



# wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jul 24, 2017 – 04:23 PM EDT

PDB ID : 4V8Z  
EMDB ID: : EMD-2422  
Title : Cryo-EM reconstruction of the 80S-eIF5B-Met-itRNAMet Eukaryotic Translation Initiation Complex  
Authors : Fernandez, I.S.; Bai, X.C.; Hussain, T.; Kelley, A.C.; Lorsch, J.R.; Ramakrishnan, V.; Scheres, S.H.W.  
Deposited on : unknown  
Resolution : 6.60 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report for a publicly released PDB/EMDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

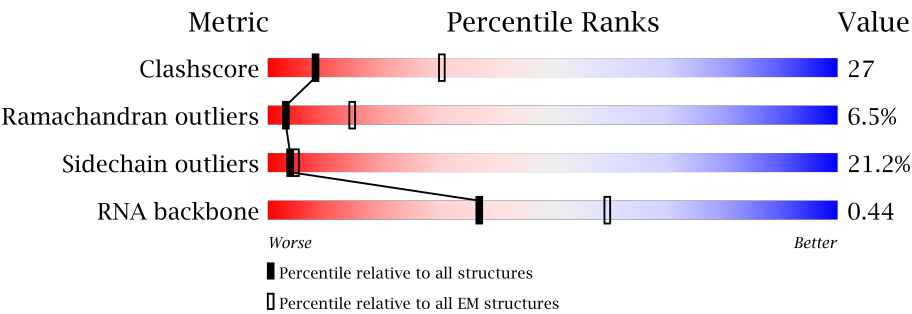
MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20029824

# 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 6.60 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.



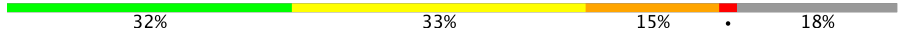


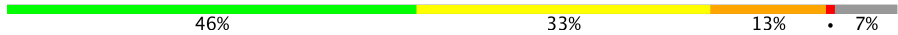
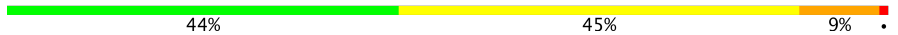
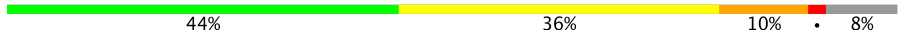
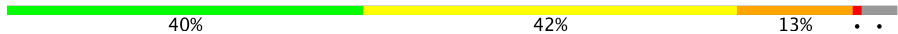
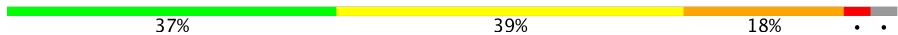
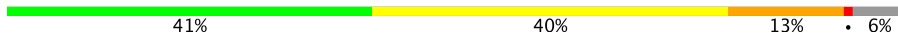
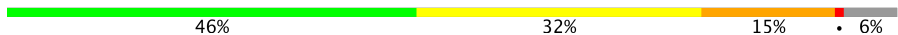
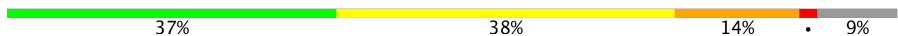
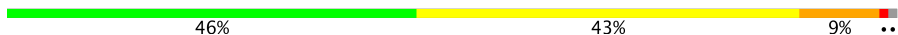
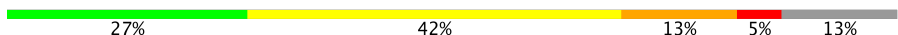







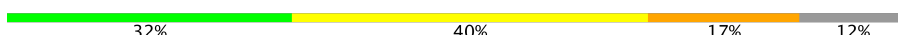




Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A0	119	31% 34% 13% • 18%
2	A1	82	55% 34% 9% ••
3	A2	67	28% 43% 22% 6%
4	A3	56	39% 45% 7% • 5%
5	A4	63	54% 33% 8% 5%
6	A5	152	19% 19% 7% • 53%
7	A6	319	58% 36% 5% •
8	A7	273	34% 15% 7% • 42%








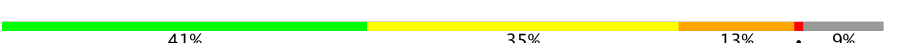
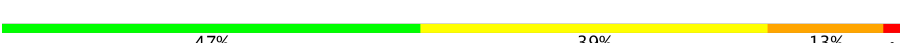

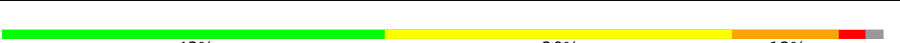
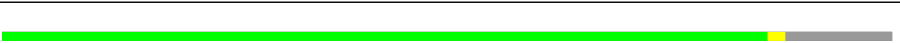




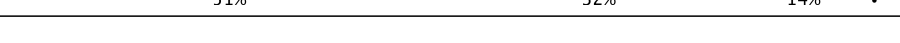
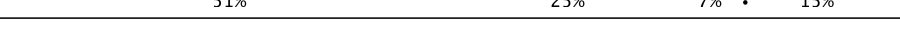



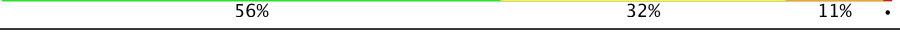



Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	AA	252	
10	AB	255	
11	AC	254	
12	AD	240	
13	AE	261	
14	AF	225	
15	AG	236	
16	AH	190	
17	AI	200	
18	AJ	197	
19	AK	105	
20	AL	156	
21	AM	143	
22	AN	151	
23	AO	137	
24	AP	142	
25	AQ	143	
26	AR	136	
27	AS	146	
28	AT	144	
29	AU	121	
30	AV	87	
31	AW	130	
32	AX	145	
33	AY	135	











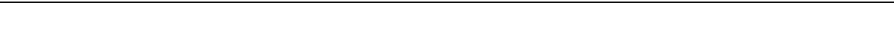

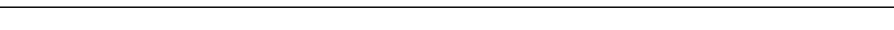
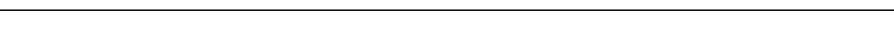





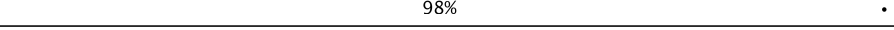
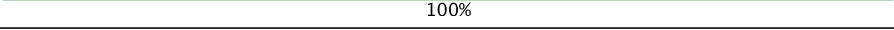



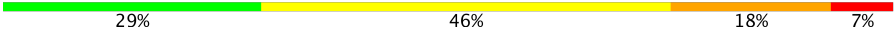
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	AZ	108	
35	BA	253	
36	BB	386	
37	BC	361	
38	BD	296	
39	BE	175	
40	BF	243	
41	BG	255	
42	BH	191	
43	BI	220	
44	BJ	173	
45	BK	174	
46	BL	198	
47	BM	137	
48	BN	203	
49	BO	218	
50	BP	183	
51	BQ	185	
52	BR	188	
53	BS	172	
54	BT	159	
55	BU	120	
56	BV	136	
57	BW	155	
58	BX	141	



Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
59	BY	126	 51% 39% 8% .
60	BZ	135	 39% 47% 10% .
61	Ba	148	 76% 22% ..
62	Bb	58	 72% 24% .
63	Bc	104	 79% 16% . .
64	Bd	112	 73% 21% . .
65	Be	129	 76% 20% . . .
66	Bf	106	 86% 12% .
67	Bg	120	 71% 22% . 7%
68	Bh	119	 76% 22% .
69	Bi	99	 68% 28% .
70	Bj	87	 75% 25%
71	Bk	77	 77% 23%
72	Bl	50	 76% 22% .
73	Bm	128	 30% 9% . 59%
74	Bn	25	 72% 20% 8%
75	Bo	105	 83% 16% .
76	Bq	312	 34% 11% . 54%
77	Br	47	 98% .
78	Bs	46	 100%
79	B2	1800	 26% 40% 26% 7% .
80	B5	3396	 21% 41% 24% 7% 7%
81	B7	121	 21% 48% 27% .
82	B8	158	 29% 46% 18% 7%
83	CV	586	 63% 26% 5% . .

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
84	CW	76	
85	CX	3	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
88	OHX	A3	102	-	-	X	-
88	OHX	AC	301	-	-	X	-
88	OHX	AL	201	-	-	X	-
88	OHX	B2	1907	-	-	X	-
88	OHX	B2	1915	-	-	X	-
88	OHX	B2	1918	-	-	X	-
88	OHX	B2	1921	-	-	X	-
88	OHX	B2	1922	-	-	X	-
88	OHX	B2	1939	-	-	X	-
88	OHX	B2	1953	-	-	X	-
88	OHX	B2	1960	-	-	X	-
88	OHX	B2	1962	-	-	X	-
88	OHX	B2	1963	-	-	X	-
88	OHX	B2	1967	-	-	X	-
88	OHX	B2	1968	-	-	X	-
88	OHX	B2	1973	-	-	X	-
88	OHX	B2	1976	-	-	X	-
88	OHX	B2	1981	-	-	X	-
88	OHX	B2	1987	-	-	X	-
88	OHX	B2	1995	-	-	X	-
88	OHX	B2	2011	-	-	X	-
88	OHX	B2	2014	-	-	X	-
88	OHX	B2	2025	-	-	X	-
88	OHX	B2	2044	-	-	X	-
88	OHX	B2	2048	-	-	X	-
88	OHX	B2	2062	-	-	X	-
88	OHX	B2	2066	-	-	X	-
88	OHX	B2	2069	-	-	X	-
88	OHX	B2	2071	-	-	X	-
88	OHX	B2	2077	-	-	X	-
88	OHX	B2	2081	-	-	X	-
88	OHX	B7	203	-	-	X	-
88	OHX	B7	219	-	-	X	-

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
88	OHX	BR	201	-	-	X	-
88	OHX	CV	601	-	-	X	-
89	GCP	CV	602	-	-	X	-

## 2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 219371 atoms, of which 8407 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 40S RIBOSOMAL PROTEIN S26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A0	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 2 is a protein called 40S RIBOSOMAL PROTEIN S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A1	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 3 is a protein called 40S RIBOSOMAL PROTEIN S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A2	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 4 is a protein called 40S RIBOSOMAL PROTEIN S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A3	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 5 is a protein called 40S RIBOSOMAL PROTEIN S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A4	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 6 is a protein called UBIQUITIN-40S RIBOSOMAL PROTEIN S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A5	71	Total	C	N	O	S	0	0
			516	328	93	91	4		



There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A5	82	UNK	LYS	SEE REMARK 999	UNP P05759
A5	83	UNK	LYS	SEE REMARK 999	UNP P05759
A5	84	UNK	VAL	SEE REMARK 999	UNP P05759
A5	85	UNK	TYR	SEE REMARK 999	UNP P05759
A5	86	UNK	THR	SEE REMARK 999	UNP P05759
A5	87	UNK	THR	SEE REMARK 999	UNP P05759
A5	88	UNK	PRO	SEE REMARK 999	UNP P05759
A5	89	UNK	LYS	SEE REMARK 999	UNP P05759
A5	90	UNK	LYS	SEE REMARK 999	UNP P05759
A5	91	UNK	ILE	SEE REMARK 999	UNP P05759
A5	92	UNK	LYS	SEE REMARK 999	UNP P05759
A5	93	UNK	HIS	SEE REMARK 999	UNP P05759
A5	94	UNK	LYS	SEE REMARK 999	UNP P05759
A5	95	UNK	HIS	SEE REMARK 999	UNP P05759
A5	96	UNK	LYS	SEE REMARK 999	UNP P05759
A5	97	UNK	LYS	SEE REMARK 999	UNP P05759
A5	98	UNK	VAL	SEE REMARK 999	UNP P05759
A5	99	UNK	LYS	SEE REMARK 999	UNP P05759
A5	100	UNK	LEU	SEE REMARK 999	UNP P05759
A5	101	UNK	ALA	SEE REMARK 999	UNP P05759

- Molecule 7 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-LIKE PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A6	318	Total	C	N	O	S	0	0
			2437	1541	418	470	8		

- Molecule 8 is a protein called SUPPRESSOR PROTEIN STM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	A7	159	Total	C	N	O	0	0
			1105	653	221	231		

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A7	9	UNK	GLY	SEE REMARK 999	UNP P39015
A7	10	UNK	ASN	SEE REMARK 999	UNP P39015
A7	11	UNK	ASP	SEE REMARK 999	UNP P39015
A7	12	UNK	VAL	SEE REMARK 999	UNP P39015

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
A7	13	UNK	GLU	SEE REMARK 999	UNP P39015
A7	14	UNK	ASP	SEE REMARK 999	UNP P39015
A7	15	UNK	ALA	SEE REMARK 999	UNP P39015
A7	16	UNK	ASP	SEE REMARK 999	UNP P39015
A7	17	UNK	VAL	SEE REMARK 999	UNP P39015
A7	18	UNK	VAL	SEE REMARK 999	UNP P39015
A7	19	UNK	VAL	SEE REMARK 999	UNP P39015
A7	20	UNK	LEU	SEE REMARK 999	UNP P39015
A7	151	UNK	LEU	SEE REMARK 999	UNP P39015
A7	152	UNK	GLN	SEE REMARK 999	UNP P39015
A7	153	UNK	ASP	SEE REMARK 999	UNP P39015
A7	154	UNK	TYR	SEE REMARK 999	UNP P39015
A7	155	UNK	LEU	SEE REMARK 999	UNP P39015
A7	156	UNK	ASN	SEE REMARK 999	UNP P39015
A7	157	UNK	GLN	SEE REMARK 999	UNP P39015
A7	158	UNK	GLN	SEE REMARK 999	UNP P39015
A7	159	UNK	ALA	SEE REMARK 999	UNP P39015
A7	160	UNK	ASN	SEE REMARK 999	UNP P39015
A7	161	UNK	ASN	SEE REMARK 999	UNP P39015
A7	162	UNK	GLN	SEE REMARK 999	UNP P39015
A7	163	UNK	PHE	SEE REMARK 999	UNP P39015
A7	164	UNK	ASN	SEE REMARK 999	UNP P39015
A7	165	UNK	LYS	SEE REMARK 999	UNP P39015
A7	166	UNK	VAL	SEE REMARK 999	UNP P39015
A7	167	UNK	PRO	SEE REMARK 999	UNP P39015
A7	168	UNK	GLU	SEE REMARK 999	UNP P39015
A7	169	UNK	ALA	SEE REMARK 999	UNP P39015
A7	170	UNK	LYS	SEE REMARK 999	UNP P39015
A7	171	UNK	LYS	SEE REMARK 999	UNP P39015
A7	172	UNK	VAL	SEE REMARK 999	UNP P39015
A7	173	UNK	GLU	SEE REMARK 999	UNP P39015
A7	174	UNK	LEU	SEE REMARK 999	UNP P39015
A7	175	UNK	ASP	SEE REMARK 999	UNP P39015

- Molecule 9 is a protein called 40S RIBOSOMAL PROTEIN S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AA	206	Total	C	N	O	S	0	0
			1577	1014	278	283	2		

- Molecule 10 is a protein called 40S RIBOSOMAL PROTEIN S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AB	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AC	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 12 is a protein called 40S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AD	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 13 is a protein called 40S RIBOSOMAL PROTEIN S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AE	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 14 is a protein called 40S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AF	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AG	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 16 is a protein called 40S RIBOSOMAL PROTEIN S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AH	184	Total	C	N	O		0	0
			1481	951	265	265			

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AI	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 18 is a protein called 40S RIBOSOMAL PROTEIN S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AK	96	Total	C	N	O	S	0	0
			772	499	126	145	2		

- Molecule 20 is a protein called 40S RIBOSOMAL PROTEIN S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AL	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AM	124	Total	C	N	O	S	0	0
			890	560	156	172	2		

- Molecule 22 is a protein called 40S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AO	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 24 is a protein called 40S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AP	124	Total	C	N	O	S	0	0
			977	622	182	166	7		

- Molecule 25 is a protein called 40S RIBOSOMAL PROTEIN S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AQ	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 26 is a protein called 40S RIBOSOMAL PROTEIN S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AR	120	Total	C	N	O	S	0	0
			926	577	177	170	2		

- Molecule 27 is a protein called 40S RIBOSOMAL PROTEIN S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 28 is a protein called 40S RIBOSOMAL PROTEIN S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AT	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 29 is a protein called 40S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AU	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 30 is a protein called 40S RIBOSOMAL PROTEIN S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 31 is a protein called 40S RIBOSOMAL PROTEIN S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 33 is a protein called 40S RIBOSOMAL PROTEIN S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AY	134	Total	C	N	O		0	0
			1073	676	208	189			

- Molecule 34 is a protein called 40S RIBOSOMAL PROTEIN S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AZ	70	Total	C	N	O		0	0
			563	360	104	99			

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN L2-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BA	252	Total	C	N	O	S	0	0
			1912	1190	388	333	1		

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BD	294	Total	C	N	O	S	0	0
			2359	1489	412	456	2		

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BE	157	Total	C	N	O	S	0	0
			1248	806	224	217	1		

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BF	223	Total	C	N	O	S	0	0
			1791	1155	325	310	1		

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BG	231	Total	C	N	O	S	0	0
			1763	1130	316	314	3		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BH	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BI	213	Total	C	N	O	S	0	0
			1722	1094	325	297	6		

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BJ	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BK	153	Total	C	H	N	O	0	3
			1509	450	756	153	150		

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	BL	194	Total	C	N	O	0	0
			1548	965	316	267		

- Molecule 47 is a protein called 60S RIBOSOMAL PROTEIN L14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BM	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BM	89	ALA	GLY	CONFLICT	UNP P38754

- Molecule 48 is a protein called 60S RIBOSOMAL PROTEIN L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 49 is a protein called 60S RIBOSOMAL PROTEIN L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BO	197	Total	C	N	O	S	197	0
			3119	2008	581	528	2		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BO	3	VAL	SER	MICROHETEROGENEITY	UNP P26784
BO	4	GLU	GLN	MICROHETEROGENEITY	UNP P26784
BO	11	GLY	ALA	MICROHETEROGENEITY	UNP P26784
BO	13	GLY	ASP	MICROHETEROGENEITY	UNP P26784
BO	16	VAL	LEU	MICROHETEROGENEITY	UNP P26784
BO	22	VAL	THR	MICROHETEROGENEITY	UNP P26784
BO	23	VAL	ILE	MICROHETEROGENEITY	UNP P26784

*Continued on next page...*



*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
BO	27	LEU	VAL	MICROHETEROGENEITY	UNP P26784
BO	40	GLU	ALA	MICROHETEROGENEITY	UNP P26784
BO	80	PHE	LEU	MICROHETEROGENEITY	UNP P26784
BO	84	LEU	ILE	MICROHETEROGENEITY	UNP P26784
BO	104	VAL	ILE	MICROHETEROGENEITY	UNP P26784
BO	158	ALA	ASP	MICROHETEROGENEITY	UNP P26784
BO	163	SER	ARG	MICROHETEROGENEITY	UNP P26784
BO	179	ALA	SER	MICROHETEROGENEITY	UNP P26784
BO	182	ASN	SER	MICROHETEROGENEITY	UNP P26784
BO	184	THR	ALA	MICROHETEROGENEITY	UNP P26784
BO	186	ALA	SER	MICROHETEROGENEITY	UNP P26784
BO	196	ALA	SER	MICROHETEROGENEITY	UNP P26784
BO	197	LEU	PHE	MICROHETEROGENEITY	UNP P26784

- Molecule 50 is a protein called 60S RIBOSOMAL PROTEIN L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	BP	155	Total	C	N	O	0	0
			1227	764	238	225		

- Molecule 51 is a protein called 60S RIBOSOMAL PROTEIN L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 52 is a protein called 60S RIBOSOMAL PROTEIN L19-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	BR	188	Total	C	N	O	0	0
			1521	935	326	260		

- Molecule 53 is a protein called 60S RIBOSOMAL PROTEIN L20-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BS	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 54 is a protein called 60S RIBOSOMAL PROTEIN L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 55 is a protein called 60S RIBOSOMAL PROTEIN L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BU	98	Total	C	N	O		0	0
			778	505	127	146			

- Molecule 56 is a protein called 60S RIBOSOMAL PROTEIN L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BV	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 57 is a protein called 60S RIBOSOMAL PROTEIN L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BW	135	Total	C	N	O	S	0	0
			1038	651	206	180	1		

- Molecule 58 is a protein called 60S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BX	120	Total	C	N	O	S	0	0
			959	617	168	172	2		

- Molecule 59 is a protein called 60S RIBOSOMAL PROTEIN L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BY	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 60 is a protein called 60S RIBOSOMAL PROTEIN L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BZ	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 61 is a protein called 60S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Ba	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 62 is a protein called 60S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Bb	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 63 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bc	100	Total	C	N	O	S	0	0
			767	492	128	146	1		

- Molecule 64 is a protein called 60S RIBOSOMAL PROTEIN L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Bd	109	Total	C	N	O	S	0	0
			883	559	167	156	1		

- Molecule 65 is a protein called 60S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Be	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 66 is a protein called 60S RIBOSOMAL PROTEIN L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bf	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 67 is a protein called 60S RIBOSOMAL PROTEIN L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bg	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 68 is a protein called 60S RIBOSOMAL PROTEIN L35-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Bh	119	Total	C	N	O	S	0	0
			965	612	185	167	1		

- Molecule 69 is a protein called 60S RIBOSOMAL PROTEIN L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Bi	99	Total	C	N	O	S	0	0
			770	481	156	131	2		

- Molecule 70 is a protein called 60S RIBOSOMAL PROTEIN L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bj	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 71 is a protein called 60S RIBOSOMAL PROTEIN L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bk	77	Total	C	N	O		0	0
			608	388	114	106			

- Molecule 72 is a protein called 60S RIBOSOMAL PROTEIN L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bl	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 73 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 74 is a protein called 60S RIBOSOMAL PROTEIN L41-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bn	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 75 is a protein called 60S RIBOSOMAL PROTEIN L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Bo	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 76 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P0.

Mol	Chain	Residues	Atoms					AltConf	Trace	
76	Bq	145	Total	C	H	N	O	S	0	2
			2185	683	1110	194	195	3		

- Molecule 77 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Br	47	Total	C	H	N	O	0	0
			473	141	237	47	48		

- Molecule 78 is a protein called 60S ACIDIC RIBOSOMAL PROTEIN P2.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bs	46	Total	C	H	N	O	0	0
			463	138	232	46	47		

- Molecule 79 is a RNA chain called 18S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	B2	1781	Total	C	N	O	P	1	0
			37835	16910	6661	12482	1782		

- Molecule 80 is a RNA chain called 25S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	B5	3147	Total	C	H	N	O	P	0	0
			67972	30066	664	12132	21965	3145		

- Molecule 81 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	B7	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 82 is a RNA chain called 5.8S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	B8	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 83 is a protein called EUKARYOTIC TRANSLATION INITIATION FACTOR 5B, PROBABLE TRANSLATION INITIATION FACTOR IF-2.

Mol	Chain	Residues	Atoms						AltConf	Trace
83	CV	570	Total	C	H	N	O	S	0	2
			9036	2819	4585	766	847	19		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CV	340	ASP	-	LINKER	UNP P39730
CV	341	LEU	-	LINKER	UNP P39730
CV	342	THR	-	LINKER	UNP P39730
CV	343	GLY	-	LINKER	UNP P39730
CV	344	LEU	-	LINKER	UNP P39730
CV	345	LEU	-	LINKER	UNP P39730
CV	346	ASP	-	LINKER	UNP P39730
CV	347	SER	-	LINKER	UNP P39730
CV	348	VAL	-	LINKER	UNP P39730
CV	349	ASP	-	LINKER	UNP P39730
CV	350	THR	-	LINKER	UNP P39730

- Molecule 84 is a RNA chain called EUKARYOTIC RIBOSOMAL PI TRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
84	CW	76	Total	C	H	N	O	P	0	0
			2403	721	789	285	533	75		

- Molecule 85 is a RNA chain called 5'-R(\*AP\*UP\*GP)-3'.

Mol	Chain	Residues	Atoms						AltConf	Trace
85	CX	3	Total	C	H	N	O	P	0	0
			96	29	34	12	19	2		

- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	A0	1	Total	Zn	0
			1	1	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		AltConf
86	A1	1	Total 1	Zn 1	0
86	Bm	1	Total 1	Zn 1	0
86	A5	1	Total 1	Zn 1	0
86	Bj	1	Total 1	Zn 1	0
86	A3	1	Total 1	Zn 1	0

- Molecule 87 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

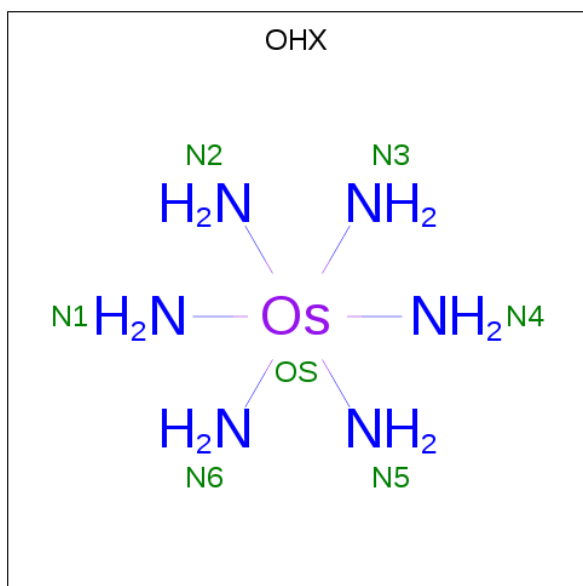
Mol	Chain	Residues	Atoms		AltConf
87	A0	2	Total 2	Mg 2	0
87	AG	1	Total 1	Mg 1	0
87	AJ	1	Total 1	Mg 1	0
87	B7	27	Total 27	Mg 27	0
87	BF	1	Total 1	Mg 1	0
87	AE	1	Total 1	Mg 1	0
87	AB	1	Total 1	Mg 1	0
87	AI	1	Total 1	Mg 1	0
87	AC	2	Total 2	Mg 2	0
87	BS	3	Total 3	Mg 3	0
87	AS	1	Total 1	Mg 1	0
87	B2	168	Total 168	Mg 168	0
87	BD	4	Total 4	Mg 4	0
87	AU	1	Total 1	Mg 1	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		AltConf
87	AN	1	Total	Mg	0
			1	1	
87	A5	1	Total	Mg	0
			1	1	
87	B5	3	Total	Mg	0
			3	3	
87	CW	1	Total	Mg	0
			1	1	
87	AL	2	Total	Mg	0
			2	2	
87	A3	3	Total	Mg	0
			3	3	
87	AP	1	Total	Mg	0
			1	1	

- Molecule 88 is osmium (III) hexammine (three-letter code: OHX) (formula:  $\text{H}_{12}\text{N}_6\text{Os}$ ).



Mol	Chain	Residues	Atoms			AltConf
88	A3	1	Total	N	Os	0
			7	6	1	
88	A6	1	Total	N	Os	0
			7	6	1	
88	AC	1	Total	N	Os	0
			7	6	1	
88	AI	1	Total	N	Os	0
			14	12	2	

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Residues	Atoms			AltConf
88	AI	1	Total 14	N 12	Os 2	0
88	AL	1	Total 7	N 6	Os 1	0
88	AN	1	Total 7	N 6	Os 1	0
88	AP	1	Total 7	N 6	Os 1	0
88	BR	1	Total 7	N 6	Os 1	0
88	Bn	1	Total 7	N 6	Os 1	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0
88	B2	1	Total 1274	N 1092	Os 182	0

*Continued on next page...*

Continued from previous page...

[illegible]

*Continued on next page...*

Continued from previous page...

[illegible]

*Continued on next page...*

Continued from previous page...

[illegible]

*Continued on next page...*

Continued from previous page...

[illegible]

*Continued on next page...*

Continued from previous page...

[illegible]

*Continued on next page...*

Continued from previous page...

[illegible]

*Continued on next page...*

Continued from previous page...

[illegible]

*Continued on next page...*



*Continued from previous page...*

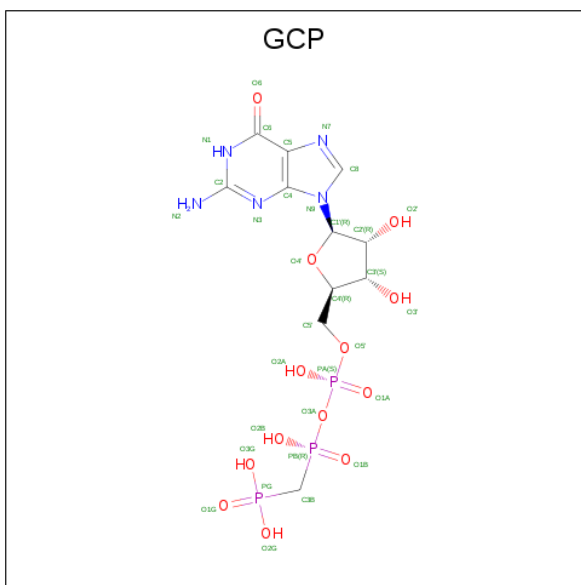
Mol	Chain	Residues	Atoms			AltConf
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B2	1	Total	N	Os	0
			1274	1092	182	
88	B5	1	Total	N	Os	0
			21	18	3	

*Continued on next page...*

*Continued from previous page...*


Mol	Chain	Residues	Atoms			AltConf
88	B5	1	Total	N	Os	0
			21	18	3	
88	B5	1	Total	N	Os	0
			21	18	3	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	B7	1	Total	N	Os	0
			91	78	13	
88	CV	1	Total	N	Os	0
			7	6	1	
88	CX	1	Total	N	Os	0
			7	6	1	

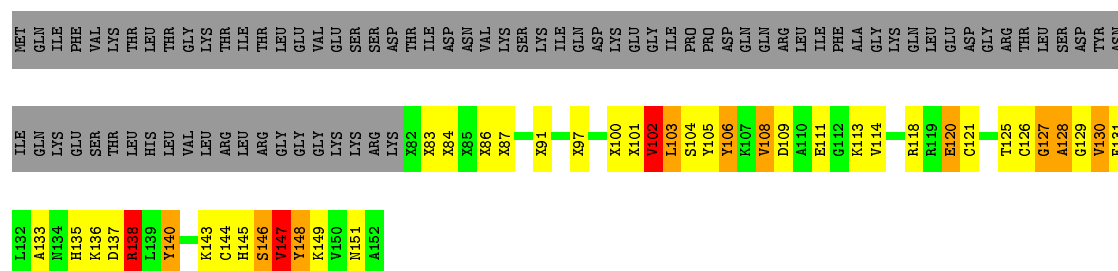
- Molecule 89 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					AltConf
89	CV	1	Total	C	N	O	P	0
			32	11	5	13	3	

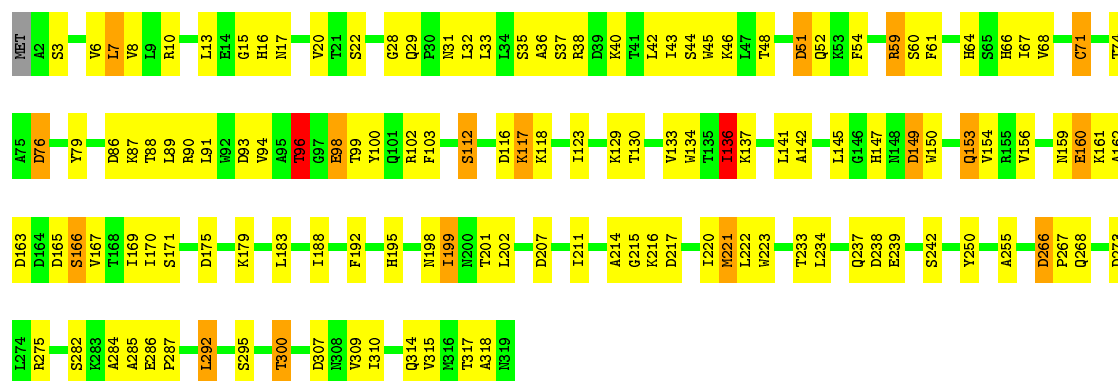


Chain A5: 




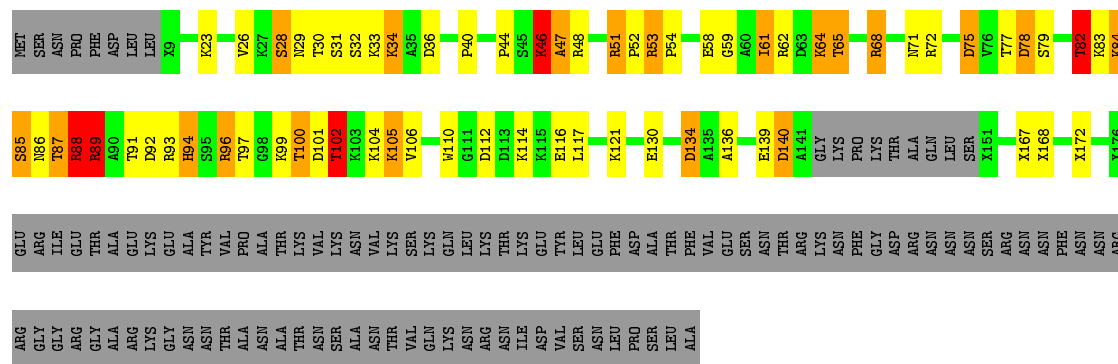
- Molecule 7: GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-LIKE PROTEIN

Chain A6: 



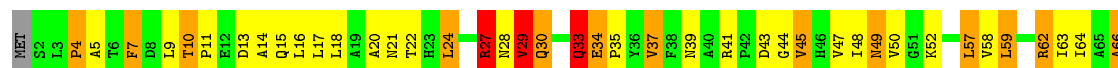
- Molecule 8: SUPPRESSOR PROTEIN STM1

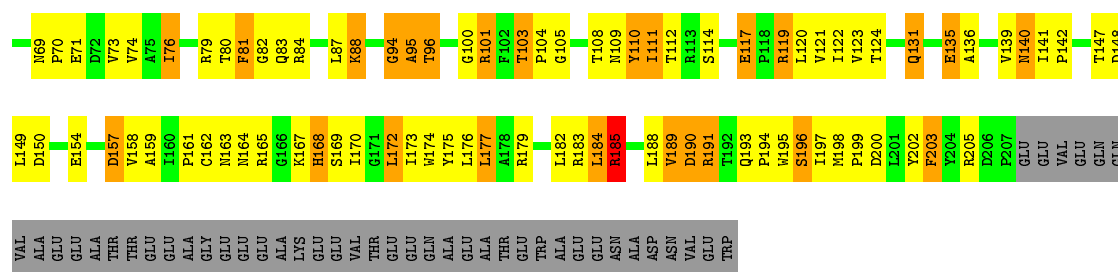
Chain A7: 



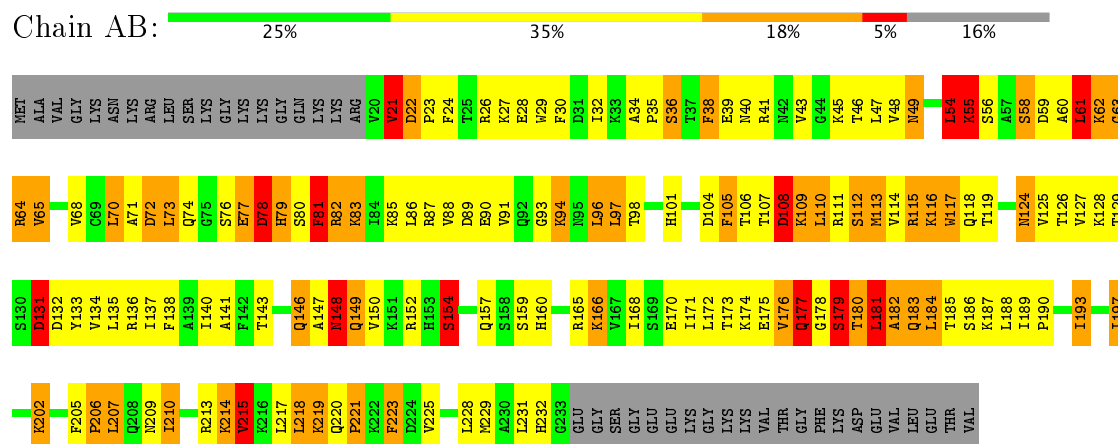
- Molecule 9: 40S RIBOSOMAL PROTEIN S0-A

Chain AA: 

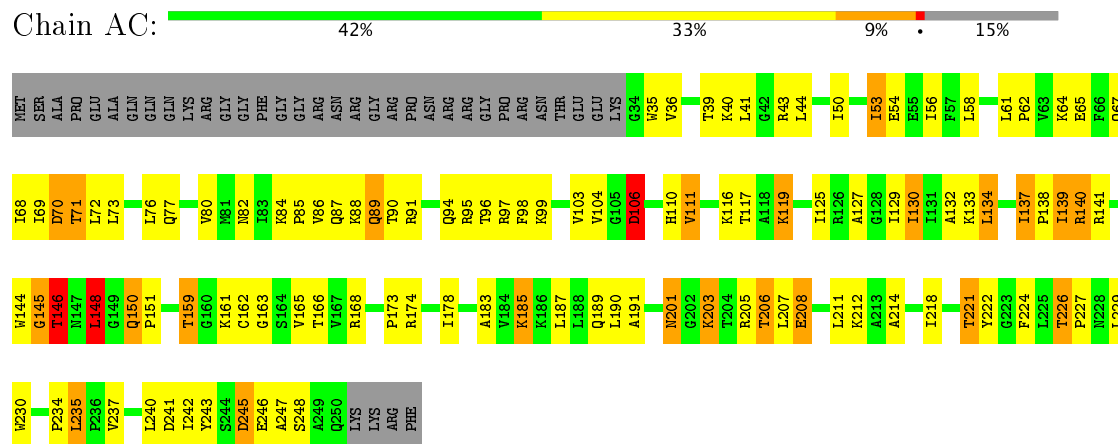




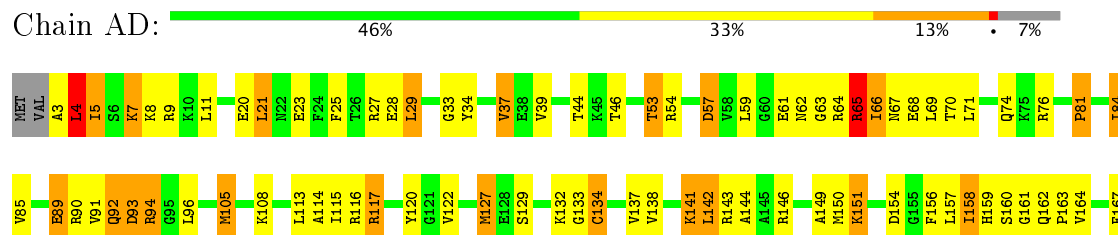
• Molecule 10: 40S RIBOSOMAL PROTEIN S1-A

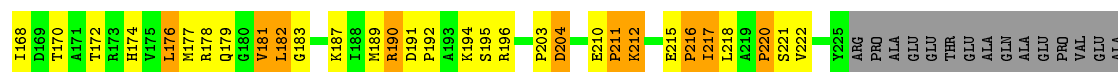


• Molecule 11: 40S RIBOSOMAL PROTEIN S2



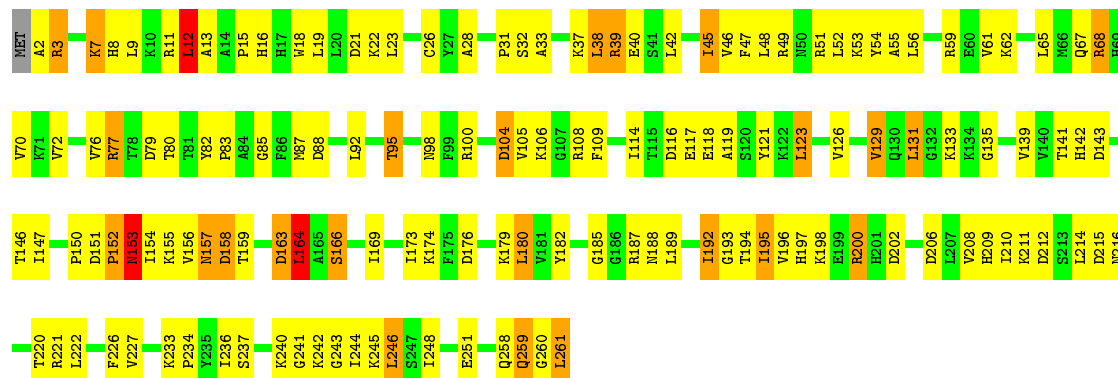
- Molecule 12: 40S RIBOSOMAL PROTEIN S3





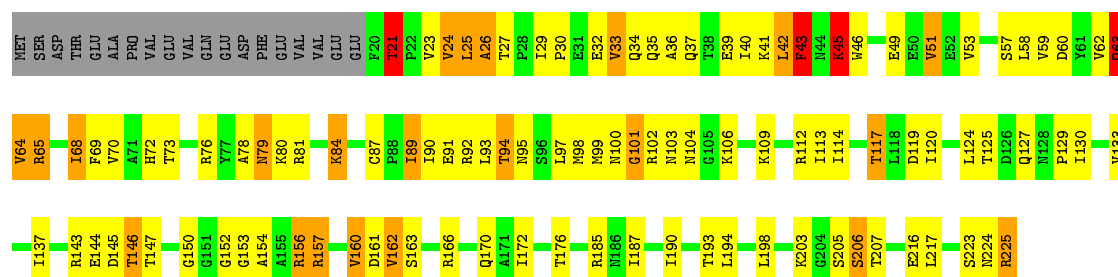
- Molecule 13: 40S RIBOSOMAL PROTEIN S4-A

Chain AE:  44% 45% 9%



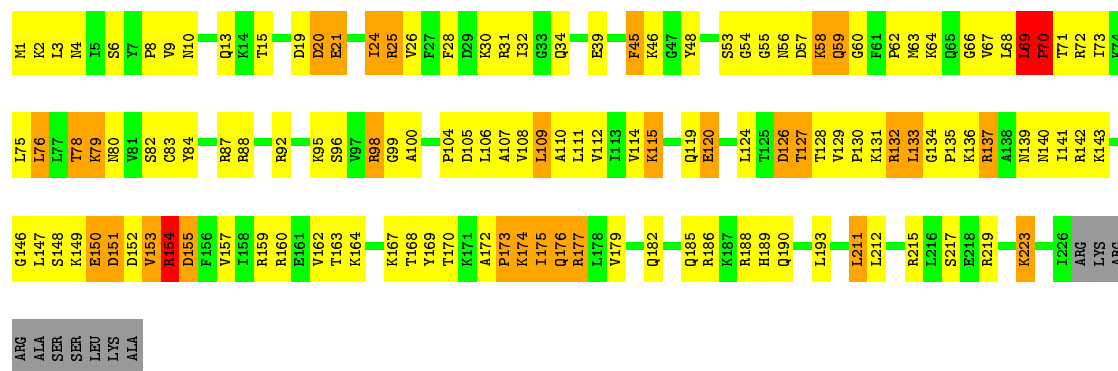
• Molecule 14: 40S RIBOSOMAL PROTEIN S5

Chain AF:  44% 36% 10% 8%



• Molecule 15: 40S RIBOSOMAL PROTEIN S6-A

Chain AG:  40% 42% 13% 3%



• Molecule 16: 40S RIBOSOMAL PROTEIN S7-A

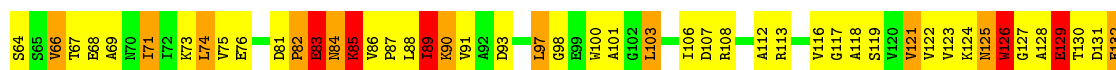
Chain AH:  37% 39% 18% 6%



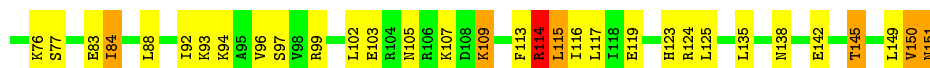
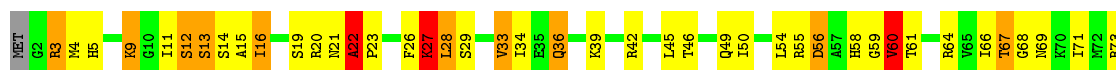




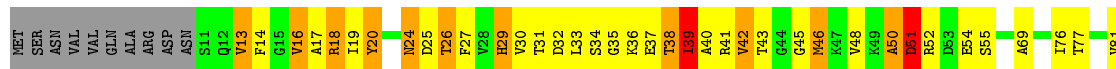
● Molecule 21: 40S RIBOSOMAL PROTEIN S12



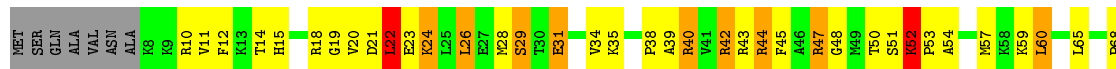
• Molecule 22: 40S RIBOSOMAL PROTEIN S13



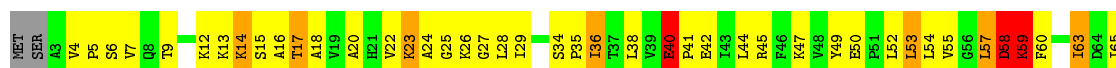
- Molecule 23: 40S RIBOSOMAL PROTEIN S14-A

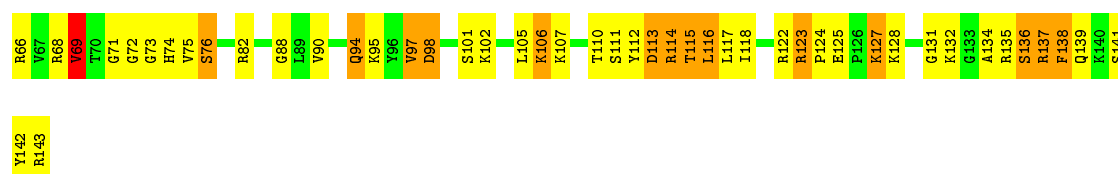


● Molecule 24: 40S RIBOSOMAL PROTEIN S15



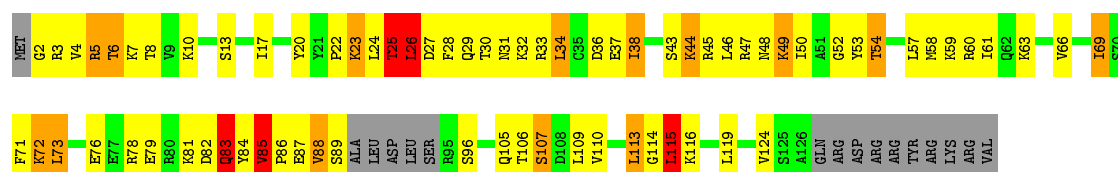
- Molecule 25: 40S RIBOSOMAL PROTEIN S16-A





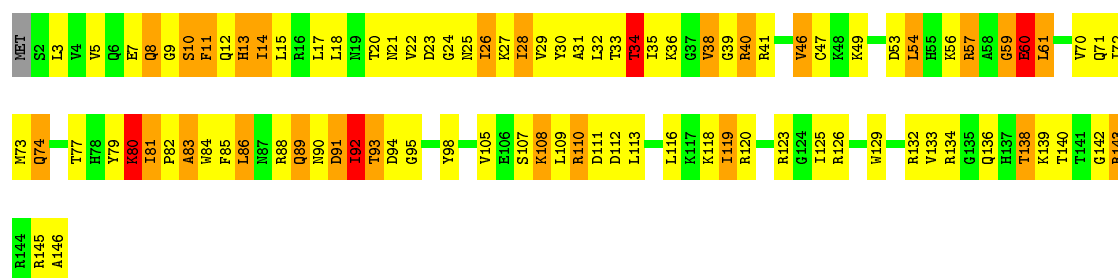
• Molecule 26: 40S RIBOSOMAL PROTEIN S17-A

Chain AR: 35% 40% 10% 12%



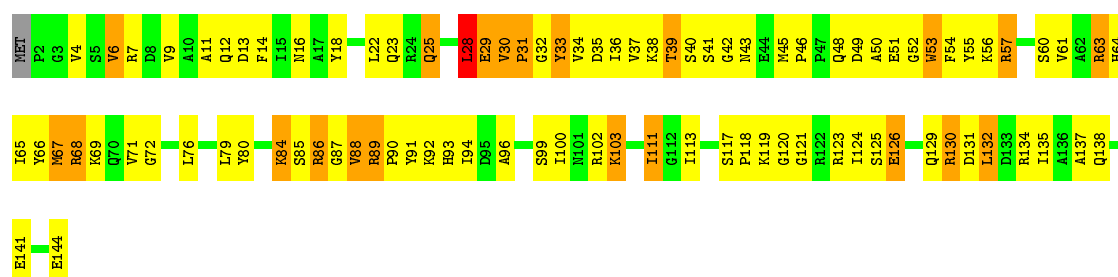
• Molecule 27: 40S RIBOSOMAL PROTEIN S18-A

Chain AS: 35% 44% 18%



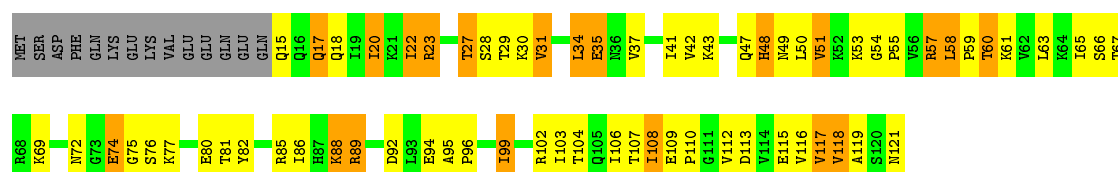
• Molecule 28: 40S RIBOSOMAL PROTEIN S19-A

Chain AT: 35% 49% 15%

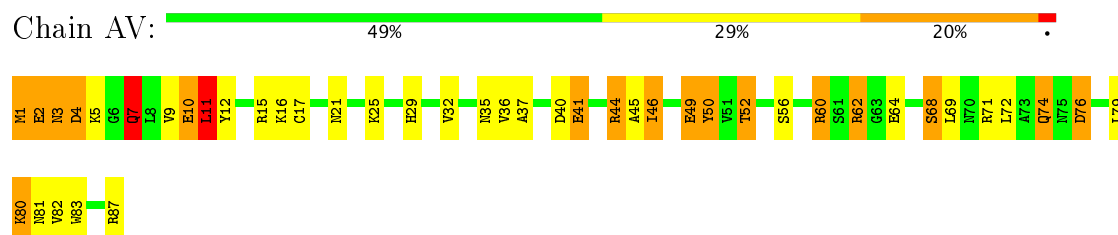


• Molecule 29: 40S RIBOSOMAL PROTEIN S20

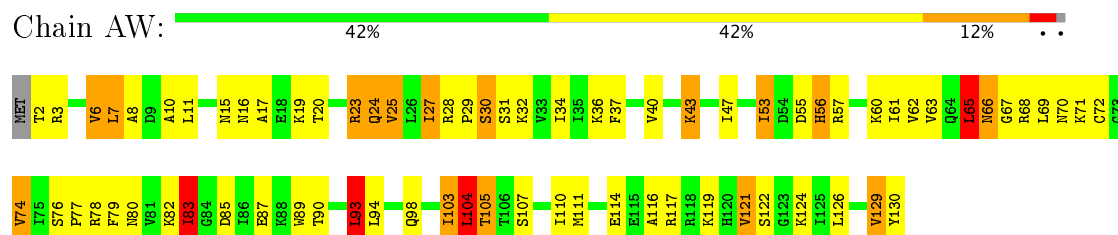
Chain AU: 32% 40% 17% 12%



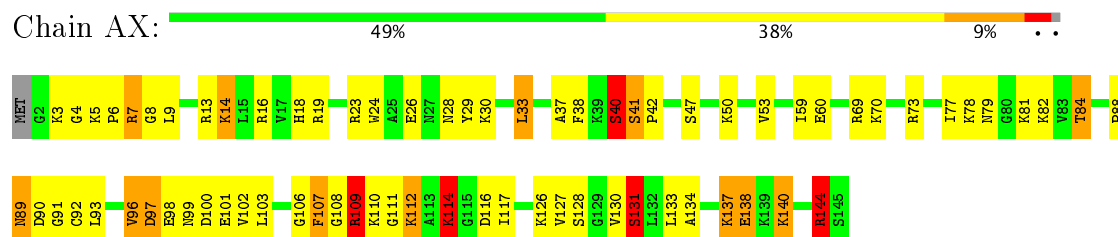
- Molecule 30: 40S RIBOSOMAL PROTEIN S21-A



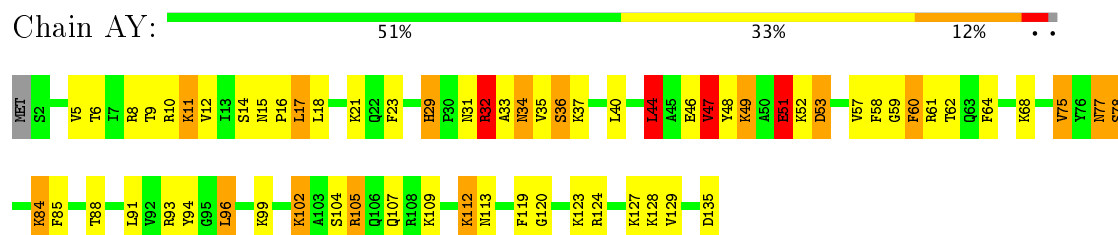
- Molecule 31: 40S RIBOSOMAL PROTEIN S22-A



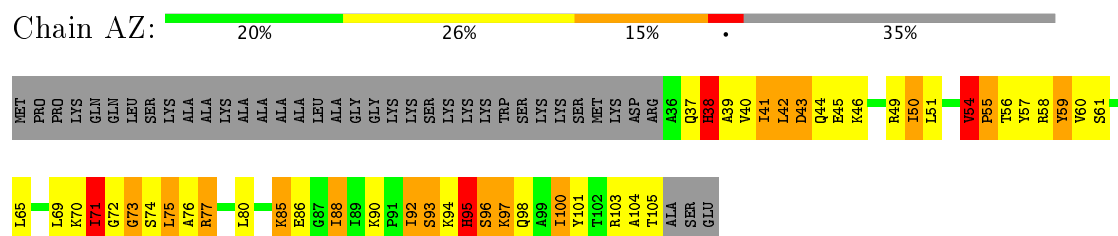
- Molecule 32: 40S RIBOSOMAL PROTEIN S23-A



- Molecule 33: 40S RIBOSOMAL PROTEIN S24-A

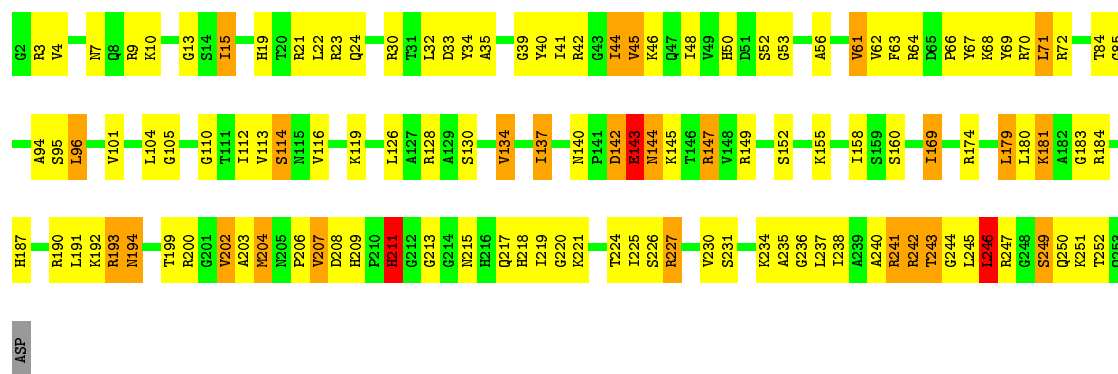


- Molecule 34: 40S RIBOSOMAL PROTEIN S25-A



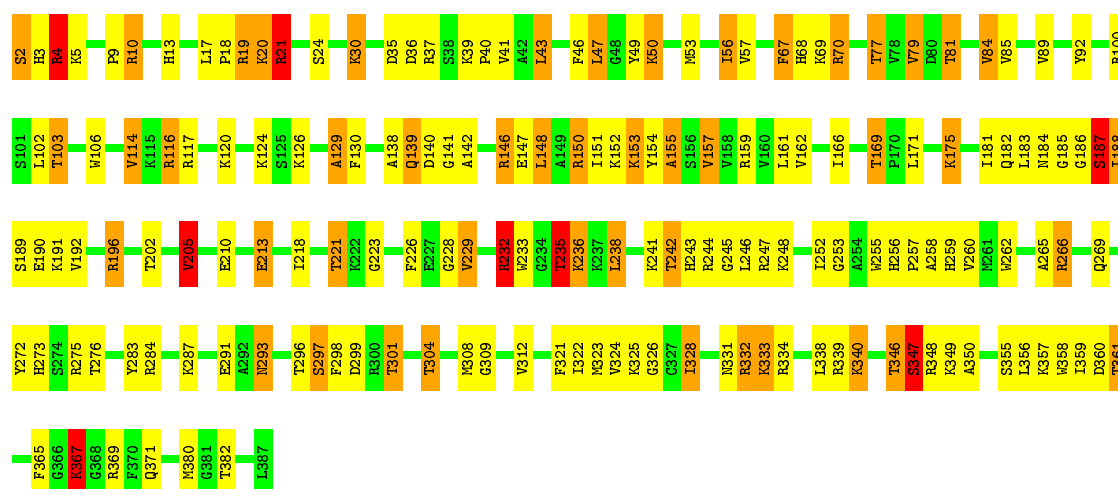
- Molecule 35: 60S RIBOSOMAL PROTEIN L2-B





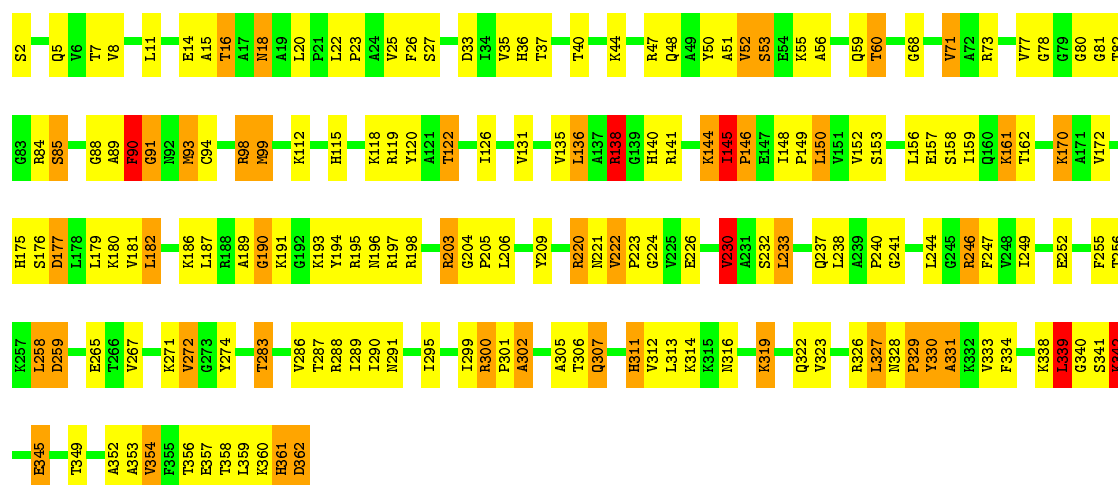
• Molecule 36: 60S RIBOSOMAL PROTEIN L3

Chain BB: 56% 30% 12%



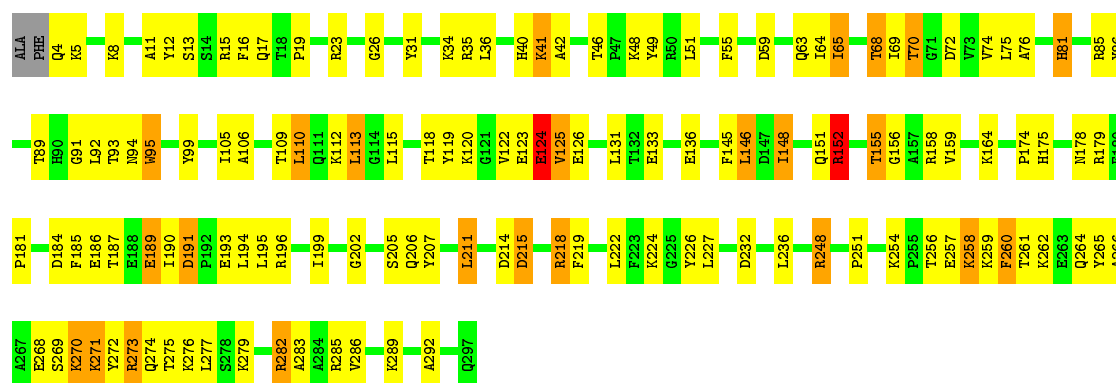
• Molecule 37: 60S RIBOSOMAL PROTEIN L4-A

Chain BC: 51% 35% 12%



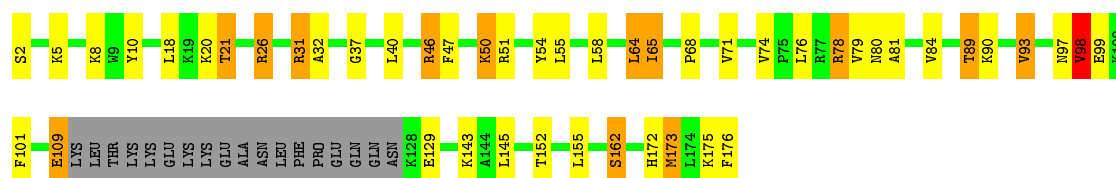
• Molecule 38: 60S RIBOSOMAL PROTEIN L5

Chain BD:



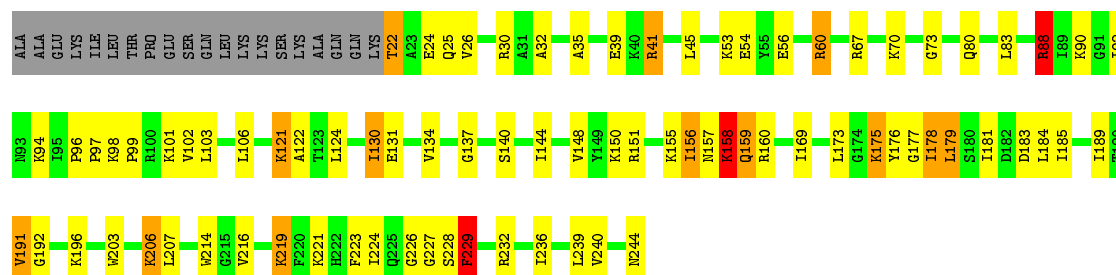
- Molecule 39: 60S RIBOSOMAL PROTEIN L6-A

Chain BE:



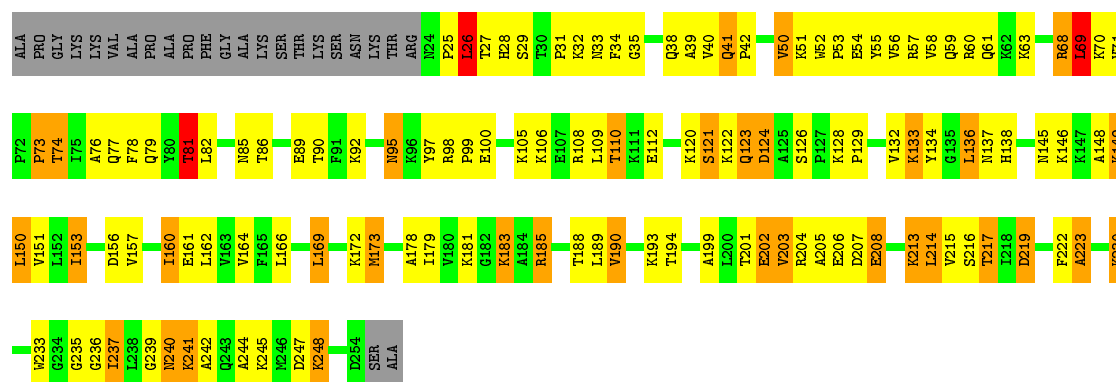
- Molecule 40: 60S RIBOSOMAL PROTEIN L7-A

Chain BF:



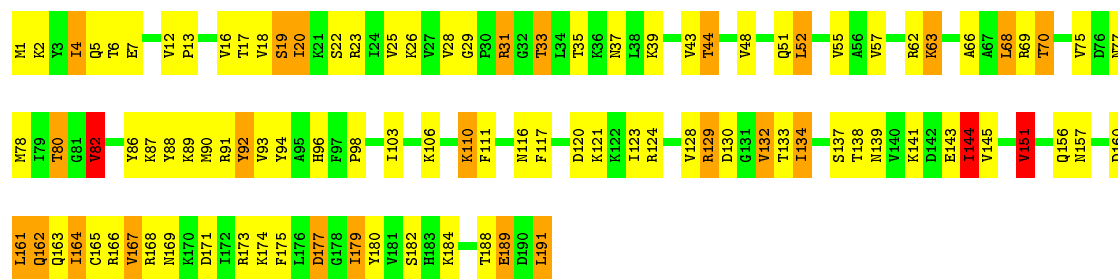
- Molecule 41: 60S RIBOSOMAL PROTEIN L8-A

Chain BG:



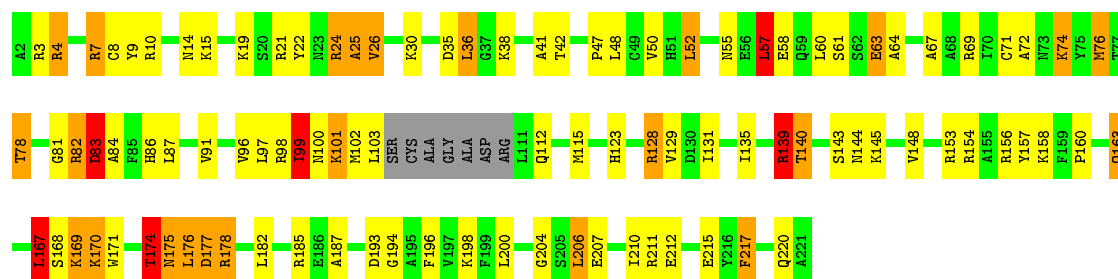
- Molecule 42: 60S RIBOSOMAL PROTEIN L9-A

Chain BH: 



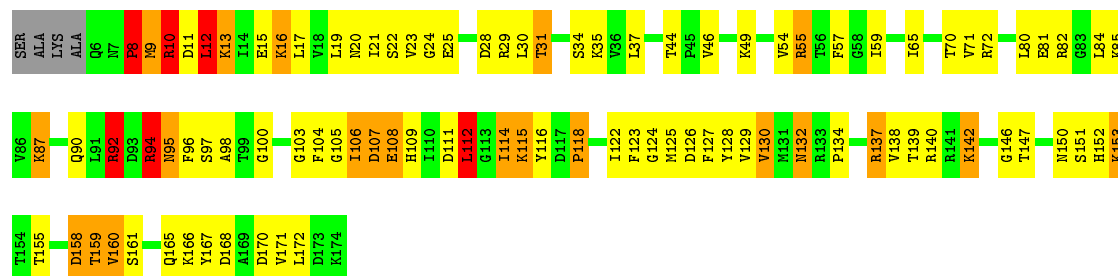
- Molecule 43: 60S RIBOSOMAL PROTEIN L10

Chain BI:  51% 32% 11% 6%

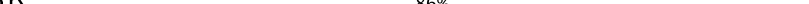


- Molecule 44: 60S RIBOSOMAL PROTEIN L11-A

Chain BJ:  43% 39% 12% . .



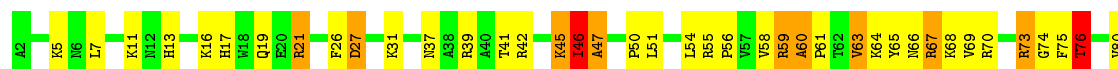
• Molecule 45: 60S RIBOSOMAL PROTEIN L11-A

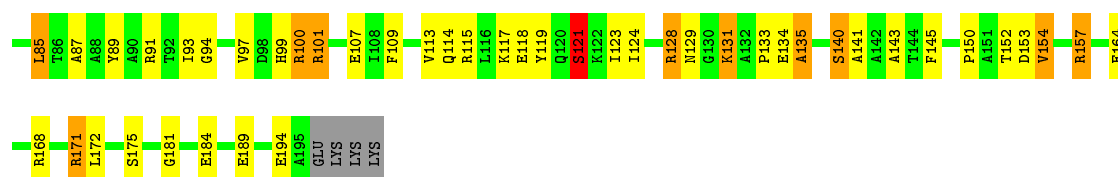
Chain BK:  86% • 12%



- Molecule 46: 60S RIBOSOMAL PROTEIN L13-A

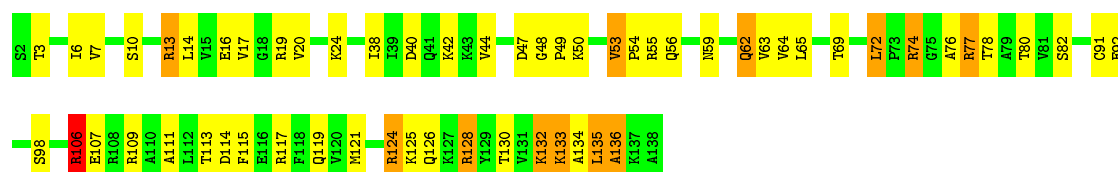
Chain BL: 





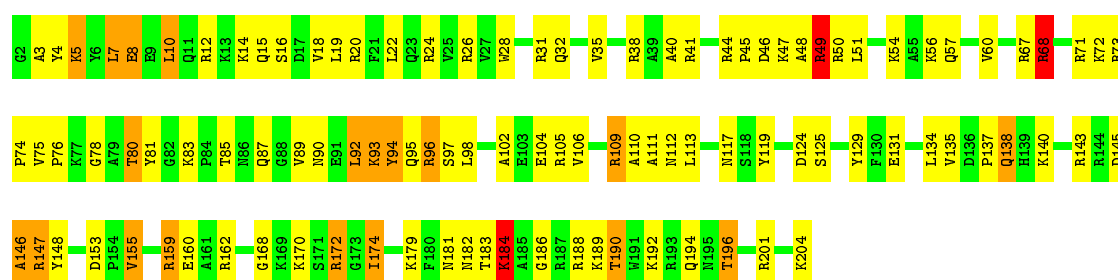
• Molecule 47: 60S RIBOSOMAL PROTEIN L14-B

Chain BM: 57% 34% 9% .



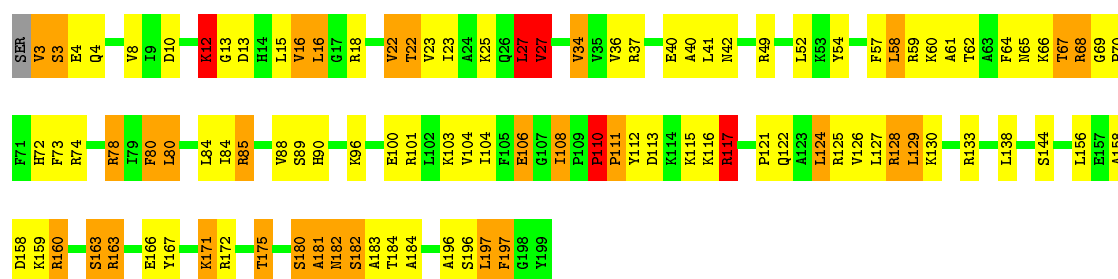
• Molecule 48: 60S RIBOSOMAL PROTEIN L15-A

Chain BN: 48% 41% 9% .



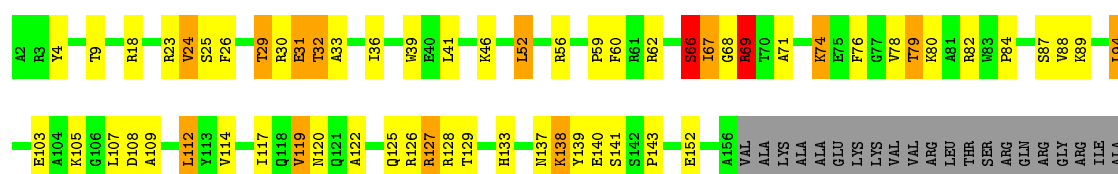
• Molecule 49: 60S RIBOSOMAL PROTEIN L16-A

Chain BO: 51% 32% 14% .



• Molecule 50: 60S RIBOSOMAL PROTEIN L17-A

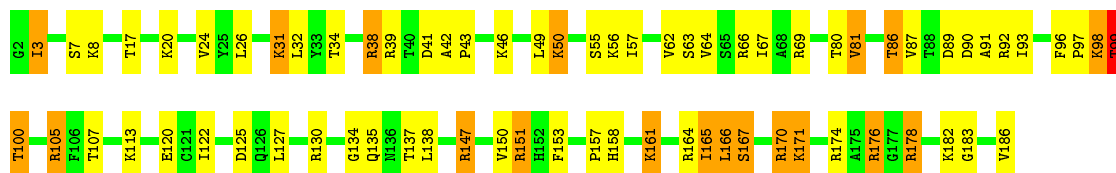
Chain BP: 51% 25% 7% 15% .



ALA  
GLN  
LYS  
ARG  
ILE  
ALA  
ALA

• Molecule 51: 60S RIBOSOMAL PROTEIN L18-A

Chain BQ:  61% 28% 10%



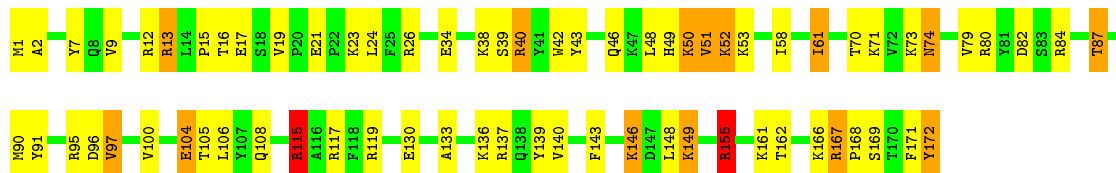
• Molecule 52: 60S RIBOSOMAL PROTEIN L19-B

Chain BR:  51% 40% 9%



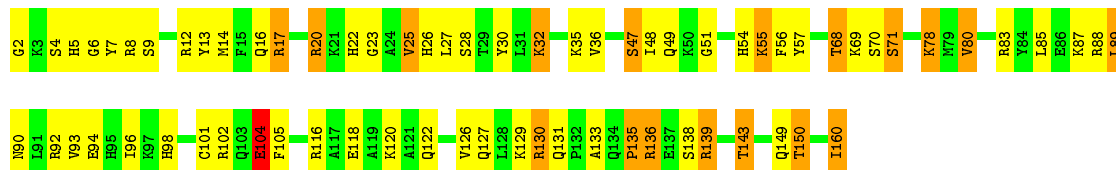
• Molecule 53: 60S RIBOSOMAL PROTEIN L20-B

Chain BS:  59% 31% 8%



• Molecule 54: 60S RIBOSOMAL PROTEIN L21-A

Chain BT:  56% 32% 11%



• Molecule 55: 60S RIBOSOMAL PROTEIN L22-A

Chain BU:  44% 26% 12% 18%

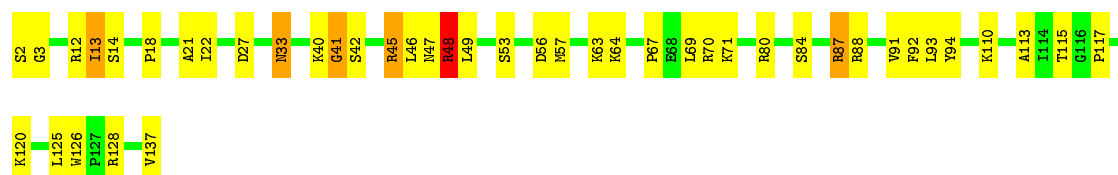






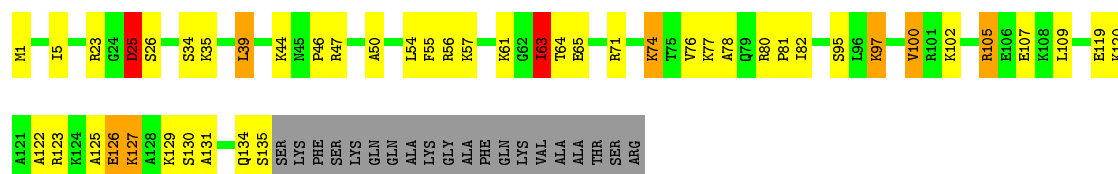
• Molecule 56: 60S RIBOSOMAL PROTEIN L23-A

Chain BV: 68% 28%



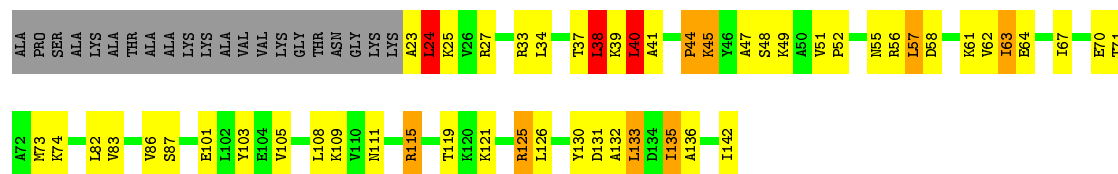
• Molecule 57: 60S RIBOSOMAL PROTEIN L24-A

Chain BW: 57% 25% 5% 13%



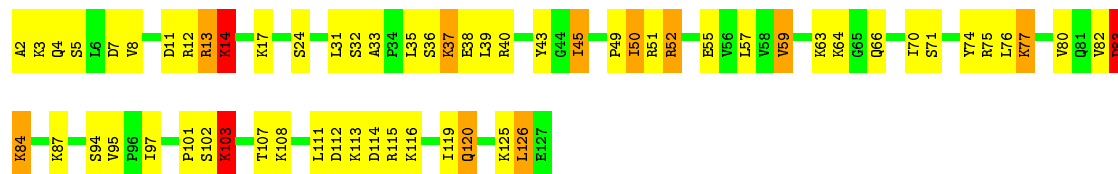
• Molecule 58: 60S RIBOSOMAL PROTEIN L25

Chain BX: 48% 30% 6% 15%



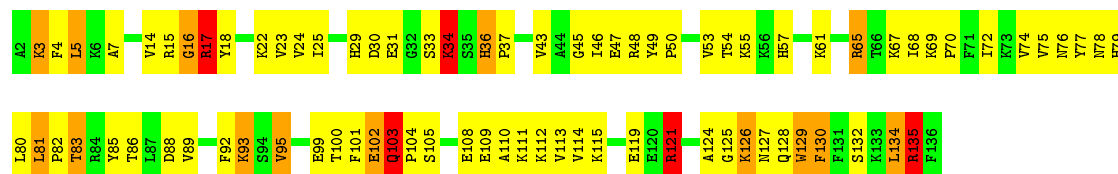
• Molecule 59: 60S RIBOSOMAL PROTEIN L26-A

Chain BY: 51% 39% 8%

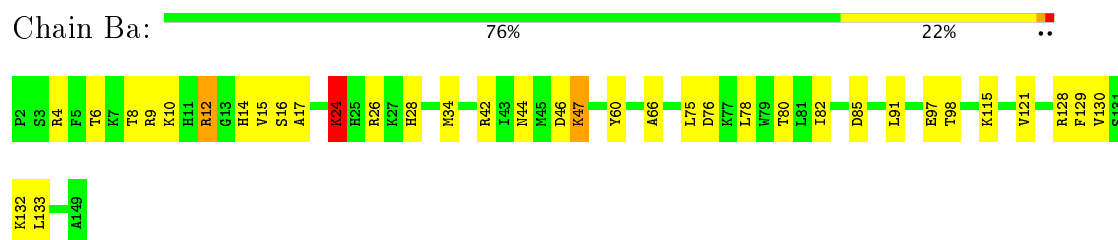


• Molecule 60: 60S RIBOSOMAL PROTEIN L27-A

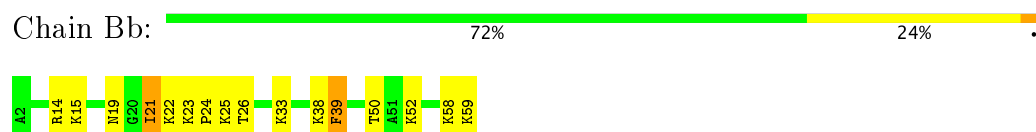
Chain BZ: 39% 47% 10%



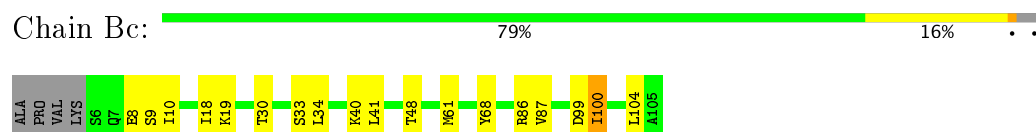
- Molecule 61: 60S RIBOSOMAL PROTEIN L28



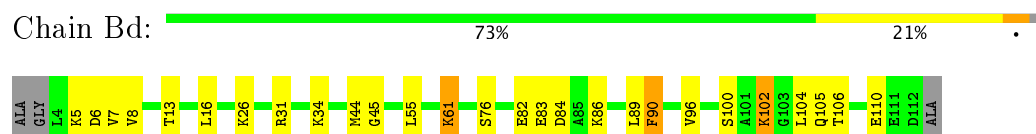
- Molecule 62: 60S RIBOSOMAL PROTEIN L29



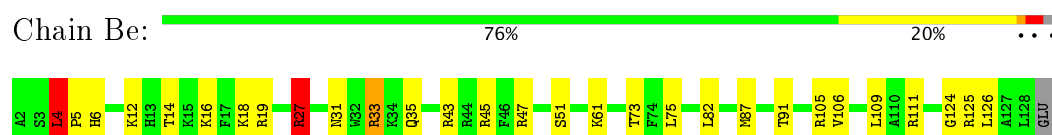
- Molecule 63: 60S RIBOSOMAL PROTEIN L30



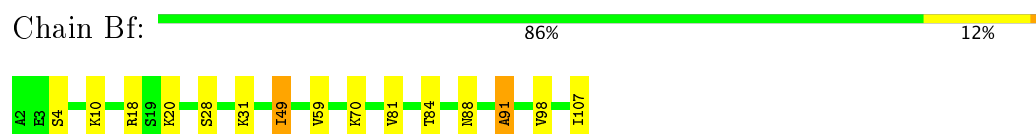
- Molecule 64: 60S RIBOSOMAL PROTEIN L31-A



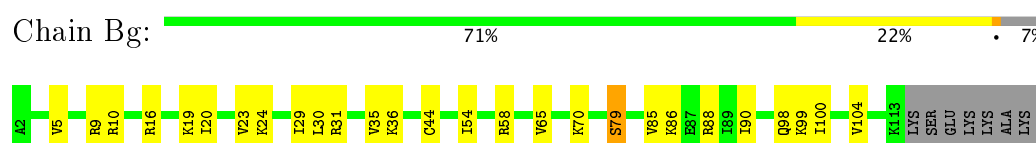
- Molecule 65: 60S RIBOSOMAL PROTEIN L32



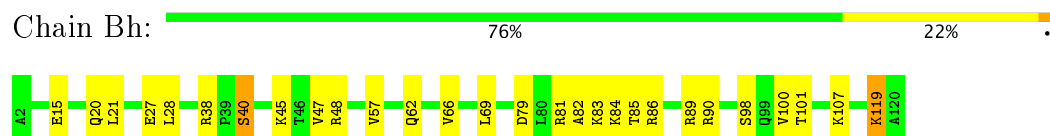
- Molecule 66: 60S RIBOSOMAL PROTEIN L33-A



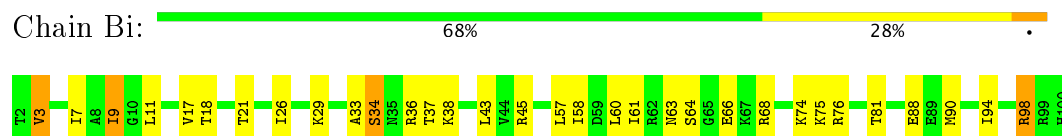
- Molecule 67: 60S RIBOSOMAL PROTEIN L34-A



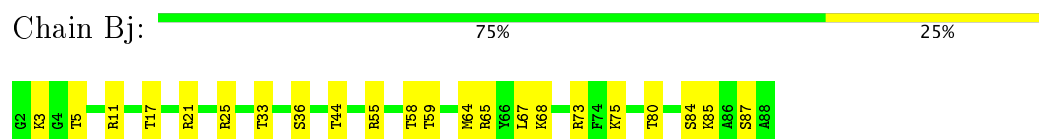
- Molecule 68: 60S RIBOSOMAL PROTEIN L35-B



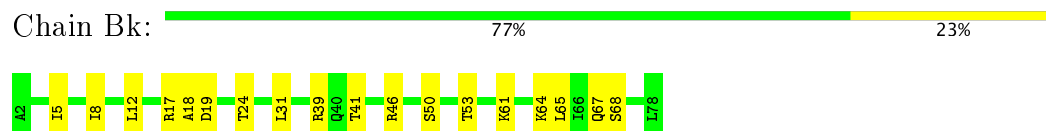
- Molecule 69: 60S RIBOSOMAL PROTEIN L36-A



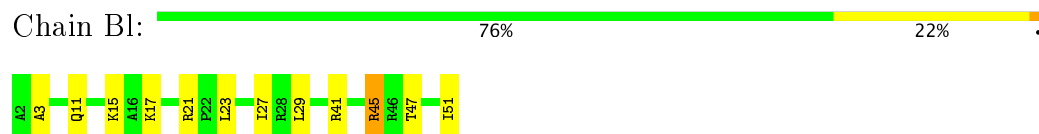
- Molecule 70: 60S RIBOSOMAL PROTEIN L37-A



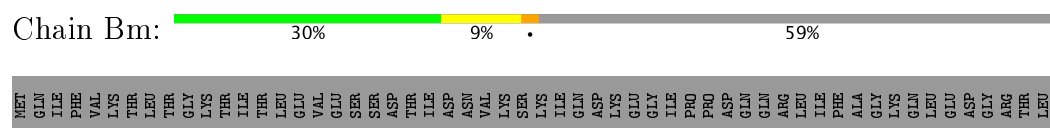
- Molecule 71: 60S RIBOSOMAL PROTEIN L38



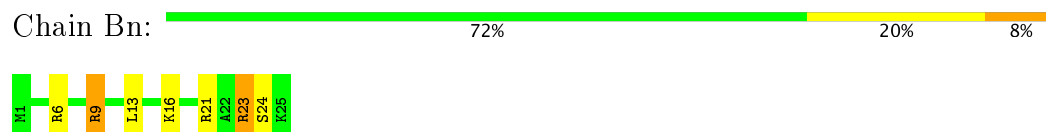
- Molecule 72: 60S RIBOSOMAL PROTEIN L39




- Molecule 73: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

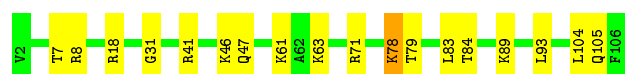


- Molecule 74: 60S RIBOSOMAL PROTEIN L41-B




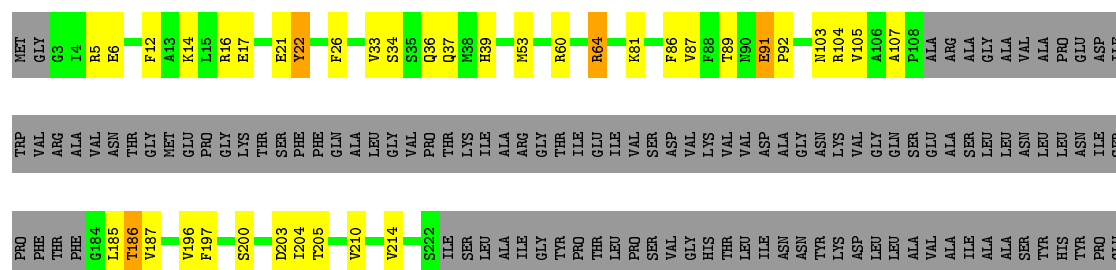
- Molecule 75: 60S RIBOSOMAL PROTEIN L42-A

Chain Bo:  83% 16% .



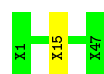
- Molecule 76: 60S ACIDIC RIBOSOMAL PROTEIN P0

Chain Bq:  34% 11% . 54%



- Molecule 77: 60S ACIDIC RIBOSOMAL PROTEIN P1

Chain Br:  98% .



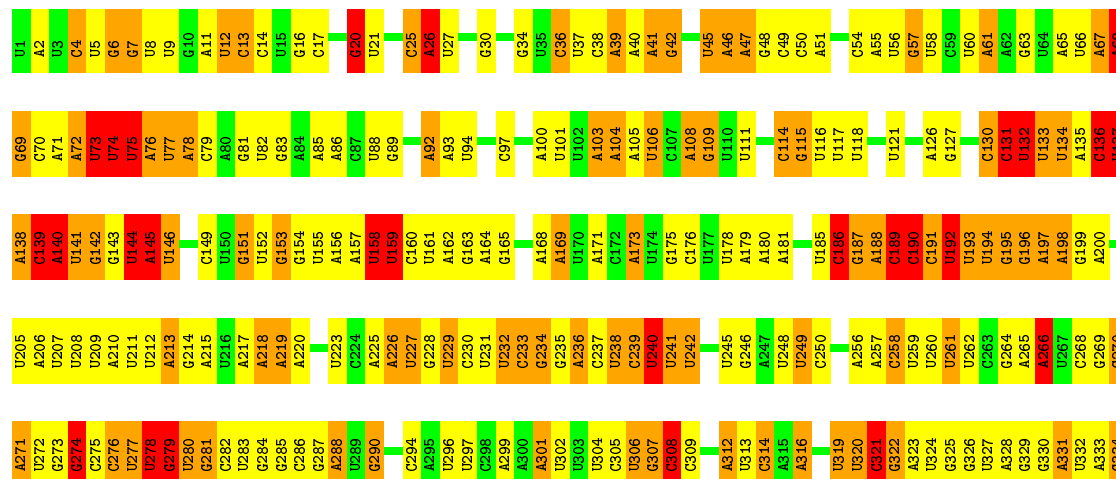
- Molecule 78: 60S ACIDIC RIBOSOMAL PROTEIN P2

Chain Bs:  100%

There are no outlier residues recorded for this chain.


- Molecule 79: 18S RIBOSOMAL RNA

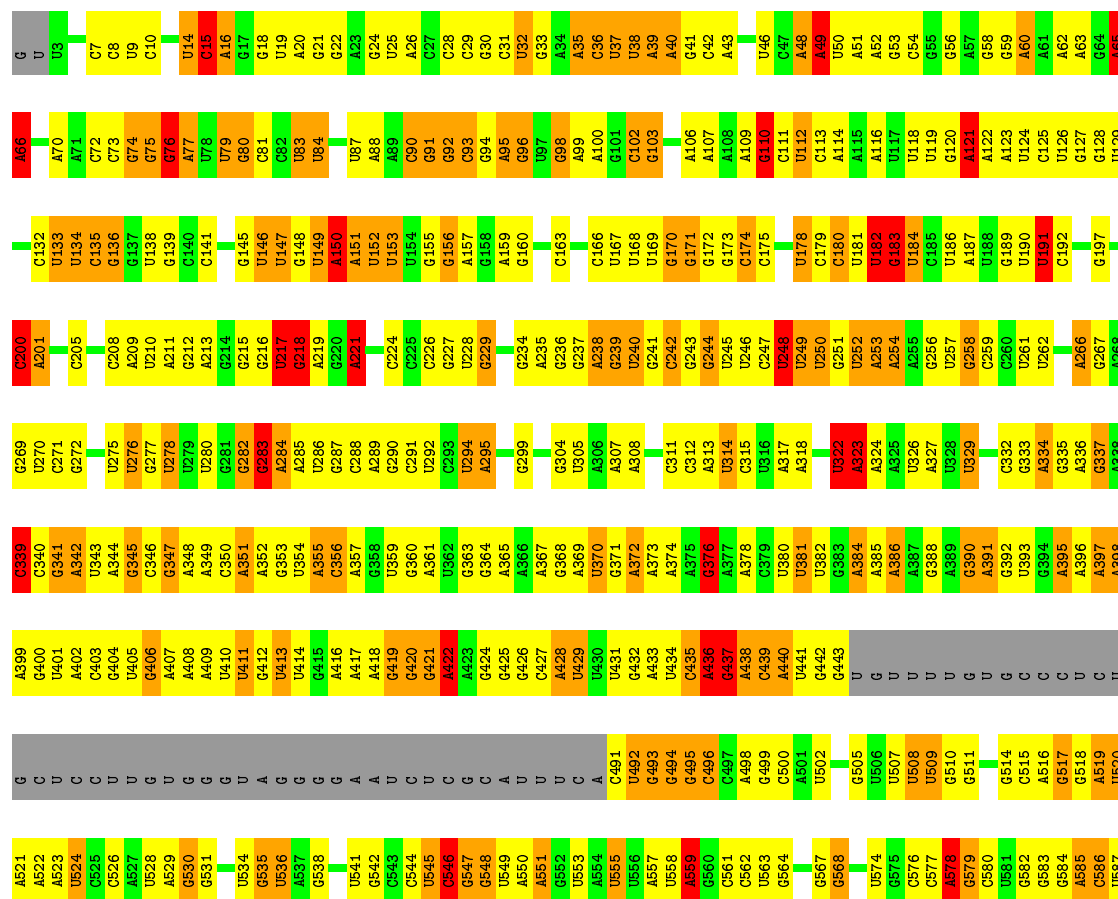
Chain B2:  26% 40% 26% 7% .



G1352	U1286	G1149	G1074	A1005	U935	G867	A803	G738	G676	U609	A541	A477	C409	U335
U1353	A1287	G1150	C1075	C1006	G936	G868	A804	G739	G677	G610	A542	A478	A410	G336
C1355	G1008	A1151	U1079	C1007	C937	A869	U805	A678	A678	U611	C543	C579	A411	C337
U1356	U1290	A1152	U1081	U1009	G938	G871	G810	C741	U680	U612	A544	G480	A412	C338
A1357	G1291	G1153	U1082	G1010	G942	G872	A811	U742	U681	G613	A545	C484	U414	C339
G1358	A1219	G1155	C1082	G1011	C943	U873	A812	U743	G682	G614	U546	A485	U415	U340
C1359	G1289	C1156	A1084	U1012	A944	C874	U813	U744	C683	A615	U547	A416	A416	A341
U1360	U1294	A1157	G1085	A1013	U945	G875	A814	U745	A684	U616	G548	G487	A417	C342
U1361	U1221	C1158	G1086	G1014	U946	G876	G815	C747	A685	A619	G553	G488	G418	C343
G1362	U1225	C1159	A1086	U1015	U947	G877	G816	C748	C686	A620	C554	C489	G419	A344
U1363	A1226	A1160	U1016	G1016	G948	G878	A817	U749	G687	A621	A555	C490	A421	U345
G1364	A1227	C1161	U1017	U1017	C949	G879	A818	U750	G688	A622	A556	C491	A422	U348
C1365	G1228	C1162	U1018	U1018	C950	G881	C818	U751	U689	A623	G557	A492	G422	U349
U1366	A1229	A1163	U1019	A1019	A951	U882	G819	A753	C692	G624	U558	U493	G423	U350
G1367	G1230	G1164	A1020	A1020	U958	G884	U820	A754	U693	G625	C559	U494	C424	C351
U1368	U1231	G1165	A1021	C1021	U959	U886	U821	A755	U694	U626	U560	G495	A425	A352
G1369	U1232	A1166	U1024	U1024	U960	A877	U822	A756	U695	G627	G561	G496	A426	U358
U1370	G1233	G1167	C1086	U1025	U961	U888	G823	A757	C696	U628	G562	G497	G427	C361
A1371	U1234	U1168	U1087	A1026	U964	A892	G824	U758	C697	U629	U563	G498	A428	G356
U1372	C1285	G1169	U1088	A1027	U965	U893	C827	U759	U698	A630	G564	U499	G429	G357
U1373	A1236	U1170	U1089	C1028	U966	U894	U828	A760	U699	U633	C565	U500	G430	U359
A1374	G1237	A1171	G1100	A1029	A966	G895	A829	G763	C700	U634	C566	C501	G431	A359
U1375	A1238	G1172	G1101	U1029	A967	G896	U830	U764	U701	G635	A567	U502	G432	A360
U1376	U1241	C1173	U1102	A1030	U968	C897	U831	G765	G702	A636	G568	G503	C433	C361
G1377	A1242	C1174	U1103	U1031	U969	C898	U832	U766	C703	U637	C569	U504	G434	G372
U1378	G1243	U1178	U1104	G1032	C969	A898	U833	U767	C704	U638	A570	A505	C435	G373
C1379	A1244	G1179	C1105	C1034	A970	G999	U834	C768	U705	U639	C572	A506	A436	A378
A1380	U1245	U1180	G1111	U1037	A971	G901	U835	A769	A706	U640	G575	U507	A437	G377
G1381	G1246	C1181	U1112	G1038	A972	G902	G837	A770	C708	U641	C576	U508	U438	A378
U1382	U1247	U1182	A1113	U1039	A973	G903	G838	A771	C709	G647	G577	G509	U439	U379
A1383	C1248	A1183	G1114	A1040	C975	A905	U839	G772	U710	U648	U578	G510	U440	U380
G1384	U1249	U1184	U1115	G1041	A976	A906	U840	C773	U711	U649	A579	U513	C443	C381
C1385	G1250	A1185	U1116	A1042	A977	U909	U841	A774	G712	U650	G580	U514	C444	C382
U1386	U1251	U1186	G1117	G1043	A978	C910	U842	G775	A713	G651	A581	A515	A445	G383
A1387	C1252	U1187	U1118	A1044	A979	C911	U843	G776	G714	G652	U582	A516	A446	G384
G1388	U1253	U1188	U1119	U1049	G980	U911	U844	C777	U715	C653	U583	U517	U447	A385
U1389	U1254	A1189	C1121	U1050	U981	U912	G845	G778	C716	C654	C584	A518	C448	G386
C1390	G1255	U1190	U1122	G1051	U982	U913	G846	U779	C717	G655	C594	A519	C449	A387
G1391	A1256	U1191	G1127	U1052	A983	C914	A847	A780	U718	U656	A585	C519	U450	G388
U1392	C1257	C1192	U1128	U1053	G984	A915	C848	U781	U719	U657	G586	A520	A451	G389
C1393	U1258	A1193	U1129	G1053	G987	U916	C849	U782	G720	C658	C590	U521	A452	G390
U1394	U1259	U1194	U1130	U1057	U987	U917	U850	G783	U721	C	G	U522	U453	A391
G1395	U1260	C1195	A1131	U1058	A988	U918	U851	C784	G722	G	A	G523	U458	G392
C1396	G1267	A1196	U1132	U1059	U989	A919	C852	U785	C723	A	U	U524	G458	C393
A1401	G1268	C1197	U1133	U1060	U990	U920	G853	C786	G724	U	U	A525	G459	C394
G1402	U1269	G1198	C1134	U1061	C991	U921	U854	G787	U725	U	U	A526	A460	A401
C1403	G1270	U1199	A1061	A1062	A992	A855	A855	G788	C726	U	U	A527	G461	C402
U1404	U1271	G1200	A1063	U1063	A993	U856	A856	A789	U727	U	U	U528	A397	G403
G1405	C1274	A1201	U1064	U1064	G994	A924	U857	U790	U728	U	U	A529	G467	G396
U1406	A1275	A1202	A1139	U1065	A995	A925	G858	U793	G729	U	U	U532	A468	A399
G1407	U1276	U1203	A1142	A1066	U996	C927	A859	U794	C730	C	U	U533	C469	A400
A1408	G1277	U1206	A1143	C1066	G997	U928	U860	U795	C731	U	U	A534	A470	A401
U1409	U1278	U1207	U1144	C1067	C1000	A929	U861	A796	G732	U	U	A535	A471	C402
A1410	G1279	A1208	U1145	C1070	A1001	C931	A862	U797	G733	G	U	A473	A472	G403
U1411	C1279	A1208	U1146	U1071	A1002	C932	A863	U800	A734	U	U	A538	A473	G404
G1412	G1280	C1209	G1146	U1072	G1003	U933	U864	G801	C735	A	U	A539	A474	A407
U1413	U1281	C1072	A1147	A1003	A1003	A933	A865	G802	C736	C	U	G540	A475	C408
A1414	G1351	U1282	C1148	G1073	U1004	C934	G866		A737	U	U		U476	



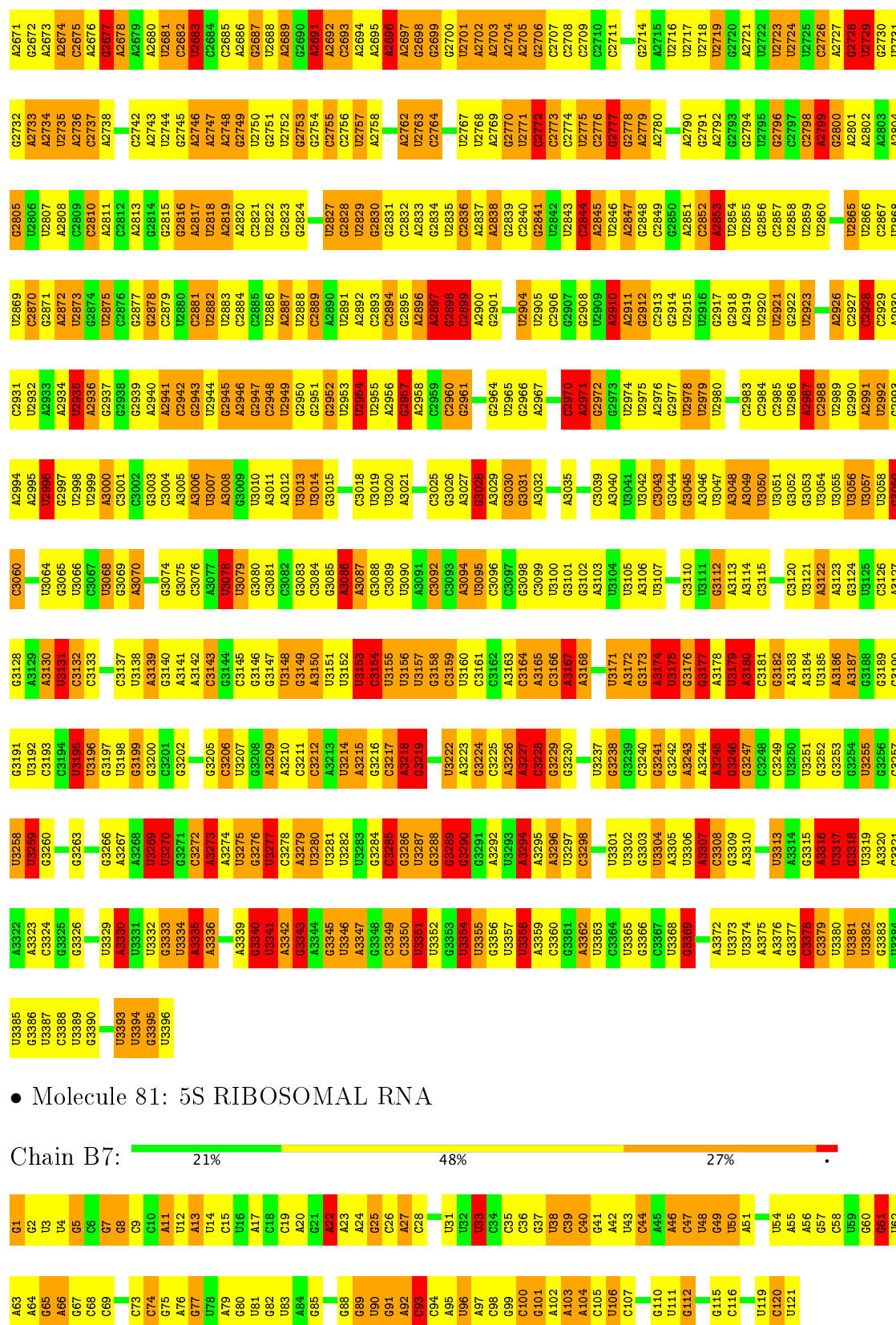
Chain B5: 



G1565	U1494	G1429	G1365	U1305	A1244	U1181	U1121	A1048	G984	U922	G860	G795	A720	G652	G588
A1566	U1495	U1430	A1366	G1306	A1245	A1182	U1122	C1049	U985	C923	C861	U796	G721	A652	A589
U1567	U1496	G1431	G1367	G1307	G1246	C1183	U1123	U1050	U986	G924	U862	U797	G722	C654	G590
U1568	C1497	U1432	U1368	A1308	U1247	A1184	U1124		U987	A925	C863	G798		C595	G591
U1569	A1499	A1433	A1369	G1309	G1248		U1125	A1054		A926	G864	G799	G725	A656	A592
U1570	G1500	G1434	G1370	G1310	G1249	C1187	U1126	A1055	U990	C927	U865	G800	G726	A657	C593
A1571		G1371	G1372	G1311	G1250	U1188	G1127	U1056	G991	C928	A866	A801	G727	G658	U984
U1572	U1501	C1437	A1373	C1312	A1251	U1189	U1128	A1057	A992	A929		C802	G728	G659	U984
U1573	U1502	U1438	G1379	G1313	A1252	C1190	U1129		G993	U930	C867	C803	G729	A660	C599
C1574	A1503	U1439	G1374	C1314	U1253	A1191	A1130	U1060	G994	G931		G805	U731	G661	G600
A1575	A1504	G1440	G1375	G1315	G1254	C1192	G1131	A1061	U995	U932	U871	C804	U730	U662	A600
G1576	A1505	G1441	C1376	G1316	G1255	A1193	C1132	A1062	A996	A933	U872	A806	C732	C663	U601
G1577	A1506	G1442	G1377	A1317	G1256	G1194	G1133	G1063	A997	A934	C873	A807	G733	U664	
C1578	G1507	G1443	U1378	A1318	C1257	A1195	G1134	A1064	A998	U935	U874	A808	C734	A665	G604
C1579	U1508	U1444	U1379	G1319	U1258	C1196	A1135	A1065	G999	A936	G875	G809	A735	A666	A607
A1580	U1509	G1445	G1380	C1320	A1259	A1197	A1136		C1000	G937	A876	A810	A736	C667	A608
C1581	G1510	A1446	A1381	G1321	G1260	C1198	C1137	U1070	G1001	C938	C877	U811	G737	G668	G609
C1582	U1511	G1447	G1382	G1322	G1261	C1199	U1138	U1071	A1002	U939	G878	G812		U669	
A1583	U1512	U1448	G1383	G1323	G1262	A1200	G1139	G1072	A1003	G940	U879	G813	U743	G670	G610
	U1513	U1449	U1384	U1324	A1263	C1201	G1140	U1073	U1004	G941	G880	U814	G742	U671	A611
G1586	G1514	G1450	U1385	U1325	G1264	A1202	C1141			U942	C881	U815	G743	A612	
A1587	C1515	C1451	A1386	A1326	U1265	A1203	G1142	U1077	U1007	U943	A882	G816	A744	U673	G613
A1588	G1516		G1387	C1327	G1266	A1204	A1143	U1078	U1008	C944	A883	C817	C745	G674	G614
A1589	G1517	A1454	U1388	G1328	U1267	A1205	U1144	A1079	A1009	C945	A884	C818		C675	U615
G1590	U1518	U1455	G1389	U1329	G1268	G1206	G1145	A1080	G1010	U946		U819	U748	G676	G616
G1591		A1456	A1390	A1330	U1269	G1207	C1146	U1081	A1011	C947	G887	A820	C749	A677	G617
G1592	U1523	U1457	C1391	U1331	A1270	U1208	G1147	U1082	C948	C948	A888	U821	G750	G678	C618
A1593	A1524	U1458	G1392	A1332	A1271	G1209	G1148	G1083	U889	C949	U889	G822	A751	U679	A619
A1594	G1525	A1459	C1393	C1333	C1272	U1210	G1149	A1084	C990	G950	A883	C823	C752	G680	G620
U1595	U1526	A1460	C1394	U1334	A1273	U1211	A1150	A1085	G891	C824	C753	C824	C753	U681	A621
G1596	G1527	A1461	C1395	C1335	A1274	U1151	U1151	C1086	U892	U825		U825	G754	U682	A622
C1597	G1528	U1462	A1399	U1336	C1275	G1213	C1152	C1087	U954	U954	C893	A828	A755	U623	
	U1529	U1463	A1400	A1337	U1276	U1214	C1153		U955	U955	G894	A828		G624	
U1601	A1534	G1464	A1401	C1338	C1277	U1215	A1154	A1093	G1019	U956	A895	U829	C758	G688	G625
A1602		A1465	C1402	C1339	A1278	C1216	C1155	U1094	G1020	C957	A896	U830	U759	U689	U626
A1603	G1538	G1466	G1403	G1340	C1279		C1156	U1095	G1021	C958	U897	G831	G760	A690	U627
G1604		A1467	C1404	U1341	G1280	U1220	G1157	U1096	U1022	C959	U898	G832		A691	A628
A1605		U1468	U1405	C1342	G1281	A1221	A1158	G1097	C1023	U960	U899	G833	C765	A692	U629
U1606	G1541	C1469	A1406	A1343	C1282	G	A1159	A1098	G1024	C961	G900	U834	C766	A693	U630
U1607	G1542	U1470	U1407	G1344	C1283	A	C1160	A1099	A1025	A962	G901	U835	U767	C694	A631
C1608	G1543	U1471	G1408	G1345	G1284	C	G1161	U1100	A1026	G963	G902	G835	C768	C695	G632
C1609	G1544	U1472	G1409	G1346	G1285	A1225	U1162	G1101	A1027	G964	U903		C769	C696	C633
G1610	A1545	G1473	U1410	U1347	A1286	G1226	A1163	A1102	U1028	A965	A904	C839	G769	C634	
	U1546		C1411	U1348	A1287	C1227	G1164	A1103	G1029	U966	U905	C840		C635	
C1614	G1547	G1476	G1412	G1349	U1288	C1228	A1165	G1104		A967	A906	A841	U776	G701	G636
C1615	U1548	A1477	G1413	A1350	G1289				C1032	G968	G907	G842	U777	C702	
U1616			G1414	U1351		G1229	U1166		U1033	C969	A843	G842	U778	G703	C637
		G1480	U1415	A1352	C1292	G1230	U1167	C1107	U1034	A970	G908	G844	U779	U704	G638
U1620	U1553	A1481	G1416	U1353	U1293	A1231	U1168	U1108	U1035	G971	G909	G845	A780	A705	G639
A1621	U1554	A1482	G1417	G1354	A1294	G1232	A1169	U1109	G1036	G972	G910	A846	A781	A706	U640
U1622	U1555	G1483	A1418	A1355	G1295	G1233	A1170	U1110	A1036	A973	G911	A847	U782	U707	C641
G1623	C1556	U1484	U1419	U1356	C1296	G1234	G1171	U1111	C1037		G912	A848	A783	G708	U642
	U1557	G1485	C1420	G1357	U1297	U1235	G1172	A1112		G974	A913	A849	A784	A709	U643
C1628	A1558	G1486	G1421	C1358	C1298	G1236	U1173	G1113	A1040	C975	A914		G785	A710	G644
U1629	U1559	G1487	G1422	C1359	U1299	G1237	U1174	U1114	U1041	U976	A915	C851	A786	A645	
U1630	G1560		C1360	G1360	G1300	G1238	G1175	G1115	U1042		G916	U852	G787	G712	A646
C1631	G1561	A1490	U1425	U1361	A1301	C1239	C1176	G1116	C1043	U979	A917		C788	A647	
C1632	U1562	A1491	U1426	A1362	A1302	A1240	G1177	G1117	U1044	A980	G918	G856	A715	C648	
C1633	U1563	G1492	U1427	A1363	A1303	U1241	G1178	C1118	C1045	U981	U919	G857	A716	A649	
G1634	U1564				A1304	G1242	A1179	C1119	A1046	C982	A920	A858	C792	G650	
						G1243	A1180	A1120	A1047	A983	A921	G859	U794	G651	







## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	5143	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	EACH PARTICLE	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	16	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	3900	Depositor
Magnification	79096	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	A0	0.54	0/782	0.77	0/1047
10	AB	0.45	0/1735	0.81	0/2335
11	AC	0.60	0/1665	0.77	0/2263
12	AD	0.59	0/1759	0.74	0/2368
13	AE	0.57	0/2109	0.86	1/2839 (0.0%)
14	AF	0.49	0/1629	0.72	0/2202
15	AG	0.55	0/1823	0.75	0/2439
16	AH	0.52	0/1506	0.77	0/2028
17	AI	0.68	0/1514	0.89	3/2021 (0.1%)
18	AJ	0.59	0/1519	0.81	0/2035
19	AK	0.55	0/789	0.83	3/1067 (0.3%)
2	A1	0.53	0/620	0.81	1/838 (0.1%)
20	AL	0.70	0/1239	0.81	0/1673
21	AM	0.49	0/898	0.76	0/1220
22	AN	0.61	0/1215	0.83	3/1638 (0.2%)
23	AO	0.48	0/901	0.82	1/1217 (0.1%)
24	AP	0.60	0/998	0.86	3/1341 (0.2%)
25	AQ	0.56	0/1125	0.85	3/1510 (0.2%)
26	AR	0.54	0/935	0.81	0/1254
27	AS	0.59	0/1211	0.80	0/1628
28	AT	0.57	0/1130	0.81	0/1517
29	AU	0.55	0/865	0.76	0/1169
3	A2	0.43	0/499	0.72	0/670
30	AV	0.52	0/693	0.75	0/935
31	AW	0.65	0/1038	0.86	3/1395 (0.2%)
32	AX	0.72	0/1139	0.91	2/1518 (0.1%)
33	AY	0.56	0/1087	0.77	1/1449 (0.1%)
34	AZ	0.50	0/571	0.85	1/768 (0.1%)
35	BA	0.87	1/1946 (0.1%)	1.05	4/2614 (0.2%)
36	BB	1.02	4/3146 (0.1%)	1.11	13/4228 (0.3%)
37	BC	0.87	0/2800	1.07	11/3790 (0.3%)
38	BD	0.89	1/2408 (0.0%)	0.96	3/3248 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	BE	0.90	1/1269 (0.1%)	1.00	3/1705 (0.2%)
4	A3	0.70	0/452	0.94	1/600 (0.2%)
40	BF	0.99	1/1828 (0.1%)	1.04	6/2461 (0.2%)
41	BG	0.64	0/1795	0.81	1/2429 (0.0%)
42	BH	0.97	2/1539 (0.1%)	1.01	1/2073 (0.0%)
43	BI	0.92	1/1758 (0.1%)	1.08	12/2358 (0.5%)
44	BJ	0.81	1/1374 (0.1%)	0.99	4/1842 (0.2%)
46	BL	0.82	0/1573	1.04	6/2113 (0.3%)
47	BM	0.96	0/1074	1.01	4/1446 (0.3%)
48	BN	0.83	1/1757 (0.1%)	1.00	6/2354 (0.3%)
49	BO	0.98	11/3159 (0.3%)	1.02	25/4205 (0.6%)
5	A4	0.50	0/483	0.71	0/643
50	BP	1.05	1/1250 (0.1%)	1.09	5/1683 (0.3%)
51	BQ	0.89	1/1465 (0.1%)	1.12	9/1965 (0.5%)
52	BR	0.78	1/1538 (0.1%)	0.87	2/2050 (0.1%)
53	BS	1.02	0/1481	1.09	7/1990 (0.4%)
54	BT	1.01	2/1300 (0.2%)	1.01	1/1743 (0.1%)
55	BU	0.56	0/794	0.77	0/1076
56	BV	0.98	0/1018	1.09	4/1369 (0.3%)
57	BW	0.80	0/1052	0.90	2/1398 (0.1%)
58	BX	0.72	0/974	0.86	0/1314
59	BY	0.79	1/1004 (0.1%)	0.98	2/1341 (0.1%)
6	A5	0.53	0/404	0.99	1/542 (0.2%)
60	BZ	0.55	0/1118	0.83	2/1497 (0.1%)
61	Ba	0.95	2/1204 (0.2%)	1.14	9/1612 (0.6%)
62	Bb	0.91	0/473	1.14	1/629 (0.2%)
63	Bc	0.61	0/775	0.77	0/1040
64	Bd	0.94	2/897 (0.2%)	0.95	1/1205 (0.1%)
65	Be	1.03	0/1041	1.27	12/1394 (0.9%)
66	Bf	1.12	0/868	1.09	3/1168 (0.3%)
67	Bg	0.72	0/890	0.92	0/1189
68	Bh	0.67	0/974	0.80	0/1297
69	Bi	0.67	0/777	0.85	0/1033
7	A6	0.49	0/2490	0.70	0/3389
70	Bj	0.87	0/696	1.04	3/923 (0.3%)
71	Bk	0.50	0/614	0.70	0/822
72	Bl	0.90	0/443	1.02	1/588 (0.2%)
73	Bm	1.08	2/423 (0.5%)	1.13	1/562 (0.2%)
74	Bn	0.90	0/234	1.15	1/300 (0.3%)
75	Bo	0.83	0/860	0.89	1/1136 (0.1%)
76	Bq	1.09	0/1090	1.31	4/1474 (0.3%)
79	B2	0.92	33/42128 (0.1%)	1.49	828/65642 (1.3%)
8	A7	0.86	2/925 (0.2%)	0.87	2/1240 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
80	B5	1.49	661/75336 (0.9%)	1.92	3722/117449 (3.2%)
81	B7	1.38	12/2883 (0.4%)	1.80	119/4491 (2.6%)
82	B8	1.16	4/3746 (0.1%)	1.70	128/5832 (2.2%)
83	CV	1.87	8/4407 (0.2%)	1.47	47/5931 (0.8%)
84	CW	2.08	51/1801 (2.8%)	3.23	250/2803 (8.9%)
85	CX	2.12	4/69 (5.8%)	3.20	11/106 (10.4%)
9	AA	0.54	0/1617	0.80	0/2215
All	All	1.14	811/222414 (0.4%)	1.53	5304/325931 (1.6%)

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
10	AB	0	1
16	AH	0	1
2	A1	0	1
20	AL	0	1
23	AO	0	1
26	AR	0	2
34	AZ	0	3
35	BA	0	2
37	BC	0	1
38	BD	0	1
39	BE	0	1
40	BF	0	2
49	BO	0	2
53	BS	0	1
56	BV	0	1
59	BY	0	1
6	A5	0	2
60	BZ	0	1
61	Ba	0	3
62	Bb	0	1
76	Bq	0	7
77	Br	0	1
8	A7	0	1
80	B5	0	35
83	CV	0	18
84	CW	0	32
85	CX	0	2
All	All	0	125

The worst 5 of 811 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	CV	63	GLU	N-CA	69.03	2.84	1.46
83	CV	210	TRP	CD2-CE3	34.76	1.92	1.40
83	CV	210	TRP	CD2-CE2	33.01	1.80	1.41
83	CV	210	TRP	CE2-CZ2	31.95	1.94	1.39
83	CV	210	TRP	CE3-CZ3	26.33	1.83	1.38

The worst 5 of 5304 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	CW	36	U	P-O3'-C3'	-59.91	47.81	119.70
80	B5	1152	G	N3-C4-C5	33.59	145.40	128.60
80	B5	1256	G	P-O3'-C3'	32.78	159.04	119.70
80	B5	1152	G	N3-C4-N9	-31.65	107.01	126.00
80	B5	1152	G	N3-C2-N2	-26.89	101.08	119.90

There are no chirality outliers.

5 of 125 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A1	42	ASN	Peptide
6	A5	105	TYR	Peptide
6	A5	138	ARG	Peptide
8	A7	134	ASP	Sidechain
10	AB	131	ASP	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A0	769	0	814	117	0
2	A1	610	0	630	53	0
3	A2	497	0	535	32	0
4	A3	442	0	428	57	0
5	A4	475	0	525	21	0
6	A5	516	0	517	41	0
7	A6	2437	0	2386	84	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A7	1105	0	933	449	0
9	AA	1577	0	1567	101	0
10	AB	1709	0	1784	197	0
11	AC	1635	0	1723	80	0
12	AD	1734	0	1817	121	0
13	AE	2068	0	2154	95	0
14	AF	1609	0	1675	114	0
15	AG	1799	0	1874	441	0
16	AH	1481	0	1572	83	0
17	AI	1489	0	1523	192	0
18	AJ	1494	0	1573	96	0
19	AK	772	0	727	45	0
20	AL	1213	0	1257	107	0
21	AM	890	0	887	48	0
22	AN	1192	0	1252	62	0
23	AO	891	0	880	295	0
24	AP	977	0	1002	76	0
25	AQ	1105	0	1164	144	0
26	AR	926	0	930	134	0
27	AS	1192	0	1220	112	0
28	AT	1112	0	1123	107	0
29	AU	855	0	917	117	0
30	AV	684	0	672	42	0
31	AW	1021	0	1060	70	0
32	AX	1121	0	1195	88	0
33	AY	1073	0	1132	113	0
34	AZ	563	0	602	52	0
35	BA	1912	0	1973	290	0
36	BB	3075	0	3142	147	0
37	BC	2748	0	2859	139	0
38	BD	2359	0	2311	266	0
39	BE	1248	0	1339	38	0
40	BF	1791	0	1869	56	0
41	BG	1763	0	1819	154	0
42	BH	1518	0	1587	82	0
43	BI	1722	0	1754	130	0
44	BJ	1353	0	1380	125	0
45	BK	753	756	195	2	0
46	BL	1548	0	1613	90	0
47	BM	1059	0	1154	51	0
48	BN	1720	0	1779	136	0
49	BO	3119	0	3302	97	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	BP	1227	0	1236	41	0
51	BQ	1441	0	1543	68	0
52	BR	1521	0	1605	197	0
53	BS	1445	0	1487	63	0
54	BT	1276	0	1323	137	0
55	BU	778	0	791	23	0
56	BV	1003	0	1048	49	0
57	BW	1038	0	1071	43	0
58	BX	959	0	1023	37	0
59	BY	993	0	1081	44	0
60	BZ	1092	0	1154	111	0
61	Ba	1173	0	1215	0	0
62	Bb	462	0	491	0	0
63	Bc	767	0	816	0	0
64	Bd	883	0	918	0	0
65	Be	1020	0	1090	0	0
66	Bf	850	0	880	0	0
67	Bg	880	0	944	0	0
68	Bh	965	0	1067	0	0
69	Bi	770	0	846	0	0
70	Bj	681	0	683	0	0
71	Bk	608	0	671	0	0
72	Bl	436	0	475	0	0
73	Bm	417	0	455	0	0
74	Bn	233	0	271	0	0
75	Bo	847	0	918	0	0
76	Bq	1075	1110	1021	0	0
77	Br	236	237	65	0	0
78	Bs	231	232	67	0	0
79	B2	37835	0	19045	3138	0
80	B5	67308	664	33785	2411	0
81	B7	2579	0	1303	190	0
82	B8	3353	0	1695	115	0
83	CV	4451	4585	4534	558	0
84	CW	1614	789	802	457	0
85	CX	62	34	34	35	0
86	A0	1	0	0	0	0
86	A1	1	0	0	0	0
86	A3	1	0	0	0	0
86	A5	1	0	0	0	0
86	Bj	1	0	0	0	0
86	Bm	1	0	0	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	A0	2	0	0	0	0
87	A3	3	0	0	0	0
87	A5	1	0	0	0	0
87	AB	1	0	0	0	0
87	AC	2	0	0	0	0
87	AE	1	0	0	0	0
87	AG	1	0	0	0	0
87	AI	1	0	0	0	0
87	AJ	1	0	0	0	0
87	AL	2	0	0	0	0
87	AN	1	0	0	0	0
87	AP	1	0	0	0	0
87	AS	1	0	0	0	0
87	AU	1	0	0	0	0
87	B2	168	0	0	0	0
87	B5	3	0	0	0	0
87	B7	27	0	0	0	0
87	BD	4	0	0	0	0
87	BF	1	0	0	0	0
87	BS	3	0	0	0	0
87	CW	1	0	0	0	0
88	A3	7	0	0	4	0
88	A6	7	0	0	2	0
88	AC	7	0	0	5	0
88	AI	14	0	0	2	0
88	AL	7	0	0	8	0
88	AN	7	0	0	2	0
88	AP	7	0	0	3	0
88	B2	1274	0	0	231	0
88	B5	21	0	0	4	0
88	B7	91	0	0	9	0
88	BR	7	0	0	9	0
88	Bn	7	0	0	0	0
88	CV	7	0	0	10	0
88	CX	7	0	0	2	0
89	CV	32	0	7	63	0
All	All	210964	8407	155586	9058	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 27.

The worst 5 of 9058 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
80:B5:2621:G:C8	84:CW:75:C:C5	1.76	1.69
8:A7:85:SER:HB2	84:CW:30:G:C8	1.24	1.66
15:AG:175:ILE:HG12	79:B2:78:A:C4	1.29	1.65
83:CV:210:TRP:CZ3	83:CV:210:TRP:CH2	1.78	1.63
83:CV:210:TRP:CE3	83:CV:210:TRP:CZ3	1.83	1.61

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A0	95/119 (80%)	57 (60%)	21 (22%)	17 (18%)	0	3
2	A1	79/82 (96%)	62 (78%)	13 (16%)	4 (5%)	2	26
3	A2	61/67 (91%)	47 (77%)	9 (15%)	5 (8%)	1	16
4	A3	51/56 (91%)	43 (84%)	6 (12%)	2 (4%)	3	31
5	A4	58/63 (92%)	49 (84%)	7 (12%)	2 (3%)	4	35
6	A5	50/152 (33%)	30 (60%)	9 (18%)	11 (22%)	0	2
7	A6	316/319 (99%)	273 (86%)	30 (10%)	13 (4%)	3	30
8	A7	120/273 (44%)	92 (77%)	17 (14%)	11 (9%)	1	15
9	AA	204/252 (81%)	143 (70%)	35 (17%)	26 (13%)	0	7
10	AB	212/255 (83%)	132 (62%)	42 (20%)	38 (18%)	0	3
11	AC	215/254 (85%)	187 (87%)	16 (7%)	12 (6%)	2	24
12	AD	221/240 (92%)	180 (81%)	27 (12%)	14 (6%)	1	22
13	AE	258/261 (99%)	201 (78%)	36 (14%)	21 (8%)	1	16
14	AF	204/225 (91%)	155 (76%)	30 (15%)	19 (9%)	1	14
15	AG	224/236 (95%)	190 (85%)	23 (10%)	11 (5%)	2	27
16	AH	182/190 (96%)	128 (70%)	27 (15%)	27 (15%)	0	5

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	AI	184/200 (92%)	155 (84%)	14 (8%)	15 (8%)	1	16
18	AJ	183/197 (93%)	153 (84%)	18 (10%)	12 (7%)	1	21
19	AK	94/105 (90%)	66 (70%)	18 (19%)	10 (11%)	0	10
20	AL	153/156 (98%)	125 (82%)	19 (12%)	9 (6%)	2	23
21	AM	122/143 (85%)	66 (54%)	23 (19%)	33 (27%)	0	1
22	AN	148/151 (98%)	125 (84%)	15 (10%)	8 (5%)	2	25
23	AO	125/137 (91%)	94 (75%)	16 (13%)	15 (12%)	0	7
24	AP	122/142 (86%)	92 (75%)	15 (12%)	15 (12%)	0	7
25	AQ	139/143 (97%)	114 (82%)	14 (10%)	11 (8%)	1	17
26	AR	116/136 (85%)	87 (75%)	17 (15%)	12 (10%)	0	11
27	AS	143/146 (98%)	110 (77%)	19 (13%)	14 (10%)	1	13
28	AT	141/144 (98%)	111 (79%)	18 (13%)	12 (8%)	1	15
29	AU	105/121 (87%)	87 (83%)	13 (12%)	5 (5%)	2	27
30	AV	85/87 (98%)	64 (75%)	11 (13%)	10 (12%)	0	7
31	AW	127/130 (98%)	114 (90%)	10 (8%)	3 (2%)	7	42
32	AX	142/145 (98%)	111 (78%)	13 (9%)	18 (13%)	0	7
33	AY	132/135 (98%)	106 (80%)	13 (10%)	13 (10%)	1	13
34	AZ	68/108 (63%)	46 (68%)	11 (16%)	11 (16%)	0	4
35	BA	250/253 (99%)	213 (85%)	30 (12%)	7 (3%)	6	39
36	BB	384/386 (100%)	341 (89%)	34 (9%)	9 (2%)	7	43
37	BC	359/361 (99%)	306 (85%)	32 (9%)	21 (6%)	2	24
38	BD	292/296 (99%)	267 (91%)	19 (6%)	6 (2%)	8	45
39	BE	153/175 (87%)	134 (88%)	15 (10%)	4 (3%)	6	40
40	BF	221/243 (91%)	201 (91%)	16 (7%)	4 (2%)	10	49
41	BG	229/255 (90%)	180 (79%)	28 (12%)	21 (9%)	1	15
42	BH	189/191 (99%)	172 (91%)	13 (7%)	4 (2%)	8	45
43	BI	209/220 (95%)	175 (84%)	22 (10%)	12 (6%)	2	24
44	BJ	167/173 (96%)	135 (81%)	19 (11%)	13 (8%)	1	17
46	BL	192/198 (97%)	161 (84%)	20 (10%)	11 (6%)	2	24
47	BM	135/137 (98%)	124 (92%)	10 (7%)	1 (1%)	25	68
48	BN	201/203 (99%)	182 (90%)	13 (6%)	6 (3%)	5	37

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	BO	352/218 (162%)	324 (92%)	18 (5%)	10 (3%)	6	39
50	BP	153/183 (84%)	142 (93%)	9 (6%)	2 (1%)	14	56
51	BQ	183/185 (99%)	168 (92%)	9 (5%)	6 (3%)	4	35
52	BR	186/188 (99%)	167 (90%)	16 (9%)	3 (2%)	11	51
53	BS	170/172 (99%)	163 (96%)	6 (4%)	1 (1%)	28	71
54	BT	157/159 (99%)	146 (93%)	9 (6%)	2 (1%)	14	56
55	BU	96/120 (80%)	80 (83%)	13 (14%)	3 (3%)	5	36
56	BV	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	12	53
57	BW	133/155 (86%)	106 (80%)	19 (14%)	8 (6%)	2	22
58	BX	118/141 (84%)	104 (88%)	6 (5%)	8 (7%)	1	20
59	BY	124/126 (98%)	107 (86%)	12 (10%)	5 (4%)	3	31
60	BZ	133/135 (98%)	107 (80%)	13 (10%)	13 (10%)	1	13
61	Ba	146/148 (99%)	123 (84%)	18 (12%)	5 (3%)	4	35
62	Bb	56/58 (97%)	44 (79%)	7 (12%)	5 (9%)	1	15
63	Bc	98/104 (94%)	87 (89%)	8 (8%)	3 (3%)	5	36
64	Bd	107/112 (96%)	88 (82%)	13 (12%)	6 (6%)	2	24
65	Be	125/129 (97%)	110 (88%)	9 (7%)	6 (5%)	2	27
66	Bf	104/106 (98%)	96 (92%)	5 (5%)	3 (3%)	5	38
67	Bg	110/120 (92%)	93 (84%)	13 (12%)	4 (4%)	4	33
68	Bh	117/119 (98%)	99 (85%)	14 (12%)	4 (3%)	4	35
69	Bi	97/99 (98%)	77 (79%)	13 (13%)	7 (7%)	1	19
70	Bj	85/87 (98%)	75 (88%)	8 (9%)	2 (2%)	7	42
71	Bk	75/77 (97%)	61 (81%)	10 (13%)	4 (5%)	2	25
72	Bl	48/50 (96%)	41 (85%)	6 (12%)	1 (2%)	8	45
73	Bm	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	9	46
74	Bn	23/25 (92%)	22 (96%)	0	1 (4%)	3	29
75	Bo	103/105 (98%)	90 (87%)	11 (11%)	2 (2%)	9	47
76	Bq	141/312 (45%)	105 (74%)	14 (10%)	22 (16%)	0	4
83	CV	555/586 (95%)	450 (81%)	61 (11%)	44 (8%)	1	17
All	All	11839/12944 (92%)	9833 (83%)	1245 (10%)	761 (6%)	3	22

5 of 761 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A0	19	LYS
1	A0	45	VAL
1	A0	46	GLU
1	A0	62	TYR
1	A0	65	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A0	83/101 (82%)	65 (78%)	18 (22%)	1	7
2	A1	70/71 (99%)	62 (89%)	8 (11%)	7	28
3	A2	56/60 (93%)	38 (68%)	18 (32%)	0	2
4	A3	47/49 (96%)	38 (81%)	9 (19%)	2	11
5	A4	51/54 (94%)	43 (84%)	8 (16%)	3	18
6	A5	43/116 (37%)	32 (74%)	11 (26%)	0	5
7	A6	259/262 (99%)	221 (85%)	38 (15%)	3	21
8	A7	97/195 (50%)	74 (76%)	23 (24%)	1	5
9	AA	164/210 (78%)	122 (74%)	42 (26%)	0	5
10	AB	191/224 (85%)	137 (72%)	54 (28%)	0	3
11	AC	176/205 (86%)	130 (74%)	46 (26%)	0	4
12	AD	182/195 (93%)	138 (76%)	44 (24%)	1	5
13	AE	221/222 (100%)	166 (75%)	55 (25%)	1	5
14	AF	173/191 (91%)	137 (79%)	36 (21%)	1	8
15	AG	188/201 (94%)	149 (79%)	39 (21%)	1	8
16	AH	165/170 (97%)	124 (75%)	41 (25%)	1	5
17	AI	150/161 (93%)	118 (79%)	32 (21%)	1	8
18	AJ	158/166 (95%)	117 (74%)	41 (26%)	0	4
19	AK	77/98 (79%)	58 (75%)	19 (25%)	1	5
20	AL	129/137 (94%)	105 (81%)	24 (19%)	2	11

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	AM	88/119 (74%)	55 (62%)	33 (38%)	0	1
22	AN	127/128 (99%)	91 (72%)	36 (28%)	0	3
23	AO	81/105 (77%)	57 (70%)	24 (30%)	0	3
24	AP	101/118 (86%)	82 (81%)	19 (19%)	2	11
25	AQ	117/119 (98%)	83 (71%)	34 (29%)	0	3
26	AR	94/124 (76%)	70 (74%)	24 (26%)	0	5
27	AS	128/129 (99%)	87 (68%)	41 (32%)	0	2
28	AT	115/116 (99%)	84 (73%)	31 (27%)	0	4
29	AU	100/114 (88%)	71 (71%)	29 (29%)	0	3
30	AV	74/74 (100%)	56 (76%)	18 (24%)	1	5
31	AW	110/111 (99%)	84 (76%)	26 (24%)	1	5
32	AX	119/120 (99%)	97 (82%)	22 (18%)	2	12
33	AY	112/113 (99%)	84 (75%)	28 (25%)	1	5
34	AZ	61/89 (68%)	43 (70%)	18 (30%)	0	3
35	BA	192/195 (98%)	153 (80%)	39 (20%)	1	9
36	BB	320/322 (99%)	250 (78%)	70 (22%)	1	7
37	BC	288/288 (100%)	223 (77%)	65 (23%)	1	7
38	BD	243/244 (100%)	196 (81%)	47 (19%)	1	10
39	BE	135/152 (89%)	115 (85%)	20 (15%)	3	20
40	BF	187/204 (92%)	158 (84%)	29 (16%)	3	19
41	BG	177/207 (86%)	138 (78%)	39 (22%)	1	7
42	BH	171/171 (100%)	132 (77%)	39 (23%)	1	6
43	BI	179/186 (96%)	142 (79%)	37 (21%)	1	8
44	BJ	147/149 (99%)	114 (78%)	33 (22%)	1	7
46	BL	154/158 (98%)	124 (80%)	30 (20%)	1	10
47	BM	108/108 (100%)	84 (78%)	24 (22%)	1	7
48	BN	175/175 (100%)	143 (82%)	32 (18%)	2	12
49	BO	323/178 (182%)	267 (83%)	56 (17%)	2	14
50	BP	125/145 (86%)	103 (82%)	22 (18%)	2	14
51	BQ	150/150 (100%)	123 (82%)	27 (18%)	2	13
52	BR	153/153 (100%)	121 (79%)	32 (21%)	1	8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	BS	156/156 (100%)	123 (79%)	33 (21%)	1	8
54	BT	136/136 (100%)	109 (80%)	27 (20%)	1	9
55	BU	85/106 (80%)	62 (73%)	23 (27%)	0	4
56	BV	104/104 (100%)	96 (92%)	8 (8%)	15	47
57	BW	100/129 (78%)	85 (85%)	15 (15%)	3	20
58	BX	104/117 (89%)	81 (78%)	23 (22%)	1	7
59	BY	109/109 (100%)	85 (78%)	24 (22%)	1	7
60	BZ	115/115 (100%)	89 (77%)	26 (23%)	1	7
61	Ba	118/118 (100%)	95 (80%)	23 (20%)	1	10
62	Bb	46/46 (100%)	35 (76%)	11 (24%)	1	5
63	Bc	84/87 (97%)	68 (81%)	16 (19%)	2	11
64	Bd	94/96 (98%)	73 (78%)	21 (22%)	1	7
65	Be	109/110 (99%)	89 (82%)	20 (18%)	2	12
66	Bf	90/90 (100%)	79 (88%)	11 (12%)	6	26
67	Bg	95/102 (93%)	71 (75%)	24 (25%)	0	5
68	Bh	103/104 (99%)	77 (75%)	26 (25%)	0	5
69	Bi	80/81 (99%)	51 (64%)	29 (36%)	0	1
70	Bj	70/70 (100%)	53 (76%)	17 (24%)	1	5
71	Bk	67/68 (98%)	53 (79%)	14 (21%)	1	8
72	Bl	45/45 (100%)	34 (76%)	11 (24%)	1	5
73	Bm	47/116 (40%)	34 (72%)	13 (28%)	0	3
74	Bn	23/23 (100%)	16 (70%)	7 (30%)	0	2
75	Bo	90/90 (100%)	74 (82%)	16 (18%)	2	13
76	Bq	101/254 (40%)	91 (90%)	10 (10%)	9	34
83	CV	481/497 (97%)	450 (94%)	31 (6%)	20	53
All	All	9986/10821 (92%)	7877 (79%)	2109 (21%)	4	8

5 of 2109 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	AY	61	ARG
38	BD	118	THR
68	Bh	79	ASP

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
34	AZ	85	LYS
36	BB	232	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
32	AX	48	HIS
38	BD	40	HIS
83	CV	65	GLN
35	BA	50	HIS
35	BA	215	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
79	B2	1764/1800 (98%)	545 (30%)	86 (4%)
80	B5	3140/3396 (92%)	741 (23%)	131 (4%)
81	B7	120/121 (99%)	18 (15%)	0
82	B8	157/158 (99%)	32 (20%)	3 (1%)
84	CW	74/76 (97%)	23 (31%)	5 (6%)
85	CX	2/3 (66%)	0	0
All	All	5257/5554 (94%)	1359 (25%)	225 (4%)

5 of 1359 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
79	B2	2	A
79	B2	4	C
79	B2	8	U
79	B2	16	G
79	B2	20	G

5 of 225 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
80	B5	588	G
80	B5	1094	U
80	B5	3228	C
80	B5	647	A
80	B5	896	A

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

9 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
83	HSO	CV	105	83	6,10,10	2.41	2 (33%)	4,12,12	1.81	2 (50%)
83	HSO	CV	13	83	6,10,10	2.26	1 (16%)	4,12,12	1.53	1 (25%)
83	HSO	CV	229	83	6,10,10	2.10	1 (16%)	4,12,12	1.73	1 (25%)
83	HSO	CV	295	83	6,10,10	2.21	1 (16%)	4,12,12	1.47	1 (25%)
83	HSO	CV	296	83	6,10,10	2.42	2 (33%)	4,12,12	2.18	2 (50%)
83	HSO	CV	541	83	6,10,10	2.77	2 (33%)	4,12,12	1.63	2 (50%)
83	HSO	CV	554	83	6,10,10	2.63	3 (50%)	4,12,12	1.52	1 (25%)
83	HSO	CV	556	83	6,10,10	2.44	2 (33%)	4,12,12	2.01	2 (50%)
83	HSO	CV	80	83	6,10,10	2.54	3 (50%)	4,12,12	1.39	1 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
83	HSO	CV	105	83	-	0/5/6/6	0/1/1/1
83	HSO	CV	13	83	-	0/5/6/6	0/1/1/1
83	HSO	CV	229	83	-	0/5/6/6	0/1/1/1
83	HSO	CV	295	83	-	0/5/6/6	0/1/1/1
83	HSO	CV	296	83	-	0/5/6/6	0/1/1/1
83	HSO	CV	541	83	-	0/5/6/6	0/1/1/1
83	HSO	CV	554	83	-	0/5/6/6	0/1/1/1
83	HSO	CV	556	83	-	0/5/6/6	0/1/1/1
83	HSO	CV	80	83	-	0/5/6/6	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	CV	296	HSO	O-C	-4.65	1.22	1.42
83	CV	556	HSO	O-C	-4.64	1.22	1.42
83	CV	541	HSO	O-C	-4.63	1.22	1.42
83	CV	295	HSO	O-C	-4.62	1.22	1.42
83	CV	13	HSO	O-C	-4.59	1.23	1.42

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	CV	296	HSO	CB-CA-C	-3.40	105.49	112.16
83	CV	556	HSO	CB-CA-C	-2.60	107.07	112.16
83	CV	105	HSO	CB-CA-C	-2.41	107.44	112.16
83	CV	541	HSO	CB-CA-C	-2.08	108.09	112.16
83	CV	80	HSO	O-C-CA	2.12	119.21	111.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
83	CV	13	HSO	1	0
83	CV	541	HSO	1	0
83	CV	554	HSO	1	0
83	CV	556	HSO	1	0
83	CV	80	HSO	3	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 443 ligands modelled in this entry, 232 are monoatomic - leaving 211 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected

value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
88	OHX	A3	102	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	A6	401	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	AC	301	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	AI	301	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	AI	302	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	AL	201	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	AN	201	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	AP	201	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1901	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1902	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1903	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1904	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1905	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1906	87	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1907	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1908	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1909	88	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1910	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1911	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1912	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1913	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1914	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1915	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1916	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1917	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1918	88	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1919	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1920	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1921	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1922	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1923	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1924	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1925	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1926	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1927	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1928	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1929	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1930	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1931	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1932	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
88	OHX	B2	1933	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1934	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1935	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1936	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1937	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1938	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1939	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1940	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1941	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1942	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1943	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1944	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1945	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1946	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1947	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1948	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1949	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1950	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1951	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1952	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1953	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1954	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1955	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1956	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1957	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1958	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1959	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1960	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1961	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1962	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1963	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1964	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1965	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1966	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1967	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1968	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1969	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1970	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1971	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1972	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1973	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1974	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1975	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
88	OHX	B2	1976	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1977	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1978	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1979	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1980	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1981	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1982	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1983	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1984	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1985	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1986	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1987	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1988	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1989	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1990	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1991	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1992	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1993	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1994	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1995	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1996	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1997	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1998	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	1999	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2000	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2001	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2002	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2003	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2004	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2005	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2006	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2007	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2008	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2009	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2010	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2011	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2012	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2013	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2014	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2015	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2016	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2017	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2018	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
88	OHX	B2	2019	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2020	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2021	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2022	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2023	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2024	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2025	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2026	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2027	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2028	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2029	88	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2030	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2031	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2032	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2033	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2034	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2035	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2036	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2037	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2038	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2039	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2040	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2041	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2042	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2043	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2044	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2045	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2046	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2047	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2048	87	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2049	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2050	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2051	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2052	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2053	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2054	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2055	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2056	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2057	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2058	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2059	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2060	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2061	-	0,6,6	0.00	-	0,15,15	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
88	OHX	B2	2062	88,87	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2063	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2064	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2065	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2066	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2067	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2068	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2069	79	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2070	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2071	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2072	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2073	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2074	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2075	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2076	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2077	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2078	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2079	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2080	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2081	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B2	2082	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B5	3401	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B5	3402	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B5	3403	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	201	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	202	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	203	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	204	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	205	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	206	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	210	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	212	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	214	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	215	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	219	87	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	220	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	B7	221	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	BR	201	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	Bn	101	-	0,6,6	0.00	-	0,15,15	0.00	-
88	OHX	CV	601	-	0,6,6	0.00	-	0,15,15	0.00	-
89	GCP	CV	602	-	25,34,34	2.82	6 (24%)	28,54,54	2.11	5 (17%)
88	OHX	CX	101	-	0,6,6	0.00	-	0,15,15	0.00	-



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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	OHX	A3	102	-	-	0/0/0/0	0/0/0/0
88	OHX	A6	401	-	-	0/0/0/0	0/0/0/0
88	OHX	AC	301	-	-	0/0/0/0	0/0/0/0
88	OHX	AI	301	-	-	0/0/0/0	0/0/0/0
88	OHX	AI	302	-	-	0/0/0/0	0/0/0/0
88	OHX	AL	201	-	-	0/0/0/0	0/0/0/0
88	OHX	AN	201	-	-	0/0/0/0	0/0/0/0
88	OHX	AP	201	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1901	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1902	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1903	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1904	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1905	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1906	87	-	0/0/0/0	0/0/0/0
88	OHX	B2	1907	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1908	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1909	88	-	0/0/0/0	0/0/0/0
88	OHX	B2	1910	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1911	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1912	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1913	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1914	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1915	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1916	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1917	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1918	88	-	0/0/0/0	0/0/0/0
88	OHX	B2	1919	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1920	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1921	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1922	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1923	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1924	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1925	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1926	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1927	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1928	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1929	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1930	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1931	-	-	0/0/0/0	0/0/0/0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	OHX	B2	1932	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1933	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1934	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1935	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1936	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1937	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1938	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1939	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1940	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1941	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1942	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1943	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1944	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1945	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1946	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1947	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1948	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1949	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1950	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1951	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1952	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1953	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1954	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1955	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1956	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1957	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1958	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1959	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1960	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1961	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1962	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1963	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1964	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1965	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1966	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1967	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1968	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1969	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1970	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1971	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1972	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1973	-	-	0/0/0/0	0/0/0/0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	OHX	B2	1974	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1975	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1976	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1977	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1978	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1979	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1980	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1981	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1982	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1983	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1984	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1985	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1986	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1987	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1988	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1989	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1990	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1991	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1992	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1993	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1994	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1995	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1996	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1997	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1998	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	1999	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2000	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2001	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2002	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2003	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2004	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2005	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2006	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2007	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2008	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2009	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2010	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2011	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2012	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2013	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2014	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2015	-	-	0/0/0/0	0/0/0/0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	OHX	B2	2016	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2017	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2018	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2019	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2020	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2021	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2022	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2023	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2024	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2025	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2026	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2027	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2028	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2029	88	-	0/0/0/0	0/0/0/0
88	OHX	B2	2030	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2031	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2032	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2033	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2034	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2035	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2036	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2037	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2038	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2039	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2040	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2041	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2042	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2043	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2044	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2045	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2046	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2047	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2048	87	-	0/0/0/0	0/0/0/0
88	OHX	B2	2049	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2050	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2051	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2052	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2053	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2054	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2055	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2056	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2057	-	-	0/0/0/0	0/0/0/0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	OHX	B2	2058	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2059	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2060	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2061	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2062	88,87	-	0/0/0/0	0/0/0/0
88	OHX	B2	2063	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2064	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2065	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2066	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2067	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2068	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2069	79	-	0/0/0/0	0/0/0/0
88	OHX	B2	2070	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2071	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2072	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2073	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2074	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2075	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2076	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2077	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2078	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2079	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2080	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2081	-	-	0/0/0/0	0/0/0/0
88	OHX	B2	2082	-	-	0/0/0/0	0/0/0/0
88	OHX	B5	3401	-	-	0/0/0/0	0/0/0/0
88	OHX	B5	3402	-	-	0/0/0/0	0/0/0/0
88	OHX	B5	3403	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	201	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	202	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	203	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	204	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	205	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	206	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	210	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	212	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	214	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	215	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	219	87	-	0/0/0/0	0/0/0/0
88	OHX	B7	220	-	-	0/0/0/0	0/0/0/0
88	OHX	B7	221	-	-	0/0/0/0	0/0/0/0
88	OHX	BR	201	-	-	0/0/0/0	0/0/0/0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	OHX	Bn	101	-	-	0/0/0/0	0/0/0/0
88	OHX	CV	601	-	-	0/0/0/0	0/0/0/0
89	GCP	CV	602	-	-	0/18/38/38	0/3/3/3
88	OHX	CX	101	-	-	0/0/0/0	0/0/0/0

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	CV	602	GCP	C4-N9	-9.57	1.35	1.47
89	CV	602	GCP	C5-C6	-4.99	1.44	1.53
89	CV	602	GCP	C8-N9	-3.56	1.36	1.46
89	CV	602	GCP	C2'-C1'	-3.04	1.43	1.53
89	CV	602	GCP	PB-O3A	-2.31	1.55	1.58

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	CV	602	GCP	O3G-PG-C3B	-7.36	88.55	106.40
89	CV	602	GCP	O6-C6-N1	-2.64	119.18	122.70
89	CV	602	GCP	O2G-PG-O1G	2.69	119.54	112.32
89	CV	602	GCP	O1B-PB-C3B	3.13	116.72	108.97
89	CV	602	GCP	O6-C6-C5	3.84	127.03	119.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

131 monomers are involved in 342 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	A3	102	OHX	4	0
88	A6	401	OHX	2	0
88	AC	301	OHX	5	0
88	AI	302	OHX	2	0
88	AL	201	OHX	8	0
88	AN	201	OHX	2	0
88	AP	201	OHX	3	0
88	B2	1901	OHX	1	0
88	B2	1906	OHX	3	0
88	B2	1907	OHX	6	0
88	B2	1909	OHX	2	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	B2	1910	OHX	2	0
88	B2	1914	OHX	3	0
88	B2	1915	OHX	6	0
88	B2	1916	OHX	1	0
88	B2	1917	OHX	2	0
88	B2	1918	OHX	8	0
88	B2	1919	OHX	1	0
88	B2	1921	OHX	6	0
88	B2	1922	OHX	7	0
88	B2	1923	OHX	1	0
88	B2	1924	OHX	1	0
88	B2	1925	OHX	1	0
88	B2	1927	OHX	1	0
88	B2	1928	OHX	1	0
88	B2	1929	OHX	1	0
88	B2	1932	OHX	1	0
88	B2	1936	OHX	1	0
88	B2	1937	OHX	1	0
88	B2	1939	OHX	5	0
88	B2	1941	OHX	1	0
88	B2	1942	OHX	2	0
88	B2	1944	OHX	1	0
88	B2	1945	OHX	1	0
88	B2	1947	OHX	1	0
88	B2	1948	OHX	1	0
88	B2	1949	OHX	2	0
88	B2	1951	OHX	2	0
88	B2	1952	OHX	2	0
88	B2	1953	OHX	6	0
88	B2	1954	OHX	1	0
88	B2	1956	OHX	1	0
88	B2	1959	OHX	1	0
88	B2	1960	OHX	4	0
88	B2	1961	OHX	1	0
88	B2	1962	OHX	4	0
88	B2	1963	OHX	6	0
88	B2	1964	OHX	2	0
88	B2	1967	OHX	4	0
88	B2	1968	OHX	7	0
88	B2	1969	OHX	1	0
88	B2	1971	OHX	2	0
88	B2	1972	OHX	1	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	B2	1973	OHX	7	0
88	B2	1974	OHX	3	0
88	B2	1976	OHX	7	0
88	B2	1977	OHX	1	0
88	B2	1978	OHX	1	0
88	B2	1981	OHX	5	0
88	B2	1982	OHX	1	0
88	B2	1985	OHX	3	0
88	B2	1986	OHX	1	0
88	B2	1987	OHX	8	0
88	B2	1988	OHX	1	0
88	B2	1989	OHX	1	0
88	B2	1990	OHX	3	0
88	B2	1995	OHX	6	0
88	B2	1999	OHX	3	0
88	B2	2002	OHX	1	0
88	B2	2004	OHX	1	0
88	B2	2006	OHX	1	0
88	B2	2007	OHX	2	0
88	B2	2009	OHX	2	0
88	B2	2010	OHX	1	0
88	B2	2011	OHX	11	0
88	B2	2012	OHX	1	0
88	B2	2013	OHX	1	0
88	B2	2014	OHX	7	0
88	B2	2020	OHX	3	0
88	B2	2022	OHX	1	0
88	B2	2023	OHX	2	0
88	B2	2024	OHX	2	0
88	B2	2025	OHX	7	0
88	B2	2028	OHX	1	0
88	B2	2029	OHX	1	0
88	B2	2032	OHX	1	0
88	B2	2033	OHX	2	0
88	B2	2036	OHX	1	0
88	B2	2037	OHX	1	0
88	B2	2038	OHX	1	0
88	B2	2040	OHX	1	0
88	B2	2041	OHX	1	0
88	B2	2042	OHX	1	0
88	B2	2043	OHX	1	0
88	B2	2044	OHX	5	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
88	B2	2045	OHX	1	0
88	B2	2046	OHX	1	0
88	B2	2047	OHX	3	0
88	B2	2048	OHX	7	0
88	B2	2051	OHX	1	0
88	B2	2056	OHX	1	0
88	B2	2057	OHX	1	0
88	B2	2058	OHX	1	0
88	B2	2059	OHX	1	0
88	B2	2061	OHX	1	0
88	B2	2062	OHX	6	0
88	B2	2063	OHX	2	0
88	B2	2066	OHX	6	0
88	B2	2067	OHX	2	0
88	B2	2068	OHX	1	0
88	B2	2069	OHX	17	0
88	B2	2071	OHX	6	0
88	B2	2073	OHX	1	0
88	B2	2074	OHX	1	0
88	B2	2075	OHX	2	0
88	B2	2076	OHX	1	0
88	B2	2077	OHX	5	0
88	B2	2078	OHX	3	0
88	B2	2080	OHX	1	0
88	B2	2081	OHX	11	0
88	B2	2082	OHX	1	0
88	B5	3401	OHX	1	0
88	B5	3402	OHX	3	0
88	B7	202	OHX	2	0
88	B7	203	OHX	6	0
88	B7	219	OHX	6	0
88	B7	220	OHX	2	0
88	BR	201	OHX	9	0
88	CV	601	OHX	10	0
89	CV	602	GCP	63	0
88	CX	101	OHX	2	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
80	B5	1
84	CW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B5	1285:G	O3'	1286:A	P	6.77
1	CW	33:U	O3'	34:C	P	4.25