1:A:2635:G:N3	2.48	0.43
1:A:3049:U:O4	1:A:3053:A:N7	2.51	0.43
22:X:28:TYR:OH	22:X:206:LEU:O	2.31	0.43
51:r:85:ASP:OD1	51:r:85:ASP:N	2.50	0.43
55:AA:1262:C:N3	55:AA:1334:G:N1	2.66	0.43
67:AM:105:THR:HG21	75:AU:56:LEU:HD13	2.00	0.43
70:AP:125:LYS:NZ	70:AP:132:ASP:OD1	2.51	0.43
71:AQ:30:LEU:HD23	71:AQ:35:LEU:HB2	2.00	0.43
1:A:2694:A:N3	1:A:2942:C:O2'	2.43	0.43
18:T:203:LEU:O	18:T:206:ARG:NE	2.50	0.43
19:U:10:TYR:OH	19:U:12:LEU:O	2.30	0.43
55:AA:991:G:HO2'	55:AA:992:U:C5'	2.31	0.43
55:AA:1207:U:O4	55:AA:1358:A:N6	2.52	0.43
75:AU:57:MET:HE2	81:A0:201:TRP:CB	2.47	0.43
1:A:2846:G:N3	1:A:2895:U:N3	2.67	0.43
1:A:3131:G:H2'	1:A:3132:G:O4'	2.19	0.43
55:AA:1134:G:OP2	64:AJ:38:ARG:NH1	2.50	0.43
67:AM:97:PHE:CD1	75:AU:70:LEU:HD13	2.53	0.43
81:A0:192:ASN:OD1	81:A0:192:ASN:N	2.49	0.43
1:A:2157:U:OP1	51:r:182:ARG:NH1	2.51	0.43
13:O:82:GLU:O	13:O:84:ASP:N	2.48	0.43
22:X:160:ASP:OD1	22:X:163:ARG:NH1	2.51	0.43
27:2:82:ARG:NH1	27:2:89:SER:O	2.51	0.43
43:i:105:ASP:OD1	43:i:106:ASP:N	2.51	0.43
55:AA:1154:A:N6	55:AA:1579:C:OP1	2.46	0.43
55:AA:1372:C:HO2'	55:AA:1373:U:H6	1.63	0.43
80:AZ:23:THR:OG1	80:AZ:24:ARG:N	2.51	0.43
1:A:2233:U:N3	1:A:2688:C:OP1	2.47	0.43
1:A:2363:A:HO2'	1:A:2364:C:P	2.41	0.43
18:T:55:ASN:O	38:d:227:ARG:NH1	2.51	0.43
52:s:347:SER:OG	52:s:348:GLU:N	2.49	0.43
55:AA:1441:A:N6	55:AA:1447:G:OP2	2.51	0.43
58:AD:250:GLY:N	58:AD:326:LEU:O	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
68:AN:19:GLY:O	68:AN:27:LYS:N	2.48	0.43
5:F:66:VAL:O	5:F:77:VAL:N	2.51	0.43
16:R:32:ARG:NH1	25:0:88:GLU:OE1	2.50	0.43
16:R:83:TYR:OH	16:R:99:ARG:NH1	2.51	0.43
55:AA:1508:C:O2'	55:AA:1509:U:O5'	2.32	0.43
1:A:1915:C:O2'	1:A:1916:G:O5'	2.33	0.43
1:A:2525:C:OP2	1:A:2526:C:O2'	2.32	0.43
4:E:231:HIS:N	4:E:232:GLY:HA2	2.34	0.43
24:Z:113:VAL:O	24:Z:116:LEU:N	2.46	0.43
67:AM:105:THR:HG21	75:AU:56:LEU:HD22	2.00	0.43
85:A4:331:UNK:N	85:A4:359:UNK:O	2.52	0.43
1:A:1805:A:H4'	1:A:1806:U:OP1	2.18	0.43
1:A:2562:U:O2'	3:D:284:ARG:N	2.51	0.43
42:h:64:GLU:O	42:h:65:ASP:HB2	2.19	0.43
45:k:80:HIS:O	51:r:36:ARG:NE	2.51	0.43
55:AA:713:C:H2'	55:AA:714:A:O5'	2.19	0.43
55:AA:1125:A:OP2	59:AE:123:ARG:NH2	2.52	0.43
65:AK:125:ARG:O	65:AK:127:THR:N	2.52	0.43
1:A:1806:U:H1'	1:A:1807:U:OP2	2.19	0.43
20:V:197:GLU:OE1	23:Y:95:ASN:ND2	2.52	0.43
55:AA:1017:A:P	55:AA:1018:G:HO2'	2.29	0.43
55:AA:1464:G:H2'	55:AA:1465:C:C6	2.54	0.43
1:A:1939:G:N3	1:A:1939:G:H3'	2.34	0.42
1:A:2684:C:P	25:0:86:THR:HG21	2.59	0.42
17:S:201:ALA:O	17:S:203:CYS:N	2.52	0.42
62:AH:123:SER:OG	62:AH:124:VAL:N	2.51	0.42
1:A:1740:A:OP2	1:A:1741:A:O2'	2.29	0.42
22:X:54:PRO:O	22:X:56:ASN:N	2.52	0.42
55:AA:713:C:H42	75:AU:27:ARG:HB2	1.84	0.42
57:AC:117:LEU:HD22	57:AC:151:VAL:HG13	1.99	0.42
79:AY:314:PRO:O	79:AY:316:ASN:N	2.52	0.42
12:N:211:ASN:ND2	12:N:213:TRP:O	2.50	0.42
30:5:377:ASP:OD2	30:5:413:LYS:NZ	2.51	0.42
6:H:57:GLU:O	6:H:81:LYS:N	2.52	0.42
17:S:102:ALA:O	17:S:104:ARG:N	2.49	0.42
34:9:18:MET:SD	34:9:18:MET:N	2.92	0.42
76:AV:102:TRP:CG	76:AV:103:TYR:H	2.38	0.42
1:A:2326:C:O2'	13:O:31:ASN:OD1	2.26	0.42
1:A:2756:C:OP1	6:H:121:ASN:ND2	2.44	0.42
10:L:75:LEU:HD23	10:L:77:ILE:HD11	2.02	0.42
10:L:123:ILE:HD12	10:L:141:ALA:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:9:87:THR:OG1	34:9:88:ALA:N	2.53	0.42
55:AA:986:G:O2'	55:AA:987:A:O4'	2.38	0.42
56:AB:103:GLU:OE1	73:AS:52:ARG:NH2	2.51	0.42
72:AR:265:THR:OG1	72:AR:266:ARG:N	2.52	0.42
1:A:2441:C:O2'	52:s:85:LYS:O	2.37	0.42
61:AG:301:GLN:HG2	78:AX:390:LEU:HD21	2.01	0.42
66:AL:209:LEU:HD11	84:A3:177:TRP:NE1	2.34	0.42
69:AO:90:THR:HG23	69:AO:138:PRO:HA	2.00	0.42
79:AY:312:GLU:N	79:AY:312:GLU:OE1	2.52	0.42
1:A:1984:A:N3	1:A:1984:A:H2'	2.34	0.42
1:A:2017:U:OP1	11:M:54:LYS:NZ	2.35	0.42
1:A:2060:A:O2'	1:A:2061:C:O5'	2.38	0.42
23:Y:94:SER:OG	23:Y:95:ASN:N	2.53	0.42
30:5:380:GLN:O	30:5:381:LEU:O	2.37	0.42
32:7:308:ALA:O	32:7:310:PHE:N	2.53	0.42
48:o:88:ILE:O	48:o:88:ILE:HG22	2.19	0.42
55:AA:704:U:N3	81:A0:138:ASP:OD2	2.52	0.42
1:A:1721:C:O2'	43:i:123:ARG:NH2	2.53	0.42
57:AC:70:SER:OG	65:AK:119:GLN:O	2.16	0.42
82:A1:125:ALA:HB2	85:A4:77:THR:HG21	2.01	0.42
1:A:1847:U:O2'	1:A:1848:U:O5'	2.38	0.42
1:A:2254:C:O2'	44:j:38:SER:O	2.38	0.42
1:A:2319:A:H4'	13:O:42:ILE:HG23	2.01	0.42
1:A:2692:G:N1	1:A:2696:A:OP2	2.50	0.42
1:A:3170:C:O2	1:A:3170:C:O4'	2.37	0.42
3:D:66:TRP:O	3:D:68:SER:N	2.52	0.42
31:6:192:GLU:N	31:6:192:GLU:OE1	2.53	0.42
66:AL:143:LEU:HD12	66:AL:156:LEU:HD13	2.02	0.42
73:AS:110:GLY:O	73:AS:112:THR:N	2.45	0.42
78:AX:282:ILE:HG22	78:AX:283:ALA:N	2.35	0.42
78:AX:340:PHE:CD1	82:A1:316:VAL:HG11	2.55	0.42
82:A1:77:LYS:O	82:A1:81:VAL:HG23	2.20	0.42
1:A:1690:C:O2	23:Y:216:ARG:NH1	2.53	0.42
5:F:289:PRO:O	5:F:291:SER:N	2.53	0.42
65:AK:62:ILE:O	65:AK:63:LEU:O	2.38	0.42
1:A:2909:G:O2'	54:u:1:C:N4	2.52	0.41
5:F:284:TYR:HD2	5:F:288:LEU:HD22	1.84	0.41
24:Z:108:ALA:O	24:Z:112:VAL:HG23	2.20	0.41
55:AA:797:C:O2	55:AA:798:C:C5	2.73	0.41
82:A1:83:LEU:O	82:A1:85:VAL:N	2.53	0.41
11:M:153:ASN:ND2	11:M:255:MET:SD	2.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:5:277:THR:OG1	30:5:278:GLY:N	2.53	0.41
55:AA:1012:A:N3	55:AA:1065:C:N4	2.68	0.41
55:AA:1138:G:O2'	55:AA:1139:A:C5'	2.69	0.41
75:AU:117:HIS:CE1	75:AU:121:ILE:HD11	2.55	0.41
76:AV:235:GLU:OE1	76:AV:255:TYR:OH	2.37	0.41
1:A:1939:G:O2'	1:A:1973:G:O5'	2.38	0.41
1:A:2898:U:O2	1:A:2898:U:O4'	2.37	0.41
36:b:115:ILE:O	36:b:116:ARG:O	2.39	0.41
55:AA:749:G:H2'	55:AA:750:A:H8	1.84	0.41
57:AC:77:ASP:OD1	57:AC:77:ASP:N	2.52	0.41
58:AD:331:ASP:N	58:AD:331:ASP:OD1	2.51	0.41
68:AN:95:VAL:O	68:AN:96:THR:OG1	2.34	0.41
81:A0:97:LEU:HD12	81:A0:100:VAL:HG22	2.02	0.41
1:A:3040:G:O4'	1:A:3069:A:O2'	2.38	0.41
1:A:3093:C:N4	1:A:3094:G:O6	2.53	0.41
5:F:282:PRO:O	5:F:284:TYR:N	2.48	0.41
7:I:167:ILE:O	7:I:170:THR:HG22	2.21	0.41
11:M:140:LEU:HD23	11:M:141:VAL:N	2.35	0.41
12:N:137:GLY:O	12:N:138:HIS:ND1	2.53	0.41
30:5:203:CYS:O	52:s:179:GLN:NE2	2.49	0.41
52:s:239:ASN:OD1	52:s:239:ASN:N	2.53	0.41
52:s:408:ASN:N	52:s:408:ASN:OD1	2.54	0.41
55:AA:833:A:HO2'	55:AA:834:G:P	2.38	0.41
55:AA:1031:G:C2	55:AA:1032:C:C6	3.08	0.41
55:AA:1151:C:O2	55:AA:1151:C:O4'	2.37	0.41
1:A:2481:A:H2'	1:A:2482:A:C2	2.56	0.41
1:A:3036:G:C6	1:A:3047:G:O6	2.74	0.41
1:A:3175:A:OP2	1:A:3187:C:N4	2.51	0.41
55:AA:1261:C:O2'	58:AD:100:LYS:O	2.39	0.41
81:A0:63:ARG:NE	81:A0:135:MET:O	2.54	0.41
1:A:1837:C:O2	1:A:1837:C:O4'	2.38	0.41
4:E:323:GLY:CA	4:E:324:ASP:C	2.93	0.41
18:T:211:THR:O	18:T:211:THR:HG23	2.21	0.41
37:c:265:THR:O	37:c:265:THR:HG22	2.20	0.41
52:s:228:ASP:N	52:s:228:ASP:OD1	2.54	0.41
55:AA:892:A:OP1	64:AJ:77:ASN:ND2	2.53	0.41
55:AA:985:U:O4	55:AA:986:G:N1	2.53	0.41
55:AA:1308:U:H5	55:AA:1309:A:H62	1.69	0.41
56:AB:224:ASP:N	56:AB:227:CYS:SG	2.94	0.41
59:AE:41:ASN:ND2	75:AU:180:ALA:O	2.54	0.41
61:AG:248:VAL:HG23	61:AG:249:THR:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2237:A:O4'	1:A:2701:G:O2'	2.39	0.41
1:A:2481:A:H4'	1:A:2482:A:OP1	2.21	0.41
1:A:2508:C:H2'	1:A:2509:A:O4'	2.20	0.41
4:E:243:VAL:HG11	4:E:251:VAL:HG22	2.02	0.41
6:H:85:ASP:OD1	6:H:86:THR:N	2.54	0.41
36:b:115:ILE:O	36:b:116:ARG:HG2	2.20	0.41
43:i:64:GLY:O	43:i:65:ASN:ND2	2.54	0.41
55:AA:953:U:C2'	55:AA:954:C:OP2	2.67	0.41
55:AA:1014:A:C5	55:AA:1031:G:N7	2.89	0.41
55:AA:1101:U:OP2	55:AA:1104:A:N6	2.53	0.41
79:AY:349:HIS:NE2	80:AZ:24:ARG:O	2.44	0.41
81:A0:82:ARG:O	81:A0:86:LEU:HD13	2.20	0.41
81:A0:184:THR:OG1	81:A0:185:SER:N	2.54	0.41
1:A:1953:A:N6	1:A:1965:A:H61	2.19	0.41
1:A:2371:U:O2	1:A:2371:U:O2'	2.34	0.41
1:A:2530:A:C4'	1:A:2531:U:OP2	2.69	0.41
1:A:3043:C:O2	1:A:3043:C:H2'	2.21	0.41
3:D:194:ASN:O	3:D:243:THR:OG1	2.38	0.41
4:E:133:THR:OG1	4:E:144:THR:OG1	2.38	0.41
44:j:28:ARG:NH1	44:j:35:ALA:O	2.49	0.41
52:s:98:PHE:HA	52:s:306:LEU:HD11	2.02	0.41
55:AA:819:A:OP1	55:AA:829:C:N4	2.54	0.41
55:AA:996:A:H61	55:AA:1075:A:H4'	1.84	0.41
55:AA:1052:C:O3'	55:AA:1053:A:O4'	2.39	0.41
55:AA:1190:C:C2'	55:AA:1191:C:O5'	2.68	0.41
62:AH:87:VAL:HG22	82:A1:109:PRO:HG3	2.02	0.41
69:AO:228:SER:OG	69:AO:229:GLY:N	2.53	0.41
74:AT:20:ASN:OD1	74:AT:20:ASN:N	2.52	0.41
75:AU:34:LEU:O	75:AU:34:LEU:HD12	2.21	0.41
1:A:2083:U:H2'	1:A:2084:A:O4'	2.20	0.41
1:A:2135:A:N3	1:A:2135:A:H2'	2.35	0.41
1:A:2144:A:N6	1:A:2257:C:H42	2.19	0.41
45:k:61:GLU:O	45:k:63:CYS:N	2.54	0.41
55:AA:1056:A:O2'	55:AA:1577:U:O2'	1.94	0.41
1:A:1742:G:O2'	1:A:1754:G:O6	2.36	0.40
1:A:1800:G:N2	1:A:1803:A:OP2	2.52	0.40
1:A:1818:A:O2'	18:T:95:ARG:NH2	2.54	0.40
1:A:1994:A:N6	1:A:2736:C:O4'	2.53	0.40
1:A:2825:G:O6	1:A:2844:G:C6	2.74	0.40
1:A:2961:C:O2	1:A:2961:C:H2'	2.20	0.40
9:K:13:THR:OG1	36:b:130:TRP:O	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:3:110:VAL:HG13	28:3:158:LEU:HD22	2.03	0.40
55:AA:700:A:H61	55:AA:712:C:H5	1.67	0.40
55:AA:1574:G:N1	55:AA:1592:U:O4	2.54	0.40
61:AG:305:PRO:O	61:AG:310:ARG:NH2	2.53	0.40
1:A:3212:C:O2	1:A:3212:C:O4'	2.40	0.40
5:F:187:LEU:O	42:h:114:ASN:ND2	2.54	0.40
61:AG:112:PHE:N	61:AG:113:PRO:HD3	2.36	0.40
65:AK:38:VAL:HG22	80:AZ:52:TYR:HB2	2.04	0.40
80:AZ:90:GLY:CA	80:AZ:91:LYS:HB2	2.51	0.40
1:A:2317:G:O6	1:A:2450:A:N6	2.55	0.40
1:A:2400:C:O2'	1:A:2401:A:O5'	2.39	0.40
1:A:3051:A:N6	1:A:3115:U:O2'	2.54	0.40
55:AA:974:U:O4	55:AA:1031:G:O6	2.39	0.40
79:AY:318:GLU:O	79:AY:320:GLY:N	2.54	0.40
1:A:1851:G:C1'	1:A:2134:A:N6	2.84	0.40
1:A:3212:C:O2'	25:0:106:ASN:OD1	2.17	0.40
14:P:103:SER:O	14:P:134:ARG:NH1	2.49	0.40
38:d:137:PHE:N	38:d:138:PRO:CD	2.84	0.40
52:s:243:ILE:N	52:s:294:TYR:O	2.49	0.40
55:AA:991:G:H2'	55:AA:992:U:C6	2.56	0.40
55:AA:1017:A:N3	70:AP:108:THR:OG1	2.55	0.40
72:AR:135:ARG:NH1	72:AR:236:GLU:OE2	2.55	0.40
5:F:106:PHE:CD2	5:F:106:PHE:C	2.99	0.40
10:L:89:HIS:ND1	10:L:91:MET:O	2.51	0.40
12:N:191:SER:OG	12:N:192:ARG:N	2.54	0.40
55:AA:840:A:N3	75:AU:27:ARG:NH1	2.69	0.40
55:AA:1204:C:C4	55:AA:1205:U:C4	3.09	0.40
55:AA:1391:U:H2'	55:AA:1392:A:O4'	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	234/305 (77%)	197 (84%)	35 (15%)	2 (1%)	14	49
4	E	296/348 (85%)	253 (86%)	34 (12%)	9 (3%)	3	22
5	F	248/311 (80%)	209 (84%)	30 (12%)	9 (4%)	2	20
6	H	93/267 (35%)	85 (91%)	7 (8%)	1 (1%)	11	45
7	I	154/261 (59%)	140 (91%)	12 (8%)	2 (1%)	9	41
8	J	138/192 (72%)	119 (86%)	16 (12%)	3 (2%)	5	29
9	K	175/178 (98%)	152 (87%)	18 (10%)	5 (3%)	3	23
10	L	113/145 (78%)	93 (82%)	17 (15%)	3 (3%)	4	25
11	M	285/296 (96%)	240 (84%)	36 (13%)	9 (3%)	3	21
12	N	203/251 (81%)	181 (89%)	20 (10%)	2 (1%)	12	47
13	O	150/175 (86%)	132 (88%)	15 (10%)	3 (2%)	6	31
14	P	129/180 (72%)	114 (88%)	12 (9%)	3 (2%)	5	28
15	Q	217/219 (99%)	180 (83%)	29 (13%)	8 (4%)	2	19
16	R	138/149 (93%)	125 (91%)	12 (9%)	1 (1%)	18	55
17	S	154/205 (75%)	132 (86%)	19 (12%)	3 (2%)	6	32
18	T	164/206 (80%)	148 (90%)	12 (7%)	4 (2%)	4	27
19	U	109/153 (71%)	92 (84%)	15 (14%)	2 (2%)	6	33
20	V	183/216 (85%)	151 (82%)	24 (13%)	8 (4%)	2	17
21	W	109/148 (74%)	94 (86%)	12 (11%)	3 (3%)	4	24
22	X	241/243 (99%)	201 (83%)	32 (13%)	8 (3%)	3	21
23	Y	174/250 (70%)	157 (90%)	14 (8%)	3 (2%)	7	35
24	Z	118/161 (73%)	100 (85%)	14 (12%)	4 (3%)	3	20
25	0	106/188 (56%)	89 (84%)	14 (13%)	3 (3%)	4	24
26	1	50/65 (77%)	43 (86%)	4 (8%)	3 (6%)	1	13
27	2	44/92 (48%)	40 (91%)	4 (9%)	0	100	100
28	3	93/188 (50%)	86 (92%)	7 (8%)	0	100	100
29	4	34/103 (33%)	33 (97%)	1 (3%)	0	100	100
30	5	368/394 (93%)	308 (84%)	47 (13%)	13 (4%)	3	20
31	6	313/380 (82%)	258 (82%)	45 (14%)	10 (3%)	3	21
32	7	258/338 (76%)	217 (84%)	36 (14%)	5 (2%)	6	32
33	8	97/206 (47%)	88 (91%)	9 (9%)	0	100	100
34	9	105/137 (77%)	90 (86%)	12 (11%)	3 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	a	78/142 (55%)	72 (92%)	5 (6%)	1 (1%)	9	41
36	b	146/215 (68%)	128 (88%)	16 (11%)	2 (1%)	9	39
37	c	271/332 (82%)	233 (86%)	31 (11%)	7 (3%)	4	25
38	d	156/306 (51%)	132 (85%)	20 (13%)	4 (3%)	4	25
39	e	211/279 (76%)	188 (89%)	20 (10%)	3 (1%)	9	39
40	f	125/212 (59%)	106 (85%)	17 (14%)	2 (2%)	7	36
41	g	127/166 (76%)	106 (84%)	18 (14%)	3 (2%)	4	27
42	h	96/158 (61%)	80 (83%)	11 (12%)	5 (5%)	1	15
43	i	95/128 (74%)	76 (80%)	16 (17%)	3 (3%)	3	21
44	j	83/123 (68%)	77 (93%)	5 (6%)	1 (1%)	10	42
45	k	82/112 (73%)	62 (76%)	12 (15%)	8 (10%)	0	7
46	l	21/138 (15%)	21 (100%)	0	0	100	100
47	m	43/128 (34%)	38 (88%)	5 (12%)	0	100	100
48	o	92/102 (90%)	80 (87%)	8 (9%)	4 (4%)	2	17
49	p	119/206 (58%)	109 (92%)	10 (8%)	0	100	100
50	q	126/222 (57%)	118 (94%)	8 (6%)	0	100	100
51	r	140/196 (71%)	121 (86%)	13 (9%)	6 (4%)	2	17
52	s	366/439 (83%)	315 (86%)	44 (12%)	7 (2%)	6	32
56	AB	215/296 (73%)	186 (86%)	27 (13%)	2 (1%)	14	49
57	AC	130/167 (78%)	97 (75%)	31 (24%)	2 (2%)	8	38
58	AD	316/430 (74%)	255 (81%)	46 (15%)	15 (5%)	2	16
59	AE	120/125 (96%)	87 (72%)	25 (21%)	8 (7%)	1	12
60	AF	197/242 (81%)	168 (85%)	25 (13%)	4 (2%)	6	31
61	AG	301/396 (76%)	245 (81%)	45 (15%)	11 (4%)	2	19
62	AH	120/201 (60%)	93 (78%)	24 (20%)	3 (2%)	4	26
63	AI	134/194 (69%)	106 (79%)	24 (18%)	4 (3%)	3	22
64	AJ	106/138 (77%)	83 (78%)	20 (19%)	3 (3%)	4	24
65	AK	99/128 (77%)	86 (87%)	7 (7%)	6 (6%)	1	13
66	AL	162/257 (63%)	137 (85%)	19 (12%)	6 (4%)	2	19
67	AM	114/137 (83%)	93 (82%)	17 (15%)	4 (4%)	3	20
68	AN	105/130 (81%)	82 (78%)	19 (18%)	4 (4%)	2	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	AO	183/185 (99%)	141 (77%)	33 (18%)	9 (5%)	1	16
70	AP	94/142 (66%)	73 (78%)	18 (19%)	3 (3%)	3	21
71	AQ	84/86 (98%)	77 (92%)	6 (7%)	1 (1%)	10	42
72	AR	240/360 (67%)	171 (71%)	55 (23%)	14 (6%)	1	14
73	AS	124/190 (65%)	102 (82%)	14 (11%)	8 (6%)	1	13
74	AT	160/173 (92%)	130 (81%)	21 (13%)	9 (6%)	1	14
75	AU	171/205 (83%)	152 (89%)	13 (8%)	6 (4%)	3	20
76	AV	320/414 (77%)	267 (83%)	43 (13%)	10 (3%)	3	22
77	AW	95/187 (51%)	65 (68%)	23 (24%)	7 (7%)	1	10
78	AX	310/398 (78%)	253 (82%)	46 (15%)	11 (4%)	3	20
79	AY	106/395 (27%)	86 (81%)	14 (13%)	6 (6%)	1	14
80	AZ	85/106 (80%)	74 (87%)	9 (11%)	2 (2%)	4	27
81	A0	197/225 (88%)	152 (77%)	29 (15%)	16 (8%)	1	9
82	A1	252/323 (78%)	198 (79%)	45 (18%)	9 (4%)	2	20
83	A2	114/118 (97%)	89 (78%)	20 (18%)	5 (4%)	2	17
84	A3	67/199 (34%)	58 (87%)	8 (12%)	1 (2%)	8	38
85	A4	237/474 (50%)	222 (94%)	12 (5%)	3 (1%)	9	41
All	All	12628/17575 (72%)	10637 (84%)	1611 (13%)	380 (3%)	5	22

All (380) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	W	73	PHE
22	X	69	ILE
22	X	149	PRO
30	5	263	ILE
30	5	296	LYS
30	5	381	LEU
30	5	383	TYR
32	7	251	ILE
36	b	116	ARG
39	e	174	PRO
40	f	90	VAL
42	h	65	ASP
45	k	38	SER
58	AD	290	ILE

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Mol	Chain	Res	Type
59	AE	15	ARG
59	AE	71	PRO
61	AG	137	ALA
64	AJ	70	PRO
70	AP	130	LEU
72	AR	259	TYR
73	AS	29	PRO
74	AT	137	ARG
75	AU	34	LEU
80	AZ	41	PRO
82	A1	97	MET
83	A2	112	PRO
85	A4	536	ALA
4	E	317	PRO
4	E	325	GLU
5	F	193	LEU
5	F	291	SER
7	I	102	VAL
8	J	27	GLY
8	J	70	ILE
11	M	280	LYS
15	Q	106	LEU
15	Q	127	SER
18	T	81	LYS
20	V	105	ARG
22	X	18	GLU
22	X	81	GLY
24	Z	133	ASN
25	0	113	CYS
25	0	116	LEU
34	9	133	ARG
37	c	65	ASN
37	c	123	GLN
38	d	272	PRO
39	e	84	TYR
40	f	190	THR
41	g	145	GLY
42	h	147	ASN
45	k	18	VAL
48	o	81	LYS
48	o	101	TRP
51	r	187	TYR

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Mol	Chain	Res	Type
52	s	250	PHE
52	s	407	ASP
56	AB	173	GLY
58	AD	129	GLY
58	AD	233	ALA
61	AG	256	LEU
61	AG	325	LYS
61	AG	392	THR
65	AK	82	SER
65	AK	126	ALA
66	AL	120	GLU
66	AL	199	ALA
67	AM	62	GLY
67	AM	124	LYS
69	AO	55	PRO
69	AO	82	LYS
72	AR	163	TYR
72	AR	204	ILE
72	AR	256	ARG
73	AS	30	LEU
73	AS	46	PHE
73	AS	56	ALA
73	AS	112	THR
74	AT	133	LYS
74	AT	144	GLU
75	AU	30	ARG
75	AU	38	LYS
76	AV	216	LYS
77	AW	153	PHE
78	AX	60	GLY
78	AX	156	PRO
78	AX	257	HIS
78	AX	301	TRP
78	AX	342	PRO
78	AX	345	VAL
79	AY	333	PHE
79	AY	343	LYS
81	A0	147	GLU
81	A0	151	THR
82	A1	138	ASP
82	A1	208	LYS
82	A1	249	GLU

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Mol	Chain	Res	Type
83	A2	42	GLU
85	A4	60	PRO
3	D	179	GLY
4	E	79	PRO
4	E	326	GLU
5	F	290	TYR
10	L	37	ARG
11	M	47	ARG
11	M	134	ARG
11	M	242	TYR
13	O	128	ASN
15	Q	76	LEU
16	R	134	ASP
19	U	38	ASP
20	V	100	LYS
20	V	101	THR
20	V	117	HIS
21	W	72	HIS
21	W	127	TYR
23	Y	162	ARG
24	Z	134	MET
24	Z	143	GLY
26	1	60	LYS
30	5	35	VAL
30	5	297	ALA
30	5	419	LEU
31	6	72	ARG
31	6	359	HIS
32	7	309	HIS
32	7	310	PHE
37	c	183	GLU
37	c	311	ARG
38	d	187	GLU
39	e	117	ALA
41	g	55	THR
41	g	70	SER
42	h	77	VAL
45	k	39	SER
45	k	59	GLY
45	k	73	ARG
48	o	61	GLY
56	AB	174	GLY

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Mol	Chain	Res	Type
57	AC	47	GLY
58	AD	94	THR
58	AD	127	ASN
58	AD	128	ARG
58	AD	193	TRP
58	AD	283	GLU
58	AD	288	HIS
58	AD	299	LYS
58	AD	428	ALA
59	AE	67	ASP
59	AE	101	GLU
60	AF	37	TYR
60	AF	129	ALA
60	AF	198	ARG
61	AG	387	ALA
62	AH	147	HIS
63	AI	60	PHE
63	AI	145	ILE
65	AK	47	TYR
65	AK	58	ARG
66	AL	86	ASP
66	AL	96	GLU
67	AM	56	PRO
68	AN	59	THR
68	AN	74	ALA
69	AO	53	ASP
69	AO	97	ARG
72	AR	162	SER
72	AR	200	GLU
72	AR	202	ARG
72	AR	238	ASP
74	AT	20	ASN
74	AT	52	ILE
74	AT	132	ARG
75	AU	37	SER
76	AV	196	PHE
76	AV	215	GLN
76	AV	327	LEU
77	AW	116	PHE
77	AW	144	LEU
78	AX	64	GLU
78	AX	234	ARG

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Mol	Chain	Res	Type
78	AX	276	ARG
79	AY	315	ILE
79	AY	329	HIS
81	A0	9	ARG
81	A0	45	PHE
81	A0	149	ALA
81	A0	163	SER
81	A0	195	ARG
82	A1	100	GLU
82	A1	137	LEU
82	A1	302	GLU
83	A2	39	GLU
85	A4	66	ASP
4	E	77	LEU
4	E	126	ASP
4	E	127	CYS
5	F	59	ARG
5	F	123	GLY
6	H	64	LEU
8	J	36	GLY
9	K	24	LYS
9	K	151	ILE
9	K	153	LYS
10	L	112	GLY
11	M	260	LYS
11	M	279	ASP
11	M	287	ASP
13	O	15	PHE
13	O	111	PRO
14	P	173	GLU
15	Q	212	ASN
18	T	69	ARG
19	U	34	ALA
20	V	53	ASP
20	V	118	ARG
20	V	141	GLY
22	X	34	GLU
22	X	220	GLU
23	Y	183	GLN
25	0	163	GLU
30	5	272	ASP
30	5	348	ASP

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Mol	Chain	Res	Type
30	5	420	HIS
31	6	130	VAL
31	6	307	HIS
31	6	314	ALA
31	6	373	HIS
32	7	62	THR
32	7	270	PRO
34	9	39	LYS
35	a	44	ASN
38	d	269	TRP
42	h	66	LEU
43	i	84	LYS
44	j	40	TYR
45	k	48	ASN
45	k	60	SER
48	o	13	PRO
51	r	55	ALA
51	r	61	PRO
51	r	158	SER
52	s	254	ASP
52	s	272	PRO
57	AC	81	HIS
58	AD	104	ALA
58	AD	147	PRO
59	AE	106	GLU
61	AG	232	GLN
61	AG	261	GLN
62	AH	64	THR
62	AH	75	ARG
63	AI	183	HIS
67	AM	95	GLY
72	AR	184	ALA
72	AR	291	ARG
72	AR	292	ASP
73	AS	59	PRO
73	AS	108	LYS
74	AT	138	GLU
76	AV	173	PHE
76	AV	174	GLU
76	AV	242	ALA
76	AV	325	SER
77	AW	130	ASP

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Mol	Chain	Res	Type
77	AW	166	ASN
78	AX	54	ASN
81	A0	129	ARG
82	A1	96	PRO
5	F	91	PRO
9	K	148	PRO
11	M	38	ARG
12	N	111	ARG
14	P	87	HIS
15	Q	171	VAL
17	S	94	ARG
17	S	138	ALA
18	T	79	GLN
18	T	158	TYR
20	V	171	ILE
22	X	52	ILE
31	6	165	ALA
37	c	64	PRO
37	c	314	TRP
38	d	208	VAL
42	h	139	LYS
43	i	82	GLY
43	i	127	PHE
51	r	64	PRO
52	s	152	GLN
58	AD	213	GLU
59	AE	32	ARG
61	AG	146	PRO
61	AG	336	GLY
61	AG	375	ARG
64	AJ	75	SER
64	AJ	116	GLN
65	AK	63	LEU
65	AK	99	GLY
66	AL	69	PRO
66	AL	123	ARG
69	AO	92	LYS
69	AO	219	LEU
72	AR	86	ASN
73	AS	94	SER
75	AU	167	PHE
76	AV	176	PRO

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Mol	Chain	Res	Type
77	AW	146	ASP
79	AY	294	LEU
79	AY	337	HIS
81	A0	32	GLN
81	A0	111	HIS
81	A0	143	PRO
81	A0	165	PRO
81	A0	185	SER
4	E	329	PRO
5	F	124	GLY
5	F	128	TRP
11	M	265	ILE
12	N	56	ALA
17	S	202	PRO
23	Y	81	SER
24	Z	146	VAL
26	1	63	ARG
31	6	228	PRO
31	6	351	HIS
52	s	203	ARG
52	s	264	ILE
59	AE	33	GLY
59	AE	122	LYS
68	AN	56	GLN
70	AP	63	LYS
72	AR	93	PRO
76	AV	102	TRP
77	AW	156	ALA
81	A0	92	PRO
81	A0	124	THR
83	A2	60	GLU
3	D	207	ILE
5	F	86	VAL
7	I	61	HIS
9	K	129	PRO
10	L	132	GLY
14	P	177	ILE
15	Q	124	PRO
15	Q	226	PRO
15	Q	228	PRO
30	5	286	PRO
34	9	121	PRO

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Mol	Chain	Res	Type
61	AG	154	GLY
74	AT	74	PRO
81	A0	80	VAL
82	A1	75	PRO
4	E	228	PRO
26	1	62	ILE
30	5	270	ILE
31	6	378	GLY
36	b	20	GLY
51	r	185	VAL
58	AD	389	GLY
70	AP	61	PRO
71	AQ	83	PRO
72	AR	173	VAL
75	AU	39	ILE
84	A3	181	GLY
22	X	181	PRO
30	5	68	PRO
37	c	162	GLY
60	AF	165	GLY
63	AI	144	VAL
68	AN	70	PRO
69	AO	200	TYR
69	AO	209	PRO
74	AT	105	ILE
80	AZ	90	GLY
45	k	78	GLY
69	AO	198	PRO
78	AX	56	PRO
83	A2	14	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	190/245 (78%)	190 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	255/290 (88%)	255 (100%)	0	100	100
5	F	217/262 (83%)	217 (100%)	0	100	100
6	H	86/228 (38%)	84 (98%)	2 (2%)	44	63
7	I	145/232 (62%)	145 (100%)	0	100	100
8	J	113/150 (75%)	113 (100%)	0	100	100
9	K	155/156 (99%)	155 (100%)	0	100	100
10	L	98/124 (79%)	98 (100%)	0	100	100
11	M	245/249 (98%)	245 (100%)	0	100	100
12	N	172/211 (82%)	170 (99%)	2 (1%)	63	73
13	O	133/150 (89%)	132 (99%)	1 (1%)	73	77
14	P	115/155 (74%)	115 (100%)	0	100	100
15	Q	201/201 (100%)	201 (100%)	0	100	100
16	R	118/126 (94%)	117 (99%)	1 (1%)	73	77
17	S	141/180 (78%)	140 (99%)	1 (1%)	76	79
18	T	146/176 (83%)	146 (100%)	0	100	100
19	U	99/135 (73%)	98 (99%)	1 (1%)	68	76
20	V	169/191 (88%)	169 (100%)	0	100	100
21	W	91/119 (76%)	91 (100%)	0	100	100
22	X	219/219 (100%)	219 (100%)	0	100	100
23	Y	159/223 (71%)	159 (100%)	0	100	100
24	Z	111/147 (76%)	111 (100%)	0	100	100
25	0	97/164 (59%)	97 (100%)	0	100	100
26	1	49/60 (82%)	49 (100%)	0	100	100
27	2	40/72 (56%)	40 (100%)	0	100	100
28	3	88/166 (53%)	88 (100%)	0	100	100
29	4	35/89 (39%)	35 (100%)	0	100	100
30	5	337/353 (96%)	335 (99%)	2 (1%)	78	80
31	6	266/332 (80%)	266 (100%)	0	100	100
32	7	242/303 (80%)	241 (100%)	1 (0%)	84	82
33	8	91/190 (48%)	91 (100%)	0	100	100
34	9	91/112 (81%)	91 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	a	78/133 (59%)	78 (100%)	0	100	100
36	b	130/186 (70%)	130 (100%)	0	100	100
37	c	241/288 (84%)	241 (100%)	0	100	100
38	d	151/274 (55%)	151 (100%)	0	100	100
39	e	188/236 (80%)	188 (100%)	0	100	100
40	f	117/188 (62%)	117 (100%)	0	100	100
41	g	119/148 (80%)	118 (99%)	1 (1%)	73	77
42	h	95/148 (64%)	95 (100%)	0	100	100
43	i	86/110 (78%)	85 (99%)	1 (1%)	63	73
44	j	68/97 (70%)	68 (100%)	0	100	100
45	k	74/90 (82%)	74 (100%)	0	100	100
46	l	23/116 (20%)	23 (100%)	0	100	100
47	m	40/113 (35%)	40 (100%)	0	100	100
48	o	80/87 (92%)	79 (99%)	1 (1%)	61	72
49	p	117/181 (65%)	117 (100%)	0	100	100
50	q	110/178 (62%)	110 (100%)	0	100	100
51	r	133/169 (79%)	133 (100%)	0	100	100
52	s	326/381 (86%)	326 (100%)	0	100	100
56	AB	191/249 (77%)	190 (100%)	1 (0%)	81	81
57	AC	115/143 (80%)	115 (100%)	0	100	100
58	AD	269/357 (75%)	269 (100%)	0	100	100
59	AE	104/107 (97%)	104 (100%)	0	100	100
60	AF	178/209 (85%)	178 (100%)	0	100	100
61	AG	265/342 (78%)	265 (100%)	0	100	100
62	AH	112/180 (62%)	112 (100%)	0	100	100
63	AI	104/147 (71%)	104 (100%)	0	100	100
64	AJ	93/118 (79%)	93 (100%)	0	100	100
65	AK	91/113 (80%)	90 (99%)	1 (1%)	65	74
66	AL	152/226 (67%)	151 (99%)	1 (1%)	76	79
67	AM	95/113 (84%)	95 (100%)	0	100	100
68	AN	93/115 (81%)	91 (98%)	2 (2%)	45	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	AO	166/166 (100%)	164 (99%)	2 (1%)	63	73
70	AP	87/123 (71%)	87 (100%)	0	100	100
71	AQ	78/78 (100%)	77 (99%)	1 (1%)	61	72
72	AR	224/318 (70%)	224 (100%)	0	100	100
73	AS	109/164 (66%)	109 (100%)	0	100	100
74	AT	150/157 (96%)	149 (99%)	1 (1%)	76	79
75	AU	149/174 (86%)	149 (100%)	0	100	100
76	AV	295/364 (81%)	294 (100%)	1 (0%)	86	84
77	AW	84/158 (53%)	84 (100%)	0	100	100
78	AX	275/351 (78%)	275 (100%)	0	100	100
79	AY	99/357 (28%)	99 (100%)	0	100	100
80	AZ	80/95 (84%)	80 (100%)	0	100	100
81	A0	176/196 (90%)	175 (99%)	1 (1%)	78	80
82	A1	237/291 (81%)	236 (100%)	1 (0%)	84	82
83	A2	99/101 (98%)	98 (99%)	1 (1%)	68	76
84	A3	63/166 (38%)	62 (98%)	1 (2%)	55	69
85	A4	226/291 (78%)	225 (100%)	1 (0%)	84	82
All	All	11349/15102 (75%)	11320 (100%)	29 (0%)	84	84

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	H	56	VAL
6	H	64	LEU
12	N	59	VAL
12	N	87	PHE
13	O	144	LEU
16	R	45	THR
17	S	103	SER
19	U	17	LEU
30	5	98	LEU
30	5	382	LEU
32	7	251	ILE
41	g	108	THR
43	i	35	ARG
48	o	27	VAL

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Mol	Chain	Res	Type
56	AB	257	ILE
65	AK	63	LEU
66	AL	185	LEU
68	AN	25	THR
68	AN	95	VAL
69	AO	94	CYS
69	AO	143	CYS
71	AQ	49	CYS
74	AT	71	THR
76	AV	266	VAL
81	A0	64	LEU
82	A1	68	SER
83	A2	70	ILE
84	A3	194	ILE
85	A4	463	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (80) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	263	ASN
4	E	72	GLN
7	I	43	GLN
7	I	193	ASN
8	J	48	GLN
9	K	94	GLN
10	L	33	GLN
10	L	103	ASN
11	M	264	GLN
12	N	202	GLN
15	Q	158	GLN
15	Q	258	GLN
16	R	12	ASN
17	S	105	GLN
18	T	62	GLN
18	T	109	ASN
18	T	132	HIS
18	T	159	HIS
20	V	119	GLN
22	X	175	GLN
23	Y	122	GLN
23	Y	179	HIS
23	Y	195	ASN

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Mol	Chain	Res	Type
23	Y	225	ASN
31	6	354	GLN
32	7	84	ASN
32	7	284	HIS
34	9	52	GLN
34	9	134	ASN
35	a	111	GLN
36	b	120	HIS
37	c	315	ASN
39	e	67	GLN
39	e	95	ASN
41	g	81	ASN
41	g	93	ASN
41	g	121	GLN
42	h	110	HIS
45	k	46	ASN
46	l	135	ASN
47	m	59	GLN
49	p	104	HIS
49	p	163	GLN
51	r	79	HIS
52	s	339	GLN
52	s	420	GLN
56	AB	69	HIS
57	AC	81	HIS
57	AC	130	HIS
58	AD	165	GLN
58	AD	308	GLN
58	AD	317	HIS
58	AD	415	GLN
58	AD	424	ASN
59	AE	54	HIS
61	AG	90	ASN
61	AG	127	HIS
61	AG	261	GLN
62	AH	109	HIS
63	AI	163	HIS
64	AJ	77	ASN
66	AL	99	ASN
67	AM	106	ASN
69	AO	114	HIS
72	AR	76	GLN

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Mol	Chain	Res	Type
74	AT	51	ASN
75	AU	31	HIS
76	AV	380	GLN
77	AW	106	HIS
77	AW	135	GLN
78	AX	66	GLN
78	AX	349	ASN
79	AY	316	ASN
80	AZ	56	HIS
81	A0	111	HIS
82	A1	217	GLN
82	A1	218	ASN
83	A2	90	GLN
84	A3	190	GLN
85	A4	417	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1458/1472 (99%)	332 (22%)	23 (1%)
2	B	51/56 (91%)	9 (17%)	1 (1%)
54	u	1/2 (50%)	0	0
55	AA	914/923 (99%)	366 (40%)	24 (2%)
All	All	2424/2453 (98%)	707 (29%)	48 (1%)

All (707) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1672	C
1	A	1676	A
1	A	1677	C
1	A	1678	C
1	A	1679	U
1	A	1680	A
1	A	1689	C
1	A	1694	U
1	A	1700	U
1	A	1702	A
1	A	1704	U
1	A	1708	A
1	A	1709	G

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Mol	Chain	Res	Type
1	A	1713	A
1	A	1714	C
1	A	1715	C
1	A	1716	U
1	A	1717	U
1	A	1724	A
1	A	1725	C
1	A	1727	A
1	A	1728	U
1	A	1731	A
1	A	1732	C
1	A	1748	G
1	A	1750	G
1	A	1751	A
1	A	1767	G
1	A	1770	G
1	A	1781	A
1	A	1782	G
1	A	1794	A
1	A	1800	G
1	A	1803	A
1	A	1804	A
1	A	1805	A
1	A	1806	U
1	A	1807	U
1	A	1808	A
1	A	1809	U
1	A	1810	A
1	A	1812	C
1	A	1817	C
1	A	1818	A
1	A	1823	A
1	A	1824	U
1	A	1827	C
1	A	1828	A
1	A	1829	A
1	A	1832	A
1	A	1836	A
1	A	1839	C
1	A	1844	A
1	A	1849	C
1	A	1852	C

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Mol	Chain	Res	Type
1	A	1853	A
1	A	1854	U
1	A	1855	A
1	A	1856	A
1	A	1867	A
1	A	1869	A
1	A	1871	A
1	A	1872	U
1	A	1882	A
1	A	1883	G
1	A	1886	G
1	A	1893	A
1	A	1902	C
1	A	1903	C
1	A	1909	A
1	A	1915	C
1	A	1917	A
1	A	1918	G
1	A	1940	A
1	A	1944	C
1	A	1946	C
1	A	1985	G
1	A	1987	G
1	A	1992	C
1	A	1994	A
1	A	1995	A
1	A	2000	C
1	A	2010	U
1	A	2015	G
1	A	2016	C
1	A	2021	U
1	A	2022	G
1	A	2029	A
1	A	2031	A
1	A	2037	U
1	A	2039	A
1	A	2053	U
1	A	2055	U
1	A	2058	C
1	A	2060	A
1	A	2061	C
1	A	2065	A

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Mol	Chain	Res	Type
1	A	2066	C
1	A	2074	A
1	A	2079	C
1	A	2090	A
1	A	2093	U
1	A	2094	G
1	A	2096	U
1	A	2097	A
1	A	2098	G
1	A	2111	C
1	A	2113	G
1	A	2124	A
1	A	2125	C
1	A	2126	U
1	A	2142	A
1	A	2147	G
1	A	2160	A
1	A	2163	A
1	A	2166	C
1	A	2170	G
1	A	2171	U
1	A	2172	A
1	A	2173	G
1	A	2174	G
1	A	2180	A
1	A	2182	G
1	A	2183	C
1	A	2184	A
1	A	2187	C
1	A	2190	C
1	A	2192	A
1	A	2193	U
1	A	2194	U
1	A	2197	G
1	A	2198	A
1	A	2201	G
1	A	2204	U
1	A	2210	C
1	A	2229	A
1	A	2230	A
1	A	2237	A
1	A	2239	A

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Mol	Chain	Res	Type
1	A	2241	A
1	A	2243	A
1	A	2244	U
1	A	2245	A
1	A	2246	A
1	A	2262	C
1	A	2263	C
1	A	2264	A
1	A	2284	C
1	A	2297	A
1	A	2300	G
1	A	2315	A
1	A	2322	C
1	A	2331	C
1	A	2332	C
1	A	2335	A
1	A	2342	U
1	A	2345	G
1	A	2364	C
1	A	2370	A
1	A	2371	U
1	A	2374	A
1	A	2379	C
1	A	2384	A
1	A	2387	U
1	A	2390	A
1	A	2393	C
1	A	2396	C
1	A	2404	U
1	A	2407	U
1	A	2426	C
1	A	2434	A
1	A	2443	C
1	A	2444	A
1	A	2447	A
1	A	2458	A
1	A	2469	A
1	A	2473	A
1	A	2478	G
1	A	2482	A
1	A	2484	C
1	A	2485	U

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Mol	Chain	Res	Type
1	A	2493	C
1	A	2500	A
1	A	2501	C
1	A	2508	C
1	A	2511	C
1	A	2520	C
1	A	2521	A
1	A	2522	U
1	A	2524	A
1	A	2527	A
1	A	2530	A
1	A	2531	U
1	A	2540	C
1	A	2544	C
1	A	2546	G
1	A	2556	A
1	A	2557	C
1	A	2558	A
1	A	2559	U
1	A	2560	G
1	A	2564	A
1	A	2570	C
1	A	2592	G
1	A	2593	G
1	A	2594	U
1	A	2599	U
1	A	2601	A
1	A	2603	C
1	A	2607	U
1	A	2618	U
1	A	2623	A
1	A	2625	C
1	A	2626	U
1	A	2627	G
1	A	2629	A
1	A	2630	U
1	A	2632	A
1	A	2633	A
1	A	2634	U
1	A	2635	G
1	A	2645	G
1	A	2656	U

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Mol	Chain	Res	Type
1	A	2660	U
1	A	2683	C
1	A	2686	G
1	A	2693	A
1	A	2694	A
1	A	2696	A
1	A	2706	A
1	A	2709	A
1	A	2718	C
1	A	2719	G
1	A	2722	A
1	A	2723	A
1	A	2724	G
1	A	2725	A
1	A	2731	U
1	A	2732	G
1	A	2738	U
1	A	2740	A
1	A	2744	U
1	A	2748	A
1	A	2757	A
1	A	2758	G
1	A	2803	A
1	A	2804	A
1	A	2808	U
1	A	2810	G
1	A	2814	G
1	A	2831	G
1	A	2832	A
1	A	2833	A
1	A	2844	G
1	A	2847	C
1	A	2853	A
1	A	2854	U
1	A	2859	A
1	A	2864	U
1	A	2865	C
1	A	2871	U
1	A	2900	C
1	A	2906	C
1	A	2910	A
1	A	2912	C

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Mol	Chain	Res	Type
1	A	2913	A
1	A	2916	G
1	A	2917	G
1	A	2918	A
1	A	2923	G
1	A	2926	A
1	A	2928	C
1	A	2935	A
1	A	2936	U
1	A	2946	A
1	A	2955	U
1	A	2962	C
1	A	2963	A
1	A	2977	G
1	A	2986	C
1	A	2989	G
1	A	2990	A
1	A	2991	U
1	A	2994	U
1	A	3000	A
1	A	3005	A
1	A	3007	C
1	A	3010	G
1	A	3016	G
1	A	3021	C
1	A	3022	G
1	A	3029	A
1	A	3040	G
1	A	3041	U
1	A	3042	U
1	A	3043	C
1	A	3049	U
1	A	3052	A
1	A	3053	A
1	A	3054	G
1	A	3060	C
1	A	3065	U
1	A	3069	A
1	A	3070	G
1	A	3072	U
1	A	3073	C
1	A	3093	C

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Mol	Chain	Res	Type
1	A	3096	U
1	A	3098	U
1	A	3100	U
1	A	3109	U
1	A	3114	U
1	A	3123	G
1	A	3129	A
1	A	3140	A
1	A	3150	U
1	A	3155	C
1	A	3157	C
1	A	3158	A
1	A	3160	A
1	A	3168	C
1	A	3169	C
1	A	3172	C
1	A	3180	A
1	A	3184	C
1	A	3189	C
1	A	3190	A
1	A	3196	G
1	A	3202	U
1	A	3217	A
1	A	3218	A
1	A	3228	U
2	B	1608	G
2	B	1611	G
2	B	1614	U
2	B	1615	A
2	B	1624	C
2	B	1625	A
2	B	1644	G
2	B	1645	A
2	B	1659	U
55	AA	650	U
55	AA	652	G
55	AA	655	U
55	AA	662	U
55	AA	667	U
55	AA	668	U
55	AA	671	U
55	AA	675	A

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Mol	Chain	Res	Type
55	AA	679	C
55	AA	680	U
55	AA	686	A
55	AA	688	A
55	AA	689	U
55	AA	690	U
55	AA	691	A
55	AA	692	C
55	AA	696	U
55	AA	700	A
55	AA	704	U
55	AA	705	C
55	AA	706	C
55	AA	710	U
55	AA	711	U
55	AA	712	C
55	AA	714	A
55	AA	718	A
55	AA	720	U
55	AA	721	U
55	AA	722	C
55	AA	723	A
55	AA	724	C
55	AA	729	U
55	AA	730	A
55	AA	734	C
55	AA	742	U
55	AA	745	A
55	AA	746	A
55	AA	753	A
55	AA	760	A
55	AA	761	A
55	AA	764	A
55	AA	770	C
55	AA	771	A
55	AA	773	U
55	AA	776	A
55	AA	781	A
55	AA	782	A
55	AA	787	C
55	AA	791	G
55	AA	792	C

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Mol	Chain	Res	Type
55	AA	793	C
55	AA	795	A
55	AA	796	G
55	AA	797	C
55	AA	803	C
55	AA	805	C
55	AA	806	C
55	AA	807	A
55	AA	808	C
55	AA	812	A
55	AA	814	A
55	AA	816	A
55	AA	826	A
55	AA	828	C
55	AA	829	C
55	AA	831	U
55	AA	832	U
55	AA	834	G
55	AA	836	A
55	AA	837	A
55	AA	838	U
55	AA	839	A
55	AA	840	A
55	AA	843	G
55	AA	846	A
55	AA	847	G
55	AA	851	A
55	AA	852	A
55	AA	861	U
55	AA	865	A
55	AA	868	C
55	AA	871	A
55	AA	877	G
55	AA	878	G
55	AA	879	U
55	AA	882	A
55	AA	883	U
55	AA	884	U
55	AA	886	C
55	AA	887	G
55	AA	890	C
55	AA	891	C

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Mol	Chain	Res	Type
55	AA	892	A
55	AA	895	C
55	AA	896	A
55	AA	897	C
55	AA	904	C
55	AA	905	A
55	AA	909	G
55	AA	919	A
55	AA	922	C
55	AA	925	U
55	AA	934	G
55	AA	938	A
55	AA	939	A
55	AA	942	A
55	AA	944	U
55	AA	945	G
55	AA	947	U
55	AA	948	U
55	AA	950	A
55	AA	953	U
55	AA	954	C
55	AA	955	A
55	AA	966	A
55	AA	967	A
55	AA	969	A
55	AA	973	C
55	AA	975	A
55	AA	980	U
55	AA	983	C
55	AA	984	C
55	AA	986	G
55	AA	987	A
55	AA	990	U
55	AA	991	G
55	AA	992	U
55	AA	993	A
55	AA	994	A
55	AA	995	A
55	AA	997	A
55	AA	998	A
55	AA	1001	C
55	AA	1003	A

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Mol	Chain	Res	Type
55	AA	1004	G
55	AA	1007	G
55	AA	1012	A
55	AA	1014	A
55	AA	1015	A
55	AA	1016	U
55	AA	1019	A
55	AA	1022	A
55	AA	1031	G
55	AA	1039	A
55	AA	1041	A
55	AA	1042	U
55	AA	1046	A
55	AA	1048	C
55	AA	1049	A
55	AA	1054	A
55	AA	1055	U
55	AA	1065	C
55	AA	1066	C
55	AA	1068	A
55	AA	1069	A
55	AA	1070	C
55	AA	1071	U
55	AA	1074	G
55	AA	1075	A
55	AA	1078	A
55	AA	1079	G
55	AA	1080	A
55	AA	1081	U
55	AA	1082	A
55	AA	1085	C
55	AA	1086	C
55	AA	1093	C
55	AA	1098	C
55	AA	1099	C
55	AA	1102	A
55	AA	1103	A
55	AA	1105	C
55	AA	1106	C
55	AA	1107	U
55	AA	1109	A
55	AA	1113	G

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Mol	Chain	Res	Type
55	AA	1121	A
55	AA	1124	A
55	AA	1125	A
55	AA	1126	A
55	AA	1138	G
55	AA	1142	A
55	AA	1143	C
55	AA	1151	C
55	AA	1152	A
55	AA	1153	C
55	AA	1154	A
55	AA	1157	U
55	AA	1163	C
55	AA	1166	A
55	AA	1167	A
55	AA	1175	G
55	AA	1178	G
55	AA	1179	G
55	AA	1180	U
55	AA	1185	C
55	AA	1187	U
55	AA	1189	U
55	AA	1191	C
55	AA	1193	U
55	AA	1194	C
55	AA	1195	U
55	AA	1199	G
55	AA	1200	G
55	AA	1206	G
55	AA	1214	A
55	AA	1215	U
55	AA	1216	C
55	AA	1217	G
55	AA	1218	A
55	AA	1219	U
55	AA	1220	A
55	AA	1222	A
55	AA	1223	C
55	AA	1225	C
55	AA	1226	C
55	AA	1228	A
55	AA	1229	U

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Mol	Chain	Res	Type
55	AA	1230	C
55	AA	1231	A
55	AA	1232	A
55	AA	1233	C
55	AA	1234	C
55	AA	1235	U
55	AA	1238	C
55	AA	1240	A
55	AA	1242	C
55	AA	1243	U
55	AA	1245	U
55	AA	1246	U
55	AA	1247	G
55	AA	1248	C
55	AA	1250	C
55	AA	1251	A
55	AA	1254	C
55	AA	1258	A
55	AA	1259	U
55	AA	1260	A
55	AA	1269	U
55	AA	1271	C
55	AA	1272	A
55	AA	1273	G
55	AA	1282	G
55	AA	1283	A
55	AA	1284	U
55	AA	1285	G
55	AA	1287	A
55	AA	1291	U
55	AA	1292	A
55	AA	1293	C
55	AA	1294	A
55	AA	1299	A
55	AA	1300	A
55	AA	1303	G
55	AA	1306	A
55	AA	1307	G
55	AA	1309	A
55	AA	1312	C
55	AA	1314	C
55	AA	1315	G

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Mol	Chain	Res	Type
55	AA	1319	A
55	AA	1320	G
55	AA	1321	A
55	AA	1325	U
55	AA	1326	A
55	AA	1327	G
55	AA	1328	G
55	AA	1330	C
55	AA	1331	A
55	AA	1332	A
55	AA	1333	G
55	AA	1337	U
55	AA	1342	C
55	AA	1343	A
55	AA	1344	U
55	AA	1346	A
55	AA	1347	G
55	AA	1354	A
55	AA	1355	G
55	AA	1356	A
55	AA	1357	A
55	AA	1362	G
55	AA	1369	U
55	AA	1371	U
55	AA	1372	C
55	AA	1374	A
55	AA	1375	C
55	AA	1376	C
55	AA	1377	C
55	AA	1378	C
55	AA	1379	A
55	AA	1390	A
55	AA	1391	U
55	AA	1397	U
55	AA	1399	A
55	AA	1404	A
55	AA	1408	A
55	AA	1416	A
55	AA	1418	G
55	AA	1420	U
55	AA	1421	G
55	AA	1424	U

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Mol	Chain	Res	Type
55	AA	1425	U
55	AA	1427	A
55	AA	1430	A
55	AA	1431	G
55	AA	1438	A
55	AA	1441	A
55	AA	1442	G
55	AA	1443	U
55	AA	1461	A
55	AA	1478	A
55	AA	1479	C
55	AA	1481	C
55	AA	1482	A
55	AA	1483	C
55	AA	1485	G
55	AA	1487	C
55	AA	1492	A
55	AA	1493	C
55	AA	1494	C
55	AA	1495	C
55	AA	1512	A
55	AA	1516	G
55	AA	1517	A
55	AA	1523	A
55	AA	1524	A
55	AA	1525	C
55	AA	1526	U
55	AA	1527	A
55	AA	1528	A
55	AA	1529	A
55	AA	1531	C
55	AA	1532	C
55	AA	1533	C
55	AA	1535	U
55	AA	1536	A
55	AA	1537	C
55	AA	1538	G
55	AA	1539	C
55	AA	1540	A
55	AA	1542	U
55	AA	1543	U
55	AA	1547	U

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Mol	Chain	Res	Type
55	AA	1549	G
55	AA	1554	G
55	AA	1555	A
55	AA	1561	C
55	AA	1563	U
55	AA	1564	A
55	AA	1567	A
55	AA	1568	U
55	AA	1569	G
55	AA	1571	U
55	AA	1572	A
55	AA	1577	U
55	AA	1578	A
55	AA	1583	A
55	AA	1585	A
55	AA	1588	G
55	AA	1590	A
55	AA	1592	U
55	AA	1594	G
55	AA	1595	G
55	AA	1598	G
55	AA	1599	A

All (48) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1703	C
1	A	1713	A
1	A	1805	A
1	A	1806	U
1	A	1807	U
1	A	1809	U
1	A	1823	A
1	A	1870	A
1	A	1871	A
1	A	2165	C
1	A	2182	G
1	A	2243	A
1	A	2369	A
1	A	2457	A
1	A	2481	A
1	A	2507	A

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Mol	Chain	Res	Type
1	A	2530	A
1	A	2559	U
1	A	2905	A
1	A	2989	G
1	A	3041	U
1	A	3092	U
1	A	3201	A
2	B	1607	U
55	AA	661	C
55	AA	678	U
55	AA	685	A
55	AA	717	G
55	AA	833	A
55	AA	878	G
55	AA	918	A
55	AA	921	U
55	AA	943	G
55	AA	947	U
55	AA	953	U
55	AA	982	A
55	AA	986	G
55	AA	1102	A
55	AA	1162	A
55	AA	1174	U
55	AA	1190	C
55	AA	1198	A
55	AA	1234	C
55	AA	1314	C
55	AA	1336	G
55	AA	1355	G
55	AA	1522	U
55	AA	1562	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 134 ligands modelled in this entry, 134 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	14
85	A4	13
55	AA	8
2	B	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	2218:C	O3'	2228:A	P	41.52
1	A4	399:UNK	C	414:LYS	N	32.07
1	A	2760:A	O3'	2792:A	P	25.98
1	A	1760:G	O3'	1766:U	P	24.98
1	AA	955:A	O3'	965:C	P	24.64
1	A4	143:GLU	C	145:UNK	N	23.21
1	A4	345:UNK	C	353:UNK	N	20.50
1	A	3207:A	O3'	3212:C	P	20.24
1	A	2881:C	O3'	2889:C	P	19.29
1	A4	380:ASP	C	386:UNK	N	18.85
1	A	1732:C	O3'	1737:A	P	17.69
1	B	1651:A	O3'	1658:U	P	17.24
1	A	2067:C	O3'	2072:A	P	17.21

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	734:C	O3'	740:G	P	16.74
1	A4	326:UNK	C	331:UNK	N	16.54
1	AA	1518:C	O3'	1521:U	P	15.33
1	A4	300:UNK	C	311:UNK	N	14.86
1	A4	250:UNK	C	255:UNK	N	14.70
1	A	3196:G	O3'	3201:A	P	13.63
1	A	2351:U	O3'	2357:C	P	13.54
1	A	2575:U	O3'	2580:U	P	12.99
1	B	1616:A	O3'	1621:A	P	12.85
1	AA	1115:U	O3'	1120:C	P	12.23
1	A4	232:UNK	C	237:UNK	N	12.04
1	A	1935:A	O3'	1938:A	P	11.62
1	A4	269:UNK	C	272:UNK	N	11.20
1	A	3109:U	O3'	3113:A	P	10.96
1	A4	173:UNK	C	220:UNK	N	10.30
1	AA	928:A	O3'	931:C	P	9.92
1	A	2359:C	O3'	2363:A	P	9.53
1	A4	285:UNK	C	290:UNK	N	8.56
1	A4	362:UNK	C	368:SER	N	8.29
1	AA	1404:A	O3'	1407:U	P	7.70
1	AA	1556:C	O3'	1559:G	P	6.97
1	A	1709:G	O3'	1711:C	P	6.47
1	A4	156:UNK	C	161:UNK	N	6.24
1	AA	1383:A	O3'	1388:C	P	5.39
1	B	1646:U	O3'	1648:U	P	5.31
1	B	1661:A	O3'	1663:C	P	5.30

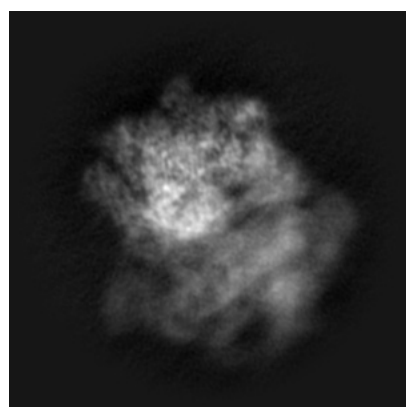
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0515. These allow visual inspection of the internal detail of the map and identification of artifacts.

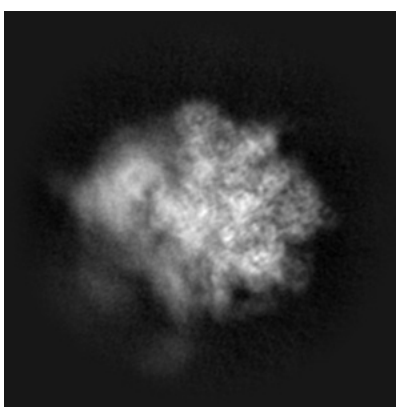
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

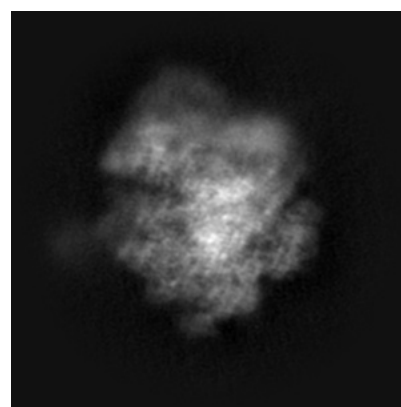
6.1.1 Primary map



X



Y

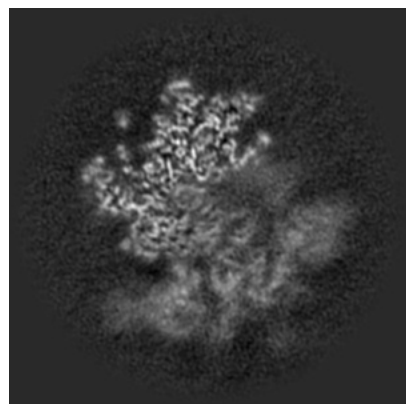


Z

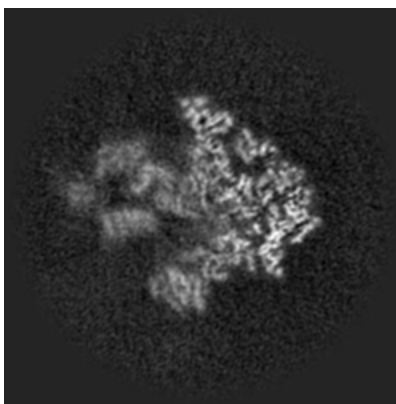
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

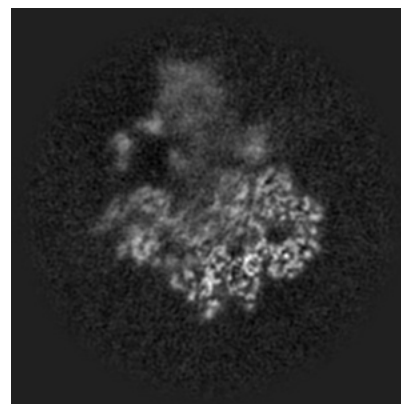
6.2.1 Primary map



X Index: 190



Y Index: 190

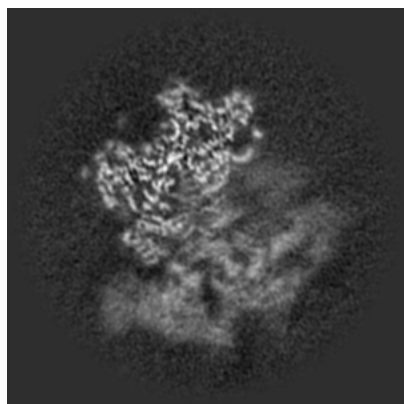


Z Index: 190

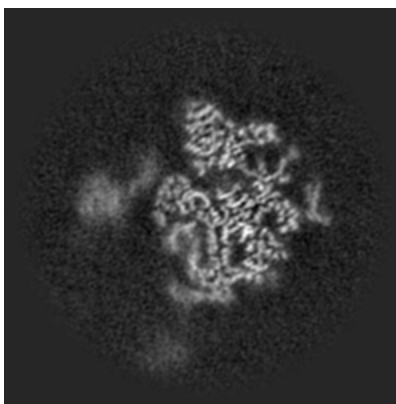
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

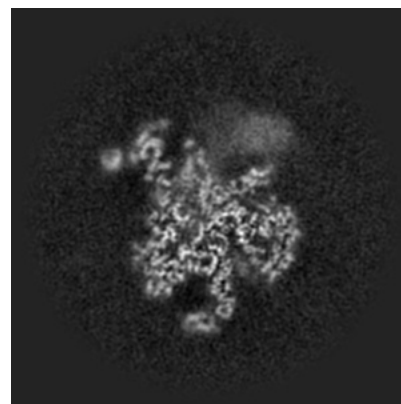
6.3.1 Primary map



X Index: 197



Y Index: 147

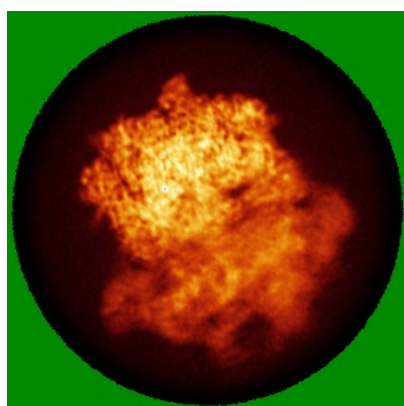


Z Index: 228

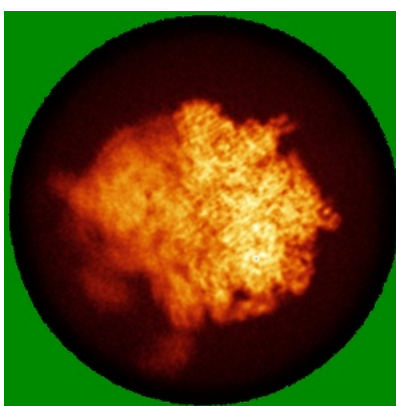
The images above show the largest variance slices of the map in three orthogonal directions.

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

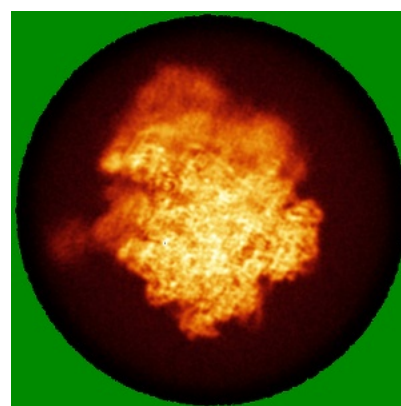
6.4.1 Primary map



X



Y



Z

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

This section was not generated.

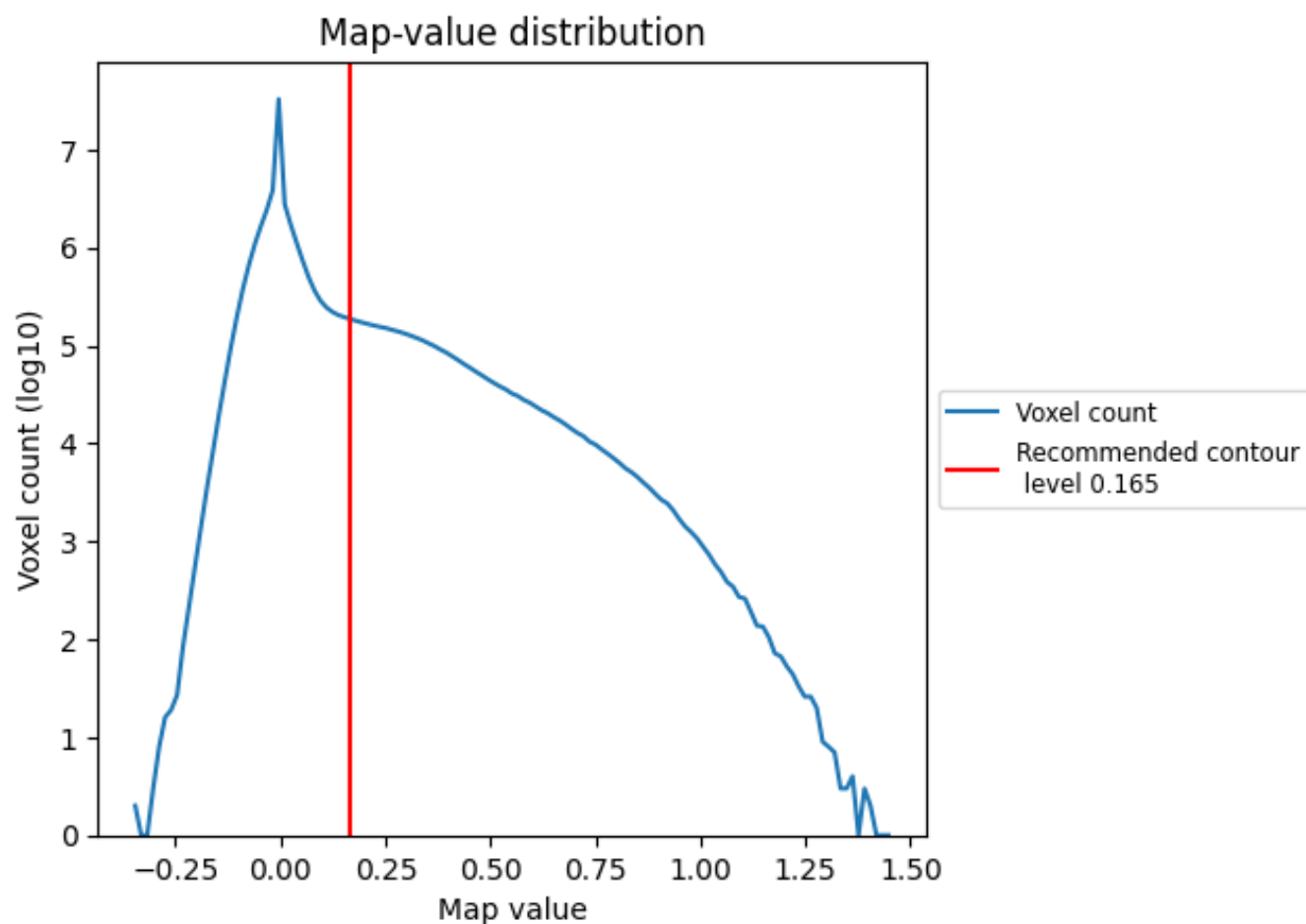
6.6 Mask visualisation

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

7 Map analysis [i](#)

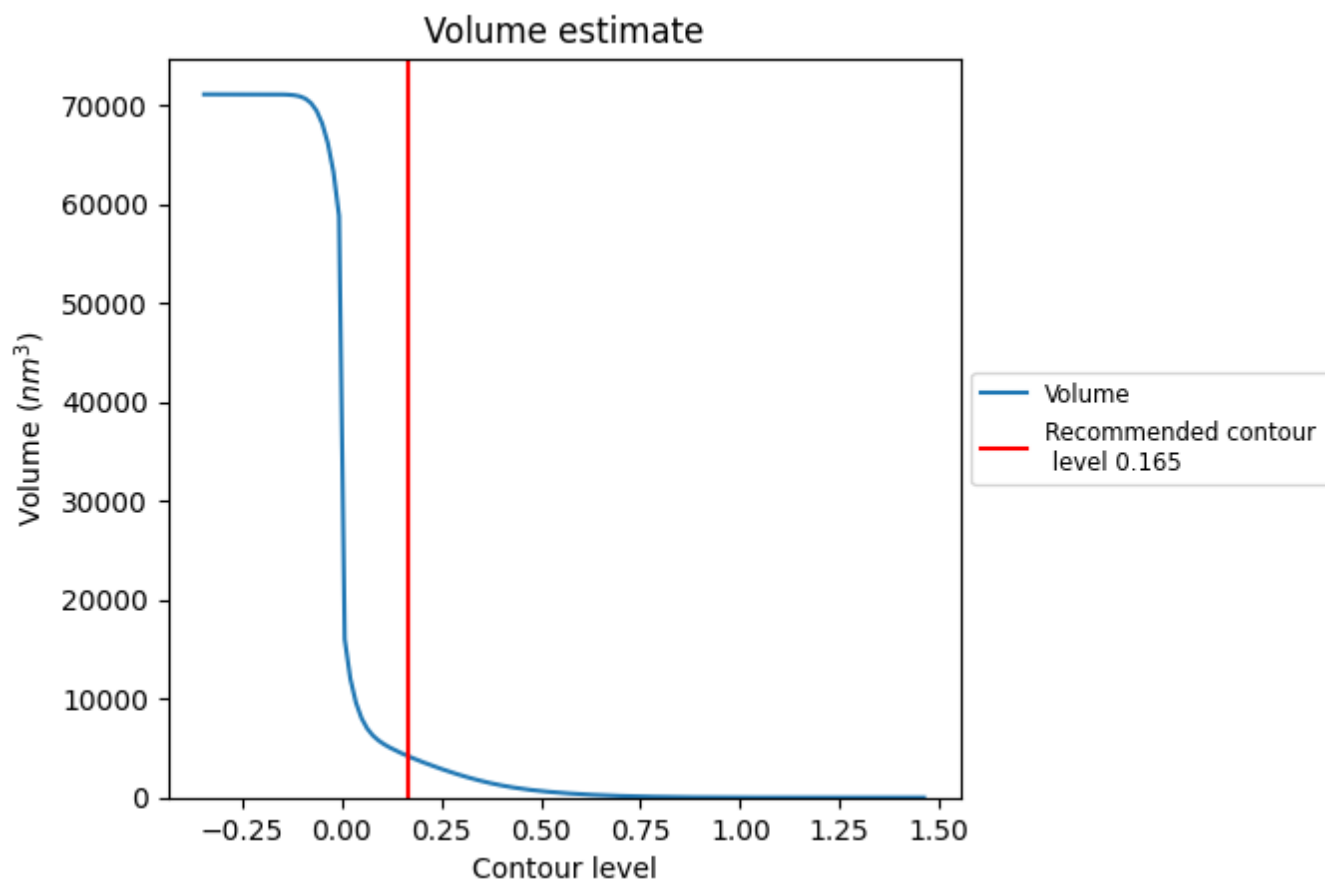
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

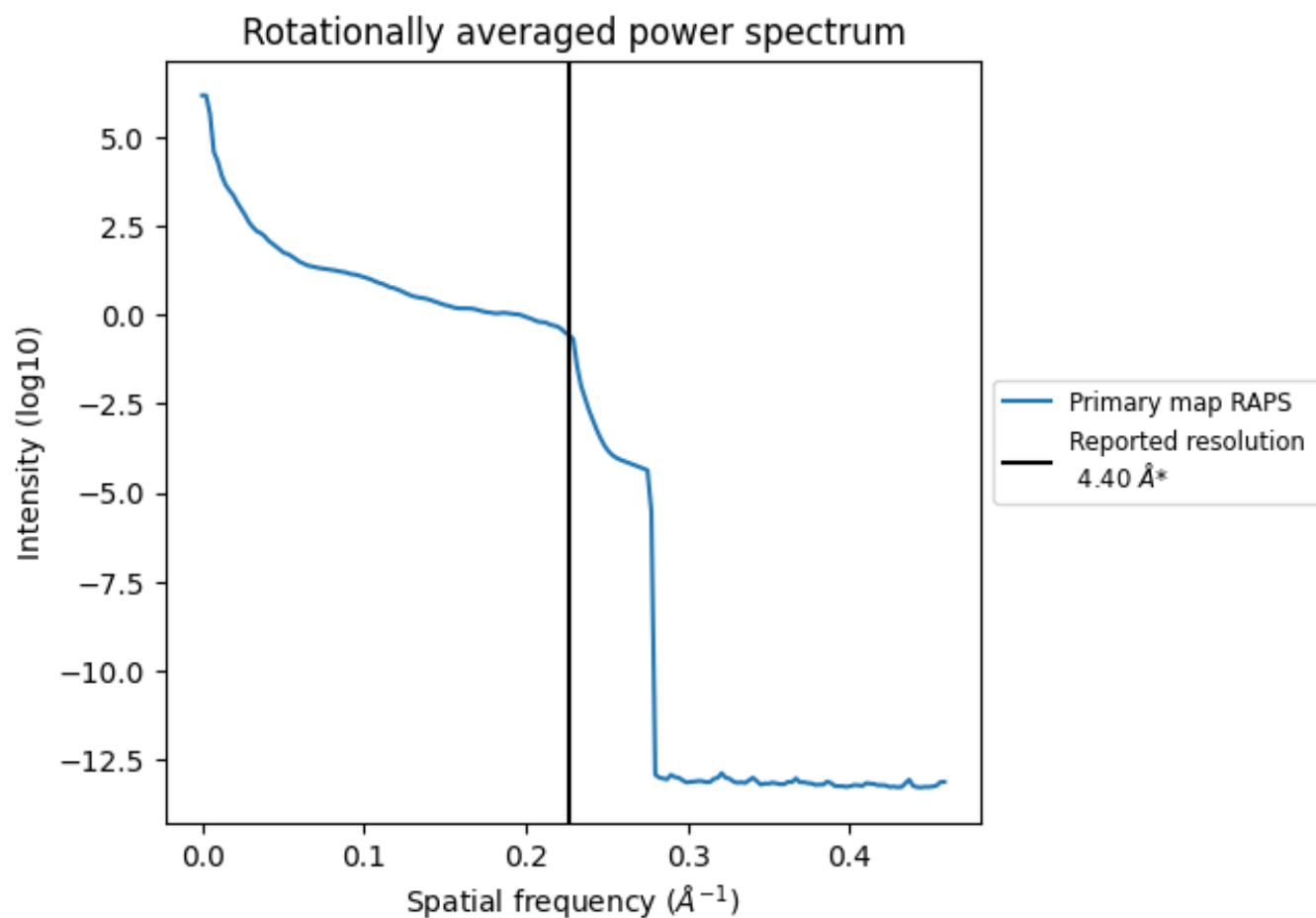
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4210 nm³; this corresponds to an approximate mass of 3803 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

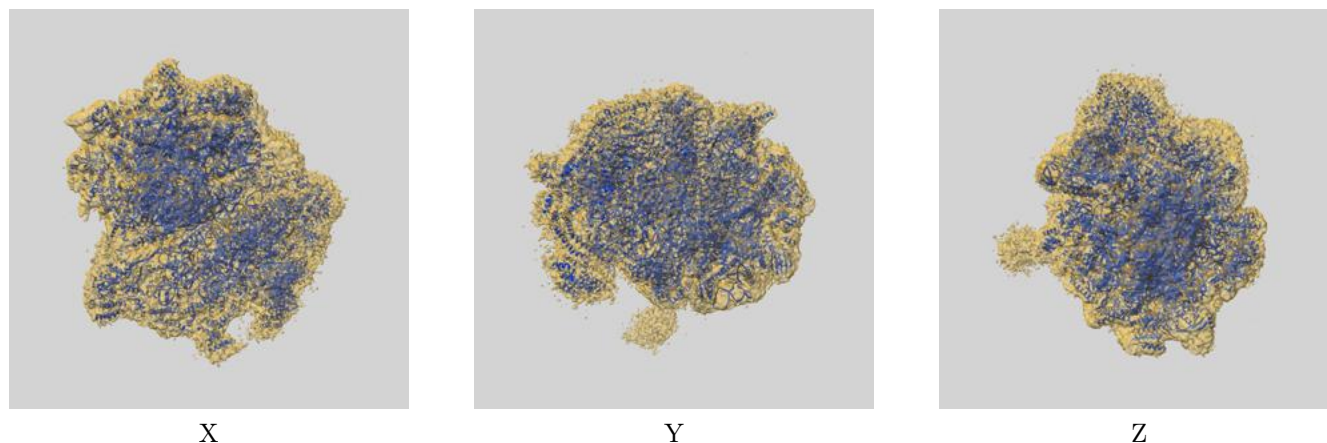
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

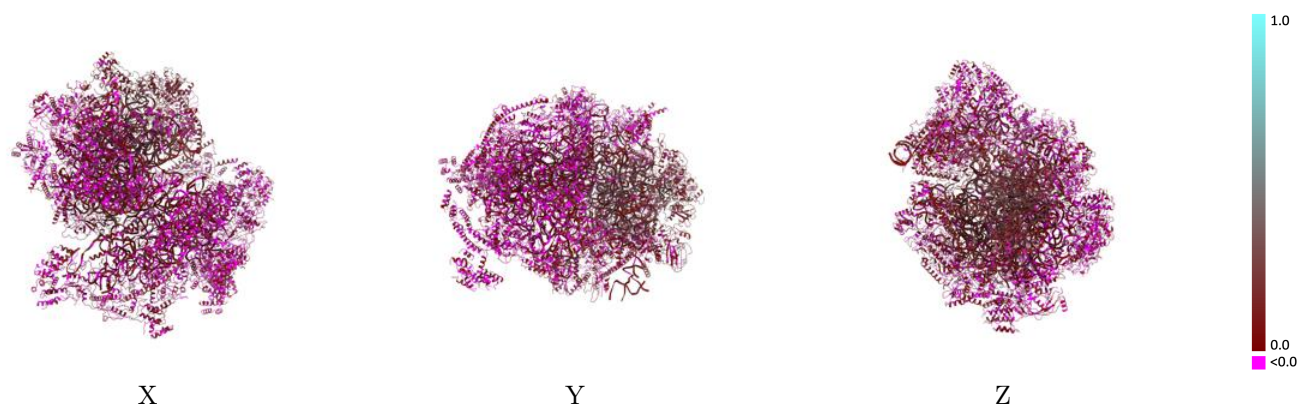
This section contains information regarding the fit between EMDB map EMD-0515 and PDB model 6NU3. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



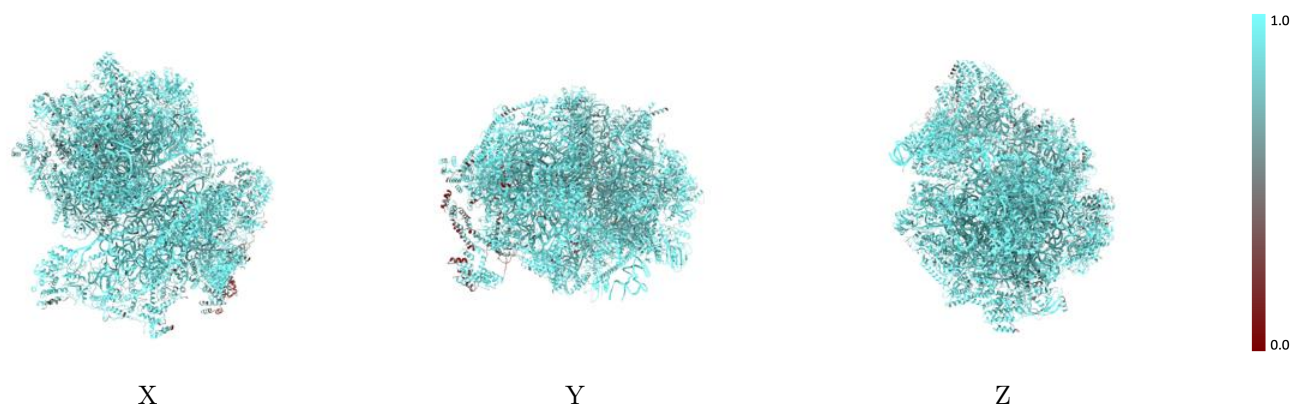
The images above show the 3D surface view of the map at the recommended contour level 0.165 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



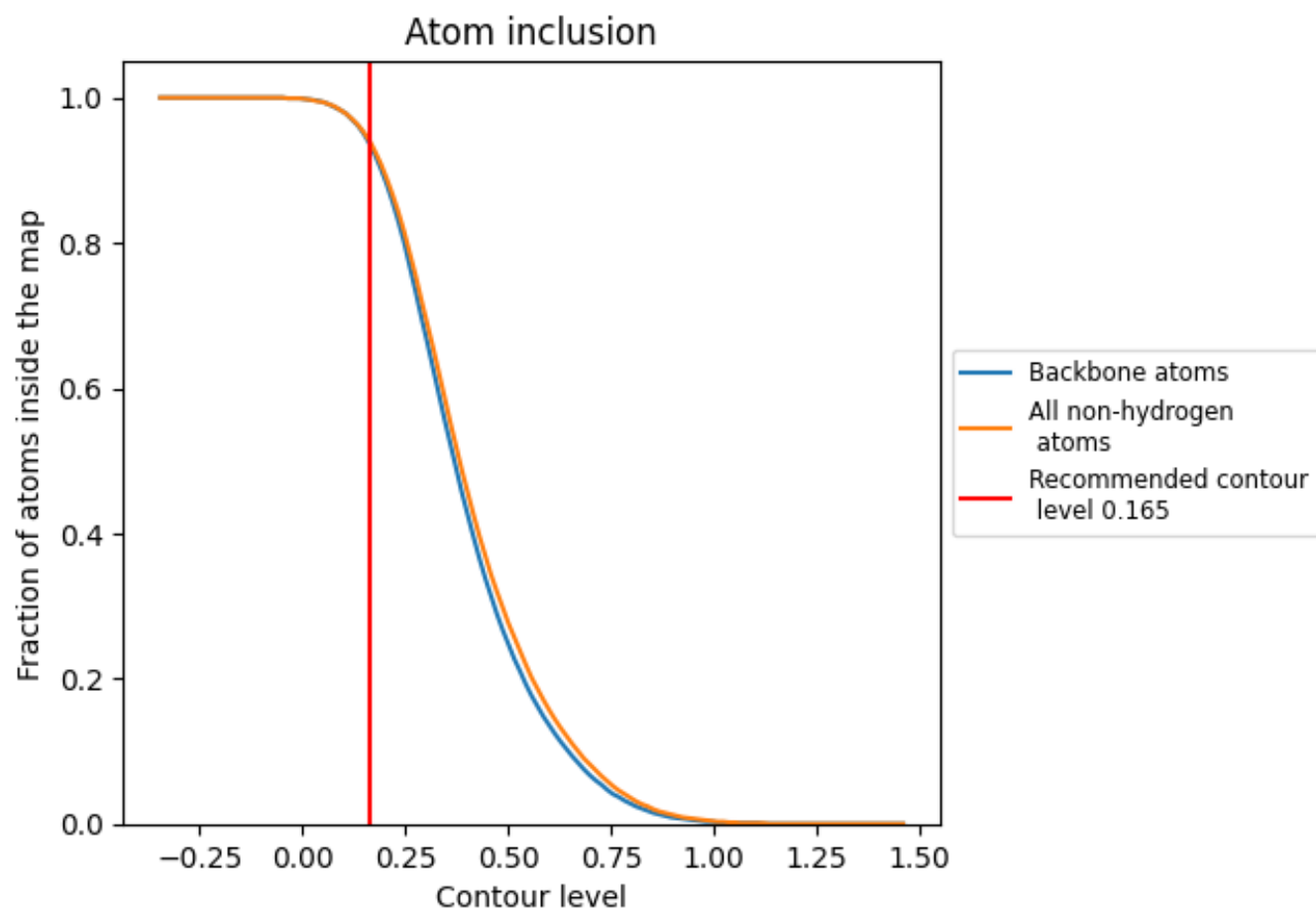
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.165).

9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 94% 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 (0.165) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9390	 0.0950
0	 0.8660	 0.0450
1	 0.9810	 0.1250
2	 0.8690	 0.0330
3	 0.9500	 0.2510
4	 0.9410	 0.1000
5	 0.9100	 0.0200
6	 0.9570	 0.1670
7	 0.8850	 0.0280
8	 0.9240	 0.0990
9	 0.9060	 0.0340
A	 0.9780	 0.1740
A0	 0.9520	 0.0590
A1	 0.8970	 0.0470
A2	 0.9270	 0.0240
A3	 0.9570	 0.0840
A4	 0.7080	 0.0270
AA	 0.9850	 0.0790
AB	 0.9610	 0.0160
AC	 0.9530	 0.0000
AD	 0.9070	 0.0320
AE	 0.9040	 -0.0190
AF	 0.9200	 0.0140
AG	 0.8240	 0.0350
AH	 0.8380	 0.0050
AI	 0.9470	 0.0130
AJ	 0.9460	 0.1030
AK	 0.9460	 0.0230
AL	 0.9670	 0.0120
AM	 0.9720	 0.0370
AN	 0.9920	 0.0210
AO	 0.9260	 0.0690
AP	 0.9660	 0.0040
AQ	 0.9520	 0.0530
AR	 0.8990	 0.0570



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Chain	Atom inclusion	Q-score
AS	 0.9610	 0.0230
AT	 0.9560	 0.0710
AU	 0.9500	 0.0690
AV	 0.9300	 0.0550
AW	 0.9320	 -0.0190
AX	 0.8930	 0.0250
AY	 0.8230	 0.0330
AZ	 0.9650	 0.0100
B	 0.9740	 0.1320
D	 0.9090	 0.0250
E	 0.9580	 0.1030
F	 0.9260	 0.1950
H	 0.9040	 0.1250
I	 0.9470	 0.0830
J	 0.9460	 0.0510
K	 0.9300	 0.1070
L	 0.8850	 0.1580
M	 0.9590	 0.2250
N	 0.9480	 0.1690
O	 0.8850	 0.0200
P	 0.9370	 0.1170
Q	 0.9210	 0.1340
R	 0.9210	 0.1100
S	 0.9190	 0.1070
T	 0.8280	 0.0650
U	 0.8770	 -0.0080
V	 0.8630	 0.0610
W	 0.9280	 0.1280
X	 0.9050	 0.1050
Y	 0.9160	 0.0380
Z	 0.9330	 0.1410
a	 0.9430	 0.0870
b	 0.8960	 0.0910
c	 0.8840	 0.0590
d	 0.8810	 0.0520
e	 0.9700	 0.1010
f	 0.8940	 0.1190
g	 0.9690	 0.2690
h	 0.9440	 0.1650
i	 0.9080	 0.1780
j	 0.9210	 0.1190
k	 0.9240	 0.0440

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Chain	Atom inclusion	Q-score
l	 0.9900	 0.1070
m	 0.9210	 0.0360
o	 0.9630	 0.1550
p	 0.9650	 0.1770
q	 0.9390	 0.1990
r	 0.9600	 0.1020
s	 0.8940	 -0.0050
t	 0.9790	 0.1730
u	 1.0000	 0.0970