Full wwPDB EM Validation Report (i)

Aug 7, 2023 – 05:43 PM EDT

PDB ID	:	5T2C
EMDB ID	:	EMD-8345
Title	:	CryoEM structure of the human ribosome at 3.6 Angstrom resolution
Authors	:	Zhang, X.; Lai, M.; Zhou, Z.H.
Deposited on	:	2016-08-23
Resolution	:	3.60 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

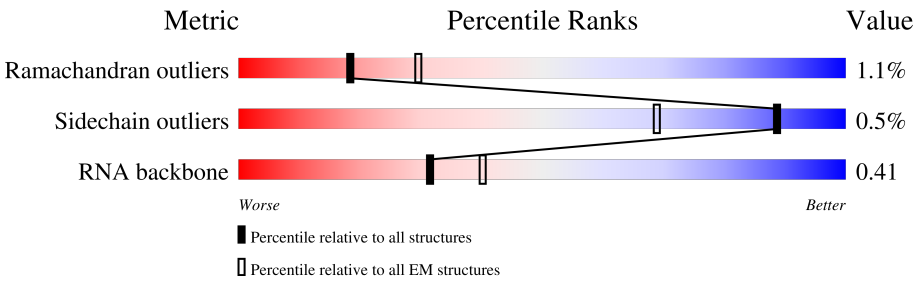
EMDB validation analysis	:	0.0.1.dev50
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	B	121	86% 13%
2	C	157	7% 77% 22%
3	D	257	7% 96%
4	E	403	9% 100%
5	F	427	9% 85% 14%
6	G	297	13% 98%
7	I	203	99%
8	J	160	5% 95%

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Mol	Chain	Length	Quality of chain
9	L	196	24% 95% 5%
10	N	160	15% 99%
11	O	128	25% 78% 21%
12	P	140	11% 94% 6%
13	Q	157	9% 41% 59%
14	S	145	9% 92% 8%
15	T	136	13% 99%
16	U	148	6% 99%
17	V	159	18% 47% 53%
18	X	125	12% 86% 14%
19	Y	135	8% 95% 5%
20	Z	110	7% 99%
21	a	117	12% 97%
22	b	123	18% 99%
23	c	105	28% 97%
24	d	97	89% 11%
25	e	70	44% 97%
26	f	51	16% 98%
27	g	128	7% 41% 59%
28	j	92	11% 99%
29	k	137	8% 91% 9%
30	m	248	6% 91% 9%
31	n	266	41% 91% 9%
32	o	192	12% 99%
33	s	215	7% 64% 35%

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Mol	Chain	Length	Quality of chain
34	t	204	99%
35	h	25	40%, 92%
36	r	211	35%, 97%
37	A	5070	11%, 53%, 21%, 26%
38	H	288	26%, 79%, 16%
39	i	106	12%, 97%
40	K	188	7%, 98%
41	l	217	100%, 98%
42	M	176	6%, 97%
43	p	214	23%, 98%
44	q	178	34%, 96%
45	R	156	13%, 76%, 23%
46	W	115	17%, 85%, 15%
47	AA	1869	41%, 31%, 51%, 12%, 7%
48	AC	83	89%, 95%, 5%
49	AD	143	65%, 96%
50	AE	115	54%, 88%, 12%
51	AF	69	86%, 90%, 9%
52	AH	156	46%, 42%, 54%
53	AJ	293	50%, 74%, 24%
54	AK	249	91%, 92%, 5%
55	AL	194	72%, 94%, 5%
56	AN	151	70%, 97%
57	AP	130	68%, 95%, 5%
58	AQ	133	85%, 95%

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Mol	Chain	Length	Quality of chain
59	AR	125	60% 58% 40%
60	AT	59	86% 93% 5%
61	AV	84	85% 95%
62	An	75	67% 29% 59% 12%
63	Ap	264	64% 78% 19%
64	Aq	243	92% 89% 7%
65	Ar	263	85% 97%
66	At	194	91% 93%
67	Au	208	78% 97%
68	Av	165	59% 58% 41%
69	Ay	146	95% 95% 5%
70	A0	152	92% 91% 7%
71	Ao	295	61% 73% 25%
72	As	204	82% 86% 6% 6%
73	Aw	158	77% 94%
74	Ax	145	66% 56% 10% 33%
75	Az	135	93% 85% 10%
76	AB	119	82% 76% 8% 14%
77	AG	56	93% 89% 5% 5%
78	AI	317	99% 95%
79	AM	132	92% 88% 8%
80	AO	151	78% 88% 5% 7%
81	AU	145	87% 90% 7%

2 Entry composition (i)

There are 81 unique types of molecules in this entry. The entry contains 217989 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	B	120	2558	1141	456	842	119	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	C	156	3314	1480	585	1094	155	0	0

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	248	1898	1189	389	314	6	0	0

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	402	3238	2060	608	556	14	0	0

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	367	2919	1835	582	488	14	0	0

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	293	2382	1507	434	427	14	0	0

- Molecule 7 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	I	201	1650	1063	321	261	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	J	153	1242	776	241	216	9	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	L	187	1566	971	336	250	9	0	0

- Molecule 10 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	N	159	1298	823	252	217	6	0	0

- Molecule 11 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	O	101	825	529	144	150	2	0	0

- Molecule 12 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	P	131	979	618	184	172	5	0	0

- Molecule 13 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	Q	64	534	340	104	87	3	0	0

- Molecule 14 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	S	134	1115	700	226	186	3	0	0

- Molecule 15 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	T	135	1107	714	208	182	3	0	0

- Molecule 16 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	U	147	1162	736	237	186	3	0	0

- Molecule 17 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	V	75	610	378	130	99	3	0	0

- Molecule 18 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	X	107	888	560	171	155	2	0	0

- Molecule 19 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	Y	128	1053	667	216	165	5	0	0

- Molecule 20 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	Z	109	876	555	174	144	3	0	0

- Molecule 21 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	a	114	906	566	187	147	6	0	0

- Molecule 22 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	b	122	1015	641	205	168	1	0	0

- Molecule 23 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	c	102	832	521	177	129	5	0	0

- Molecule 24 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	d	86	705	434	155	111	5	0	0

- Molecule 25 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	e	69	569	366	103	99	1	0	0

- Molecule 26 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	f	50	444	281	98	64	1	0	0

- Molecule 27 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	g	52	429	266	90	67	6	0	0

- Molecule 28 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	j	91	708	445	136	120	7	0	0

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	k	125	1002	622	207	168	5	0	0

- Molecule 30 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	m	225	1870	1202	358	301	9	0	0

- Molecule 31 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	n	241	1927	1228	371	324	4	0	0

- Molecule 32 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	o	190	1518	956	284	272	6	0	0

- Molecule 33 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	s	139	1138	730	218	183	7	0	0

- Molecule 34 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	t	203	1701	1072	359	266	4	0	0

- Molecule 35 is a protein called 60S Ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	h	24	230	139	62	26	3	0	0

- Molecule 36 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	r	210	1701	1064	352	281	4	0	0

- Molecule 37 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
37	A	3776	80184	35672	14597	26140	3775	0	0

- Molecule 38 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	H	242	1958	1257	372	325	4	0	0

- Molecule 39 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	i	105	862	542	175	139	6	0	0

- Molecule 40 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	K	187	1513	944	314	250	5	0	0

- Molecule 41 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	l	217	1741	1113	312	307	9	0	0

- Molecule 42 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	M	175	1453	925	283	235	10	0	0

- Molecule 43 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	p	213	1711	1082	329	285	15	0	0

- Molecule 44 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	q	176	1410	888	263	253	6	0	0

- Molecule 45 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	R	120	985	630	185	169	1	0	0

- Molecule 46 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	W	98	764	485	135	138	6	0	0

- Molecule 47 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
47	AA	1742	36900	16458	6595	12106	1741	0	0

- Molecule 48 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	AC	83	636	393	117	121	5	0	0

- Molecule 49 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	AD	141	1098	693	219	183	3	0	0

- Molecule 50 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	AE	101	814	507	170	132	5	0	0

- Molecule 51 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	AF	63	498	302	101	93	2	0	0

- Molecule 52 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	AH	71	581	367	109	98	7	0	0

- Molecule 53 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	AJ	222	1725	1115	298	302	10	0	0

- Molecule 54 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	AK	237	1923	1200	387	329	7	0	0

- Molecule 55 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	AL	185	1525	969	306	248	2	0	0

- Molecule 56 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	AN	149	1202	770	228	203	1	0	0

- Molecule 57 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	AP	129	1034	659	193	176	6	0	0

- Molecule 58 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	AQ	131	1065	673	209	178	5	0	0

- Molecule 59 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	AR	75	598	382	111	104	1	0	0

- Molecule 60 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	AT	58	459	284	100	74	1	0	0

- Molecule 61 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	AV	83	651	408	121	115	7	0	0

- Molecule 62 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
62	An	75	1604	717	298	515	74	0	0

- Molecule 63 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	Ap	214	1738	1103	310	311	14	0	0

- Molecule 64 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	Aq	227	1765	1125	317	315	8	0	0

- Molecule 65 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	Ar	262	2076	1324	386	358	8	0	0

- Molecule 66 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	At	189	1521	969	280	271	1	0	0

- Molecule 67 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Au	206	1686	1058	332	291	5	0	0

- Molecule 68 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	Av	98	827	539	148	134	6	0	0

- Molecule 69 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Ay	146	1158	736	218	200	4	0	0

- Molecule 70 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	A0	150	1235	776	250	208	1	0	0

- Molecule 71 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	Ao	222	1747	1109	306	324	8	0	0

- Molecule 72 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	As	191	1509	943	286	273	7	0	0

- Molecule 73 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	Aw	153	1247	793	234	214	6	0	0

- Molecule 74 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	Ax	97	804	505	155	138	6	0	0

- Molecule 75 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	Az	132	1072	673	199	195	5	0	0

- Molecule 76 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	AB	102	807	507	153	143	4	0	0

- Molecule 77 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	AG	53	445	278	90	72	5	0	0

- Molecule 78 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	AI	313	2436	1535	424	465	12	0	0

- Molecule 79 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	AM	122	952	596	169	179	8	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AM	52	GLN	LEU	conflict	UNP P25398
AM	69	LEU	CYS	conflict	UNP P25398
AM	99	ASN	LYS	conflict	UNP P25398

- Molecule 80 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	AO	140	1049	642	204	197	6	0	0

- Molecule 81 is a protein called 40S ribosomal protein S19.

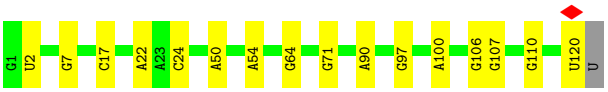
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
81	AU	143	1112	697	214	198	3	0	0

3 Residue-property plots (i)

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

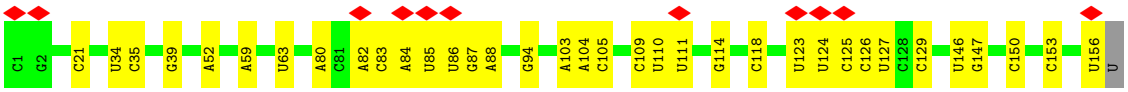
- Molecule 1: 5S rRNA

Chain B:



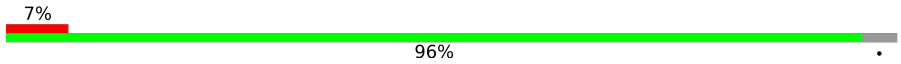
- Molecule 2: 5.8S rRNA

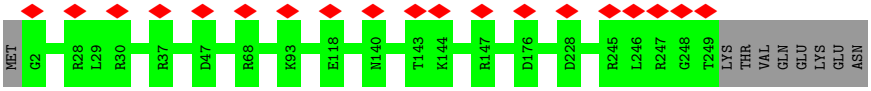
Chain C:



- Molecule 3: 60S ribosomal protein L8

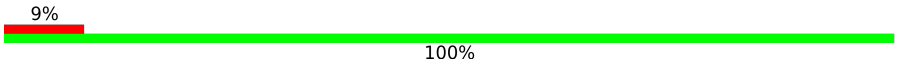
Chain D:

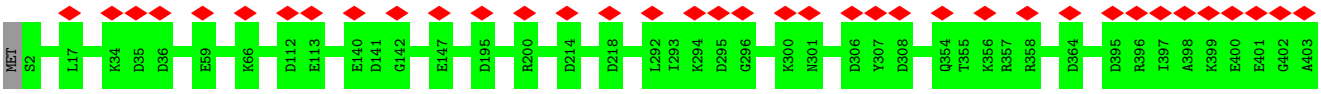




- Molecule 4: 60S ribosomal protein L3

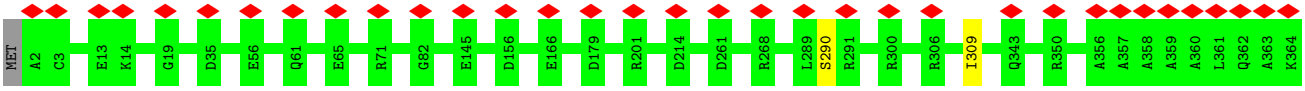
Chain E:

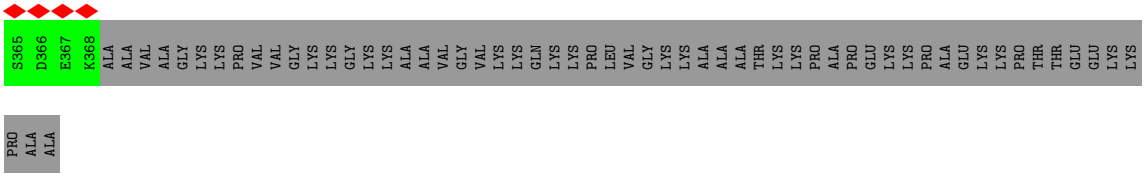




- Molecule 5: 60S ribosomal protein L4

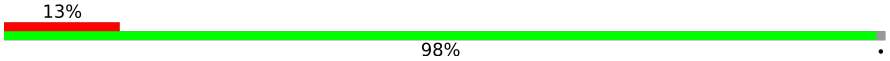
Chain F:

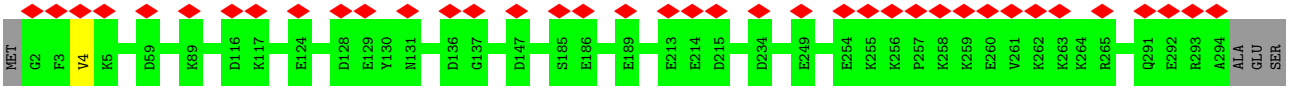




• Molecule 6: 60S ribosomal protein L5

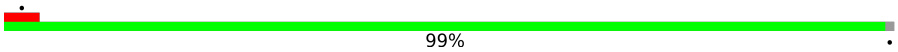
Chain G:

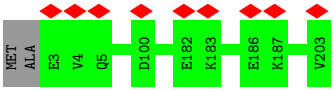




• Molecule 7: 60S ribosomal protein L13a

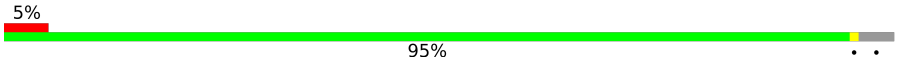
Chain I:

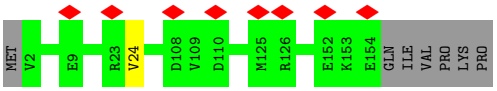




• Molecule 8: 60S ribosomal protein L17

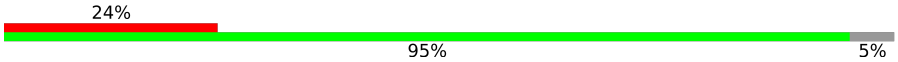
Chain J:

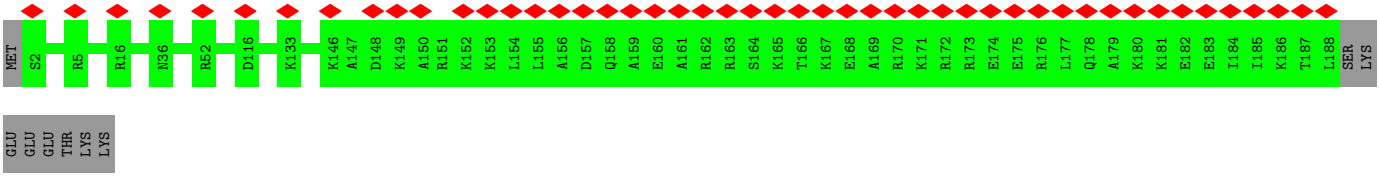




• Molecule 9: 60S ribosomal protein L19

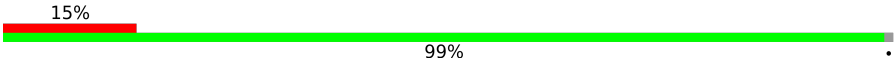
Chain L:

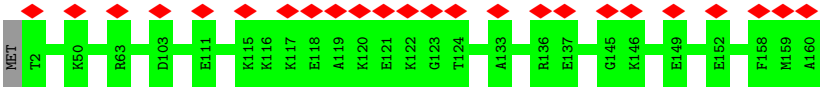




• Molecule 10: 60S ribosomal protein L21

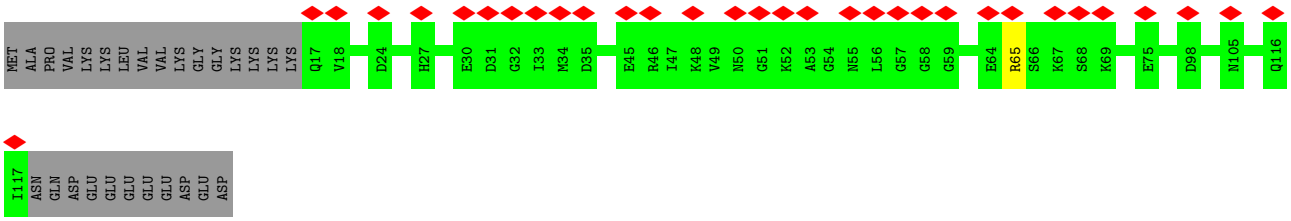
Chain N:





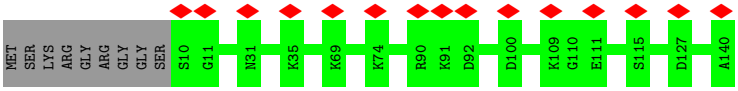
• Molecule 11: 60S ribosomal protein L22

Chain O:



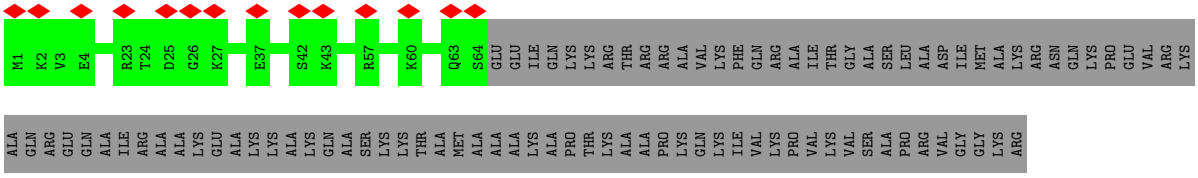
• Molecule 12: 60S ribosomal protein L23

Chain P: 11% 94% 6%



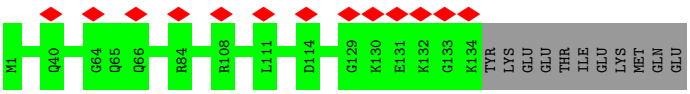
• Molecule 13: 60S ribosomal protein L24

Chain Q: 9% 41% 59%



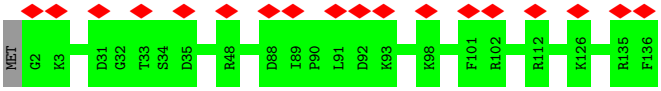
• Molecule 14: 60S ribosomal protein L26

Chain S: 9% 92% 8%



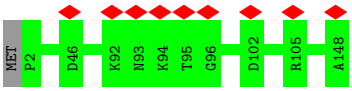
• Molecule 15: 60S ribosomal protein L27

Chain T: 13% 99%



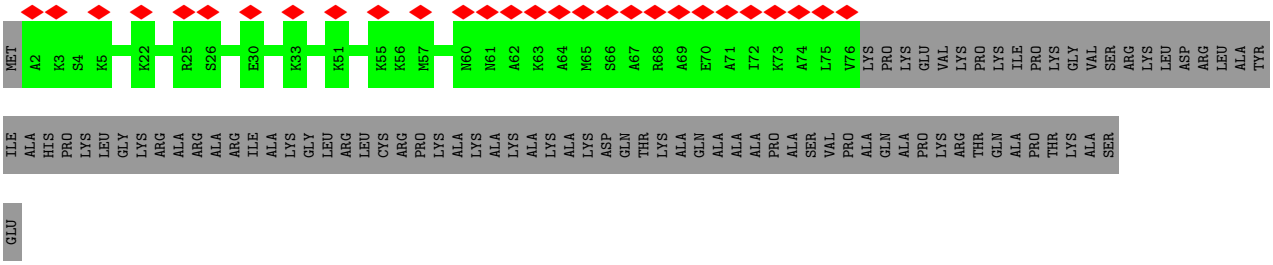
• Molecule 16: 60S ribosomal protein L27a

Chain U: 6% 99%



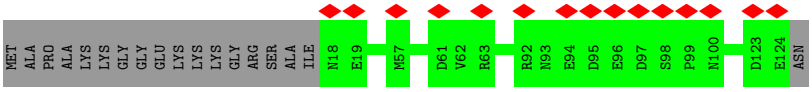
• Molecule 17: 60S ribosomal protein L29

Chain V:

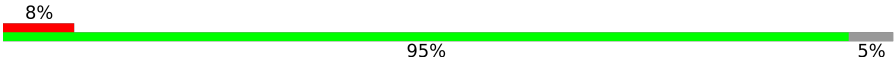


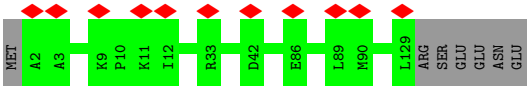
- Molecule 18: 60S ribosomal protein L31

Chain X:

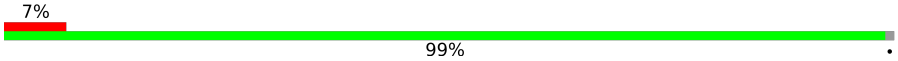


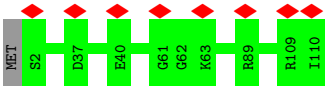
- Molecule 19: 60S ribosomal protein L32

Chain Y: 

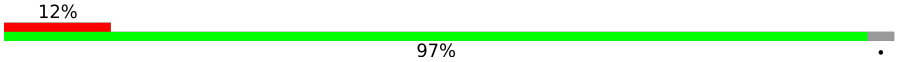


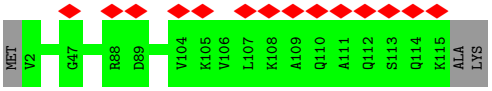
- Molecule 20: 60S ribosomal protein L35a

Chain Z: 

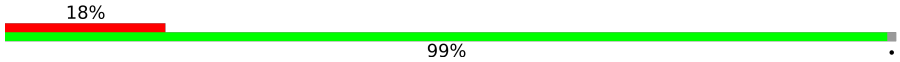


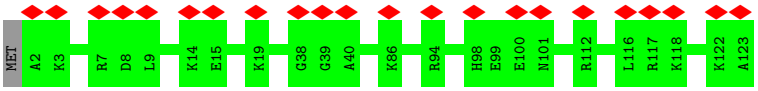
- Molecule 21: 60S ribosomal protein L34

Chain a: 



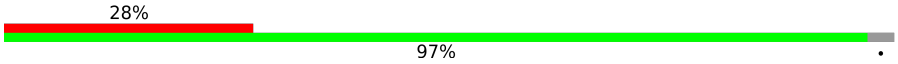
- Molecule 22: 60S ribosomal protein L35

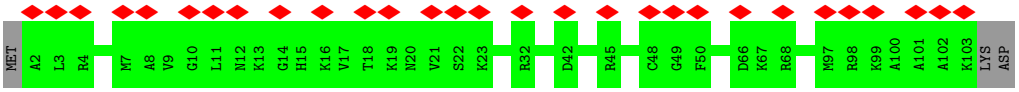
Chain b: 



- Molecule 23: 60S ribosomal protein L36

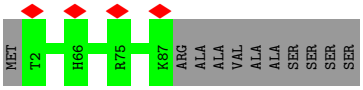
Chain c:





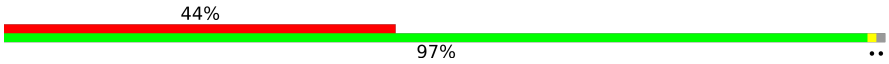
• Molecule 24: 60S ribosomal protein L37

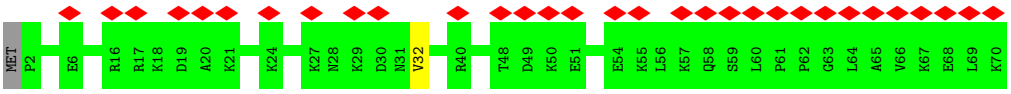
Chain d:



• Molecule 25: 60S ribosomal protein L38

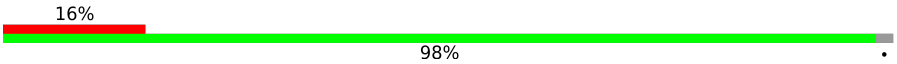
Chain e:

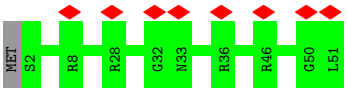




• Molecule 26: 60S ribosomal protein L39

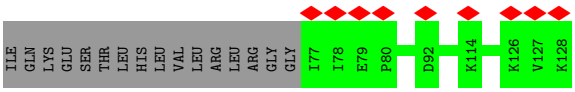
Chain f:





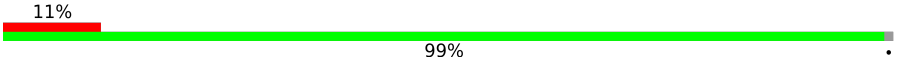
• Molecule 27: Ubiquitin-60S ribosomal protein L40

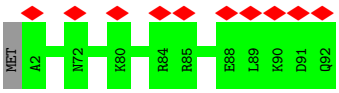
Chain g:



• Molecule 28: 60S ribosomal protein L37a

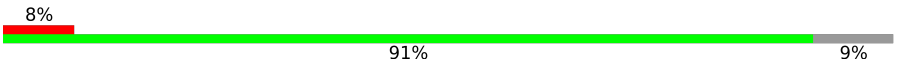
Chain j:

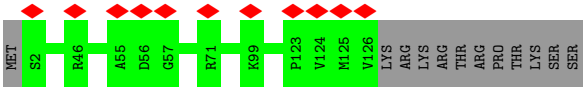




• Molecule 29: 60S ribosomal protein L28

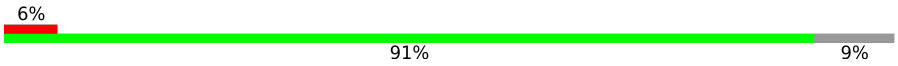
Chain k:

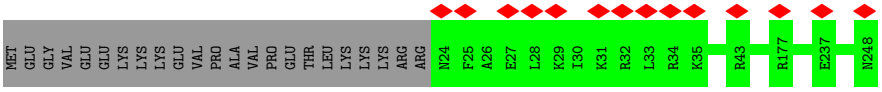




• Molecule 30: 60S ribosomal protein L7

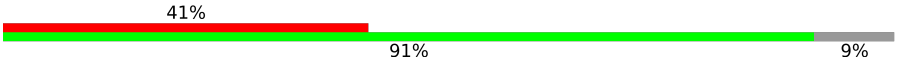
Chain m:

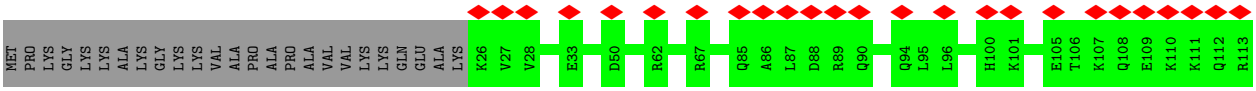


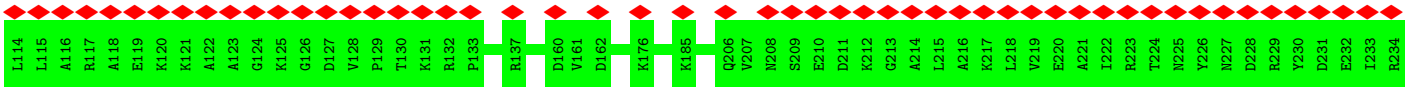


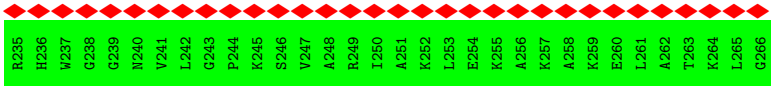
• Molecule 31: 60S ribosomal protein L7a

Chain n:



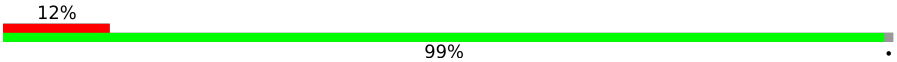


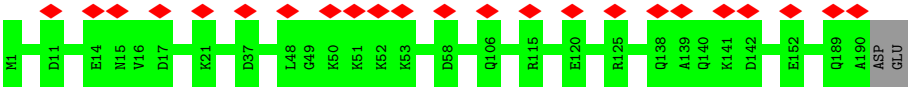




• Molecule 32: 60S ribosomal protein L9

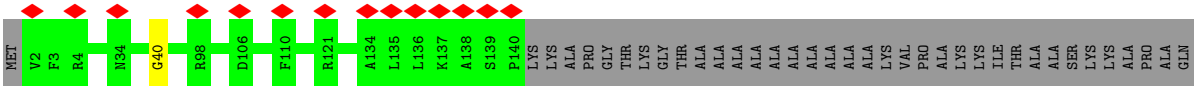
Chain o:

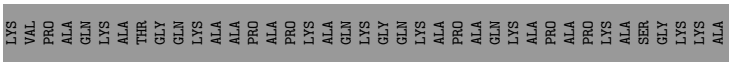




• Molecule 33: 60S ribosomal protein L14

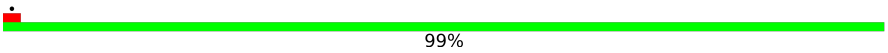
Chain s:

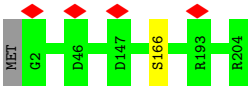




• Molecule 34: 60S ribosomal protein L15

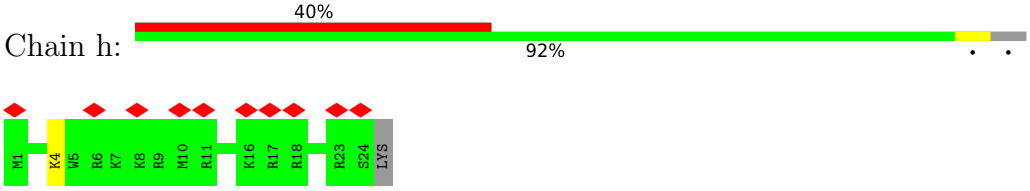
Chain t:





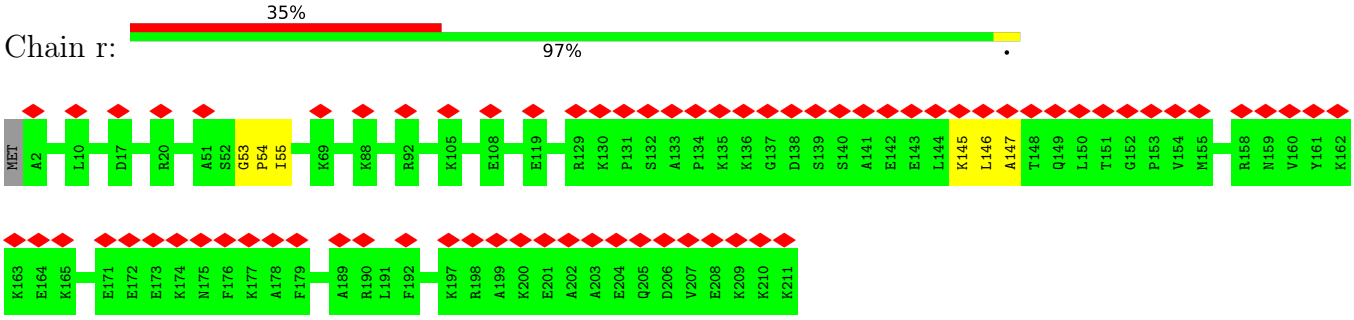
- Molecule 35: 60S Ribosomal protein L41

Chain h:



- Molecule 36: 60S ribosomal protein L13

Chain r:



- Molecule 37: 28S rRNA

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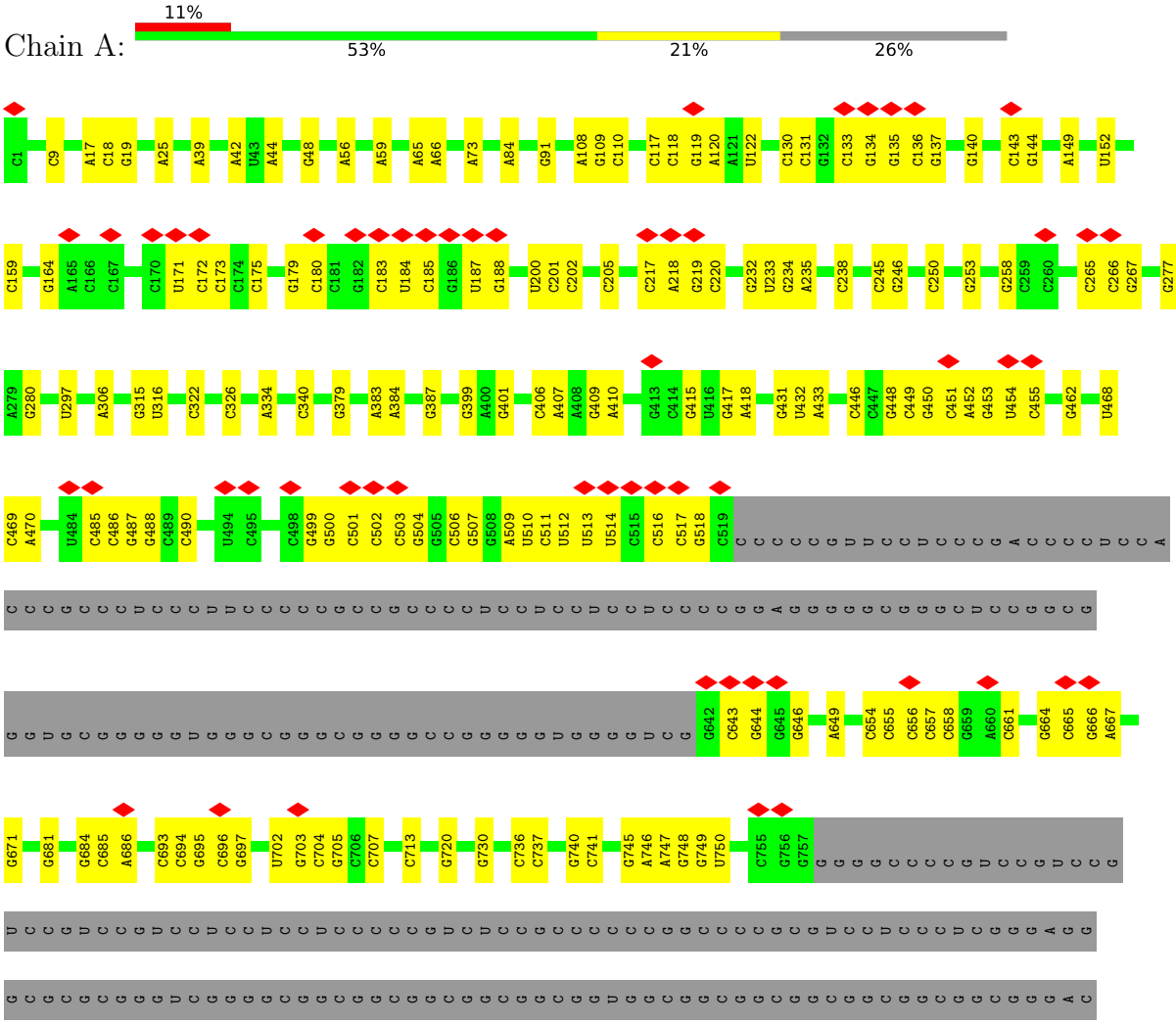

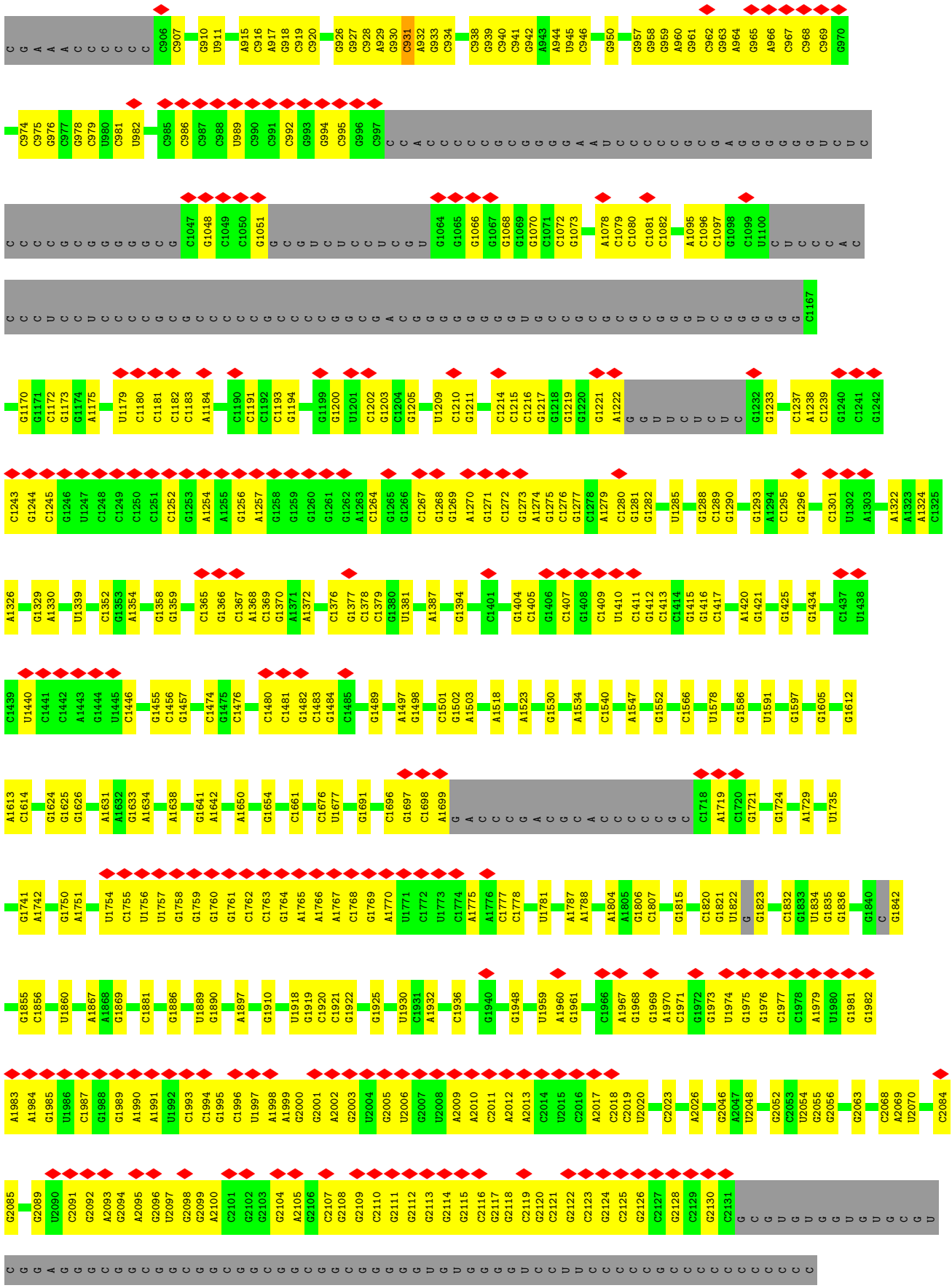
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C974 C975 G976 G977 G978 C979 U980 C981 U982 C985 C986 C987 C988 U989 C990 C991 C992 G993 G994 C995 G996 C997
C1047 G1048 C1049 C1050 G1051 G1064 G1065 G1066 G1067 G1068 G1069 G1070 C1071 C1072 G1073 A1078 C1079 C1080 C1081 C1082 A1095 C1096 C1097 G1098 C1099 U1100
C1167
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C1243 G1244 C1245 G1246 U1247 C1248 C1249 C1250 C1251 C1252 G1253 A1254 A1255 G1256 A1257 G1258 G1259 G1260 G1261 G1262 A1263 C1264 G1265 G1266 C1267 G1268 G1269 A1270 G1271 C1272 G1273 A1274 G1275 C1276 G1277 C1278 A1279 C1280 G1281 G1282 U1285 G1288 C1289 G1290 G1293 A1294 C1295 G1296 C1301 U1302 A1303 A1322 A1323 A1324 C1325
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C1439 U1440 C1441 C1442 A1443 G1444 U1445 C1446 G1455 C1456 G1457 C1474 G1475 C1476 C1480 C1481 G1482 C1483 G1484 C1485 G1489 A1497 G1498 C1501 G1502 A1503 A1518 A1523 G1530 A1534 C1540 A1547 G1552 C1566 U1578 G1586 U1591 G1597 G1605 G1612
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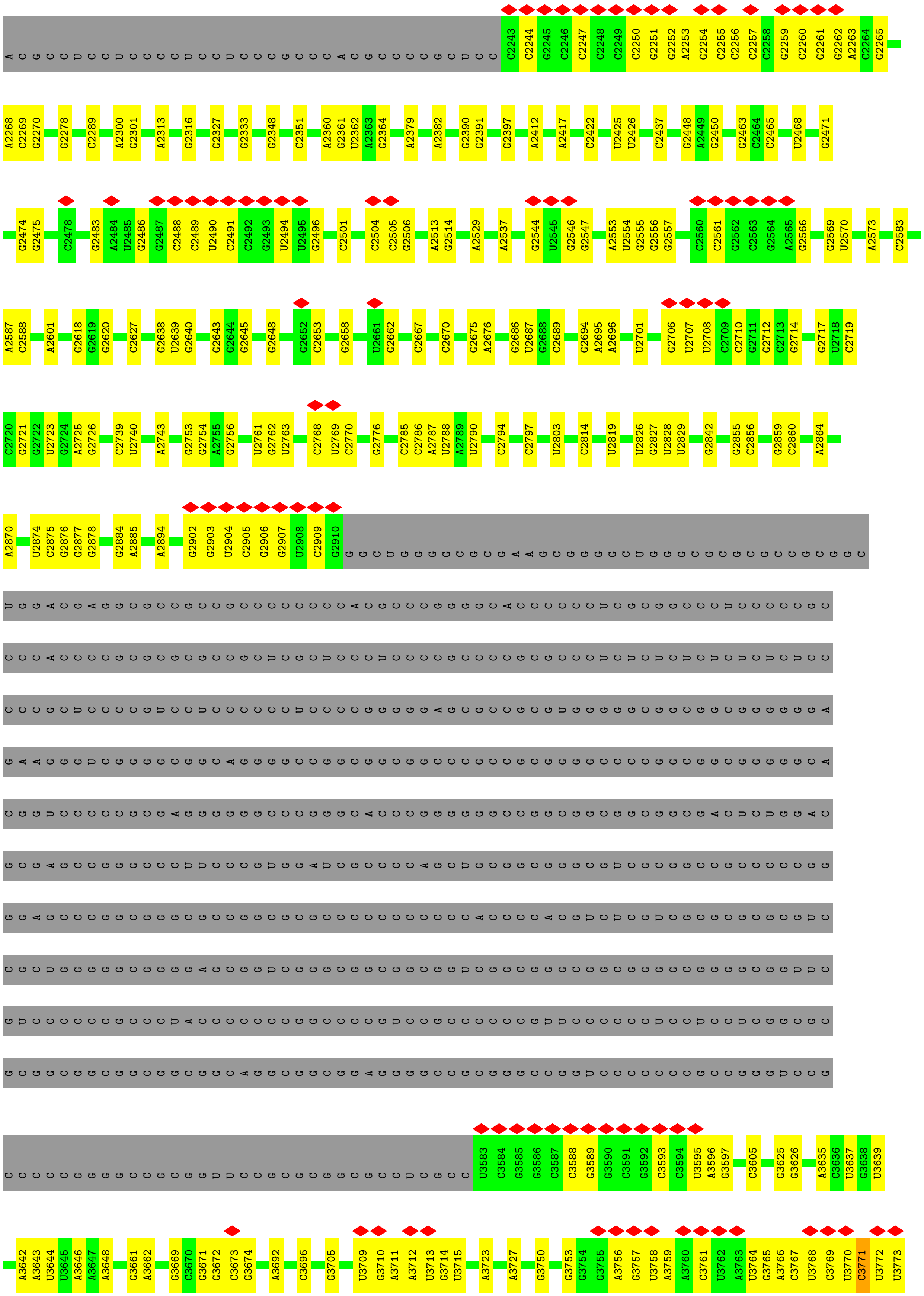
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C G C U G G G G C G G G G A G C G G U C G G C G C C G G C G G U C G G C G G G G G C G C G G C G C G C G C G G G U U C
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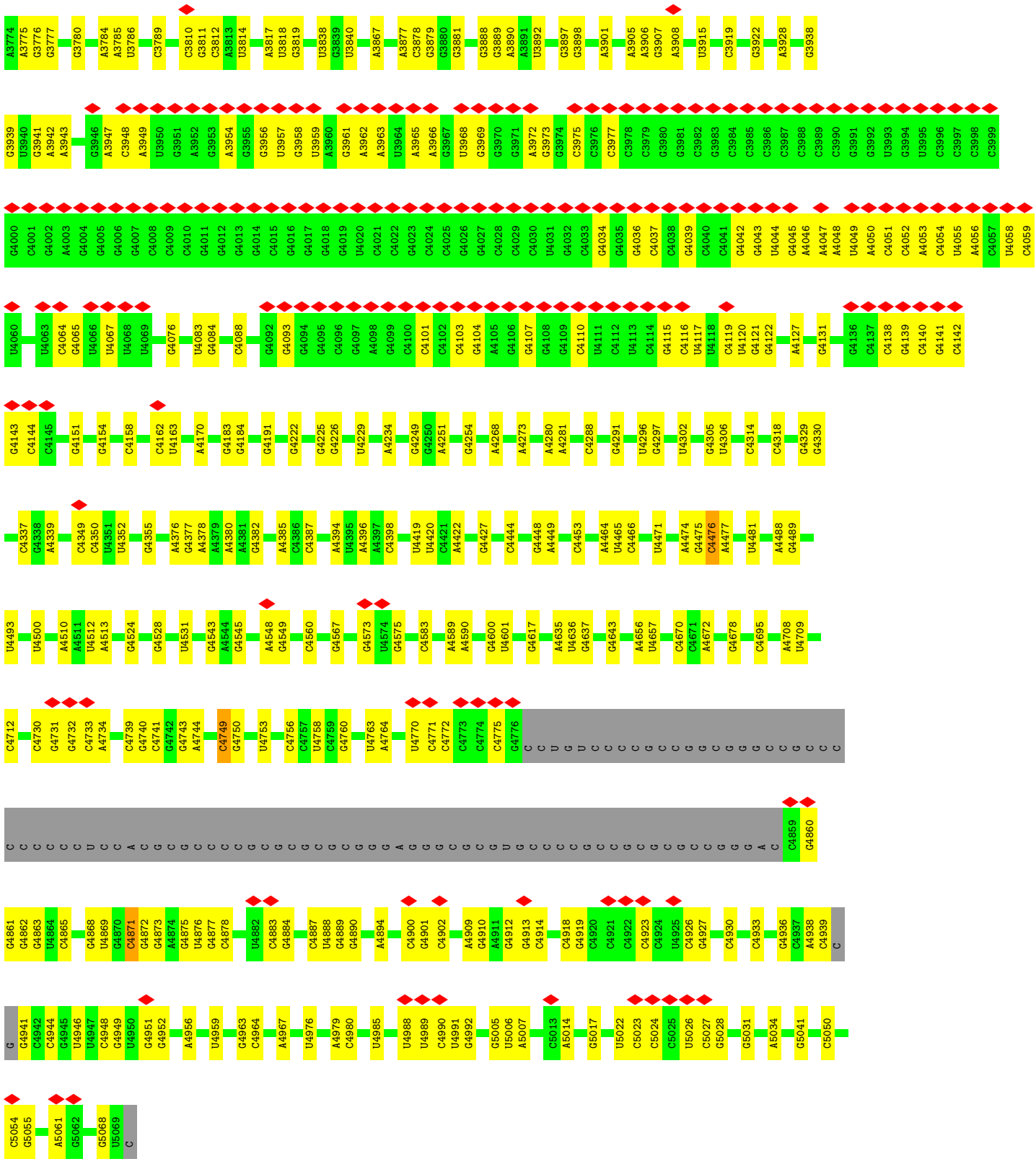
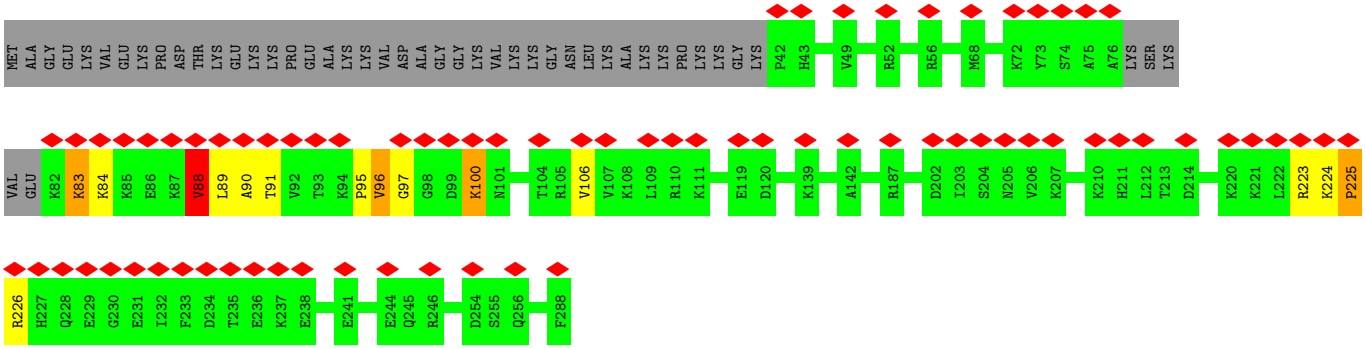


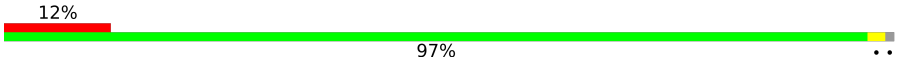
• Molecule 38: 60S ribosomal protein L6

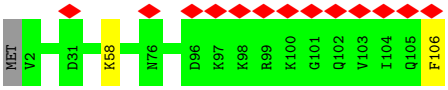
Chain H:



- Molecule 39: 60S ribosomal protein L36a

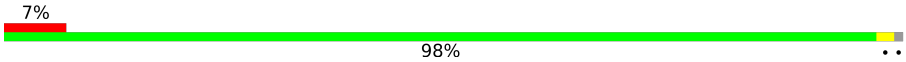
Chain i:

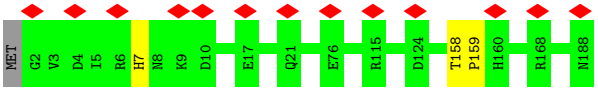




- Molecule 40: 60S ribosomal protein L18

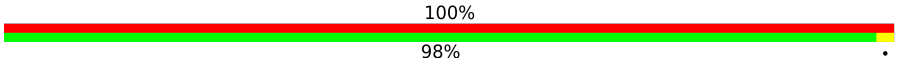
Chain K:

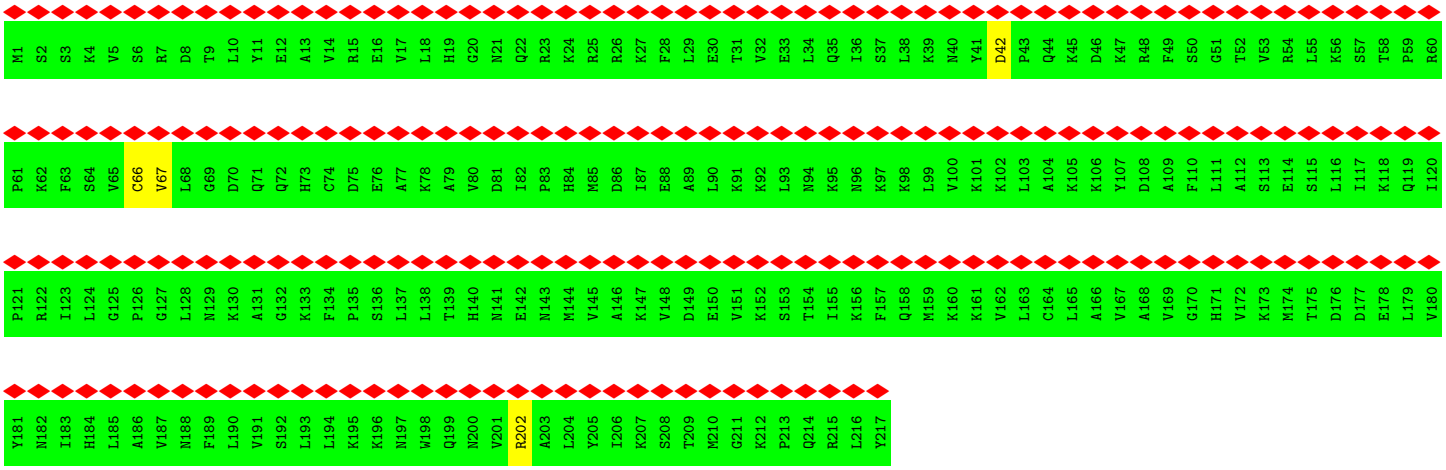




- Molecule 41: 60S ribosomal protein L10a

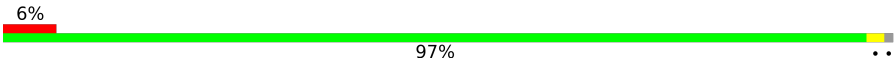
Chain l:

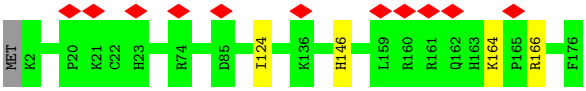




- Molecule 42: 60S ribosomal protein L18a

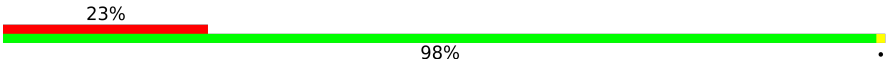
Chain M:

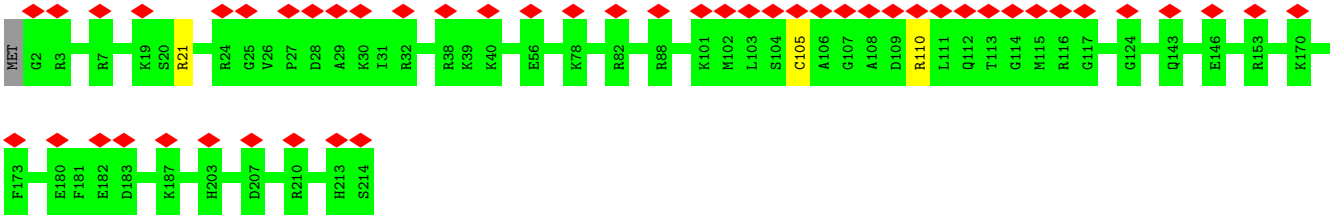




- Molecule 43: 60S ribosomal protein L10-like

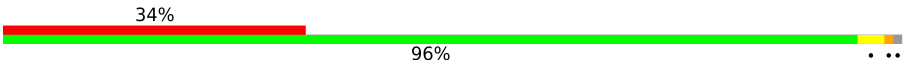
Chain p:

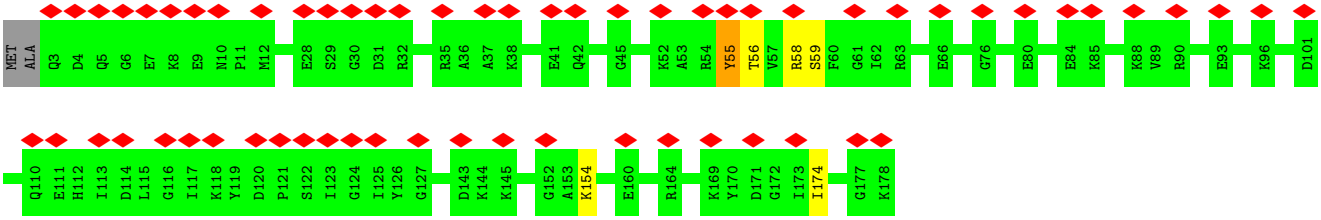




- Molecule 44: 60S ribosomal protein L11

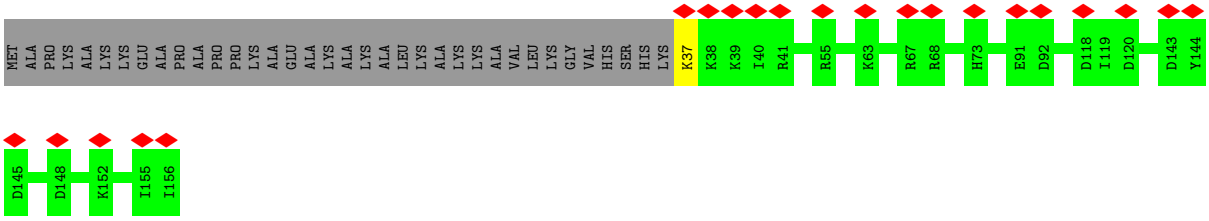
Chain q:





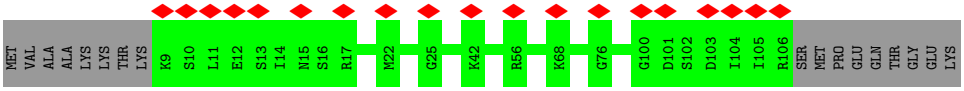
- Molecule 45: 60S ribosomal protein L23a

Chain R:



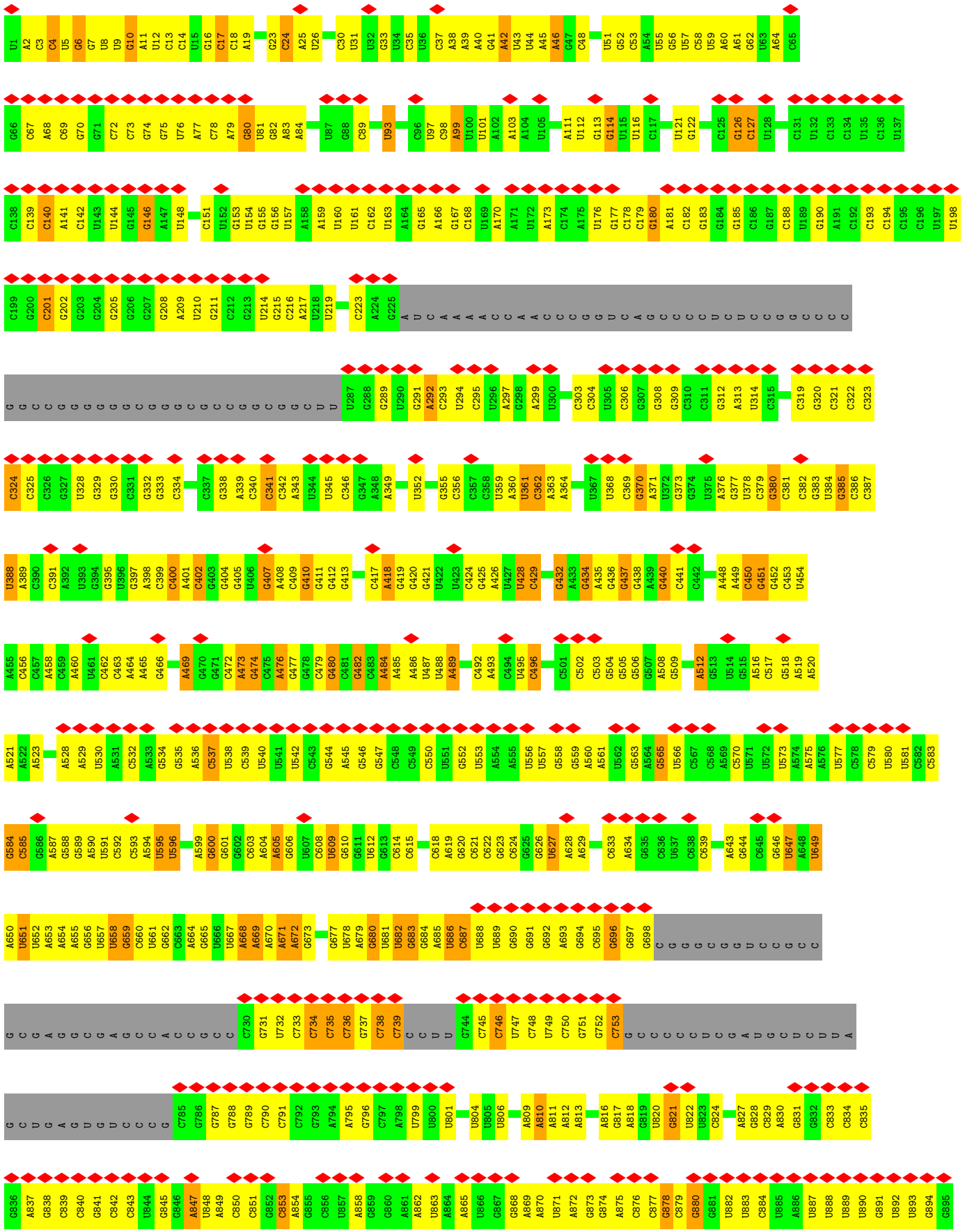
- Molecule 46: 60S ribosomal protein L30

Chain W:



- Molecule 47: 18S rRNA

Chain AA: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G66 C67 A68 C69 G70 G71 C72 C73 G74 G75 U76 A77 C78 A79 G80 U81 G82 A83 A84 U87 G88 C89 U93 C96 U97 C98 A99 U100 U101 A102 A103 A104 U105 A111 U112 G113 G114 U115 U116 C117 U121 G122 C125 G126 C127 U128 C131 U132 C133 C134 U135 C136 U137
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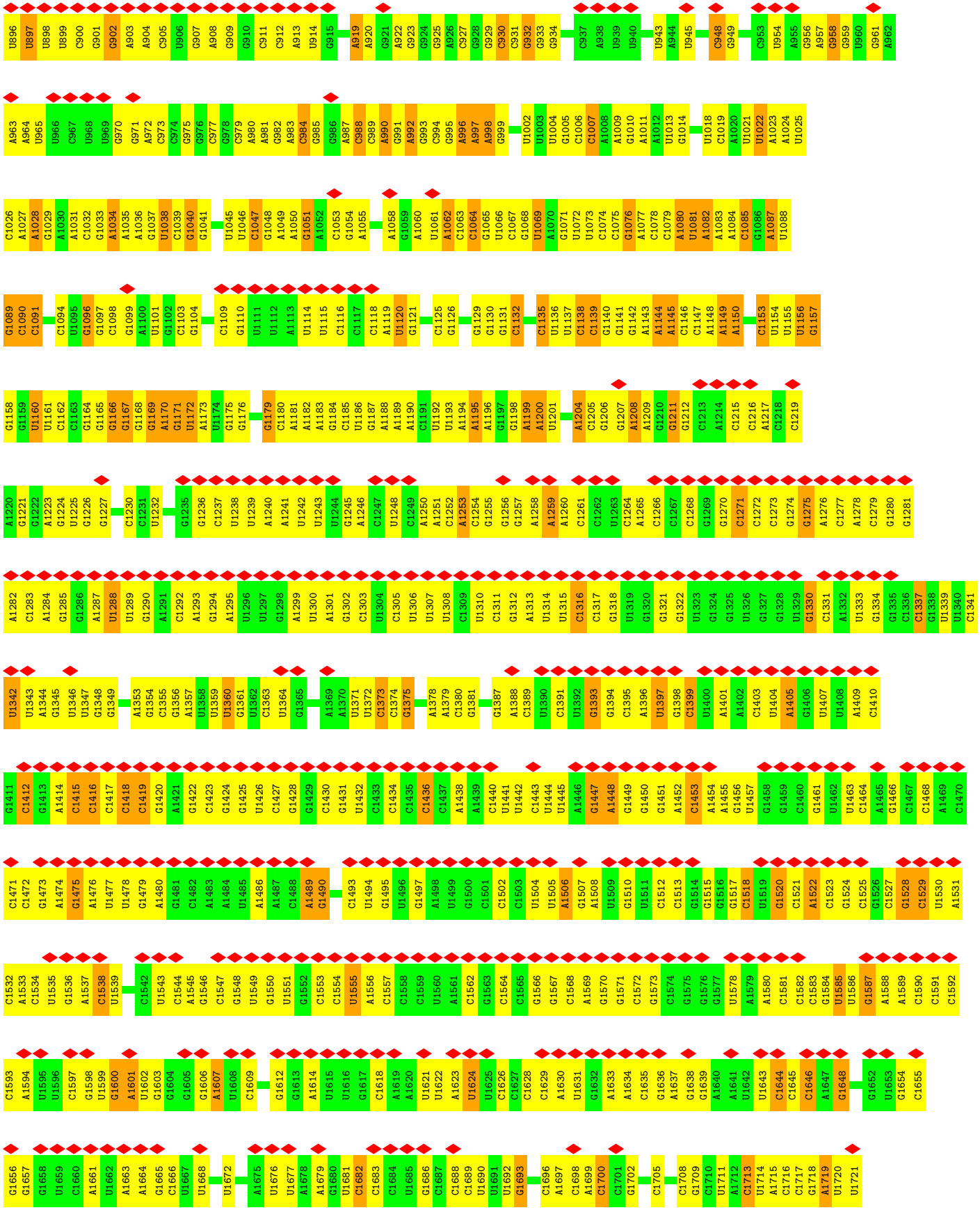
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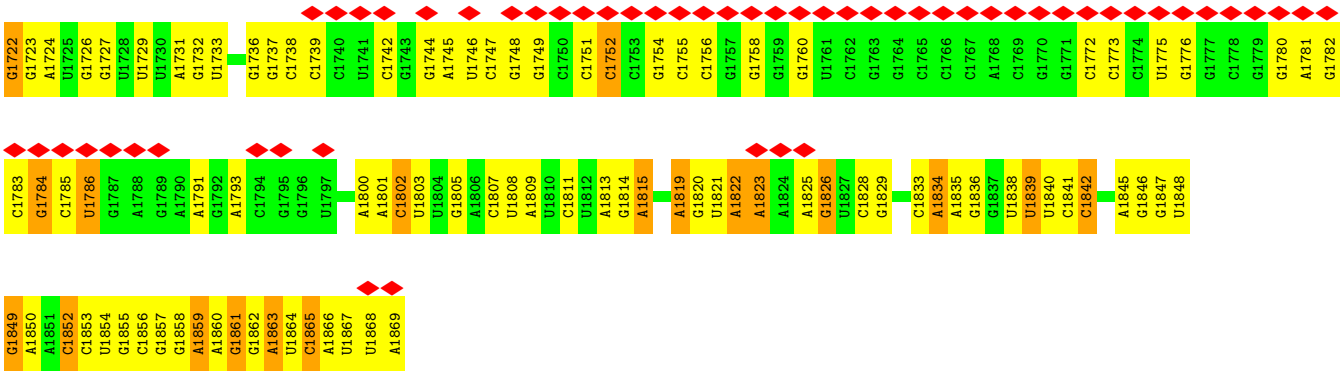
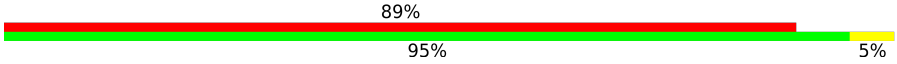
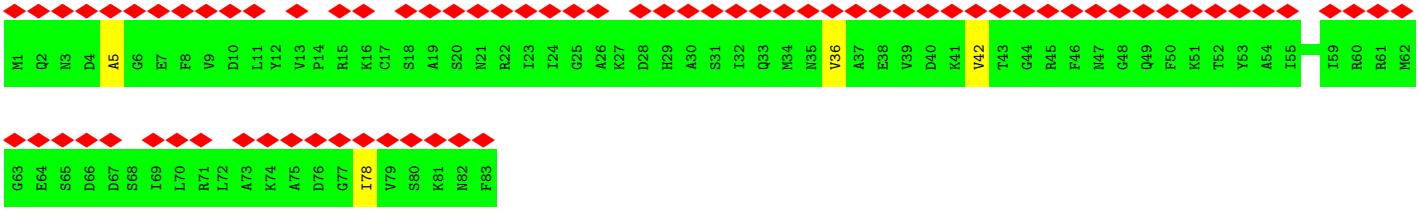


- Molecule 48: 40S ribosomal protein S21

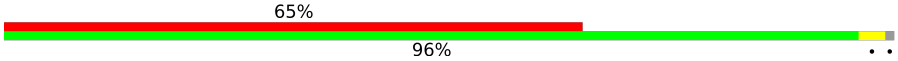
Chain AC:

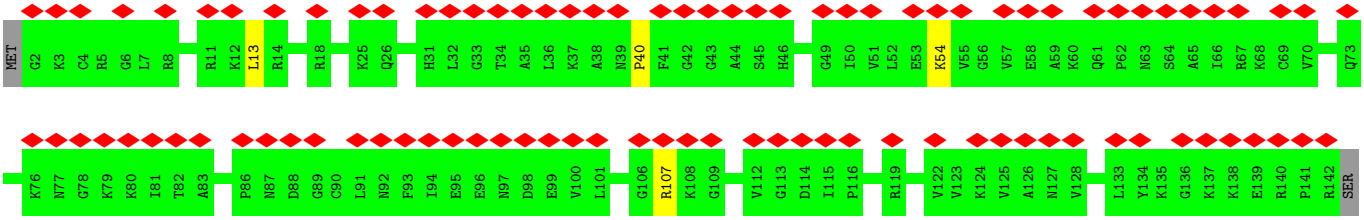




- Molecule 49: 40S ribosomal protein S23

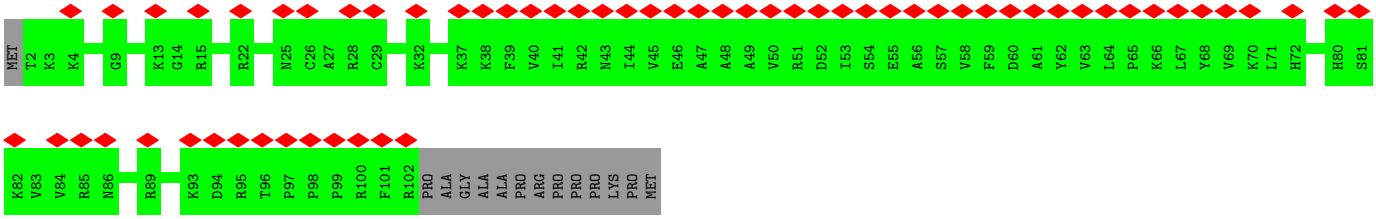
Chain AD:





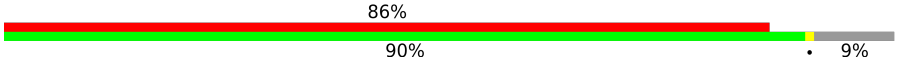
- Molecule 50: 40S ribosomal protein S26

Chain AE:



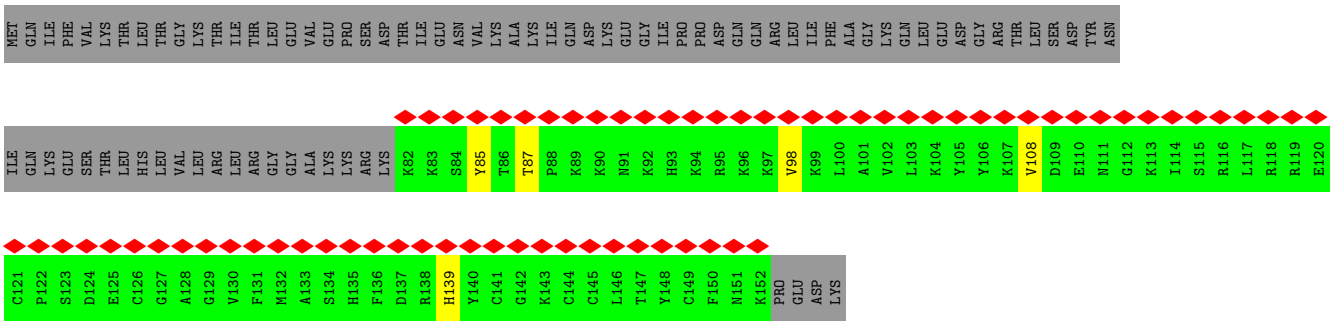
- Molecule 51: 40S ribosomal protein S28

Chain AF:



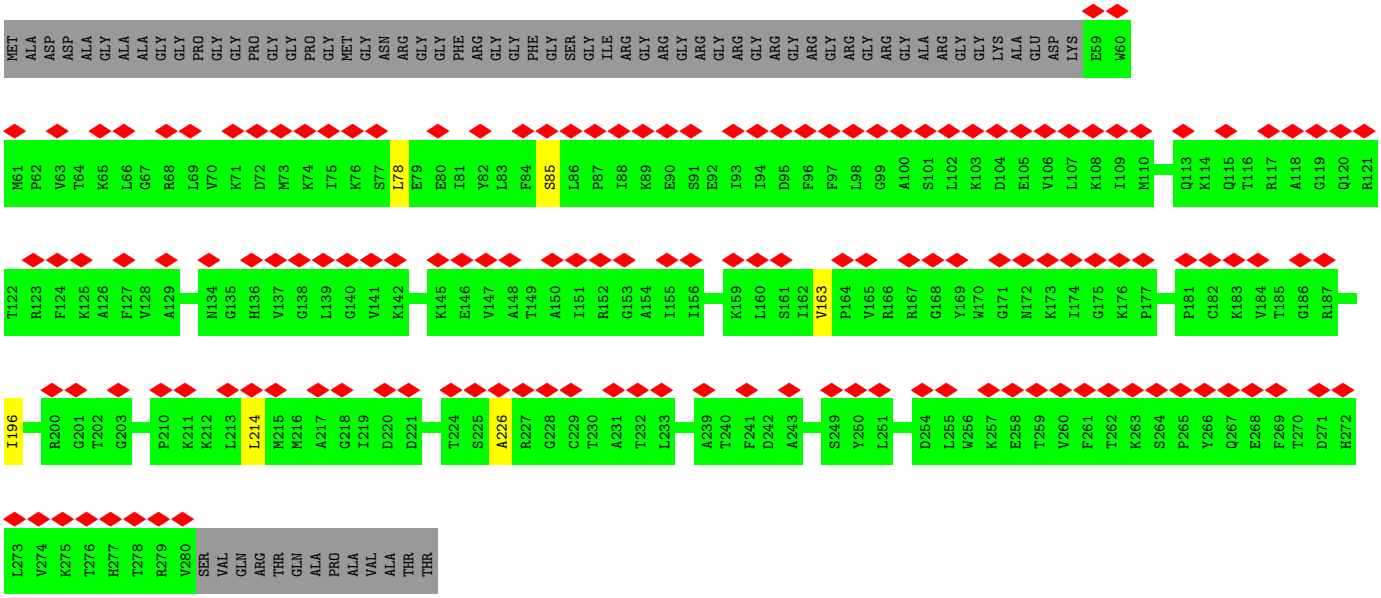
- Molecule 52: Ubiquitin-40S ribosomal protein S27a

Chain AH:



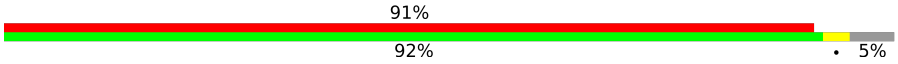
- Molecule 53: 40S ribosomal protein S2

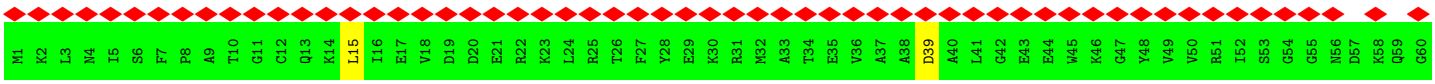
Chain AJ:

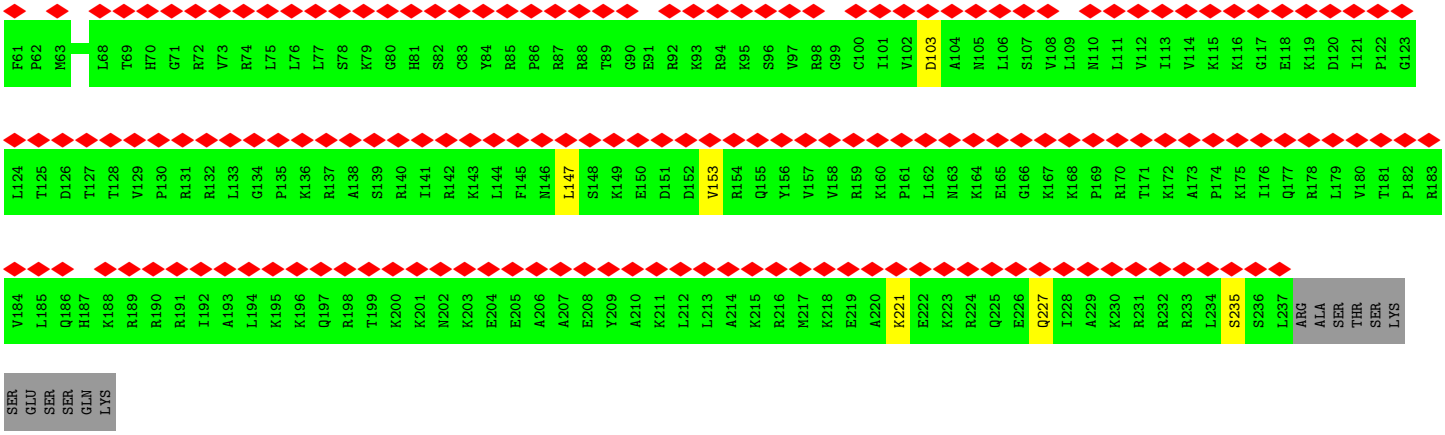


- Molecule 54: 40S ribosomal protein S6

Chain AK:

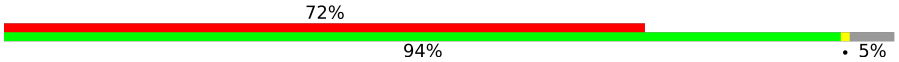


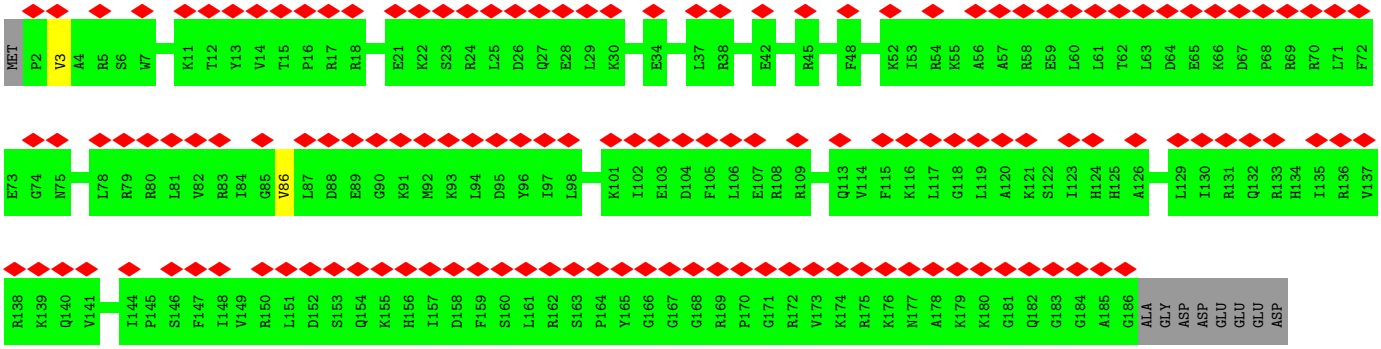




- Molecule 55: 40S ribosomal protein S9

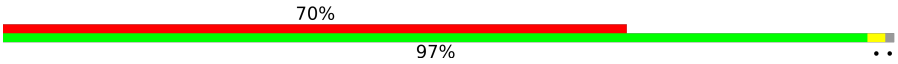
Chain AL:





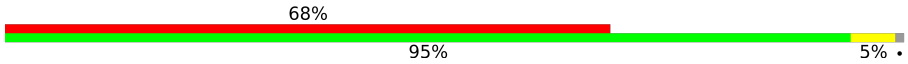
- Molecule 56: 40S ribosomal protein S13

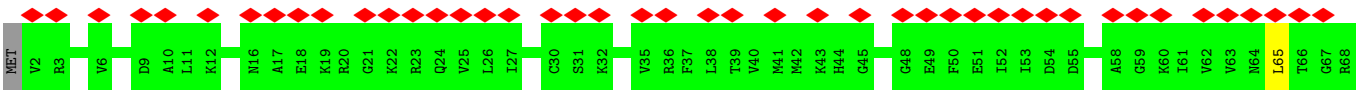
Chain AN:

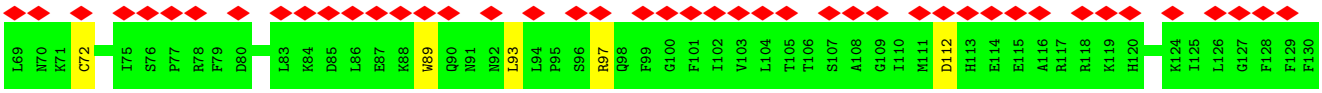


- Molecule 57: 40S ribosomal protein S15a

Chain AP:

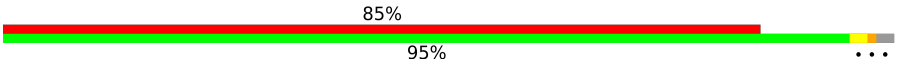






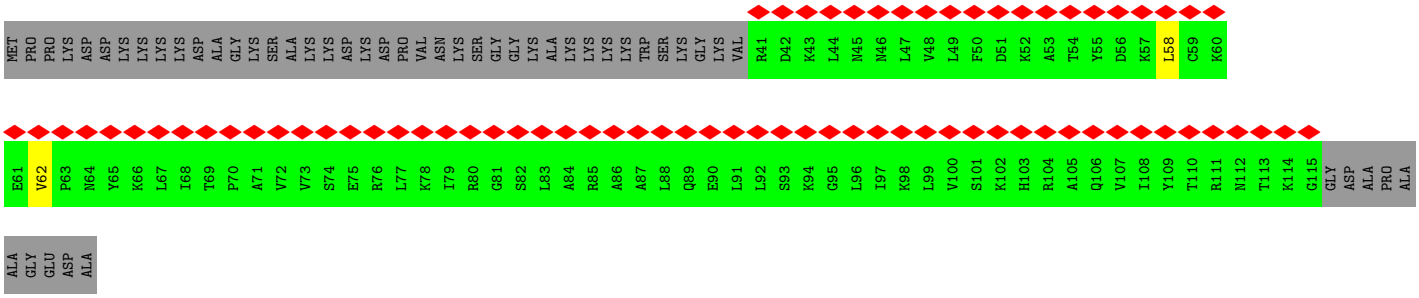
- Molecule 58: 40S ribosomal protein S24

Chain AQ:



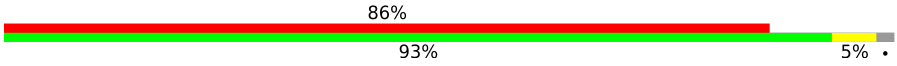
- Molecule 59: 40S ribosomal protein S25

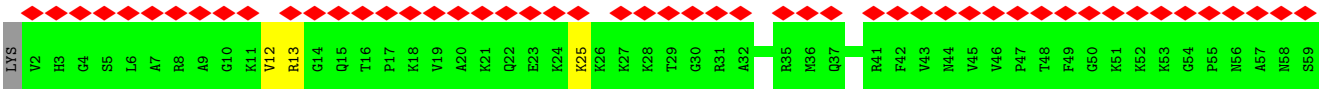
Chain AR:



- Molecule 60: 40S ribosomal protein S30

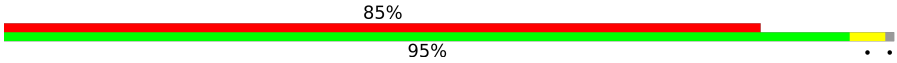
Chain AT:

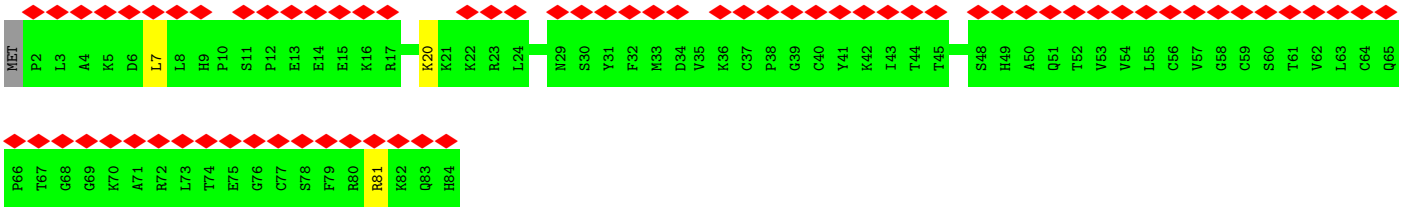




- Molecule 61: 40S ribosomal protein S27

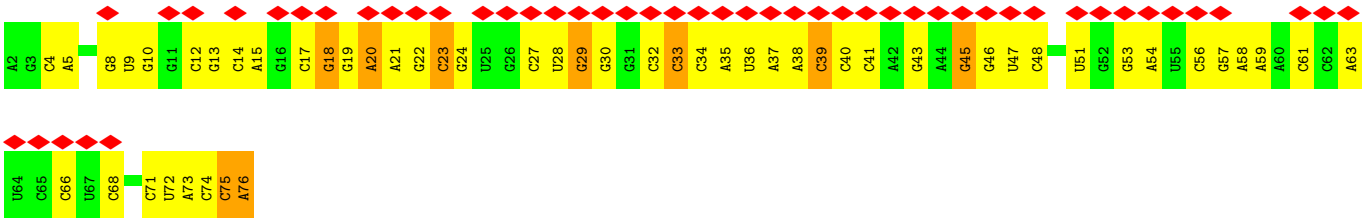
Chain AV:





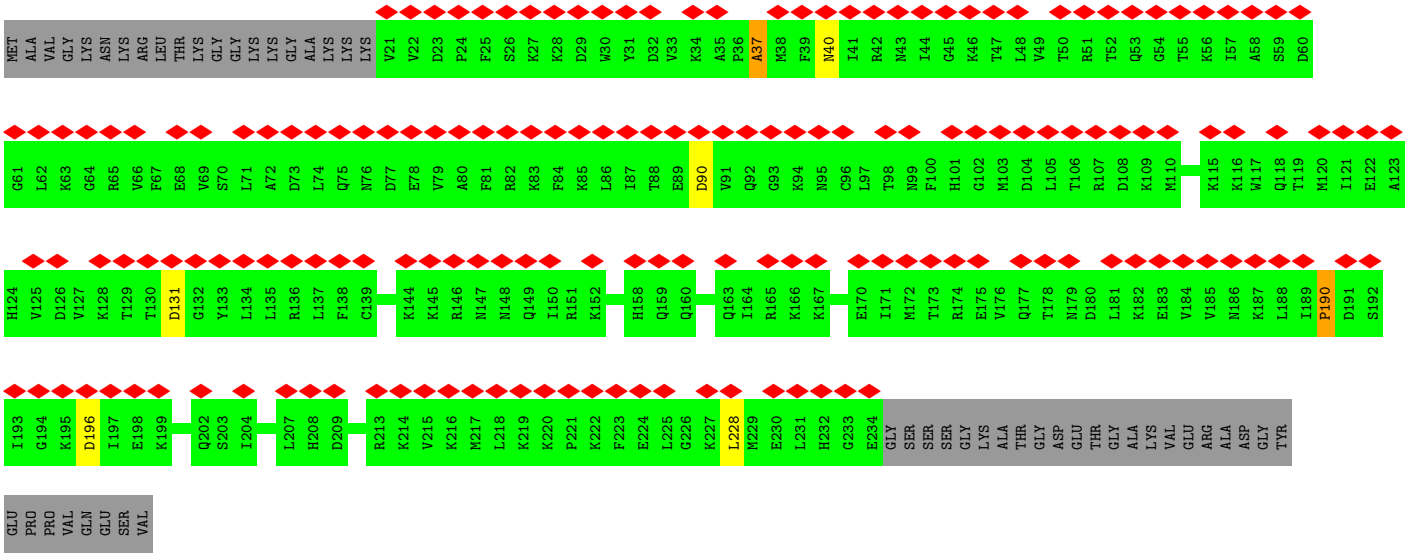
- Molecule 62: tRNA

Chain An:



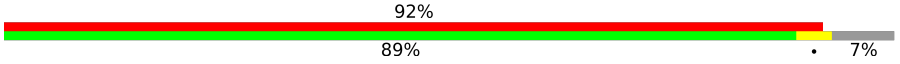
- Molecule 63: 40S ribosomal protein S3a

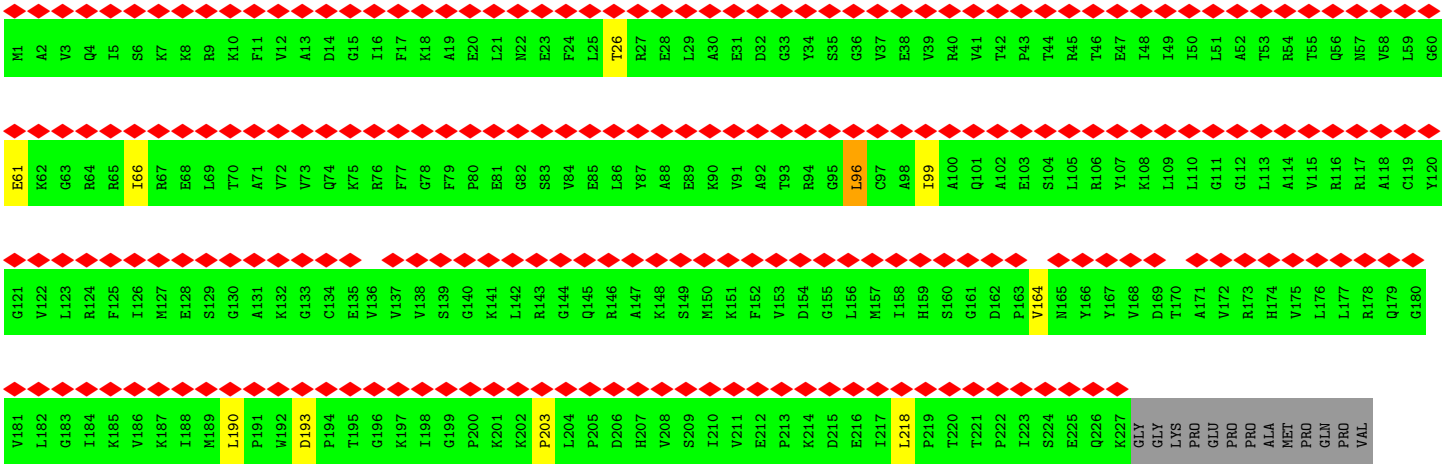
Chain Ap:



- Molecule 64: 40S ribosomal protein S3

Chain Aq:

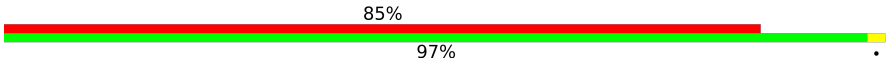




PRO
THR
ALA

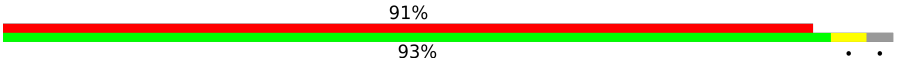
- Molecule 65: 40S ribosomal protein S4, X isoform

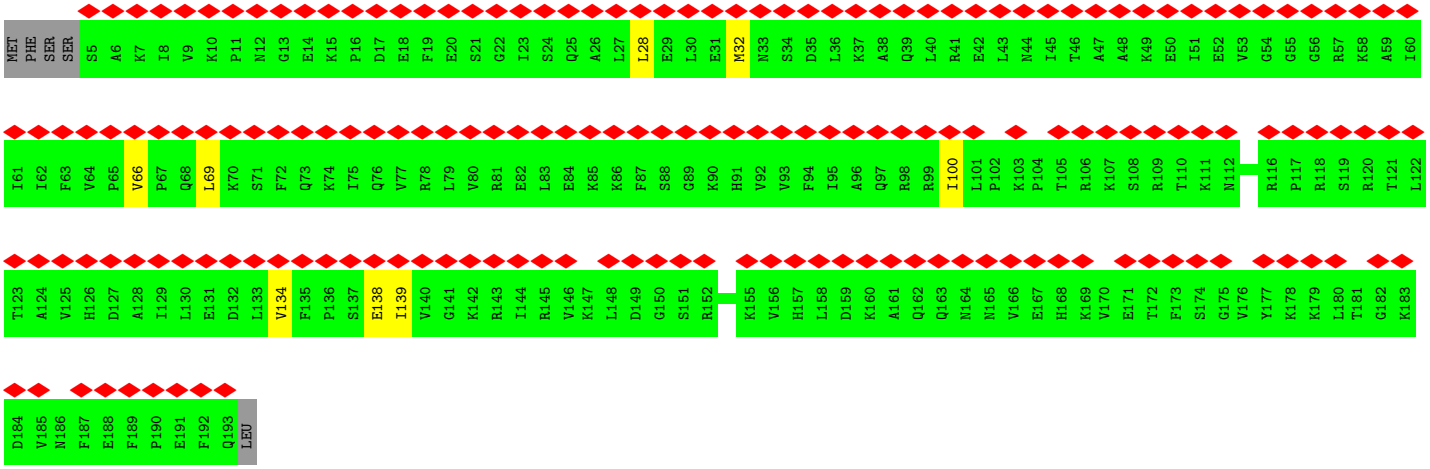
Chain Ar:



- Molecule 66: 40S ribosomal protein S7

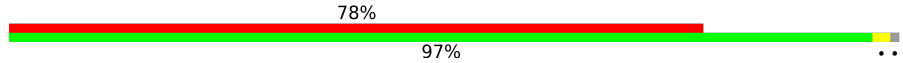
Chain At:

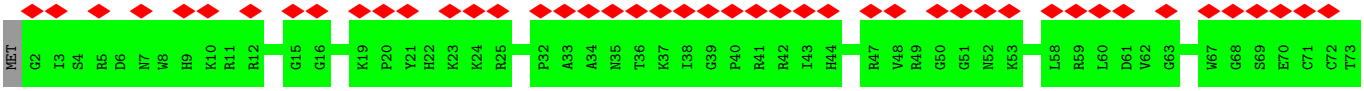




- Molecule 67: 40S ribosomal protein S8

Chain Au:





R74 K75 T76 R77 I78 I79 D80 V81 V82 Y83 N84 A85 S86 N87 N88 E89 L90 V91 R92 T93 K94 T95 L96 V97 K98 N99 C100 I101 V102 L103 I104 D105 S106 Y109 R110 Q111 W112 Y113 E114 S115 H116 Y117 A118 L119 P120 L121 G122 R123 K124 K125 G126 A127 K128 L129 T130 P131 E132 E133 E134

E135 I136 L137 N138 K139 K140 R141 S142 K143 K144 I145 Q146 K147 K148 Y149 D150 E151 R152 K153 K154 N155 A156 K157 I158 S159 S160 L161 L162 E163 E164 Q165 F166 Q167 Q168 G169 K170 L171 L172 A176 S177 R178 Q181 A185 D186 G187 L190 E191 G192 K193 E194 L195 E196 F197 Y198 L199 R200

K201 I202 K203 A204 R205 K206 G207 LYS

- Molecule 68: 40S ribosomal protein S10

Chain Av: 59% 58% 41%

M1 L2 M3 P4 K5 K6 N7 R8 I9 A10 I11 Y12 E13 L14 L15 F16 K17 E18 G19 V20 M21 V22 A23 K24 K25 D26 V27 H28 M29 P30 K31 H32 P33 E34 L35 A36 D37 K38 N39 V40 P41 N42 L43 H44 V45 M46 K47 A48 M49 Q50 S51 L52 K53 S54 R55 G56 Y57 V58 K59 E60

Q61 F62 A63 W64 R65 H66 F67 Y68 W69 Y70 L71 T72 N73 E74 G75 I76 Q77 Y78 L79 R80 D81 Y82 L83 H84 L85 P86 P87 E88 I89 V90 P91 A92 T93 L94 R95 R96 S97 R98 PRO GLU THR GLY ARG PRO ARG PRO LYS GLY LEU GLU GLY GLU ARG PRO ALA ARG LEU THR ARG GLY

GLU ALA ASP ARG ASP THR TYR ARG ARG SER ALA VAL PRO PRO GLY ALA ASP LYS LYS ALA GLU ALA GLY ALA GLY SER ALA THR GLU PHE GLN PHE ARG GLY GLY PHE GLY ARG GLY ARG GLY GLN PRO PRO GLN

- Molecule 69: 40S ribosomal protein S16

Chain Ay: 95% 95% 5%

M1 P2 S3 K4 G5 P6 L7 Q8 S9 V10 Q11 V12 F13 G14 R15 K16 K17 T18 A19 T20 A21 V22 A23 H24 C25 K26 R27 G28 N29 G30 L31 I32 K33 V34 N35 G36 R37 P38 L39 E40 M41 I42 E43 P44 R45 T46 L47 Q48 Y49 K50 L51 L52 E53 P54 V55 L56 L57 L58 G59 K60

E61 R62 F63 A64 G65 V66 D67 I68 R69 V70 R71 V72 K73 G74 G75 G76 H77 Q80 I81 Y82 A83 I84 R85 Q86 S87 I88 S89 K90 A91 L92 V93 A94 Y95 Y96 Q97 K98 Y99 V100 D101 E102 A103 S104 K105 K106 E107 I108 K109 D110 I111 L112 I113 Q114 Y115 D116 R117 T118 L119 L120 V121

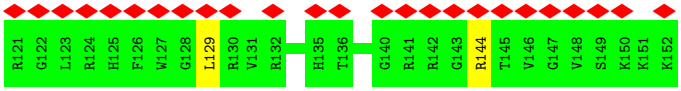
A122 D123 P124 R125 R126 C127 E128 S129 K130 G133 G134 P135 G136 A137 R138 A139 R140 Y141 Q142 K143 S144 Y145 R146

- Molecule 70: 40S ribosomal protein S18

Chain A0: 92% 91% 7%

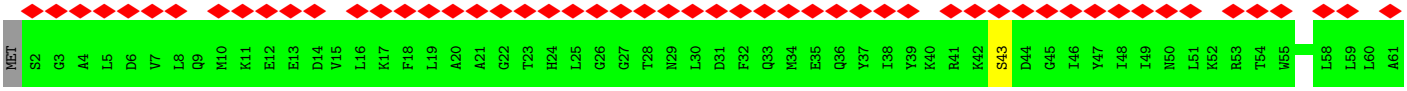
MET SER L3 V4 I5 P6 E7 K8 F9 Q10 H11 I12 L13 R14 V15 L16 N17 T18 N19 I20 D21 G22 R23 R24 K25 I26 A27 F28 A29 I30 T31 A32 I33 K34 G35 V36 G37 R38 R39 Y40 A41 H42 V43 V44 L45 R46 K47 A48 D49 I50 D51 L52 T53 K54 R55 A56 G57 E58 L59 T60

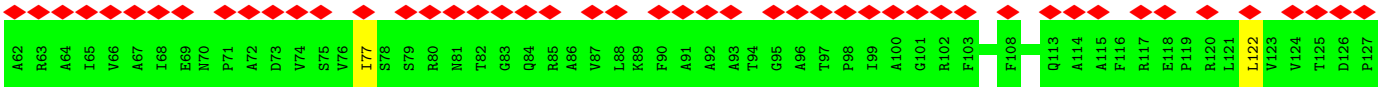
E61 D62 E63 V64 E65 R66 V67 I68 T69 I70 M71 Q72 N73 P74 R75 Q76 Y77 K78 I79 P80 D81 W82 F83 L84 N85 R86 Q87 K88 D89 V90 K91 D92 G93 K94 Y95 S96 Q97 V98 L99 A100 N101 G102 L103 D104 N105 K106 L107 R108 E109 D110 L111 E112 R113 L114 K115 K116 I117 R118 A119 H120

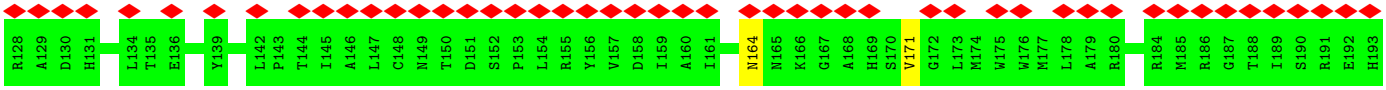


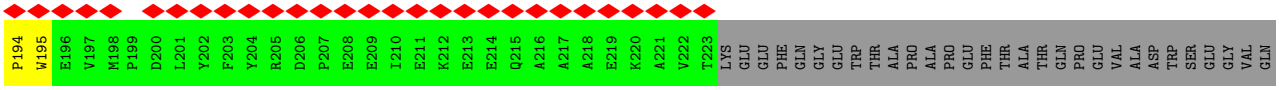
- Molecule 71: 40S ribosomal protein SA

Chain Ao:



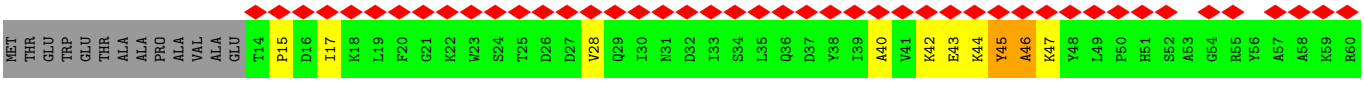


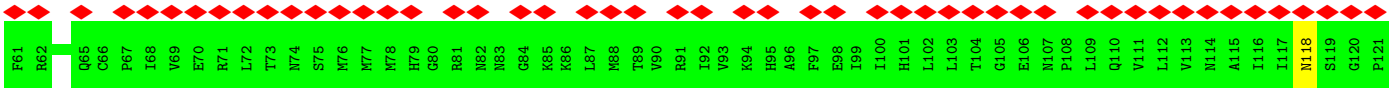


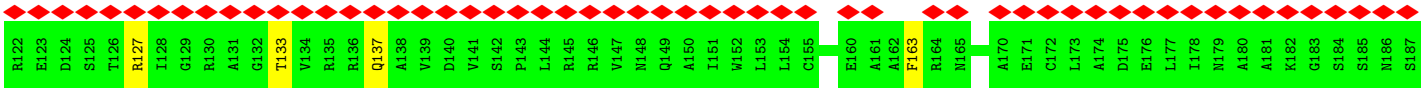


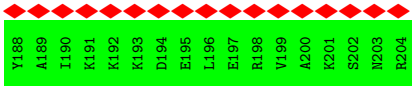
- Molecule 72: 40S ribosomal protein S5

Chain As:



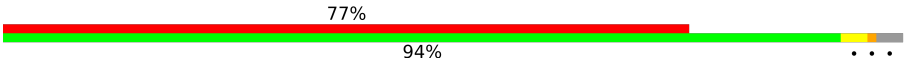


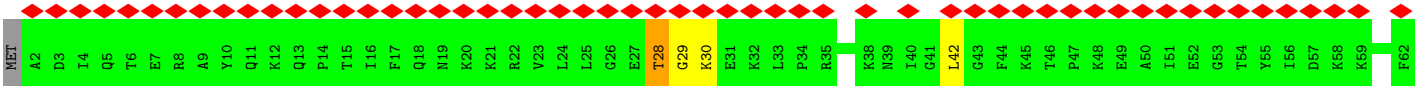


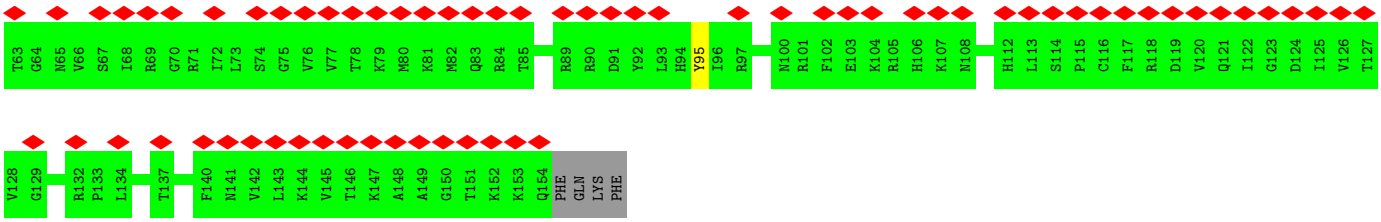


- Molecule 73: 40S ribosomal protein S11

Chain Aw:

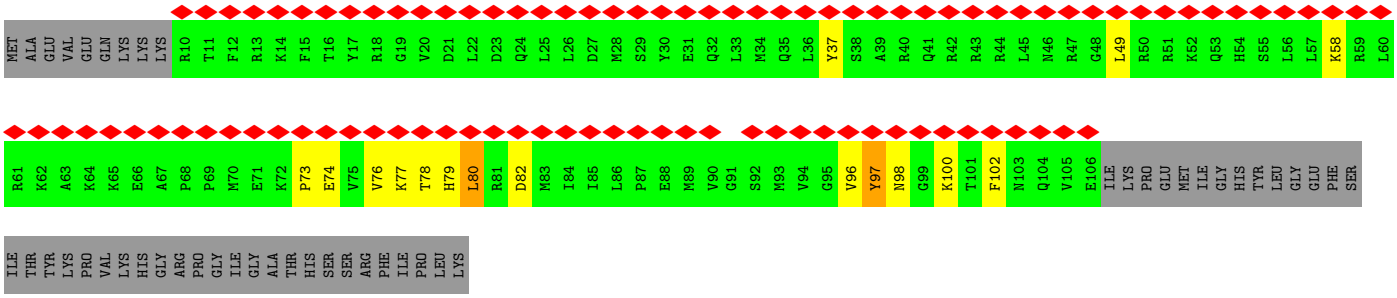






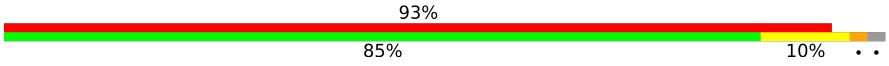
• Molecule 74: 40S ribosomal protein S15

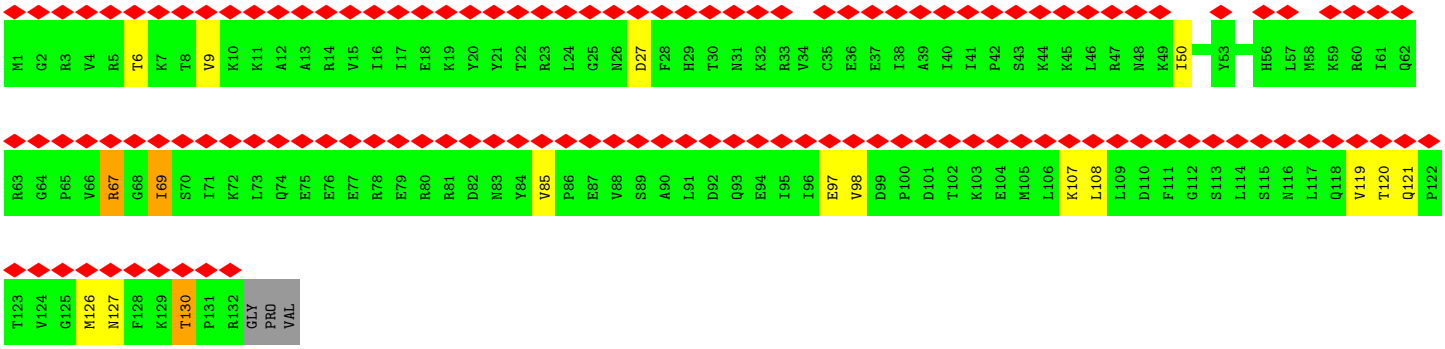
Chain Ax:



• Molecule 75: 40S ribosomal protein S17

Chain Az:



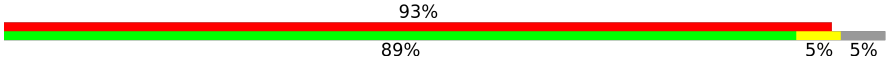


• Molecule 76: 40S ribosomal protein S20

Chain AB:

• Molecule 77: 40S ribosomal protein S29

Chain AG:



MET GLY HIS Q4 Q5 L6 Y7 W8 S9 H10 P11 R12 K13 F14 G15 Q16 G17 S18 R19 S20 C21 R22 V23 C24 S25 N26 R27 H28 G29 L30 I31 R32 K33 Y34 G35 L36 N37 M38 C39 R40 Q41 C42 F43 R44 Q45 Y46 A47 K48 D49 I50 G51 F52 I53 K54 L55 D56

- Molecule 78: Receptor of activated protein C kinase 1

Chain AI: 99% 95%

MET T2 E3 Q4 M5 T6 L7 R8 G9 T10 L11 K12 G13 H14 N15 G16 W17 V18 T19 Q20 I21 A22 T23 T24 P25 Q26 F27 P28 D29 M30 I31 L32 S33 A34 S35 R36 D37 K38 T39 I40 I41 M42 W43 K44 L45 T46 R47 D48 E49 T50 N51 Y52 G53 I54 P55 Q56 R57 A58 L59 R60

G61 H62 S63 H64 F65 V66 S67 D68 V69 V70 I71 S72 S73 D74 G75 Q76 F77 A78 L79 S80 G81 S82 W83 D84 G85 T86 L87 R88 L89 W90 D91 L92 T93 T94 G95 T96 T97 T98 R99 R100 F101 V102 G103 H104 T105 K106 D107 V108 L109 S110 V111 A112 F113 S114 S115 D116 N117 R118 Q119 I120

V121 S122 G123 S124 R125 D126 K127 T128 I129 K130 L131 W132 N133 T134 L135 G136 V137 C138 K139 Y140 T141 V142 Q143 D144 E145 S146 H147 S148 E149 W150 V151 S152 C153 V154 R155 F156 S157 P158 N159 S160 S161 N162 P163 I164 I165 V166 S167 C168 G169 W170 D171 K172 L173 V174 K175 V176 W177 N178 L179 A180

N181 C182 K183 L184 K185 T186 N187 H188 I189 G190 H191 T192 G193 Y194 L195 N196 T197 V198 T199 V200 S201 P202 D203 G204 S205 L206 C207 A208 S209 G210 G211 K212 D213 G214 Q215 A216 M217 L218 W219 D220 L221 N222 E223 G224 K225 H226 L227 Y228 T229 L230 D231 G232 G233 D234 I235 I236 N237 A238 L239 C240

F241 S242 P243 N244 R245 Y246 W247 L248 C249 A250 A251 T252 G253 P254 S255 I256 K257 I258 W259 D260 L261 E262 G263 K264 I265 I266 V267 D268 E269 L270 K271 Q272 E273 V274 I275 S276 T277 S278 S279 K280 A281 E282 P283 P284 Q285 C286 T287 S288 L289 A290 W291 S292 A293 D294 G295 Q296 T297 L298 F299 A300

G301 Y302 T303 D304 N305 L306 V307 R308 V309 W310 Q311 V312 T313 I314 GLY THR ARG

- Molecule 79: 40S ribosomal protein S12

Chain AM: 92% 88% 8%

MET ALA GLU GLU GLY ILE ALA ALA GLY GLY V11 M12 D13 V14 N15 T16 A17 L18 Q19 E20 V21 L22 K23 T24 A25 L26 I27 H28 D29 G30 L31 A32 R33 G34 I35 R36 E37 A38 A39 K40 A41 L42 D43 K44 R45 Q46 A47 H48 L49 C50 V51 Q52 A53 S54 N55 C56 D57 E58 P59 M60

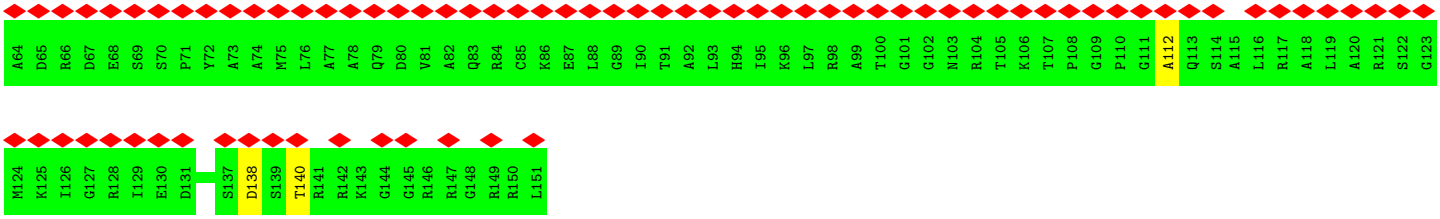
Y61 V62 K63 L64 V65 E66 A67 L68 L69 A70 E71 H72 Q73 I74 N75 L76 I77 K78 V79 D80 D81 N82 K83 K84 L85 G86 E87 W88 V89 G90 L91 C92 K93 I94 D95 R96 E97 G98 N99 P100 R101 K102 V103 V104 G105 C106 S107 C108 V109 V110 V111 K112 D113 Y114 G115 K116 E117 S118 Q119 A120

K121 D122 V123 I124 E125 E126 Y127 F128 K129 C130 K131 K132

- Molecule 80: 40S ribosomal protein S14

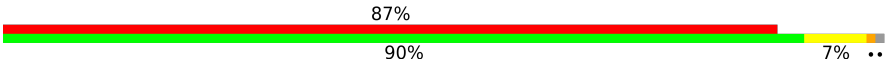
Chain AO: 78% 88% 5% 7%

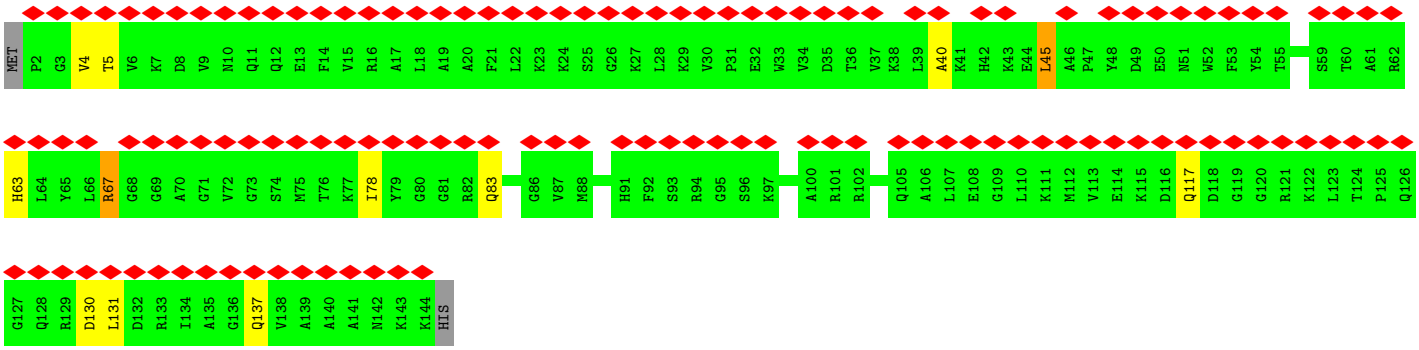
MET ALA PRO ARG LYS GLY LYS GLU LYS LYS GLU E12 Q13 V14 I15 S16 L17 G18 P19 Q20 V21 A22 E23 G24 E25 N26 V27 F28 G29 V30 I33 S36 F37 N38 F41 V42 H43 V44 T45 D46 L47 S48 G49 K50 E51 T52 I53 C54 R55 V56 T57 G58 G59 M60 K61 V62 K63



• Molecule 81: 40S ribosomal protein S19

Chain AU:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	175708	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	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	0.127	Depositor
Minimum map value	-0.052	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	374.50003, 374.50003, 374.50003	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	B	0.22	0/2858	0.68	0/4455
2	C	0.23	0/3701	0.71	3/5766 (0.1%)
3	D	0.28	0/1936	0.50	0/2596
4	E	0.26	0/3306	0.49	0/4424
5	F	0.25	0/2973	0.47	0/3992
6	G	0.26	0/2428	0.45	0/3252
7	I	0.26	0/1682	0.45	0/2250
8	J	0.26	0/1268	0.45	0/1701
9	L	0.24	0/1582	0.45	0/2091
10	N	0.26	0/1326	0.44	0/1770
11	O	0.27	0/839	0.46	0/1126
12	P	0.27	0/993	0.47	0/1332
13	Q	0.26	0/547	0.44	0/728
14	S	0.25	0/1132	0.46	0/1504
15	T	0.27	0/1130	0.47	0/1507
16	U	0.28	0/1191	0.51	0/1591
17	V	0.24	0/620	0.41	0/819
18	X	0.25	0/903	0.44	0/1216
19	Y	0.26	0/1071	0.46	0/1429
20	Z	0.27	0/895	0.50	0/1198
21	a	0.25	0/916	0.46	0/1220
22	b	0.24	0/1023	0.43	0/1351
23	c	0.25	0/843	0.44	0/1115
24	d	0.25	0/720	0.48	0/952
25	e	0.26	0/575	0.51	0/761
26	f	0.24	0/454	0.41	0/599
27	g	0.23	0/435	0.44	0/575
28	j	0.29	0/718	0.45	0/953
29	k	0.26	0/1017	0.49	0/1364
30	m	0.26	0/1905	0.42	0/2539
31	n	0.25	0/1960	0.45	0/2637
32	o	0.25	0/1537	0.49	0/2066
33	s	0.28	0/1161	0.45	0/1554
34	t	0.26	0/1746	0.48	1/2338 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	h	0.21	0/231	0.36	0/294
36	r	0.29	0/1732	0.51	2/2315 (0.1%)
37	A	0.24	0/89645	0.73	17/139764 (0.0%)
38	H	0.34	0/1996	0.86	9/2673 (0.3%)
39	i	0.26	0/876	0.47	0/1156
40	K	0.27	0/1537	0.70	1/2052 (0.0%)
41	l	0.29	0/1769	0.52	1/2371 (0.0%)
42	M	0.32	0/1493	0.50	0/2003
43	p	0.26	0/1751	0.48	0/2340
44	q	0.25	0/1432	0.46	0/1912
45	R	0.25	0/1002	0.44	0/1345
46	W	0.26	0/774	0.46	0/1038
47	AA	1.45	406/41243 (1.0%)	1.53	695/64257 (1.1%)
48	AC	0.64	0/643	0.79	0/860
49	AD	0.83	0/1116	0.85	1/1490 (0.1%)
50	AE	0.75	0/828	0.78	0/1109
51	AF	0.50	0/500	0.83	1/669 (0.1%)
52	AH	0.51	0/593	0.80	1/786 (0.1%)
53	AJ	0.75	0/1762	0.83	3/2381 (0.1%)
54	AK	0.48	0/1946	0.75	1/2590 (0.0%)
55	AL	0.61	0/1550	0.77	0/2069
56	AN	0.67	0/1226	0.79	2/1649 (0.1%)
57	AP	0.74	0/1051	0.93	4/1406 (0.3%)
58	AQ	0.59	1/1083 (0.1%)	0.79	1/1438 (0.1%)
59	AR	0.42	0/604	0.80	1/810 (0.1%)
60	AT	0.54	0/465	0.73	0/612
61	AV	0.58	0/665	0.75	1/891 (0.1%)
62	An	1.24	10/1795 (0.6%)	1.64	46/2798 (1.6%)
63	Ap	0.66	0/1765	0.78	1/2362 (0.0%)
64	Aq	0.54	2/1793 (0.1%)	0.77	2/2414 (0.1%)
65	Ar	0.60	0/2118	0.72	0/2849
66	At	0.53	0/1544	0.79	3/2068 (0.1%)
67	Au	0.69	0/1715	0.76	1/2287 (0.0%)
68	Av	0.45	0/851	0.79	0/1147
69	Ay	0.49	0/1177	0.74	0/1575
70	A0	0.50	0/1253	0.84	1/1676 (0.1%)
71	Ao	0.68	0/1784	0.76	1/2424 (0.0%)
72	As	0.48	0/1531	0.76	1/2059 (0.0%)
73	Aw	0.79	1/1268 (0.1%)
74	Ax	0.44	0/815	0.78	1/1087 (0.1%)
75	Az	0.55	0/1086	0.84	0/1457
76	AB	0.47	0/817	0.84	2/1097 (0.2%)
77	AG	0.52	0/455	0.68	0/603

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	AI	0.46	0/2493	0.75	3/3394 (0.1%)
79	AM	0.41	0/962	0.80	1/1290 (0.1%)
80	AO	0.61	0/1062	0.83	0/1425
81	AU	0.52	0/1131	0.82	2/1515 (0.1%)
All	All	0.69	420/234319 (0.2%)	0.92	811/344274 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	F	0	1
11	O	0	1
33	s	0	1
38	H	0	1
39	i	0	1
40	K	0	1
48	AC	0	1
49	AD	0	3
52	AH	0	2
53	AJ	0	1
54	AK	0	5
55	AL	0	1
56	AN	0	1
59	AR	0	1
60	AT	0	3
61	AV	0	1
63	Ap	0	3
64	Aq	0	3
65	Ar	0	2
66	At	0	3
67	Au	0	1
68	Av	0	1
69	Ay	0	5
70	A0	0	4
71	Ao	0	4
72	As	0	6
75	Az	0	4
76	AB	0	4
78	AI	0	5
79	AM	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
80	AO	0	2
81	AU	0	4
All	All	0	78

All (420) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	1031	A	N9-C4	-10.37	1.31	1.37
47	AA	1170	A	N9-C4	-9.35	1.32	1.37
47	AA	1815	A	N9-C4	-9.17	1.32	1.37
47	AA	1815	A	N3-C4	-8.95	1.29	1.34
47	AA	1173	A	N9-C4	-8.77	1.32	1.37
47	AA	1357	A	N9-C4	-8.60	1.32	1.37
47	AA	1828	C	N1-C6	-8.48	1.32	1.37
47	AA	1861	G	N1-C2	-8.36	1.31	1.37
47	AA	997	A	N7-C5	-8.32	1.34	1.39
47	AA	1189	A	N9-C4	-8.21	1.32	1.37
47	AA	1815	A	C5-C4	-8.01	1.33	1.38
47	AA	1717	C	N1-C6	-7.97	1.32	1.37
47	AA	1813	A	N9-C4	-7.95	1.33	1.37
47	AA	1130	G	N9-C4	-7.88	1.31	1.38
47	AA	1173	A	C5-C4	-7.86	1.33	1.38
47	AA	1861	G	C6-N1	-7.82	1.34	1.39
47	AA	1144	A	N9-C4	-7.80	1.33	1.37
47	AA	1173	A	C5-C6	-7.70	1.34	1.41
47	AA	1144	A	N3-C4	-7.67	1.30	1.34
47	AA	1353	A	N9-C4	-7.62	1.33	1.37
47	AA	1719	A	C6-N1	-7.62	1.30	1.35
47	AA	1863	A	N3-C4	-7.60	1.30	1.34
47	AA	1173	A	N7-C5	-7.59	1.34	1.39
47	AA	1863	A	N9-C4	-7.57	1.33	1.37
47	AA	1089	G	N3-C4	-7.49	1.30	1.35
47	AA	1024	A	N9-C4	-7.47	1.33	1.37
47	AA	1076	G	N9-C4	-7.37	1.32	1.38
47	AA	1846	G	N3-C4	-7.34	1.30	1.35
47	AA	1726	G	N9-C4	-7.32	1.32	1.38
47	AA	1814	G	C5-C4	-7.28	1.33	1.38
47	AA	1031	A	N3-C4	-7.28	1.30	1.34
47	AA	16	G	N3-C4	-7.26	1.30	1.35
47	AA	670	A	N9-C4	-7.25	1.33	1.37
47	AA	1719	A	N3-C4	-7.22	1.30	1.34
47	AA	1719	A	C5-C4	-7.18	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	996	A	C5-C6	-7.17	1.34	1.41
47	AA	659	G	C6-N1	-7.14	1.34	1.39
47	AA	1834	A	N7-C5	-7.13	1.34	1.39
47	AA	997	A	N3-C4	-7.12	1.30	1.34
47	AA	1846	G	C5-C4	-7.12	1.33	1.38
47	AA	653	A	N9-C4	-7.11	1.33	1.37
47	AA	1199	A	N9-C4	-7.07	1.33	1.37
47	AA	668	A	C5-C4	-7.05	1.33	1.38
47	AA	1173	A	N3-C4	-7.03	1.30	1.34
47	AA	1189	A	N3-C4	-7.03	1.30	1.34
47	AA	99	A	N9-C4	-6.97	1.33	1.37
47	AA	1170	A	N3-C4	-6.95	1.30	1.34
47	AA	1171	G	C5-C4	-6.94	1.33	1.38
47	AA	398	A	N9-C4	-6.94	1.33	1.37
47	AA	665	G	C5-C4	-6.94	1.33	1.38
47	AA	1087	A	N9-C4	-6.93	1.33	1.37
47	AA	1819	A	N9-C4	-6.92	1.33	1.37
47	AA	1815	A	C6-N1	-6.89	1.30	1.35
47	AA	1855	G	C5-C4	-6.89	1.33	1.38
47	AA	389	A	N9-C4	-6.86	1.33	1.37
47	AA	1189	A	C5-C4	-6.84	1.33	1.38
47	AA	1144	A	N7-C5	-6.83	1.35	1.39
47	AA	1813	A	N3-C4	-6.83	1.30	1.34
62	An	5	A	N9-C4	-6.82	1.33	1.37
47	AA	1198	G	N9-C4	-6.81	1.32	1.38
47	AA	669	A	N3-C4	-6.80	1.30	1.34
47	AA	1145	A	N9-C4	-6.80	1.33	1.37
47	AA	1082	A	N7-C5	-6.80	1.35	1.39
47	AA	1196	A	N9-C4	-6.79	1.33	1.37
47	AA	460	A	N9-C4	-6.78	1.33	1.37
47	AA	1198	G	N3-C4	-6.78	1.30	1.35
47	AA	1172	U	C2-N3	-6.76	1.33	1.37
47	AA	11	A	N9-C4	-6.72	1.33	1.37
47	AA	1028	A	N9-C4	-6.71	1.33	1.37
47	AA	16	G	C5-C4	-6.70	1.33	1.38
47	AA	995	G	N9-C4	-6.63	1.32	1.38
47	AA	1184	G	C6-N1	-6.62	1.34	1.39
47	AA	7	G	N9-C4	-6.61	1.32	1.38
47	AA	1187	G	N7-C5	-6.60	1.35	1.39
47	AA	1096	G	N9-C4	-6.58	1.32	1.38
47	AA	1034	A	N9-C4	-6.56	1.33	1.37
47	AA	1791	A	N9-C4	-6.56	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	1176	G	N3-C4	-6.55	1.30	1.35
47	AA	1722	G	C5-C4	-6.55	1.33	1.38
47	AA	1169	G	C5-C4	-6.53	1.33	1.38
47	AA	1717	C	N1-C2	-6.52	1.33	1.40
47	AA	1169	G	N3-C4	-6.52	1.30	1.35
47	AA	16	G	N9-C4	-6.50	1.32	1.38
47	AA	990	A	N9-C4	-6.50	1.33	1.37
47	AA	1199	A	N3-C4	-6.49	1.30	1.34
47	AA	1184	G	C5-C4	-6.47	1.33	1.38
47	AA	1200	A	N9-C4	-6.46	1.33	1.37
47	AA	1175	G	N3-C4	-6.44	1.30	1.35
47	AA	996	A	N7-C5	-6.43	1.35	1.39
47	AA	1814	G	N1-C2	-6.40	1.32	1.37
47	AA	1028	A	N7-C5	-6.40	1.35	1.39
47	AA	1029	G	N3-C4	-6.40	1.30	1.35
47	AA	1055	A	N9-C4	-6.39	1.34	1.37
47	AA	1187	G	C5-C4	-6.38	1.33	1.38
47	AA	1029	G	C5-C4	-6.38	1.33	1.38
47	AA	996	A	N9-C4	-6.38	1.34	1.37
47	AA	1854	U	C2-N3	-6.37	1.33	1.37
47	AA	668	A	C5-C6	-6.37	1.35	1.41
47	AA	664	A	N3-C4	-6.34	1.31	1.34
47	AA	1182	A	N9-C4	-6.33	1.34	1.37
47	AA	1066	U	N1-C2	-6.32	1.32	1.38
47	AA	1856	C	N1-C6	-6.30	1.33	1.37
47	AA	1847	G	N3-C4	-6.29	1.31	1.35
47	AA	659	G	N7-C5	-6.28	1.35	1.39
47	AA	1144	A	C6-N1	-6.28	1.31	1.35
47	AA	1103	C	N1-C6	-6.28	1.33	1.37
47	AA	1034	A	C5-C4	-6.25	1.34	1.38
47	AA	1165	G	N7-C5	-6.24	1.35	1.39
47	AA	1085	C	N1-C6	-6.24	1.33	1.37
62	An	75	C	N1-C6	-6.24	1.33	1.37
47	AA	673	G	N9-C8	-6.23	1.33	1.37
58	AQ	51	THR	C-N	-6.22	1.22	1.34
47	AA	668	A	N7-C5	-6.22	1.35	1.39
47	AA	42	A	C5-C6	-6.21	1.35	1.41
47	AA	1065	G	N3-C4	-6.21	1.31	1.35
47	AA	1175	G	C6-N1	-6.20	1.35	1.39
47	AA	1089	G	N9-C4	-6.20	1.32	1.38
47	AA	1834	A	N3-C4	-6.20	1.31	1.34
47	AA	11	A	N3-C4	-6.19	1.31	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	1185	C	N1-C6	-6.18	1.33	1.37
47	AA	1846	G	C6-N1	-6.18	1.35	1.39
62	An	72	U	N1-C2	-6.17	1.33	1.38
47	AA	473	A	N9-C4	-6.13	1.34	1.37
47	AA	1150	A	N9-C4	-6.13	1.34	1.37
47	AA	964	A	N9-C4	-6.13	1.34	1.37
47	AA	1037	G	N3-C4	-6.12	1.31	1.35
47	AA	1158	G	C5-C4	-6.11	1.34	1.38
47	AA	669	A	N7-C5	-6.10	1.35	1.39
47	AA	668	A	N3-C4	-6.10	1.31	1.34
47	AA	1190	A	N3-C4	-6.09	1.31	1.34
47	AA	1175	G	C5-C4	-6.08	1.34	1.38
47	AA	619	A	N9-C4	-6.07	1.34	1.37
47	AA	1031	A	N7-C5	-6.07	1.35	1.39
47	AA	1723	G	C5-C4	-6.07	1.34	1.38
47	AA	1693	G	N9-C4	-6.06	1.33	1.38
47	AA	1164	G	C5-C4	-6.06	1.34	1.38
47	AA	1036	A	N3-C4	-6.05	1.31	1.34
47	AA	618	C	N1-C6	-6.05	1.33	1.37
47	AA	1814	G	N9-C8	-6.05	1.33	1.37
47	AA	672	A	N9-C4	-6.04	1.34	1.37
47	AA	1190	A	N9-C4	-6.03	1.34	1.37
47	AA	1179	G	C5-C4	-6.03	1.34	1.38
47	AA	1196	A	C5-C4	-6.03	1.34	1.38
47	AA	1033	G	C6-N1	-6.01	1.35	1.39
47	AA	1175	G	N9-C4	-6.01	1.33	1.38
47	AA	670	A	C5-C4	-6.01	1.34	1.38
47	AA	982	G	N3-C4	-6.01	1.31	1.35
47	AA	670	A	N7-C5	-6.01	1.35	1.39
47	AA	682	U	C2-N3	-6.01	1.33	1.37
47	AA	42	A	N9-C4	-5.99	1.34	1.37
47	AA	669	A	N9-C4	-5.99	1.34	1.37
47	AA	601	G	C6-N1	-5.98	1.35	1.39
47	AA	662	G	C5-C4	-5.98	1.34	1.38
47	AA	1080	A	N9-C4	-5.98	1.34	1.37
47	AA	987	A	N9-C4	-5.97	1.34	1.37
47	AA	677	G	C5-C4	-5.97	1.34	1.38
47	AA	1813	A	C5-C4	-5.95	1.34	1.38
47	AA	1190	A	C5-C4	-5.94	1.34	1.38
47	AA	1194	A	N3-C4	-5.94	1.31	1.34
47	AA	1049	A	C5-C6	-5.94	1.35	1.41
47	AA	1096	G	N3-C4	-5.94	1.31	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	14	C	N1-C2	-5.94	1.34	1.40
47	AA	361	U	C2-N3	-5.93	1.33	1.37
47	AA	1081	U	C2-N3	-5.92	1.33	1.37
64	Aq	190	LEU	C-N	-5.91	1.23	1.34
47	AA	1182	A	N7-C5	-5.91	1.35	1.39
47	AA	1164	G	C6-N1	-5.89	1.35	1.39
47	AA	670	A	N3-C4	-5.89	1.31	1.34
47	AA	1167	G	C6-N1	-5.89	1.35	1.39
47	AA	389	A	N3-C4	-5.89	1.31	1.34
47	AA	1169	G	C6-N1	-5.88	1.35	1.39
47	AA	649	U	C2-N3	-5.87	1.33	1.37
47	AA	668	A	N9-C8	-5.86	1.33	1.37
47	AA	1187	G	C5-C6	-5.86	1.36	1.42
47	AA	1062	A	N9-C4	-5.85	1.34	1.37
62	An	71	C	N1-C6	-5.85	1.33	1.37
47	AA	1096	G	C5-C4	-5.84	1.34	1.38
47	AA	13	C	N1-C6	-5.83	1.33	1.37
47	AA	14	C	N3-C4	-5.83	1.29	1.33
47	AA	1083	A	N9-C4	-5.83	1.34	1.37
47	AA	1354	G	C5-C4	-5.83	1.34	1.38
47	AA	1724	A	N9-C4	-5.81	1.34	1.37
47	AA	1719	A	C5-C6	-5.81	1.35	1.41
47	AA	1693	G	N3-C4	-5.80	1.31	1.35
47	AA	1164	G	N1-C2	-5.80	1.33	1.37
47	AA	1719	A	N7-C5	-5.80	1.35	1.39
47	AA	664	A	C5-C6	-5.80	1.35	1.41
47	AA	1198	G	N7-C5	-5.79	1.35	1.39
47	AA	605	A	N9-C4	-5.79	1.34	1.37
47	AA	1823	A	N9-C4	-5.78	1.34	1.37
47	AA	1186	U	C2-N3	-5.77	1.33	1.37
47	AA	1855	G	N9-C8	-5.76	1.33	1.37
47	AA	1353	A	N3-C4	-5.75	1.31	1.34
47	AA	659	G	C5-C4	-5.75	1.34	1.38
47	AA	1198	G	C2-N3	-5.75	1.28	1.32
47	AA	1055	A	C5-C4	-5.75	1.34	1.38
47	AA	363	A	N9-C4	-5.74	1.34	1.37
47	AA	1172	U	N1-C2	-5.74	1.33	1.38
47	AA	657	U	N1-C2	-5.74	1.33	1.38
47	AA	410	G	N3-C4	-5.73	1.31	1.35
47	AA	1801	A	N9-C4	-5.73	1.34	1.37
47	AA	1142	G	C5-C4	-5.72	1.34	1.38
47	AA	1846	G	N7-C5	-5.72	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	664	A	N7-C5	-5.71	1.35	1.39
47	AA	1169	G	N7-C5	-5.71	1.35	1.39
47	AA	667	U	N1-C2	-5.70	1.33	1.38
47	AA	880	G	N3-C4	-5.70	1.31	1.35
64	Aq	218	LEU	C-N	5.70	1.45	1.34
47	AA	397	G	N9-C4	-5.69	1.33	1.38
47	AA	1182	A	C5-C4	-5.69	1.34	1.38
47	AA	476	A	C6-N1	-5.68	1.31	1.35
47	AA	512	A	N9-C4	-5.68	1.34	1.37
47	AA	672	A	N7-C5	-5.68	1.35	1.39
47	AA	1814	G	C6-N1	-5.68	1.35	1.39
47	AA	1147	C	N1-C6	-5.67	1.33	1.37
47	AA	1846	G	N9-C4	-5.67	1.33	1.38
47	AA	14	C	N1-C6	-5.67	1.33	1.37
47	AA	964	A	N3-C4	-5.66	1.31	1.34
47	AA	1713	C	N1-C6	-5.66	1.33	1.37
47	AA	653	A	N3-C4	-5.66	1.31	1.34
47	AA	1175	G	N1-C2	-5.66	1.33	1.37
47	AA	659	G	N3-C4	-5.66	1.31	1.35
47	AA	1840	U	C2-N3	-5.65	1.33	1.37
47	AA	1809	A	C5-C4	-5.65	1.34	1.38
47	AA	1854	U	N1-C2	-5.65	1.33	1.38
47	AA	1171	G	N9-C8	-5.65	1.33	1.37
47	AA	1165	G	N3-C4	-5.65	1.31	1.35
47	AA	11	A	C5-C4	-5.65	1.34	1.38
47	AA	432	G	C5-C4	-5.64	1.34	1.38
47	AA	880	G	C2-N3	-5.64	1.28	1.32
47	AA	1853	C	N1-C6	-5.64	1.33	1.37
47	AA	1065	G	N9-C4	-5.64	1.33	1.38
47	AA	1845	A	N9-C4	-5.63	1.34	1.37
47	AA	1847	G	C5-C4	-5.61	1.34	1.38
47	AA	919	A	N7-C5	-5.61	1.35	1.39
47	AA	1803	U	C2-N3	-5.61	1.33	1.37
47	AA	1722	G	N3-C4	-5.61	1.31	1.35
47	AA	997	A	N9-C4	-5.61	1.34	1.37
47	AA	173	A	C5-C6	-5.60	1.36	1.41
47	AA	420	G	N9-C4	-5.59	1.33	1.38
47	AA	1169	G	N9-C4	-5.59	1.33	1.38
47	AA	1198	G	N9-C8	-5.59	1.33	1.37
47	AA	1852	C	N1-C6	-5.59	1.33	1.37
47	AA	1149	A	N7-C5	-5.59	1.35	1.39
47	AA	362	C	N1-C6	-5.59	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	1828	C	N1-C2	-5.58	1.34	1.40
47	AA	1029	G	C6-N1	-5.58	1.35	1.39
47	AA	1144	A	C5-C4	-5.58	1.34	1.38
47	AA	379	C	N1-C6	-5.57	1.33	1.37
47	AA	662	G	N9-C8	-5.56	1.33	1.37
47	AA	1201	U	C2-N3	-5.55	1.33	1.37
47	AA	410	G	C6-N1	-5.55	1.35	1.39
62	An	4	C	N1-C6	-5.55	1.33	1.37
47	AA	19	A	N9-C4	-5.54	1.34	1.37
47	AA	1033	G	N7-C5	-5.54	1.35	1.39
47	AA	1700	C	N1-C6	-5.53	1.33	1.37
47	AA	1144	A	C5-C6	-5.53	1.36	1.41
47	AA	1863	A	C6-N1	-5.53	1.31	1.35
47	AA	1071	G	N7-C5	-5.53	1.35	1.39
47	AA	1087	A	N3-C4	-5.53	1.31	1.34
47	AA	1176	G	N9-C4	-5.52	1.33	1.38
47	AA	1863	A	C5-C6	-5.52	1.36	1.41
47	AA	1142	G	C6-N1	-5.51	1.35	1.39
47	AA	98	C	N1-C6	-5.50	1.33	1.37
47	AA	1379	A	N7-C5	-5.50	1.35	1.39
47	AA	665	G	N9-C4	-5.49	1.33	1.38
47	AA	997	A	C5-C6	-5.49	1.36	1.41
47	AA	404	G	C5-C4	-5.49	1.34	1.38
47	AA	1847	G	N9-C4	-5.49	1.33	1.38
47	AA	1198	G	C5-C4	-5.48	1.34	1.38
47	AA	997	A	C6-N1	-5.48	1.31	1.35
47	AA	1165	G	C5-C4	-5.47	1.34	1.38
47	AA	669	A	C6-N1	-5.46	1.31	1.35
47	AA	1166	G	C5-C4	-5.45	1.34	1.38
47	AA	1184	G	N3-C4	-5.45	1.31	1.35
47	AA	1150	A	N3-C4	-5.45	1.31	1.34
47	AA	349	A	N9-C4	-5.44	1.34	1.37
47	AA	1026	C	C2-N3	-5.44	1.31	1.35
47	AA	1834	A	C6-N1	-5.43	1.31	1.35
47	AA	1050	A	N3-C4	-5.42	1.31	1.34
47	AA	1173	A	N9-C8	-5.42	1.33	1.37
47	AA	428	U	N1-C2	-5.42	1.33	1.38
47	AA	1033	G	C5-C6	-5.42	1.36	1.42
47	AA	1731	A	C5-C4	-5.41	1.34	1.38
47	AA	7	G	C5-C4	-5.41	1.34	1.38
47	AA	1355	C	N1-C6	-5.41	1.33	1.37
47	AA	1726	G	N3-C4	-5.40	1.31	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	16	G	C2-N3	-5.40	1.28	1.32
47	AA	1083	A	C5-C4	-5.39	1.34	1.38
47	AA	1199	A	C5-C4	-5.39	1.34	1.38
47	AA	1139	C	N1-C6	-5.39	1.33	1.37
47	AA	1036	A	C5-C4	-5.39	1.34	1.38
62	An	15	A	N9-C4	-5.39	1.34	1.37
47	AA	659	G	C5-C6	-5.38	1.36	1.42
47	AA	1143	A	N7-C5	-5.38	1.36	1.39
47	AA	1141	G	C6-N1	-5.38	1.35	1.39
47	AA	1141	G	C5-C4	-5.37	1.34	1.38
47	AA	1176	G	C2-N3	-5.37	1.28	1.32
47	AA	1173	A	C6-N1	-5.37	1.31	1.35
47	AA	469	A	N9-C4	-5.36	1.34	1.37
47	AA	1855	G	N9-C4	-5.35	1.33	1.38
47	AA	1815	A	N7-C5	-5.35	1.36	1.39
47	AA	670	A	C6-N1	-5.34	1.31	1.35
47	AA	1855	G	C5-C6	-5.34	1.37	1.42
47	AA	1065	G	C6-N1	-5.33	1.35	1.39
47	AA	995	G	C5-C4	-5.33	1.34	1.38
47	AA	679	A	C5-C4	-5.33	1.35	1.38
47	AA	1140	G	N3-C4	-5.33	1.31	1.35
47	AA	1727	G	C5-C4	-5.33	1.34	1.38
47	AA	1845	A	N3-C4	-5.31	1.31	1.34
47	AA	16	G	C6-N1	-5.31	1.35	1.39
62	An	75	C	N1-C2	-5.31	1.34	1.40
47	AA	1356	G	C6-N1	-5.30	1.35	1.39
47	AA	1361	G	C5-C4	-5.29	1.34	1.38
47	AA	610	G	N9-C4	-5.29	1.33	1.38
47	AA	990	A	N3-C4	-5.29	1.31	1.34
47	AA	669	A	C5-C6	-5.29	1.36	1.41
47	AA	683	G	N9-C4	-5.29	1.33	1.38
47	AA	945	U	C2-N3	-5.29	1.34	1.37
47	AA	1855	G	N1-C2	-5.28	1.33	1.37
47	AA	1379	A	N9-C4	-5.28	1.34	1.37
47	AA	1062	A	C5-C4	-5.28	1.35	1.38
73	Aw	95	TYR	CD2-CE2	-5.28	1.31	1.39
47	AA	1709	G	N9-C4	-5.27	1.33	1.38
47	AA	1195	A	N3-C4	-5.27	1.31	1.34
47	AA	1031	A	C5-C4	-5.27	1.35	1.38
47	AA	1822	A	N9-C4	-5.26	1.34	1.37
47	AA	388	U	C2-N3	-5.26	1.34	1.37
47	AA	402	C	C2-N3	-5.26	1.31	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	434	G	N9-C4	-5.25	1.33	1.38
62	An	75	C	C2-N3	-5.25	1.31	1.35
47	AA	1846	G	N1-C2	-5.25	1.33	1.37
47	AA	1143	A	N3-C4	-5.25	1.31	1.34
47	AA	1836	G	C5-C4	-5.25	1.34	1.38
47	AA	14	C	C2-N3	-5.24	1.31	1.35
62	An	73	A	N9-C4	-5.24	1.34	1.37
47	AA	1165	G	C5-C6	-5.24	1.37	1.42
47	AA	1182	A	N3-C4	-5.24	1.31	1.34
47	AA	982	G	N9-C4	-5.23	1.33	1.38
47	AA	1198	G	C6-N1	-5.23	1.35	1.39
47	AA	1813	A	C5-C6	-5.23	1.36	1.41
47	AA	1722	G	N9-C4	-5.23	1.33	1.38
47	AA	1176	G	C6-N1	-5.23	1.35	1.39
47	AA	1828	C	N3-C4	-5.22	1.30	1.33
47	AA	1183	A	C5-C6	-5.22	1.36	1.41
47	AA	450	C	N1-C6	-5.21	1.34	1.37
47	AA	1014	G	N1-C2	-5.21	1.33	1.37
47	AA	1814	G	N3-C4	-5.21	1.31	1.35
47	AA	1188	A	N9-C4	-5.21	1.34	1.37
47	AA	679	A	N9-C4	-5.21	1.34	1.37
47	AA	405	G	C5-C4	-5.20	1.34	1.38
47	AA	1709	G	N3-C4	-5.20	1.31	1.35
47	AA	46	A	N9-C4	-5.20	1.34	1.37
47	AA	1205	C	N3-C4	-5.20	1.30	1.33
47	AA	1209	A	N9-C4	-5.20	1.34	1.37
47	AA	1040	G	N7-C5	-5.20	1.36	1.39
47	AA	1170	A	C5-C4	-5.20	1.35	1.38
47	AA	1171	G	N9-C4	-5.20	1.33	1.38
47	AA	667	U	C2-N3	-5.19	1.34	1.37
47	AA	1189	A	N7-C5	-5.19	1.36	1.39
47	AA	1096	G	N9-C8	-5.18	1.34	1.37
47	AA	1143	A	C6-N1	-5.18	1.31	1.35
47	AA	1356	G	C5-C4	-5.18	1.34	1.38
47	AA	1856	C	N3-C4	-5.17	1.30	1.33
47	AA	1036	A	N9-C4	-5.17	1.34	1.37
47	AA	1089	G	N7-C5	-5.17	1.36	1.39
47	AA	1096	G	N7-C5	-5.17	1.36	1.39
47	AA	919	A	N9-C4	-5.17	1.34	1.37
47	AA	677	G	N7-C5	-5.16	1.36	1.39
47	AA	929	G	N3-C4	-5.16	1.31	1.35
47	AA	679	A	N9-C8	-5.16	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	42	A	N7-C5	-5.16	1.36	1.39
47	AA	1089	G	N9-C8	-5.15	1.34	1.37
47	AA	671	A	N9-C4	-5.15	1.34	1.37
47	AA	664	A	C6-N1	-5.15	1.31	1.35
47	AA	1853	C	N3-C4	-5.14	1.30	1.33
47	AA	97	U	N1-C2	-5.13	1.33	1.38
47	AA	677	G	C5-C6	-5.13	1.37	1.42
47	AA	1014	G	C6-N1	-5.13	1.35	1.39
47	AA	1145	A	N3-C4	-5.13	1.31	1.34
47	AA	1185	C	N1-C2	-5.12	1.35	1.40
47	AA	1135	C	N1-C6	-5.12	1.34	1.37
47	AA	1708	C	N1-C6	-5.12	1.34	1.37
47	AA	665	G	C5-C6	-5.12	1.37	1.42
47	AA	673	G	N7-C5	-5.11	1.36	1.39
47	AA	23	G	N9-C4	-5.11	1.33	1.38
47	AA	7	G	C8-N7	-5.11	1.27	1.30
47	AA	12	U	N1-C2	-5.11	1.33	1.38
47	AA	1204	A	N7-C5	-5.10	1.36	1.39
47	AA	1815	A	N9-C8	-5.10	1.33	1.37
47	AA	659	G	C8-N7	-5.10	1.27	1.30
47	AA	1200	A	N3-C4	-5.10	1.31	1.34
47	AA	1187	G	C6-N1	-5.09	1.35	1.39
47	AA	1724	A	N7-C5	-5.08	1.36	1.39
47	AA	402	C	N3-C4	-5.08	1.30	1.33
47	AA	389	A	C5-C4	-5.07	1.35	1.38
47	AA	1129	G	C6-N1	-5.07	1.35	1.39
47	AA	1063	C	N1-C6	-5.07	1.34	1.37
47	AA	1077	A	N9-C4	-5.07	1.34	1.37
47	AA	1855	G	C8-N7	-5.06	1.27	1.30
47	AA	520	A	N9-C4	-5.05	1.34	1.37
47	AA	1811	C	N1-C6	-5.05	1.34	1.37
47	AA	1199	A	N7-C5	-5.05	1.36	1.39
47	AA	1813	A	N7-C5	-5.05	1.36	1.39
47	AA	1026	C	N3-C4	-5.04	1.30	1.33
47	AA	1194	A	C5-C4	-5.04	1.35	1.38
47	AA	1208	A	N9-C4	-5.04	1.34	1.37
47	AA	1716	C	N1-C6	-5.04	1.34	1.37
47	AA	1858	G	N9-C8	-5.03	1.34	1.37
47	AA	1149	A	N9-C4	-5.02	1.34	1.37
47	AA	609	U	N1-C2	-5.02	1.34	1.38
47	AA	1175	G	C2-N3	-5.02	1.28	1.32
47	AA	146	G	C5-C6	-5.01	1.37	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	1354	G	N9-C4	-5.01	1.33	1.38
47	AA	1697	A	N3-C4	-5.01	1.31	1.34
47	AA	1718	G	C5-C4	-5.01	1.34	1.38
47	AA	1357	A	N3-C4	-5.00	1.31	1.34
62	An	75	C	N3-C4	-5.00	1.30	1.33
47	AA	957	A	N7-C5	-5.00	1.36	1.39
47	AA	1193	U	C2-N3	-5.00	1.34	1.37

All (811) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
40	K	158	THR	C-N-CD	-21.62	73.03	120.60
38	H	96	VAL	N-CA-C	-18.95	59.84	111.00
38	H	89	LEU	N-CA-C	-15.05	70.37	111.00
47	AA	1130	G	N3-C4-C5	12.10	134.65	128.60
47	AA	1861	G	N3-C4-C5	-11.49	122.85	128.60
38	H	83	LYS	N-CA-C	-11.16	80.86	111.00
47	AA	1130	G	N3-C4-N9	-11.05	119.37	126.00
47	AA	1861	G	N3-C4-N9	10.85	132.51	126.00
62	An	39	C	N1-C2-O2	10.63	125.28	118.90
47	AA	1075	C	C6-N1-C2	10.60	124.54	120.30
47	AA	1717	C	N1-C2-O2	-10.53	112.58	118.90
62	An	39	C	N3-C2-O2	-10.30	114.69	121.90
47	AA	880	G	N3-C2-N2	-10.26	112.72	119.90
47	AA	997	A	N7-C8-N9	10.11	118.86	113.80
47	AA	1091	C	N3-C4-C5	9.88	125.85	121.90
47	AA	1861	G	C4-N9-C1'	9.84	139.29	126.50
38	H	88	VAL	N-CA-C	-9.80	84.54	111.00
47	AA	1682	C	C6-N1-C2	9.55	124.12	120.30
47	AA	201	C	C6-N1-C2	-9.50	116.50	120.30
47	AA	1085	C	C6-N1-C2	9.50	124.10	120.30
47	AA	1518	C	N1-C2-O2	9.38	124.53	118.90
47	AA	1863	A	C2-N3-C4	-9.29	105.95	110.60
47	AA	736	C	N1-C2-O2	9.16	124.39	118.90
47	AA	997	A	C8-N9-C4	-9.03	102.19	105.80
47	AA	146	G	C4-C5-N7	8.98	114.39	110.80
47	AA	1024	A	C8-N9-C4	8.90	109.36	105.80
64	Aq	203	PRO	C-N-CA	8.87	143.88	121.70
47	AA	1861	G	N1-C2-N2	-8.84	108.24	116.20
47	AA	1130	G	C4-N9-C1'	-8.83	115.02	126.50
47	AA	405	G	C8-N9-C4	8.77	109.91	106.40
47	AA	400	C	C6-N1-C2	8.75	123.80	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	An	23	C	C2-N1-C1'	8.71	128.38	118.80
47	AA	682	U	O5'-P-OP1	-8.66	97.91	105.70
47	AA	1855	G	N9-C4-C5	-8.65	101.94	105.40
47	AA	1022	U	N1-C2-O2	8.62	128.83	122.80
47	AA	1157	G	C4-N9-C1'	8.59	137.67	126.50
47	AA	1518	C	C2-N1-C1'	8.58	128.24	118.80
47	AA	1518	C	N3-C2-O2	-8.52	115.94	121.90
47	AA	1855	G	C4-C5-N7	8.48	114.19	110.80
38	H	97	GLY	N-CA-C	-8.48	91.90	113.10
47	AA	1834	A	N1-C2-N3	8.46	133.53	129.30
47	AA	1453	C	C5-C6-N1	8.45	125.22	121.00
62	An	76	A	N1-C6-N6	-8.43	113.55	118.60
47	AA	1453	C	C2-N1-C1'	8.42	128.06	118.80
47	AA	1453	C	C6-N1-C2	-8.34	116.97	120.30
47	AA	1861	G	C8-N9-C1'	-8.30	116.20	127.00
47	AA	880	G	N9-C4-C5	8.21	108.68	105.40
47	AA	45	A	N1-C6-N6	-8.21	113.68	118.60
47	AA	1153	C	C6-N1-C2	8.17	123.57	120.30
47	AA	1834	A	C4-C5-C6	8.16	121.08	117.00
47	AA	1833	C	C4-C5-C6	8.12	121.46	117.40
47	AA	997	A	C5-N7-C8	-7.98	99.91	103.90
47	AA	173	A	N1-C6-N6	7.94	123.37	118.60
47	AA	1646	C	C6-N1-C2	7.93	123.47	120.30
47	AA	1022	U	N3-C2-O2	-7.90	116.67	122.20
47	AA	42	A	N1-C6-N6	7.88	123.33	118.60
47	AA	624	C	C6-N1-C2	-7.87	117.15	120.30
47	AA	1337	C	C6-N1-C2	7.84	123.44	120.30
47	AA	738	C	C2-N1-C1'	7.83	127.41	118.80
47	AA	992	A	O5'-P-OP1	-7.82	98.66	105.70
47	AA	1834	A	C6-C5-N7	-7.78	126.85	132.30
47	AA	1157	G	C8-N9-C1'	-7.77	116.90	127.00
47	AA	1201	U	C5-C6-N1	-7.75	118.82	122.70
47	AA	1354	G	C8-N9-C4	7.74	109.50	106.40
47	AA	1121	G	C8-N9-C4	7.73	109.49	106.40
47	AA	1518	C	C6-N1-C2	-7.71	117.22	120.30
47	AA	1732	G	C8-N9-C4	7.69	109.48	106.40
37	A	931	C	C2-N1-C1'	7.68	127.24	118.80
47	AA	434	G	N3-C4-C5	7.66	132.43	128.60
47	AA	1085	C	C5-C6-N1	-7.66	117.17	121.00
47	AA	678	U	C5-C6-N1	7.64	126.52	122.70
47	AA	1863	A	C5-N7-C8	-7.60	100.10	103.90
47	AA	1855	G	C8-N9-C4	7.55	109.42	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
53	AJ	78	LEU	CA-CB-CG	-7.55	97.94	115.30
47	AA	878	G	C5-C6-N1	7.51	115.26	111.50
47	AA	639	C	C6-N1-C2	7.50	123.30	120.30
47	AA	1031	A	C2-N3-C4	-7.45	106.88	110.60
47	AA	997	A	C6-C5-N7	-7.44	127.09	132.30
47	AA	397	G	C8-N9-C4	7.44	109.37	106.40
47	AA	1138	C	C2-N1-C1'	7.42	126.96	118.80
62	An	23	C	C5-C6-N1	7.40	124.70	121.00
47	AA	1130	G	C2-N3-C4	-7.40	108.20	111.90
47	AA	1157	G	C6-C5-N7	-7.39	125.97	130.40
47	AA	18	C	N3-C4-C5	7.36	124.84	121.90
47	AA	126	G	N3-C2-N2	-7.33	114.77	119.90
47	AA	1803	U	C5-C6-N1	-7.32	119.04	122.70
47	AA	14	C	N1-C2-O2	-7.31	114.51	118.90
47	AA	930	C	C2-N1-C1'	7.31	126.84	118.80
47	AA	460	A	C8-N9-C4	7.29	108.72	105.80
47	AA	428	U	C2-N1-C1'	-7.29	108.96	117.70
47	AA	1104	G	C8-N9-C4	7.28	109.31	106.40
47	AA	847	A	N1-C6-N6	7.26	122.96	118.60
47	AA	126	G	N3-C4-N9	-7.25	121.65	126.00
47	AA	880	G	N1-C2-N2	7.25	122.72	116.20
47	AA	585	C	N1-C2-O2	7.24	123.24	118.90
47	AA	1158	G	N9-C4-C5	-7.23	102.51	105.40
47	AA	1176	G	C2-N3-C4	-7.22	108.29	111.90
62	An	33	C	N1-C2-O2	-7.20	114.58	118.90
62	An	23	C	C6-N1-C1'	-7.19	112.17	120.80
47	AA	1157	G	N3-C4-N9	7.17	130.30	126.00
47	AA	1726	G	C2-N3-C4	-7.17	108.31	111.90
47	AA	1861	G	C6-N1-C2	-7.16	120.80	125.10
37	A	931	C	N1-C2-O2	7.16	123.19	118.90
47	AA	1842	C	N3-C4-C5	7.14	124.76	121.90
76	AB	88	LEU	CA-CB-CG	7.14	131.72	115.30
47	AA	806	U	C5-C6-N1	7.14	126.27	122.70
47	AA	1130	G	C8-N9-C1'	7.13	136.27	127.00
47	AA	477	G	C8-N9-C4	7.10	109.24	106.40
47	AA	958	G	C6-C5-N7	-7.10	126.14	130.40
47	AA	1031	A	N3-C4-N9	-7.09	121.72	127.40
47	AA	1138	C	N1-C2-O2	7.09	123.16	118.90
47	AA	1271	C	C6-N1-C2	-7.07	117.47	120.30
47	AA	1198	G	C2-N3-C4	-7.06	108.37	111.90
47	AA	1049	A	N9-C4-C5	-7.05	102.98	105.80
47	AA	1689	C	C6-N1-C2	7.05	123.12	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	1288	U	C2-N1-C1'	7.04	126.15	117.70
47	AA	1861	G	N1-C6-O6	-7.04	115.68	119.90
47	AA	13	C	N1-C2-O2	-7.03	114.68	118.90
47	AA	1607	A	C5-N7-C8	-7.02	100.39	103.90
47	AA	462	C	C5-C6-N1	7.00	124.50	121.00
37	A	4083	U	C2-N1-C1'	7.00	126.10	117.70
47	AA	1120	U	C2-N1-C1'	6.99	126.09	117.70
47	AA	1506	A	N1-C2-N3	6.98	132.79	129.30
47	AA	565	G	C4-N9-C1'	6.97	135.57	126.50
57	AP	93	LEU	CA-CB-CG	-6.97	99.27	115.30
62	An	71	C	C6-N1-C2	6.95	123.08	120.30
37	A	4083	U	N1-C2-O2	6.95	127.67	122.80
47	AA	1808	U	C5-C6-N1	-6.93	119.23	122.70
47	AA	1047	C	C5-C4-N4	-6.93	115.35	120.20
47	AA	1836	G	C8-N9-C4	6.92	109.17	106.40
47	AA	1024	A	C2-N3-C4	-6.92	107.14	110.60
47	AA	615	C	N1-C2-O2	6.90	123.04	118.90
47	AA	1855	G	N3-C2-N2	6.88	124.72	119.90
47	AA	878	G	N3-C4-N9	6.88	130.13	126.00
47	AA	1682	C	C5-C6-N1	-6.87	117.57	121.00
62	An	33	C	C2-N1-C1'	-6.85	111.26	118.80
67	Au	103	LEU	CA-CB-CG	6.84	131.03	115.30
47	AA	930	C	C6-N1-C1'	-6.83	112.60	120.80
62	An	18	G	C5-C6-O6	-6.83	124.50	128.60
47	AA	1148	A	O4'-C1'-N9	6.82	113.65	108.20
47	AA	1726	G	N3-C4-C5	6.82	132.01	128.60
47	AA	512	A	C8-N9-C4	6.80	108.52	105.80
47	AA	1607	A	C5-C6-N6	-6.80	118.26	123.70
47	AA	1834	A	C2-N3-C4	-6.80	107.20	110.60
47	AA	1784	G	N9-C4-C5	-6.79	102.68	105.40
47	AA	496	C	C2-N1-C1'	-6.79	111.34	118.80
47	AA	1076	G	N3-C4-C5	6.78	131.99	128.60
2	C	111	U	C2-N1-C1'	6.78	125.84	117.70
47	AA	7	G	C4-C5-N7	6.78	113.51	110.80
47	AA	1173	A	N9-C4-C5	-6.77	103.09	105.80
47	AA	847	A	C4-C5-N7	6.76	114.08	110.70
47	AA	1014	G	N3-C4-C5	-6.75	125.22	128.60
47	AA	1607	A	C4-C5-N7	6.75	114.07	110.70
47	AA	1158	G	C8-N9-C4	6.74	109.10	106.40
47	AA	1091	C	C6-N1-C2	6.74	123.00	120.30
47	AA	736	C	N3-C2-O2	-6.74	117.19	121.90
47	AA	1747	C	C5-C6-N1	6.73	124.36	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	341	C	N1-C2-O2	6.72	122.93	118.90
47	AA	1688	C	C6-N1-C2	6.72	122.99	120.30
47	AA	428	U	C5-C6-N1	-6.72	119.34	122.70
47	AA	1039	C	C6-N1-C2	6.72	122.99	120.30
47	AA	292	A	C8-N9-C4	6.71	108.49	105.80
47	AA	173	A	C4-C5-N7	6.71	114.06	110.70
47	AA	178	C	N3-C2-O2	-6.70	117.21	121.90
78	AI	109	LEU	CA-CB-CG	6.70	130.71	115.30
47	AA	146	G	N9-C4-C5	-6.70	102.72	105.40
47	AA	1022	U	C2-N1-C1'	6.68	125.72	117.70
47	AA	1032	C	C6-N1-C2	-6.68	117.63	120.30
37	A	4083	U	N3-C2-O2	-6.67	117.53	122.20
47	AA	1160	U	O5'-P-OP1	-6.67	99.70	105.70
47	AA	1682	C	N3-C4-C5	6.66	124.57	121.90
47	AA	1208	A	C8-N9-C4	6.66	108.46	105.80
47	AA	996	A	C6-C5-N7	-6.65	127.65	132.30
47	AA	1147	C	C6-N1-C2	6.64	122.96	120.30
47	AA	412	G	C6-C5-N7	-6.63	126.42	130.40
47	AA	659	G	C6-C5-N7	-6.63	126.42	130.40
47	AA	565	G	C6-C5-N7	-6.63	126.42	130.40
47	AA	997	A	C2-N3-C4	-6.63	107.28	110.60
47	AA	489	A	O4'-C1'-N9	-6.62	102.90	108.20
47	AA	982	G	C2-N3-C4	-6.62	108.59	111.90
47	AA	93	U	C5-C6-N1	6.61	126.01	122.70
37	A	3771	C	C2-N1-C1'	6.61	126.07	118.80
47	AA	1049	A	N1-C6-N6	6.61	122.56	118.60
47	AA	477	G	N9-C4-C5	-6.61	102.76	105.40
47	AA	1173	A	C2-N3-C4	-6.60	107.30	110.60
47	AA	1275	G	N3-C4-C5	6.60	131.90	128.60
47	AA	1156	U	C5-C6-N1	-6.59	119.40	122.70
47	AA	1158	G	C4-C5-N7	6.59	113.44	110.80
47	AA	1717	C	C2-N3-C4	-6.59	116.60	119.90
47	AA	679	A	C8-N9-C4	6.59	108.44	105.80
70	A0	129	LEU	CB-CG-CD1	-6.59	99.80	111.00
47	AA	1380	C	C5-C6-N1	-6.58	117.71	121.00
47	AA	1157	G	N1-C2-N2	-6.57	110.29	116.20
47	AA	1074	C	N3-C4-C5	6.57	124.53	121.90
47	AA	997	A	N1-C2-N3	6.56	132.58	129.30
62	An	40	C	C2-N1-C1'	6.56	126.02	118.80
47	AA	1173	A	C6-C5-N7	-6.55	127.71	132.30
47	AA	1201	U	C2-N3-C4	-6.54	123.07	127.00
47	AA	1120	U	C6-N1-C1'	-6.54	112.04	121.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
66	At	134	VAL	C-N-CA	-6.54	105.34	121.70
47	AA	16	G	N3-C4-N9	-6.54	122.08	126.00
47	AA	1360	U	C5-C6-N1	-6.54	119.43	122.70
47	AA	1592	C	C5-C6-N1	6.53	124.27	121.00
47	AA	561	A	C8-N9-C4	6.53	108.41	105.80
47	AA	1826	G	C8-N9-C1'	-6.53	118.52	127.00
47	AA	652	U	C6-N1-C2	-6.52	117.09	121.00
47	AA	1427	C	C5-C6-N1	6.52	124.26	121.00
47	AA	686	U	C2-N1-C1'	6.51	125.51	117.70
47	AA	1026	C	C2-N1-C1'	-6.51	111.64	118.80
47	AA	1380	C	C2-N3-C4	-6.51	116.64	119.90
47	AA	4	C	C2-N1-C1'	6.50	125.95	118.80
47	AA	993	G	C8-N9-C4	6.48	108.99	106.40
47	AA	1089	G	C2-N3-C4	-6.48	108.66	111.90
47	AA	1648	G	N9-C4-C5	6.48	107.99	105.40
47	AA	1089	G	N1-C2-N3	6.46	127.78	123.90
47	AA	1847	G	C2-N3-C4	-6.46	108.67	111.90
47	AA	428	U	N1-C2-O2	-6.46	118.28	122.80
47	AA	1826	G	C4-N9-C1'	6.46	134.90	126.50
47	AA	1522	A	N7-C8-N9	6.45	117.03	113.80
47	AA	1049	A	C4-C5-N7	6.45	113.92	110.70
47	AA	405	G	N9-C4-C5	-6.45	102.82	105.40
47	AA	997	A	C4-C5-C6	6.45	120.22	117.00
47	AA	1784	G	C4-C5-N7	6.43	113.37	110.80
47	AA	1709	G	C2-N3-C4	-6.43	108.69	111.90
47	AA	619	A	C4-C5-N7	6.42	113.91	110.70
62	An	40	C	N1-C2-O2	6.42	122.75	118.90
47	AA	1096	G	N3-C2-N2	-6.42	115.41	119.90
47	AA	201	C	C2-N1-C1'	6.41	125.84	118.80
62	An	18	G	N1-C6-O6	6.41	123.74	119.90
47	AA	1597	C	C6-N1-C2	6.40	122.86	120.30
47	AA	379	C	O5'-P-OP1	-6.40	99.94	105.70
47	AA	1859	A	N1-C6-N6	-6.40	114.76	118.60
47	AA	1442	U	N3-C2-O2	-6.39	117.73	122.20
47	AA	847	A	N9-C4-C5	-6.38	103.25	105.80
47	AA	1140	G	N9-C4-C5	-6.38	102.85	105.40
47	AA	988	C	C6-N1-C2	6.38	122.85	120.30
47	AA	1393	G	C4-N9-C1'	-6.38	118.21	126.50
47	AA	1029	G	N1-C2-N3	6.37	127.72	123.90
47	AA	1399	C	C2-N1-C1'	6.37	125.81	118.80
47	AA	1096	G	N3-C4-N9	-6.37	122.18	126.00
47	AA	1048	G	C6-C5-N7	-6.36	126.58	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	1529	C	C6-N1-C2	-6.34	117.76	120.30
47	AA	1173	A	C4-C5-N7	6.34	113.87	110.70
47	AA	1077	A	C8-N9-C4	6.33	108.33	105.80
47	AA	601	G	N1-C2-N2	-6.32	110.51	116.20
2	C	111	U	N1-C2-O2	6.32	127.22	122.80
47	AA	1031	A	N3-C4-C5	6.32	131.22	126.80
47	AA	434	G	C2-N3-C4	-6.31	108.74	111.90
47	AA	930	C	N1-C2-O2	6.31	122.69	118.90
47	AA	1288	U	N3-C2-O2	-6.31	117.78	122.20
47	AA	1140	G	C2-N3-C4	-6.31	108.75	111.90
47	AA	1475	G	N3-C4-N9	-6.31	122.22	126.00
47	AA	1138	C	C6-N1-C1'	-6.29	113.25	120.80
37	A	4871	C	C2-N1-C1'	6.29	125.71	118.80
47	AA	662	G	C8-N9-C4	6.28	108.91	106.40
47	AA	341	C	C6-N1-C1'	-6.28	113.27	120.80
47	AA	1007	C	N3-C4-C5	6.28	124.41	121.90
47	AA	42	A	C4-C5-N7	6.27	113.84	110.70
47	AA	429	C	O5'-P-OP2	-6.27	100.06	105.70
47	AA	1085	C	C2-N3-C4	-6.27	116.77	119.90
47	AA	1861	G	N1-C2-N3	6.26	127.66	123.90
47	AA	451	G	C4-C5-N7	6.26	113.30	110.80
51	AF	18	LEU	CA-CB-CG	-6.26	100.91	115.30
47	AA	565	G	C8-N9-C1'	-6.25	118.87	127.00
47	AA	1275	G	C8-N9-C4	6.25	108.90	106.40
47	AA	201	C	N3-C2-O2	-6.24	117.53	121.90
47	AA	565	G	N3-C4-N9	6.24	129.75	126.00
47	AA	1436	C	N3-C2-O2	-6.24	117.53	121.90
38	H	95	PRO	C-N-CA	-6.24	106.11	121.70
62	An	45	G	C4-N9-C1'	6.24	134.61	126.50
47	AA	1185	C	C6-N1-C2	6.23	122.79	120.30
47	AA	1399	C	C6-N1-C1'	-6.23	113.32	120.80
47	AA	407	G	C2-N3-C4	6.23	115.02	111.90
47	AA	1085	C	N3-C4-C5	6.23	124.39	121.90
47	AA	14	C	C2-N1-C1'	-6.22	111.95	118.80
47	AA	356	C	C2-N1-C1'	6.22	125.65	118.80
47	AA	17	C	N1-C2-O2	-6.21	115.17	118.90
47	AA	1176	G	N1-C2-N3	6.21	127.63	123.90
47	AA	659	G	C4-N9-C1'	6.21	134.57	126.50
47	AA	418	A	N9-C4-C5	-6.21	103.32	105.80
47	AA	1547	C	C6-N1-C2	6.21	122.78	120.30
47	AA	736	C	C2-N1-C1'	6.20	125.62	118.80
62	An	19	G	O4'-C1'-N9	6.20	113.16	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	1747	C	C6-N1-C2	-6.19	117.82	120.30
47	AA	420	G	C4-N9-C1'	-6.19	118.45	126.50
47	AA	1861	G	C6-C5-N7	-6.19	126.69	130.40
47	AA	1489	A	C8-N9-C4	6.19	108.27	105.80
37	A	4476	C	C2-N1-C1'	6.18	125.60	118.80
47	AA	619	A	N9-C4-C5	-6.18	103.33	105.80
47	AA	6	G	N1-C6-O6	-6.18	116.19	119.90
47	AA	1852	C	N3-C4-C5	6.18	124.37	121.90
47	AA	1173	A	C8-N9-C4	6.17	108.27	105.80
47	AA	404	G	C4-C5-N7	6.17	113.27	110.80
47	AA	1253	A	C8-N9-C4	6.16	108.27	105.80
62	An	75	C	N3-C4-C5	6.16	124.36	121.90
47	AA	1135	C	N3-C2-O2	-6.15	117.60	121.90
47	AA	1732	G	N9-C4-C5	-6.15	102.94	105.40
47	AA	1162	C	C6-N1-C2	-6.14	117.84	120.30
47	AA	1330	G	N3-C4-N9	6.13	129.68	126.00
47	AA	829	C	C6-N1-C2	6.13	122.75	120.30
47	AA	1334	G	C4-N9-C1'	-6.12	118.54	126.50
62	An	63	A	C8-N9-C4	6.12	108.25	105.80
47	AA	820	U	O4'-C1'-N1	6.11	113.09	108.20
47	AA	7	G	N9-C4-C5	-6.10	102.96	105.40
62	An	75	C	C6-N1-C2	6.10	122.74	120.30
47	AA	659	G	C8-N9-C1'	-6.09	119.09	127.00
47	AA	474	G	C2-N3-C4	-6.09	108.86	111.90
47	AA	880	G	N3-C4-N9	-6.08	122.35	126.00
47	AA	1693	G	N3-C4-N9	-6.08	122.35	126.00
47	AA	380	G	C8-N9-C4	6.08	108.83	106.40
47	AA	1354	G	N9-C4-C5	-6.08	102.97	105.40
62	An	28	U	C2-N1-C1'	6.08	125.00	117.70
47	AA	371	A	O5'-P-OP2	-6.08	100.23	105.70
47	AA	1847	G	N3-C4-N9	-6.08	122.35	126.00
47	AA	434	G	N1-C6-O6	6.07	123.54	119.90
47	AA	42	A	C6-C5-N7	-6.07	128.06	132.30
47	AA	173	A	C5-C6-N6	-6.07	118.85	123.70
47	AA	114	G	O4'-C1'-N9	6.05	113.04	108.20
47	AA	418	A	C8-N9-C4	6.05	108.22	105.80
47	AA	1648	G	N3-C4-N9	-6.05	122.37	126.00
2	C	111	U	N3-C2-O2	-6.04	117.97	122.20
78	AI	109	LEU	CB-CG-CD2	-6.03	100.75	111.00
47	AA	1803	U	C6-N1-C2	6.02	124.61	121.00
47	AA	1397	U	O5'-P-OP2	-6.02	100.28	105.70
47	AA	1609	C	C2-N3-C4	6.02	122.91	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	1064	C	N3-C4-C5	6.01	124.31	121.90
47	AA	1120	U	N1-C2-O2	6.01	127.01	122.80
36	r	147	ALA	N-CA-C	-6.00	94.79	111.00
47	AA	1399	C	N1-C2-O2	6.00	122.50	118.90
47	AA	341	C	C2-N1-C1'	6.00	125.40	118.80
47	AA	355	G	C8-N9-C4	6.00	108.80	106.40
47	AA	1624	U	C2-N1-C1'	6.00	124.90	117.70
47	AA	1682	C	N3-C4-N4	-6.00	113.80	118.00
47	AA	1436	C	N1-C2-O2	6.00	122.50	118.90
47	AA	1861	G	N3-C2-N2	6.00	124.10	119.90
47	AA	1416	C	N1-C2-O2	6.00	122.50	118.90
47	AA	1696	C	N3-C2-O2	-5.99	117.70	121.90
47	AA	127	C	N1-C2-O2	5.99	122.50	118.90
47	AA	1158	G	C5-C6-N1	5.99	114.50	111.50
47	AA	931	C	C6-N1-C2	5.99	122.69	120.30
47	AA	804	U	C5-C6-N1	5.98	125.69	122.70
59	AR	58	LEU	CA-CB-CG	5.97	129.04	115.30
64	Aq	96	LEU	CA-CB-CG	5.97	129.04	115.30
47	AA	402	C	C2-N1-C1'	5.97	125.37	118.80
47	AA	651	U	C5-C6-N1	5.97	125.68	122.70
47	AA	1866	A	N7-C8-N9	5.97	116.78	113.80
47	AA	303	C	N3-C2-O2	-5.97	117.72	121.90
47	AA	484	A	C8-N9-C4	5.97	108.19	105.80
47	AA	42	A	N9-C4-C5	-5.96	103.42	105.80
47	AA	662	G	N7-C8-N9	-5.95	110.12	113.10
47	AA	482	G	N3-C4-N9	-5.95	122.43	126.00
47	AA	1076	G	C8-N9-C4	5.95	108.78	106.40
47	AA	1157	G	N1-C2-N3	5.95	127.47	123.90
47	AA	1448	A	C8-N9-C4	5.94	108.18	105.80
47	AA	1578	U	N1-C2-O2	5.94	126.96	122.80
47	AA	324	C	C2-N1-C1'	5.94	125.33	118.80
47	AA	1436	C	C2-N1-C1'	5.93	125.33	118.80
38	H	90	ALA	C-N-CA	-5.93	106.87	121.70
47	AA	753	C	C6-N1-C2	5.93	122.67	120.30
47	AA	4	C	C6-N1-C2	-5.93	117.93	120.30
47	AA	1054	G	C6-N1-C2	-5.93	121.54	125.10
56	AN	72	LEU	CA-CB-CG	-5.93	101.67	115.30
47	AA	1259	A	O4'-C1'-N9	5.92	112.94	108.20
47	AA	996	A	C4-C5-N7	5.92	113.66	110.70
38	H	223	ARG	N-CA-C	5.92	126.98	111.00
47	AA	18	C	C6-N1-C2	5.92	122.67	120.30
47	AA	1136	U	C6-N1-C2	5.92	124.55	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	1726	G	N3-C4-N9	-5.90	122.46	126.00
53	AJ	214	LEU	CA-CB-CG	-5.90	101.73	115.30
47	AA	1250	A	N7-C8-N9	5.89	116.74	113.80
62	An	76	A	C5-C6-N1	5.89	120.64	117.70
62	An	4	C	C6-N1-C2	5.88	122.65	120.30
47	AA	542	U	C2-N1-C1'	5.87	124.75	117.70
47	AA	14	C	C2-N3-C4	-5.87	116.97	119.90
62	An	45	G	C6-C5-N7	-5.86	126.88	130.40
62	An	15	A	N1-C6-N6	-5.86	115.08	118.60
47	AA	679	A	N9-C4-C5	-5.86	103.46	105.80
47	AA	179	C	C6-N1-C2	5.85	122.64	120.30
47	AA	460	A	N3-C4-C5	5.85	130.89	126.80
47	AA	687	C	N3-C2-O2	-5.85	117.81	121.90
37	A	4476	C	N1-C2-O2	5.85	122.41	118.90
47	AA	1096	G	N3-C4-C5	5.85	131.52	128.60
47	AA	665	G	C4-C5-N7	5.84	113.14	110.80
47	AA	1140	G	C4-C5-N7	5.84	113.14	110.80
47	AA	984	C	C6-N1-C2	-5.83	117.97	120.30
47	AA	1863	A	C4-C5-N7	5.83	113.61	110.70
47	AA	1049	A	C5-C6-N6	-5.83	119.04	123.70
62	An	76	A	C6-C5-N7	5.83	136.38	132.30
47	AA	437	G	C2-N3-C4	-5.82	108.99	111.90
47	AA	460	A	N9-C4-C5	-5.82	103.47	105.80
47	AA	1096	G	C2-N3-C4	-5.82	108.99	111.90
47	AA	738	C	N1-C2-O2	5.82	122.39	118.90
47	AA	1140	G	C8-N9-C4	5.82	108.73	106.40
47	AA	657	U	C6-N1-C2	5.82	124.49	121.00
62	An	45	G	C8-N9-C1'	-5.82	119.44	127.00
47	AA	14	C	C6-N1-C1'	5.82	127.78	120.80
47	AA	1861	G	C5-C6-N1	5.81	114.41	111.50
37	A	3771	C	N1-C2-O2	5.80	122.38	118.90
47	AA	1648	G	C4-C5-N7	-5.80	108.48	110.80
62	An	53	G	O4'-C1'-N9	-5.79	103.56	108.20
47	AA	1193	U	C2-N3-C4	-5.79	123.53	127.00
47	AA	1622	U	C5-C6-N1	-5.79	119.81	122.70
47	AA	1865	C	N1-C2-O2	5.79	122.38	118.90
38	H	225	PRO	CA-N-CD	-5.79	103.40	111.50
62	An	28	U	N1-C2-O2	5.79	126.85	122.80
47	AA	1190	A	C8-N9-C4	5.78	108.11	105.80
47	AA	1211	G	C8-N9-C4	5.78	108.71	106.40
47	AA	1442	U	C2-N1-C1'	5.78	124.63	117.70
47	AA	595	U	N1-C2-O2	-5.77	118.76	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	AA	450	C	C6-N1-C2	5.77	122.61	120.30
47	AA	1190	A	N7-C8-N9	-5.76	110.92	113.80
47	AA	1855	G	C5-C6-N1	5.76	114.38	111.50
47	AA	1205	C	C6-N1-C2	-5.75	118.00	120.30
47	AA	173	A	N9-C4-C5	-5.75	103.50	105.80
47	AA	1834	A	N7-C8-N9	5.74	116.67	113.80
47	AA	173	A	C6-C5-N7	-5.74	128.28	132.30
47	AA	1648	G	N3-C2-N2	-5.74	115.88	119.90
47	AA	683	G	C8-N9-C4	5.74	108.70	106.40
47	AA	619	A	N1-C6-N6	5.74	122.04	118.60
62	An	43	G	N9-C4-C5	-5.73	103.11	105.40
47	AA	1130	G	C8-N9-C4	5.73	108.69	106.40
47	AA	40	A	O5'-P-OP1	-5.73	100.54	105.70
47	AA	402	C	N3-C4-C5	5.73	124.19	121.90
47	AA	1144	A	C2-N3-C4	-5.72	107.74	110.60
47	AA	1022	U	O4'-C1'-N1	5.72	112.78	108.20
47	AA	1032	C	N3-C2-O2	-5.72	117.90	121.90
47	AA	1737	G	C6-C5-N7	-5.71	126.97	130.40
47	AA	1334	G	N3-C4-C5	5.71	131.46	128.60
47	AA	46	A	C8-N9-C4	5.70	108.08	105.80
47	AA	537	C	C6-N1-C2	-5.70	118.02	120.30
74	Ax	49	LEU	CA-CB-CG	5.70	128.42	115.30
47	AA	359	U	N1-C2-O2	5.70	126.79	122.80
47	AA	1607	A	N1-C6-N6	5.70	122.02	118.60
47	AA	359	U	N3-C2-O2	-5.69	118.21	122.20
47	AA	1158	G	O5'-P-OP2	-5.69	100.58	105.70
81	AU	131	LEU	CA-CB-CG	5.69	128.39	115.30
47	AA	746	C	C6-N1-C2	-5.69	118.02	120.30
47	AA	1700	C	C6-N1-C2	5.68	122.57	120.30
47	AA	619	A	C5-N7-C8	-5.68	101.06	103.90
47	AA	1461	G	N3-C4-C5	5.68	131.44	128.60
47	AA	897	U	C2-N1-C1'	5.67	124.51	117.70
47	AA	1731	A	C8-N9-C4	5.67	108.07	105.80
53	AJ	85	SER	C-N-CA	-5.67	107.53	121.70
47	AA	810	A	C5-N7-C8	-5.66	101.07	103.90
71	Ao	122	LEU	CA-CB-CG	5.66	128.31	115.30
47	AA	16	G	C2-N3-C4	-5.66	109.07	111.90
47	AA	1090	C	C2-N1-C1'	-5.66	112.58	118.80
47	AA	1538	C	N3-C4-C5	5.66	124.16	121.90
66	At	28	LEU	CA-CB-CG	5.65	128.30	115.30
47	AA	1866	A	C8-N9-C4	-5.64	103.54	105.80
47	AA	820	U	C2-N1-C1'	-5.64	110.93	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
37	A	4871	C	C6-N1-C1'	-5.63	114.04	120.80
47	AA	1316	C	C5-C4-N4	-5.63	116.26	120.20
47	AA	821	G	N3-C4-C5	5.63	131.42	128.60
47	AA	1393	G	C8-N9-C1'	5.63	134.32	127.00
62	An	4	C	C5-C6-N1	-5.63	118.19	121.00
47	AA	601	G	C6-C5-N7	-5.63	127.02	130.40
47	AA	1075	C	N3-C4-C5	5.63	124.15	121.90
47	AA	668	A	C8-N9-C4	5.62	108.05	105.80
47	AA	114	G	N3-C4-N9	-5.62	122.63	126.00
47	AA	677	G	C4-C5-N7	5.62	113.05	110.80
47	AA	1261	C	C6-N1-C2	-5.62	118.05	120.30
47	AA	419	G	N1-C6-O6	5.61	123.27	119.90
47	AA	738	C	C6-N1-C1'	-5.61	114.06	120.80
47	AA	37	C	C2-N1-C1'	5.61	124.97	118.80
72	As	46	ALA	N-CA-C	5.61	126.15	111.00
47	AA	1069	U	N1-C2-O2	5.61	126.73	122.80
47	AA	1157	G	N3-C4-C5	-5.61	125.80	128.60
66	At	69	LEU	CA-CB-CG	5.61	128.19	115.30
47	AA	450	C	C5-C6-N1	-5.60	118.20	121.00
47	AA	1140	G	C6-C5-N7	-5.60	127.04	130.40
76	AB	39	LEU	CA-CB-CG	-5.60	102.42	115.30
47	AA	1447	G	C5-C6-O6	-5.60	125.24	128.60
37	A	931	C	C6-N1-C1'	-5.59	114.09	120.80
47	AA	996	A	N1-C6-N6	5.59	121.95	118.60
47	AA	146	G	C6-C5-N7	-5.59	127.05	130.40
47	AA	1049	A	C6-C5-N7	-5.59	128.39	132.30
47	AA	847	A	C6-C5-N7	-5.58	128.39	132.30
63	Ap	228	LEU	CA-CB-CG	5.58	128.14	115.30
47	AA	1520	G	C4-C5-N7	5.58	113.03	110.80
47	AA	1857	G	N1-C2-N3	5.57	127.25	123.90
47	AA	932	G	N9-C4-C5	-5.57	103.17	105.40
47	AA	610	G	C8-N9-C4	5.57	108.63	106.40
47	AA	1010	G	C4-C5-N7	5.57	113.03	110.80
47	AA	615	C	C2-N1-C1'	5.56	124.92	118.80
47	AA	1624	U	N3-C2-O2	-5.56	118.31	122.20
47	AA	680	G	C6-C5-N7	-5.55	127.07	130.40
47	AA	1024	A	N7-C8-N9	-5.55	111.03	113.80
47	AA	1348	G	N3-C4-C5	5.55	131.38	128.60
47	AA	1029	G	C6-N1-C2	-5.54	121.77	125.10
47	AA	356	C	N1-C2-O2	5.54	122.22	118.90
47	AA	146	G	C5-N7-C8	-5.54	101.53	104.30
47	AA	1600	G	C4-N9-C1'	5.54	133.70	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	1375	G	C8-N9-C4	5.53	108.61	106.40
47	AA	356	C	C6-N1-C2	-5.53	118.09	120.30
47	AA	361	U	N3-C4-O4	-5.52	115.53	119.40
47	AA	1737	G	C4-N9-C1'	5.52	133.68	126.50
47	AA	930	C	N3-C2-O2	-5.52	118.04	121.90
47	AA	1187	G	C5-C6-O6	-5.52	125.29	128.60
47	AA	1719	A	C6-N1-C2	-5.52	115.29	118.60
47	AA	361	U	C5-C4-O4	5.52	129.21	125.90
47	AA	622	C	C6-N1-C2	5.51	122.50	120.30
47	AA	734	C	C2-N1-C1'	5.51	124.86	118.80
47	AA	1013	U	C6-N1-C2	-5.51	117.69	121.00
47	AA	958	G	N1-C6-O6	5.51	123.21	119.90
47	AA	1033	G	C6-C5-N7	-5.51	127.09	130.40
47	AA	996	A	C5-N7-C8	-5.50	101.15	103.90
62	An	33	C	C6-N1-C1'	5.50	127.40	120.80
47	AA	847	A	C5-C6-N6	-5.50	119.30	123.70
47	AA	606	G	C4-C5-N7	5.49	112.99	110.80
47	AA	880	G	C8-N9-C4	-5.49	104.21	106.40
47	AA	948	C	C2-N1-C1'	5.49	124.83	118.80
81	AU	67	ARG	NE-CZ-NH2	5.49	123.04	120.30
47	AA	23	G	N3-C4-N9	-5.48	122.71	126.00
47	AA	882	U	C5-C6-N1	5.48	125.44	122.70
47	AA	1211	G	C2-N3-C4	-5.48	109.16	111.90
47	AA	377	G	C8-N9-C4	-5.48	104.21	106.40
47	AA	16	G	N3-C4-C5	5.48	131.34	128.60
47	AA	1005	G	C4-C5-N7	5.48	112.99	110.80
47	AA	1198	G	N3-C4-C5	5.48	131.34	128.60
47	AA	407	G	O4'-C1'-N9	-5.48	103.82	108.20
47	AA	14	C	N1-C2-N3	5.47	123.03	119.20
47	AA	1054	G	N3-C4-C5	-5.47	125.86	128.60
47	AA	1090	C	C5-C6-N1	-5.47	118.26	121.00
47	AA	1010	G	N9-C4-C5	-5.47	103.21	105.40
47	AA	653	A	N1-C6-N6	-5.46	115.32	118.60
47	AA	1807	C	N3-C4-C5	5.46	124.08	121.90
47	AA	1644	C	C2-N1-C1'	5.46	124.81	118.80
47	AA	1342	U	N1-C2-O2	5.46	126.62	122.80
47	AA	647	U	N3-C2-O2	-5.45	118.38	122.20
47	AA	1054	G	C5-C6-N1	5.45	114.22	111.50
47	AA	850	C	O4'-C1'-N1	5.45	112.56	108.20
47	AA	1600	G	O4'-C1'-N9	5.45	112.56	108.20
47	AA	400	C	C5-C6-N1	-5.45	118.28	121.00
47	AA	665	G	C8-N9-C4	5.45	108.58	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	AA	420	G	C8-N9-C4	5.44	108.58	106.40
47	AA	1075	C	C5-C6-N1	-5.44	118.28	121.00
37	A	931	C	N3-C2-O2	-5.44	118.09	121.90
47	AA	1192	U	C5-C6-N1	-5.44	119.98	122.70
47	AA	1026	C	N3-C4-N4	-5.43	114.20	118.00
47	AA	1033	G	C4-C5-N7	5.43	112.97	110.80
47	AA	223	C	N1-C2-O2	5.43	122.16	118.90
47	AA	303	C	N1-C2-O2	5.43	122.16	118.90
47	AA	1528	G	C4-N9-C1'	5.42	133.55	126.50
47	AA	495	U	C6-N1-C2	5.42	124.25	121.00
47	AA	412	G	N3-C4-N9	5.42	129.25	126.00
47	AA	809	A	C2-N3-C4	-5.42	107.89	110.60
47	AA	1060	A	C6-C5-N7	-5.42	128.51	132.30
47	AA	1839	U	C5-C4-O4	5.42	129.15	125.90
57	AP	89	TRP	CA-CB-CG	-5.42	103.40	113.70
47	AA	370	G	C5-C6-N1	5.42	114.21	111.50
62	An	53	G	N9-C4-C5	-5.42	103.23	105.40
47	AA	1475	G	N3-C2-N2	-5.42	116.11	119.90
47	AA	649	U	C5-C6-N1	-5.41	119.99	122.70
47	AA	1601	A	C8-N9-C4	5.41	107.97	105.80
47	AA	658	U	O4'-C1'-N1	-5.41	103.87	108.20
47	AA	1091	C	C6-N1-C1'	-5.41	114.31	120.80
47	AA	1171	G	P-O3'-C3'	5.41	126.19	119.70
47	AA	984	C	C2-N1-C1'	5.41	124.75	118.80
47	AA	1826	G	N3-C4-N9	5.41	129.25	126.00
47	AA	1866	A	C6-C5-N7	-5.41	128.51	132.30
47	AA	622	C	O5'-P-OP1	-5.41	100.83	105.70
47	AA	1490	G	C8-N9-C4	-5.41	104.24	106.40
47	AA	1186	U	N3-C4-O4	-5.41	115.62	119.40
57	AP	97	ARG	NE-CZ-NH1	-5.41	117.60	120.30
47	AA	878	G	C4-C5-N7	5.40	112.96	110.80
78	AI	54	ILE	C-N-CD	5.40	139.75	128.40
47	AA	738	C	N3-C2-O2	-5.40	118.12	121.90
47	AA	1164	G	N1-C6-O6	-5.40	116.66	119.90
47	AA	1415	C	N1-C2-O2	5.40	122.14	118.90
47	AA	1164	G	C6-N1-C2	-5.39	121.86	125.10
62	An	23	C	C5-C4-N4	-5.39	116.42	120.20
47	AA	1693	G	N3-C4-C5	5.39	131.30	128.60
47	AA	424	C	C6-N1-C2	5.39	122.46	120.30
47	AA	932	G	C8-N9-C4	5.39	108.56	106.40
47	AA	958	G	C4-N9-C1'	5.39	133.51	126.50
34	t	166	SER	C-N-CA	5.38	135.16	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	AA	958	G	C5-C6-O6	-5.38	125.37	128.60
47	AA	958	G	N3-C4-N9	5.38	129.23	126.00
47	AA	370	G	C6-N1-C2	-5.38	121.87	125.10
62	An	66	C	C6-N1-C2	5.38	122.45	120.30
47	AA	1037	G	N1-C2-N3	5.38	127.12	123.90
47	AA	1393	G	C6-C5-N7	5.37	133.62	130.40
47	AA	12	U	C2-N1-C1'	-5.37	111.25	117.70
54	AK	147	LEU	CA-CB-CG	5.37	127.65	115.30
47	AA	440	G	N9-C4-C5	-5.37	103.25	105.40
62	An	13	G	N3-C2-N2	-5.37	116.14	119.90
47	AA	1009	A	C8-N9-C4	5.37	107.95	105.80
47	AA	1090	C	C2-N3-C4	-5.37	117.22	119.90
57	AP	65	LEU	CB-CG-CD2	-5.36	101.88	111.00
47	AA	998	A	O4'-C1'-N9	-5.36	103.91	108.20
47	AA	1447	G	C6-C5-N7	-5.36	127.18	130.40
47	AA	1644	C	N1-C2-O2	5.36	122.11	118.90
47	AA	1187	G	C4-C5-N7	5.35	112.94	110.80
47	AA	672	A	C5-N7-C8	-5.35	101.22	103.90
47	AA	949	G	N3-C4-C5	5.35	131.28	128.60
47	AA	1522	A	C5-N7-C8	-5.35	101.22	103.90
47	AA	1028	A	N1-C6-N6	5.35	121.81	118.60
47	AA	1803	U	C2-N1-C1'	-5.35	111.28	117.70
47	AA	1271	C	C5-C6-N1	5.34	123.67	121.00
47	AA	1288	U	N1-C2-O2	5.34	126.54	122.80
47	AA	389	A	C8-N9-C4	5.34	107.94	105.80
47	AA	1130	G	N3-C2-N2	-5.34	116.16	119.90
47	AA	387	C	N1-C2-O2	5.34	122.10	118.90
47	AA	672	A	C2-N3-C4	-5.34	107.93	110.60
47	AA	385	G	O4'-C1'-N9	-5.33	103.93	108.20
47	AA	1784	G	C5-C6-O6	-5.33	125.40	128.60
62	An	29	G	N3-C4-N9	-5.33	122.80	126.00
47	AA	114	G	C8-N9-C1'	5.33	133.93	127.00
47	AA	1010	G	N3-C4-N9	5.33	129.20	126.00
47	AA	361	U	O4'-C1'-N1	-5.32	103.94	108.20
47	AA	809	A	C4-C5-N7	5.32	113.36	110.70
47	AA	1125	C	C6-N1-C2	5.32	122.43	120.30
47	AA	907	G	N9-C4-C5	-5.32	103.27	105.40
47	AA	1147	C	C5-C6-N1	-5.32	118.34	121.00
47	AA	1395	C	C6-N1-C2	-5.32	118.17	120.30
47	AA	1014	G	C5-C6-N1	5.32	114.16	111.50
47	AA	1729	U	C6-N1-C2	5.32	124.19	121.00
47	AA	1800	A	C8-N9-C4	5.32	107.93	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	AA	1855	G	C5-C6-O6	-5.31	125.41	128.60
47	AA	565	G	C4-C5-N7	5.31	112.92	110.80
47	AA	1051	G	C2-N3-C4	-5.30	109.25	111.90
47	AA	1014	G	C6-N1-C2	-5.30	121.92	125.10
47	AA	1208	A	N9-C4-C5	-5.30	103.68	105.80
47	AA	361	U	C5-C6-N1	-5.30	120.05	122.70
47	AA	686	U	C6-N1-C1'	-5.30	113.78	121.20
47	AA	1373	C	O5'-P-OP2	-5.30	100.93	105.70
47	AA	1518	C	C6-N1-C1'	-5.30	114.44	120.80
37	A	3715	U	C2-N1-C1'	5.29	124.05	117.70
47	AA	1002	U	C2-N1-C1'	5.29	124.05	117.70
47	AA	7	G	C8-N9-C4	5.29	108.51	106.40
62	An	39	C	C2-N1-C1'	5.29	124.61	118.80
47	AA	1857	G	C4-C5-C6	5.28	121.97	118.80
47	AA	42	A	C2-N3-C4	-5.28	107.96	110.60
47	AA	1164	G	C5-C6-N1	5.28	114.14	111.50
47	AA	1834	A	C4-N9-C1'	5.28	135.81	126.30
62	An	45	G	N1-C2-N3	5.28	127.07	123.90
47	AA	127	C	C2-N1-C1'	5.28	124.60	118.80
62	An	20	A	N1-C6-N6	-5.27	115.44	118.60
62	An	71	C	N3-C4-C5	5.27	124.01	121.90
47	AA	1170	A	N3-C4-N9	-5.27	123.19	127.40
47	AA	1349	G	C6-N1-C2	-5.27	121.94	125.10
37	A	4749	C	C2-N1-C1'	5.27	124.59	118.80
47	AA	127	C	C6-N1-C1'	-5.26	114.48	120.80
47	AA	627	U	C5-C6-N1	-5.26	120.07	122.70
47	AA	1419	C	C2-N1-C1'	-5.26	113.01	118.80
47	AA	1405	A	O5'-P-OP1	-5.26	100.96	105.70
47	AA	1288	U	O4'-C1'-N1	5.26	112.41	108.20
47	AA	996	A	C2-N3-C4	-5.26	107.97	110.60
47	AA	1784	G	N3-C4-N9	5.25	129.15	126.00
47	AA	1808	U	C2-N1-C1'	-5.25	111.39	117.70
47	AA	1842	C	C6-N1-C2	5.25	122.40	120.30
36	r	53	GLY	C-N-CD	5.25	139.43	128.40
47	AA	579	C	C2-N1-C1'	-5.25	113.02	118.80
47	AA	993	G	C4-N9-C1'	-5.25	119.67	126.50
47	AA	80	G	N7-C8-N9	5.25	115.72	113.10
47	AA	1426	U	C2-N1-C1'	5.25	124.00	117.70
47	AA	1538	C	C6-N1-C2	5.24	122.40	120.30
47	AA	696	G	N3-C4-C5	5.24	131.22	128.60
47	AA	402	C	C4-C5-C6	-5.24	114.78	117.40
47	AA	596	U	O5'-P-OP1	-5.24	100.99	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	1288	U	C6-N1-C2	-5.23	117.86	121.00
47	AA	126	G	N3-C4-C5	5.23	131.21	128.60
47	AA	1607	A	N7-C8-N9	5.23	116.41	113.80
47	AA	664	A	C6-C5-N7	-5.23	128.64	132.30
47	AA	994	C	N3-C4-C5	5.22	123.99	121.90
62	An	72	U	C2-N1-C1'	-5.22	111.43	117.70
47	AA	30	C	N3-C4-C5	5.22	123.99	121.90
47	AA	10	G	N1-C6-O6	-5.21	116.77	119.90
47	AA	1866	A	C4-C5-C6	5.21	119.61	117.00
47	AA	1863	A	N7-C8-N9	5.21	116.41	113.80
47	AA	496	C	C6-N1-C1'	5.21	127.05	120.80
47	AA	923	G	N3-C4-N9	5.21	129.12	126.00
47	AA	1564	C	C2-N1-C1'	5.21	124.53	118.80
47	AA	739	C	N1-C2-O2	-5.21	115.78	118.90
47	AA	1836	G	N9-C4-C5	-5.21	103.32	105.40
47	AA	1775	U	N1-C2-O2	5.21	126.44	122.80
47	AA	1854	U	C5-C6-N1	-5.21	120.10	122.70
47	AA	1040	G	C6-C5-N7	-5.20	127.28	130.40
47	AA	1130	G	C5-C6-N1	-5.20	108.90	111.50
47	AA	1518	C	C5-C6-N1	5.20	123.60	121.00
47	AA	1811	C	N3-C4-C5	5.20	123.98	121.90
47	AA	878	G	N9-C4-C5	-5.20	103.32	105.40
47	AA	1004	U	C4-C5-C6	-5.20	116.58	119.70
49	AD	13	LEU	CA-CB-CG	-5.20	103.34	115.30
47	AA	810	A	O4'-C1'-N9	-5.20	104.04	108.20
79	AM	99	ASN	C-N-CD	5.20	139.31	128.40
62	An	29	G	C4-N9-C1'	-5.19	119.75	126.50
47	AA	1053	C	C2-N1-C1'	-5.19	113.09	118.80
47	AA	1717	C	N1-C2-N3	5.19	122.83	119.20
47	AA	584	G	C8-N9-C4	5.19	108.48	106.40
47	AA	880	G	C4-C5-N7	-5.19	108.72	110.80
47	AA	480	G	C8-N9-C4	5.19	108.47	106.40
47	AA	477	G	C2-N3-C4	-5.18	109.31	111.90
47	AA	680	G	N9-C4-C5	-5.18	103.33	105.40
47	AA	902	G	N3-C2-N2	-5.18	116.27	119.90
47	AA	1011	A	C8-N9-C4	-5.18	103.73	105.80
47	AA	1007	C	C6-N1-C2	5.18	122.37	120.30
47	AA	201	C	N3-C4-C5	-5.17	119.83	121.90
47	AA	1823	A	N9-C4-C5	-5.17	103.73	105.80
47	AA	1692	U	C5-C6-N1	-5.17	120.11	122.70
47	AA	30	C	C2-N3-C4	-5.17	117.31	119.90
47	AA	1524	G	C6-C5-N7	-5.16	127.30	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	1585	U	C6-N1-C2	5.16	124.09	121.00
47	AA	853	C	O4'-C1'-N1	5.16	112.32	108.20
47	AA	1014	G	N3-C4-N9	5.16	129.09	126.00
47	AA	1436	C	C6-N1-C2	-5.15	118.24	120.30
47	AA	194	C	C6-N1-C2	-5.15	118.24	120.30
47	AA	671	A	O4'-C1'-N9	-5.15	104.08	108.20
47	AA	519	A	C8-N9-C4	5.14	107.86	105.80
47	AA	850	C	C2-N1-C1'	-5.14	113.14	118.80
47	AA	1849	G	C6-C5-N7	-5.14	127.31	130.40
47	AA	1187	G	C6-C5-N7	-5.14	127.31	130.40
47	AA	1337	C	N3-C4-C5	5.14	123.96	121.90
47	AA	1752	C	N3-C2-O2	-5.14	118.30	121.90
47	AA	12	U	C5-C6-N1	-5.14	120.13	122.70
47	AA	1415	C	C2-N1-C1'	5.14	124.45	118.80
62	An	18	G	O4'-C1'-N9	5.14	112.31	108.20
47	AA	6	G	C5-C6-N1	5.13	114.07	111.50
47	AA	1475	G	N3-C4-C5	5.13	131.17	128.60
47	AA	680	G	C4-C5-N7	5.13	112.85	110.80
47	AA	1555	U	C5-C6-N1	5.13	125.27	122.70
47	AA	1334	G	C8-N9-C1'	5.13	133.67	127.00
47	AA	1786	U	N1-C2-O2	-5.13	119.21	122.80
47	AA	600	G	C5-C6-O6	-5.12	125.53	128.60
47	AA	399	C	N3-C4-C5	5.12	123.95	121.90
47	AA	39	A	O4'-C1'-N9	5.12	112.30	108.20
47	AA	1490	G	N7-C8-N9	5.12	115.66	113.10
47	AA	1150	A	C8-N9-C4	5.12	107.85	105.80
47	AA	1657	G	N1-C6-O6	5.12	122.97	119.90
47	AA	1802	C	N3-C4-C5	5.12	123.95	121.90
47	AA	923	G	N3-C4-C5	-5.11	126.05	128.60
47	AA	1138	C	N3-C2-O2	-5.11	118.33	121.90
47	AA	1211	G	N3-C4-C5	5.10	131.15	128.60
47	AA	1047	C	C6-N1-C2	-5.10	118.26	120.30
47	AA	1049	A	C8-N9-C4	5.10	107.84	105.80
47	AA	1038	U	C6-N1-C2	5.10	124.06	121.00
47	AA	1528	G	C8-N9-C1'	-5.10	120.38	127.00
47	AA	7	G	C5-N7-C8	-5.09	101.75	104.30
56	AN	149	LEU	CA-CB-CG	5.09	127.01	115.30
47	AA	1418	C	C6-N1-C2	-5.09	118.26	120.30
62	An	28	U	C6-N1-C1'	-5.09	114.08	121.20
47	AA	361	U	C2-N1-C1'	-5.09	111.60	117.70
47	AA	1791	A	C8-N9-C4	5.09	107.83	105.80
47	AA	1801	A	C8-N9-C4	5.09	107.83	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	1841	C	C6-N1-C2	5.09	122.33	120.30
62	An	61	C	C6-N1-C2	-5.08	118.27	120.30
47	AA	180	G	N3-C4-C5	5.08	131.14	128.60
47	AA	1227	G	N3-C4-C5	-5.08	126.06	128.60
47	AA	1205	C	N1-C2-N3	5.08	122.76	119.20
47	AA	1062	A	C8-N9-C4	5.08	107.83	105.80
73	Aw	42	LEU	CA-CB-CG	5.08	126.98	115.30
41	l	42	ASP	C-N-CD	5.08	139.06	128.40
47	AA	1099	G	C6-C5-N7	-5.08	127.35	130.40
47	AA	304	C	C5-C6-N1	5.07	123.54	121.00
47	AA	897	U	C5-C6-N1	5.07	125.24	122.70
47	AA	997	A	N1-C6-N6	5.07	121.64	118.60
47	AA	639	C	N3-C4-C5	5.07	123.93	121.90
47	AA	1158	G	N3-C4-N9	5.07	129.04	126.00
47	AA	661	U	N1-C2-O2	5.07	126.35	122.80
47	AA	907	G	N3-C4-N9	5.07	129.04	126.00
47	AA	1193	U	C5-C6-N1	-5.07	120.17	122.70
47	AA	622	C	N3-C4-C5	5.07	123.93	121.90
47	AA	948	C	C6-N1-C1'	-5.07	114.72	120.80
47	AA	1587	G	N3-C4-C5	-5.07	126.07	128.60
47	AA	1094	C	C6-N1-C2	5.06	122.33	120.30
47	AA	1863	A	N1-C2-N3	5.06	131.83	129.30
58	AQ	17	LEU	CA-CB-CG	-5.06	103.66	115.30
37	A	3771	C	N3-C2-O2	-5.06	118.36	121.90
47	AA	1146	C	C2-N3-C4	-5.06	117.37	119.90
62	An	40	C	N3-C2-O2	-5.06	118.36	121.90
47	AA	657	U	C5-C6-N1	-5.05	120.17	122.70
47	AA	24	C	N1-C2-O2	-5.05	115.87	118.90
52	AH	85	TYR	CA-CB-CG	-5.05	103.81	113.40
47	AA	1132	C	C6-N1-C2	-5.05	118.28	120.30
47	AA	324	C	C6-N1-C1'	-5.04	114.75	120.80
47	AA	1047	C	N3-C4-N4	5.04	121.53	118.00
47	AA	420	G	N3-C4-C5	5.04	131.12	128.60
47	AA	1415	C	N3-C2-O2	-5.04	118.37	121.90
47	AA	496	C	N1-C2-O2	-5.04	115.88	118.90
47	AA	685	A	N1-C6-N6	5.04	121.62	118.60
47	AA	1461	G	C8-N9-C4	5.04	108.41	106.40
37	A	4749	C	N1-C2-O2	5.03	121.92	118.90
47	AA	735	C	N1-C2-O2	5.03	121.92	118.90
47	AA	1585	U	C5-C6-N1	-5.03	120.18	122.70
47	AA	1853	C	C2-N1-C1'	5.03	124.34	118.80
47	AA	1185	C	N1-C2-O2	-5.03	115.88	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
47	AA	460	A	C4-C5-N7	5.03	113.21	110.70
61	AV	7	LEU	CA-CB-CG	-5.03	103.73	115.30
47	AA	1026	C	C5-C6-N1	-5.03	118.49	121.00
62	An	27	C	C2-N1-C1'	-5.02	113.27	118.80
47	AA	140	C	C6-N1-C2	5.02	122.31	120.30
47	AA	1082	A	C4-C5-C6	5.02	119.51	117.00
47	AA	1572	C	N3-C2-O2	-5.02	118.38	121.90
47	AA	1626	C	N3-C4-C5	5.02	123.91	121.90
47	AA	927	C	N3-C2-O2	-5.02	118.39	121.90
47	AA	509	G	N9-C4-C5	-5.02	103.39	105.40
47	AA	1412	C	N1-C2-O2	5.02	121.91	118.90
47	AA	1823	A	C4-C5-N7	5.02	113.21	110.70
47	AA	1732	G	C4-C5-N7	5.02	112.81	110.80
47	AA	654	A	C8-N9-C4	5.01	107.81	105.80
47	AA	847	A	C5-N7-C8	-5.01	101.39	103.90
47	AA	1600	G	C8-N9-C1'	-5.01	120.48	127.00
47	AA	381	C	C4-C5-C6	-5.01	114.89	117.40
47	AA	657	U	N3-C2-O2	5.01	125.71	122.20
47	AA	1295	A	C8-N9-C4	-5.01	103.80	105.80
47	AA	1847	G	N3-C4-C5	5.01	131.10	128.60
47	AA	984	C	N3-C2-O2	-5.00	118.40	121.90
47	AA	1447	G	N1-C6-O6	5.00	122.90	119.90
47	AA	657	U	N1-C2-O2	-5.00	119.30	122.80
47	AA	1201	U	C6-N1-C2	5.00	124.00	121.00

There are no chirality outliers.

All (78) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
70	A0	110	ASP	Peptide
70	A0	144	ARG	Peptide
70	A0	34	LYS	Peptide
70	A0	72	GLN	Peptide
76	AB	107	GLU	Peptide
76	AB	110	VAL	Peptide
76	AB	60	THR	Peptide
76	AB	96	GLU	Peptide
48	AC	5	ALA	Peptide
49	AD	107	ARG	Peptide
49	AD	40	PRO	Peptide
49	AD	54	LYS	Peptide
52	AH	139	HIS	Peptide

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Mol	Chain	Res	Type	Group
52	AH	87	THR	Peptide
78	AI	101	PHE	Peptide
78	AI	140	TYR	Peptide
78	AI	152	SER	Peptide
78	AI	245	ARG	Peptide
78	AI	262	GLU	Peptide
53	AJ	226	ALA	Peptide
54	AK	103	ASP	Peptide
54	AK	15	LEU	Peptide
54	AK	221	LYS	Peptide
54	AK	227	GLN	Peptide
54	AK	39	ASP	Peptide
55	AL	3	VAL	Peptide
79	AM	28	HIS	Peptide
79	AM	40	LYS	Peptide
56	AN	23	PRO	Peptide
80	AO	138	ASP	Peptide
80	AO	47	LEU	Peptide
59	AR	62	VAL	Peptide
60	AT	12	VAL	Peptide
60	AT	13	ARG	Peptide
60	AT	25	LYS	Peptide
81	AU	117	GLN	Peptide
81	AU	40	ALA	Peptide
81	AU	63	HIS	Peptide
81	AU	83	GLN	Peptide
61	AV	81	ARG	Peptide
71	Ao	164	ASN	Peptide
71	Ao	195	TRP	Peptide
71	Ao	43	SER	Peptide
71	Ao	77	ILE	Peptide
63	Ap	131	ASP	Peptide
63	Ap	190	PRO	Peptide
63	Ap	37	ALA	Peptide
64	Aq	164	VAL	Peptide
64	Aq	193	ASP	Peptide
64	Aq	96	LEU	Peptide
65	Ar	144	ALA	Peptide
65	Ar	194	VAL	Peptide
72	As	118	ASN	Peptide
72	As	133	THR	Peptide
72	As	137	GLN	Peptide

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Mol	Chain	Res	Type	Group
72	As	163	PHE	Peptide
72	As	28	VAL	Peptide
72	As	40	ALA	Peptide
66	At	138	GLU	Peptide
66	At	32	MET	Peptide
66	At	66	VAL	Peptide
67	Au	127	ALA	Peptide
68	Av	3	MET	Peptide
69	Ay	110	ASP	Peptide
69	Ay	118	THR	Peptide
69	Ay	37	ARG	Peptide
69	Ay	38	PRO	Peptide
69	Ay	43	GLU	Peptide
75	Az	107	LYS	Peptide
75	Az	27	ASP	Peptide
75	Az	6	THR	Peptide
75	Az	85	VAL	Peptide
5	F	290	SER	Peptide
38	H	88	VAL	Mainchain
40	K	7	HIS	Peptide
11	O	65	ARG	Peptide
39	i	58	LYS	Peptide
33	s	40	GLY	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	246/257 (96%)	227 (92%)	19 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	E	400/403 (99%)	378 (94%)	22 (6%)	0	100	100
5	F	365/427 (86%)	331 (91%)	33 (9%)	1 (0%)	41	75
6	G	291/297 (98%)	270 (93%)	20 (7%)	1 (0%)	41	75
7	I	199/203 (98%)	195 (98%)	4 (2%)	0	100	100
8	J	151/160 (94%)	145 (96%)	5 (3%)	1 (1%)	22	61
9	L	185/196 (94%)	177 (96%)	8 (4%)	0	100	100
10	N	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
11	O	99/128 (77%)	94 (95%)	5 (5%)	0	100	100
12	P	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
13	Q	62/157 (40%)	58 (94%)	4 (6%)	0	100	100
14	S	132/145 (91%)	121 (92%)	11 (8%)	0	100	100
15	T	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
16	U	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
17	V	73/159 (46%)	65 (89%)	8 (11%)	0	100	100
18	X	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
19	Y	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
20	Z	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
21	a	112/117 (96%)	109 (97%)	3 (3%)	0	100	100
22	b	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
23	c	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
24	d	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
25	e	67/70 (96%)	62 (92%)	4 (6%)	1 (2%)	10	47
26	f	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
27	g	50/128 (39%)	45 (90%)	5 (10%)	0	100	100
28	j	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
29	k	123/137 (90%)	110 (89%)	13 (11%)	0	100	100
30	m	223/248 (90%)	212 (95%)	11 (5%)	0	100	100
31	n	239/266 (90%)	228 (95%)	11 (5%)	0	100	100
32	o	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
33	s	137/215 (64%)	124 (90%)	13 (10%)	0	100	100
34	t	201/204 (98%)	191 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	h	22/25 (88%)	19 (86%)	2 (9%)	1 (4%)	2	23
36	r	208/211 (99%)	189 (91%)	17 (8%)	2 (1%)	15	55
38	H	238/288 (83%)	203 (85%)	30 (13%)	5 (2%)	7	40
39	i	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
40	K	185/188 (98%)	177 (96%)	7 (4%)	1 (0%)	29	68
41	l	215/217 (99%)	188 (87%)	25 (12%)	2 (1%)	17	57
42	M	173/176 (98%)	158 (91%)	13 (8%)	2 (1%)	13	51
43	p	211/214 (99%)	196 (93%)	14 (7%)	1 (0%)	29	68
44	q	172/178 (97%)	163 (95%)	6 (4%)	3 (2%)	9	45
45	R	118/156 (76%)	112 (95%)	6 (5%)	0	100	100
46	W	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
48	AC	81/83 (98%)	70 (86%)	8 (10%)	3 (4%)	3	28
49	AD	139/143 (97%)	117 (84%)	22 (16%)	0	100	100
50	AE	99/115 (86%)	93 (94%)	6 (6%)	0	100	100
51	AF	61/69 (88%)	55 (90%)	6 (10%)	0	100	100
52	AH	69/156 (44%)	54 (78%)	13 (19%)	2 (3%)	4	33
53	AJ	220/293 (75%)	195 (89%)	25 (11%)	0	100	100
54	AK	235/249 (94%)	206 (88%)	27 (12%)	2 (1%)	17	57
55	AL	183/194 (94%)	161 (88%)	21 (12%)	1 (0%)	29	68
56	AN	147/151 (97%)	125 (85%)	22 (15%)	0	100	100
57	AP	127/130 (98%)	112 (88%)	15 (12%)	0	100	100
58	AQ	129/133 (97%)	118 (92%)	8 (6%)	3 (2%)	6	38
59	AR	73/125 (58%)	61 (84%)	12 (16%)	0	100	100
60	AT	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
61	AV	81/84 (96%)	73 (90%)	7 (9%)	1 (1%)	13	51
63	Ap	212/264 (80%)	184 (87%)	25 (12%)	3 (1%)	11	48
64	Aq	225/243 (93%)	195 (87%)	26 (12%)	4 (2%)	8	43
65	Ar	260/263 (99%)	226 (87%)	31 (12%)	3 (1%)	13	51
66	At	187/194 (96%)	155 (83%)	30 (16%)	2 (1%)	14	53
67	Au	204/208 (98%)	179 (88%)	22 (11%)	3 (2%)	10	47
68	Av	96/165 (58%)	77 (80%)	18 (19%)	1 (1%)	15	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	Ay	144/146 (99%)	123 (85%)	18 (12%)	3 (2%)	7	40
70	A0	148/152 (97%)	121 (82%)	21 (14%)	6 (4%)	3	26
71	Ao	220/295 (75%)	190 (86%)	28 (13%)	2 (1%)	17	57
72	As	189/204 (93%)	158 (84%)	23 (12%)	8 (4%)	3	25
73	Aw	151/158 (96%)	130 (86%)	18 (12%)	3 (2%)	7	41
74	Ax	95/145 (66%)	60 (63%)	21 (22%)	14 (15%)	0	3
75	Az	130/135 (96%)	93 (72%)	26 (20%)	11 (8%)	1	10
76	AB	100/119 (84%)	82 (82%)	14 (14%)	4 (4%)	3	26
77	AG	51/56 (91%)	43 (84%)	6 (12%)	2 (4%)	3	27
78	AI	311/317 (98%)	261 (84%)	44 (14%)	6 (2%)	8	42
79	AM	120/132 (91%)	91 (76%)	26 (22%)	3 (2%)	5	36
80	AO	138/151 (91%)	112 (81%)	21 (15%)	5 (4%)	3	29
81	AU	141/145 (97%)	116 (82%)	18 (13%)	7 (5%)	2	21
All	All	11449/12881 (89%)	10266 (90%)	1060 (9%)	123 (1%)	18	53

All (123) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	H	100	LYS
38	H	225	PRO
40	K	159	PRO
44	q	55	TYR
44	q	59	SER
54	AK	153	VAL
70	A0	90	VAL
72	As	43	GLU
72	As	45	TYR
72	As	46	ALA
72	As	47	LYS
74	Ax	73	PRO
74	Ax	78	THR
74	Ax	98	ASN
74	Ax	100	LYS
74	Ax	102	PHE
75	Az	67	ARG
75	Az	97	GLU
75	Az	119	VAL

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Mol	Chain	Res	Type
75	Az	127	ASN
76	AB	49	LYS
76	AB	51	LYS
78	AI	54	ILE
78	AI	57	ARG
80	AO	13	GLN
80	AO	14	VAL
81	AU	78	ILE
41	l	67	VAL
70	A0	117	ILE
72	As	42	LYS
73	Aw	28	THR
73	Aw	29	GLY
74	Ax	77	LYS
74	Ax	79	HIS
74	Ax	80	LEU
75	Az	98	VAL
75	Az	130	THR
81	AU	4	VAL
6	G	4	VAL
35	h	4	LYS
36	r	55	ILE
38	H	91	THR
38	H	226	ARG
48	AC	36	VAL
69	Ay	100	VAL
70	A0	12	ILE
74	Ax	74	GLU
74	Ax	76	VAL
74	Ax	97	TYR
77	AG	7	TYR
77	AG	8	TRP
78	AI	53	GLY
80	AO	140	THR
43	p	21	ARG
48	AC	78	ILE
61	AV	20	LYS
63	Ap	40	ASN
64	Aq	61	GLU
66	At	139	ILE
67	Au	97	VAL
68	Av	4	PRO

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Mol	Chain	Res	Type
70	A0	16	LEU
70	A0	71	MET
72	As	17	ILE
74	Ax	37	TYR
74	Ax	58	LYS
75	Az	108	LEU
75	Az	121	GLN
81	AU	5	THR
81	AU	45	LEU
81	AU	130	ASP
81	AU	137	GLN
42	M	146	HIS
58	AQ	33	ALA
63	Ap	37	ALA
63	Ap	190	PRO
67	Au	140	LYS
67	Au	177	SER
72	As	127	ARG
78	AI	284	PRO
79	AM	100	PRO
80	AO	112	ALA
81	AU	67	ARG
41	l	202	ARG
54	AK	235	SER
55	AL	86	VAL
58	AQ	52	PRO
64	Aq	26	THR
70	A0	17	ASN
73	Aw	30	LYS
74	Ax	96	VAL
79	AM	123	VAL
8	J	24	VAL
42	M	124	ILE
52	AH	108	VAL
64	Aq	99	ILE
75	Az	9	VAL
75	Az	69	ILE
76	AB	17	ILE
76	AB	50	VAL
48	AC	42	VAL
65	Ar	80	ILE
65	Ar	131	VAL

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Mol	Chain	Res	Type
71	Ao	171	VAL
71	Ao	194	PRO
78	AI	28	PRO
52	AH	98	VAL
69	Ay	42	ILE
69	Ay	93	VAL
79	AM	103	VAL
80	AO	56	VAL
36	r	54	PRO
38	H	106	VAL
44	q	174	ILE
65	Ar	76	VAL
66	At	100	ILE
75	Az	50	ILE
5	F	309	ILE
25	e	32	VAL
58	AQ	51	THR
64	Aq	66	ILE
78	AI	163	PRO
72	As	15	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D	190/199 (96%)	190 (100%)	0	100	100
4	E	348/349 (100%)	348 (100%)	0	100	100
5	F	305/348 (88%)	305 (100%)	0	100	100
6	G	246/250 (98%)	246 (100%)	0	100	100
7	I	173/174 (99%)	173 (100%)	0	100	100
8	J	134/141 (95%)	134 (100%)	0	100	100
9	L	166/175 (95%)	166 (100%)	0	100	100
10	N	139/140 (99%)	139 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	O	91/115 (79%)	91 (100%)	0	100	100
12	P	101/107 (94%)	101 (100%)	0	100	100
13	Q	56/126 (44%)	56 (100%)	0	100	100
14	S	124/135 (92%)	124 (100%)	0	100	100
15	T	117/118 (99%)	117 (100%)	0	100	100
16	U	120/121 (99%)	120 (100%)	0	100	100
17	V	63/126 (50%)	63 (100%)	0	100	100
18	X	98/110 (89%)	98 (100%)	0	100	100
19	Y	114/121 (94%)	114 (100%)	0	100	100
20	Z	88/89 (99%)	88 (100%)	0	100	100
21	a	98/100 (98%)	98 (100%)	0	100	100
22	b	109/110 (99%)	109 (100%)	0	100	100
23	c	86/89 (97%)	86 (100%)	0	100	100
24	d	73/80 (91%)	73 (100%)	0	100	100
25	e	64/65 (98%)	64 (100%)	0	100	100
26	f	47/48 (98%)	47 (100%)	0	100	100
27	g	48/116 (41%)	48 (100%)	0	100	100
28	j	74/75 (99%)	74 (100%)	0	100	100
29	k	109/121 (90%)	109 (100%)	0	100	100
30	m	194/215 (90%)	194 (100%)	0	100	100
31	n	203/223 (91%)	203 (100%)	0	100	100
32	o	169/171 (99%)	169 (100%)	0	100	100
33	s	118/161 (73%)	118 (100%)	0	100	100
34	t	171/172 (99%)	171 (100%)	0	100	100
35	h	23/24 (96%)	23 (100%)	0	100	100
36	r	176/177 (99%)	174 (99%)	2 (1%)	73	88
38	H	215/252 (85%)	209 (97%)	6 (3%)	43	72
39	i	93/94 (99%)	92 (99%)	1 (1%)	73	88
40	K	164/165 (99%)	164 (100%)	0	100	100
41	l	195/196 (100%)	194 (100%)	1 (0%)	88	95
42	M	156/157 (99%)	154 (99%)	2 (1%)	69	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	p	180/181 (99%)	178 (99%)	2 (1%)	73	88
44	q	148/149 (99%)	144 (97%)	4 (3%)	44	73
45	R	108/133 (81%)	107 (99%)	1 (1%)	78	90
46	W	83/97 (86%)	83 (100%)	0	100	100
48	AC	67/67 (100%)	67 (100%)	0	100	100
49	AD	113/115 (98%)	113 (100%)	0	100	100
50	AE	88/98 (90%)	88 (100%)	0	100	100
51	AF	56/62 (90%)	56 (100%)	0	100	100
52	AH	64/140 (46%)	64 (100%)	0	100	100
53	AJ	188/225 (84%)	186 (99%)	2 (1%)	73	88
54	AK	207/218 (95%)	207 (100%)	0	100	100
55	AL	161/168 (96%)	161 (100%)	0	100	100
56	AN	130/131 (99%)	130 (100%)	0	100	100
57	AP	112/113 (99%)	110 (98%)	2 (2%)	59	81
58	AQ	113/115 (98%)	113 (100%)	0	100	100
59	AR	66/103 (64%)	66 (100%)	0	100	100
60	AT	47/48 (98%)	47 (100%)	0	100	100
61	AV	75/76 (99%)	75 (100%)	0	100	100
63	Ap	195/231 (84%)	193 (99%)	2 (1%)	76	88
64	Aq	190/202 (94%)	190 (100%)	0	100	100
65	Ar	224/225 (100%)	223 (100%)	1 (0%)	91	97
66	At	169/174 (97%)	169 (100%)	0	100	100
67	Au	178/180 (99%)	178 (100%)	0	100	100
68	Av	89/136 (65%)	89 (100%)	0	100	100
69	Ay	121/121 (100%)	120 (99%)	1 (1%)	81	91
70	A0	130/132 (98%)	130 (100%)	0	100	100
71	Ao	184/243 (76%)	184 (100%)	0	100	100
72	As	161/170 (95%)	159 (99%)	2 (1%)	71	87
73	Aw	137/142 (96%)	136 (99%)	1 (1%)	84	93
74	Ax	87/130 (67%)	84 (97%)	3 (3%)	37	69
75	Az	120/122 (98%)	115 (96%)	5 (4%)	30	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
76	AB	93/107 (87%)	89 (96%)	4 (4%)	29	63
77	AG	47/49 (96%)	46 (98%)	1 (2%)	53	78
78	AI	272/275 (99%)	270 (99%)	2 (1%)	84	93
79	AM	104/108 (96%)	103 (99%)	1 (1%)	76	88
80	AO	110/119 (92%)	110 (100%)	0	100	100
81	AU	113/115 (98%)	112 (99%)	1 (1%)	78	90
All	All	9988/10975 (91%)	9941 (100%)	47 (0%)	89	95

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	r	145	LYS
36	r	146	LEU
38	H	83	LYS
38	H	84	LYS
38	H	88	VAL
38	H	96	VAL
38	H	100	LYS
38	H	224	LYS
39	i	106	PHE
41	l	66	CYS
42	M	164	LYS
42	M	166	ARG
43	p	105	CYS
43	p	110	ARG
44	q	55	TYR
44	q	56	THR
44	q	58	ARG
44	q	154	LYS
45	R	37	LYS
53	AJ	163	VAL
53	AJ	196	ILE
57	AP	72	CYS
57	AP	112	ASP
63	Ap	90	ASP
63	Ap	196	ASP
65	Ar	98	ASN
69	Ay	100	VAL
72	As	44	LYS
72	As	45	TYR

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Mol	Chain	Res	Type
73	Aw	28	THR
74	Ax	80	LEU
74	Ax	82	ASP
74	Ax	97	TYR
75	Az	67	ARG
75	Az	69	ILE
75	Az	120	THR
75	Az	126	MET
75	Az	130	THR
76	AB	46	LYS
76	AB	48	LEU
76	AB	49	LYS
76	AB	88	LEU
77	AG	4	GLN
78	AI	54	ILE
78	AI	107	ASP
79	AM	99	ASN
81	AU	45	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	86	GLN
4	E	302	ASN
5	F	142	HIS
5	F	276	ASN
5	F	286	ASN
8	J	75	GLN
8	J	80	GLN
8	J	97	ASN
9	L	58	HIS
10	N	98	HIS
13	Q	59	HIS
14	S	96	HIS
16	U	19	HIS
16	U	25	HIS
16	U	28	HIS
17	V	49	HIS
18	X	118	GLN
19	Y	23	HIS
28	j	33	GLN
29	k	6	GLN

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Mol	Chain	Res	Type
30	m	63	GLN
30	m	110	GLN
30	m	116	GLN
30	m	119	ASN
32	o	188	GLN
34	t	37	HIS
34	t	201	HIS
36	r	15	HIS
38	H	128	HIS
38	H	167	GLN
38	H	191	GLN
38	H	228	GLN
39	i	19	GLN
39	i	45	GLN
39	i	51	GLN
40	K	57	ASN
41	l	35	GLN
41	l	119	GLN
41	l	143	ASN
41	l	200	ASN
42	M	50	GLN
42	M	117	HIS
42	M	146	HIS
43	p	51	HIS
44	q	155	HIS
45	R	93	ASN
49	AD	87	ASN
49	AD	92	ASN
50	AE	19	GLN
51	AF	26	GLN
52	AH	139	HIS
54	AK	13	GLN
54	AK	225	GLN
55	AL	75	ASN
55	AL	113	GLN
55	AL	140	GLN
55	AL	156	HIS
56	AN	105	ASN
57	AP	113	HIS
61	AV	19	HIS
63	Ap	92	GLN
63	Ap	101	HIS

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Mol	Chain	Res	Type
63	Ap	186	ASN
63	Ap	208	HIS
65	Ar	214	ASN
66	At	44	ASN
68	Av	39	ASN
68	Av	42	ASN
68	Av	44	HIS
68	Av	66	HIS
70	A0	87	GLN
70	A0	125	HIS
71	Ao	193	HIS
72	As	51	HIS
72	As	179	ASN
73	Aw	13	GLN
75	Az	48	ASN
76	AB	28	ASN
77	AG	37	ASN
78	AI	14	HIS
78	AI	20	GLN
78	AI	62	HIS
78	AI	64	HIS
78	AI	76	GLN
78	AI	147	HIS
78	AI	187	ASN
78	AI	191	HIS
78	AI	237	ASN
78	AI	285	GLN
79	AM	52	GLN
80	AO	26	ASN
80	AO	113	GLN
81	AU	63	HIS
81	AU	105	GLN
81	AU	128	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	119/121 (98%)	16 (13%)	0
2	C	155/157 (98%)	34 (21%)	1 (0%)
37	A	3707/5070 (73%)	1071 (28%)	50 (1%)
47	AA	1716/1869 (91%)	906 (52%)	48 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
62	An	74/75 (98%)	37 (50%)	0
All	All	5771/7292 (79%)	2064 (35%)	99 (1%)

All (2064) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	2	U
1	B	7	G
1	B	17	C
1	B	22	A
1	B	24	C
1	B	50	A
1	B	54	A
1	B	64	G
1	B	71	G
1	B	90	A
1	B	97	G
1	B	100	A
1	B	106	G
1	B	107	G
1	B	110	G
1	B	120	U
2	C	21	C
2	C	34	U
2	C	35	C
2	C	39	G
2	C	52	A
2	C	59	A
2	C	63	U
2	C	80	A
2	C	82	A
2	C	83	C
2	C	84	A
2	C	85	U
2	C	86	U
2	C	87	G
2	C	88	A
2	C	94	G
2	C	103	A
2	C	104	A
2	C	105	C
2	C	109	C

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Mol	Chain	Res	Type
2	C	110	U
2	C	114	G
2	C	118	C
2	C	123	U
2	C	124	U
2	C	125	C
2	C	126	C
2	C	127	U
2	C	129	C
2	C	146	U
2	C	147	G
2	C	150	C
2	C	153	C
2	C	156	U
37	A	9	C
37	A	17	A
37	A	18	C
37	A	19	G
37	A	25	A
37	A	39	A
37	A	42	A
37	A	44	A
37	A	48	G
37	A	56	A
37	A	59	A
37	A	65	A
37	A	66	A
37	A	73	A
37	A	84	A
37	A	91	G
37	A	108	A
37	A	109	G
37	A	110	C
37	A	117	C
37	A	118	C
37	A	119	G
37	A	120	A
37	A	122	U
37	A	130	C
37	A	131	C
37	A	133	C
37	A	134	G

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Mol	Chain	Res	Type
37	A	135	G
37	A	136	C
37	A	137	G
37	A	140	G
37	A	143	C
37	A	144	G
37	A	149	A
37	A	152	U
37	A	159	C
37	A	164	G
37	A	171	U
37	A	172	C
37	A	173	C
37	A	175	C
37	A	179	G
37	A	180	C
37	A	183	C
37	A	184	U
37	A	185	C
37	A	187	U
37	A	188	G
37	A	200	U
37	A	201	C
37	A	202	C
37	A	205	C
37	A	217	C
37	A	218	A
37	A	219	G
37	A	220	C
37	A	232	G
37	A	233	U
37	A	234	G
37	A	235	A
37	A	238	C
37	A	245	C
37	A	246	G
37	A	250	C
37	A	253	G
37	A	258	G
37	A	265	C
37	A	266	C
37	A	267	G

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Mol	Chain	Res	Type
37	A	277	G
37	A	278	G
37	A	280	G
37	A	297	U
37	A	306	A
37	A	315	G
37	A	316	U
37	A	322	C
37	A	326	C
37	A	334	A
37	A	340	C
37	A	379	G
37	A	383	A
37	A	384	A
37	A	387	G
37	A	399	G
37	A	401	G
37	A	407	A
37	A	409	G
37	A	410	A
37	A	415	G
37	A	417	G
37	A	418	A
37	A	431	G
37	A	432	U
37	A	433	A
37	A	446	C
37	A	448	G
37	A	449	C
37	A	450	G
37	A	451	C
37	A	452	A
37	A	453	G
37	A	454	U
37	A	455	C
37	A	462	G
37	A	468	U
37	A	469	C
37	A	470	A
37	A	485	C
37	A	486	C
37	A	487	G

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Mol	Chain	Res	Type
37	A	488	G
37	A	490	C
37	A	499	G
37	A	500	G
37	A	501	C
37	A	502	C
37	A	503	C
37	A	504	G
37	A	506	C
37	A	507	G
37	A	509	A
37	A	510	U
37	A	511	C
37	A	512	U
37	A	513	U
37	A	514	U
37	A	516	C
37	A	517	C
37	A	518	G
37	A	643	C
37	A	644	G
37	A	646	G
37	A	649	A
37	A	654	C
37	A	655	C
37	A	656	C
37	A	657	C
37	A	658	C
37	A	661	C
37	A	664	G
37	A	665	C
37	A	666	G
37	A	667	A
37	A	671	G
37	A	681	G
37	A	684	G
37	A	685	C
37	A	686	A
37	A	694	C
37	A	695	G
37	A	696	C
37	A	697	G

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Mol	Chain	Res	Type
37	A	702	U
37	A	703	G
37	A	704	C
37	A	705	G
37	A	707	C
37	A	713	C
37	A	720	G
37	A	730	G
37	A	736	C
37	A	737	C
37	A	740	G
37	A	741	C
37	A	745	G
37	A	746	A
37	A	747	A
37	A	748	G
37	A	749	G
37	A	750	U
37	A	907	C
37	A	910	G
37	A	911	U
37	A	915	A
37	A	916	C
37	A	917	A
37	A	918	G
37	A	919	C
37	A	920	C
37	A	926	G
37	A	927	G
37	A	928	C
37	A	929	A
37	A	930	G
37	A	931	C
37	A	932	A
37	A	933	G
37	A	934	C
37	A	938	C
37	A	939	G
37	A	940	C
37	A	941	C
37	A	942	G
37	A	944	A

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Mol	Chain	Res	Type
37	A	945	U
37	A	946	C
37	A	950	G
37	A	957	G
37	A	958	G
37	A	959	G
37	A	960	A
37	A	961	G
37	A	962	C
37	A	963	G
37	A	964	A
37	A	965	G
37	A	966	A
37	A	967	C
37	A	968	C
37	A	969	C
37	A	975	C
37	A	976	G
37	A	978	G
37	A	979	C
37	A	981	C
37	A	982	U
37	A	986	C
37	A	989	U
37	A	992	C
37	A	994	G
37	A	995	C
37	A	1048	G
37	A	1051	G
37	A	1066	G
37	A	1068	G
37	A	1070	G
37	A	1072	C
37	A	1073	G
37	A	1078	A
37	A	1079	C
37	A	1080	C
37	A	1081	C
37	A	1082	C
37	A	1095	A
37	A	1096	C
37	A	1097	C

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Mol	Chain	Res	Type
37	A	1170	G
37	A	1172	C
37	A	1173	G
37	A	1175	A
37	A	1179	U
37	A	1180	C
37	A	1181	C
37	A	1182	C
37	A	1183	C
37	A	1184	A
37	A	1191	C
37	A	1193	C
37	A	1194	G
37	A	1200	G
37	A	1202	C
37	A	1203	G
37	A	1205	G
37	A	1209	U
37	A	1210	C
37	A	1211	G
37	A	1214	C
37	A	1215	C
37	A	1216	C
37	A	1217	G
37	A	1219	G
37	A	1221	G
37	A	1222	A
37	A	1233	G
37	A	1237	C
37	A	1238	A
37	A	1239	C
37	A	1243	C
37	A	1244	G
37	A	1245	C
37	A	1252	C
37	A	1254	A
37	A	1256	G
37	A	1257	A
37	A	1264	C
37	A	1267	C
37	A	1268	G
37	A	1269	G

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Mol	Chain	Res	Type
37	A	1270	A
37	A	1271	G
37	A	1272	C
37	A	1273	G
37	A	1274	A
37	A	1275	G
37	A	1276	C
37	A	1277	G
37	A	1279	A
37	A	1280	C
37	A	1281	G
37	A	1282	G
37	A	1285	U
37	A	1288	G
37	A	1289	C
37	A	1290	G
37	A	1293	G
37	A	1295	C
37	A	1296	G
37	A	1301	C
37	A	1322	A
37	A	1324	A
37	A	1326	A
37	A	1330	A
37	A	1339	U
37	A	1352	C
37	A	1354	A
37	A	1358	G
37	A	1359	G
37	A	1365	C
37	A	1366	G
37	A	1367	C
37	A	1368	A
37	A	1369	C
37	A	1370	G
37	A	1372	A
37	A	1376	C
37	A	1377	G
37	A	1378	C
37	A	1379	C
37	A	1381	U
37	A	1387	A

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Mol	Chain	Res	Type
37	A	1394	G
37	A	1404	G
37	A	1405	C
37	A	1407	C
37	A	1409	C
37	A	1410	U
37	A	1411	C
37	A	1412	G
37	A	1413	C
37	A	1415	G
37	A	1416	G
37	A	1417	C
37	A	1420	A
37	A	1421	G
37	A	1425	G
37	A	1434	G
37	A	1440	U
37	A	1446	C
37	A	1456	C
37	A	1457	G
37	A	1474	C
37	A	1476	C
37	A	1480	C
37	A	1481	C
37	A	1482	G
37	A	1483	C
37	A	1484	G
37	A	1489	G
37	A	1497	A
37	A	1498	G
37	A	1501	C
37	A	1502	G
37	A	1503	A
37	A	1518	A
37	A	1523	A
37	A	1530	G
37	A	1534	A
37	A	1540	C
37	A	1547	A
37	A	1552	G
37	A	1566	C
37	A	1578	U

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Mol	Chain	Res	Type
37	A	1586	G
37	A	1591	U
37	A	1597	G
37	A	1605	G
37	A	1612	G
37	A	1613	A
37	A	1614	C
37	A	1624	G
37	A	1625	G
37	A	1626	G
37	A	1631	A
37	A	1633	G
37	A	1634	A
37	A	1638	A
37	A	1641	G
37	A	1642	A
37	A	1650	A
37	A	1654	G
37	A	1661	C
37	A	1676	C
37	A	1677	U
37	A	1691	G
37	A	1696	C
37	A	1697	G
37	A	1698	C
37	A	1699	A
37	A	1719	A
37	A	1721	G
37	A	1724	G
37	A	1729	A
37	A	1735	U
37	A	1741	G
37	A	1742	A
37	A	1750	G
37	A	1751	A
37	A	1754	U
37	A	1755	C
37	A	1756	U
37	A	1757	U
37	A	1758	G
37	A	1759	G
37	A	1760	G

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Mol	Chain	Res	Type
37	A	1761	G
37	A	1762	C
37	A	1763	C
37	A	1764	G
37	A	1765	A
37	A	1766	A
37	A	1767	A
37	A	1768	C
37	A	1769	G
37	A	1770	A
37	A	1775	A
37	A	1777	C
37	A	1778	C
37	A	1781	U
37	A	1787	A
37	A	1788	A
37	A	1804	A
37	A	1806	G
37	A	1807	C
37	A	1815	G
37	A	1820	C
37	A	1822	U
37	A	1823	G
37	A	1832	C
37	A	1834	U
37	A	1835	G
37	A	1836	G
37	A	1842	G
37	A	1855	G
37	A	1856	C
37	A	1860	U
37	A	1867	A
37	A	1869	G
37	A	1881	C
37	A	1886	G
37	A	1889	U
37	A	1890	G
37	A	1897	A
37	A	1910	G
37	A	1918	U
37	A	1919	G
37	A	1920	C

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Mol	Chain	Res	Type
37	A	1921	C
37	A	1922	G
37	A	1925	G
37	A	1930	U
37	A	1932	A
37	A	1936	C
37	A	1948	G
37	A	1959	U
37	A	1960	A
37	A	1961	G
37	A	1967	A
37	A	1968	G
37	A	1969	G
37	A	1970	A
37	A	1971	C
37	A	1973	G
37	A	1974	U
37	A	1975	G
37	A	1976	G
37	A	1977	C
37	A	1979	A
37	A	1981	G
37	A	1982	G
37	A	1983	A
37	A	1984	A
37	A	1985	G
37	A	1987	C
37	A	1989	G
37	A	1990	A
37	A	1991	A
37	A	1993	C
37	A	1994	C
37	A	1995	G
37	A	1996	C
37	A	1997	U
37	A	1998	A
37	A	1999	A
37	A	2000	G
37	A	2001	G
37	A	2002	A
37	A	2003	G
37	A	2005	G

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Mol	Chain	Res	Type
37	A	2006	U
37	A	2009	A
37	A	2010	A
37	A	2011	C
37	A	2012	A
37	A	2013	A
37	A	2017	A
37	A	2018	C
37	A	2019	C
37	A	2020	U
37	A	2023	C
37	A	2026	A
37	A	2046	G
37	A	2048	U
37	A	2052	G
37	A	2054	U
37	A	2055	G
37	A	2056	G
37	A	2063	G
37	A	2068	C
37	A	2069	A
37	A	2070	U
37	A	2084	C
37	A	2085	G
37	A	2089	G
37	A	2091	C
37	A	2092	G
37	A	2093	A
37	A	2094	G
37	A	2095	A
37	A	2096	G
37	A	2097	U
37	A	2098	G
37	A	2099	G
37	A	2100	A
37	A	2104	G
37	A	2105	A
37	A	2107	C
37	A	2108	G
37	A	2109	G
37	A	2110	C
37	A	2111	G

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Mol	Chain	Res	Type
37	A	2112	G
37	A	2113	G
37	A	2114	G
37	A	2115	G
37	A	2116	C
37	A	2117	G
37	A	2118	G
37	A	2119	C
37	A	2120	G
37	A	2121	C
37	A	2122	G
37	A	2123	C
37	A	2124	G
37	A	2125	C
37	A	2126	G
37	A	2128	G
37	A	2130	G
37	A	2244	C
37	A	2247	C
37	A	2250	C
37	A	2251	G
37	A	2252	G
37	A	2253	A
37	A	2254	G
37	A	2255	C
37	A	2256	C
37	A	2257	C
37	A	2259	G
37	A	2260	C
37	A	2261	G
37	A	2262	G
37	A	2263	A
37	A	2265	G
37	A	2268	A
37	A	2270	G
37	A	2278	G
37	A	2289	C
37	A	2300	A
37	A	2301	G
37	A	2313	A
37	A	2316	G
37	A	2327	G

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Mol	Chain	Res	Type
37	A	2333	G
37	A	2348	G
37	A	2351	C
37	A	2360	A
37	A	2361	G
37	A	2362	U
37	A	2364	G
37	A	2379	A
37	A	2382	A
37	A	2390	G
37	A	2391	G
37	A	2397	G
37	A	2412	A
37	A	2417	A
37	A	2422	C
37	A	2425	U
37	A	2426	U
37	A	2437	C
37	A	2448	G
37	A	2450	G
37	A	2463	G
37	A	2465	C
37	A	2468	U
37	A	2471	G
37	A	2474	G
37	A	2475	G
37	A	2483	G
37	A	2486	G
37	A	2488	C
37	A	2489	C
37	A	2490	U
37	A	2491	C
37	A	2494	U
37	A	2496	G
37	A	2501	C
37	A	2504	C
37	A	2505	C
37	A	2506	G
37	A	2513	A
37	A	2514	G
37	A	2529	A
37	A	2537	A

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Mol	Chain	Res	Type
37	A	2544	G
37	A	2546	G
37	A	2547	G
37	A	2553	A
37	A	2554	U
37	A	2555	G
37	A	2556	G
37	A	2557	G
37	A	2561	C
37	A	2566	G
37	A	2569	G
37	A	2570	U
37	A	2573	A
37	A	2583	C
37	A	2587	A
37	A	2588	C
37	A	2601	A
37	A	2618	G
37	A	2620	G
37	A	2627	C
37	A	2638	G
37	A	2640	G
37	A	2643	G
37	A	2645	G
37	A	2648	G
37	A	2653	C
37	A	2658	G
37	A	2662	G
37	A	2667	C
37	A	2670	C
37	A	2675	G
37	A	2676	A
37	A	2686	G
37	A	2687	U
37	A	2689	C
37	A	2694	G
37	A	2696	A
37	A	2701	U
37	A	2706	G
37	A	2707	U
37	A	2708	U
37	A	2710	C

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Mol	Chain	Res	Type
37	A	2712	G
37	A	2714	G
37	A	2717	G
37	A	2719	C
37	A	2721	G
37	A	2723	U
37	A	2725	A
37	A	2726	G
37	A	2739	C
37	A	2740	U
37	A	2743	A
37	A	2753	G
37	A	2754	G
37	A	2756	G
37	A	2761	U
37	A	2762	G
37	A	2763	U
37	A	2768	C
37	A	2769	U
37	A	2770	C
37	A	2776	G
37	A	2786	C
37	A	2787	A
37	A	2788	U
37	A	2790	U
37	A	2794	C
37	A	2797	C
37	A	2803	U
37	A	2814	C
37	A	2819	U
37	A	2826	U
37	A	2827	G
37	A	2829	U
37	A	2842	G
37	A	2855	G
37	A	2856	C
37	A	2859	G
37	A	2860	C
37	A	2864	A
37	A	2870	A
37	A	2874	U
37	A	2875	C

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Mol	Chain	Res	Type
37	A	2876	G
37	A	2877	G
37	A	2878	G
37	A	2884	G
37	A	2885	A
37	A	2894	A
37	A	2902	G
37	A	2903	G
37	A	2904	U
37	A	2905	C
37	A	2906	G
37	A	2907	G
37	A	2909	C
37	A	3588	C
37	A	3589	G
37	A	3593	C
37	A	3595	U
37	A	3596	A
37	A	3597	G
37	A	3605	C
37	A	3626	G
37	A	3635	A
37	A	3637	U
37	A	3639	U
37	A	3642	A
37	A	3643	A
37	A	3644	U
37	A	3646	A
37	A	3648	A
37	A	3661	G
37	A	3662	A
37	A	3669	G
37	A	3671	G
37	A	3672	G
37	A	3673	C
37	A	3674	G
37	A	3692	A
37	A	3696	C
37	A	3705	G
37	A	3709	U
37	A	3710	G
37	A	3711	A

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Mol	Chain	Res	Type
37	A	3712	A
37	A	3713	U
37	A	3714	G
37	A	3723	A
37	A	3727	A
37	A	3750	G
37	A	3753	G
37	A	3756	A
37	A	3757	G
37	A	3758	U
37	A	3759	A
37	A	3761	C
37	A	3764	U
37	A	3765	G
37	A	3766	A
37	A	3767	C
37	A	3768	U
37	A	3769	C
37	A	3770	U
37	A	3771	C
37	A	3772	U
37	A	3773	U
37	A	3775	A
37	A	3776	G
37	A	3777	G
37	A	3780	G
37	A	3785	A
37	A	3786	U
37	A	3789	C
37	A	3811	G
37	A	3812	C
37	A	3814	U
37	A	3817	A
37	A	3818	U
37	A	3819	G
37	A	3838	U
37	A	3840	U
37	A	3867	A
37	A	3877	A
37	A	3878	C
37	A	3879	G
37	A	3881	G

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Mol	Chain	Res	Type
37	A	3889	G
37	A	3890	A
37	A	3892	U
37	A	3897	G
37	A	3898	G
37	A	3901	A
37	A	3905	A
37	A	3906	A
37	A	3907	G
37	A	3908	A
37	A	3915	U
37	A	3919	C
37	A	3922	G
37	A	3928	A
37	A	3938	G
37	A	3939	G
37	A	3941	G
37	A	3942	A
37	A	3943	A
37	A	3947	A
37	A	3948	C
37	A	3949	A
37	A	3954	A
37	A	3956	G
37	A	3957	U
37	A	3958	G
37	A	3959	U
37	A	3961	G
37	A	3962	A
37	A	3963	A
37	A	3965	A
37	A	3966	A
37	A	3968	U
37	A	3969	G
37	A	3972	A
37	A	3973	G
37	A	3975	C
37	A	3977	C
37	A	4034	G
37	A	4036	G
37	A	4037	C
37	A	4039	G

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Mol	Chain	Res	Type
37	A	4042	G
37	A	4043	G
37	A	4044	U
37	A	4045	G
37	A	4046	A
37	A	4047	A
37	A	4048	A
37	A	4049	U
37	A	4050	A
37	A	4051	C
37	A	4052	C
37	A	4053	A
37	A	4054	C
37	A	4055	U
37	A	4056	A
37	A	4058	U
37	A	4059	C
37	A	4064	C
37	A	4065	G
37	A	4067	U
37	A	4076	G
37	A	4084	G
37	A	4088	C
37	A	4093	G
37	A	4101	C
37	A	4103	C
37	A	4104	G
37	A	4107	G
37	A	4110	C
37	A	4115	G
37	A	4116	C
37	A	4117	U
37	A	4119	C
37	A	4120	U
37	A	4121	G
37	A	4122	G
37	A	4127	A
37	A	4131	G
37	A	4138	C
37	A	4139	G
37	A	4140	C
37	A	4141	G

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Mol	Chain	Res	Type
37	A	4142	C
37	A	4143	G
37	A	4144	C
37	A	4151	G
37	A	4154	G
37	A	4158	C
37	A	4162	C
37	A	4163	U
37	A	4170	A
37	A	4183	G
37	A	4184	G
37	A	4191	G
37	A	4222	G
37	A	4225	G
37	A	4226	G
37	A	4229	U
37	A	4234	A
37	A	4249	G
37	A	4251	A
37	A	4254	G
37	A	4268	A
37	A	4273	A
37	A	4280	A
37	A	4281	A
37	A	4288	C
37	A	4291	G
37	A	4296	U
37	A	4297	G
37	A	4302	U
37	A	4305	G
37	A	4306	U
37	A	4314	C
37	A	4318	C
37	A	4329	G
37	A	4330	G
37	A	4337	C
37	A	4339	A
37	A	4349	C
37	A	4350	C
37	A	4352	U
37	A	4355	G
37	A	4376	A

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Mol	Chain	Res	Type
37	A	4377	G
37	A	4378	A
37	A	4380	A
37	A	4382	G
37	A	4385	A
37	A	4387	C
37	A	4394	A
37	A	4396	A
37	A	4398	C
37	A	4419	U
37	A	4420	U
37	A	4422	A
37	A	4427	G
37	A	4444	C
37	A	4448	G
37	A	4449	A
37	A	4453	C
37	A	4464	A
37	A	4465	U
37	A	4466	C
37	A	4471	U
37	A	4474	A
37	A	4475	G
37	A	4476	C
37	A	4477	A
37	A	4481	U
37	A	4488	A
37	A	4489	G
37	A	4493	U
37	A	4500	U
37	A	4510	A
37	A	4512	U
37	A	4513	A
37	A	4524	G
37	A	4528	G
37	A	4531	U
37	A	4543	G
37	A	4545	G
37	A	4548	A
37	A	4549	G
37	A	4560	C
37	A	4567	G

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Mol	Chain	Res	Type
37	A	4573	G
37	A	4575	G
37	A	4583	C
37	A	4589	A
37	A	4590	A
37	A	4600	G
37	A	4601	U
37	A	4617	G
37	A	4635	A
37	A	4636	U
37	A	4637	G
37	A	4643	G
37	A	4656	A
37	A	4657	U
37	A	4670	C
37	A	4672	A
37	A	4678	G
37	A	4695	C
37	A	4708	A
37	A	4709	U
37	A	4712	C
37	A	4730	C
37	A	4731	G
37	A	4732	G
37	A	4733	C
37	A	4734	A
37	A	4739	C
37	A	4740	G
37	A	4741	C
37	A	4743	G
37	A	4744	A
37	A	4749	C
37	A	4750	G
37	A	4753	U
37	A	4756	C
37	A	4758	U
37	A	4760	G
37	A	4763	U
37	A	4764	A
37	A	4770	U
37	A	4771	C
37	A	4772	C

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Mol	Chain	Res	Type
37	A	4775	C
37	A	4860	G
37	A	4861	G
37	A	4862	G
37	A	4863	G
37	A	4865	C
37	A	4868	G
37	A	4869	U
37	A	4871	C
37	A	4872	G
37	A	4873	G
37	A	4875	G
37	A	4876	U
37	A	4877	G
37	A	4878	C
37	A	4883	C
37	A	4884	G
37	A	4887	C
37	A	4888	U
37	A	4889	G
37	A	4890	G
37	A	4894	A
37	A	4900	C
37	A	4901	G
37	A	4902	C
37	A	4910	G
37	A	4912	G
37	A	4913	G
37	A	4914	C
37	A	4918	C
37	A	4919	G
37	A	4923	C
37	A	4926	C
37	A	4927	G
37	A	4930	C
37	A	4933	C
37	A	4936	G
37	A	4938	A
37	A	4939	C
37	A	4941	G
37	A	4944	C
37	A	4946	U

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Mol	Chain	Res	Type
37	A	4949	G
37	A	4951	G
37	A	4952	G
37	A	4956	A
37	A	4959	U
37	A	4963	G
37	A	4964	C
37	A	4967	A
37	A	4976	U
37	A	4979	A
37	A	4980	C
37	A	4985	U
37	A	4988	U
37	A	4989	U
37	A	4990	C
37	A	4991	U
37	A	4992	G
37	A	5006	U
37	A	5007	A
37	A	5014	A
37	A	5017	G
37	A	5022	U
37	A	5023	C
37	A	5024	C
37	A	5026	U
37	A	5027	C
37	A	5028	G
37	A	5031	G
37	A	5034	A
37	A	5041	G
37	A	5050	C
37	A	5054	C
37	A	5055	G
37	A	5061	A
37	A	5068	G
47	AA	2	A
47	AA	3	C
47	AA	4	C
47	AA	5	U
47	AA	6	G
47	AA	8	U
47	AA	9	U

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Mol	Chain	Res	Type
47	AA	10	G
47	AA	17	C
47	AA	25	A
47	AA	26	U
47	AA	31	U
47	AA	33	G
47	AA	35	C
47	AA	38	A
47	AA	41	G
47	AA	42	A
47	AA	43	U
47	AA	44	U
47	AA	46	A
47	AA	48	C
47	AA	51	U
47	AA	52	G
47	AA	53	C
47	AA	55	U
47	AA	56	G
47	AA	57	U
47	AA	58	C
47	AA	59	U
47	AA	60	A
47	AA	61	A
47	AA	62	G
47	AA	64	A
47	AA	67	C
47	AA	68	A
47	AA	69	C
47	AA	70	G
47	AA	72	C
47	AA	73	C
47	AA	74	G
47	AA	75	G
47	AA	76	U
47	AA	77	A
47	AA	78	C
47	AA	79	A
47	AA	80	G
47	AA	81	U
47	AA	82	G
47	AA	83	A

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Mol	Chain	Res	Type
47	AA	84	A
47	AA	89	C
47	AA	93	U
47	AA	99	A
47	AA	101	U
47	AA	103	A
47	AA	111	A
47	AA	112	U
47	AA	113	G
47	AA	114	G
47	AA	116	U
47	AA	121	U
47	AA	122	G
47	AA	126	G
47	AA	127	C
47	AA	139	C
47	AA	140	C
47	AA	141	A
47	AA	142	C
47	AA	144	U
47	AA	146	G
47	AA	148	U
47	AA	151	C
47	AA	153	G
47	AA	154	U
47	AA	155	G
47	AA	156	G
47	AA	157	U
47	AA	159	A
47	AA	160	U
47	AA	161	U
47	AA	162	C
47	AA	163	U
47	AA	165	G
47	AA	166	A
47	AA	167	G
47	AA	168	C
47	AA	170	A
47	AA	176	U
47	AA	177	G
47	AA	180	G
47	AA	181	A

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Mol	Chain	Res	Type
47	AA	182	C
47	AA	183	G
47	AA	185	G
47	AA	188	C
47	AA	190	G
47	AA	193	C
47	AA	198	U
47	AA	201	C
47	AA	202	G
47	AA	205	G
47	AA	208	G
47	AA	209	A
47	AA	210	U
47	AA	211	G
47	AA	214	U
47	AA	215	G
47	AA	216	C
47	AA	217	A
47	AA	219	U
47	AA	289	G
47	AA	291	G
47	AA	292	A
47	AA	293	C
47	AA	294	U
47	AA	295	C
47	AA	297	A
47	AA	299	A
47	AA	306	C
47	AA	308	G
47	AA	309	G
47	AA	312	G
47	AA	313	A
47	AA	314	U
47	AA	319	C
47	AA	320	G
47	AA	321	C
47	AA	322	C
47	AA	323	C
47	AA	324	C
47	AA	325	C
47	AA	328	U
47	AA	329	G

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Mol	Chain	Res	Type
47	AA	330	G
47	AA	332	G
47	AA	333	G
47	AA	334	C
47	AA	338	G
47	AA	339	A
47	AA	340	C
47	AA	341	C
47	AA	342	C
47	AA	343	A
47	AA	345	U
47	AA	346	C
47	AA	352	U
47	AA	360	A
47	AA	361	U
47	AA	362	C
47	AA	364	A
47	AA	368	U
47	AA	369	C
47	AA	370	G
47	AA	373	G
47	AA	376	A
47	AA	378	U
47	AA	380	G
47	AA	382	C
47	AA	383	G
47	AA	384	U
47	AA	385	G
47	AA	386	C
47	AA	388	U
47	AA	391	C
47	AA	395	G
47	AA	401	A
47	AA	402	C
47	AA	407	G
47	AA	408	A
47	AA	409	C
47	AA	410	G
47	AA	411	G
47	AA	413	G
47	AA	417	C
47	AA	418	A

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Mol	Chain	Res	Type
47	AA	421	G
47	AA	425	G
47	AA	426	A
47	AA	428	U
47	AA	429	C
47	AA	432	G
47	AA	434	G
47	AA	435	A
47	AA	436	G
47	AA	437	G
47	AA	438	G
47	AA	440	G
47	AA	441	C
47	AA	448	A
47	AA	449	A
47	AA	450	C
47	AA	452	G
47	AA	453	C
47	AA	454	U
47	AA	456	C
47	AA	458	A
47	AA	463	C
47	AA	464	A
47	AA	465	A
47	AA	466	G
47	AA	469	A
47	AA	472	C
47	AA	473	A
47	AA	474	G
47	AA	476	A
47	AA	479	C
47	AA	480	G
47	AA	482	G
47	AA	484	A
47	AA	485	A
47	AA	486	A
47	AA	487	U
47	AA	488	U
47	AA	489	A
47	AA	492	C
47	AA	493	A
47	AA	496	C

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Mol	Chain	Res	Type
47	AA	502	C
47	AA	503	C
47	AA	504	G
47	AA	505	G
47	AA	506	G
47	AA	508	A
47	AA	512	A
47	AA	516	A
47	AA	517	C
47	AA	518	G
47	AA	521	A
47	AA	523	A
47	AA	528	A
47	AA	529	A
47	AA	530	U
47	AA	532	C
47	AA	534	G
47	AA	535	G
47	AA	536	A
47	AA	537	C
47	AA	538	U
47	AA	539	C
47	AA	540	U
47	AA	544	G
47	AA	545	A
47	AA	546	G
47	AA	547	G
47	AA	550	C
47	AA	552	G
47	AA	553	U
47	AA	556	U
47	AA	557	U
47	AA	559	G
47	AA	560	A
47	AA	563	G
47	AA	565	G
47	AA	566	U
47	AA	570	C
47	AA	573	U
47	AA	575	A
47	AA	577	U
47	AA	580	U

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Mol	Chain	Res	Type
47	AA	581	U
47	AA	583	C
47	AA	584	G
47	AA	585	C
47	AA	587	A
47	AA	588	G
47	AA	589	G
47	AA	590	A
47	AA	591	U
47	AA	592	C
47	AA	593	C
47	AA	594	A
47	AA	595	U
47	AA	596	U
47	AA	599	A
47	AA	600	G
47	AA	603	C
47	AA	604	A
47	AA	605	A
47	AA	608	C
47	AA	609	U
47	AA	612	U
47	AA	614	C
47	AA	620	G
47	AA	621	C
47	AA	623	G
47	AA	626	G
47	AA	627	U
47	AA	628	A
47	AA	629	A
47	AA	633	C
47	AA	634	A
47	AA	643	A
47	AA	644	G
47	AA	646	G
47	AA	647	U
47	AA	649	U
47	AA	650	A
47	AA	651	U
47	AA	655	A
47	AA	656	G
47	AA	658	U

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Mol	Chain	Res	Type
47	AA	659	G
47	AA	660	C
47	AA	668	A
47	AA	669	A
47	AA	671	A
47	AA	672	A
47	AA	680	G
47	AA	682	U
47	AA	683	G
47	AA	684	G
47	AA	686	U
47	AA	687	C
47	AA	688	U
47	AA	689	U
47	AA	690	G
47	AA	691	G
47	AA	692	G
47	AA	693	A
47	AA	694	G
47	AA	695	C
47	AA	696	G
47	AA	697	G
47	AA	698	G
47	AA	731	G
47	AA	732	U
47	AA	733	C
47	AA	734	C
47	AA	735	C
47	AA	736	C
47	AA	737	G
47	AA	738	C
47	AA	739	C
47	AA	746	C
47	AA	747	U
47	AA	748	C
47	AA	749	U
47	AA	750	C
47	AA	751	G
47	AA	752	G
47	AA	753	C
47	AA	787	G
47	AA	788	G

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Mol	Chain	Res	Type
47	AA	789	G
47	AA	790	C
47	AA	791	C
47	AA	795	A
47	AA	796	G
47	AA	799	U
47	AA	801	U
47	AA	810	A
47	AA	811	A
47	AA	812	A
47	AA	813	A
47	AA	816	A
47	AA	817	G
47	AA	818	A
47	AA	821	G
47	AA	822	U
47	AA	824	C
47	AA	827	A
47	AA	828	G
47	AA	830	A
47	AA	831	G
47	AA	833	C
47	AA	834	C
47	AA	835	C
47	AA	837	A
47	AA	838	G
47	AA	839	C
47	AA	840	C
47	AA	841	G
47	AA	842	C
47	AA	843	C
47	AA	845	G
47	AA	847	A
47	AA	848	U
47	AA	849	A
47	AA	851	C
47	AA	853	C
47	AA	854	A
47	AA	858	A
47	AA	862	A
47	AA	863	U
47	AA	865	A

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Mol	Chain	Res	Type
47	AA	869	A
47	AA	870	A
47	AA	871	U
47	AA	872	A
47	AA	873	G
47	AA	874	G
47	AA	875	A
47	AA	876	C
47	AA	877	C
47	AA	878	G
47	AA	879	C
47	AA	880	G
47	AA	883	U
47	AA	884	C
47	AA	887	U
47	AA	888	U
47	AA	889	U
47	AA	890	U
47	AA	891	G
47	AA	892	U
47	AA	893	U
47	AA	894	G
47	AA	896	U
47	AA	897	U
47	AA	898	U
47	AA	899	U
47	AA	900	C
47	AA	901	G
47	AA	902	G
47	AA	903	A
47	AA	904	A
47	AA	905	C
47	AA	908	A
47	AA	909	G
47	AA	911	C
47	AA	912	C
47	AA	913	A
47	AA	914	U
47	AA	919	A
47	AA	920	A
47	AA	922	A
47	AA	925	G

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Mol	Chain	Res	Type
47	AA	930	C
47	AA	932	G
47	AA	933	G
47	AA	934	G
47	AA	943	U
47	AA	948	C
47	AA	954	U
47	AA	956	G
47	AA	958	G
47	AA	959	G
47	AA	961	G
47	AA	963	A
47	AA	965	U
47	AA	970	G
47	AA	971	G
47	AA	972	A
47	AA	973	C
47	AA	975	G
47	AA	977	C
47	AA	979	C
47	AA	980	A
47	AA	981	A
47	AA	983	A
47	AA	984	C
47	AA	985	G
47	AA	988	C
47	AA	989	C
47	AA	990	A
47	AA	992	A
47	AA	996	A
47	AA	997	A
47	AA	998	A
47	AA	999	G
47	AA	1006	C
47	AA	1007	C
47	AA	1018	U
47	AA	1019	C
47	AA	1021	U
47	AA	1022	U
47	AA	1023	A
47	AA	1025	U
47	AA	1027	A

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Mol	Chain	Res	Type
47	AA	1028	A
47	AA	1034	A
47	AA	1035	A
47	AA	1038	U
47	AA	1040	G
47	AA	1041	G
47	AA	1045	U
47	AA	1046	U
47	AA	1047	C
47	AA	1051	G
47	AA	1058	A
47	AA	1061	U
47	AA	1062	A
47	AA	1064	C
47	AA	1067	C
47	AA	1068	G
47	AA	1069	U
47	AA	1072	U
47	AA	1073	U
47	AA	1076	G
47	AA	1078	C
47	AA	1079	C
47	AA	1080	A
47	AA	1081	U
47	AA	1082	A
47	AA	1084	A
47	AA	1085	C
47	AA	1087	A
47	AA	1088	U
47	AA	1089	G
47	AA	1090	C
47	AA	1091	C
47	AA	1096	G
47	AA	1097	G
47	AA	1098	C
47	AA	1101	U
47	AA	1109	C
47	AA	1110	G
47	AA	1114	U
47	AA	1115	U
47	AA	1116	C
47	AA	1118	C

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Mol	Chain	Res	Type
47	AA	1119	A
47	AA	1120	U
47	AA	1126	G
47	AA	1131	G
47	AA	1132	C
47	AA	1135	C
47	AA	1138	C
47	AA	1139	C
47	AA	1144	A
47	AA	1145	A
47	AA	1149	A
47	AA	1150	A
47	AA	1153	C
47	AA	1154	U
47	AA	1155	U
47	AA	1156	U
47	AA	1157	G
47	AA	1160	U
47	AA	1161	U
47	AA	1166	G
47	AA	1167	G
47	AA	1168	G
47	AA	1169	G
47	AA	1170	A
47	AA	1171	G
47	AA	1172	U
47	AA	1179	G
47	AA	1180	C
47	AA	1181	A
47	AA	1195	A
47	AA	1199	A
47	AA	1200	A
47	AA	1204	A
47	AA	1206	G
47	AA	1207	G
47	AA	1208	A
47	AA	1211	G
47	AA	1212	G
47	AA	1215	C
47	AA	1216	C
47	AA	1217	A
47	AA	1219	C

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Mol	Chain	Res	Type
47	AA	1221	G
47	AA	1223	A
47	AA	1224	G
47	AA	1225	U
47	AA	1226	G
47	AA	1230	C
47	AA	1232	U
47	AA	1236	G
47	AA	1237	C
47	AA	1238	U
47	AA	1239	U
47	AA	1240	A
47	AA	1241	A
47	AA	1242	U
47	AA	1243	U
47	AA	1245	G
47	AA	1246	A
47	AA	1248	U
47	AA	1251	A
47	AA	1252	C
47	AA	1253	A
47	AA	1254	C
47	AA	1255	G
47	AA	1256	G
47	AA	1257	G
47	AA	1258	A
47	AA	1259	A
47	AA	1260	A
47	AA	1264	C
47	AA	1265	A
47	AA	1266	C
47	AA	1268	C
47	AA	1270	G
47	AA	1271	C
47	AA	1272	C
47	AA	1273	C
47	AA	1274	G
47	AA	1275	G
47	AA	1276	A
47	AA	1277	C
47	AA	1278	A
47	AA	1279	C

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Mol	Chain	Res	Type
47	AA	1280	G
47	AA	1281	G
47	AA	1282	A
47	AA	1283	C
47	AA	1284	A
47	AA	1285	G
47	AA	1287	A
47	AA	1288	U
47	AA	1289	U
47	AA	1290	G
47	AA	1292	C
47	AA	1293	A
47	AA	1294	G
47	AA	1299	A
47	AA	1300	U
47	AA	1301	A
47	AA	1302	G
47	AA	1303	C
47	AA	1305	C
47	AA	1306	U
47	AA	1307	U
47	AA	1308	U
47	AA	1310	U
47	AA	1311	C
47	AA	1312	G
47	AA	1313	A
47	AA	1314	U
47	AA	1315	U
47	AA	1316	C
47	AA	1317	C
47	AA	1318	G
47	AA	1321	G
47	AA	1322	G
47	AA	1330	G
47	AA	1331	C
47	AA	1333	U
47	AA	1337	C
47	AA	1339	U
47	AA	1341	C
47	AA	1342	U
47	AA	1343	U
47	AA	1344	A

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Mol	Chain	Res	Type
47	AA	1345	G
47	AA	1346	U
47	AA	1347	U
47	AA	1359	U
47	AA	1360	U
47	AA	1363	C
47	AA	1364	U
47	AA	1371	U
47	AA	1372	U
47	AA	1373	C
47	AA	1374	C
47	AA	1375	G
47	AA	1378	A
47	AA	1381	G
47	AA	1387	G
47	AA	1388	A
47	AA	1389	C
47	AA	1391	C
47	AA	1393	G
47	AA	1394	G
47	AA	1396	A
47	AA	1397	U
47	AA	1398	G
47	AA	1399	C
47	AA	1401	A
47	AA	1403	C
47	AA	1404	U
47	AA	1405	A
47	AA	1407	U
47	AA	1409	A
47	AA	1410	C
47	AA	1412	C
47	AA	1414	A
47	AA	1415	C
47	AA	1416	C
47	AA	1417	C
47	AA	1418	C
47	AA	1419	C
47	AA	1420	G
47	AA	1422	G
47	AA	1423	C
47	AA	1424	G

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Mol	Chain	Res	Type
47	AA	1425	G
47	AA	1428	G
47	AA	1430	C
47	AA	1431	G
47	AA	1432	U
47	AA	1434	C
47	AA	1436	C
47	AA	1438	A
47	AA	1440	C
47	AA	1441	U
47	AA	1443	C
47	AA	1444	U
47	AA	1445	U
47	AA	1447	G
47	AA	1448	A
47	AA	1449	G
47	AA	1450	G
47	AA	1451	G
47	AA	1452	A
47	AA	1453	C
47	AA	1454	A
47	AA	1455	A
47	AA	1456	G
47	AA	1457	U
47	AA	1463	U
47	AA	1464	C
47	AA	1466	G
47	AA	1468	C
47	AA	1471	C
47	AA	1472	C
47	AA	1473	G
47	AA	1474	A
47	AA	1475	G
47	AA	1476	A
47	AA	1477	U
47	AA	1478	U
47	AA	1479	G
47	AA	1480	A
47	AA	1486	A
47	AA	1489	A
47	AA	1490	G
47	AA	1493	C

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Mol	Chain	Res	Type
47	AA	1494	U
47	AA	1495	G
47	AA	1497	G
47	AA	1502	C
47	AA	1504	U
47	AA	1505	U
47	AA	1506	A
47	AA	1507	G
47	AA	1508	A
47	AA	1510	G
47	AA	1512	C
47	AA	1513	C
47	AA	1515	G
47	AA	1517	G
47	AA	1518	C
47	AA	1520	G
47	AA	1521	C
47	AA	1522	A
47	AA	1523	C
47	AA	1525	C
47	AA	1527	C
47	AA	1528	G
47	AA	1529	C
47	AA	1530	U
47	AA	1531	A
47	AA	1532	C
47	AA	1533	A
47	AA	1534	C
47	AA	1535	U
47	AA	1536	G
47	AA	1537	A
47	AA	1538	C
47	AA	1539	U
47	AA	1543	U
47	AA	1544	C
47	AA	1545	A
47	AA	1546	G
47	AA	1548	G
47	AA	1549	U
47	AA	1550	G
47	AA	1551	U
47	AA	1553	C

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Mol	Chain	Res	Type
47	AA	1554	C
47	AA	1555	U
47	AA	1556	A
47	AA	1557	C
47	AA	1562	C
47	AA	1566	G
47	AA	1567	G
47	AA	1568	C
47	AA	1569	A
47	AA	1570	G
47	AA	1571	G
47	AA	1573	G
47	AA	1580	A
47	AA	1581	C
47	AA	1582	C
47	AA	1583	C
47	AA	1584	G
47	AA	1585	U
47	AA	1586	U
47	AA	1587	G
47	AA	1588	A
47	AA	1589	A
47	AA	1590	C
47	AA	1591	C
47	AA	1593	C
47	AA	1594	A
47	AA	1598	G
47	AA	1599	U
47	AA	1600	G
47	AA	1601	A
47	AA	1602	U
47	AA	1603	G
47	AA	1607	A
47	AA	1612	G
47	AA	1614	A
47	AA	1618	C
47	AA	1621	U
47	AA	1623	A
47	AA	1624	U
47	AA	1628	C
47	AA	1629	C
47	AA	1630	A

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Mol	Chain	Res	Type
47	AA	1631	U
47	AA	1633	A
47	AA	1634	A
47	AA	1635	C
47	AA	1636	G
47	AA	1637	A
47	AA	1638	G
47	AA	1639	G
47	AA	1643	U
47	AA	1644	C
47	AA	1645	C
47	AA	1646	C
47	AA	1648	G
47	AA	1654	G
47	AA	1655	C
47	AA	1656	G
47	AA	1661	A
47	AA	1664	A
47	AA	1665	G
47	AA	1666	C
47	AA	1668	U
47	AA	1672	U
47	AA	1676	U
47	AA	1677	U
47	AA	1679	A
47	AA	1681	U
47	AA	1682	C
47	AA	1683	C
47	AA	1686	G
47	AA	1690	U
47	AA	1693	G
47	AA	1698	C
47	AA	1699	A
47	AA	1700	C
47	AA	1702	G
47	AA	1705	C
47	AA	1711	U
47	AA	1713	C
47	AA	1714	U
47	AA	1715	A
47	AA	1719	A
47	AA	1720	U

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Mol	Chain	Res	Type
47	AA	1721	U
47	AA	1722	G
47	AA	1733	U
47	AA	1736	G
47	AA	1738	C
47	AA	1739	C
47	AA	1742	C
47	AA	1744	G
47	AA	1745	A
47	AA	1746	U
47	AA	1748	G
47	AA	1749	G
47	AA	1751	C
47	AA	1752	C
47	AA	1754	G
47	AA	1755	C
47	AA	1756	C
47	AA	1758	G
47	AA	1760	G
47	AA	1772	C
47	AA	1773	C
47	AA	1776	G
47	AA	1780	G
47	AA	1781	A
47	AA	1782	G
47	AA	1783	C
47	AA	1784	G
47	AA	1785	C
47	AA	1786	U
47	AA	1793	A
47	AA	1802	C
47	AA	1805	G
47	AA	1815	A
47	AA	1819	A
47	AA	1820	G
47	AA	1821	U
47	AA	1822	A
47	AA	1823	A
47	AA	1825	A
47	AA	1826	G
47	AA	1829	G
47	AA	1834	A

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Mol	Chain	Res	Type
47	AA	1835	A
47	AA	1838	U
47	AA	1839	U
47	AA	1842	C
47	AA	1849	G
47	AA	1850	A
47	AA	1852	C
47	AA	1859	A
47	AA	1860	A
47	AA	1861	G
47	AA	1862	G
47	AA	1863	A
47	AA	1864	U
47	AA	1865	C
47	AA	1867	U
47	AA	1868	U
47	AA	1869	A
62	An	8	G
62	An	9	U
62	An	10	G
62	An	12	C
62	An	14	C
62	An	17	C
62	An	18	G
62	An	20	A
62	An	21	A
62	An	22	G
62	An	23	C
62	An	24	G
62	An	29	G
62	An	30	G
62	An	32	C
62	An	33	C
62	An	34	C
62	An	35	A
62	An	36	U
62	An	37	A
62	An	38	A
62	An	39	C
62	An	41	C
62	An	45	G
62	An	46	G

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Mol	Chain	Res	Type
62	An	47	U
62	An	48	C
62	An	51	U
62	An	54	A
62	An	56	C
62	An	57	G
62	An	58	A
62	An	59	A
62	An	68	C
62	An	74	C
62	An	75	C
62	An	76	A

All (99) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	C	87	G
37	A	172	C
37	A	406	C
37	A	417	G
37	A	693	C
37	A	930	G
37	A	931	C
37	A	957	G
37	A	958	G
37	A	974	C
37	A	1072	C
37	A	1238	A
37	A	1329	G
37	A	1410	U
37	A	1455	G
37	A	1633	G
37	A	1821	G
37	A	2019	C
37	A	2055	G
37	A	2068	C
37	A	2096	G
37	A	2116	C
37	A	2119	C
37	A	2120	G
37	A	2124	G
37	A	2269	C

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Mol	Chain	Res	Type
37	A	2587	A
37	A	2639	U
37	A	2675	G
37	A	2695	A
37	A	2785	C
37	A	2828	U
37	A	3625	G
37	A	3673	C
37	A	3767	C
37	A	3784	A
37	A	3810	C
37	A	3888	G
37	A	3956	G
37	A	4419	U
37	A	4600	G
37	A	4730	C
37	A	4731	G
37	A	4860	G
37	A	4889	G
37	A	4909	A
37	A	4913	G
37	A	4948	C
37	A	4991	U
37	A	5005	G
37	A	5027	C
47	AA	24	C
47	AA	291	G
47	AA	324	C
47	AA	385	G
47	AA	400	C
47	AA	417	C
47	AA	428	U
47	AA	451	G
47	AA	465	A
47	AA	473	A
47	AA	558	G
47	AA	589	G
47	AA	604	A
47	AA	656	G
47	AA	681	U
47	AA	688	U
47	AA	734	C

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Mol	Chain	Res	Type
47	AA	745	C
47	AA	833	C
47	AA	868	G
47	AA	912	C
47	AA	913	A
47	AA	971	G
47	AA	980	A
47	AA	991	G
47	AA	1027	A
47	AA	1061	U
47	AA	1137	U
47	AA	1138	C
47	AA	1153	C
47	AA	1171	G
47	AA	1251	A
47	AA	1342	U
47	AA	1396	A
47	AA	1397	U
47	AA	1404	U
47	AA	1506	A
47	AA	1507	G
47	AA	1580	A
47	AA	1585	U
47	AA	1606	G
47	AA	1663	A
47	AA	1664	A
47	AA	1699	A
47	AA	1713	C
47	AA	1785	C
47	AA	1848	U
47	AA	1860	A

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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
44	q	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	q	151:ILE	C	152:GLY	N	2.01

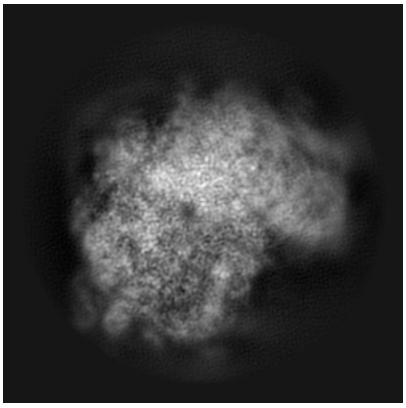
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-8345. These allow visual inspection of the internal detail of the map and identification of artifacts.

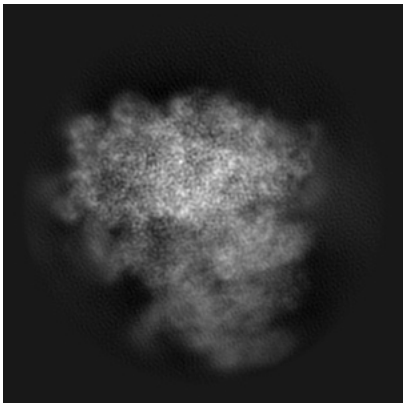
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

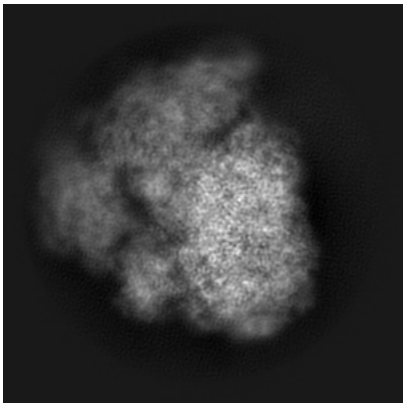
6.1.1 Primary map



X



Y

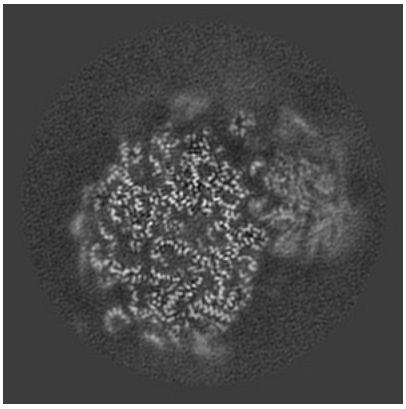


Z

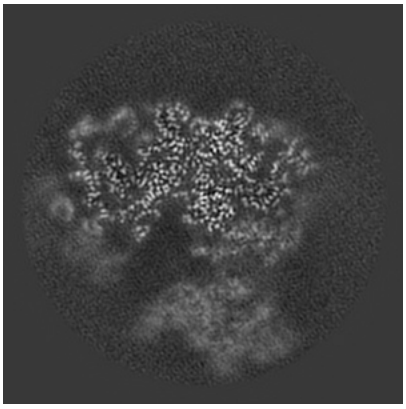
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

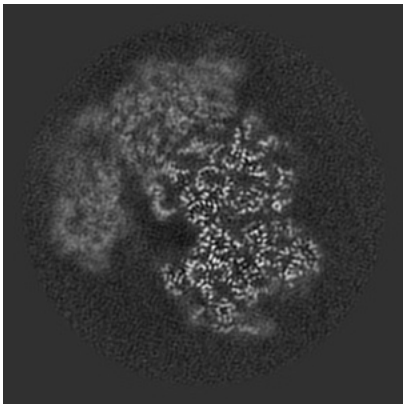
6.2.1 Primary map



X Index: 175



Y Index: 175

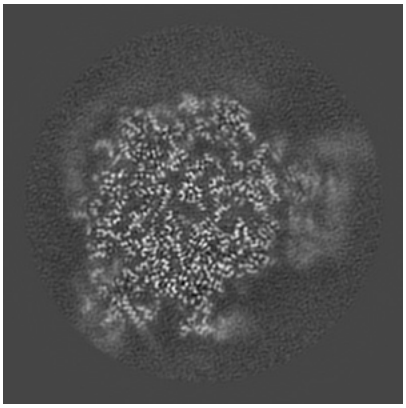


Z Index: 175

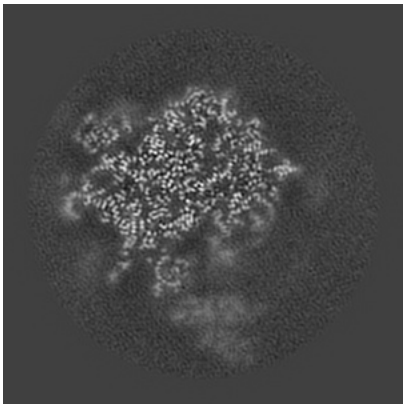
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

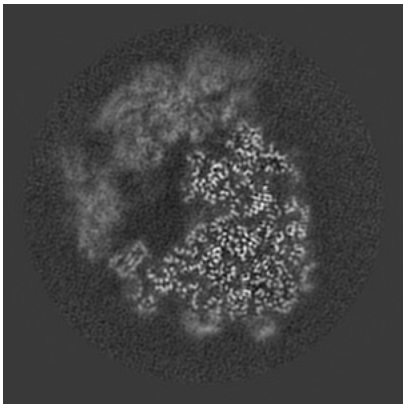
6.3.1 Primary map



X Index: 202



Y Index: 132

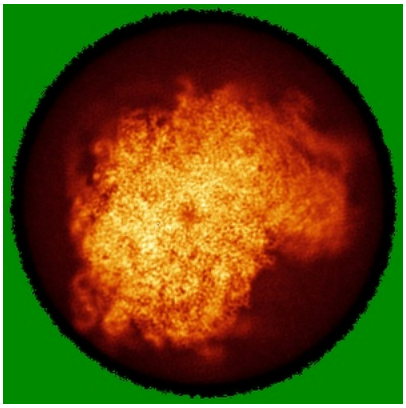


Z Index: 156

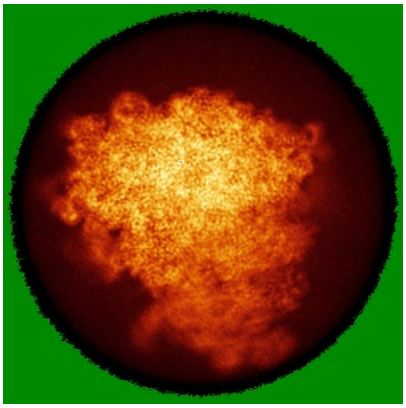
The images above show the largest variance slices of the map in three orthogonal directions.

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

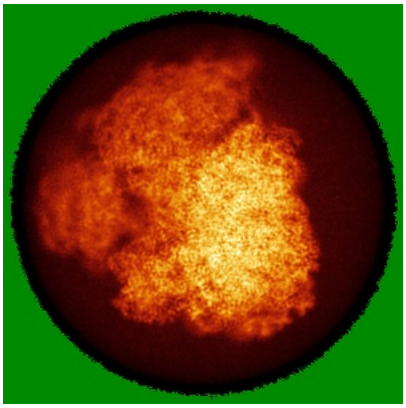
6.4.1 Primary map



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 (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

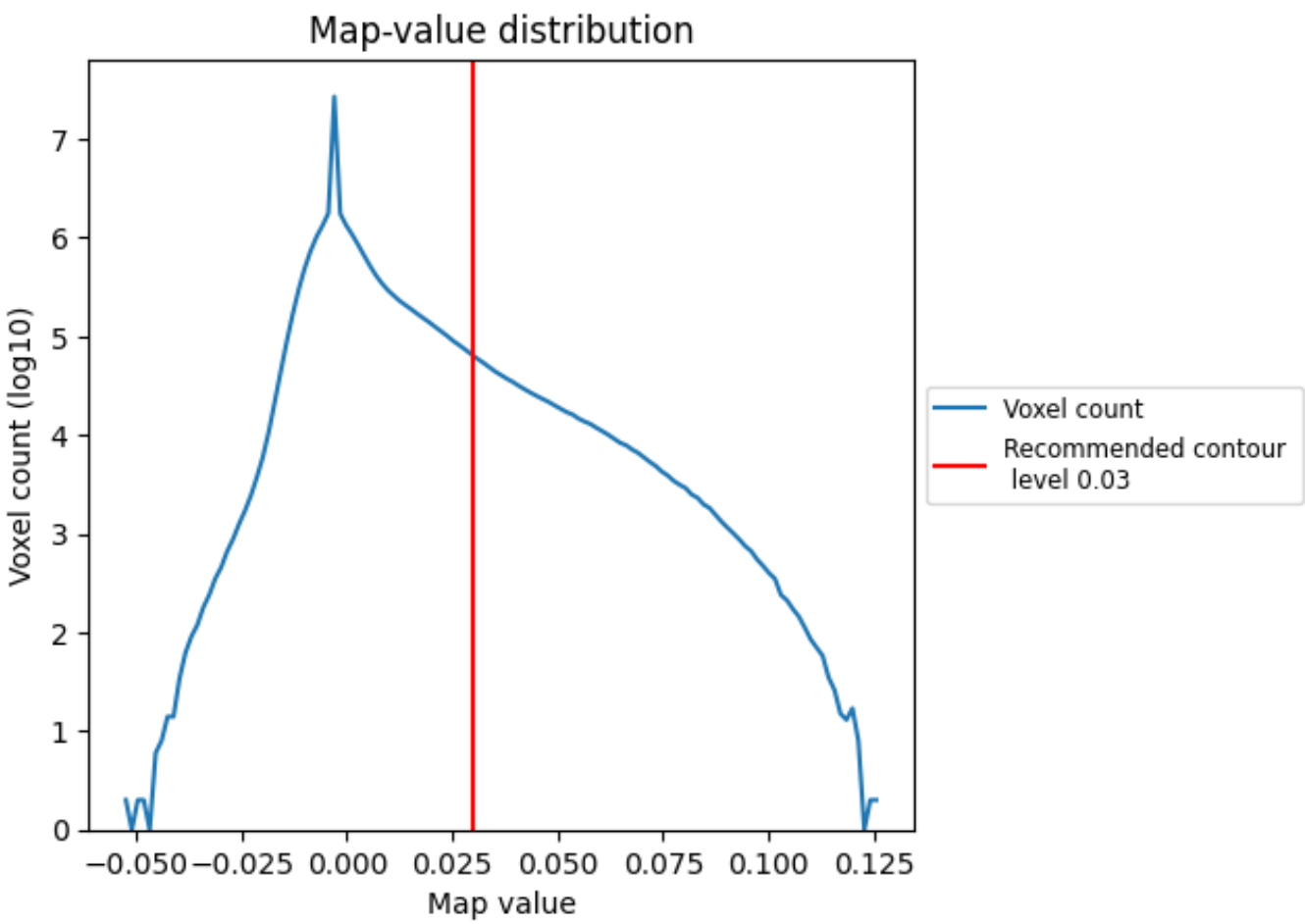
6.6 Mask visualisation (i)

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

7 Map analysis (i)

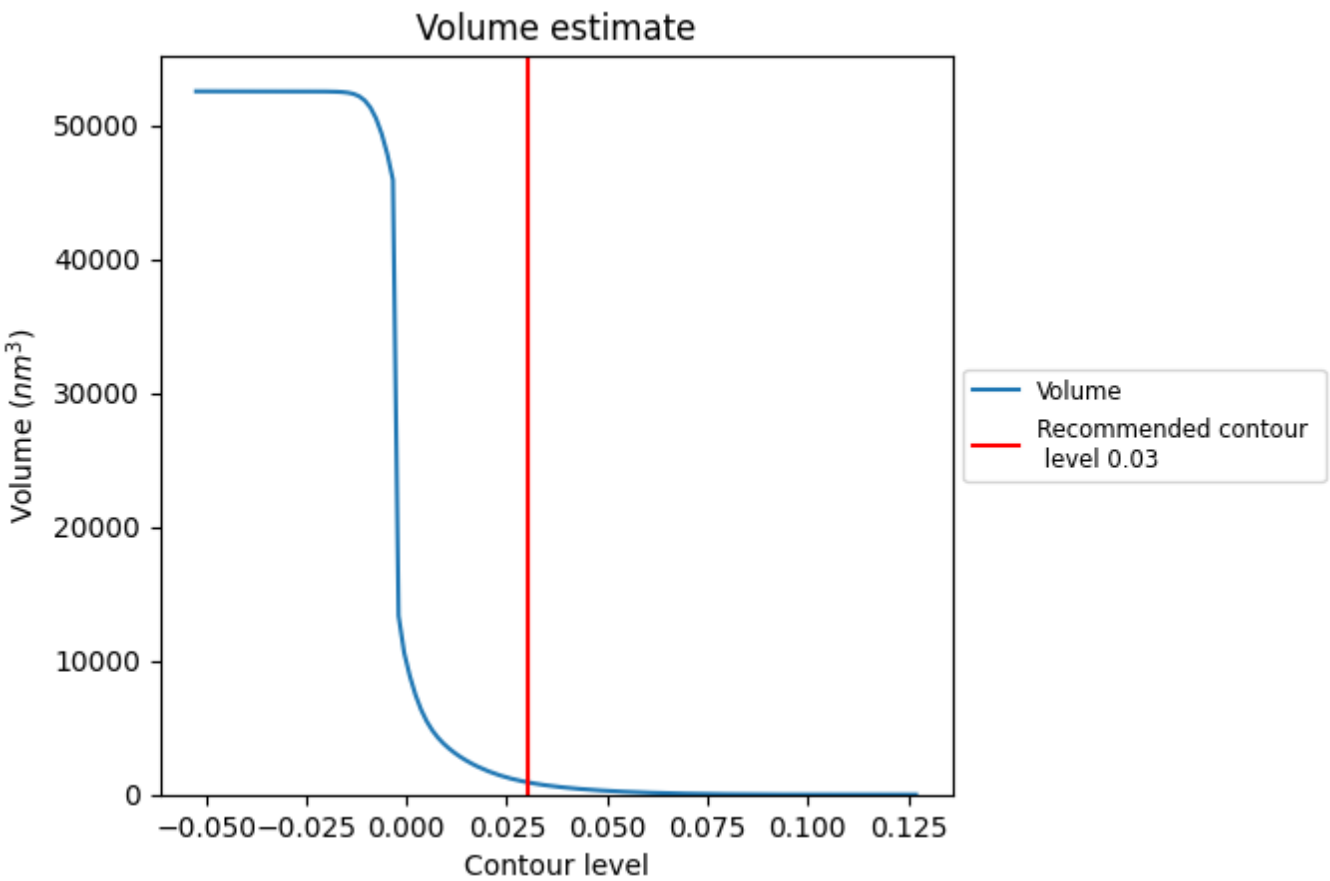
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

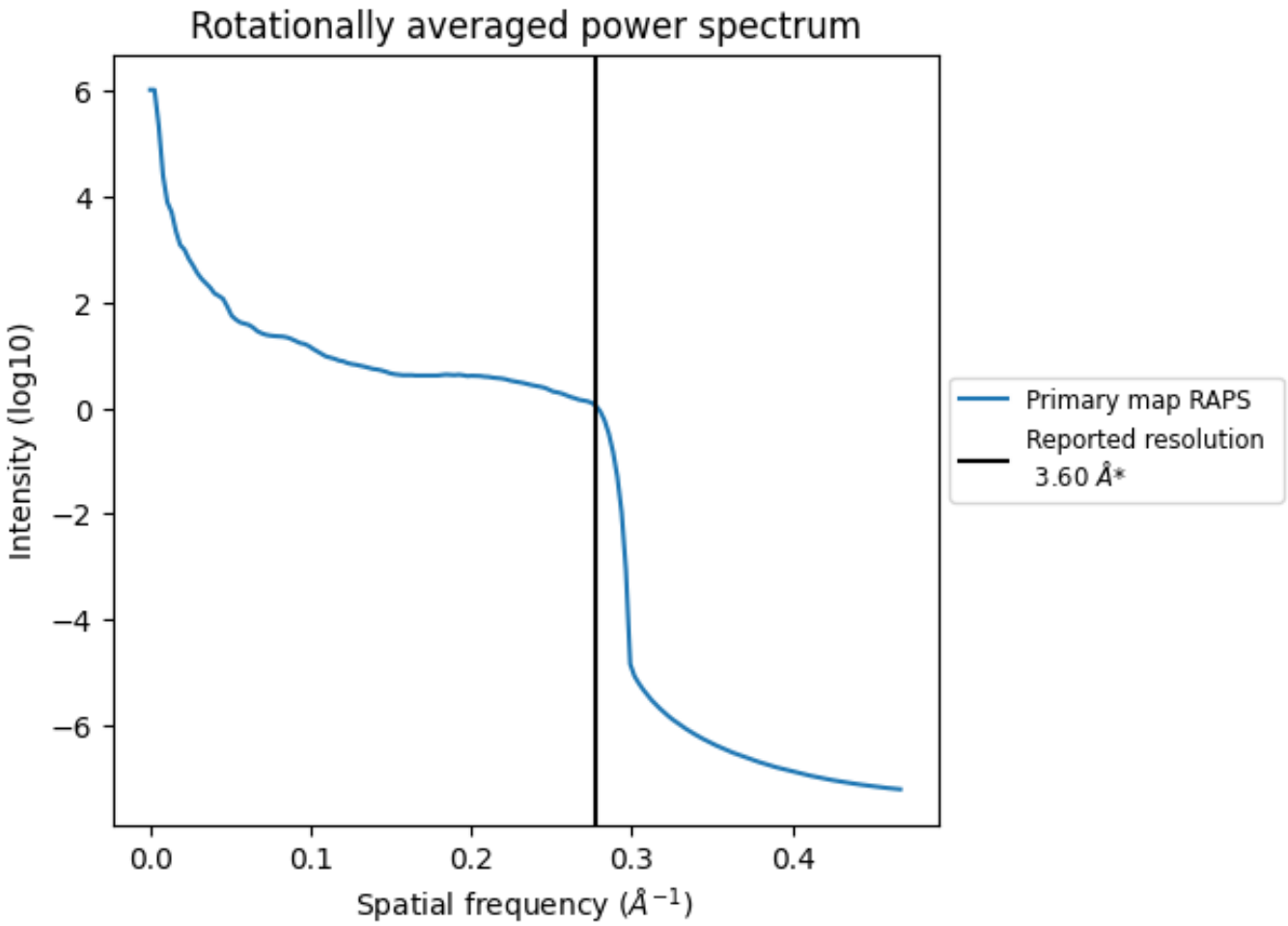
7.2 Volume estimate (i)



The volume at the recommended contour level is 928 nm^3; this corresponds to an approximate mass of 838 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

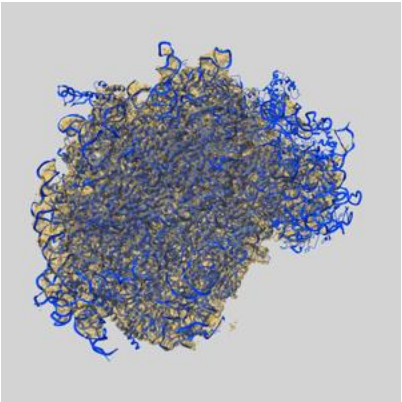
8 Fourier-Shell correlation (i)

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

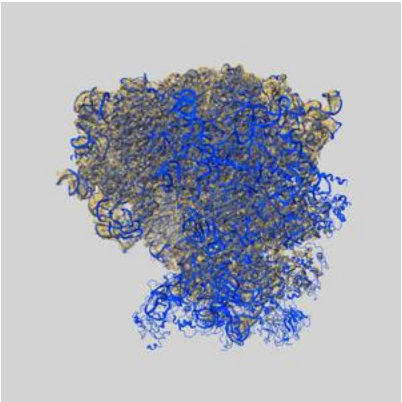
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-8345 and PDB model 5T2C. Per-residue inclusion information can be found in section 3 on page 18.

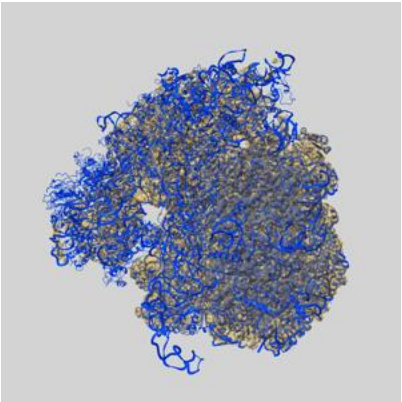
9.1 Map-model overlay (i)



X



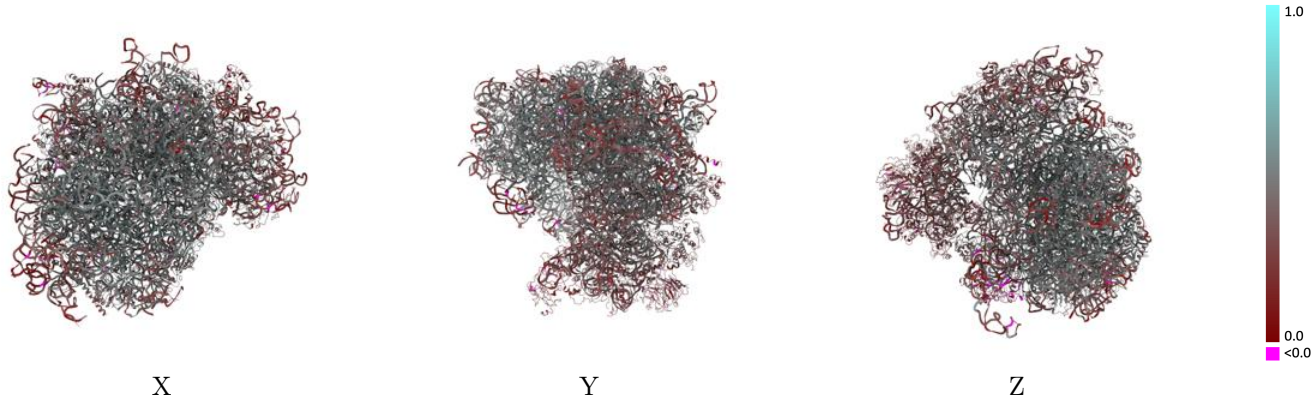
Y



Z

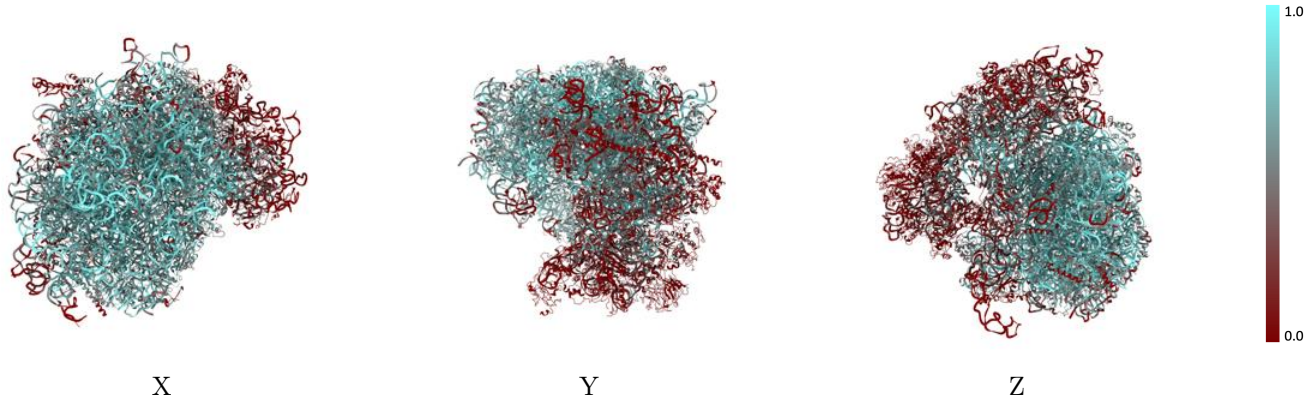
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



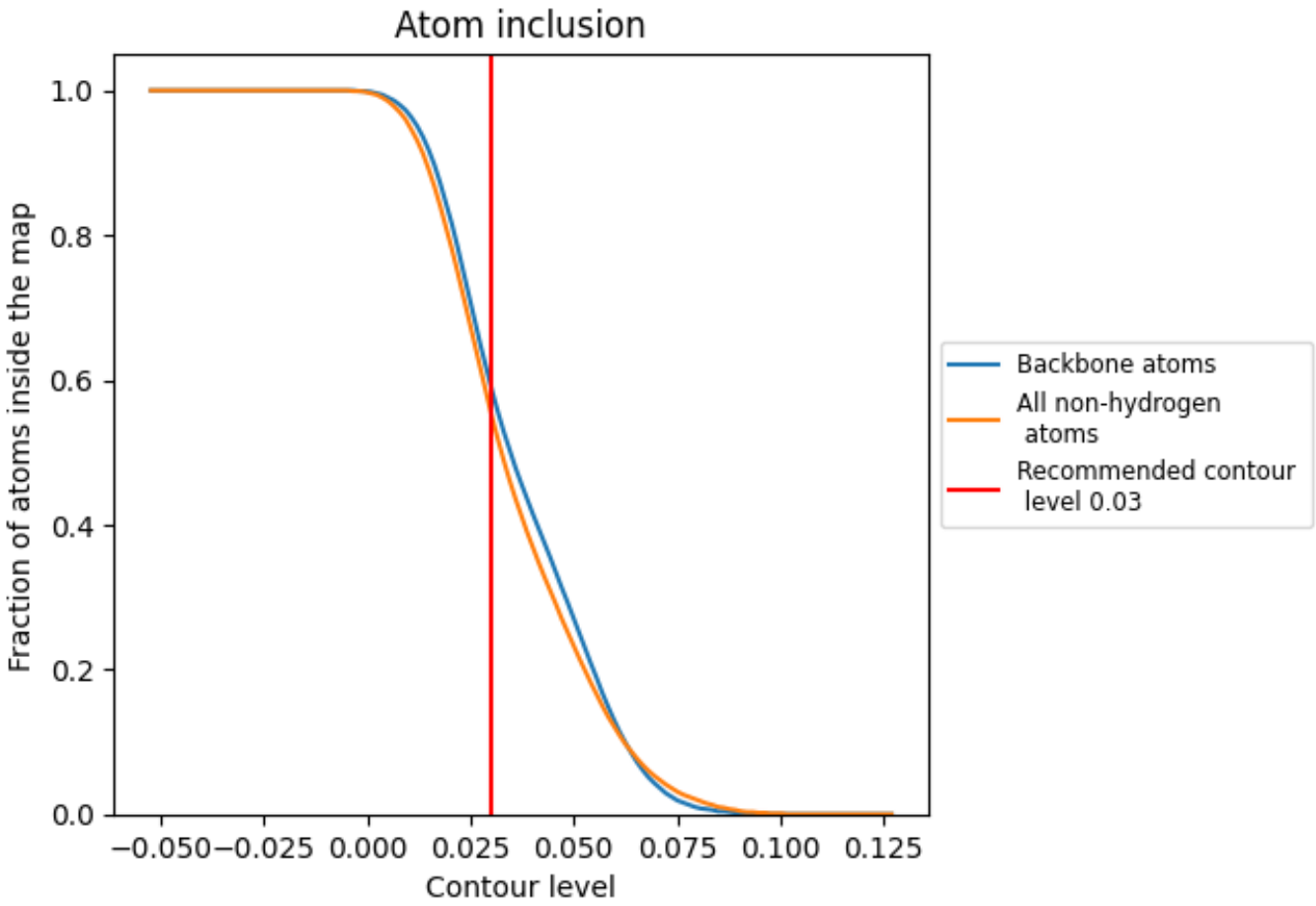
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion (i)



At the recommended contour level, 59% of all backbone atoms, 55% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5530	0.4190
A	0.7530	0.4420
A0	0.0820	0.2900
AA	0.4670	0.3940
AB	0.0480	0.3020
AC	0.1670	0.3780
AD	0.3240	0.4300
AE	0.3230	0.4420
AF	0.0710	0.3370
AG	0.0610	0.3260
AH	0.0040	0.2180
AI	0.0050	0.2700
AJ	0.2980	0.4100
AK	0.0650	0.3290
AL	0.2460	0.3850
AM	0.0000	0.2500
AN	0.2860	0.4450
AO	0.1830	0.4010
AP	0.3010	0.4190
AQ	0.1450	0.3330
AR	0.0070	0.2640
AT	0.1400	0.3800
AU	0.1390	0.2840
AV	0.1450	0.4080
An	0.3200	0.3210
Ao	0.2080	0.3830
Ap	0.1910	0.4150
Aq	0.0240	0.3290
Ar	0.1870	0.4020
As	0.1180	0.3070
At	0.0800	0.3510
Au	0.2030	0.4180
Av	0.0090	0.2770
Aw	0.1960	0.4350
Ax	0.0390	0.2670

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Chain	Atom inclusion	Q-score
Ay	0.0650	0.3010
Az	0.0630	0.3070
B	0.8980	0.4870
C	0.8290	0.4720
D	0.6560	0.4920
E	0.6320	0.4730
F	0.6400	0.4710
G	0.6210	0.4260
H	0.4890	0.3930
I	0.6480	0.4870
J	0.6750	0.4910
K	0.6530	0.4830
L	0.5470	0.4320
M	0.6810	0.4810
N	0.6220	0.4670
O	0.5010	0.4070
P	0.6100	0.4860
Q	0.5090	0.4620
R	0.5970	0.4380
S	0.6380	0.4550
T	0.5980	0.4590
U	0.6930	0.4890
V	0.4970	0.4210
W	0.5290	0.4210
X	0.6220	0.4610
Y	0.6620	0.4880
Z	0.6720	0.4970
a	0.5860	0.4600
b	0.5800	0.4290
c	0.5280	0.4330
d	0.7200	0.5010
e	0.4330	0.3730
f	0.6290	0.4800
g	0.6190	0.4610
h	0.4830	0.4250
i	0.5910	0.4570
j	0.5920	0.4690
k	0.6490	0.4770
l	0.0010	0.1070
m	0.6570	0.4770
n	0.3950	0.3930
o	0.6100	0.4550

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Chain	Atom inclusion	Q-score
p	0.5470	0.4470
q	0.4980	0.3960
r	0.4960	0.4350
s	0.6210	0.4520
t	0.7200	0.5050