



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 10:22 am BST

PDB ID : 4V8P
Title : T.thermophila 60S ribosomal subunit in complex with initiation factor 6.
Authors : Klinge, S.; Voigts-Hoffmann, F.; Leibundgut, M.; Arpagaus, S.; Ban, N.
Deposited on : 2011-09-14
Resolution : 3.52 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

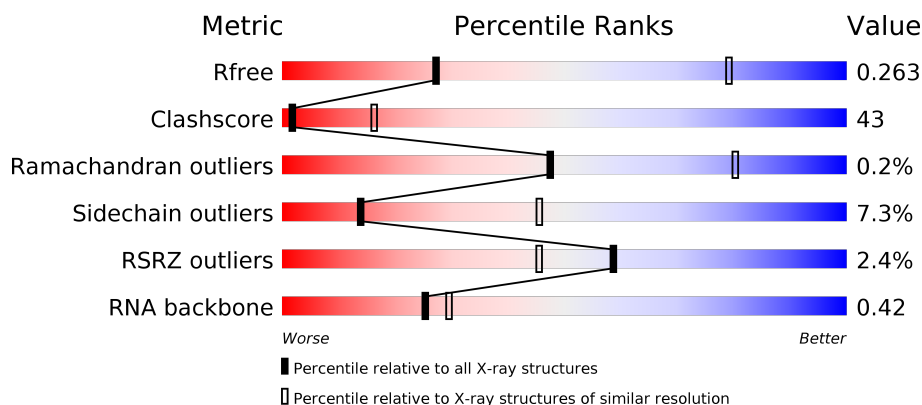
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.52 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1161 (3.60-3.44)
Clashscore	141614	1244 (3.60-3.44)
Ramachandran outliers	138981	1206 (3.60-3.44)
Sidechain outliers	138945	1207 (3.60-3.44)
RSRZ outliers	127900	1080 (3.60-3.44)
RNA backbone	3102	1003 (4.02-3.00)

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

Mol	Chain	Length	Quality of chain
1	A1	3354	<div> <div>3%</div> <div>18% 44% 29% 7%</div> </div>
1	D1	3354	<div> <div>%</div> <div>18% 44% 28% 7%</div> </div>
1	F1	3354	<div> <div>2%</div> <div>18% 44% 28% 7%</div> </div>
1	H1	3354	<div> <div>4%</div> <div>17% 43% 29% 7%</div> </div>

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Mol	Chain	Length	Quality of chain
2	AA	94	
2	DA	94	
2	FA	94	
2	HA	94	
3	AB	52	
3	DB	52	
3	FB	52	
3	HB	52	
4	AC	109	
4	DC	109	
4	FC	109	
4	HC	109	
5	AE	191	
5	DE	191	
5	FE	191	
5	HE	191	
6	AF	126	
6	DF	126	
6	FF	126	
6	HF	126	
7	AG	104	
7	DG	104	
7	FG	104	
7	HG	104	
8	AH	113	

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Mol	Chain	Length	Quality of chain
8	DH	113	
8	FH	113	
8	HH	113	
9	AJ	248	
9	DJ	248	
9	FJ	248	
9	HJ	248	
10	AK	129	
10	DK	129	
10	FK	129	
10	HK	129	
11	AL	123	
11	DL	123	
11	FL	123	
11	HL	123	
12	AM	118	
12	DM	118	
12	FM	118	
12	HM	118	
13	AN	144	
13	DN	144	
13	FN	144	
13	HN	144	
14	AO	134	
14	DO	134	

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Mol	Chain	Length	Quality of chain
14	FO	134	
14	HO	134	
15	AP	89	
15	DP	89	
15	FP	89	
15	HP	89	
16	AQ	104	
16	DQ	104	
16	FQ	104	
16	HQ	104	
17	AT	66	
17	DT	66	
17	FT	66	
17	HT	66	
18	AU	206	
18	DU	206	
18	FU	206	
18	HU	206	
19	AX	189	
19	DX	189	
19	FX	189	
19	HX	189	
20	B2	154	
20	C2	154	
20	E2	154	

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Mol	Chain	Length	Quality of chain
20	G2	154	
21	B3	120	
21	C3	120	
21	E3	120	
21	G3	120	
22	BA	264	
22	CA	264	
22	EA	264	
22	GA	264	
23	BB	391	
23	CB	391	
23	EB	391	
23	GB	391	
24	BC	410	
24	CC	410	
24	EC	410	
24	GC	410	
25	BD	172	
25	CD	172	
25	ED	172	
25	GD	172	
26	BE	188	
26	CE	188	
26	EE	188	
26	GE	188	


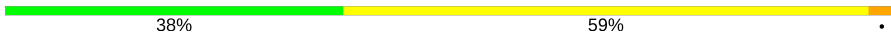
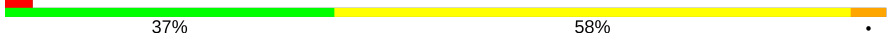


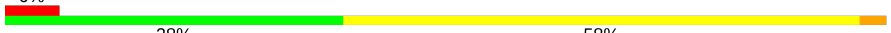
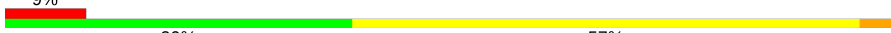







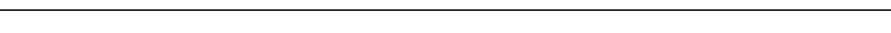




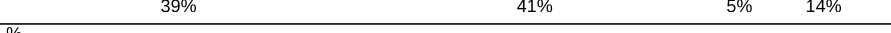

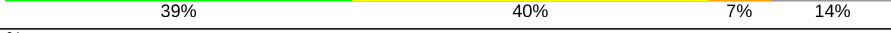



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Mol	Chain	Length	Quality of chain
27	BF	255	
27	CF	255	
27	EF	255	
27	GF	255	
28	BG	123	
28	CG	123	
28	EG	123	
28	GG	123	
29	BH	215	
29	CH	215	
29	EH	215	
29	GH	215	
30	BI	198	
30	CI	198	
30	EI	198	
30	GI	198	
31	BJ	141	
31	CJ	141	
31	EJ	141	
31	GJ	141	
32	BK	149	
32	CK	149	
32	EK	149	
32	GK	149	
33	BL	204	

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Mol	Chain	Length	Quality of chain
33	CL	204	
33	EL	204	
33	GL	204	
34	BM	301	
34	CM	301	
34	EM	301	
34	GM	301	
35	BN	181	
35	CN	181	
35	EN	181	
35	GN	181	
36	BO	185	
36	EO	185	
36	GO	185	
37	BP	157	
37	CP	157	
37	EP	157	
37	GP	157	
38	BQ	183	
38	CQ	183	
38	EQ	183	
38	GQ	183	
39	BR	150	
39	CR	150	
39	ER	150	

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Mol	Chain	Length	Quality of chain
39	GR	150	
40	BS	135	
40	CS	135	
40	ES	135	
40	GS	135	
41	BT	158	
41	CT	158	
41	ET	158	
41	GT	158	
42	BU	124	
42	CU	124	
42	EU	124	
42	GU	124	
43	BV	239	
43	CV	239	
43	EV	239	
43	GV	239	
44	BW	111	
44	CW	111	
44	EW	111	
44	GW	111	
45	BX	134	
45	CX	134	
45	EX	134	
45	GX	134	

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Mol	Chain	Length	Quality of chain
46	BY	103	
46	CY	103	
46	EY	103	
46	GY	103	
47	CO	185	

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
48	MG	A1	3422	-	-	-	X
48	MG	A1	3428	-	-	-	X
48	MG	A1	3430	-	-	-	X
48	MG	A1	3435	-	-	-	X
48	MG	A1	3437	-	-	-	X
48	MG	A1	3472	-	-	-	X
48	MG	A1	3522	-	-	-	X
48	MG	A1	3530	-	-	-	X
48	MG	A1	3555	-	-	-	X
48	MG	A1	3573	-	-	-	X
48	MG	A1	3579	-	-	-	X
48	MG	A1	3583	-	-	-	X
48	MG	A1	3585	-	-	-	X
48	MG	A1	3587	-	-	-	X
48	MG	A1	3593	-	-	-	X
48	MG	A1	3595	-	-	-	X
48	MG	C3	205	-	-	-	X
48	MG	C3	207	-	-	-	X
48	MG	D1	3424	-	-	-	X
48	MG	D1	3434	-	-	-	X
48	MG	D1	3446	-	-	-	X
48	MG	D1	3463	-	-	-	X
48	MG	D1	3497	-	-	-	X
48	MG	D1	3548	-	-	-	X
48	MG	D1	3550	-	-	-	X
48	MG	D1	3571	-	-	-	X
48	MG	D1	3576	-	-	-	X
48	MG	D1	3592	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
48	MG	D1	3596	-	-	-	X
48	MG	D1	3597	-	-	-	X
48	MG	D1	3600	-	-	-	X
48	MG	D1	3603	-	-	-	X
48	MG	D1	3606	-	-	-	X
48	MG	D1	3611	-	-	-	X
48	MG	D1	3624	-	-	-	X
48	MG	DJ	301	-	-	-	X
48	MG	E2	205	-	-	-	X
48	MG	E3	204	-	-	-	X
48	MG	F1	3411	-	-	-	X
48	MG	F1	3451	-	-	-	X
48	MG	F1	3493	-	-	-	X
48	MG	F1	3511	-	-	-	X
48	MG	F1	3515	-	-	-	X
48	MG	F1	3539	-	-	-	X
48	MG	F1	3560	-	-	-	X
48	MG	F1	3565	-	-	-	X
48	MG	F1	3566	-	-	-	X
48	MG	F1	3574	-	-	-	X
48	MG	F1	3576	-	-	-	X
48	MG	F1	3578	-	-	-	X
48	MG	G2	204	-	-	-	X
48	MG	G2	206	-	-	-	X
48	MG	G3	202	-	-	-	X
48	MG	G3	205	-	-	-	X
48	MG	GN	201	-	-	-	X
48	MG	GP	201	-	-	-	X
48	MG	H1	3409	-	-	-	X
48	MG	H1	3410	-	-	-	X
48	MG	H1	3412	-	-	-	X
48	MG	H1	3414	-	-	-	X
48	MG	H1	3450	-	-	-	X
48	MG	H1	3479	-	-	-	X
48	MG	H1	3489	-	-	-	X
48	MG	H1	3524	-	-	-	X
48	MG	H1	3531	-	-	-	X
48	MG	H1	3533	-	-	-	X
48	MG	H1	3534	-	-	-	X
48	MG	H1	3535	-	-	-	X
48	MG	H1	3536	-	-	-	X
48	MG	H1	3543	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
48	MG	H1	3544	-	-	-	X
48	MG	H1	3550	-	-	-	X
48	MG	H1	3551	-	-	-	X
48	MG	H1	3554	-	-	-	X

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 511395 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 26S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A1	3119	Total	C	N	O	P	0	0	0
			66769	29861	12195	21594	3119			
1	D1	3119	Total	C	N	O	P	0	0	0
			66769	29861	12195	21594	3119			
1	F1	3119	Total	C	N	O	P	0	0	0
			66769	29861	12195	21594	3119			
1	H1	3119	Total	C	N	O	P	0	0	0
			66769	29861	12195	21594	3119			

- Molecule 2 is a protein called RIBOSOMAL PROTEIN L37.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AA	91	Total	C	N	O	S	0	0	0
			721	440	158	116	7			
2	DA	91	Total	C	N	O	S	0	0	0
			721	440	158	116	7			
2	FA	91	Total	C	N	O	S	0	0	0
			721	440	158	116	7			
2	HA	91	Total	C	N	O	S	0	0	0
			721	440	158	116	7			

- Molecule 3 is a protein called RPL39.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AB	51	Total	C	N	O	S	0	0	0
			456	288	97	70	1			
3	DB	51	Total	C	N	O	S	0	0	0
			456	288	97	70	1			
3	FB	51	Total	C	N	O	S	0	0	0
			456	288	97	70	1			
3	HB	51	Total	C	N	O	S	0	0	0
			456	288	97	70	1			

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L36A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AC	103	Total	C	N	O	S	0	0	0
			836	526	163	140	7			
4	DC	103	Total	C	N	O	S	0	0	0
			836	526	163	140	7			
4	FC	103	Total	C	N	O	S	0	0	0
			836	526	163	140	7			
4	HC	103	Total	C	N	O	S	0	0	0
			836	526	163	140	7			

- Molecule 5 is a protein called RPL6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	190	Total	C	N	O	S	0	0	0
			1525	966	286	272	1			
5	DE	190	Total	C	N	O	S	0	0	0
			1525	966	286	272	1			
5	FE	190	Total	C	N	O	S	0	0	0
			1525	966	286	272	1			
5	HE	190	Total	C	N	O	S	0	0	0
			1525	966	286	272	1			

- Molecule 6 is a protein called RPL14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	125	Total	C	N	O	S	0	0	0
			1021	659	192	169	1			
6	DF	125	Total	C	N	O	S	0	0	0
			1021	659	192	169	1			
6	FF	125	Total	C	N	O	S	0	0	0
			1021	659	192	169	1			
6	HF	125	Total	C	N	O	S	0	0	0
			1021	659	192	169	1			

- Molecule 7 is a protein called RPL30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	96	Total	C	N	O	S	0	0	0
			727	455	129	138	5			
7	DG	96	Total	C	N	O	S	0	0	0
			727	455	129	138	5			
7	FG	96	Total	C	N	O	S	0	0	0
			727	455	129	138	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	HG	96	Total	C	N	O	S	0	0	0
			727	455	129	138	5			

- Molecule 8 is a protein called RPL35A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	107	Total	C	N	O	S	0	0	0
			850	540	167	142	1			
8	DH	107	Total	C	N	O	S	0	0	0
			850	540	167	142	1			
8	FH	107	Total	C	N	O	S	0	0	0
			850	540	167	142	1			
8	HH	107	Total	C	N	O	S	0	0	0
			850	540	167	142	1			

- Molecule 9 is a protein called TRANSLATION INITIATION FACTOR EIF-6, PUTATIVE FAMILY PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AJ	226	Total	C	N	O	S	0	0	0
			1716	1068	302	336	10			
9	DJ	226	Total	C	N	O	S	0	0	0
			1716	1068	302	336	10			
9	FJ	226	Total	C	N	O	S	0	0	0
			1716	1068	302	336	10			
9	HJ	226	Total	C	N	O	S	0	0	0
			1716	1068	302	336	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AJ	-2	GLY	-	expression tag	UNP Q245F2
AJ	-1	THR	-	expression tag	UNP Q245F2
AJ	0	SER	-	expression tag	UNP Q245F2
DJ	-2	GLY	-	expression tag	UNP Q245F2
DJ	-1	THR	-	expression tag	UNP Q245F2
DJ	0	SER	-	expression tag	UNP Q245F2
FJ	-2	GLY	-	expression tag	UNP Q245F2
FJ	-1	THR	-	expression tag	UNP Q245F2
FJ	0	SER	-	expression tag	UNP Q245F2
HJ	-2	GLY	-	expression tag	UNP Q245F2
HJ	-1	THR	-	expression tag	UNP Q245F2

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Chain	Residue	Modelled	Actual	Comment	Reference
HJ	0	SER	-	expression tag	UNP Q245F2

- Molecule 10 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AK	52	Total	C	N	O	S	0	0	0
			415	257	83	69	6			
10	DK	52	Total	C	N	O	S	0	0	0
			415	257	83	69	6			
10	FK	52	Total	C	N	O	S	0	0	0
			415	257	83	69	6			
10	HK	52	Total	C	N	O	S	0	0	0
			415	257	83	69	6			

- Molecule 11 is a protein called RPL34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AL	108	Total	C	N	O	S	0	0	0
			852	529	170	147	6			
11	DL	108	Total	C	N	O	S	0	0	0
			852	529	170	147	6			
11	FL	108	Total	C	N	O	S	0	0	0
			852	529	170	147	6			
11	HL	108	Total	C	N	O	S	0	0	0
			852	529	170	147	6			

- Molecule 12 is a protein called RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AM	100	Total	C	N	O	S	0	0	0
			819	530	137	151	1			
12	DM	100	Total	C	N	O	S	0	0	0
			819	530	137	151	1			
12	FM	100	Total	C	N	O	S	0	0	0
			819	530	137	151	1			
12	HM	100	Total	C	N	O	S	0	0	0
			819	530	137	151	1			

- Molecule 13 is a protein called RPL27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AN	143	Total	C	N	O	S	0	0	0
			1170	755	213	199	3			
13	DN	143	Total	C	N	O	S	0	0	0
			1170	755	213	199	3			
13	FN	143	Total	C	N	O	S	0	0	0
			1170	755	213	199	3			
13	HN	143	Total	C	N	O	S	0	0	0
			1170	755	213	199	3			

- Molecule 14 is a protein called RPL28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AO	134	Total	C	N	O	S	0	0	0
			1034	650	204	179	1			
14	DO	134	Total	C	N	O	S	0	0	0
			1034	650	204	179	1			
14	FO	134	Total	C	N	O	S	0	0	0
			1034	650	204	179	1			
14	HO	134	Total	C	N	O	S	0	0	0
			1034	650	204	179	1			

- Molecule 15 is a protein called RPL38.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AP	66	Total	C	N	O	S	0	0	0
			551	367	93	90	1			
15	DP	66	Total	C	N	O	S	0	0	0
			551	367	93	90	1			
15	FP	66	Total	C	N	O	S	0	0	0
			551	367	93	90	1			
15	HP	66	Total	C	N	O	S	0	0	0
			551	367	93	90	1			

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
16	AQ	102	Total	C	N	O	0	0	0
			803	506	165	132			
16	DQ	102	Total	C	N	O	0	0	0
			803	506	165	132			
16	FQ	102	Total	C	N	O	0	0	0
			803	506	165	132			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
16	HQ	102	Total	C	N	O	0	0	0
			803	506	165	132			

- Molecule 17 is a protein called RPL29.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	AT	65	Total	C	N	O	0	0	0
			533	324	117	92			
17	DT	65	Total	C	N	O	0	0	0
			533	324	117	92			
17	FT	65	Total	C	N	O	0	0	0
			533	324	117	92			
17	HT	65	Total	C	N	O	0	0	0
			533	324	117	92			

- Molecule 18 is a protein called RPL13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	AU	203	Total	C	N	O	S	0	0	0
			1624	1015	328	279	2			
18	DU	203	Total	C	N	O	S	0	0	0
			1624	1015	328	279	2			
18	FU	203	Total	C	N	O	S	0	0	0
			1624	1015	328	279	2			
18	HU	203	Total	C	N	O	S	0	0	0
			1624	1015	328	279	2			

- Molecule 19 is a protein called RPL18A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AX	188	Total	C	N	O	S	0	0	0
			1536	972	287	271	6			
19	DX	188	Total	C	N	O	S	0	0	0
			1536	972	287	271	6			
19	FX	188	Total	C	N	O	S	0	0	0
			1536	972	287	271	6			
19	HX	188	Total	C	N	O	S	0	0	0
			1536	972	287	271	6			

- Molecule 20 is a RNA chain called 5.8S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	B2	154	Total	C	N	O	P	0	0	0
			3300	1475	602	1069	154			
20	C2	154	Total	C	N	O	P	0	0	0
			3300	1475	602	1069	154			
20	E2	154	Total	C	N	O	P	0	0	0
			3300	1475	602	1069	154			
20	G2	154	Total	C	N	O	P	0	0	0
			3300	1475	602	1069	154			

- Molecule 21 is a RNA chain called 5S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	B3	120	Total	C	N	O	P	0	0	0
			2566	1145	463	838	120			
21	C3	120	Total	C	N	O	P	0	0	0
			2566	1145	463	838	120			
21	E3	120	Total	C	N	O	P	0	0	0
			2566	1145	463	838	120			
21	G3	120	Total	C	N	O	P	0	0	0
			2566	1145	463	838	120			

- Molecule 22 is a protein called RPL8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	BA	257	Total	C	N	O	S	0	0	0
			1977	1226	400	343	8			
22	CA	257	Total	C	N	O	S	0	0	0
			1977	1226	400	343	8			
22	EA	257	Total	C	N	O	S	0	0	0
			1977	1226	400	343	8			
22	GA	257	Total	C	N	O	S	0	0	0
			1977	1226	400	343	8			

- Molecule 23 is a protein called RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	BB	386	Total	C	N	O	S	0	0	0
			3080	1944	595	530	11			
23	CB	386	Total	C	N	O	S	0	0	0
			3080	1944	595	530	11			
23	EB	386	Total	C	N	O	S	0	0	0
			3080	1944	595	530	11			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	GB	386	Total	C	N	O	S	0	0	0
			3080	1944	595	530	11			

- Molecule 24 is a protein called RPL4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	BC	409	Total	C	N	O	S	0	0	0
			3172	1975	622	571	4			
24	CC	409	Total	C	N	O	S	0	0	0
			3172	1975	622	571	4			
24	EC	409	Total	C	N	O	S	0	0	0
			3172	1975	622	571	4			
24	GC	409	Total	C	N	O	S	0	0	0
			3172	1975	622	571	4			

- Molecule 25 is a protein called 60S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BD	169	Total	C	N	O	S	0	0	0
			1357	851	254	243	9			
25	CD	169	Total	C	N	O	S	0	0	0
			1357	851	254	243	9			
25	ED	169	Total	C	N	O	S	0	0	0
			1357	851	254	243	9			
25	GD	169	Total	C	N	O	S	0	0	0
			1357	851	254	243	9			

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BE	186	Total	C	N	O	S	0	0	0
			1481	939	272	264	6			
26	CE	186	Total	C	N	O	S	0	0	0
			1481	939	272	264	6			
26	EE	186	Total	C	N	O	S	0	0	0
			1481	939	272	264	6			
26	GE	186	Total	C	N	O	S	0	0	0
			1481	939	272	264	6			

- Molecule 27 is a protein called RPL7A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BF	231	Total	C	N	O	S	0	0	0
			1860	1191	341	327	1			
27	CF	231	Total	C	N	O	S	0	0	0
			1860	1191	341	327	1			
27	EF	231	Total	C	N	O	S	0	0	0
			1860	1191	341	327	1			
27	GF	231	Total	C	N	O	S	0	0	0
			1860	1191	341	327	1			

- Molecule 28 is a protein called RPLP0.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
28	BG	123	Total	C	N	O	0	0	0
			711	465	123	123			
28	CG	123	Total	C	N	O	0	0	0
			711	465	123	123			
28	EG	123	Total	C	N	O	0	0	0
			711	465	123	123			
28	GG	123	Total	C	N	O	0	0	0
			711	465	123	123			

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BH	201	Total	C	N	O	S	0	0	0
			1620	1027	319	271	3			
29	CH	201	Total	C	N	O	S	0	0	0
			1620	1027	319	271	3			
29	EH	201	Total	C	N	O	S	0	0	0
			1620	1027	319	271	3			
29	GH	201	Total	C	N	O	S	0	0	0
			1620	1027	319	271	3			

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN L13A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BI	198	Total	C	N	O	S	0	0	0
			1594	1019	308	263	4			
30	CI	198	Total	C	N	O	S	0	0	0
			1594	1019	308	263	4			
30	EI	198	Total	C	N	O	S	0	0	0
			1594	1019	308	263	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	GI	198	Total	C	N	O	S	0	0	0
			1594	1019	308	263	4			

- Molecule 31 is a protein called RPL23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BJ	138	Total	C	N	O	S	0	0	0
			1022	643	193	179	7			
31	CJ	138	Total	C	N	O	S	0	0	0
			1022	643	193	179	7			
31	EJ	138	Total	C	N	O	S	0	0	0
			1022	643	193	179	7			
31	GJ	138	Total	C	N	O	S	0	0	0
			1022	643	193	179	7			

- Molecule 32 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BK	148	Total	C	N	O	S	0	0	0
			1161	739	234	182	6			
32	CK	148	Total	C	N	O	S	0	0	0
			1161	739	234	182	6			
32	EK	148	Total	C	N	O	S	0	0	0
			1161	739	234	182	6			
32	GK	148	Total	C	N	O	S	0	0	0
			1161	739	234	182	6			

- Molecule 33 is a protein called RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BL	203	Total	C	N	O	S	0	0	0
			1691	1061	351	275	4			
33	CL	203	Total	C	N	O	S	0	0	0
			1691	1061	351	275	4			
33	EL	203	Total	C	N	O	S	0	0	0
			1691	1061	351	275	4			
33	GL	203	Total	C	N	O	S	0	0	0
			1691	1061	351	275	4			

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BM	298	Total	C	N	O	S	0	0	0
			2409	1530	445	430	4			
34	CM	300	Total	C	N	O	S	0	0	0
			2424	1541	447	432	4			
34	EM	300	Total	C	N	O	S	0	0	0
			2424	1541	447	432	4			
34	GM	300	Total	C	N	O	S	0	0	0
			2424	1541	447	432	4			

- Molecule 35 is a protein called RPL18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BN	180	Total	C	N	O	S	0	0	0
			1441	909	280	249	3			
35	CN	180	Total	C	N	O	S	0	0	0
			1441	909	280	249	3			
35	EN	180	Total	C	N	O	S	0	0	0
			1441	909	280	249	3			
35	GN	180	Total	C	N	O	S	0	0	0
			1441	909	280	249	3			

- Molecule 36 is a protein called RPL19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BO	184	Total	C	N	O	S	0	0	0
			1491	924	311	251	5			
36	EO	146	Total	C	N	O	S	0	0	0
			1192	745	249	193	5			
36	GO	153	Total	C	N	O	S	0	0	0
			1234	772	256	201	5			

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BP	156	Total	C	N	O	S	0	0	0
			1272	804	251	215	2			
37	CP	156	Total	C	N	O	S	0	0	0
			1272	804	251	215	2			
37	EP	156	Total	C	N	O	S	0	0	0
			1272	804	251	215	2			
37	GP	156	Total	C	N	O	S	0	0	0
			1272	804	251	215	2			

- Molecule 38 is a protein called RPL17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BQ	157	Total	C	N	O	S	0	0	0
			1239	771	249	216	3			
38	CQ	157	Total	C	N	O	S	0	0	0
			1239	771	249	216	3			
38	EQ	157	Total	C	N	O	S	0	0	0
			1239	771	249	216	3			
38	GQ	157	Total	C	N	O	S	0	0	0
			1239	771	249	216	3			

- Molecule 39 is a protein called RPL23A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BR	121	Total	C	N	O	S	0	0	0
			965	613	176	173	3			
39	CR	121	Total	C	N	O	S	0	0	0
			965	613	176	173	3			
39	ER	121	Total	C	N	O	S	0	0	0
			965	613	176	173	3			
39	GR	121	Total	C	N	O	S	0	0	0
			965	613	176	173	3			

- Molecule 40 is a protein called RPL26.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BS	126	Total	C	N	O	S	0	0	0
			1013	638	200	173	2			
40	CS	126	Total	C	N	O	S	0	0	0
			1013	638	200	173	2			
40	ES	126	Total	C	N	O	S	0	0	0
			1013	638	200	173	2			
40	GS	126	Total	C	N	O	S	0	0	0
			1013	638	200	173	2			

- Molecule 41 is a protein called RPL24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BT	61	Total	C	N	O	S	0	0	0
			510	331	100	76	3			
41	CT	61	Total	C	N	O	S	0	0	0
			510	331	100	76	3			
41	ET	61	Total	C	N	O	S	0	0	0
			510	331	100	76	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	GT	61	Total	C	N	O	S	0	0	0
			510	331	100	76	3			

- Molecule 42 is a protein called RPL35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BU	123	Total	C	N	O		0	0	0
			990	629	196	165				
42	CU	123	Total	C	N	O		0	0	0
			990	629	196	165				
42	EU	123	Total	C	N	O		0	0	0
			990	629	196	165				
42	GU	123	Total	C	N	O		0	0	0
			990	629	196	165				

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BV	234	Total	C	N	O	S	0	0	0
			1910	1221	362	323	4			
43	CV	234	Total	C	N	O	S	0	0	0
			1910	1221	362	323	4			
43	EV	234	Total	C	N	O	S	0	0	0
			1910	1221	362	323	4			
43	GV	234	Total	C	N	O	S	0	0	0
			1910	1221	362	323	4			

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BW	110	Total	C	N	O	S	0	0	0
			901	563	171	164	3			
44	CW	110	Total	C	N	O	S	0	0	0
			901	563	171	164	3			
44	EW	110	Total	C	N	O	S	0	0	0
			901	563	171	164	3			
44	GW	110	Total	C	N	O	S	0	0	0
			901	563	171	164	3			

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BX	125	Total	C	N	O	S	0	0	0
			1012	639	205	165	3			
45	CX	125	Total	C	N	O	S	0	0	0
			1012	639	205	165	3			
45	EX	125	Total	C	N	O	S	0	0	0
			1012	639	205	165	3			
45	GX	125	Total	C	N	O	S	0	0	0
			1012	639	205	165	3			

- Molecule 46 is a protein called RPL37A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	BY	102	Total	C	N	O	S	0	0	0
			786	502	148	131	5			
46	CY	102	Total	C	N	O	S	0	0	0
			786	502	148	131	5			
46	EY	102	Total	C	N	O	S	0	0	0
			786	502	148	131	5			
46	GY	102	Total	C	N	O	S	0	0	0
			786	502	148	131	5			

- Molecule 47 is a protein called RPL19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	CO	175	Total	C	N	O	S	0	0	0
			1366	861	278	222	5			

- Molecule 48 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
48	DK	1	Total	Mg	0	0
			1	1		
48	AK	1	Total	Mg	0	0
			1	1		
48	DQ	1	Total	Mg	0	0
			1	1		
48	G3	5	Total	Mg	0	0
			5	5		
48	E3	6	Total	Mg	0	0
			6	6		
48	EN	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
48	BL	1	Total 1	Mg 1	0	0
48	GJ	1	Total 1	Mg 1	0	0
48	GA	1	Total 1	Mg 1	0	0
48	FK	1	Total 1	Mg 1	0	0
48	CD	1	Total 1	Mg 1	0	0
48	BP	1	Total 1	Mg 1	0	0
48	GN	1	Total 1	Mg 1	0	0
48	EQ	1	Total 1	Mg 1	0	0
48	CY	1	Total 1	Mg 1	0	0
48	G2	6	Total 6	Mg 6	0	0
48	E2	7	Total 7	Mg 7	0	0
48	B2	8	Total 8	Mg 8	0	0
48	AA	2	Total 2	Mg 2	0	0
48	BQ	2	Total 2	Mg 2	0	0
48	CQ	2	Total 2	Mg 2	0	0
48	BJ	1	Total 1	Mg 1	0	0
48	EW	2	Total 2	Mg 2	0	0
48	FA	2	Total 2	Mg 2	0	0
48	H1	155	Total 155	Mg 155	0	0
48	A1	200	Total 200	Mg 200	0	0
48	CN	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
48	BN	1	Total 1	Mg 1	0	0
48	GQ	1	Total 1	Mg 1	0	0
48	B3	3	Total 3	Mg 3	0	0
48	CJ	1	Total 1	Mg 1	0	0
48	GL	1	Total 1	Mg 1	0	0
48	DA	2	Total 2	Mg 2	0	0
48	HT	1	Total 1	Mg 1	0	0
48	C3	7	Total 7	Mg 7	0	0
48	GW	1	Total 1	Mg 1	0	0
48	EL	2	Total 2	Mg 2	0	0
48	D1	232	Total 232	Mg 232	0	0
48	DJ	1	Total 1	Mg 1	0	0
48	GP	2	Total 2	Mg 2	0	0
48	FT	1	Total 1	Mg 1	0	0
48	CW	1	Total 1	Mg 1	0	0
48	F1	184	Total 184	Mg 184	0	0
48	EJ	1	Total 1	Mg 1	0	0
48	C2	6	Total 6	Mg 6	0	0
48	BW	1	Total 1	Mg 1	0	0
48	GO	1	Total 1	Mg 1	0	0
48	CL	2	Total 2	Mg 2	0	0

- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
49	FA	1	Total	Zn	0	0
			1	1		
49	HK	1	Total	Zn	0	0
			1	1		
49	DK	1	Total	Zn	0	0
			1	1		
49	AK	1	Total	Zn	0	0
			1	1		
49	DC	1	Total	Zn	0	0
			1	1		
49	BY	1	Total	Zn	0	0
			1	1		
49	AC	1	Total	Zn	0	0
			1	1		
49	DL	1	Total	Zn	0	0
			1	1		
49	HL	1	Total	Zn	0	0
			1	1		
49	FK	1	Total	Zn	0	0
			1	1		
49	AA	1	Total	Zn	0	0
			1	1		
49	DA	1	Total	Zn	0	0
			1	1		
49	EY	1	Total	Zn	0	0
			1	1		
49	HC	1	Total	Zn	0	0
			1	1		
49	GY	1	Total	Zn	0	0
			1	1		
49	FC	1	Total	Zn	0	0
			1	1		
49	FL	1	Total	Zn	0	0
			1	1		
49	AL	1	Total	Zn	0	0
			1	1		
49	CY	1	Total	Zn	0	0
			1	1		
49	HA	1	Total	Zn	0	0
			1	1		

- Molecule 50 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
50	A1	1134	Total 1134	O 1134	0	0
50	AA	8	Total 8	O 8	0	0
50	AB	5	Total 5	O 5	0	0
50	AH	1	Total 1	O 1	0	0
50	AK	3	Total 3	O 3	0	0
50	AM	1	Total 1	O 1	0	0
50	AP	2	Total 2	O 2	0	0
50	AT	3	Total 3	O 3	0	0
50	AU	4	Total 4	O 4	0	0
50	B2	54	Total 54	O 54	0	0
50	B3	23	Total 23	O 23	0	0
50	BA	12	Total 12	O 12	0	0
50	BB	4	Total 4	O 4	0	0
50	BC	7	Total 7	O 7	0	0
50	BE	1	Total 1	O 1	0	0
50	BI	3	Total 3	O 3	0	0
50	BJ	5	Total 5	O 5	0	0
50	BK	3	Total 3	O 3	0	0
50	BL	8	Total 8	O 8	0	0
50	BM	2	Total 2	O 2	0	0
50	BN	5	Total 5	O 5	0	0
50	BO	2	Total 2	O 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
50	BP	5	Total	O	0	0
			5	5		
50	BQ	7	Total	O	0	0
			7	7		
50	BU	1	Total	O	0	0
			1	1		
50	BV	7	Total	O	0	0
			7	7		
50	BW	5	Total	O	0	0
			5	5		
50	BX	6	Total	O	0	0
			6	6		
50	BY	5	Total	O	0	0
			5	5		
50	C2	46	Total	O	0	0
			46	46		
50	C3	39	Total	O	0	0
			39	39		
50	CA	11	Total	O	0	0
			11	11		
50	CB	4	Total	O	0	0
			4	4		
50	CC	7	Total	O	0	0
			7	7		
50	CD	4	Total	O	0	0
			4	4		
50	CE	2	Total	O	0	0
			2	2		
50	CI	1	Total	O	0	0
			1	1		
50	CJ	4	Total	O	0	0
			4	4		
50	CK	3	Total	O	0	0
			3	3		
50	CL	12	Total	O	0	0
			12	12		
50	CM	6	Total	O	0	0
			6	6		
50	CN	7	Total	O	0	0
			7	7		
50	CO	2	Total	O	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
50	CP	6	Total 6	O 6	0	0
50	CQ	7	Total 7	O 7	0	0
50	CU	1	Total 1	O 1	0	0
50	CV	4	Total 4	O 4	0	0
50	CW	5	Total 5	O 5	0	0
50	CX	6	Total 6	O 6	0	0
50	CY	5	Total 5	O 5	0	0
50	D1	1341	Total 1341	O 1341	0	0
50	DA	10	Total 10	O 10	0	0
50	DB	4	Total 4	O 4	0	0
50	DE	1	Total 1	O 1	0	0
50	DJ	2	Total 2	O 2	0	0
50	DK	2	Total 2	O 2	0	0
50	DP	1	Total 1	O 1	0	0
50	DQ	2	Total 2	O 2	0	0
50	DT	4	Total 4	O 4	0	0
50	DU	3	Total 3	O 3	0	0
50	DX	2	Total 2	O 2	0	0
50	E2	44	Total 44	O 44	0	0
50	E3	34	Total 34	O 34	0	0
50	EA	4	Total 4	O 4	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
50	EB	3	Total 3	O 3	0	0
50	EC	2	Total 2	O 2	0	0
50	EE	2	Total 2	O 2	0	0
50	EJ	4	Total 4	O 4	0	0
50	EK	5	Total 5	O 5	0	0
50	EL	10	Total 10	O 10	0	0
50	EM	2	Total 2	O 2	0	0
50	EN	7	Total 7	O 7	0	0
50	EP	6	Total 6	O 6	0	0
50	EQ	4	Total 4	O 4	0	0
50	EV	6	Total 6	O 6	0	0
50	EW	7	Total 7	O 7	0	0
50	EX	5	Total 5	O 5	0	0
50	EY	5	Total 5	O 5	0	0
50	F1	1076	Total 1076	O 1076	0	0
50	FA	7	Total 7	O 7	0	0
50	FB	4	Total 4	O 4	0	0
50	FE	1	Total 1	O 1	0	0
50	FH	1	Total 1	O 1	0	0
50	FK	2	Total 2	O 2	0	0
50	FL	3	Total 3	O 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
50	FP	2	Total	O	0	0
			2	2		
50	FT	4	Total	O	0	0
			4	4		
50	FU	4	Total	O	0	0
			4	4		
50	G2	34	Total	O	0	0
			34	34		
50	G3	26	Total	O	0	0
			26	26		
50	GA	6	Total	O	0	0
			6	6		
50	GB	3	Total	O	0	0
			3	3		
50	GC	2	Total	O	0	0
			2	2		
50	GE	2	Total	O	0	0
			2	2		
50	GI	1	Total	O	0	0
			1	1		
50	GJ	4	Total	O	0	0
			4	4		
50	GK	2	Total	O	0	0
			2	2		
50	GL	5	Total	O	0	0
			5	5		
50	GM	1	Total	O	0	0
			1	1		
50	GN	2	Total	O	0	0
			2	2		
50	GO	2	Total	O	0	0
			2	2		
50	GP	5	Total	O	0	0
			5	5		
50	GQ	4	Total	O	0	0
			4	4		
50	GV	3	Total	O	0	0
			3	3		
50	GW	4	Total	O	0	0
			4	4		
50	GX	5	Total	O	0	0
			5	5		

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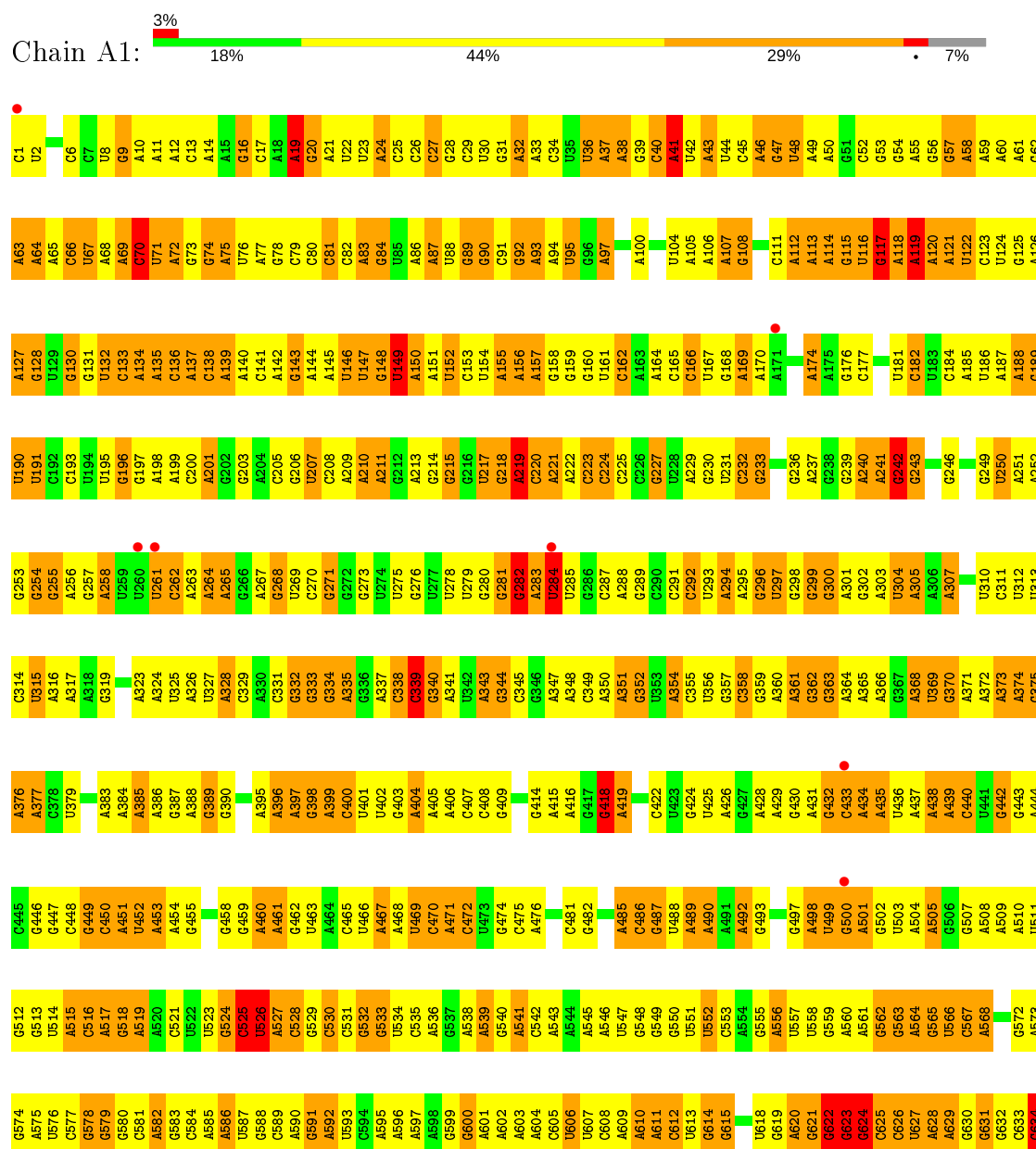
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
50	GY	1	Total 1	O 1	0	0
50	H1	924	Total 924	O 924	0	0
50	HA	4	Total 4	O 4	0	0
50	HB	4	Total 4	O 4	0	0
50	HJ	2	Total 2	O 2	0	0
50	HK	2	Total 2	O 2	0	0
50	HP	1	Total 1	O 1	0	0
50	HT	5	Total 5	O 5	0	0
50	HU	2	Total 2	O 2	0	0

3 Residue-property plots

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

• Molecule 1: 26S rRNA



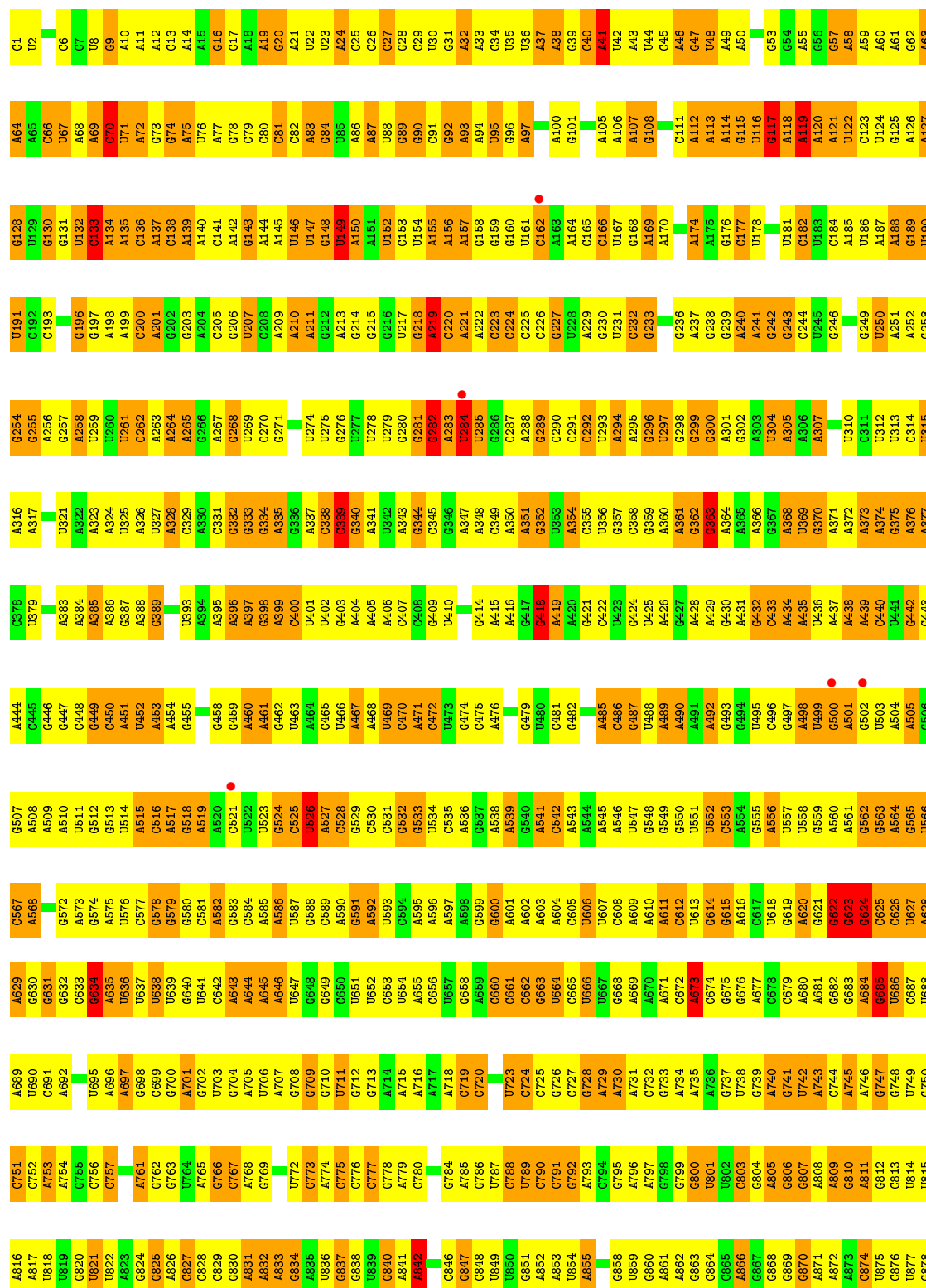

A1459	G1392	G1332	A	A1207	C1146	U1083	A1022	U960	C885	U821	C757	A697	A635
G1460	A1393	U1332	U	U1208	A1147	G1084	A1023	A961	C886	U822		G698	U636
U1461	G1394	G1333	G	G1209	U1148	G1085	A1024	G962		A823	A761	C699	U637
U1462	U1395	G1334	G	C1210	U1149	G1086	G1025	C963	G894	G824	G762	G700	U638
C1463	A1396	U1335	A	A1211	U1150	A1087	C1026	U964	A895	G825	G763	G701	U639
U1464	G1397	U1336	A	C1212	U1151	A1088	G1027	U965	U896	A826	G764	G702	G640
U1465	G1398	G1337	G	G1213	U1152	G1089	A1028	G966	A897	C827	A765	U703	U641
G1466	A1399	G1338	U	C1214	G1153	A1090	A1029	U967	C898	C828	G766	G704	C642
G1467	G1400	G1339	U	U1215	G1154	G1091	U1030	U968	U899	G829	G767	A705	A643
U1468	G1401	G1340	U	C1216	U1155	G1092	G1031	C970		G830	A768	U706	A644
G1469	G1402	C1341	G	A1217		C1093		C971	U904	G831	G769	A707	A645
G1470	G1403	U1342	A	U1218	G1158	G1094	U1034	C972	G905	A832	U772	G708	A646
U1471	A	G1343	A	C1219	C1159	C1095	A1035	U972	C906	U833		G709	U647
U1472	U	A1344	U	A1220	A1160	G1096	G1036	C973	A907		G773	G710	G648
G1473	C	A1345	C	G1221	G1161	G1097	A1037	C974	A908	U836	A774	U711	G649
U1474	C		C	A1222	G1162	A1098	G1038	C975	A909	G837	G775	G712	C650
A1475	G		G	C1223	A1163	G1099	G1039	A976	U910	G838	G776	G713	U651
G1476	C		C	U1224	C1164	U1000	A1040	C978	C911	U839	G777	A714	U652
C1477	G		G	C1225	U1165	U1001	C1041	U979	G912	G840	G778	A715	C653
U1478	U		U	A1226	G1166	U1002	U1042	U980		A841	A779	A716	U654
U1479	A		A	C1227	G1167	U1003	U1043	U981	C915	A842	G780	A717	A655
U1480	G		G	C1228	C1168	C1104	U1044	C982	G916	C846		A718	U656
U1481	G		G	A1229	G1169	U1005	G1045	C983	U917	C847	G781	C719	U657
A1482	C		C	A1230	U1170	U1006	G1046	U984	U918	C848		G720	G658
	G		G	A1231	A1171	A1007	U1047	C984	A919	C849	G785	C721	A659
	U		U	A1232	G1172	A1008	U1048	U985	A920	U849	G786	G722	C660
	G		G	G1233	A1173	A1009	U1049	C986	A921	U850	U787	U723	C661
	U		U	A1234	G1174	U1110	C1050	C987	U922	G851	C788	C724	C662
	G		G	U1235	G1175	G1111	C1051	G988		A852	U789	C725	G663
	U		U	G1236	G1176	A1112	A1052	G989	G925	A853	G790	G726	U664
	C		C	U1237	A1177	A1113	A1053	A990	A926	U854	C791	C727	C665
	A		A	U1238	U1178	C1114	G1054	U991	C927	A855	G792	U666	U667
	C		C	G1239	G1179	U1115	A1055	A992	U928	G856	A793	A729	A668
	A		A	G1240	A1180	C1116	U1056	C993	G929	G857	G794	A730	A669
	C		C	U1241	A1181	U1057	A1057	C994	U930	G858	G795	A731	A670
	U		U	U1242	C1182	C1058	U1058	A995	A931	U859	A796	C732	C671
	C		C	A1243	G1183	U1059	U1059	G997	G932	G860	A797	G733	C672
	A		A	A1244	U1184	A1122	C1060	A998	G933	A861	G798	A734	A673
	U		U	U1245	A1185	A1123	G1061	G999	G934	A862	G799	A735	G674
	C		C	A1246	A1186	G1124	A1062		G935	G863	G800	G736	G675
	G		G	C1247	C1187	A1125	C1063		C936	C864	U801	U737	G676
	U		U	G1248	G1188	A1126	U1064		C937	C865	U802	U738	
	C		C	A1249	U1189	U1127	U1065		A938	A866	C803	G739	
	A		A	C1250	U1190	G1128	A1066		A939	G867	G804	A740	C679
	U		U	U1251	G1191	C1129	U1067		A940	C868	A805	G741	A680
	C		C	A1252	A1192	A1130	U1068		G941	G869	G806	U742	A681
	G		G	G1253	G1193	G1131	C1069		A942	G870	G807	A743	G682
	U		U	C1254	A1194	U1132	U1070		C943	A871	A808	C744	G683
	C		C	A1255	U1195	G1133	C1071		U944	A872	A809	A745	A684
	G		G	G1256	A1196	C1134	A1072		A945	A873	G810	A746	G685
	U		U	G1257	A1197	U1135	A1073		A946	C874	A811	G747	U686
	A		A	A	G1198	C1136	A1074		U947	U875	G812	G748	C687
	C		C	C	G1199	U1137	C1075		C948	C876	G813	U749	U688
	G		G	U	C1200	U1138	U1076		C949	U877	U814	G750	A689
	U		U	U	G1201		U1077		A950		U815	C751	U690
	C		C	G	C1202	U1141	U1078		A951	U880	A816	C752	C691
	U		U	G	C1203		A1079			G881	A817	A753	A692
	C		C	U	C1204	G1142	A1080			G882	U818	A754	U695
	G		G	G	A1205	G1143	A1081			A883	U819	G755	A696
	U		U	U	A1206	C1145	U1082			A884	G820	C756	

G2371	U2309	G2246	A2178	A2113	U	A	G1926	U1854	C	A1721	A1853	G1592
G2372	G2310	A2247	U2179	C2114	U	A	U1927	U1855	C		G1654	U1526
U2375	G2311	G2248	G2180	A2115	U	A	C1928	C1856	U	U1724	A1655	A1593
A2376	A2312	U2249	U2181	A2116	G	G	G1929	G1857	A	A1725	G1656	A1527
G2377	U2313	G2250	G2182	G2117	C	A	G1930	U1858	A	C1726	C1657	U1596
A2378		A2251	A2183	G2118	U	U	C1931			U1727	G1658	U1597
U2379	A2316	C2252	U2184	G2119	A	A	A1932	C1861	G1792	A1728	G1659	U1598
U2380	G2317	U2253	U2185	U2120	G	U	A1933	C1862	A1793	U1729	U1660	G1599
A2381	U2318	U2254	U2186	A2121	G	C		A1863	C1795	G1730	A1601	A1535
A2382	A2319	U2255	C2187	A2122	U	C	U1936	A1864	G1796	G1731	G1602	A1536
U2383	G2320	G2256	U2188	U2123	A	A	G1937	A1865	G1797	C1732	U1603	U1537
U2384	A2321	A2257	G2189	C2124	G	A	G1938	A1866	U1798	C1733	G1604	U1538
A2385	C2322	C2258	C2190	C2125	G	G		A1867	C1799	A1734	G1605	G1539
A2386	U2323	U2259	C2191	G2126	U	C	C1941	C1868	A1800	U1735	U1606	U1540
A2387	A2324	C2260	C2192	A2127	U	U	G1942	G1869	G1801	A1667	G1606	U1541
G2388	C2325	U2261	A2193	C2128	U	U	G1943	C1870	U1802	A1737	U1607	U1542
G2389	C2326	C2262	G2194	U2129	C	U	U1944	A1871	U1803	A1738	G1608	C1543
G2390	A2327	U2263	U2195	G2130	G	U	G1945	U1872	G1804	A1739	U1609	A1543
G2391	G2328	U2264	G2196	U2131	C	U	A1946	C1873	C1805	U1740	C1610	U1544
G2392	U2329	A2265	C2197	U2132	G	U	C1947	A1874	A1806	U1741	G1545	G1546
A2393	G2330	A2266	U2198	U2133	C	G	U1948	G1875	A1807	G1742	A1612	
A2394	U2331	G2267	C2199	A2134	G	U	U1949	A1876	A1808	G1743	A1613	G1547
A2395	C2332	G2268	U2200	A2135	U	U	C1950	C1880	C1809	A1744	U1548	
A2396	G2333	U2269	G2201	U2136	C	A	G1951	C1881	G1810	U1745	G1615	U1549
A2397	C2334	A2270	A2202	A2137	U	G	G1952	A1882	U1811	U1746	G1616	A1550
G2398	U2335	G2271	A2203	A2138	U	U	G1953	A1883	A1812	A1747	C1617	U1551
A2399	A2336	C2272	U2204	A2139	U	G	A1954	G1884	A1813	U1748	A1618	U1552
C2400	U2339	A2273		A2140	A	U	U1955	G1885	U1814	A1619	C1563	
	A2340	A2274	A2205	A2141	U	G	A1956	U1886	A1815	U1751	U1620	G1564
U2403	U2341	A2275	A2206	C2142	A	G	A1957	C1890	A1816	G1752	A1621	
G2404	U2342	U2276	G2210	A2143	C	C	G1958	A1891	C1817	A1753	G1622	A1561
U2405	A2343	G2277	U2211	A2144	A	A		A1892	C1818	G1754		G1562
U2406	U2344	C2278	U2212	A2145	U	A	G1963	U1893	A1819	A1755	U1625	A1563
G2407	U2345	A2279	G2213	G2146	U	C	C1964	U1894	U1820	U1756	G1626	A1564
A2408	C2346	C2280	A2214	C2147	U	A	U1895	U1895	U1821	A1757	A1627	A1565
G2409	U2347	U2281	C2215	A2148	A	U	U1966	C1896	G1822	U1758	A1628	U1566
C2410	G2348	G2282	G2216	U2149	A	G	C1967	U1897	A1823	C1759	U1629	A1567
U2411	C2349	U2283	A2217		C	C			A1824	G1760	C1630	
U2412	U2350	C2285	A2218	A2150	G	U	G1971	C1901	A1825	U1697	U1631	U1570
A2413	A2351	A2286	U2220	C2154	A	G	G1972	C1902	G1972	A1766	G1632	U1571
A2414	A2352		U2221	A2155	U	A	A1973	A1903	C1828	U1767	G1633	A1572
C2415	C2353		C2222	G2156	C	U	U1974	U1904	G1768	A1700	C1634	A1573
U2416	G2354	U2289	A2223	G2157	A	A	C	A1905	U1769	A1701	U1635	C1574
A2417	U2355	A2291		C2158	A	G	G	U1906	G1833	A1770	C1636	U1575
U2418	A2356	U2292	A2227	C2159	C2097	C	G	A1907	G1834	U1771	A1637	C1576
U2419	C2357	U2293	A2228	A2162	U2098	C	U	U1908	G1772	G1772	A1638	C1577
G2420	A2358	A2294	G2229	A2163	C2099	U	A	C1909	U1840	G1773	G1639	U1578
U2421	G2359			C2164	A2100	U	U	A1910	U1841	C1774	C1640	U1579
C2422		A2298		A2165	G2101	G	U		A1841	A1775	U1641	G1580
U2423	U2361	G2299	G2235	G2166	A2102	C	A	G1913	U1842	G1776	G1642	C1581
A2424	A2362	A2237	A2237	A2167	A2103	G	A		U1843	G1777	G1643	A1582
A2425	A2363	G2300	A2238	U2168	C2104	A	A	A1917	A1844	G1778	A1644	A1583
C2426	G2364	G2302	A2239	G2169	U2105	A	G	U1918	U1845	C1779	C1645	U1584
	C2365	C2303	G2240	A2170	G2106	C	G	A1919	C1846	A1780	G1646	A1585
U2429	G2366	A2304	G2241	U2171	A2107	G	C	U1920	A1847	G1781	U1647	C1586
G2430	A2367	U2305	G2242	G2172	A2108	A	U	G1921	C1848	U1716	G1648	A1587
U2431	A2368	C2306	G2243	A2173	G2109	U	U	G1922	G1849	U1717	C1782	A1588
G2432	C2369	A2307	G2244		C2110	G	U	G1923	G1849	U1718	U1650	G1589
A2433	U2370	A2308	G2245	A2177	G2111	A	U	A1924	A1852	U1719	A1651	A1590
	C2370		G2246	A2177	C2112	A	U	A1925	C1852	A1720	G1652	A1591

C3276	G3213	U3088	A3022	A2988	G2827	U2762	A2626	A2561	A2434
A3277	A3214	U3150	C3023	C2899	A2828	U2763	C2627	U2562	A2435
U3278	G3151	G3091	A3024	G2900	G2829	A2764	U2630	G2563	U2436
	G3152	A3092	U3027	U2901	U2830	C2765	U2631	U2564	G2437
	U3153	U3093	U3028	G2902	C2832	A2766	A2632	U2565	G2438
	U3154	U3094	A3029	U2903	A2833	A2767	C2633	U2499	G2439
	A3155	A3095	A3029	G2904	U2833	G2768	C2634	C2500	A2440
	A3156	U3096	A3030	G2905	U2837	G2769	G2635	A2501	C
	G3157	G3097	U3031	G2906	G2838	U2770	A2636	A2502	G
	G3158	A3098	C3032	A2907	G2839	U2771	G2637	U2503	G
	G3159	G3099	A3033	U2908	C2840	U2772	A2638	U2504	U
	A3160	U3100	G3034	G2909	A2773	A2773	G2639	U2505	G
	A3161	G3101	A3035	U2911	G2774	G2774	C2640	U2506	G
	A3162	A3102	U3036	U2912	C2775	G2775	G2641	C2507	G
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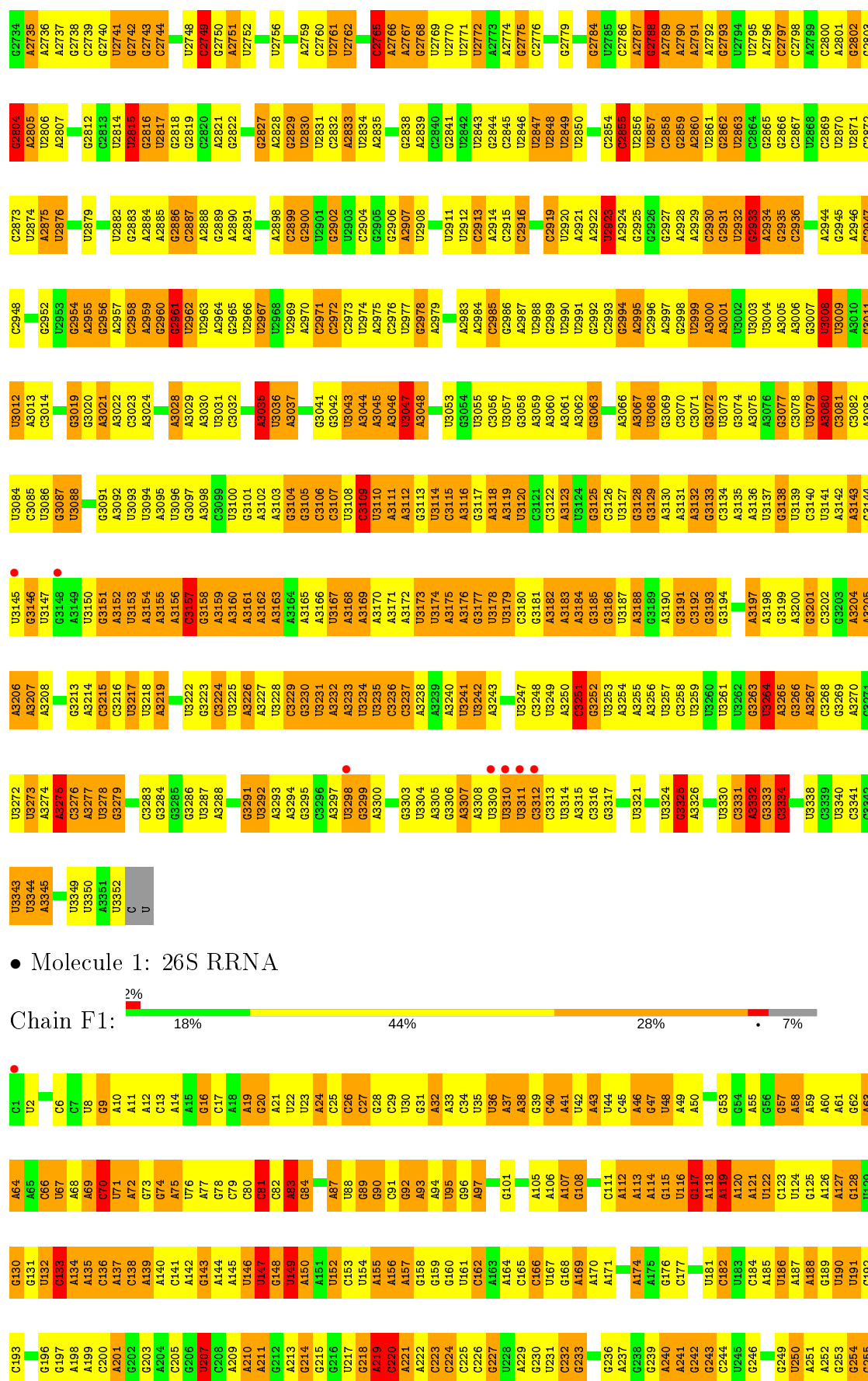
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● Molecule 1: 26S RRNA

Chain D1: 











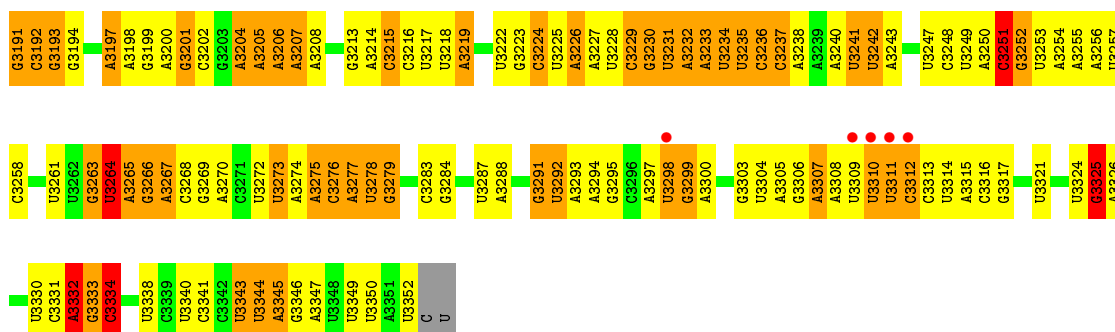




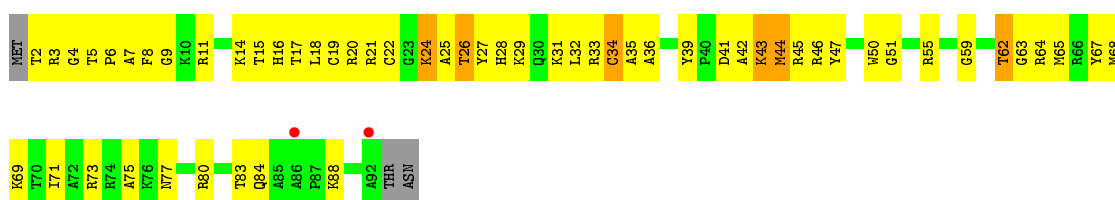




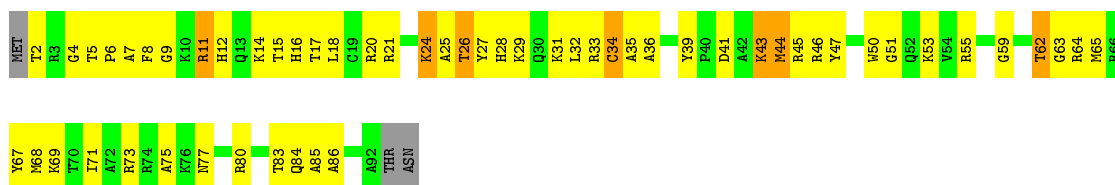
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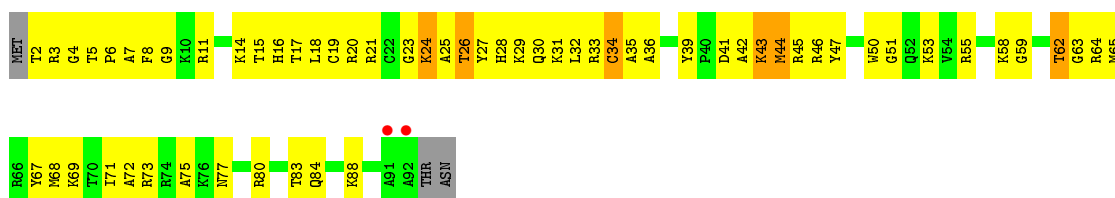
• Molecule 2: RIBOSOMAL PROTEIN L37



• Molecule 2: RIBOSOMAL PROTEIN L37



• Molecule 2: RIBOSOMAL PROTEIN L37



• Molecule 2: RIBOSOMAL PROTEIN L37

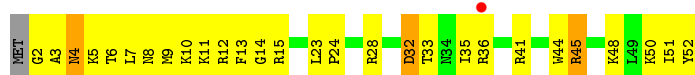




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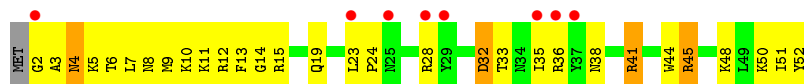
• Molecule 3: RPL39



• Molecule 3: RPL39



• Molecule 3: RPL39



• Molecule 4: 60S RIBOSOMAL PROTEIN L36A

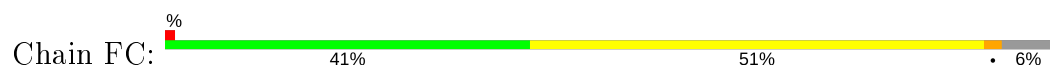


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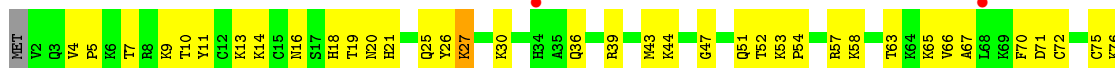
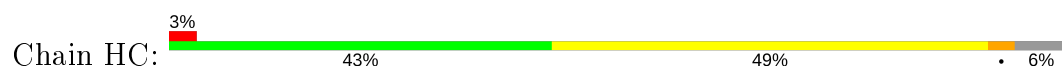




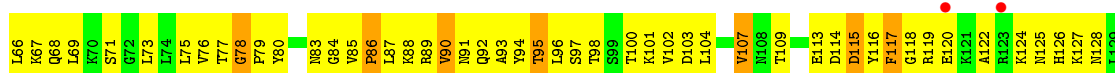
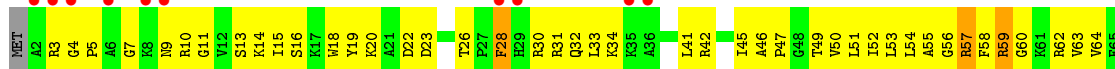
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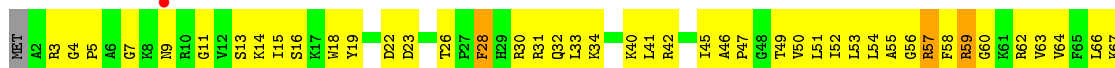
• Molecule 4: 60S RIBOSOMAL PROTEIN L36A



• Molecule 5: RPL6

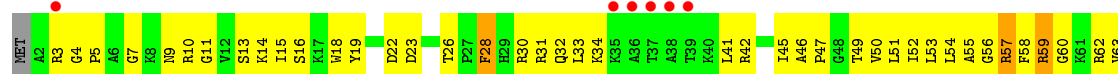


• Molecule 5: RPL6

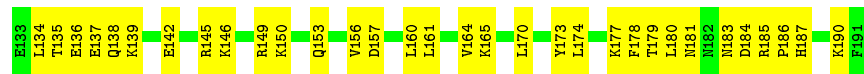
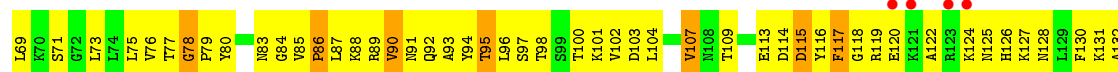
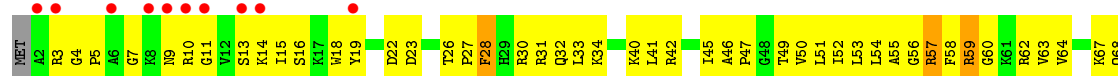




• Molecule 5: RPL6



• Molecule 5: RPL6

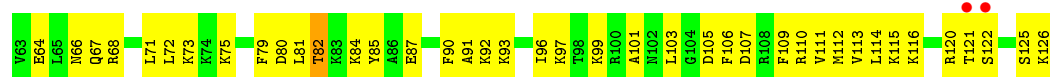


• Molecule 6: RPL14

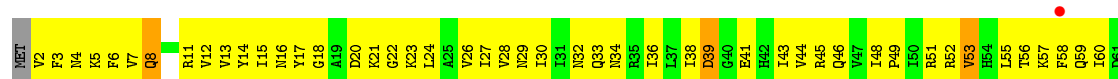


• Molecule 6: RPL14

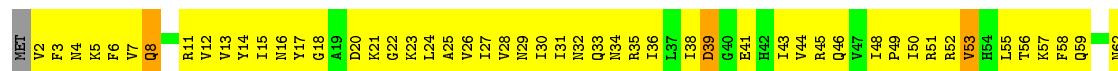
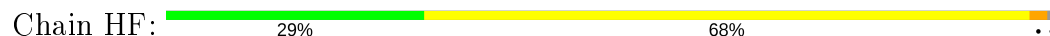




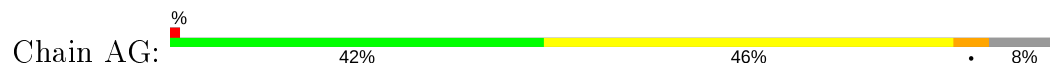
• Molecule 6: RPL14



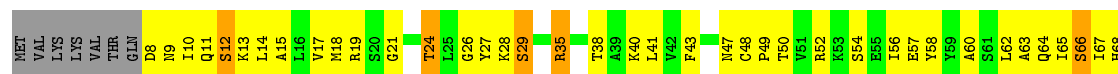
• Molecule 6: RPL14



• Molecule 7: RPL30

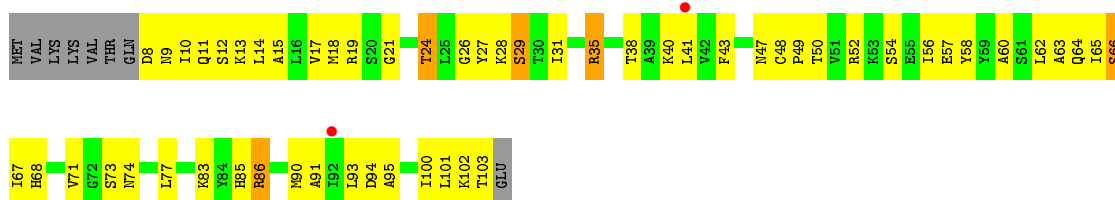


• Molecule 7: RPL30

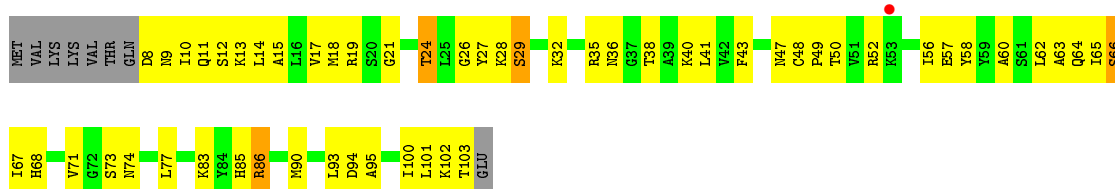


• Molecule 7: RPL30

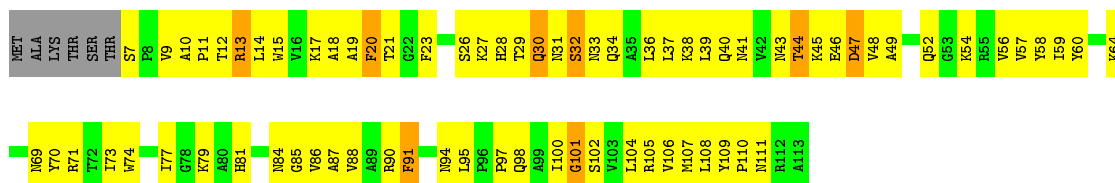




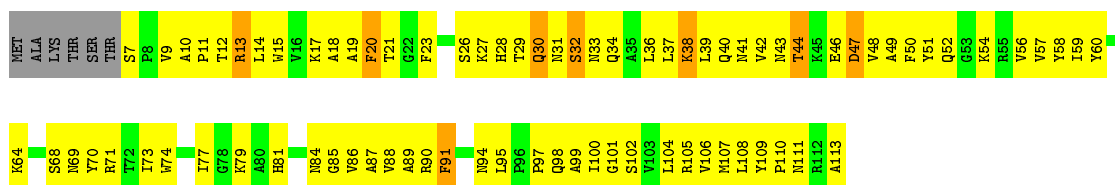
• Molecule 7: RPL30



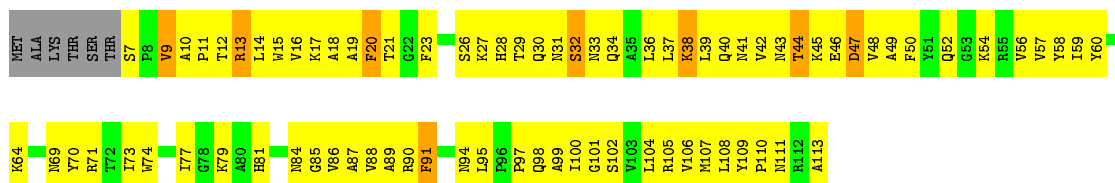
• Molecule 8: RPL35A



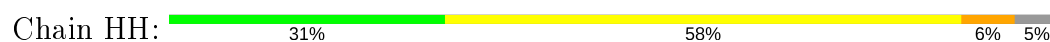
• Molecule 8: RPL35A

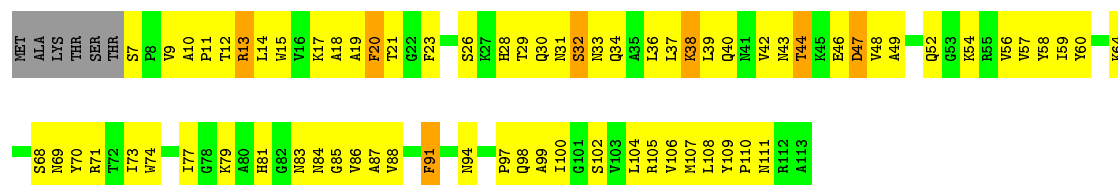


• Molecule 8: RPL35A



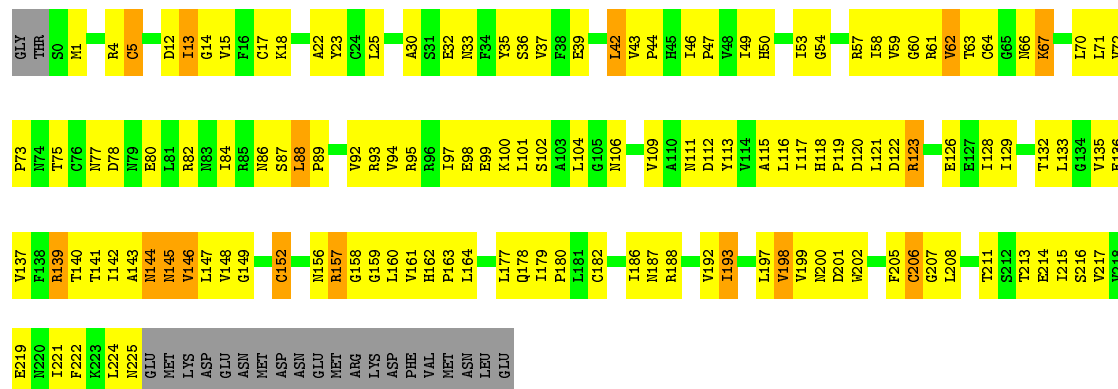
• Molecule 8: RPL35A





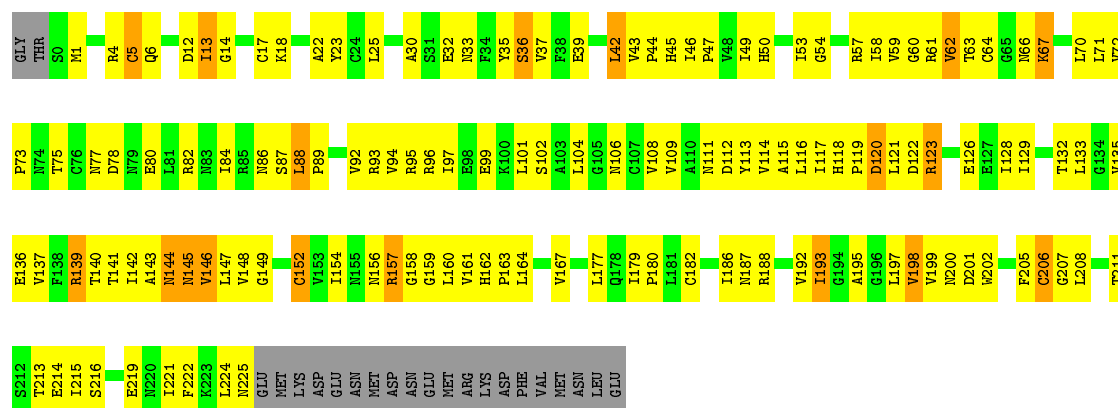
• Molecule 9: TRANSLATION INITIATION FACTOR EIF-6, PUTATIVE FAMILY PROTEIN

Chain AJ: 36% 49% 6% 9%



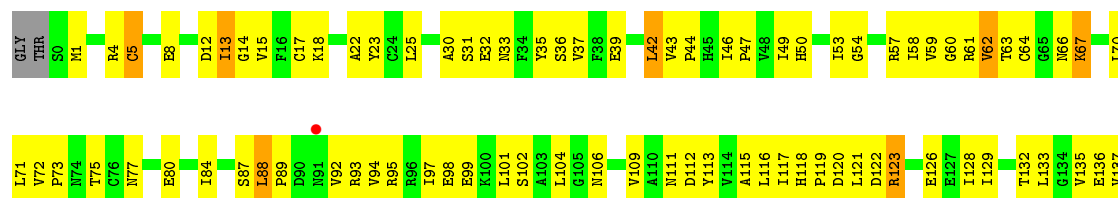
• Molecule 9: TRANSLATION INITIATION FACTOR EIF-6, PUTATIVE FAMILY PROTEIN

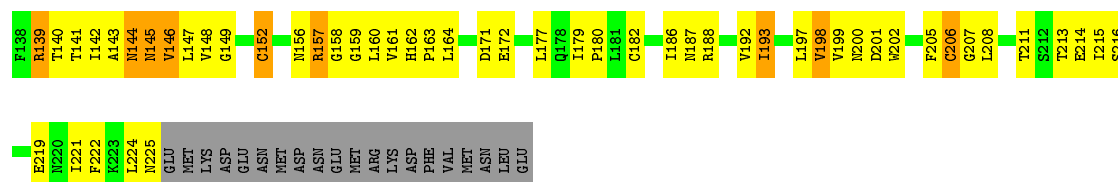
Chain DJ: 35% 49% 7% 9%



• Molecule 9: TRANSLATION INITIATION FACTOR EIF-6, PUTATIVE FAMILY PROTEIN

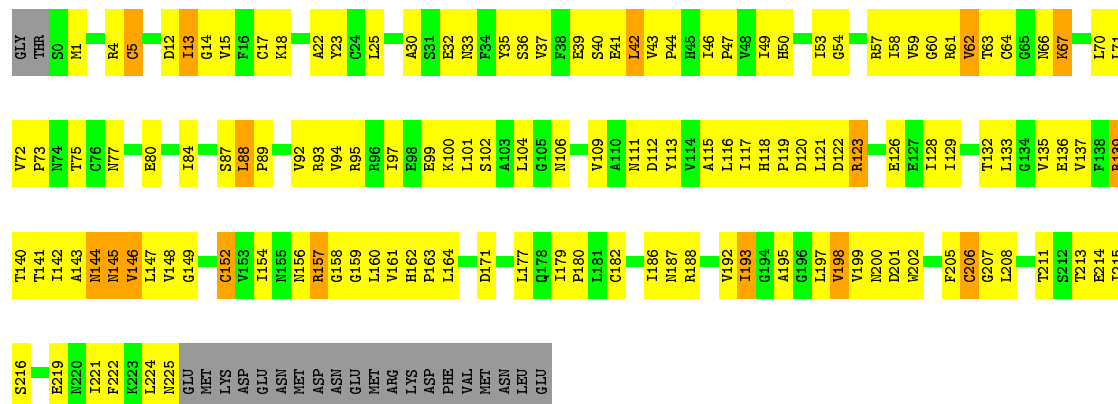
Chain FJ: 37% 48% 6% 9%





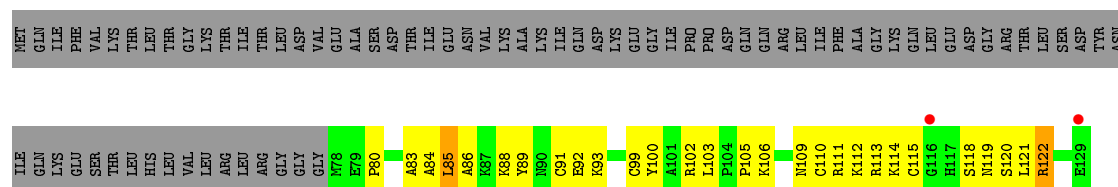
• Molecule 9: TRANSLATION INITIATION FACTOR EIF-6, PUTATIVE FAMILY PROTEIN

Chain HJ: 36% 48% 6% 9%



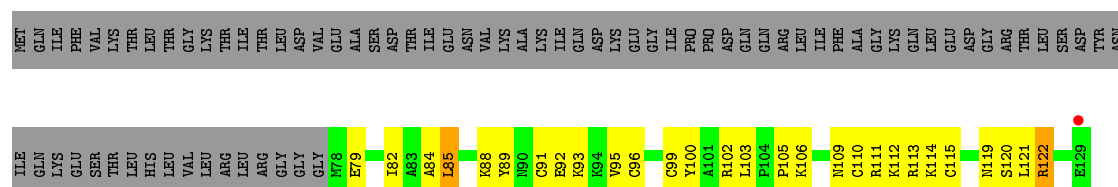
• Molecule 10: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain AK: 29% 19% 20% 60%



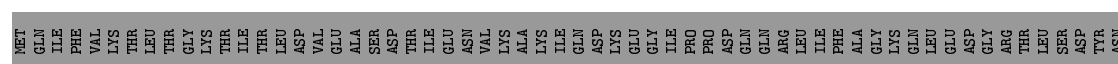
• Molecule 10: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain DK: 19% 20% 60%



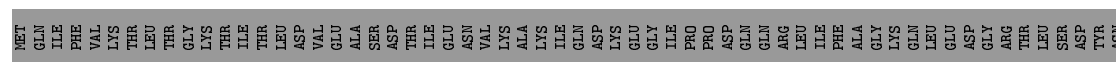
• Molecule 10: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain FK: 19% 19% 60%

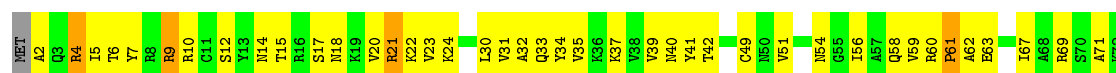




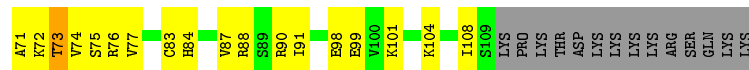
• Molecule 10: UBIQUITIN-60S RIBOSOMAL PROTEIN L40



• Molecule 11: RPL34



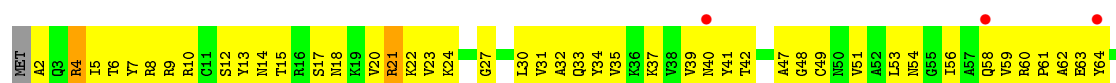
• Molecule 11: RPL34



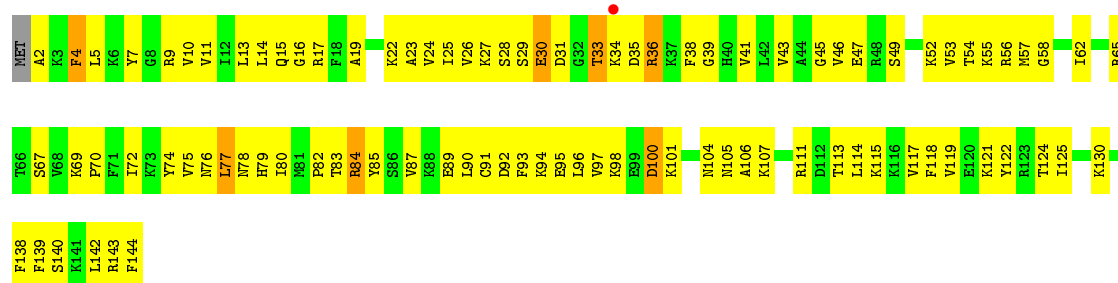
• Molecule 11: RPL34



• Molecule 11: RPL34



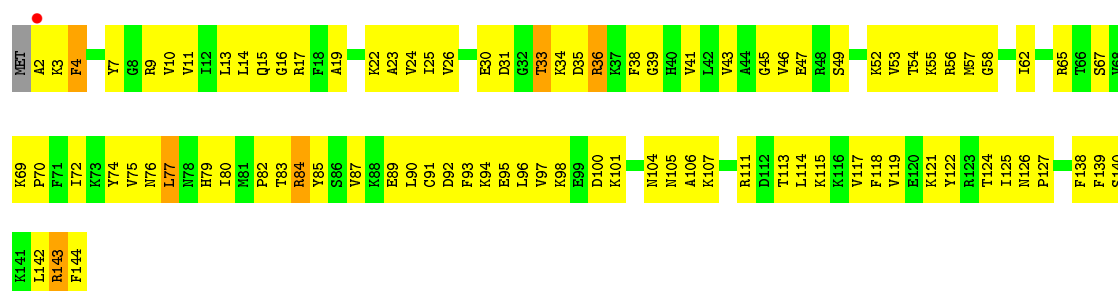




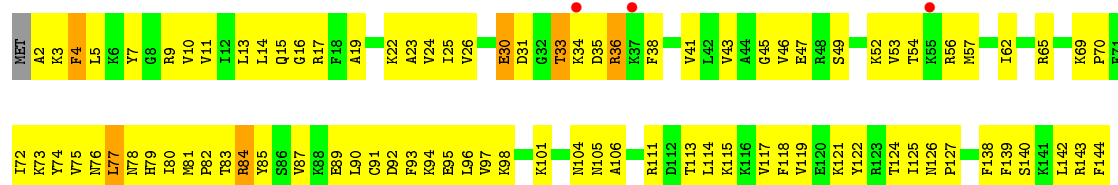
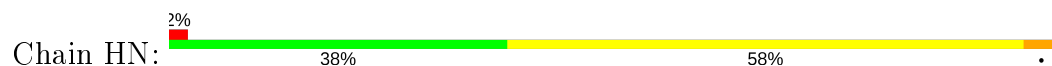
• Molecule 13: RPL27



• Molecule 13: RPL27

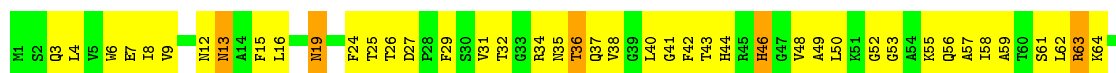


• Molecule 13: RPL27

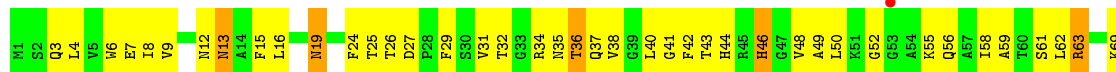
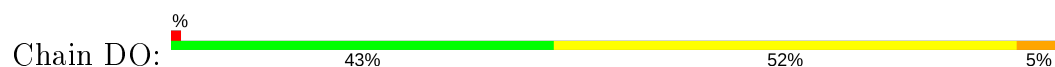


• Molecule 14: RPL28

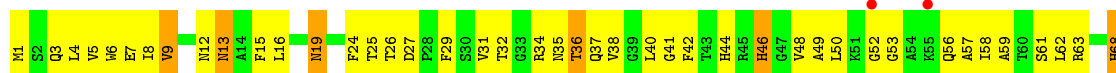
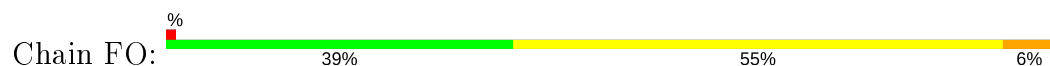




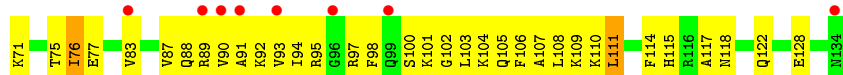
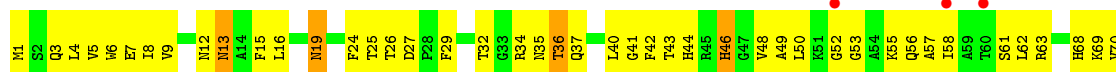
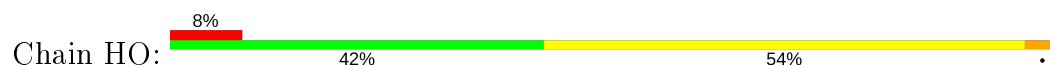
• Molecule 14: RPL28



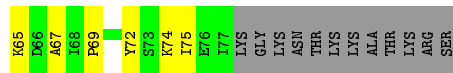
• Molecule 14: RPL28



• Molecule 14: RPL28



• Molecule 15: RPL38



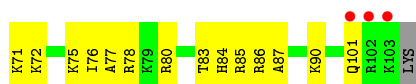
• Molecule 15: RPL38

MET	P2	K3	E4	T5	T6	D7	I8
I64	K65	D66	A67	I68	P69	A70	T71
Y72	S73	K74	I75	E76	LYS	GLY	LYS
ASN	THR	LYS	THR	ALA	ALA	LYS	THR
ARG	SER	K28	K29	V30	V31	V32	V33
K34	T35	R38	T39	T40	K41	F42	K43
L44	R45	G46	K47	K48	Y49	L50	V51
T52	F53	K54	T55	A56	D57	P58	X59
T60	A61						

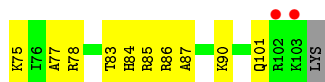
D66	A67	I68	P69	A70	T71	Y72	S73	K74	I75	E76	I77	GLY	LYS	ASN	THR	LYS	LYS	LYS	ALA	ALA	THR	LYS	ARG	ALA	GLY	ALA	K28	K29	V30	V31	V32	V33	K34	I39	T40	K41	F42	K43	L44	R45	G46	K47	K48	Y49	L50	Y51	T52	F53	K54	T55	A56	D57	P58	R59	L60	A61	L64	V65
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Label	Value	Color
D69	1	Red
S70	2	Green
K71	3	Yellow
K75	4	Green
I76	5	Yellow
R78	6	Yellow
A77	7	Yellow
R78	8	Yellow
T83	9	Green
H84	10	Yellow
R85	11	Yellow
R86	12	Yellow
A87	13	Yellow
K90	14	Yellow
Q101	15	Yellow
R102	16	Yellow
K103	17	Yellow
LNS	18	Grey
K21	19	Yellow
K22	20	Yellow
K23	21	Yellow
K24	22	Yellow
H25	23	Yellow
S26	24	Yellow
A27	25	Yellow
V28	26	Yellow
Q29	27	Yellow
R30	28	Yellow
K31	29	Yellow
G32	30	Yellow
K33	31	Yellow
L34	32	Yellow
G35	33	Yellow
K36	34	Yellow
R37	35	Yellow
L40	36	Yellow
V41	37	Yellow
R42	38	Yellow
Q43	39	Yellow
V44	40	Yellow
L45	41	Yellow
R46	42	Yellow
E47	43	Yellow
V48	44	Yellow
T49	45	Yellow
G50	46	Yellow
F51	47	Yellow
A52	48	Yellow
E55	49	Yellow
K56	50	Yellow
R57	51	Yellow
L58	52	Yellow
E59	53	Yellow
E60	54	Yellow
L61	55	Yellow
L62	56	Yellow
V63	57	Yellow

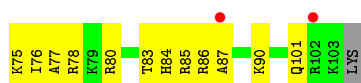
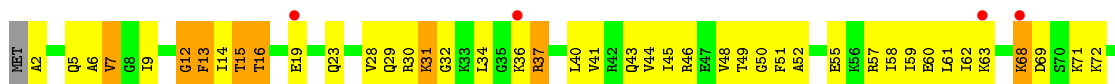
[illegible]



● Molecule 16: 60S RIBOSOMAL PROTEIN L36



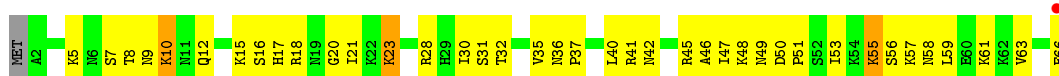
● Molecule 16: 60S RIBOSOMAL PROTEIN L36



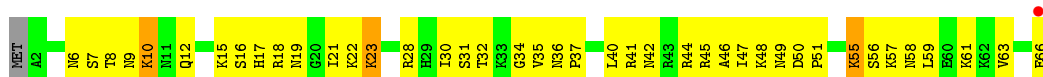
● Molecule 17: RPL29



● Molecule 17: RPL29

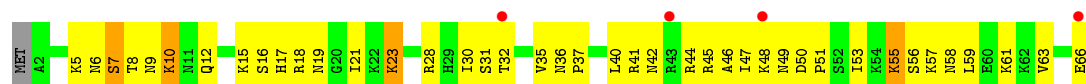


● Molecule 17: RPL29



● Molecule 17: RPL29





• Molecule 18: RPL13



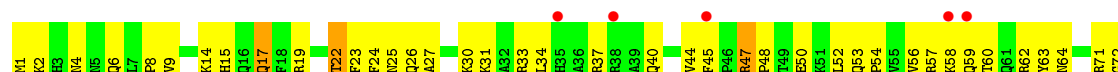
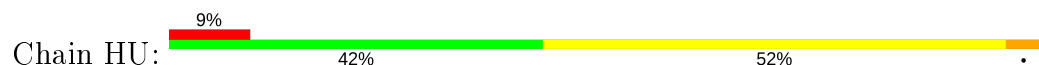
• Molecule 18: RPL13

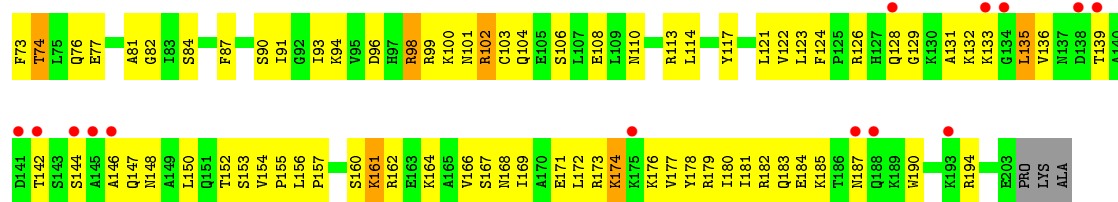


• Molecule 18: RPL13

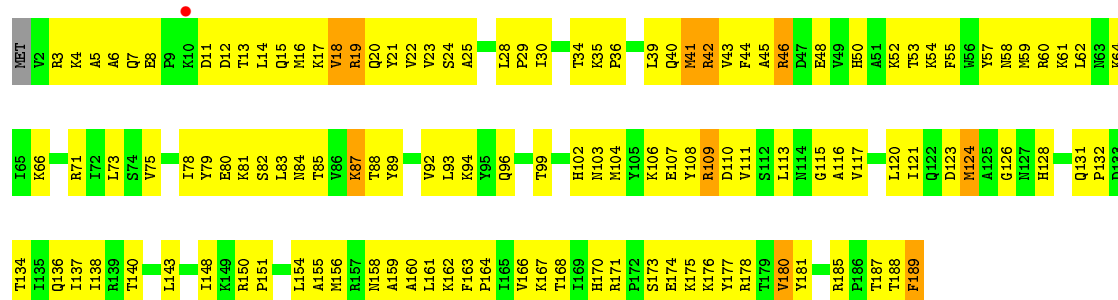


• Molecule 18: RPL13

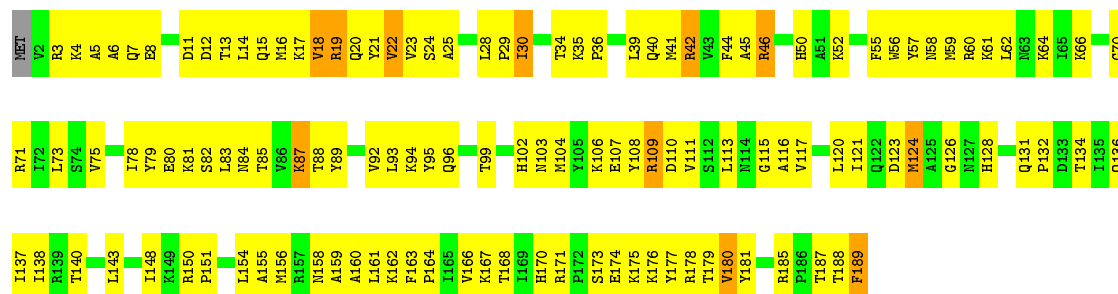




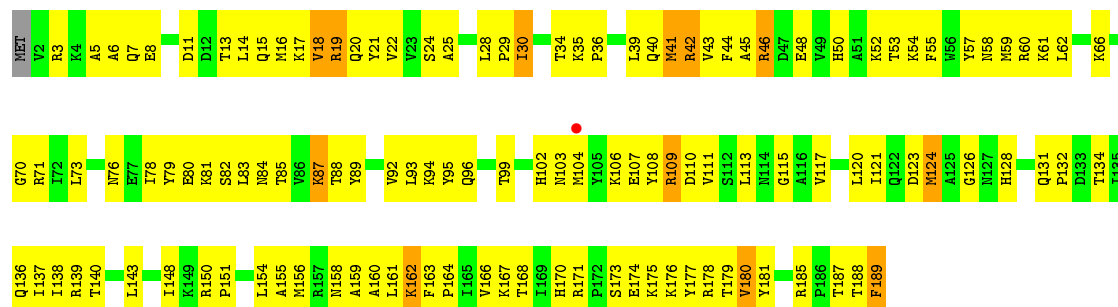
• Molecule 19: RPL18A



• Molecule 19: RPL18A

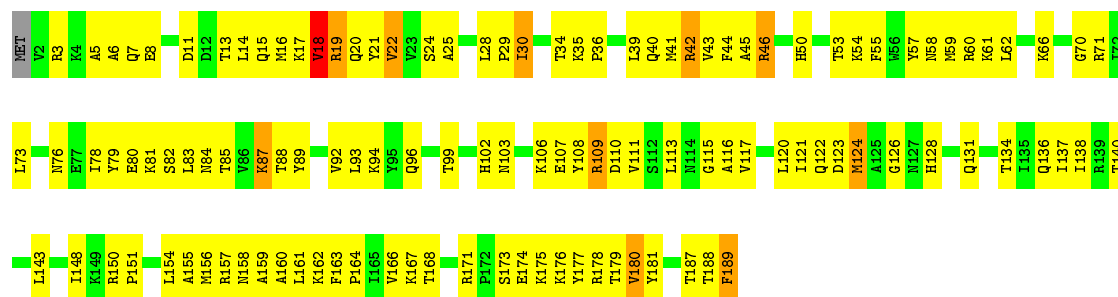


• Molecule 19: RPL18A

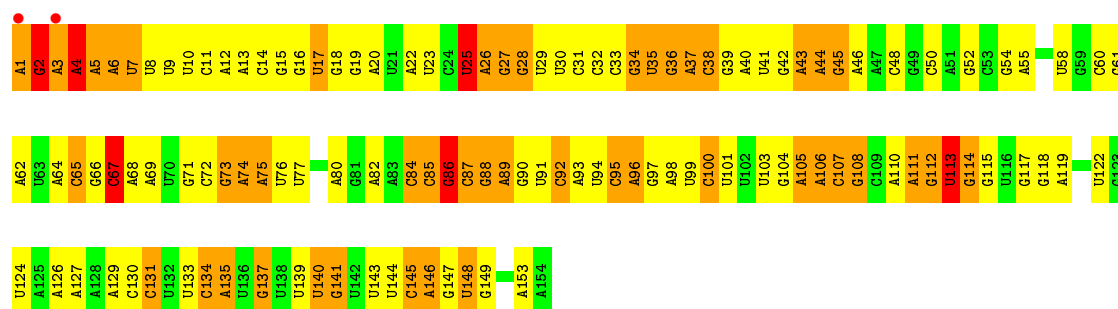
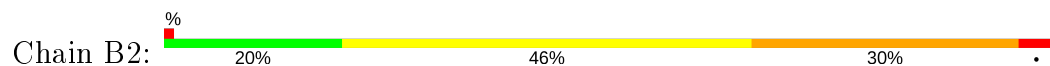


• Molecule 19: RPL18A

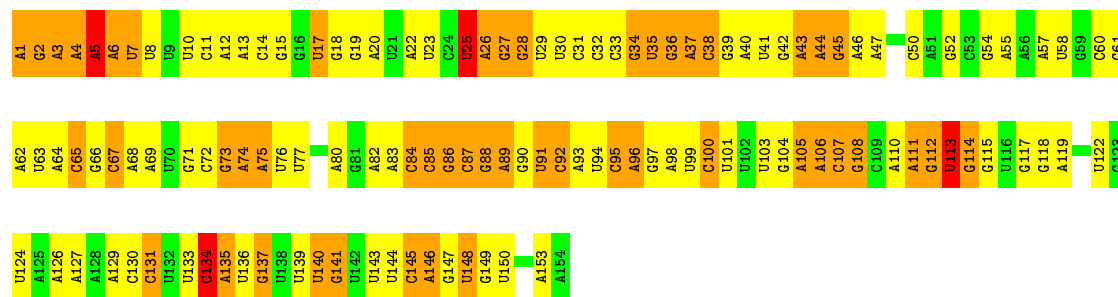
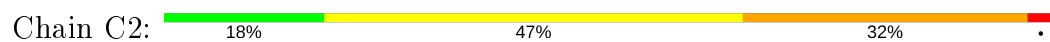




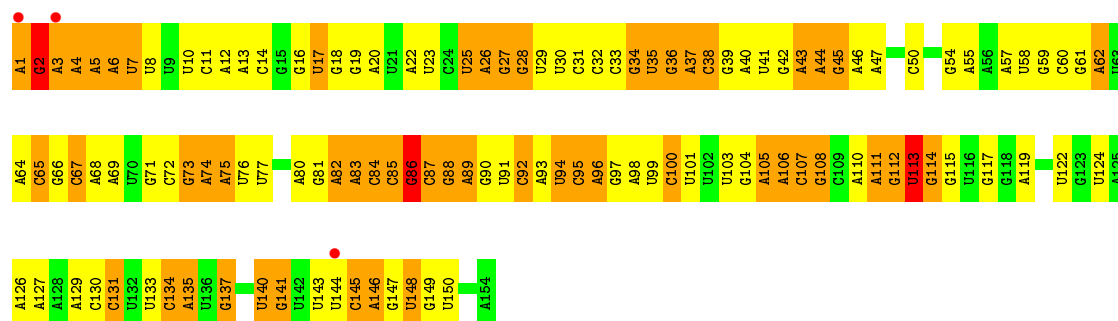
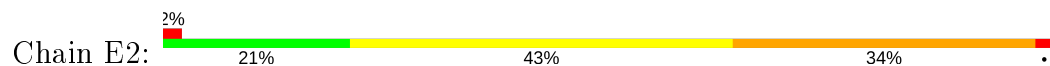
- Molecule 20: 5.8S RRNA



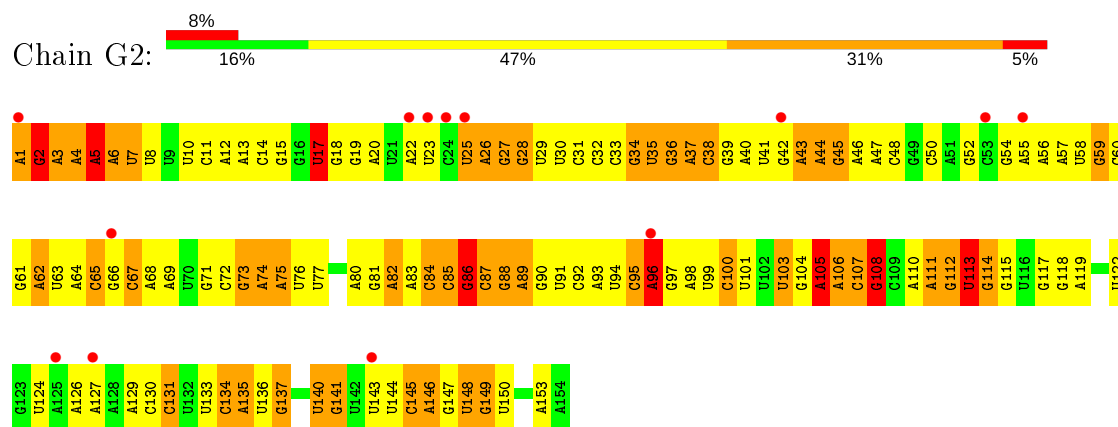
- Molecule 20: 5.8S RRNA



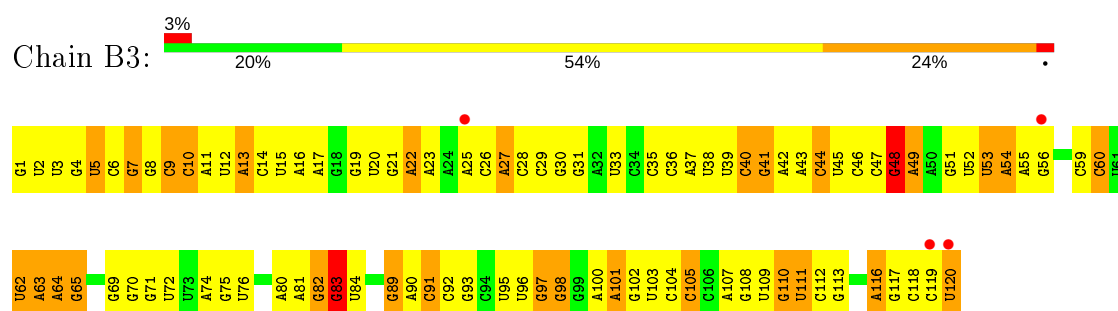
- Molecule 20: 5.8S RRNA



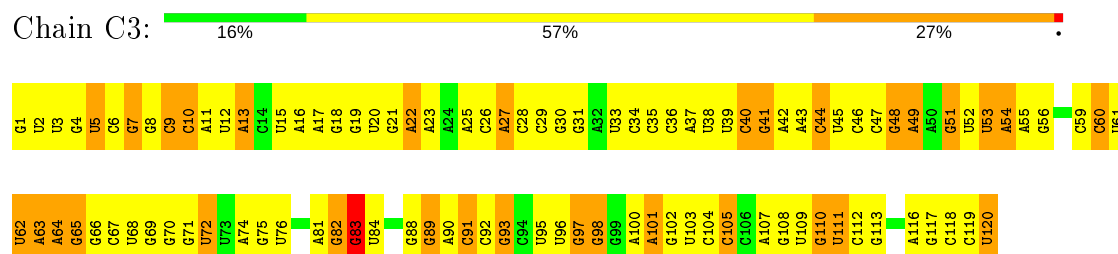
- Molecule 20: 5.8S rRNA



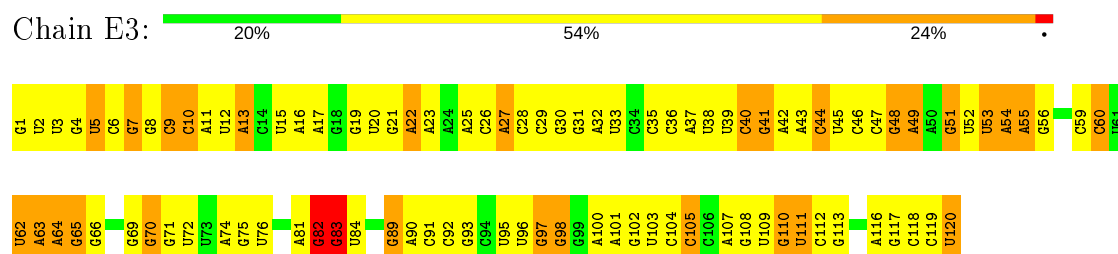
- Molecule 21: 5S rRNA



- Molecule 21: 5S rRNA

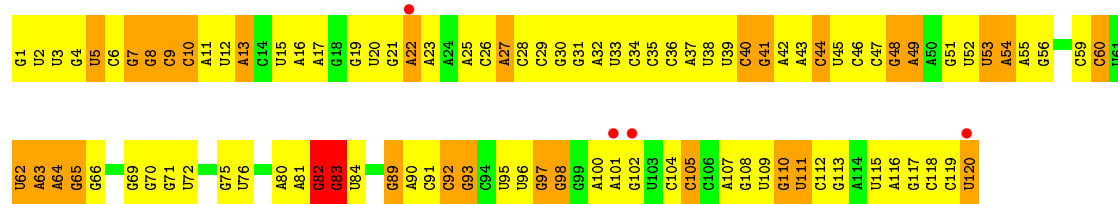


- Molecule 21: 5S rRNA

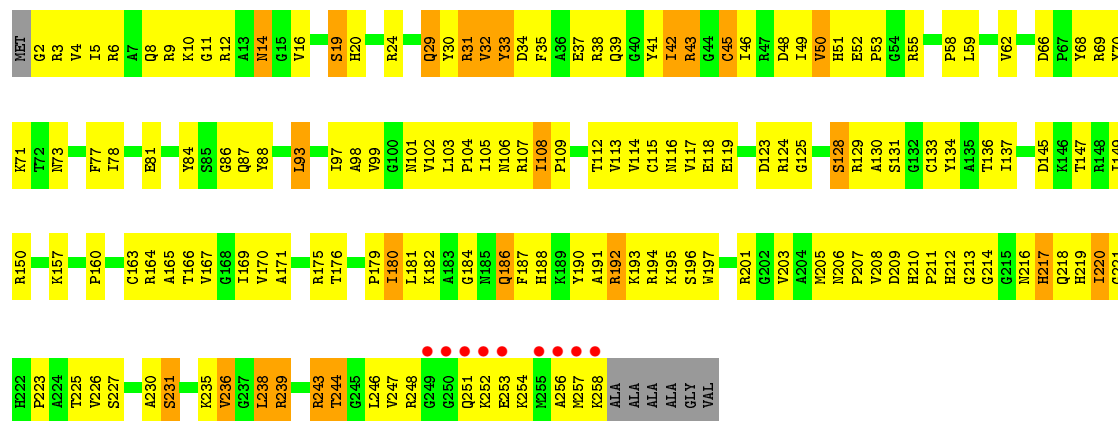


- Molecule 21: 5S rRNA

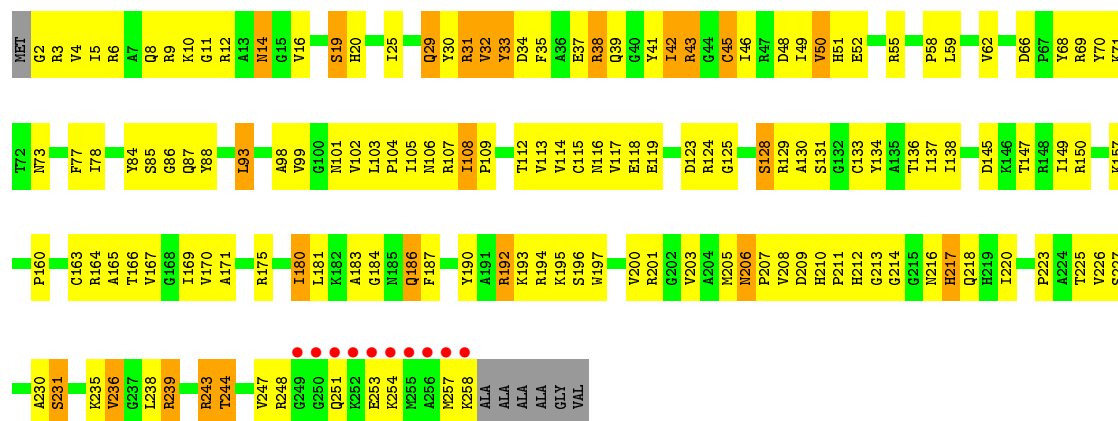
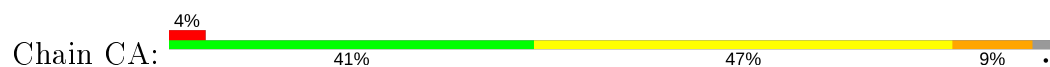




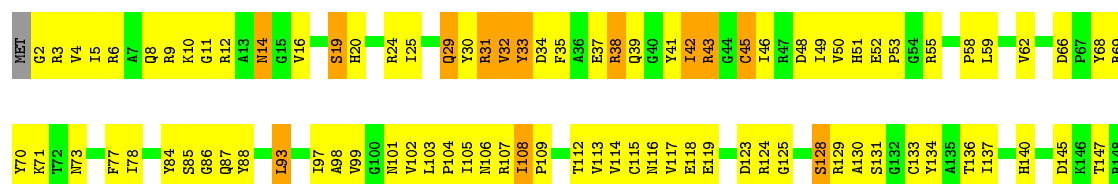
• Molecule 22: RPL8

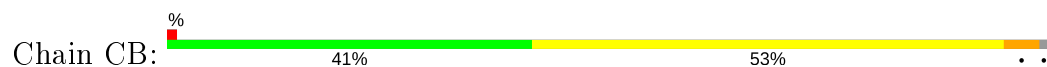


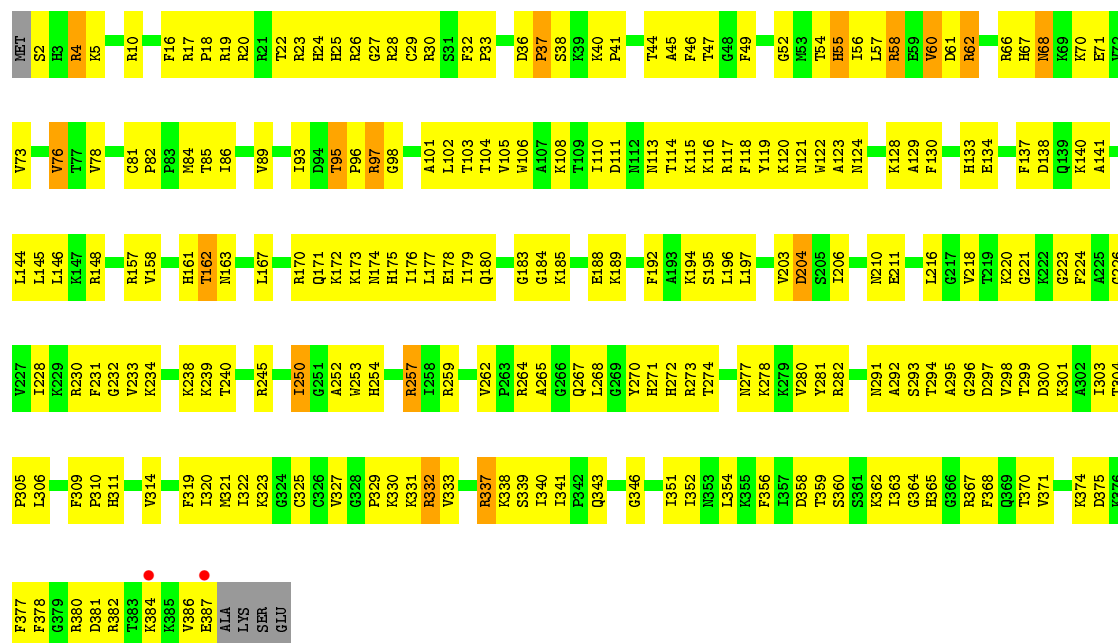
• Molecule 22: RPL8



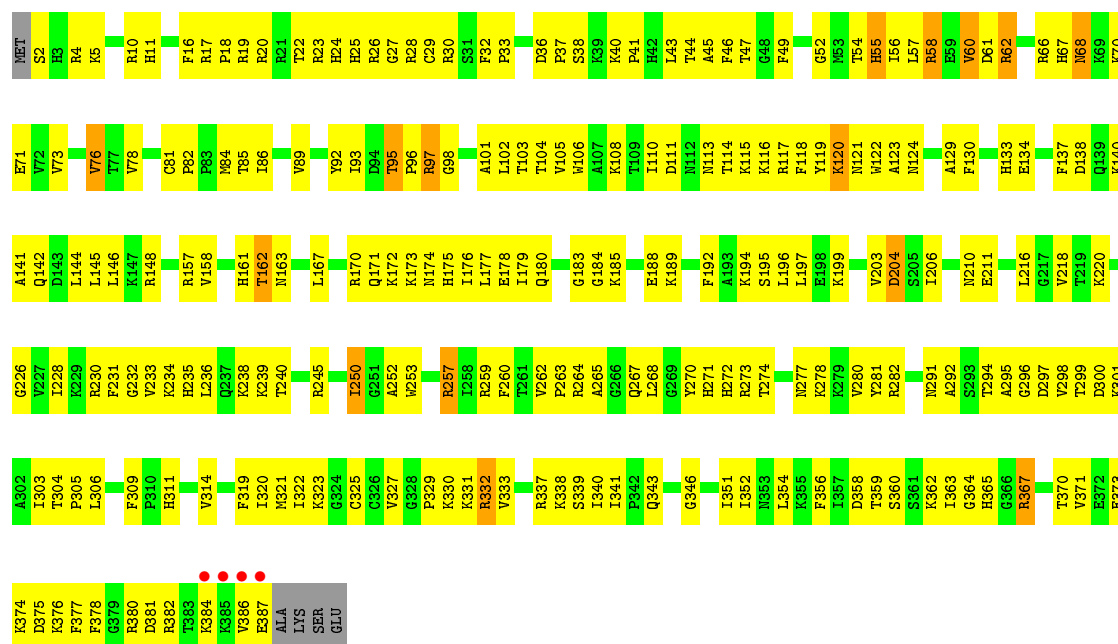
• Molecule 22: RPL8



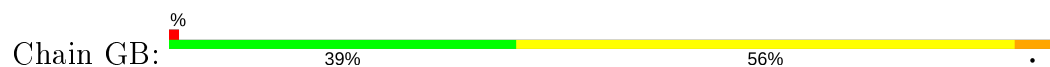


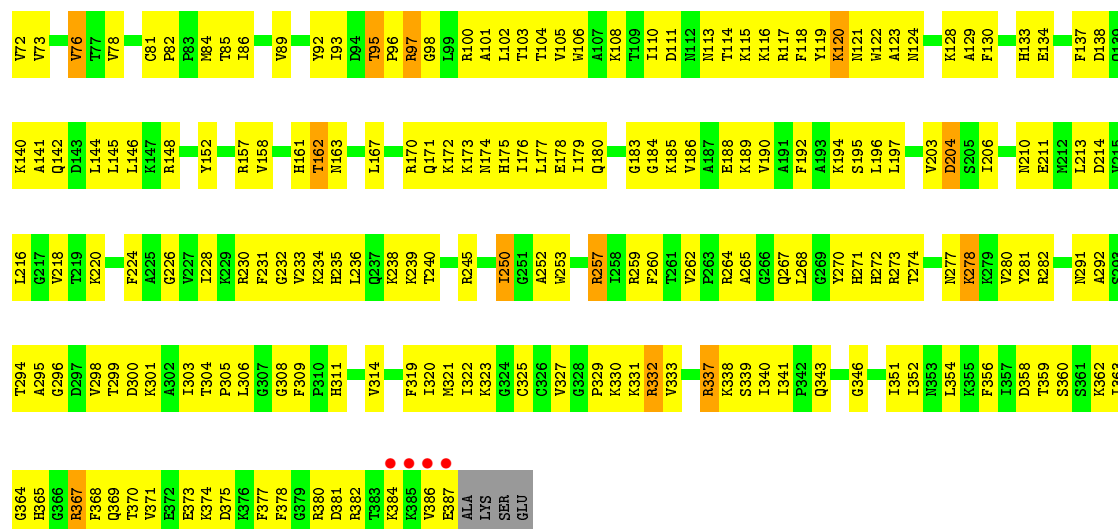


• Molecule 23: RIBOSOMAL PROTEIN L3

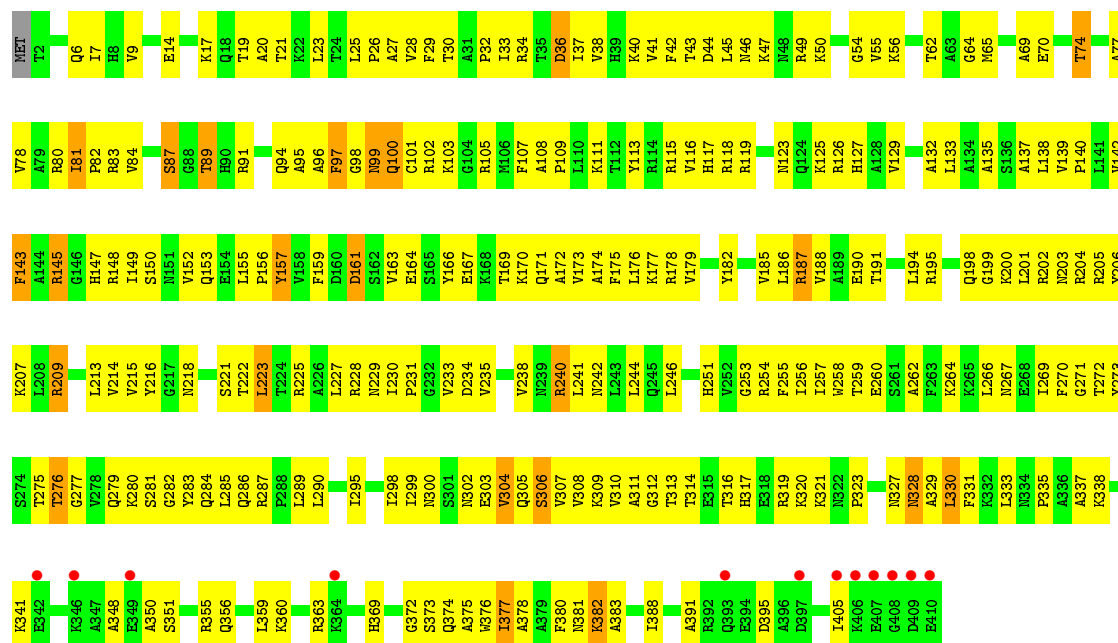
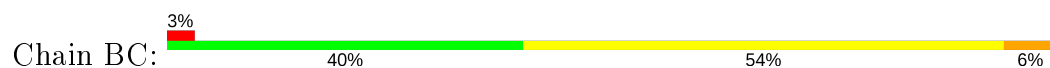


• Molecule 23: RIBOSOMAL PROTEIN L3

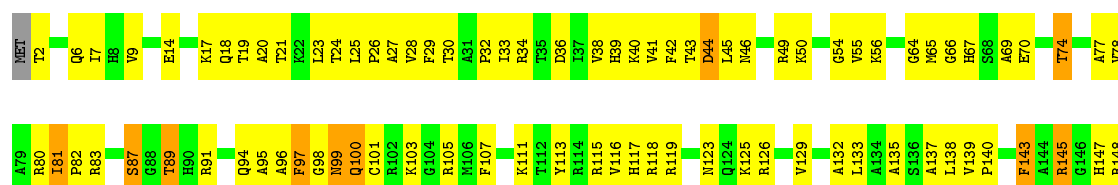


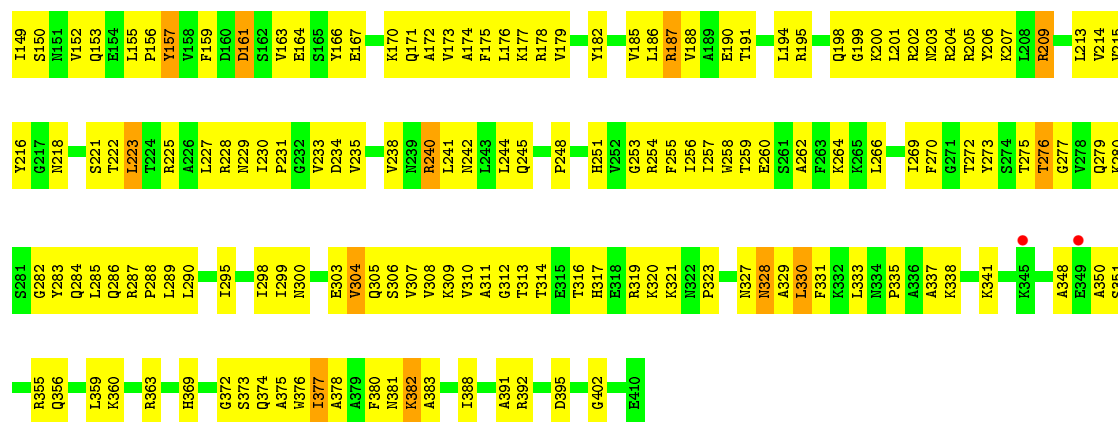


● Molecule 24: RPL4

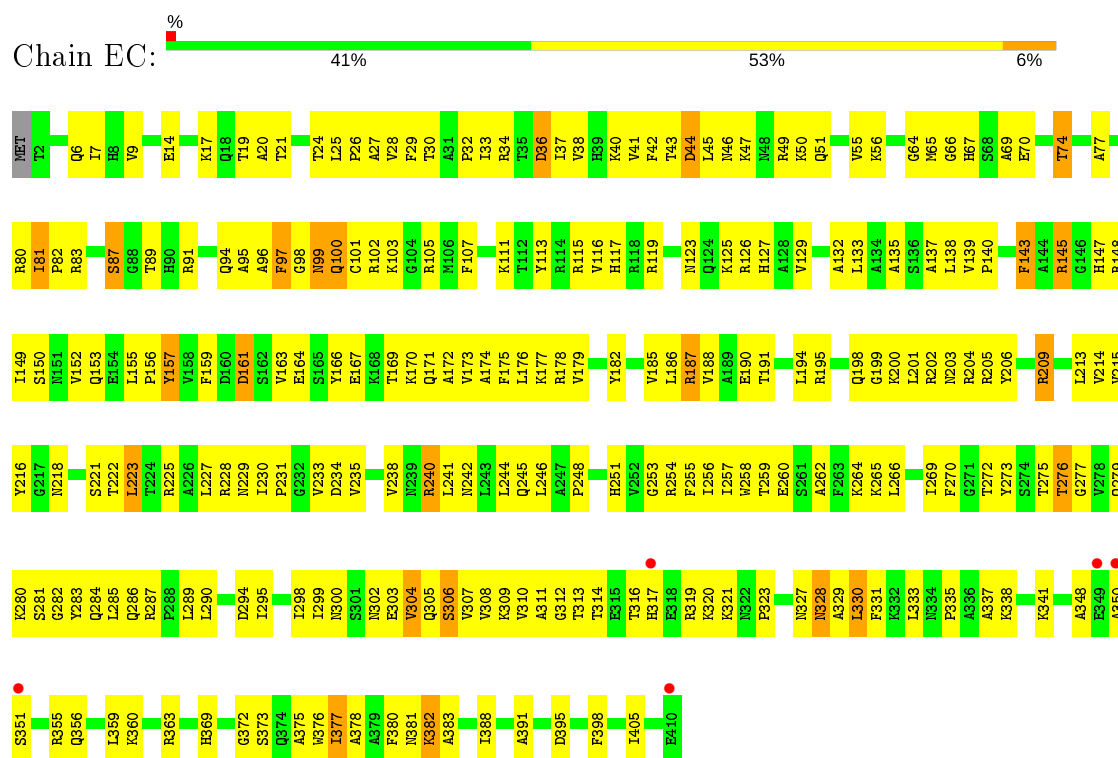


● Molecule 24: RPL4

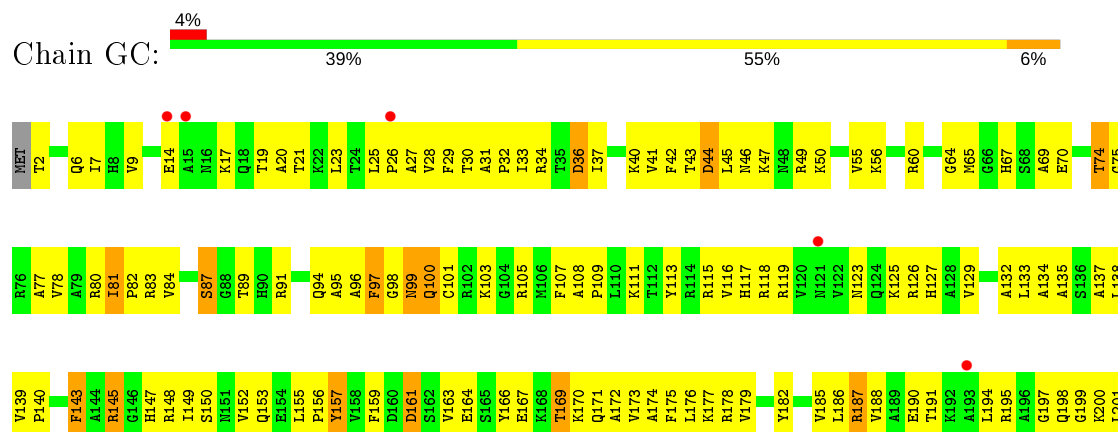


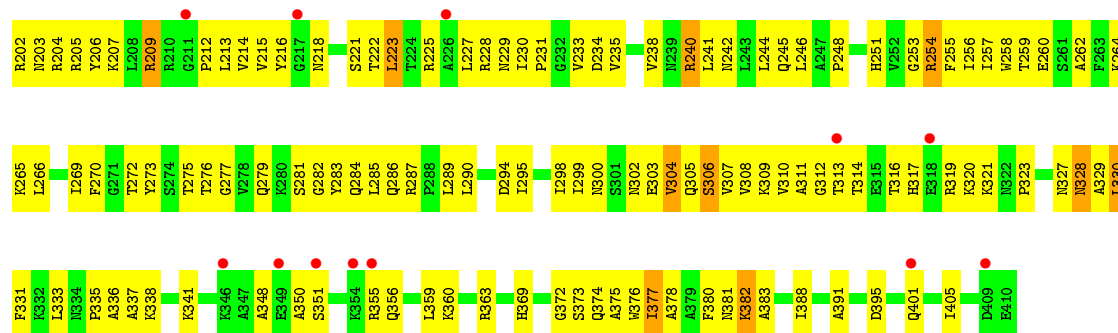


• Molecule 24: RPL4

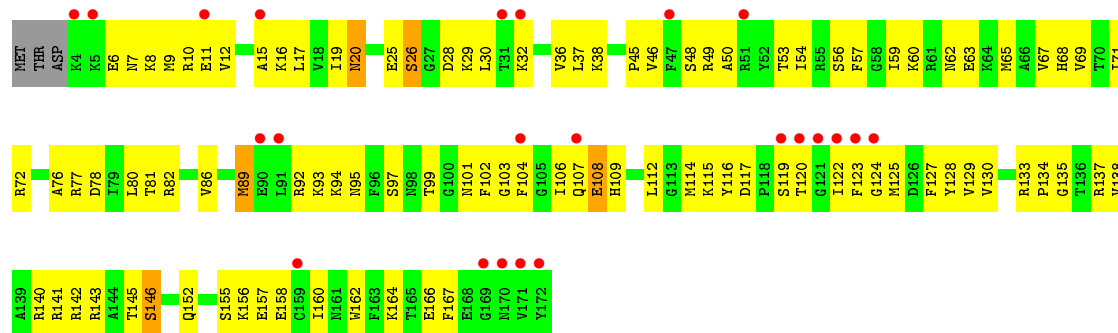
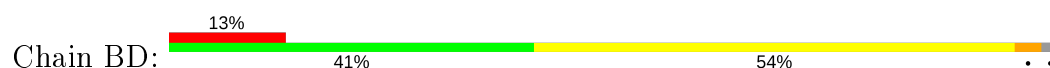


• Molecule 24: RPL4

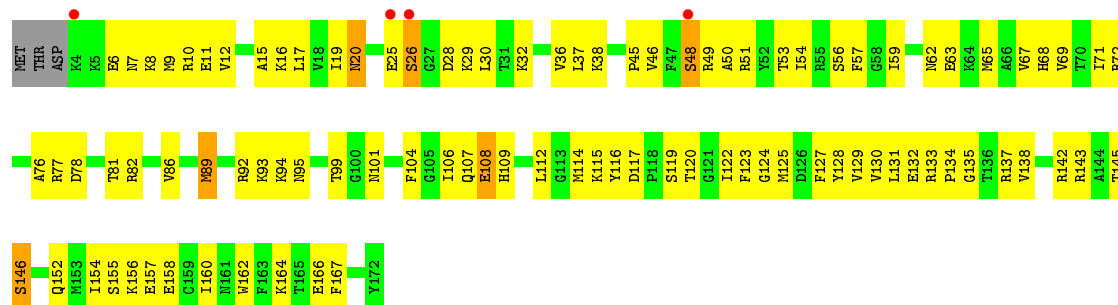
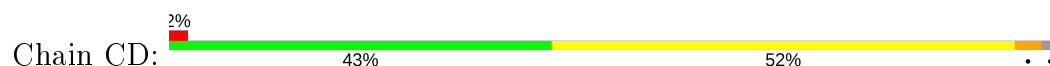




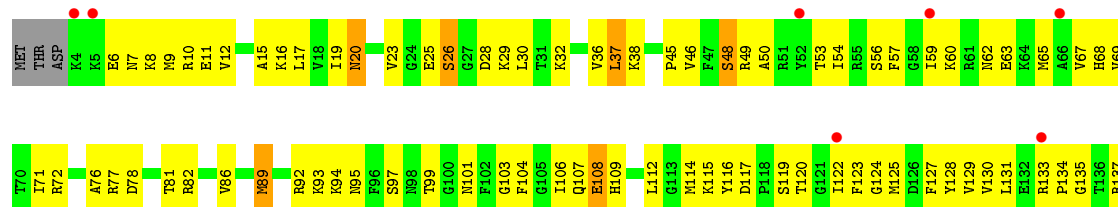
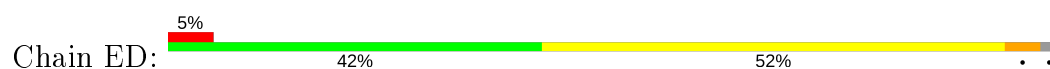
• Molecule 25: 60S RIBOSOMAL PROTEIN L11

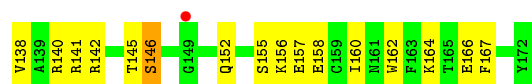


• Molecule 25: 60S RIBOSOMAL PROTEIN L11

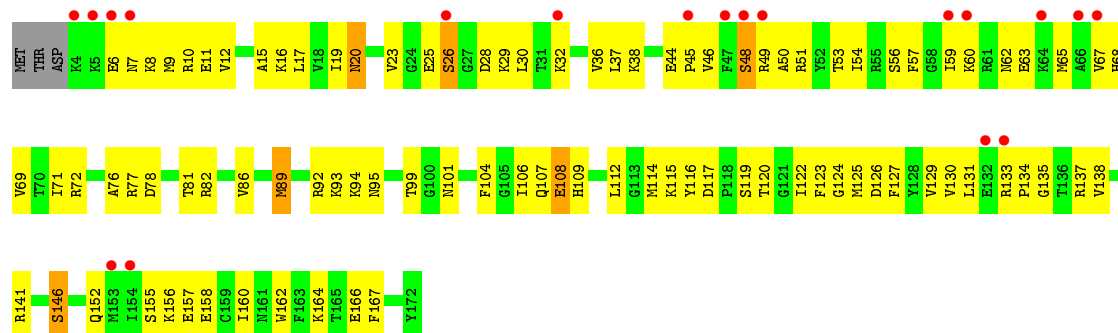


• Molecule 25: 60S RIBOSOMAL PROTEIN L11

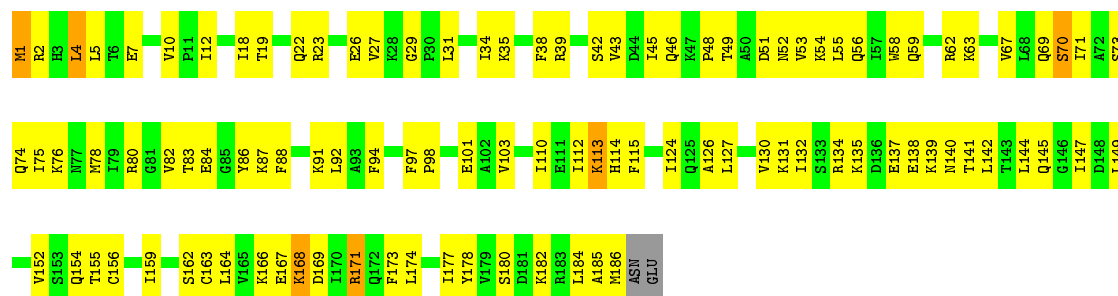




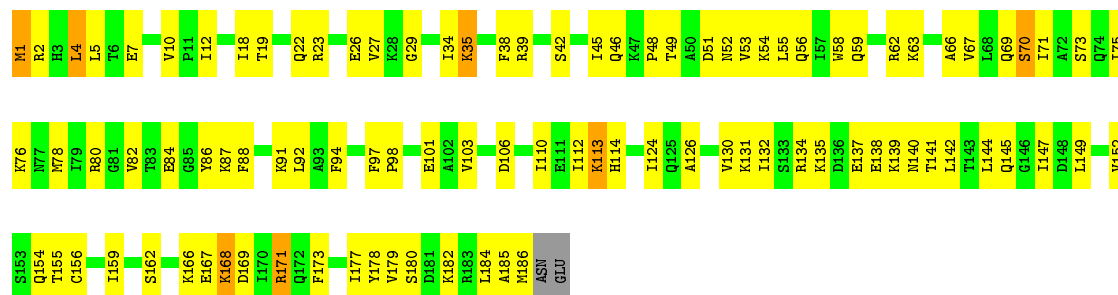
• Molecule 25: 60S RIBOSOMAL PROTEIN L11



• Molecule 26: 60S RIBOSOMAL PROTEIN L9

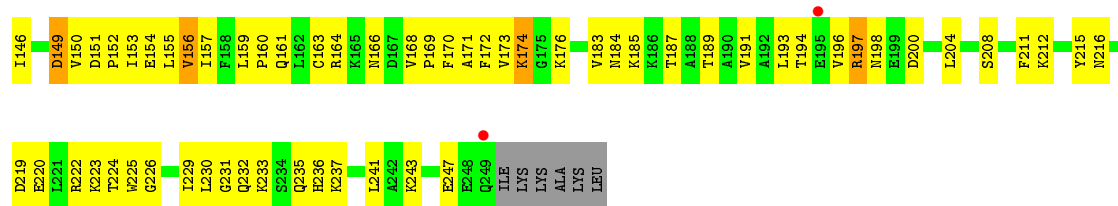


• Molecule 26: 60S RIBOSOMAL PROTEIN L9

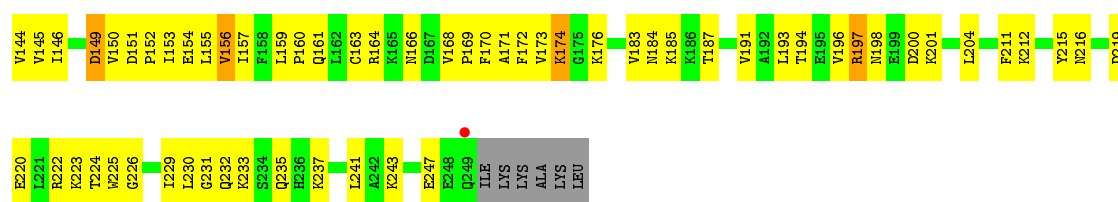
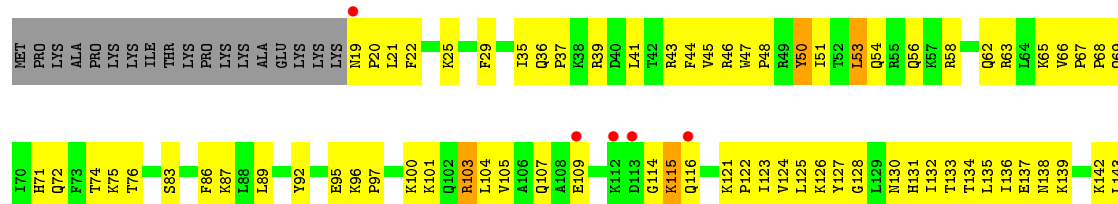


• Molecule 26: 60S RIBOSOMAL PROTEIN L9

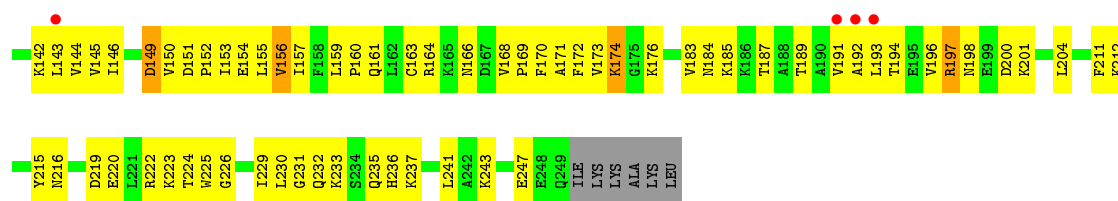
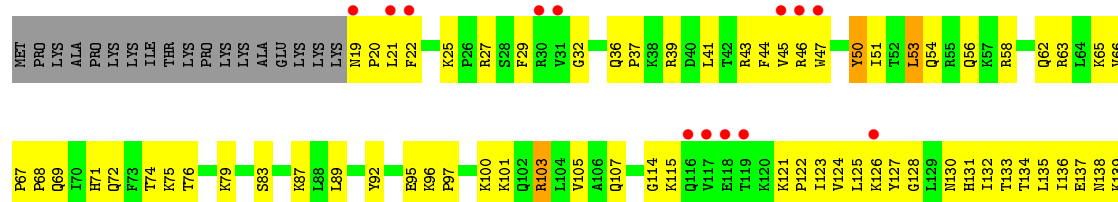




• Molecule 27: RPL7A



• Molecule 27: RPL7A

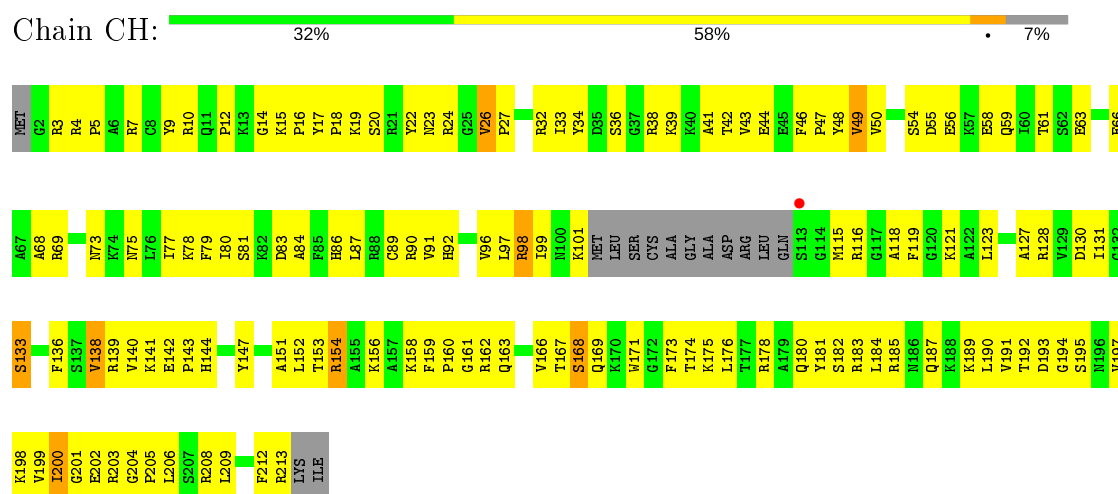


• Molecule 28: RPLP0

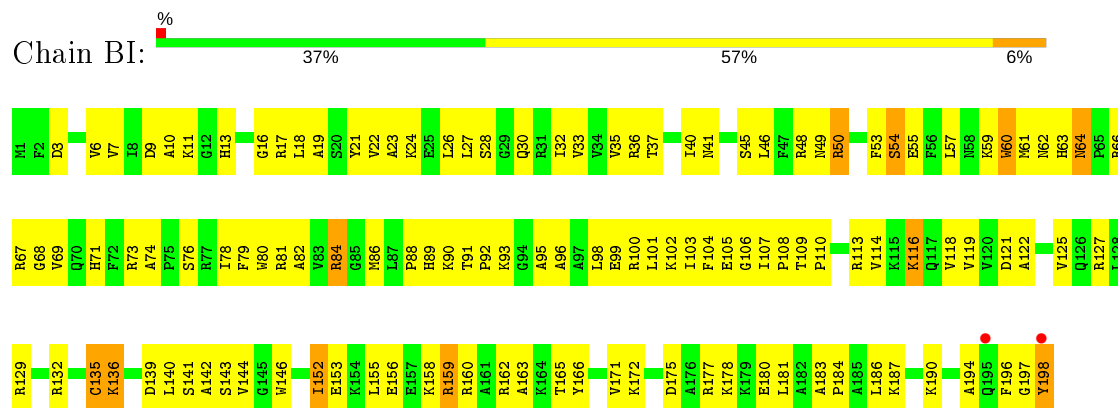


• Molecule 29: 60S RIBOSOMAL PROTEIN L10

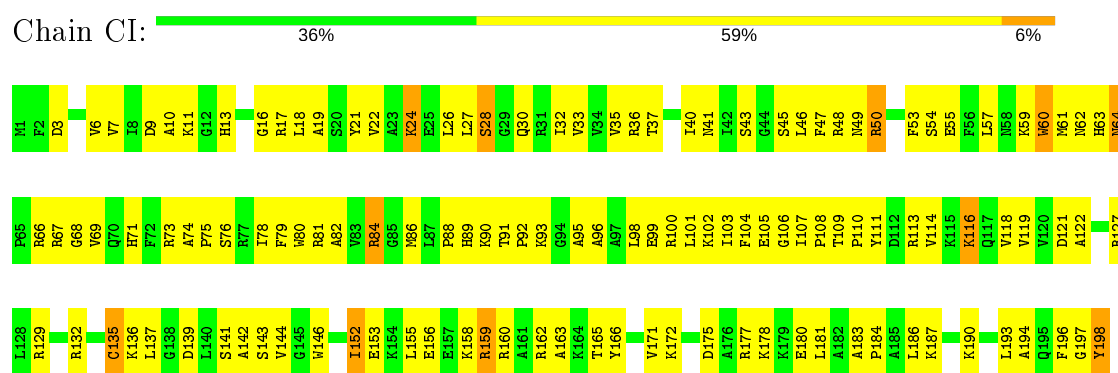
Chain CH:



- Molecule 30: 60S RIBOSOMAL PROTEIN L13A



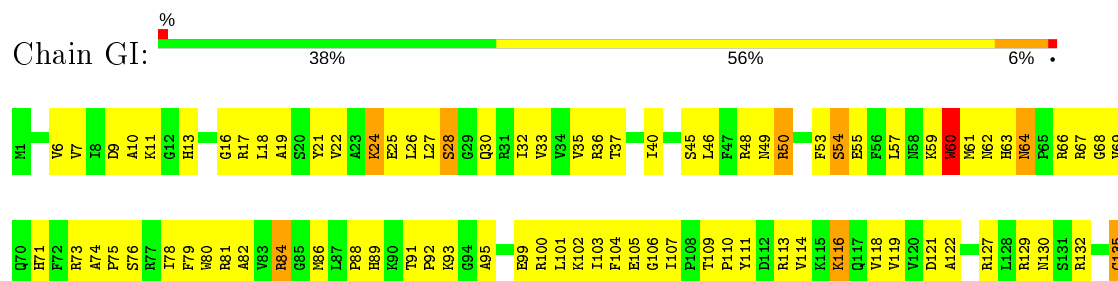
- Molecule 30: 60S RIBOSOMAL PROTEIN L13A

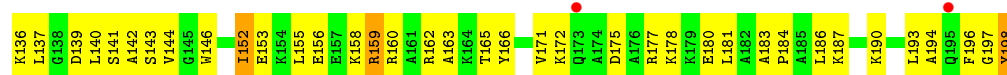


- Molecule 30: 60S RIBOSOMAL PROTEIN L13A



- Molecule 30: 60S RIBOSOMAL PROTEIN L13A

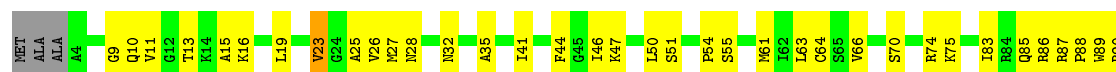




• Molecule 31: RPL23



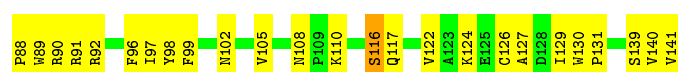
• Molecule 31: RPL23



• Molecule 31: RPL23

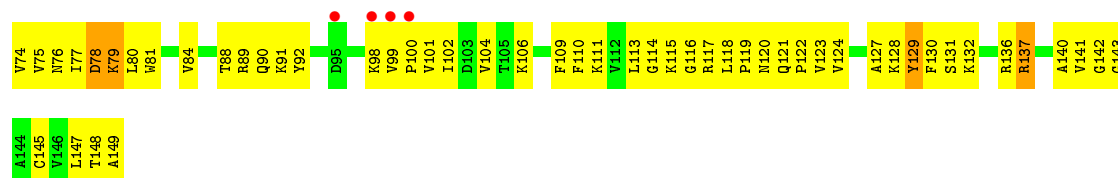


• Molecule 31: RPL23



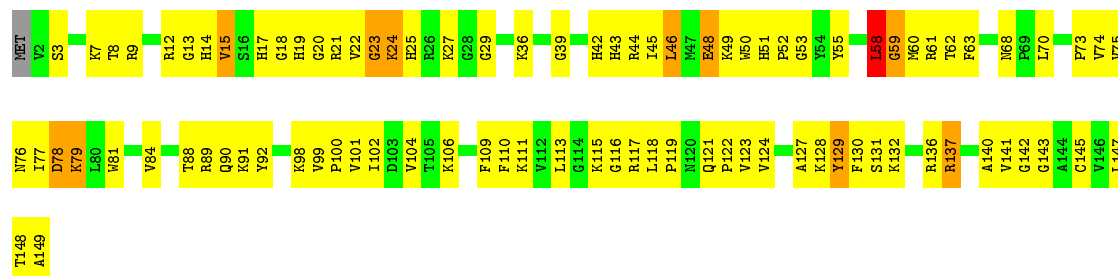
• Molecule 32: 60S RIBOSOMAL PROTEIN L27A





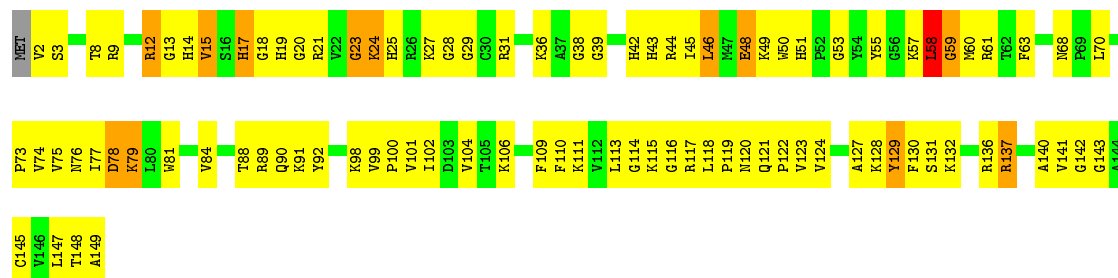
• Molecule 32: 60S RIBOSOMAL PROTEIN L27A

Chain CK: 38% 54% 7% ..



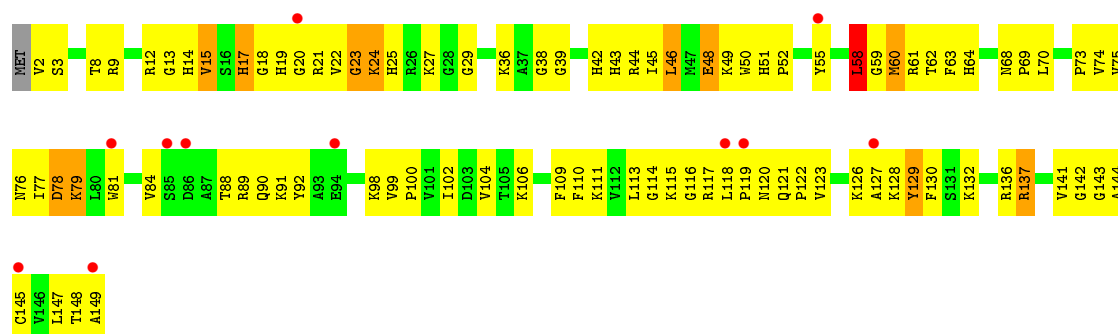
• Molecule 32: 60S RIBOSOMAL PROTEIN L27A

Chain EK: 36% 54% 8% ..



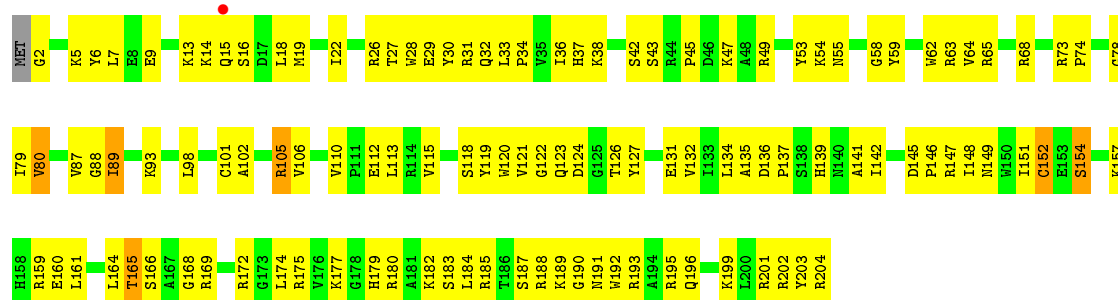
• Molecule 32: 60S RIBOSOMAL PROTEIN L27A

Chain GK: 7% 37% 54% 7% ..



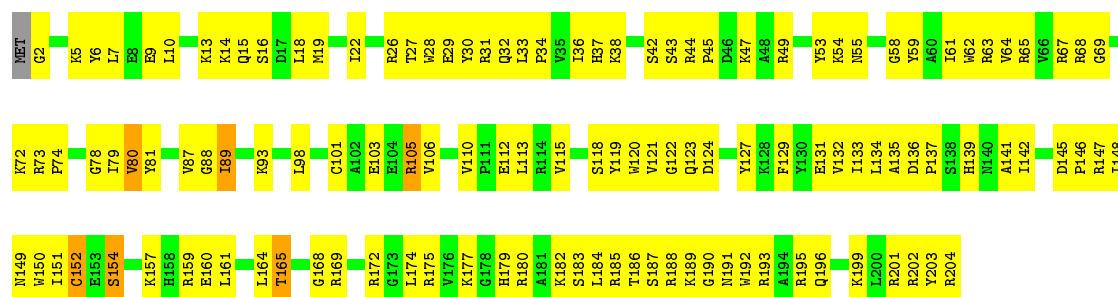
• Molecule 33: RIBOSOMAL PROTEIN L15

Chain BL: 43% 54% 3%



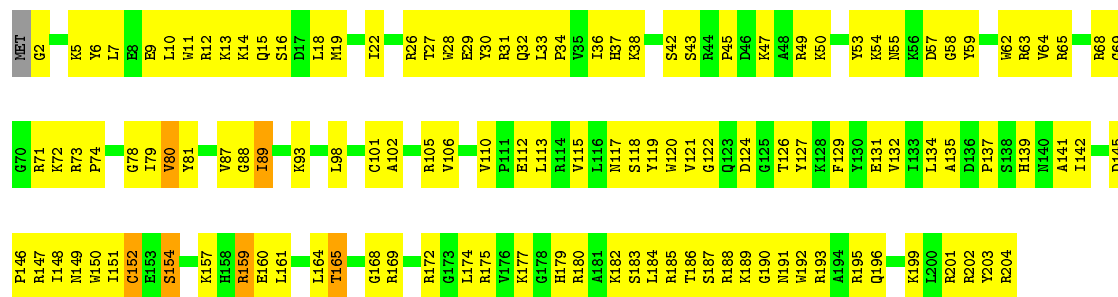
• Molecule 33: RIBOSOMAL PROTEIN L15

Chain CL: 38% 58%



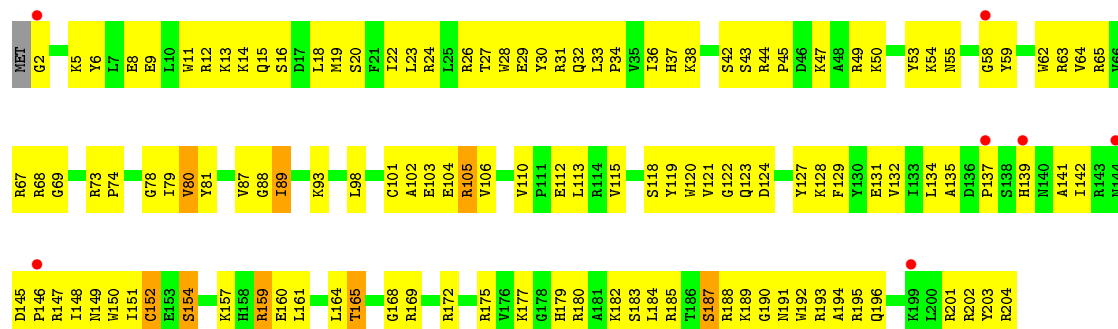
• Molecule 33: RIBOSOMAL PROTEIN L15

Chain EL: 38% 59%

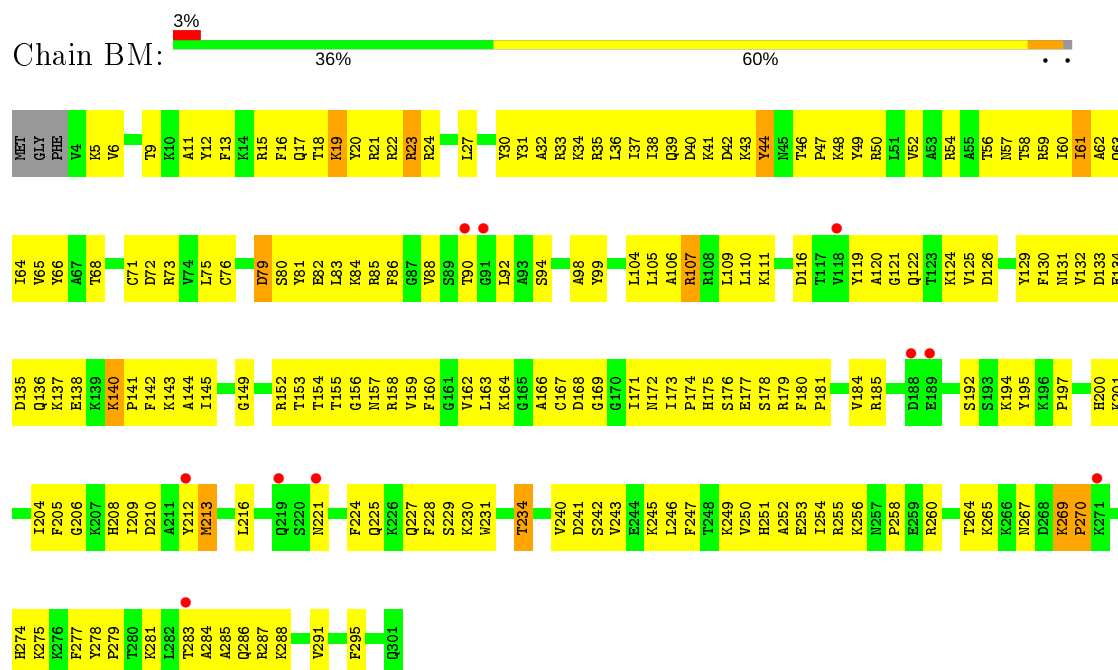


• Molecule 33: RIBOSOMAL PROTEIN L15

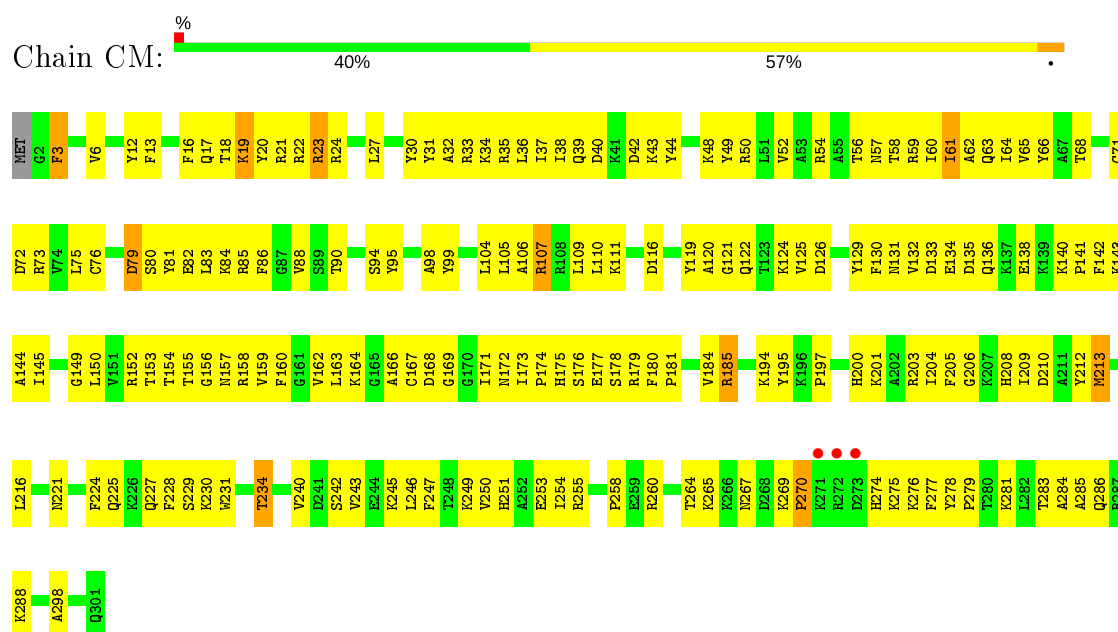
Chain GL: 3% 37% 58%



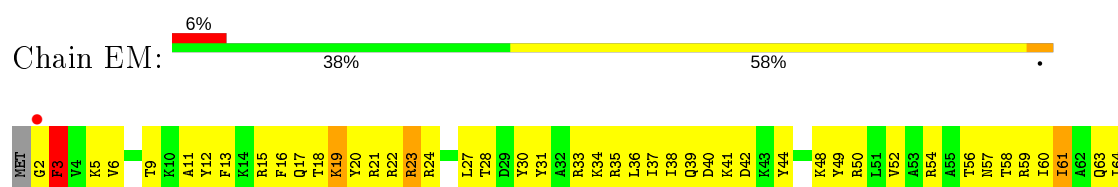
• Molecule 34: 60S RIBOSOMAL PROTEIN L5

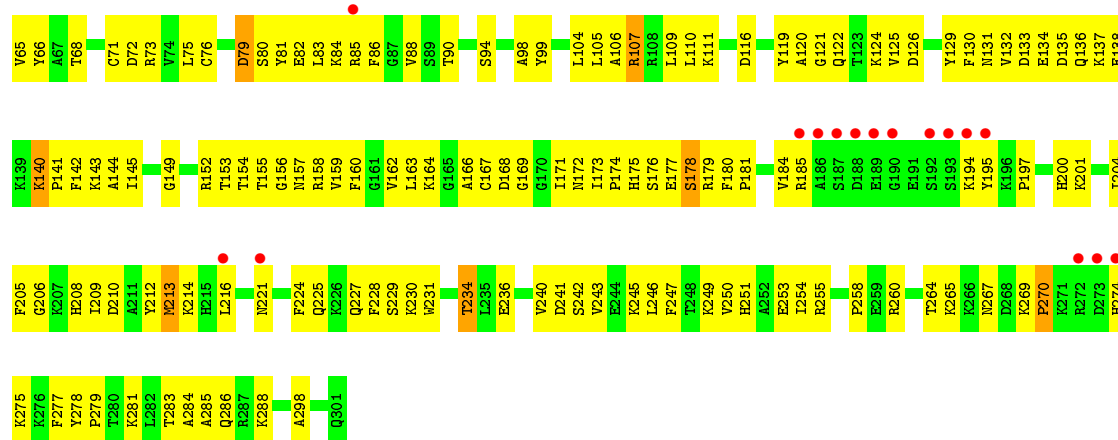


• Molecule 34: 60S RIBOSOMAL PROTEIN L5

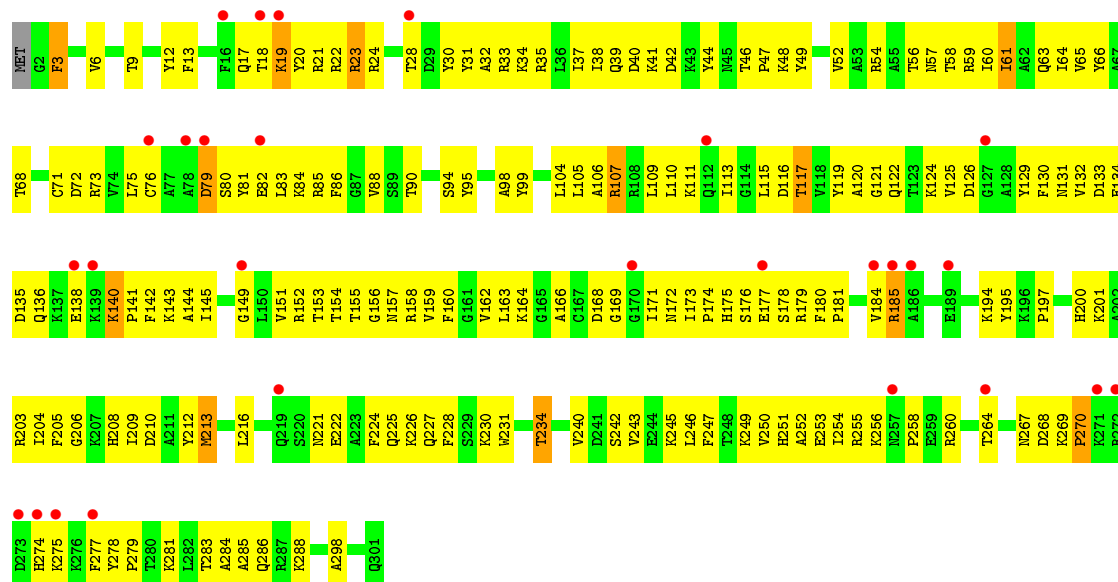


• Molecule 34: 60S RIBOSOMAL PROTEIN L5

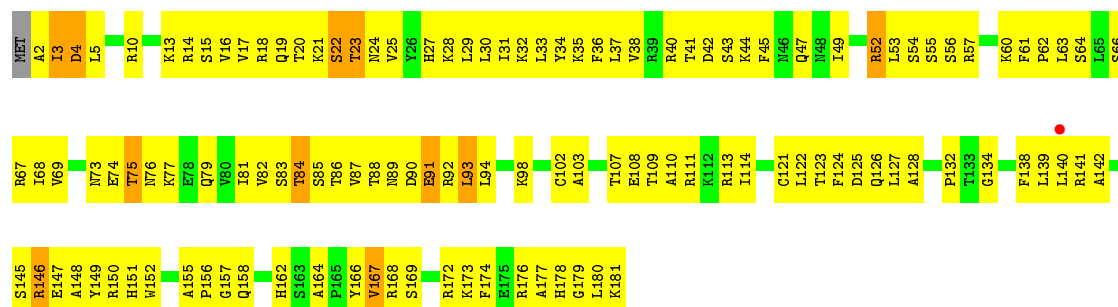




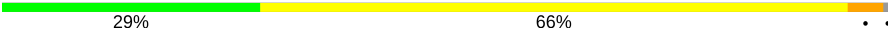
• Molecule 34: 60S RIBOSOMAL PROTEIN L5

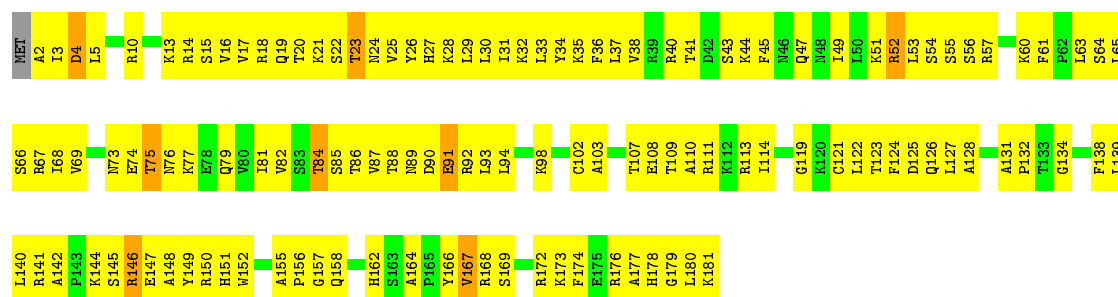


• Molecule 35: RPL18



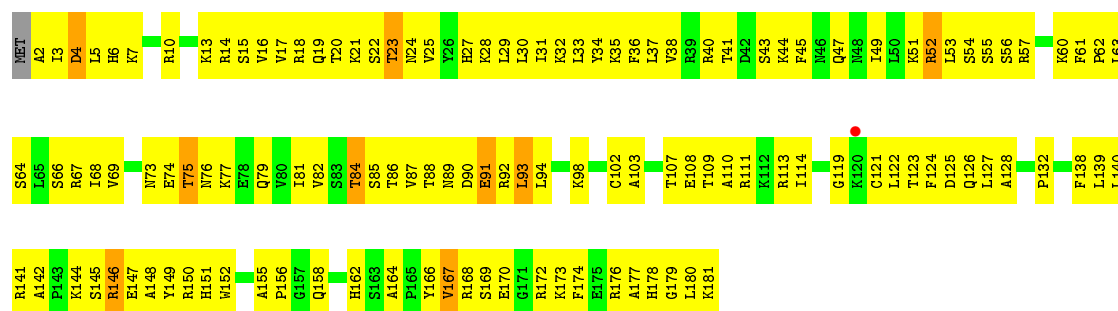
• Molecule 35: RPL18

Chain CN:  29% 66%

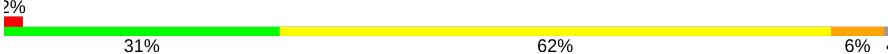


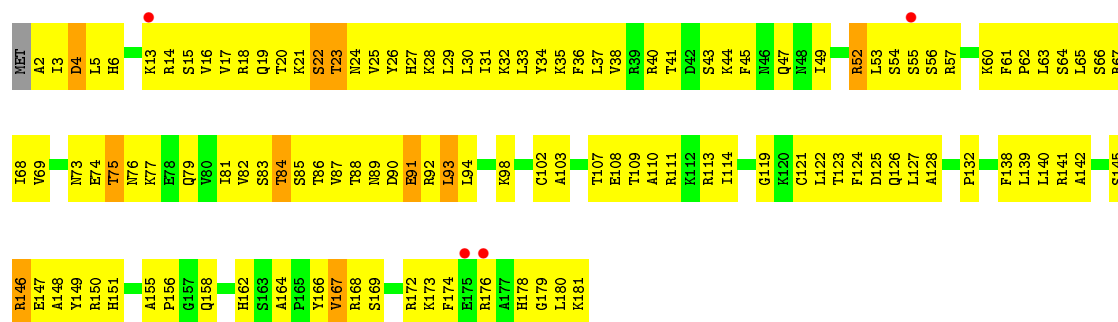
• Molecule 35: RPL18

Chain EN:  29% 65% 5%



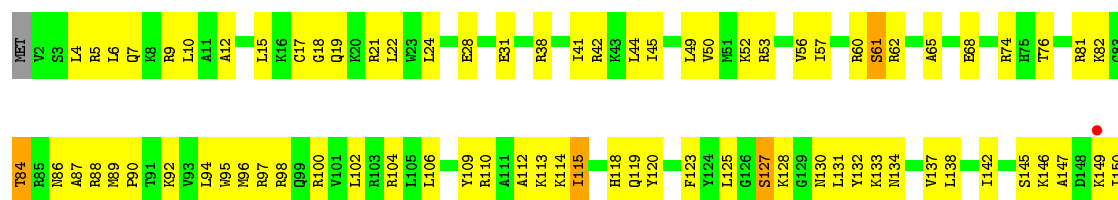
• Molecule 35: RPL18

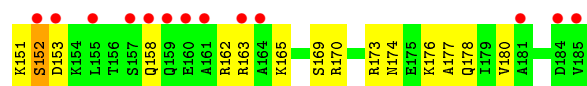
Chain GN:  31% 62% 6%



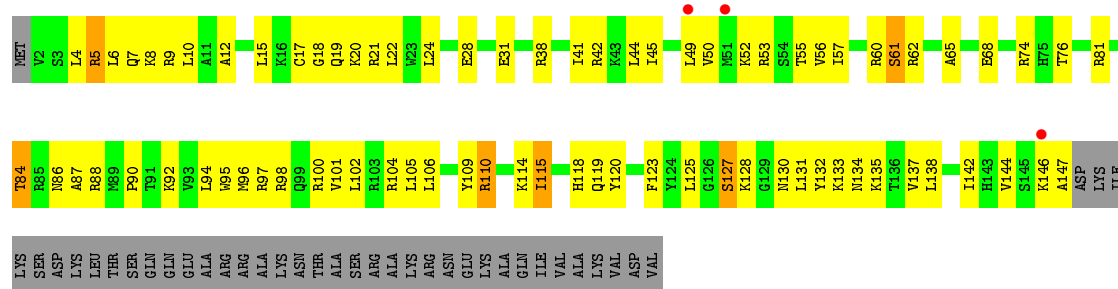
• Molecule 36: RPL19

Chain BO:  49% 48% 8%

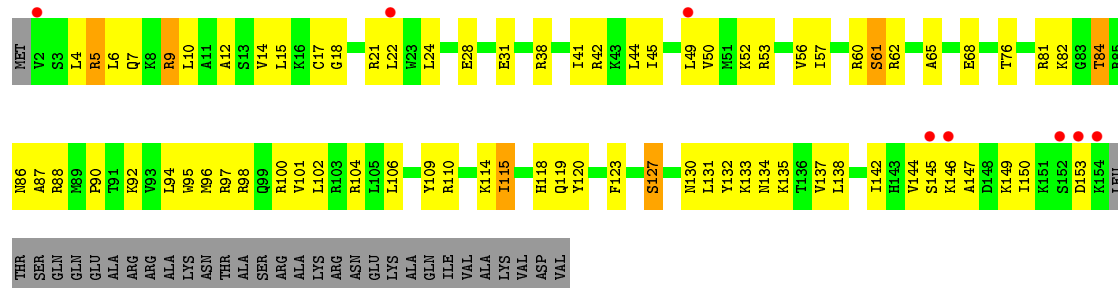
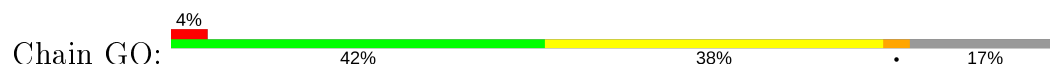




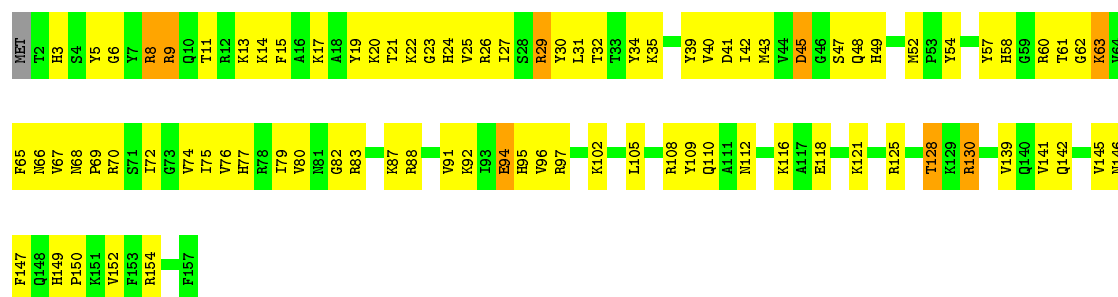
• Molecule 36: RPL19



• Molecule 36: RPL19

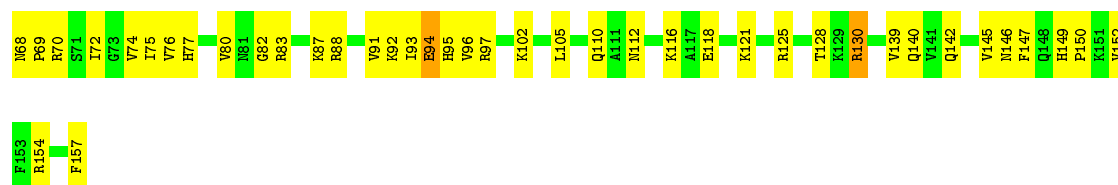


• Molecule 37: 60S RIBOSOMAL PROTEIN L21

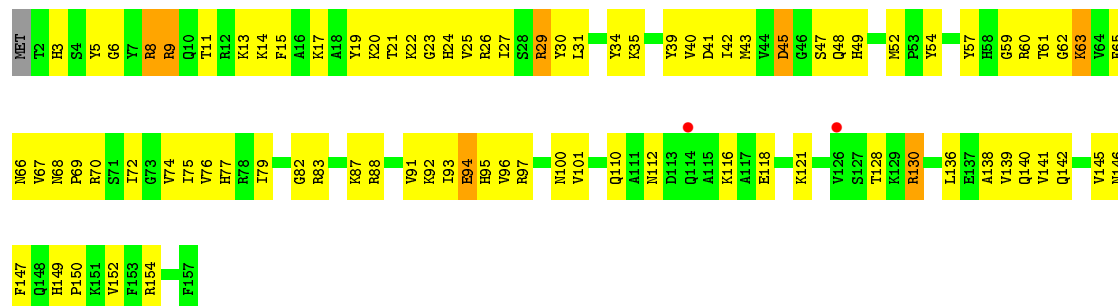


• Molecule 37: 60S RIBOSOMAL PROTEIN L21

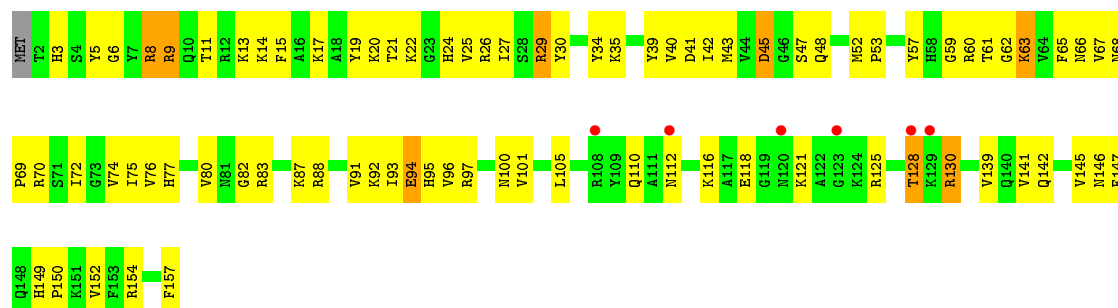




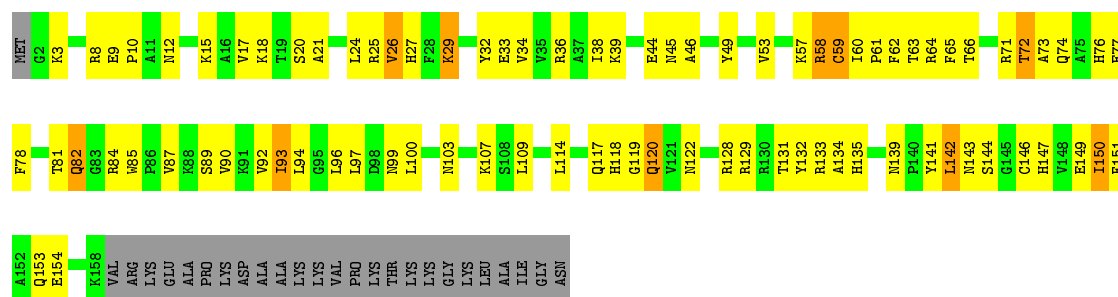
• Molecule 37: 60S RIBOSOMAL PROTEIN L21



• Molecule 37: 60S RIBOSOMAL PROTEIN L21

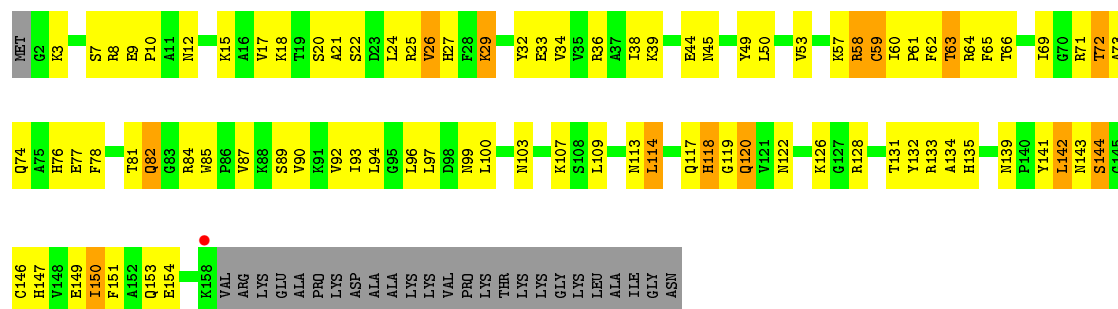


• Molecule 38: RPL17

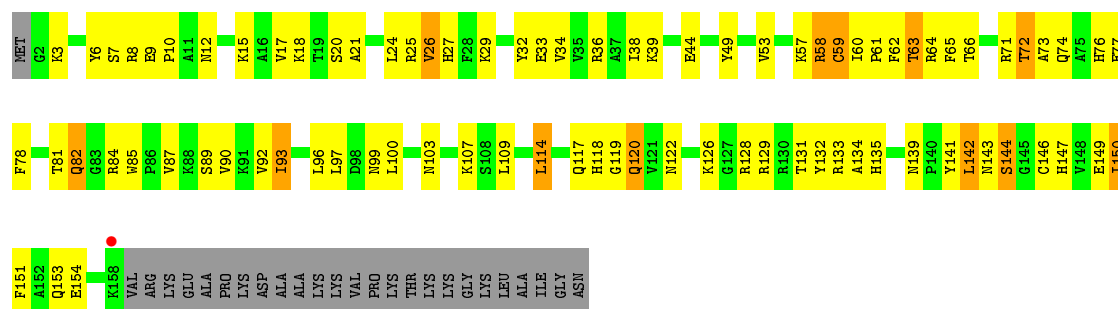


• Molecule 38: RPL17

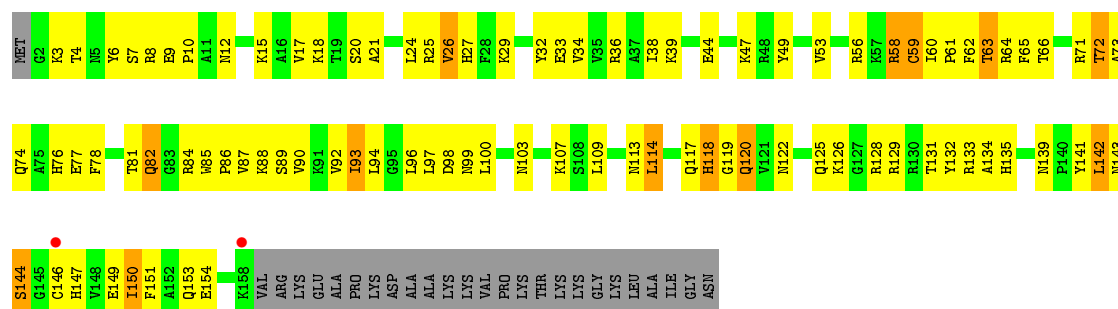
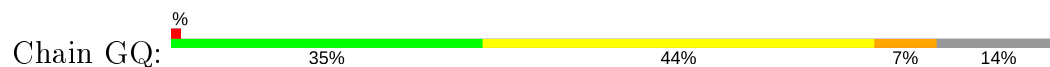




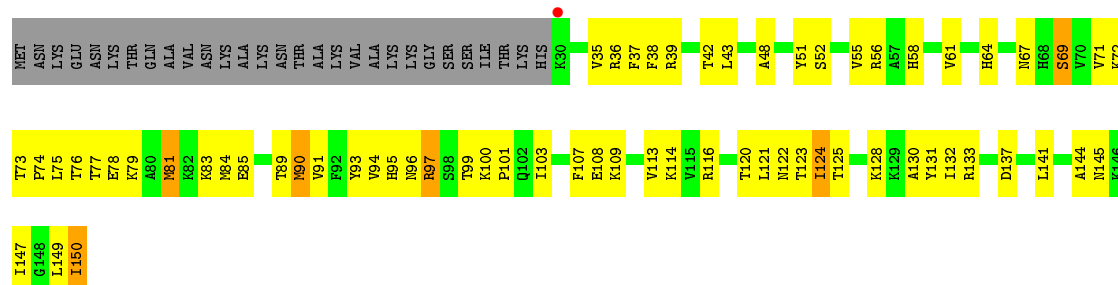
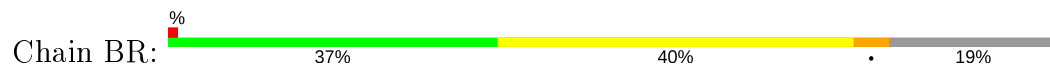
• Molecule 38: RPL17



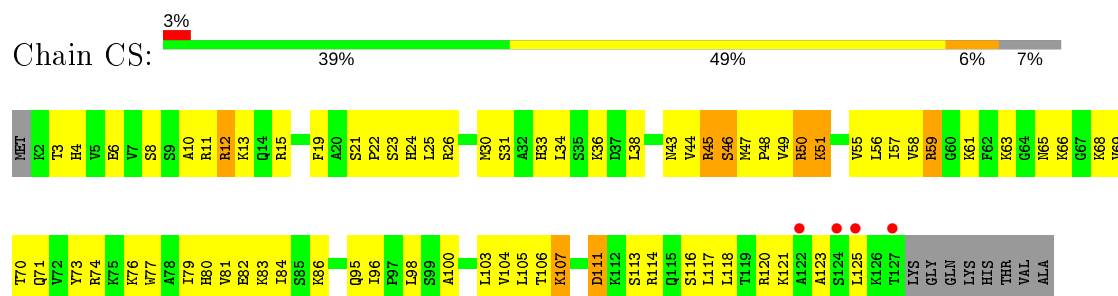
• Molecule 38: RPL17



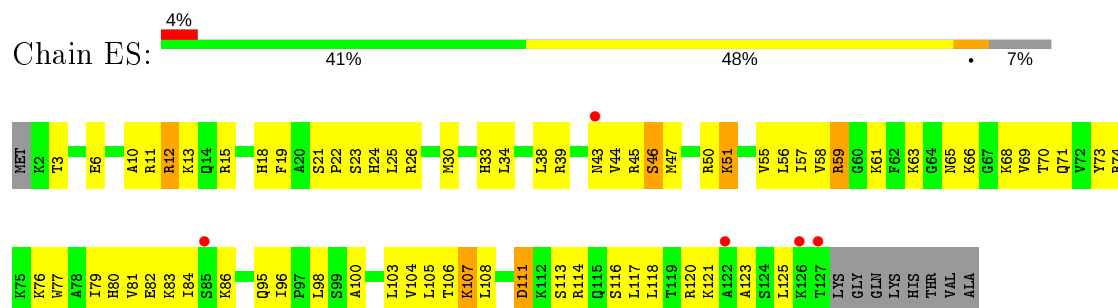
• Molecule 39: RPL23A



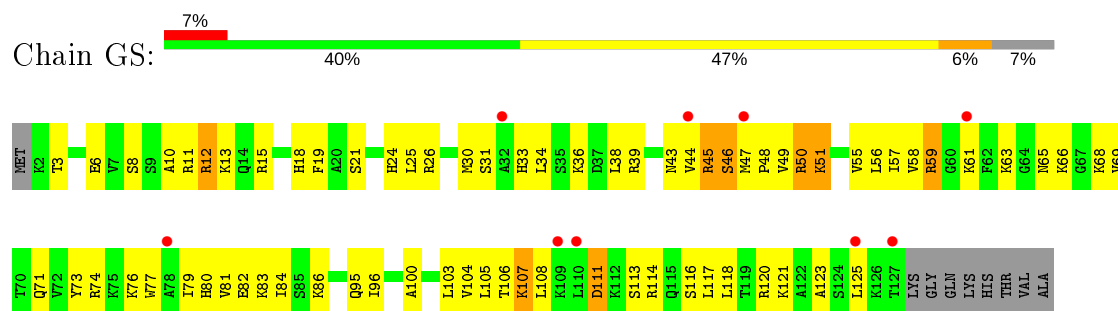
- Molecule 40: RPL26



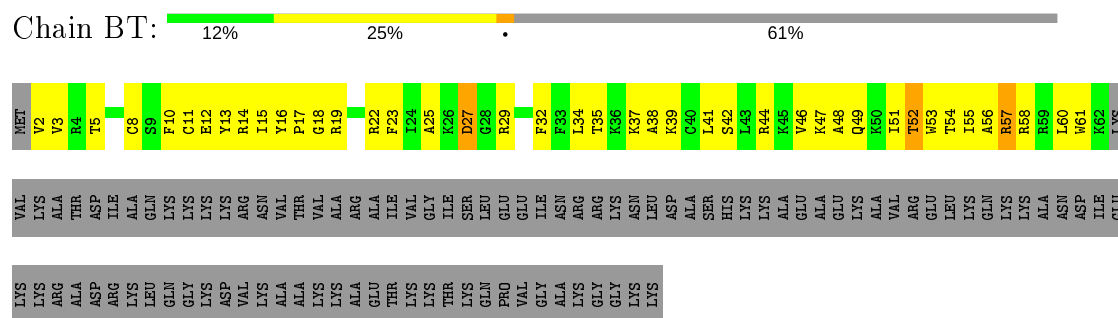
- Molecule 40: RPL26



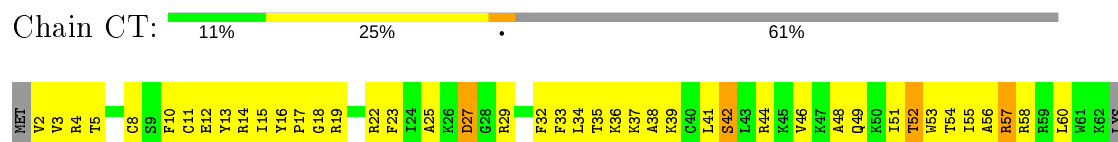
- Molecule 40: RPL26



- Molecule 41: RPL24

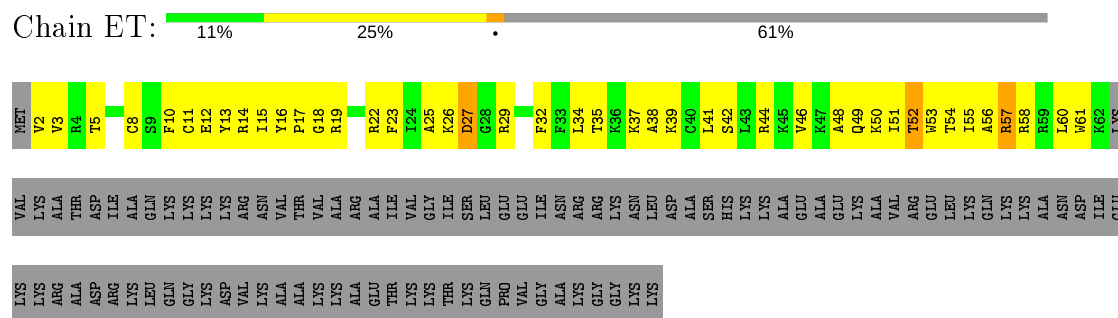


- Molecule 41: RPL24

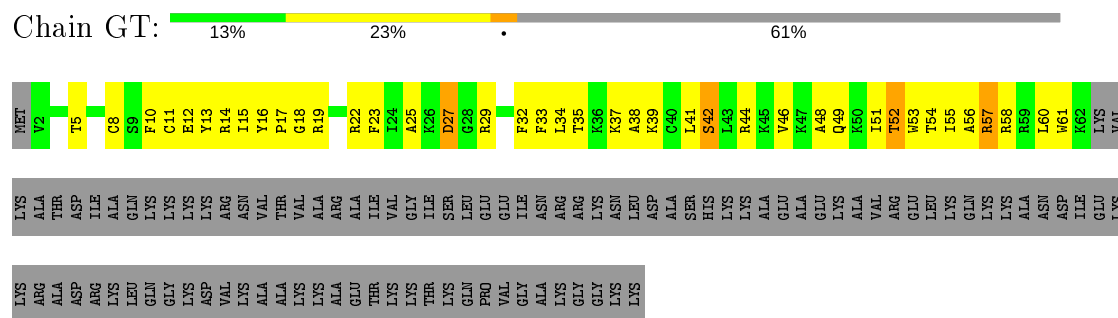




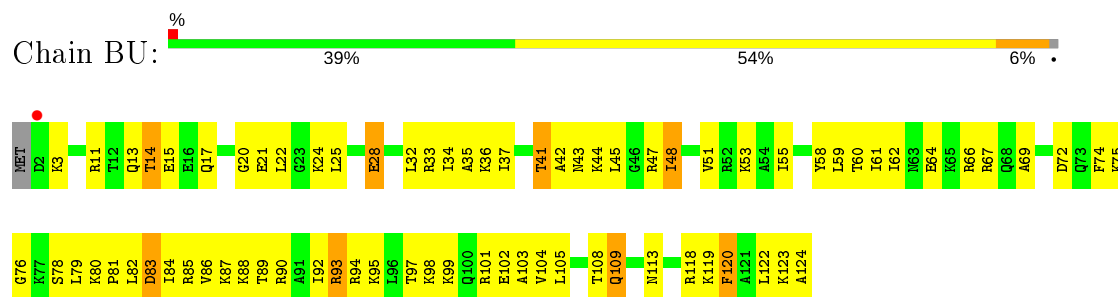
• Molecule 41: RPL24



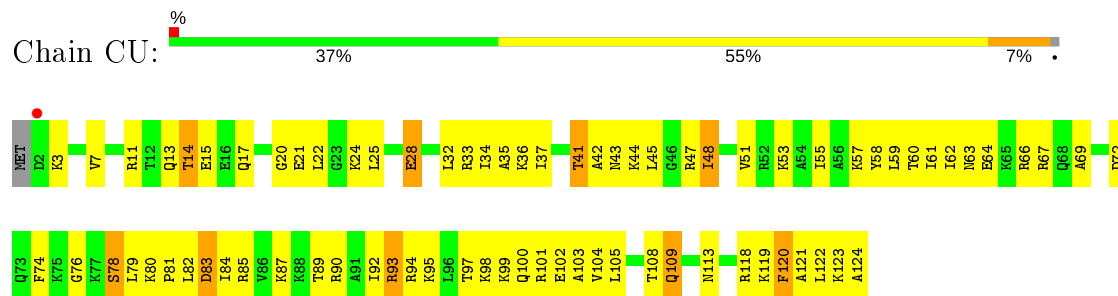
• Molecule 41: RPL24



• Molecule 42: RPL35



• Molecule 42: RPL35



• Molecule 42: RPL35

- Molecule 42: RPL35

- Molecule 43: 60S RIBOSOMAL PROTEIN L7

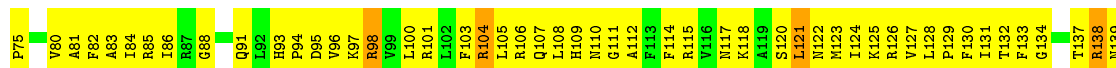
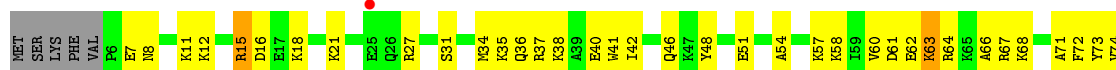
● Molecule 43: 60S RIBOSOMAL PROTEIN L7





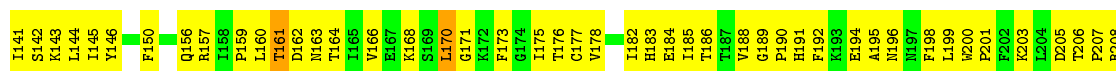
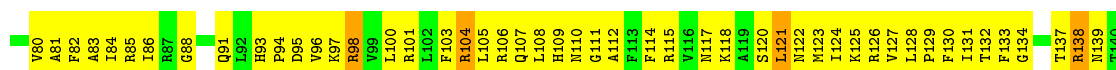
• Molecule 43: 60S RIBOSOMAL PROTEIN L7

Chain EV: 35% 59% 5%



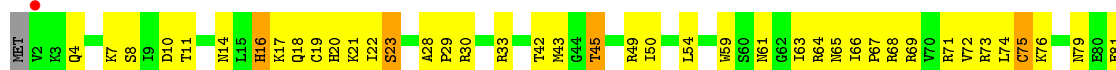
• Molecule 43: 60S RIBOSOMAL PROTEIN L7

Chain GV: 34% 59%



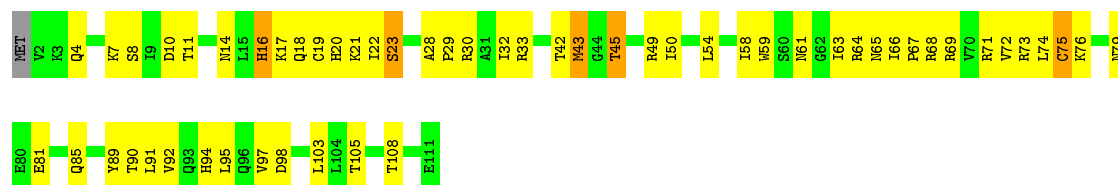
• Molecule 44: 60S RIBOSOMAL PROTEIN L31

Chain BW: 2% 53% 42%



• Molecule 44: 60S RIBOSOMAL PROTEIN L31

Chain CW: 50% 45% 5%



• Molecule 44: 60S RIBOSOMAL PROTEIN L31



• Molecule 44: 60S RIBOSOMAL PROTEIN L31



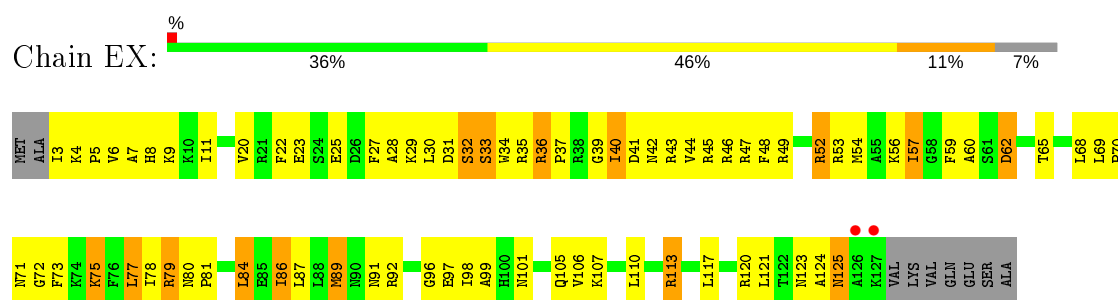
• Molecule 45: 60S RIBOSOMAL PROTEIN L32



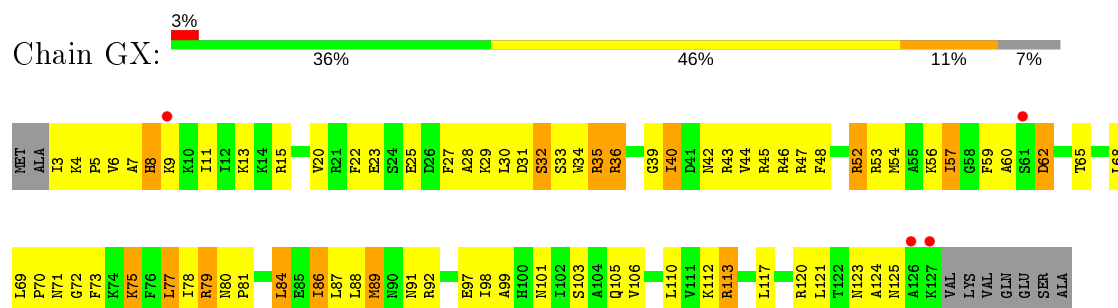
• Molecule 45: 60S RIBOSOMAL PROTEIN L32



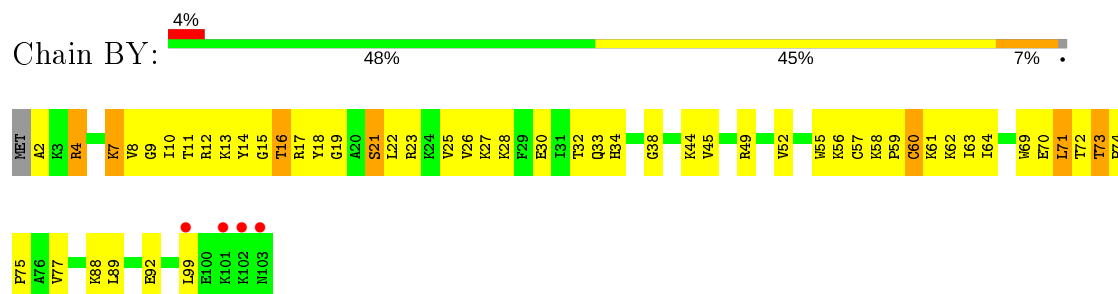
• Molecule 45: 60S RIBOSOMAL PROTEIN L32



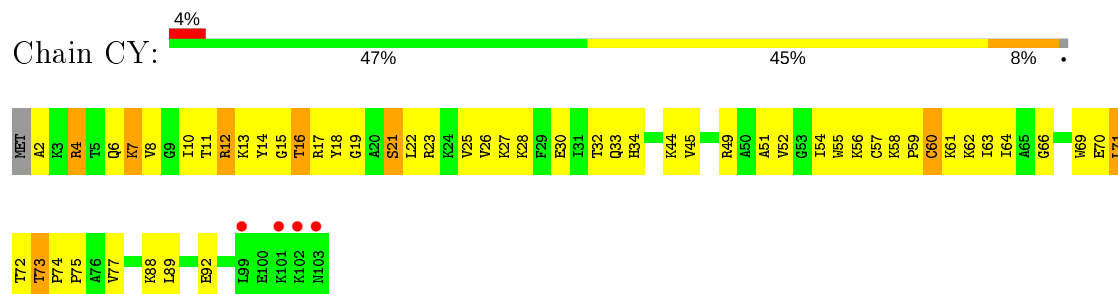
• Molecule 45: 60S RIBOSOMAL PROTEIN L32



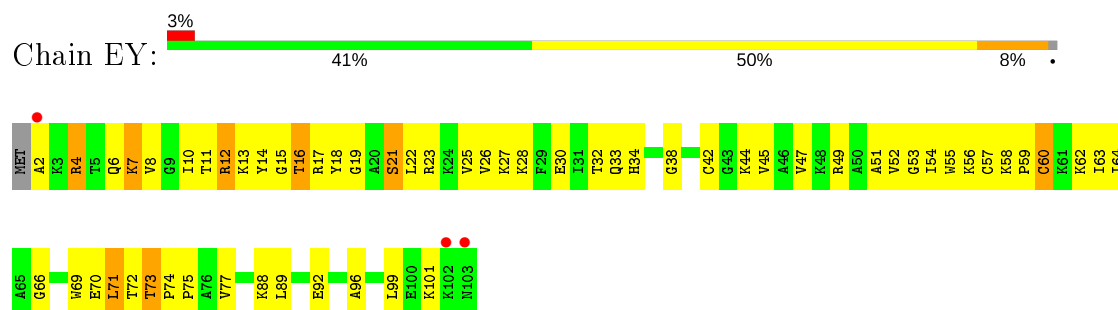
• Molecule 46: RPL37A



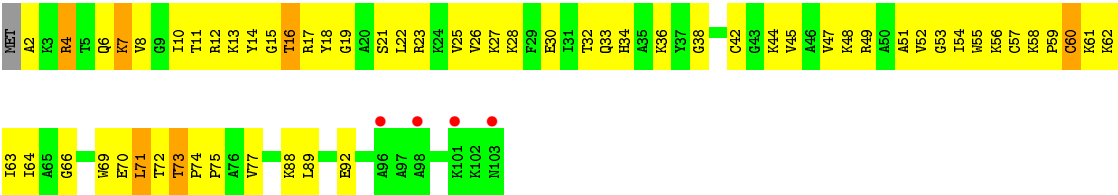
• Molecule 46: RPL37A



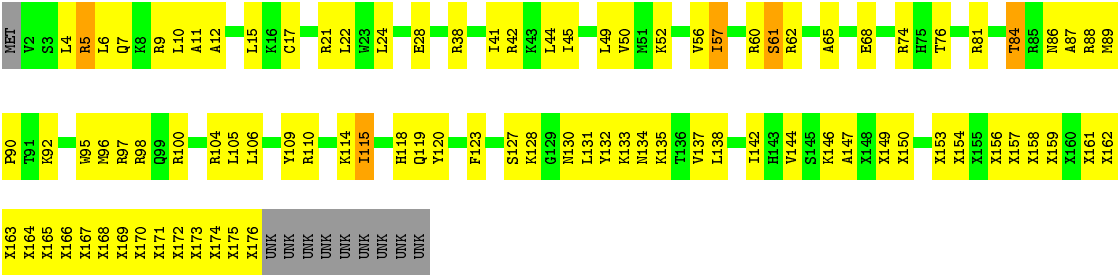
• Molecule 46: RPL37A



● Molecule 46: RPL37A



● Molecule 47: RPL19



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	320.19Å 289.25Å 535.04Å 90.00° 91.22° 90.00°	Depositor
Resolution (Å)	20.00 – 3.52 39.96 – 3.52	Depositor EDS
% Data completeness (in resolution range)	99.4 (20.00-3.52) 99.4 (39.96-3.52)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 3.48Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.216 , 0.244 0.238 , 0.263	Depositor DCC
R_{free} test set	10000 reflections (0.84%)	wwPDB-VP
Wilson B-factor (Å ²)	96.9	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 73.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	511395	wwPDB-VP
Average B, all atoms (Å ²)	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A1	0.75	14/74792 (0.0%)	1.12	353/116594 (0.3%)
1	D1	0.82	60/74792 (0.1%)	1.14	368/116594 (0.3%)
1	F1	0.74	57/74792 (0.1%)	1.12	384/116594 (0.3%)
1	H1	0.78	8/74792 (0.0%)	1.15	436/116594 (0.4%)
2	AA	0.64	1/734 (0.1%)	0.77	0/972
2	DA	0.63	0/734	0.76	0/972
2	FA	0.61	1/734 (0.1%)	0.75	0/972
2	HA	0.63	0/734	0.77	0/972
3	AB	0.54	0/466	0.62	0/619
3	DB	0.46	0/466	0.62	0/619
3	FB	0.48	0/466	0.62	0/619
3	HB	0.51	0/466	0.62	0/619
4	AC	0.58	0/848	0.71	1/1123 (0.1%)
4	DC	0.53	0/848	0.69	0/1123
4	FC	0.54	0/848	0.70	0/1123
4	HC	0.57	0/848	0.71	1/1123 (0.1%)
5	AE	0.47	0/1550	0.74	2/2077 (0.1%)
5	DE	0.47	0/1550	0.74	2/2077 (0.1%)
5	FE	0.48	0/1550	0.75	2/2077 (0.1%)
5	HE	0.47	0/1550	0.75	2/2077 (0.1%)
6	AF	0.51	0/1033	0.71	0/1380
6	DF	0.51	0/1033	0.71	0/1380
6	FF	0.53	0/1033	0.71	0/1380
6	HF	0.53	0/1033	0.72	0/1380
7	AG	0.50	0/736	0.74	0/990
7	DG	0.47	0/736	0.73	0/990
7	FG	0.47	0/736	0.72	0/990
7	HG	0.46	0/736	0.72	0/990
8	AH	0.63	0/870	0.81	0/1175
8	DH	0.62	0/870	0.82	0/1175
8	FH	0.63	0/870	0.81	0/1175
8	HH	0.58	0/870	0.81	0/1175

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	AJ	0.51	0/1739	0.70	0/2368
9	DJ	0.49	0/1739	0.70	0/2368
9	FJ	0.53	0/1739	0.70	0/2368
9	HJ	0.54	0/1739	0.70	0/2368
10	AK	0.48	0/421	0.69	0/558
10	DK	0.45	0/421	0.70	0/558
10	FK	0.46	0/421	0.69	0/558
10	HK	0.48	0/421	0.71	0/558
11	AL	0.64	0/861	0.77	1/1154 (0.1%)
11	DL	0.57	0/861	0.72	0/1154
11	FL	0.51	0/861	0.73	0/1154
11	HL	0.51	0/861	0.74	0/1154
12	AM	0.41	0/832	0.67	0/1113
12	DM	0.41	0/832	0.67	0/1113
12	FM	0.41	0/832	0.67	0/1113
12	HM	0.42	0/832	0.66	0/1113
13	AN	0.43	0/1190	0.63	1/1582 (0.1%)
13	DN	0.38	0/1190	0.58	0/1582
13	FN	0.38	0/1190	0.58	0/1582
13	HN	0.38	0/1190	0.58	0/1582
14	AO	0.47	0/1047	0.77	1/1400 (0.1%)
14	DO	0.47	0/1047	0.77	1/1400 (0.1%)
14	FO	0.46	0/1047	0.76	1/1400 (0.1%)
14	HO	0.51	0/1047	0.78	1/1400 (0.1%)
15	AP	0.41	0/561	0.61	0/745
15	DP	0.38	0/561	0.62	0/745
15	FP	0.40	0/561	0.60	0/745
15	HP	0.40	0/561	0.62	0/745
16	AQ	0.48	0/808	0.70	0/1068
16	DQ	0.48	0/808	0.69	0/1068
16	FQ	0.49	0/808	0.73	0/1068
16	HQ	0.50	0/808	0.70	0/1068
17	AT	0.48	0/539	0.72	0/711
17	DT	0.48	0/539	0.72	0/711
17	FT	0.49	0/539	0.71	0/711
17	HT	0.52	0/539	0.72	0/711
18	AU	0.53	0/1647	0.74	1/2201 (0.0%)
18	DU	0.51	0/1647	0.74	1/2201 (0.0%)
18	FU	0.54	0/1647	0.74	1/2201 (0.0%)
18	HU	0.58	0/1647	0.74	1/2201 (0.0%)
19	AX	0.48	0/1563	0.74	0/2104
19	DX	0.50	0/1563	0.75	1/2104 (0.0%)
19	FX	0.49	0/1563	0.74	0/2104

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	HX	0.50	0/1563	0.74	2/2104 (0.1%)
20	B2	0.69	0/3696	1.06	10/5761 (0.2%)
20	C2	0.69	0/3696	1.07	7/5761 (0.1%)
20	E2	0.63	0/3696	1.07	10/5761 (0.2%)
20	G2	0.86	1/3696 (0.0%)	1.17	24/5761 (0.4%)
21	B3	0.70	0/2870	0.96	7/4473 (0.2%)
21	C3	0.61	0/2870	0.97	5/4473 (0.1%)
21	E3	0.59	0/2870	0.95	4/4473 (0.1%)
21	G3	0.63	0/2870	0.98	10/4473 (0.2%)
22	BA	0.63	0/2019	0.79	1/2712 (0.0%)
22	CA	0.61	0/2019	0.77	1/2712 (0.0%)
22	EA	0.61	0/2019	0.77	1/2712 (0.0%)
22	GA	0.60	0/2019	0.76	1/2712 (0.0%)
23	BB	0.56	0/3144	0.72	0/4213
23	CB	0.54	0/3144	0.71	0/4213
23	EB	0.54	0/3144	0.71	0/4213
23	GB	0.52	0/3144	0.72	0/4213
24	BC	0.47	0/3222	0.67	0/4338
24	CC	0.49	0/3222	0.68	0/4338
24	EC	0.49	0/3222	0.68	0/4338
24	GC	0.53	0/3222	0.69	1/4338 (0.0%)
25	BD	0.48	0/1376	0.66	0/1833
25	CD	0.45	0/1376	0.66	0/1833
25	ED	0.46	0/1376	0.66	0/1833
25	GD	0.47	0/1376	0.67	0/1833
26	BE	0.49	0/1501	0.72	2/2015 (0.1%)
26	CE	0.48	0/1501	0.72	2/2015 (0.1%)
26	EE	0.50	0/1501	0.72	1/2015 (0.0%)
26	GE	0.50	0/1501	0.74	2/2015 (0.1%)
27	BF	0.48	0/1893	0.66	0/2548
27	CF	0.48	0/1893	0.66	0/2548
27	EF	0.48	0/1893	0.65	0/2548
27	GF	0.49	0/1893	0.66	0/2548
29	BH	0.48	0/1652	0.68	0/2213
29	CH	0.48	0/1652	0.66	0/2213
29	EH	0.46	0/1652	0.66	0/2213
29	GH	0.46	0/1652	0.67	0/2213
30	BI	0.48	0/1624	0.66	0/2176
30	CI	0.49	0/1624	0.68	0/2176
30	EI	0.49	0/1624	0.66	0/2176
30	GI	0.87	6/1624 (0.4%)	0.92	7/2176 (0.3%)
31	BJ	0.64	1/1038 (0.1%)	0.77	0/1394
31	CJ	0.67	1/1038 (0.1%)	0.77	1/1394 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	EJ	0.64	1/1038 (0.1%)	0.76	0/1394
31	GJ	0.68	1/1038 (0.1%)	0.77	2/1394 (0.1%)
32	BK	0.53	0/1189	0.71	0/1589
32	CK	0.53	0/1189	0.73	1/1589 (0.1%)
32	EK	0.52	0/1189	0.73	1/1589 (0.1%)
32	GK	0.58	0/1189	0.74	0/1589
33	BL	0.53	0/1727	0.71	0/2308
33	CL	0.53	0/1727	0.71	0/2308
33	EL	0.53	0/1727	0.72	0/2308
33	GL	0.59	0/1727	0.73	0/2308
34	BM	0.49	0/2453	0.70	1/3285 (0.0%)
34	CM	0.48	0/2469	0.69	1/3306 (0.0%)
34	EM	0.54	1/2469 (0.0%)	0.71	1/3306 (0.0%)
34	GM	0.53	1/2469 (0.0%)	0.72	1/3306 (0.0%)
35	BN	0.54	0/1464	0.77	1/1965 (0.1%)
35	CN	0.52	0/1464	0.77	0/1965
35	EN	0.53	0/1464	0.76	0/1965
35	GN	0.60	0/1464	0.78	1/1965 (0.1%)
36	BO	0.58	0/1507	0.67	0/2001
36	EO	0.44	0/1208	0.62	0/1604
36	GO	0.50	0/1250	0.65	0/1660
37	BP	0.53	0/1300	0.64	0/1743
37	CP	0.49	0/1300	0.62	0/1743
37	EP	0.50	0/1300	0.63	0/1743
37	GP	0.54	0/1300	0.64	0/1743
38	BQ	0.60	0/1259	0.77	0/1693
38	CQ	0.57	0/1259	0.75	1/1693 (0.1%)
38	EQ	0.55	0/1259	0.75	1/1693 (0.1%)
38	GQ	0.56	0/1259	0.78	1/1693 (0.1%)
39	BR	0.52	0/981	0.67	0/1320
39	CR	0.47	0/981	0.66	0/1320
39	ER	0.46	0/981	0.66	0/1320
39	GR	0.52	0/981	0.67	0/1320
40	BS	0.44	0/1028	0.62	0/1372
40	CS	0.42	0/1028	0.61	0/1372
40	ES	0.44	0/1028	0.61	0/1372
40	GS	0.50	0/1028	0.63	0/1372
41	BT	0.60	0/521	0.72	0/693
41	CT	0.57	0/521	0.69	0/693
41	ET	0.55	0/521	0.71	0/693
41	GT	0.53	0/521	0.70	0/693
42	BU	0.44	0/995	0.65	0/1318
42	CU	0.44	0/995	0.64	0/1318

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
42	EU	0.44	0/995	0.65	0/1318
42	GU	0.51	0/995	0.66	0/1318
43	BV	0.48	0/1950	0.66	0/2614
43	CV	0.49	0/1950	0.67	1/2614 (0.0%)
43	EV	0.50	0/1950	0.67	1/2614 (0.0%)
43	GV	0.49	0/1950	0.66	1/2614 (0.0%)
44	BW	0.60	0/913	0.68	0/1222
44	CW	0.55	0/913	0.68	0/1222
44	EW	0.51	0/913	0.67	0/1222
44	GW	0.51	0/913	0.68	0/1222
45	BX	0.48	0/1028	0.67	0/1371
45	CX	0.51	0/1028	0.67	0/1371
45	EX	0.47	0/1028	0.67	0/1371
45	GX	0.56	0/1028	0.68	0/1371
46	BY	0.60	0/799	0.79	0/1069
46	CY	0.60	0/799	0.75	0/1069
46	EY	0.57	0/799	0.76	0/1069
46	GY	0.55	0/799	0.75	0/1069
47	CO	0.46	0/1208	0.63	0/1604
All	All	0.68	154/540737 (0.0%)	0.99	1677/795620 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AA	0	1
2	DA	0	1
2	FA	0	1
2	HA	0	1
8	AH	0	1
12	AM	0	1
12	DM	0	1
12	FM	0	1
12	HM	0	1
16	AQ	0	1
16	DQ	0	1
16	FQ	0	1
16	HQ	0	1
18	FU	0	1
27	BF	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
27	CF	0	1
27	EF	0	1
27	GF	0	1
32	BK	0	2
32	CK	0	2
32	EK	0	2
32	GK	0	2
38	CQ	0	1
38	GQ	0	1
42	CU	0	1
45	GX	0	1
All	All	0	30

The worst 5 of 154 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F1	2239	A	O3'-P	25.66	1.92	1.61
30	GI	60	TRP	NE1-CE2	-18.39	1.13	1.37
1	D1	2254	A	C5-C4	17.31	1.50	1.38
1	D1	2254	A	N7-C5	15.90	1.48	1.39
1	D1	2254	A	N3-C4	15.68	1.44	1.34

The worst 5 of 1677 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F1	2253	U	C5-C6-N1	-21.57	111.92	122.70
30	GI	60	TRP	CE2-CD2-CG	-18.64	92.39	107.30
1	D1	284	U	C6-N1-C2	-15.54	111.67	121.00
1	F1	119	A	N1-C6-N6	15.41	127.85	118.60
1	H1	1053	A	C6-N1-C2	-15.06	109.57	118.60

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AA	51	GLY	Peptide
8	AH	101	GLY	Peptide
12	AM	53	GLY	Peptide
16	AQ	12	GLY	Peptide
27	BF	174	LYS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	66769	0	33570	4643	2
1	D1	66769	0	33568	4655	1
1	F1	66769	0	33568	4661	3
1	H1	66769	0	33570	4682	4
2	AA	721	0	744	102	0
2	DA	721	0	744	103	0
2	FA	721	0	744	110	0
2	HA	721	0	744	114	0
3	AB	456	0	483	51	0
3	DB	456	0	483	52	0
3	FB	456	0	483	53	0
3	HB	456	0	483	51	0
4	AC	836	0	912	64	0
4	DC	836	0	911	62	0
4	FC	836	0	911	65	0
4	HC	836	0	911	67	0
5	AE	1525	0	1600	230	0
5	DE	1525	0	1600	225	0
5	FE	1525	0	1600	221	0
5	HE	1525	0	1600	231	0
6	AF	1021	0	1119	147	0
6	DF	1021	0	1119	152	0
6	FF	1021	0	1119	152	0
6	HF	1021	0	1119	152	0
7	AG	727	0	747	103	0
7	DG	727	0	747	92	0
7	FG	727	0	747	88	0
7	HG	727	0	747	88	0
8	AH	850	0	870	134	0
8	DH	850	0	870	139	0
8	FH	850	0	870	139	0
8	HH	850	0	870	129	0
9	AJ	1716	0	1712	162	0
9	DJ	1716	0	1712	181	0
9	FJ	1716	0	1712	178	0
9	HJ	1716	0	1712	176	0
10	AK	415	0	446	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	DK	415	0	446	38	0
10	FK	415	0	446	36	0
10	HK	415	0	446	35	0
11	AL	852	0	906	90	0
11	DL	852	0	906	94	0
11	FL	852	0	906	88	0
11	HL	852	0	906	90	0
12	AM	819	0	855	75	0
12	DM	819	0	855	73	0
12	FM	819	0	855	77	0
12	HM	819	0	855	74	0
13	AN	1170	0	1259	156	0
13	DN	1170	0	1259	134	0
13	FN	1170	0	1259	155	0
13	HN	1170	0	1259	134	0
14	AO	1034	0	1101	143	0
14	DO	1034	0	1101	127	0
14	FO	1034	0	1101	130	0
14	HO	1034	0	1101	119	0
15	AP	551	0	614	53	0
15	DP	551	0	614	57	2
15	FP	551	0	614	49	0
15	HP	551	0	614	58	0
16	AQ	803	0	907	87	2
16	DQ	803	0	907	98	0
16	FQ	803	0	907	100	0
16	HQ	803	0	907	82	0
17	AT	533	0	578	65	0
17	DT	533	0	578	55	0
17	FT	533	0	578	56	0
17	HT	533	0	578	62	0
18	AU	1624	0	1733	210	0
18	DU	1624	0	1733	215	0
18	FU	1624	0	1733	209	0
18	HU	1624	0	1733	236	0
19	AX	1536	0	1613	221	0
19	DX	1536	0	1613	220	0
19	FX	1536	0	1613	222	0
19	HX	1536	0	1613	211	0
20	B2	3300	0	1657	219	1
20	C2	3300	0	1657	225	0
20	E2	3300	0	1657	227	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	G2	3300	0	1657	234	0
21	B3	2566	0	1294	179	0
21	C3	2566	0	1294	195	0
21	E3	2566	0	1294	191	0
21	G3	2566	0	1294	187	0
22	BA	1977	0	2000	233	0
22	CA	1977	0	2000	221	0
22	EA	1977	0	2000	240	0
22	GA	1977	0	2000	247	0
23	BB	3080	0	3187	338	0
23	CB	3080	0	3187	332	0
23	EB	3080	0	3187	364	0
23	GB	3080	0	3187	361	0
24	BC	3172	0	3274	422	0
24	CC	3172	0	3274	428	0
24	EC	3172	0	3274	438	0
24	GC	3172	0	3274	443	0
25	BD	1357	0	1400	124	0
25	CD	1357	0	1400	123	0
25	ED	1357	0	1400	125	0
25	GD	1357	0	1400	127	0
26	BE	1481	0	1574	124	0
26	CE	1481	0	1574	119	0
26	EE	1481	0	1574	124	0
26	GE	1481	0	1574	123	0
27	BF	1860	0	1968	208	0
27	CF	1860	0	1968	217	0
27	EF	1860	0	1968	197	1
27	GF	1860	0	1968	208	0
28	BG	711	0	644	56	0
28	CG	711	0	644	44	0
28	EG	711	0	644	46	0
28	GG	711	0	644	86	0
29	BH	1620	0	1701	159	0
29	CH	1620	0	1701	155	0
29	EH	1620	0	1701	165	0
29	GH	1620	0	1701	160	0
30	BI	1594	0	1701	172	0
30	CI	1594	0	1701	179	0
30	EI	1594	0	1701	170	0
30	GI	1594	0	1701	179	0
31	BJ	1022	0	1078	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	CJ	1022	0	1079	64	0
31	EJ	1022	0	1079	70	0
31	GJ	1022	0	1078	71	0
32	BK	1161	0	1227	189	0
32	CK	1161	0	1227	180	0
32	EK	1161	0	1227	183	0
32	GK	1161	0	1227	195	0
33	BL	1691	0	1762	183	0
33	CL	1691	0	1762	187	0
33	EL	1691	0	1762	195	0
33	GL	1691	0	1762	203	0
34	BM	2409	0	2497	327	0
34	CM	2424	0	2509	312	1
34	EM	2424	0	2509	311	4
34	GM	2424	0	2509	286	2
35	BN	1441	0	1534	218	0
35	CN	1441	0	1534	232	0
35	EN	1441	0	1534	223	0
35	GN	1441	0	1534	234	0
36	BO	1491	0	1618	106	0
36	EO	1192	0	1296	87	0
36	GO	1234	0	1323	87	0
37	BP	1272	0	1310	136	0
37	CP	1272	0	1310	129	0
37	EP	1272	0	1310	137	0
37	GP	1272	0	1310	126	0
38	BQ	1239	0	1276	126	0
38	CQ	1239	0	1276	132	0
38	EQ	1239	0	1276	125	0
38	GQ	1239	0	1276	133	0
39	BR	965	0	1020	96	0
39	CR	965	0	1020	82	0
39	ER	965	0	1020	90	0
39	GR	965	0	1020	97	0
40	BS	1013	0	1101	90	0
40	CS	1013	0	1101	96	1
40	ES	1013	0	1101	94	0
40	GS	1013	0	1101	92	0
41	BT	510	0	546	51	0
41	CT	510	0	546	51	0
41	ET	510	0	546	59	0
41	GT	510	0	546	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	BU	990	0	1123	98	0
42	CU	990	0	1123	106	0
42	EU	990	0	1123	109	0
42	GU	990	0	1123	117	0
43	BV	1910	0	1983	203	0
43	CV	1910	0	1983	202	0
43	EV	1910	0	1983	212	0
43	GV	1910	0	1983	199	0
44	BW	901	0	937	65	0
44	CW	901	0	937	68	0
44	EW	901	0	937	70	0
44	GW	901	0	937	69	0
45	BX	1012	0	1079	110	0
45	CX	1012	0	1079	108	0
45	EX	1012	0	1079	114	0
45	GX	1012	0	1079	120	0
46	BY	786	0	851	83	0
46	CY	786	0	849	90	0
46	EY	786	0	851	105	0
46	GY	786	0	851	94	0
47	CO	1366	0	1470	140	0
48	A1	200	0	0	0	0
48	AA	2	0	0	0	0
48	AK	1	0	0	0	0
48	B2	8	0	0	0	0
48	B3	3	0	0	0	0
48	BJ	1	0	0	0	0
48	BL	1	0	0	0	0
48	BN	1	0	0	0	0
48	BP	1	0	0	0	0
48	BQ	2	0	0	0	0
48	BW	1	0	0	0	0
48	C2	6	0	0	0	0
48	C3	7	0	0	0	0
48	CD	1	0	0	0	0
48	CJ	1	0	0	0	0
48	CL	2	0	0	0	0
48	CN	1	0	0	0	0
48	CQ	2	0	0	0	0
48	CW	1	0	0	0	0
48	CY	1	0	0	0	0
48	D1	232	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	DA	2	0	0	0	0
48	DJ	1	0	0	0	0
48	DK	1	0	0	0	0
48	DQ	1	0	0	0	0
48	E2	7	0	0	0	0
48	E3	6	0	0	0	0
48	EJ	1	0	0	0	0
48	EL	2	0	0	0	0
48	EN	2	0	0	0	0
48	EQ	1	0	0	0	0
48	EW	2	0	0	0	0
48	F1	184	0	0	0	0
48	FA	2	0	0	0	0
48	FK	1	0	0	0	0
48	FT	1	0	0	0	0
48	G2	6	0	0	0	0
48	G3	5	0	0	0	0
48	GA	1	0	0	0	0
48	GJ	1	0	0	0	0
48	GL	1	0	0	0	0
48	GN	1	0	0	0	0
48	GO	1	0	0	0	0
48	GP	2	0	0	0	0
48	GQ	1	0	0	0	0
48	GW	1	0	0	0	0
48	H1	155	0	0	0	0
48	HT	1	0	0	0	0
49	AA	1	0	0	0	0
49	AC	1	0	0	0	0
49	AK	1	0	0	0	0
49	AL	1	0	0	0	0
49	BY	1	0	0	0	0
49	CY	1	0	0	0	0
49	DA	1	0	0	0	0
49	DC	1	0	0	0	0
49	DK	1	0	0	0	0
49	DL	1	0	0	0	0
49	EY	1	0	0	0	0
49	FA	1	0	0	0	0
49	FC	1	0	0	0	0
49	FK	1	0	0	0	0
49	FL	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	GY	1	0	0	0	0
49	HA	1	0	0	0	0
49	HC	1	0	0	0	0
49	HK	1	0	0	0	0
49	HL	1	0	0	0	0
50	A1	1134	0	0	292	0
50	AA	8	0	0	2	0
50	AB	5	0	0	2	0
50	AH	1	0	0	0	0
50	AK	3	0	0	1	0
50	AM	1	0	0	0	0
50	AP	2	0	0	0	0
50	AT	3	0	0	3	0
50	AU	4	0	0	3	0
50	B2	54	0	0	5	0
50	B3	23	0	0	6	0
50	BA	12	0	0	3	0
50	BB	4	0	0	1	0
50	BC	7	0	0	0	0
50	BE	1	0	0	0	0
50	BI	3	0	0	1	0
50	BJ	5	0	0	1	0
50	BK	3	0	0	1	0
50	BL	8	0	0	0	0
50	BM	2	0	0	1	0
50	BN	5	0	0	0	0
50	BO	2	0	0	2	0
50	BP	5	0	0	2	0
50	BQ	7	0	0	3	0
50	BU	1	0	0	0	0
50	BV	7	0	0	1	0
50	BW	5	0	0	0	0
50	BX	6	0	0	1	0
50	BY	5	0	0	0	0
50	C2	46	0	0	3	0
50	C3	39	0	0	10	0
50	CA	11	0	0	3	0
50	CB	4	0	0	0	0
50	CC	7	0	0	0	0
50	CD	4	0	0	0	0
50	CE	2	0	0	1	0
50	CI	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	CJ	4	0	0	3	0
50	CK	3	0	0	1	0
50	CL	12	0	0	2	0
50	CM	6	0	0	1	0
50	CN	7	0	0	5	0
50	CO	2	0	0	1	0
50	CP	6	0	0	1	0
50	CQ	7	0	0	5	0
50	CU	1	0	0	0	0
50	CV	4	0	0	1	0
50	CW	5	0	0	0	0
50	CX	6	0	0	0	0
50	CY	5	0	0	0	0
50	D1	1341	0	0	313	0
50	DA	10	0	0	1	0
50	DB	4	0	0	2	0
50	DE	1	0	0	0	0
50	DJ	2	0	0	1	0
50	DK	2	0	0	0	0
50	DP	1	0	0	0	0
50	DQ	2	0	0	2	0
50	DT	4	0	0	3	0
50	DU	3	0	0	0	0
50	DX	2	0	0	0	0
50	E2	44	0	0	8	0
50	E3	34	0	0	4	0
50	EA	4	0	0	4	0
50	EB	3	0	0	0	0
50	EC	2	0	0	0	0
50	EE	2	0	0	0	0
50	EJ	4	0	0	1	0
50	EK	5	0	0	1	0
50	EL	10	0	0	1	0
50	EM	2	0	0	0	0
50	EN	7	0	0	6	0
50	EP	6	0	0	1	0
50	EQ	4	0	0	4	0
50	EV	6	0	0	1	0
50	EW	7	0	0	0	0
50	EX	5	0	0	2	0
50	EY	5	0	0	0	0
50	F1	1076	0	0	268	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	FA	7	0	0	2	0
50	FB	4	0	0	1	0
50	FE	1	0	0	0	0
50	FH	1	0	0	0	0
50	FK	2	0	0	0	0
50	FL	3	0	0	1	0
50	FP	2	0	0	0	0
50	FT	4	0	0	4	0
50	FU	4	0	0	0	0
50	G2	34	0	0	2	0
50	G3	26	0	0	9	0
50	GA	6	0	0	6	0
50	GB	3	0	0	0	0
50	GC	2	0	0	0	0
50	GE	2	0	0	0	0
50	GI	1	0	0	0	0
50	GJ	4	0	0	2	0
50	GK	2	0	0	2	0
50	GL	5	0	0	1	0
50	GM	1	0	0	1	0
50	GN	2	0	0	1	0
50	GO	2	0	0	1	0
50	GP	5	0	0	0	0
50	GQ	4	0	0	2	0
50	GV	3	0	0	0	0
50	GW	4	0	0	0	0
50	GX	5	0	0	1	0
50	GY	1	0	0	0	0
50	H1	924	0	0	217	0
50	HA	4	0	0	1	0
50	HB	4	0	0	2	0
50	HJ	2	0	0	0	0
50	HK	2	0	0	0	0
50	HP	1	0	0	0	0
50	HT	5	0	0	5	0
50	HU	2	0	0	0	0
All	All	511395	0	371708	37500	12

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 43.

The worst 5 of 37500 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)
28:GG:8:UNK:CG	1:H1:1248:G:N2	1.82	1.41
28:GG:8:UNK:HG3	1:H1:1248:G:N2	1.34	1.40
1:F1:452:U:H5'	14:FO:56:GLN:NE2	1.41	1.35
13:AN:130:LYS:HG2	1:H1:2664:C:OP1	1.22	1.33
46:CY:28:LYS:NZ	1:F1:2252:C:OP1	1.60	1.33

The worst 5 of 12 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:CM:276:LYS:NZ	1:D1:259:U:O3'[2_546]	1.54	0.66
34:GM:117:THR:OG1	1:H1:192:C:C4'[2_445]	1.57	0.63
34:EM:214:LYS:NZ	1:F1:171:A:O4'[2_456]	1.76	0.44
20:B2:87:C:N4	40:CS:82:GLU:OE2[1_545]	1.84	0.36
1:A1:1840:U:O4	15:DP:74:LYS:N[1_545]	1.88	0.32

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	
2	AA	89/94 (95%)	85 (96%)	4 (4%)	0	100	100
2	DA	89/94 (95%)	85 (96%)	4 (4%)	0	100	100
2	FA	89/94 (95%)	85 (96%)	4 (4%)	0	100	100
2	HA	89/94 (95%)	85 (96%)	4 (4%)	0	100	100
3	AB	49/52 (94%)	46 (94%)	3 (6%)	0	100	100
3	DB	49/52 (94%)	46 (94%)	3 (6%)	0	100	100
3	FB	49/52 (94%)	46 (94%)	3 (6%)	0	100	100
3	HB	49/52 (94%)	46 (94%)	3 (6%)	0	100	100
4	AC	101/109 (93%)	99 (98%)	2 (2%)	0	100	100
4	DC	101/109 (93%)	99 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	FC	101/109 (93%)	99 (98%)	2 (2%)	0	100	100
4	HC	101/109 (93%)	99 (98%)	2 (2%)	0	100	100
5	AE	188/191 (98%)	178 (95%)	9 (5%)	1 (0%)	29	67
5	DE	188/191 (98%)	176 (94%)	11 (6%)	1 (0%)	29	67
5	FE	188/191 (98%)	178 (95%)	9 (5%)	1 (0%)	29	67
5	HE	188/191 (98%)	177 (94%)	10 (5%)	1 (0%)	29	67
6	AF	123/126 (98%)	115 (94%)	8 (6%)	0	100	100
6	DF	123/126 (98%)	116 (94%)	7 (6%)	0	100	100
6	FF	123/126 (98%)	115 (94%)	8 (6%)	0	100	100
6	HF	123/126 (98%)	114 (93%)	9 (7%)	0	100	100
7	AG	94/104 (90%)	90 (96%)	4 (4%)	0	100	100
7	DG	94/104 (90%)	90 (96%)	4 (4%)	0	100	100
7	FG	94/104 (90%)	90 (96%)	4 (4%)	0	100	100
7	HG	94/104 (90%)	90 (96%)	4 (4%)	0	100	100
8	AH	105/113 (93%)	100 (95%)	5 (5%)	0	100	100
8	DH	105/113 (93%)	100 (95%)	5 (5%)	0	100	100
8	FH	105/113 (93%)	100 (95%)	4 (4%)	1 (1%)	15	54
8	HH	105/113 (93%)	100 (95%)	5 (5%)	0	100	100
9	AJ	224/248 (90%)	211 (94%)	11 (5%)	2 (1%)	17	57
9	DJ	224/248 (90%)	211 (94%)	11 (5%)	2 (1%)	17	57
9	FJ	224/248 (90%)	212 (95%)	10 (4%)	2 (1%)	17	57
9	HJ	224/248 (90%)	213 (95%)	9 (4%)	2 (1%)	17	57
10	AK	50/129 (39%)	43 (86%)	7 (14%)	0	100	100
10	DK	50/129 (39%)	44 (88%)	6 (12%)	0	100	100
10	FK	50/129 (39%)	44 (88%)	6 (12%)	0	100	100
10	HK	50/129 (39%)	43 (86%)	7 (14%)	0	100	100
11	AL	106/123 (86%)	98 (92%)	8 (8%)	0	100	100
11	DL	106/123 (86%)	98 (92%)	8 (8%)	0	100	100
11	FL	106/123 (86%)	98 (92%)	8 (8%)	0	100	100
11	HL	106/123 (86%)	98 (92%)	8 (8%)	0	100	100
12	AM	98/118 (83%)	92 (94%)	5 (5%)	1 (1%)	15	54

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	DM	98/118 (83%)	94 (96%)	3 (3%)	1 (1%)	15	54
12	FM	98/118 (83%)	93 (95%)	4 (4%)	1 (1%)	15	54
12	HM	98/118 (83%)	92 (94%)	5 (5%)	1 (1%)	15	54
13	AN	141/144 (98%)	133 (94%)	7 (5%)	1 (1%)	22	62
13	DN	141/144 (98%)	133 (94%)	7 (5%)	1 (1%)	22	62
13	FN	141/144 (98%)	133 (94%)	8 (6%)	0	100	100
13	HN	141/144 (98%)	133 (94%)	7 (5%)	1 (1%)	22	62
14	AO	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
14	DO	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
14	FO	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
14	HO	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
15	AP	62/89 (70%)	58 (94%)	4 (6%)	0	100	100
15	DP	62/89 (70%)	58 (94%)	4 (6%)	0	100	100
15	FP	62/89 (70%)	58 (94%)	4 (6%)	0	100	100
15	HP	62/89 (70%)	58 (94%)	4 (6%)	0	100	100
16	AQ	100/104 (96%)	89 (89%)	9 (9%)	2 (2%)	7	41
16	DQ	100/104 (96%)	89 (89%)	9 (9%)	2 (2%)	7	41
16	FQ	100/104 (96%)	88 (88%)	10 (10%)	2 (2%)	7	41
16	HQ	100/104 (96%)	89 (89%)	9 (9%)	2 (2%)	7	41
17	AT	63/66 (96%)	59 (94%)	3 (5%)	1 (2%)	9	45
17	DT	63/66 (96%)	60 (95%)	2 (3%)	1 (2%)	9	45
17	FT	63/66 (96%)	60 (95%)	2 (3%)	1 (2%)	9	45
17	HT	63/66 (96%)	60 (95%)	2 (3%)	1 (2%)	9	45
18	AU	201/206 (98%)	188 (94%)	12 (6%)	1 (0%)	29	67
18	DU	201/206 (98%)	187 (93%)	13 (6%)	1 (0%)	29	67
18	FU	201/206 (98%)	187 (93%)	13 (6%)	1 (0%)	29	67
18	HU	201/206 (98%)	189 (94%)	11 (6%)	1 (0%)	29	67
19	AX	186/189 (98%)	177 (95%)	8 (4%)	1 (0%)	29	67
19	DX	186/189 (98%)	178 (96%)	6 (3%)	2 (1%)	14	53
19	FX	186/189 (98%)	178 (96%)	6 (3%)	2 (1%)	14	53
19	HX	186/189 (98%)	177 (95%)	7 (4%)	2 (1%)	14	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	BA	255/264 (97%)	236 (92%)	19 (8%)	0	100	100
22	CA	255/264 (97%)	235 (92%)	20 (8%)	0	100	100
22	EA	255/264 (97%)	234 (92%)	21 (8%)	0	100	100
22	GA	255/264 (97%)	237 (93%)	18 (7%)	0	100	100
23	BB	384/391 (98%)	371 (97%)	13 (3%)	0	100	100
23	CB	384/391 (98%)	371 (97%)	13 (3%)	0	100	100
23	EB	384/391 (98%)	371 (97%)	13 (3%)	0	100	100
23	GB	384/391 (98%)	370 (96%)	14 (4%)	0	100	100
24	BC	407/410 (99%)	383 (94%)	24 (6%)	0	100	100
24	CC	407/410 (99%)	387 (95%)	20 (5%)	0	100	100
24	EC	407/410 (99%)	384 (94%)	23 (6%)	0	100	100
24	GC	407/410 (99%)	386 (95%)	21 (5%)	0	100	100
25	BD	167/172 (97%)	156 (93%)	11 (7%)	0	100	100
25	CD	167/172 (97%)	156 (93%)	11 (7%)	0	100	100
25	ED	167/172 (97%)	156 (93%)	11 (7%)	0	100	100
25	GD	167/172 (97%)	156 (93%)	11 (7%)	0	100	100
26	BE	184/188 (98%)	171 (93%)	13 (7%)	0	100	100
26	CE	184/188 (98%)	171 (93%)	13 (7%)	0	100	100
26	EE	184/188 (98%)	171 (93%)	13 (7%)	0	100	100
26	GE	184/188 (98%)	171 (93%)	13 (7%)	0	100	100
27	BF	229/255 (90%)	219 (96%)	10 (4%)	0	100	100
27	CF	229/255 (90%)	219 (96%)	10 (4%)	0	100	100
27	EF	229/255 (90%)	219 (96%)	9 (4%)	1 (0%)	34	71
27	GF	229/255 (90%)	219 (96%)	10 (4%)	0	100	100
29	BH	197/215 (92%)	186 (94%)	11 (6%)	0	100	100
29	CH	197/215 (92%)	187 (95%)	10 (5%)	0	100	100
29	EH	197/215 (92%)	186 (94%)	11 (6%)	0	100	100
29	GH	197/215 (92%)	186 (94%)	11 (6%)	0	100	100
30	BI	196/198 (99%)	189 (96%)	7 (4%)	0	100	100
30	CI	196/198 (99%)	189 (96%)	7 (4%)	0	100	100
30	EI	196/198 (99%)	189 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	GI	196/198 (99%)	189 (96%)	7 (4%)	0	100	100
31	BJ	136/141 (96%)	132 (97%)	4 (3%)	0	100	100
31	CJ	136/141 (96%)	132 (97%)	4 (3%)	0	100	100
31	EJ	136/141 (96%)	131 (96%)	5 (4%)	0	100	100
31	GJ	136/141 (96%)	132 (97%)	4 (3%)	0	100	100
32	BK	146/149 (98%)	136 (93%)	8 (6%)	2 (1%)	11	47
32	CK	146/149 (98%)	135 (92%)	8 (6%)	3 (2%)	7	39
32	EK	146/149 (98%)	137 (94%)	7 (5%)	2 (1%)	11	47
32	GK	146/149 (98%)	135 (92%)	8 (6%)	3 (2%)	7	39
33	BL	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
33	CL	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
33	EL	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
33	GL	201/204 (98%)	193 (96%)	7 (4%)	1 (0%)	29	67
34	BM	296/301 (98%)	282 (95%)	13 (4%)	1 (0%)	41	75
34	CM	298/301 (99%)	282 (95%)	15 (5%)	1 (0%)	41	75
34	EM	298/301 (99%)	283 (95%)	14 (5%)	1 (0%)	41	75
34	GM	298/301 (99%)	285 (96%)	12 (4%)	1 (0%)	41	75
35	BN	178/181 (98%)	168 (94%)	10 (6%)	0	100	100
35	CN	178/181 (98%)	168 (94%)	10 (6%)	0	100	100
35	EN	178/181 (98%)	168 (94%)	10 (6%)	0	100	100
35	GN	178/181 (98%)	168 (94%)	10 (6%)	0	100	100
36	BO	182/185 (98%)	170 (93%)	11 (6%)	1 (0%)	29	67
36	EO	144/185 (78%)	137 (95%)	7 (5%)	0	100	100
36	GO	151/185 (82%)	143 (95%)	8 (5%)	0	100	100
37	BP	154/157 (98%)	148 (96%)	6 (4%)	0	100	100
37	CP	154/157 (98%)	147 (96%)	7 (4%)	0	100	100
37	EP	154/157 (98%)	148 (96%)	6 (4%)	0	100	100
37	GP	154/157 (98%)	147 (96%)	7 (4%)	0	100	100
38	BQ	155/183 (85%)	146 (94%)	9 (6%)	0	100	100
38	CQ	155/183 (85%)	147 (95%)	8 (5%)	0	100	100
38	EQ	155/183 (85%)	147 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	GQ	155/183 (85%)	147 (95%)	8 (5%)	0	100	100
39	BR	119/150 (79%)	115 (97%)	4 (3%)	0	100	100
39	CR	119/150 (79%)	116 (98%)	3 (2%)	0	100	100
39	ER	119/150 (79%)	115 (97%)	4 (3%)	0	100	100
39	GR	119/150 (79%)	114 (96%)	5 (4%)	0	100	100
40	BS	124/135 (92%)	119 (96%)	5 (4%)	0	100	100
40	CS	124/135 (92%)	119 (96%)	5 (4%)	0	100	100
40	ES	124/135 (92%)	119 (96%)	5 (4%)	0	100	100
40	GS	124/135 (92%)	118 (95%)	6 (5%)	0	100	100
41	BT	59/158 (37%)	57 (97%)	2 (3%)	0	100	100
41	CT	59/158 (37%)	56 (95%)	3 (5%)	0	100	100
41	ET	59/158 (37%)	57 (97%)	2 (3%)	0	100	100
41	GT	59/158 (37%)	57 (97%)	2 (3%)	0	100	100
42	BU	121/124 (98%)	112 (93%)	9 (7%)	0	100	100
42	CU	121/124 (98%)	111 (92%)	10 (8%)	0	100	100
42	EU	121/124 (98%)	113 (93%)	8 (7%)	0	100	100
42	GU	121/124 (98%)	112 (93%)	9 (7%)	0	100	100
43	BV	232/239 (97%)	216 (93%)	16 (7%)	0	100	100
43	CV	232/239 (97%)	216 (93%)	16 (7%)	0	100	100
43	EV	232/239 (97%)	216 (93%)	15 (6%)	1 (0%)	34	71
43	GV	232/239 (97%)	216 (93%)	15 (6%)	1 (0%)	34	71
44	BW	108/111 (97%)	102 (94%)	6 (6%)	0	100	100
44	CW	108/111 (97%)	102 (94%)	6 (6%)	0	100	100
44	EW	108/111 (97%)	101 (94%)	7 (6%)	0	100	100
44	GW	108/111 (97%)	102 (94%)	6 (6%)	0	100	100
45	BX	123/134 (92%)	119 (97%)	4 (3%)	0	100	100
45	CX	123/134 (92%)	117 (95%)	6 (5%)	0	100	100
45	EX	123/134 (92%)	118 (96%)	5 (4%)	0	100	100
45	GX	123/134 (92%)	117 (95%)	6 (5%)	0	100	100
46	BY	100/103 (97%)	91 (91%)	9 (9%)	0	100	100
46	CY	100/103 (97%)	90 (90%)	10 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
46	EY	100/103 (97%)	90 (90%)	10 (10%)	0	100	100
46	GY	100/103 (97%)	90 (90%)	10 (10%)	0	100	100
47	CO	145/185 (78%)	138 (95%)	7 (5%)	0	100	100
All	All	26160/28348 (92%)	24720 (94%)	1378 (5%)	62 (0%)	47	80

5 of 62 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	AQ	7	VAL
32	BK	24	LYS
32	CK	24	LYS
16	DQ	7	VAL
32	EK	24	LYS

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 X-ray entries followed by that with respect to entries of similar resolution.

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	
2	AA	69/72 (96%)	58 (84%)	11 (16%)	2	15
2	DA	69/72 (96%)	58 (84%)	11 (16%)	2	15
2	FA	69/72 (96%)	59 (86%)	10 (14%)	3	19
2	HA	69/72 (96%)	58 (84%)	11 (16%)	2	15
3	AB	48/49 (98%)	44 (92%)	4 (8%)	11	40
3	DB	48/49 (98%)	44 (92%)	4 (8%)	11	40
3	FB	48/49 (98%)	44 (92%)	4 (8%)	11	40
3	HB	48/49 (98%)	44 (92%)	4 (8%)	11	40
4	AC	95/101 (94%)	92 (97%)	3 (3%)	39	69
4	DC	95/101 (94%)	92 (97%)	3 (3%)	39	69
4	FC	95/101 (94%)	92 (97%)	3 (3%)	39	69
4	HC	95/101 (94%)	92 (97%)	3 (3%)	39	69
5	AE	162/163 (99%)	152 (94%)	10 (6%)	18	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	DE	162/163 (99%)	152 (94%)	10 (6%)	18	52
5	FE	162/163 (99%)	151 (93%)	11 (7%)	16	48
5	HE	162/163 (99%)	151 (93%)	11 (7%)	16	48
6	AF	111/112 (99%)	107 (96%)	4 (4%)	35	66
6	DF	111/112 (99%)	106 (96%)	5 (4%)	27	62
6	FF	111/112 (99%)	107 (96%)	4 (4%)	35	66
6	HF	111/112 (99%)	107 (96%)	4 (4%)	35	66
7	AG	80/88 (91%)	76 (95%)	4 (5%)	24	58
7	DG	80/88 (91%)	74 (92%)	6 (8%)	13	44
7	FG	80/88 (91%)	75 (94%)	5 (6%)	18	51
7	HG	80/88 (91%)	76 (95%)	4 (5%)	24	58
8	AH	87/92 (95%)	78 (90%)	9 (10%)	7	32
8	DH	87/92 (95%)	78 (90%)	9 (10%)	7	32
8	FH	87/92 (95%)	78 (90%)	9 (10%)	7	32
8	HH	87/92 (95%)	78 (90%)	9 (10%)	7	32
9	AJ	195/216 (90%)	177 (91%)	18 (9%)	9	37
9	DJ	195/216 (90%)	176 (90%)	19 (10%)	8	34
9	FJ	195/216 (90%)	177 (91%)	18 (9%)	9	37
9	HJ	195/216 (90%)	177 (91%)	18 (9%)	9	37
10	AK	46/113 (41%)	43 (94%)	3 (6%)	17	50
10	DK	46/113 (41%)	43 (94%)	3 (6%)	17	50
10	FK	46/113 (41%)	43 (94%)	3 (6%)	17	50
10	HK	46/113 (41%)	43 (94%)	3 (6%)	17	50
11	AL	92/107 (86%)	87 (95%)	5 (5%)	22	56
11	DL	92/107 (86%)	87 (95%)	5 (5%)	22	56
11	FL	92/107 (86%)	88 (96%)	4 (4%)	29	62
11	HL	92/107 (86%)	87 (95%)	5 (5%)	22	56
12	AM	93/110 (84%)	90 (97%)	3 (3%)	39	69
12	DM	93/110 (84%)	90 (97%)	3 (3%)	39	69
12	FM	93/110 (84%)	90 (97%)	3 (3%)	39	69
12	HM	93/110 (84%)	90 (97%)	3 (3%)	39	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	AN	130/131 (99%)	123 (95%)	7 (5%)	22	56
13	DN	130/131 (99%)	122 (94%)	8 (6%)	18	52
13	FN	130/131 (99%)	123 (95%)	7 (5%)	22	56
13	HN	130/131 (99%)	123 (95%)	7 (5%)	22	56
14	AO	108/108 (100%)	102 (94%)	6 (6%)	21	55
14	DO	108/108 (100%)	102 (94%)	6 (6%)	21	55
14	FO	108/108 (100%)	100 (93%)	8 (7%)	13	45
14	HO	108/108 (100%)	102 (94%)	6 (6%)	21	55
15	AP	60/77 (78%)	56 (93%)	4 (7%)	16	49
15	DP	60/77 (78%)	56 (93%)	4 (7%)	16	49
15	FP	60/77 (78%)	56 (93%)	4 (7%)	16	49
15	HP	60/77 (78%)	56 (93%)	4 (7%)	16	49
16	AQ	81/83 (98%)	75 (93%)	6 (7%)	13	45
16	DQ	81/83 (98%)	75 (93%)	6 (7%)	13	45
16	FQ	81/83 (98%)	75 (93%)	6 (7%)	13	45
16	HQ	81/83 (98%)	75 (93%)	6 (7%)	13	45
17	AT	61/62 (98%)	55 (90%)	6 (10%)	8	34
17	DT	61/62 (98%)	57 (93%)	4 (7%)	16	50
17	FT	61/62 (98%)	57 (93%)	4 (7%)	16	50
17	HT	61/62 (98%)	57 (93%)	4 (7%)	16	50
18	AU	169/171 (99%)	159 (94%)	10 (6%)	19	53
18	DU	169/171 (99%)	161 (95%)	8 (5%)	26	60
18	FU	169/171 (99%)	160 (95%)	9 (5%)	22	56
18	HU	169/171 (99%)	161 (95%)	8 (5%)	26	60
19	AX	167/168 (99%)	153 (92%)	14 (8%)	11	40
19	DX	167/168 (99%)	152 (91%)	15 (9%)	9	38
19	FX	167/168 (99%)	151 (90%)	16 (10%)	8	35
19	HX	167/168 (99%)	154 (92%)	13 (8%)	12	43
22	BA	196/198 (99%)	165 (84%)	31 (16%)	2	16
22	CA	196/198 (99%)	164 (84%)	32 (16%)	2	14
22	EA	196/198 (99%)	164 (84%)	32 (16%)	2	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	GA	196/198 (99%)	165 (84%)	31 (16%)	2	16
23	BB	330/334 (99%)	306 (93%)	24 (7%)	14	45
23	CB	330/334 (99%)	307 (93%)	23 (7%)	15	47
23	EB	330/334 (99%)	308 (93%)	22 (7%)	16	49
23	GB	330/334 (99%)	306 (93%)	24 (7%)	14	45
24	BC	325/326 (100%)	302 (93%)	23 (7%)	14	47
24	CC	325/326 (100%)	302 (93%)	23 (7%)	14	47
24	EC	325/326 (100%)	300 (92%)	25 (8%)	13	43
24	GC	325/326 (100%)	300 (92%)	25 (8%)	13	43
25	BD	146/149 (98%)	136 (93%)	10 (7%)	16	48
25	CD	146/149 (98%)	136 (93%)	10 (7%)	16	48
25	ED	146/149 (98%)	135 (92%)	11 (8%)	13	44
25	GD	146/149 (98%)	136 (93%)	10 (7%)	16	48
26	BE	163/165 (99%)	157 (96%)	6 (4%)	34	65
26	CE	163/165 (99%)	157 (96%)	6 (4%)	34	65
26	EE	163/165 (99%)	157 (96%)	6 (4%)	34	65
26	GE	163/165 (99%)	157 (96%)	6 (4%)	34	65
27	BF	201/222 (90%)	194 (96%)	7 (4%)	36	67
27	CF	201/222 (90%)	194 (96%)	7 (4%)	36	67
27	EF	201/222 (90%)	194 (96%)	7 (4%)	36	67
27	GF	201/222 (90%)	194 (96%)	7 (4%)	36	67
29	BH	169/180 (94%)	155 (92%)	14 (8%)	11	40
29	CH	169/180 (94%)	155 (92%)	14 (8%)	11	40
29	EH	169/180 (94%)	156 (92%)	13 (8%)	13	43
29	GH	169/180 (94%)	153 (90%)	16 (10%)	8	35
30	BI	166/166 (100%)	150 (90%)	16 (10%)	8	35
30	CI	166/166 (100%)	149 (90%)	17 (10%)	7	32
30	EI	166/166 (100%)	150 (90%)	16 (10%)	8	35
30	GI	166/166 (100%)	150 (90%)	16 (10%)	8	35
31	BJ	107/108 (99%)	98 (92%)	9 (8%)	11	40
31	CJ	107/108 (99%)	99 (92%)	8 (8%)	13	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	EJ	107/108 (99%)	99 (92%)	8 (8%)	13	44
31	GJ	107/108 (99%)	99 (92%)	8 (8%)	13	44
32	BK	120/121 (99%)	110 (92%)	10 (8%)	11	40
32	CK	120/121 (99%)	111 (92%)	9 (8%)	13	44
32	EK	120/121 (99%)	110 (92%)	10 (8%)	11	40
32	GK	120/121 (99%)	110 (92%)	10 (8%)	11	40
33	BL	174/175 (99%)	165 (95%)	9 (5%)	23	57
33	CL	174/175 (99%)	165 (95%)	9 (5%)	23	57
33	EL	174/175 (99%)	165 (95%)	9 (5%)	23	57
33	GL	174/175 (99%)	166 (95%)	8 (5%)	27	61
34	BM	252/254 (99%)	239 (95%)	13 (5%)	23	57
34	CM	253/254 (100%)	242 (96%)	11 (4%)	29	62
34	EM	253/254 (100%)	242 (96%)	11 (4%)	29	62
34	GM	253/254 (100%)	240 (95%)	13 (5%)	24	58
35	BN	159/160 (99%)	145 (91%)	14 (9%)	10	39
35	CN	159/160 (99%)	146 (92%)	13 (8%)	11	41
35	EN	159/160 (99%)	145 (91%)	14 (9%)	10	39
35	GN	159/160 (99%)	146 (92%)	13 (8%)	11	41
36	BO	158/159 (99%)	148 (94%)	10 (6%)	18	51
36	EO	126/159 (79%)	116 (92%)	10 (8%)	12	42
36	GO	127/159 (80%)	117 (92%)	10 (8%)	12	42
37	BP	134/135 (99%)	124 (92%)	10 (8%)	13	44
37	CP	134/135 (99%)	126 (94%)	8 (6%)	19	53
37	EP	134/135 (99%)	125 (93%)	9 (7%)	16	49
37	GP	134/135 (99%)	125 (93%)	9 (7%)	16	49
38	BQ	128/148 (86%)	115 (90%)	13 (10%)	7	32
38	CQ	128/148 (86%)	115 (90%)	13 (10%)	7	32
38	EQ	128/148 (86%)	115 (90%)	13 (10%)	7	32
38	GQ	128/148 (86%)	115 (90%)	13 (10%)	7	32
39	BR	108/132 (82%)	101 (94%)	7 (6%)	17	50
39	CR	108/132 (82%)	101 (94%)	7 (6%)	17	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	ER	108/132 (82%)	102 (94%)	6 (6%)	21	55
39	GR	108/132 (82%)	103 (95%)	5 (5%)	27	61
40	BS	113/120 (94%)	105 (93%)	8 (7%)	14	47
40	CS	113/120 (94%)	104 (92%)	9 (8%)	12	42
40	ES	113/120 (94%)	105 (93%)	8 (7%)	14	47
40	GS	113/120 (94%)	104 (92%)	9 (8%)	12	42
41	BT	52/130 (40%)	46 (88%)	6 (12%)	5	27
41	CT	52/130 (40%)	46 (88%)	6 (12%)	5	27
41	ET	52/130 (40%)	46 (88%)	6 (12%)	5	27
41	GT	52/130 (40%)	46 (88%)	6 (12%)	5	27
42	BU	105/106 (99%)	96 (91%)	9 (9%)	10	39
42	CU	105/106 (99%)	96 (91%)	9 (9%)	10	39
42	EU	105/106 (99%)	96 (91%)	9 (9%)	10	39
42	GU	105/106 (99%)	96 (91%)	9 (9%)	10	39
43	BV	197/202 (98%)	186 (94%)	11 (6%)	21	55
43	CV	197/202 (98%)	187 (95%)	10 (5%)	24	58
43	EV	197/202 (98%)	188 (95%)	9 (5%)	27	61
43	GV	197/202 (98%)	187 (95%)	10 (5%)	24	58
44	BW	100/101 (99%)	96 (96%)	4 (4%)	31	64
44	CW	100/101 (99%)	95 (95%)	5 (5%)	24	58
44	EW	100/101 (99%)	95 (95%)	5 (5%)	24	58
44	GW	100/101 (99%)	96 (96%)	4 (4%)	31	64
45	BX	104/111 (94%)	88 (85%)	16 (15%)	2	17
45	CX	104/111 (94%)	87 (84%)	17 (16%)	2	14
45	EX	104/111 (94%)	88 (85%)	16 (15%)	2	17
45	GX	104/111 (94%)	88 (85%)	16 (15%)	2	17
46	BY	79/80 (99%)	72 (91%)	7 (9%)	9	38
46	CY	79/80 (99%)	71 (90%)	8 (10%)	7	33
46	EY	79/80 (99%)	71 (90%)	8 (10%)	7	33
46	GY	79/80 (99%)	73 (92%)	6 (8%)	13	44
47	CO	126/127 (99%)	116 (92%)	10 (8%)	12	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	22468/23988 (94%)	20823 (93%)	1645 (7%)	14 45

5 of 1645 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	DH	47	ASP
26	EE	113	LYS
46	GY	71	LEU
10	DK	85	LEU
22	EA	43	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 750 such sidechains are listed below:

Mol	Chain	Res	Type
14	DO	56	GLN
27	EF	107	GLN
6	HF	67	GLN
18	DU	3	HIS
23	EB	163	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A1	3114/3354 (92%)	1118 (35%)	209 (6%)
1	D1	3114/3354 (92%)	1113 (35%)	215 (6%)
1	F1	3114/3354 (92%)	1113 (35%)	211 (6%)
1	H1	3114/3354 (92%)	1113 (35%)	210 (6%)
20	B2	154/154 (100%)	58 (37%)	13 (8%)
20	C2	154/154 (100%)	60 (38%)	13 (8%)
20	E2	154/154 (100%)	60 (38%)	13 (8%)
20	G2	154/154 (100%)	60 (38%)	13 (8%)
21	B3	119/120 (99%)	38 (31%)	1 (0%)
21	C3	119/120 (99%)	39 (32%)	1 (0%)
21	E3	119/120 (99%)	38 (31%)	1 (0%)
21	G3	119/120 (99%)	38 (31%)	1 (0%)
All	All	13548/14512 (93%)	4848 (35%)	901 (6%)

5 of 4848 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A1	9	G
1	A1	16	G
1	A1	17	C
1	A1	19	A
1	A1	20	G

5 of 901 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	D1	2741	U
1	F1	500	G
1	H1	2300	G
1	D1	3035	A
20	E2	43	A

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 885 ligands modelled in this entry, 885 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	F1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F1	2239:A	O3'	2240:C	P	1.91

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A1	3119/3354 (92%)	0.13	90 (2%) 51 38	42, 91, 187, 390	0
1	D1	3119/3354 (92%)	0.05	34 (1%) 80 69	40, 79, 164, 330	0
1	F1	3119/3354 (92%)	0.18	62 (1%) 65 52	51, 94, 176, 357	0
1	H1	3119/3354 (92%)	0.49	136 (4%) 34 25	54, 121, 213, 367	0
2	AA	91/94 (96%)	-0.16	2 (2%) 62 48	29, 65, 120, 243	0
2	DA	91/94 (96%)	-0.09	0 100 100	34, 66, 123, 226	0
2	FA	91/94 (96%)	0.21	2 (2%) 62 48	47, 83, 132, 204	0
2	HA	91/94 (96%)	0.86	12 (13%) 3 3	74, 119, 186, 243	0
3	AB	51/52 (98%)	-0.20	1 (1%) 65 52	44, 63, 110, 148	0
3	DB	51/52 (98%)	-0.13	1 (1%) 65 52	49, 69, 111, 146	0
3	FB	51/52 (98%)	0.09	0 100 100	59, 86, 118, 167	0
3	HB	51/52 (98%)	0.79	8 (15%) 2 2	90, 114, 144, 197	0
4	AC	103/109 (94%)	0.37	3 (2%) 51 38	73, 117, 154, 228	0
4	DC	103/109 (94%)	-0.01	0 100 100	46, 84, 135, 194	0
4	FC	103/109 (94%)	0.01	1 (0%) 82 71	58, 96, 156, 192	0
4	HC	103/109 (94%)	0.32	3 (2%) 51 38	81, 130, 176, 199	0
5	AE	190/191 (99%)	0.19	12 (6%) 20 15	69, 122, 171, 214	0
5	DE	190/191 (99%)	0.08	1 (0%) 91 84	74, 124, 169, 226	0
5	FE	190/191 (99%)	0.20	8 (4%) 36 27	60, 123, 176, 227	0
5	HE	190/191 (99%)	0.35	14 (7%) 14 12	76, 141, 194, 227	0
6	AF	125/126 (99%)	0.02	5 (4%) 38 28	71, 111, 156, 213	0
6	DF	125/126 (99%)	-0.22	2 (1%) 72 59	70, 106, 157, 190	0
6	FF	125/126 (99%)	0.01	6 (4%) 30 23	63, 109, 166, 245	0
6	HF	125/126 (99%)	0.02	0 100 100	74, 113, 163, 224	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
7	AG	96/104 (92%)	0.08	1 (1%) 82 71	62, 103, 188, 218	0
7	DG	96/104 (92%)	0.06	4 (4%) 36 27	57, 114, 179, 222	0
7	FG	96/104 (92%)	0.18	2 (2%) 63 50	81, 112, 176, 199	0
7	HG	96/104 (92%)	0.21	1 (1%) 82 71	94, 134, 183, 218	0
8	AH	107/113 (94%)	-0.11	0 100 100	61, 91, 127, 159	0
8	DH	107/113 (94%)	-0.12	0 100 100	54, 89, 127, 138	0
8	FH	107/113 (94%)	-0.04	0 100 100	57, 89, 122, 164	0
8	HH	107/113 (94%)	0.14	0 100 100	68, 109, 141, 181	0
9	AJ	226/248 (91%)	-0.40	0 100 100	52, 90, 138, 190	0
9	DJ	226/248 (91%)	-0.36	0 100 100	51, 89, 136, 206	0
9	FJ	226/248 (91%)	-0.41	1 (0%) 92 87	38, 82, 130, 183	0
9	HJ	226/248 (91%)	-0.49	0 100 100	40, 78, 123, 155	0
10	AK	52/129 (40%)	0.12	2 (3%) 40 30	73, 101, 146, 182	0
10	DK	52/129 (40%)	-0.32	1 (1%) 66 53	53, 79, 134, 151	0
10	FK	52/129 (40%)	-0.40	0 100 100	56, 81, 139, 189	0
10	HK	52/129 (40%)	-0.27	0 100 100	61, 77, 118, 158	0
11	AL	108/123 (87%)	-0.12	1 (0%) 84 73	38, 73, 130, 165	0
11	DL	108/123 (87%)	-0.10	1 (0%) 84 73	47, 85, 144, 217	0
11	FL	108/123 (87%)	0.13	1 (0%) 84 73	66, 98, 135, 174	0
11	HL	108/123 (87%)	0.51	5 (4%) 32 24	90, 117, 156, 183	0
12	AM	100/118 (84%)	0.20	3 (3%) 50 37	72, 121, 155, 185	0
12	DM	100/118 (84%)	0.16	4 (4%) 38 28	73, 126, 179, 199	0
12	FM	100/118 (84%)	0.29	2 (2%) 65 52	93, 144, 196, 208	0
12	HM	100/118 (84%)	0.06	2 (2%) 65 52	98, 151, 195, 214	0
13	AN	143/144 (99%)	-0.20	1 (0%) 87 79	59, 97, 163, 189	0
13	DN	143/144 (99%)	-0.06	1 (0%) 87 79	73, 121, 179, 214	0
13	FN	143/144 (99%)	-0.02	1 (0%) 87 79	72, 122, 175, 208	0
13	HN	143/144 (99%)	0.30	3 (2%) 63 50	92, 148, 189, 217	0
14	AO	134/134 (100%)	-0.20	1 (0%) 87 79	66, 116, 162, 202	0
14	DO	134/134 (100%)	-0.11	1 (0%) 87 79	52, 99, 151, 209	0
14	FO	134/134 (100%)	0.04	2 (1%) 73 61	65, 118, 167, 219	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
14	HO	134/134 (100%)	0.48	11 (8%) 11 10	96, 143, 197, 227	0
15	AP	66/89 (74%)	0.39	3 (4%) 33 24	55, 128, 209, 241	0
15	DP	66/89 (74%)	0.32	5 (7%) 13 11	73, 116, 176, 245	0
15	FP	66/89 (74%)	0.56	4 (6%) 21 16	99, 143, 202, 214	0
15	HP	66/89 (74%)	1.03	8 (12%) 4 4	99, 149, 219, 247	0
16	AQ	102/104 (98%)	0.09	3 (2%) 51 38	72, 122, 172, 208	0
16	DQ	102/104 (98%)	-0.01	3 (2%) 51 38	63, 105, 151, 186	0
16	FQ	102/104 (98%)	0.01	2 (1%) 65 52	72, 114, 166, 190	0
16	HQ	102/104 (98%)	0.57	6 (5%) 22 16	110, 154, 195, 203	0
17	AT	65/66 (98%)	0.37	4 (6%) 20 15	76, 121, 156, 193	0
17	DT	65/66 (98%)	0.11	1 (1%) 73 61	51, 87, 122, 211	0
17	FT	65/66 (98%)	0.26	1 (1%) 73 61	51, 107, 144, 201	0
17	HT	65/66 (98%)	0.76	4 (6%) 20 15	69, 136, 171, 222	0
18	AU	203/206 (98%)	0.09	4 (1%) 65 52	74, 122, 179, 233	0
18	DU	203/206 (98%)	-0.13	0 100 100	48, 98, 158, 198	0
18	FU	203/206 (98%)	-0.07	1 (0%) 91 84	67, 116, 174, 203	0
18	HU	203/206 (98%)	0.54	19 (9%) 8 6	102, 155, 206, 240	0
19	AX	188/189 (99%)	-0.20	1 (0%) 91 84	72, 105, 145, 201	0
19	DX	188/189 (99%)	-0.29	0 100 100	54, 89, 128, 170	0
19	FX	188/189 (99%)	-0.09	1 (0%) 91 84	62, 98, 141, 179	0
19	HX	188/189 (99%)	-0.03	0 100 100	74, 106, 135, 193	0
20	B2	154/154 (100%)	-0.11	2 (1%) 77 65	61, 80, 118, 192	0
20	C2	154/154 (100%)	-0.03	0 100 100	54, 80, 120, 186	0
20	E2	154/154 (100%)	0.16	3 (1%) 66 53	74, 105, 142, 189	0
20	G2	154/154 (100%)	0.73	13 (8%) 11 9	98, 146, 182, 210	0
21	B3	120/120 (100%)	0.46	4 (3%) 46 35	90, 150, 184, 217	0
21	C3	120/120 (100%)	-0.10	0 100 100	64, 98, 116, 161	0
21	E3	120/120 (100%)	0.03	0 100 100	72, 120, 147, 172	0
21	G3	120/120 (100%)	0.45	4 (3%) 46 35	95, 138, 175, 235	0
22	BA	257/264 (97%)	-0.02	9 (3%) 44 33	30, 70, 134, 233	0
22	CA	257/264 (97%)	-0.18	10 (3%) 39 29	31, 75, 139, 238	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
22	EA	257/264 (97%)	-0.16	10 (3%) 39 29	40, 79, 136, 217	0
22	GA	257/264 (97%)	0.22	13 (5%) 28 20	60, 106, 157, 242	0
23	BB	386/391 (98%)	-0.32	5 (1%) 77 65	33, 69, 120, 227	0
23	CB	386/391 (98%)	-0.44	2 (0%) 91 84	34, 75, 123, 222	0
23	EB	386/391 (98%)	-0.36	4 (1%) 82 71	38, 75, 123, 230	0
23	GB	386/391 (98%)	-0.35	4 (1%) 82 71	51, 82, 132, 217	0
24	BC	409/410 (99%)	-0.01	12 (2%) 51 38	37, 107, 173, 241	0
24	CC	409/410 (99%)	-0.20	2 (0%) 91 84	40, 91, 151, 206	0
24	EC	409/410 (99%)	-0.07	5 (1%) 79 67	54, 107, 162, 237	0
24	GC	409/410 (99%)	0.34	17 (4%) 36 27	77, 143, 195, 252	0
25	BD	169/172 (98%)	0.96	23 (13%) 3 3	116, 159, 200, 225	0
25	CD	169/172 (98%)	0.12	4 (2%) 59 45	70, 110, 151, 188	0
25	ED	169/172 (98%)	0.49	8 (4%) 31 23	89, 133, 179, 209	0
25	GD	169/172 (98%)	0.66	19 (11%) 5 5	96, 139, 182, 216	0
26	BE	186/188 (98%)	-0.08	0 100 100	65, 109, 150, 194	0
26	CE	186/188 (98%)	-0.19	0 100 100	59, 94, 131, 171	0
26	EE	186/188 (98%)	-0.08	1 (0%) 91 84	60, 94, 139, 195	0
26	GE	186/188 (98%)	-0.12	0 100 100	53, 91, 135, 220	0
27	BF	231/255 (90%)	0.18	7 (3%) 50 37	70, 122, 176, 252	0
27	CF	231/255 (90%)	-0.14	3 (1%) 77 65	71, 115, 175, 233	0
27	EF	231/255 (90%)	0.00	6 (2%) 56 43	76, 120, 187, 241	0
27	GF	231/255 (90%)	0.60	17 (7%) 14 12	112, 166, 210, 233	0
28	BG	0/123	-	-	-	-
28	CG	0/123	-	-	-	-
28	EG	0/123	-	-	-	-
28	GG	0/123	-	-	-	-
29	BH	201/215 (93%)	0.18	6 (2%) 50 37	79, 133, 181, 221	0
29	CH	201/215 (93%)	-0.24	1 (0%) 91 84	42, 93, 139, 153	0
29	EH	201/215 (93%)	-0.15	2 (0%) 82 71	50, 105, 158, 202	0
29	GH	201/215 (93%)	0.08	2 (0%) 82 71	71, 118, 171, 203	0
30	BI	198/198 (100%)	-0.21	2 (1%) 82 71	51, 85, 152, 185	0
30	CI	198/198 (100%)	-0.36	0 100 100	48, 78, 149, 208	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
30	EI	198/198 (100%)	-0.26	2 (1%) 82 71	47, 79, 152, 174	0
30	GI	198/198 (100%)	-0.20	2 (1%) 82 71	53, 91, 151, 195	0
31	BJ	138/141 (97%)	-0.43	0 100 100	42, 68, 112, 160	0
31	CJ	138/141 (97%)	-0.47	0 100 100	40, 65, 108, 150	0
31	EJ	138/141 (97%)	-0.44	3 (2%) 62 48	40, 65, 108, 202	0
31	GJ	138/141 (97%)	-0.41	1 (0%) 87 79	30, 60, 98, 186	0
32	BK	148/149 (99%)	0.01	4 (2%) 54 41	50, 105, 158, 221	0
32	CK	148/149 (99%)	-0.27	0 100 100	36, 74, 124, 184	0
32	EK	148/149 (99%)	-0.10	0 100 100	50, 95, 140, 228	0
32	GK	148/149 (99%)	0.53	11 (7%) 14 12	78, 129, 181, 208	0
33	BL	203/204 (99%)	-0.26	1 (0%) 91 84	57, 83, 120, 153	0
33	CL	203/204 (99%)	-0.36	0 100 100	37, 74, 106, 180	0
33	EL	203/204 (99%)	-0.10	0 100 100	51, 89, 121, 160	0
33	GL	203/204 (99%)	0.39	7 (3%) 45 34	89, 133, 165, 205	0
34	BM	298/301 (99%)	0.35	10 (3%) 45 34	87, 152, 201, 240	0
34	CM	300/301 (99%)	-0.12	3 (1%) 82 71	61, 110, 166, 208	0
34	EM	300/301 (99%)	0.23	17 (5%) 23 17	76, 127, 183, 233	0
34	GM	300/301 (99%)	0.69	28 (9%) 8 7	98, 157, 204, 233	0
35	BN	180/181 (99%)	0.04	1 (0%) 89 81	68, 110, 150, 224	0
35	CN	180/181 (99%)	-0.33	0 100 100	47, 82, 125, 185	0
35	EN	180/181 (99%)	-0.10	1 (0%) 89 81	63, 101, 142, 187	0
35	GN	180/181 (99%)	0.28	4 (2%) 62 48	94, 139, 188, 248	0
36	BO	184/185 (99%)	0.27	14 (7%) 13 11	29, 78, 184, 207	0
36	EO	146/185 (78%)	0.19	3 (2%) 63 50	57, 95, 128, 194	0
36	GO	153/185 (82%)	0.39	8 (5%) 27 20	67, 109, 153, 262	0
37	BP	156/157 (99%)	0.16	0 100 100	70, 116, 169, 203	0
37	CP	156/157 (99%)	-0.27	0 100 100	42, 79, 136, 152	0
37	EP	156/157 (99%)	-0.09	2 (1%) 77 65	56, 100, 148, 183	0
37	GP	156/157 (99%)	0.46	6 (3%) 40 30	69, 122, 163, 222	0
38	BQ	157/183 (85%)	-0.34	0 100 100	31, 68, 121, 173	0
38	CQ	157/183 (85%)	-0.32	1 (0%) 89 81	26, 70, 124, 158	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
38	EQ	157/183 (85%)	-0.18	1 (0%) 89 81	48, 86, 141, 177	0
38	GQ	157/183 (85%)	0.16	2 (1%) 77 65	60, 106, 157, 200	0
39	BR	121/150 (80%)	-0.20	1 (0%) 86 75	42, 78, 129, 185	0
39	CR	121/150 (80%)	0.05	1 (0%) 86 75	54, 88, 129, 172	0
39	ER	121/150 (80%)	0.18	5 (4%) 37 27	65, 112, 146, 172	0
39	GR	121/150 (80%)	0.45	9 (7%) 14 12	97, 138, 175, 191	0
40	BS	126/135 (93%)	-0.17	0 100 100	62, 98, 133, 177	0
40	CS	126/135 (93%)	0.02	4 (3%) 47 36	46, 89, 127, 152	0
40	ES	126/135 (93%)	0.16	5 (3%) 38 28	74, 112, 151, 184	0
40	GS	126/135 (93%)	0.58	9 (7%) 16 13	101, 143, 186, 218	0
41	BT	61/158 (38%)	-0.38	0 100 100	39, 73, 127, 158	0
41	CT	61/158 (38%)	-0.31	0 100 100	37, 73, 105, 137	0
41	ET	61/158 (38%)	-0.35	0 100 100	45, 78, 113, 147	0
41	GT	61/158 (38%)	-0.20	0 100 100	42, 76, 115, 138	0
42	BU	123/124 (99%)	-0.12	1 (0%) 86 75	59, 101, 139, 204	0
42	CU	123/124 (99%)	-0.22	1 (0%) 86 75	49, 92, 143, 163	0
42	EU	123/124 (99%)	-0.06	2 (1%) 72 59	79, 114, 157, 220	0
42	GU	123/124 (99%)	0.80	19 (15%) 2 2	113, 157, 193, 233	0
43	BV	234/239 (97%)	-0.32	0 100 100	61, 107, 160, 213	0
43	CV	234/239 (97%)	-0.44	0 100 100	47, 87, 145, 213	0
43	EV	234/239 (97%)	-0.36	1 (0%) 92 87	53, 102, 159, 232	0
43	GV	234/239 (97%)	-0.15	1 (0%) 92 87	75, 121, 173, 239	0
44	BW	110/111 (99%)	-0.21	2 (1%) 68 55	36, 64, 155, 204	0
44	CW	110/111 (99%)	-0.19	0 100 100	43, 76, 138, 178	0
44	EW	110/111 (99%)	-0.00	1 (0%) 84 73	56, 88, 170, 227	0
44	GW	110/111 (99%)	0.09	1 (0%) 84 73	63, 102, 183, 216	0
45	BX	125/134 (93%)	-0.01	2 (1%) 72 59	53, 89, 128, 202	0
45	CX	125/134 (93%)	-0.27	1 (0%) 86 75	40, 78, 116, 196	0
45	EX	125/134 (93%)	-0.13	2 (1%) 72 59	49, 88, 129, 233	0
45	GX	125/134 (93%)	0.34	4 (3%) 47 36	73, 117, 162, 215	0
46	BY	102/103 (99%)	-0.11	4 (3%) 39 29	40, 74, 164, 222	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
46	CY	102/103 (99%)	-0.21	4 (3%) 39 29	41, 83, 173, 196	0
46	EY	102/103 (99%)	-0.08	3 (2%) 51 38	45, 84, 156, 193	0
46	GY	102/103 (99%)	0.05	4 (3%) 39 29	53, 102, 189, 222	0
47	CO	146/185 (78%)	-0.08	0 100 100	45, 79, 115, 148	0
All	All	40083/43352 (92%)	0.07	964 (2%) 59 45	26, 101, 177, 390	0

The worst 5 of 964 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	HA	92	ALA	14.8
1	A1	2500	C	11.2
1	H1	1597	U	11.2
1	A1	1597	U	10.4
23	BB	387	GLU	10.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
48	MG	D1	3463	1/1	-0.16	1.03	176,176,176,176	0
48	MG	G2	204	1/1	-0.14	0.92	181,181,181,181	0
48	MG	EW	201	1/1	-0.02	0.33	172,172,172,172	0
48	MG	H1	3529	1/1	0.04	0.33	214,214,214,214	0
48	MG	F1	3411	1/1	0.09	0.65	142,142,142,142	0
48	MG	H1	3489	1/1	0.10	0.45	206,206,206,206	0
48	MG	H1	3551	1/1	0.12	3.30	202,202,202,202	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	H1	3534	1/1	0.16	1.54	221,221,221,221	0
48	MG	G3	202	1/1	0.20	0.62	136,136,136,136	0
48	MG	H1	3519	1/1	0.21	0.31	151,151,151,151	0
48	MG	A1	3527	1/1	0.28	0.30	119,119,119,119	0
48	MG	F1	3561	1/1	0.30	0.24	167,167,167,167	0
48	MG	A1	3568	1/1	0.34	0.36	173,173,173,173	0
48	MG	F1	3415	1/1	0.35	0.32	118,118,118,118	0
48	MG	E3	204	1/1	0.36	1.60	199,199,199,199	0
48	MG	D1	3528	1/1	0.39	0.26	123,123,123,123	0
48	MG	H1	3548	1/1	0.40	0.38	188,188,188,188	0
48	MG	F1	3515	1/1	0.40	0.42	143,143,143,143	0
48	MG	D1	3611	1/1	0.41	0.63	205,205,205,205	0
48	MG	H1	3406	1/1	0.42	0.16	143,143,143,143	0
48	MG	H1	3525	1/1	0.42	0.39	157,157,157,157	0
48	MG	H1	3547	1/1	0.44	0.31	175,175,175,175	0
48	MG	F1	3575	1/1	0.44	0.25	130,130,130,130	0
48	MG	H1	3481	1/1	0.44	0.29	134,134,134,134	0
48	MG	A1	3422	1/1	0.44	0.58	144,144,144,144	0
48	MG	H1	3544	1/1	0.45	0.99	146,146,146,146	0
48	MG	H1	3541	1/1	0.46	0.35	154,154,154,154	0
48	MG	F1	3539	1/1	0.46	1.11	187,187,187,187	0
48	MG	A1	3585	1/1	0.47	0.45	152,152,152,152	0
48	MG	D1	3437	1/1	0.50	0.32	148,148,148,148	0
48	MG	E2	206	1/1	0.51	0.32	151,151,151,151	0
48	MG	A1	3428	1/1	0.52	0.60	159,159,159,159	0
48	MG	D1	3608	1/1	0.52	0.23	115,115,115,115	0
48	MG	H1	3543	1/1	0.52	0.46	183,183,183,183	0
48	MG	F1	3540	1/1	0.53	0.21	111,111,111,111	0
48	MG	E2	205	1/1	0.53	0.60	140,140,140,140	0
48	MG	D1	3401	1/1	0.53	0.25	109,109,109,109	0
48	MG	H1	3450	1/1	0.53	0.73	156,156,156,156	0
48	MG	H1	3479	1/1	0.53	0.43	132,132,132,132	0
48	MG	H1	3409	1/1	0.54	0.55	193,193,193,193	0
48	MG	A1	3573	1/1	0.54	0.47	186,186,186,186	0
48	MG	D1	3606	1/1	0.55	1.19	157,157,157,157	0
48	MG	F1	3490	1/1	0.55	0.22	139,139,139,139	0
48	MG	F1	3419	1/1	0.56	0.11	124,124,124,124	0
48	MG	D1	3624	1/1	0.57	0.61	162,162,162,162	0
48	MG	F1	3522	1/1	0.58	0.18	111,111,111,111	0
48	MG	A1	3430	1/1	0.58	0.50	146,146,146,146	0
48	MG	D1	3470	1/1	0.58	0.38	134,134,134,134	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	B3	201	1/1	0.59	0.29	129,129,129,129	0
48	MG	F1	3421	1/1	0.59	0.35	174,174,174,174	0
48	MG	H1	3414	1/1	0.59	0.54	169,169,169,169	0
48	MG	A1	3556	1/1	0.59	0.18	124,124,124,124	0
48	MG	H1	3538	1/1	0.59	0.27	140,140,140,140	0
48	MG	H1	3412	1/1	0.59	0.89	173,173,173,173	0
48	MG	F1	3578	1/1	0.60	0.79	161,161,161,161	0
48	MG	H1	3536	1/1	0.60	0.86	168,168,168,168	0
48	MG	D1	3598	1/1	0.61	0.24	159,159,159,159	0
48	MG	A1	3588	1/1	0.61	0.26	144,144,144,144	0
48	MG	F1	3496	1/1	0.61	0.24	122,122,122,122	0
48	MG	D1	3616	1/1	0.61	0.20	150,150,150,150	0
48	MG	F1	3430	1/1	0.61	0.15	128,128,128,128	0
48	MG	A1	3427	1/1	0.61	0.26	152,152,152,152	0
48	MG	A1	3402	1/1	0.62	0.31	143,143,143,143	0
48	MG	A1	3578	1/1	0.62	0.18	117,117,117,117	0
48	MG	H1	3554	1/1	0.62	0.68	128,128,128,128	0
48	MG	H1	3533	1/1	0.63	1.06	153,153,153,153	0
48	MG	D1	3592	1/1	0.63	0.97	159,159,159,159	0
48	MG	A1	3522	1/1	0.63	1.27	146,146,146,146	0
48	MG	H1	3540	1/1	0.63	0.20	136,136,136,136	0
48	MG	H1	3470	1/1	0.63	0.16	140,140,140,140	0
48	MG	G2	205	1/1	0.64	0.18	146,146,146,146	0
48	MG	H1	3535	1/1	0.64	0.99	150,150,150,150	0
48	MG	A1	3583	1/1	0.64	0.44	112,112,112,112	0
48	MG	G3	205	1/1	0.64	0.94	171,171,171,171	0
48	MG	F1	3509	1/1	0.65	0.34	144,144,144,144	0
48	MG	F1	3414	1/1	0.65	0.20	123,123,123,123	0
48	MG	H1	3401	1/1	0.65	0.12	146,146,146,146	0
48	MG	H1	3516	1/1	0.66	0.28	129,129,129,129	0
48	MG	D1	3521	1/1	0.66	0.28	129,129,129,129	0
48	MG	GN	201	1/1	0.66	0.52	212,212,212,212	0
48	MG	A1	3417	1/1	0.66	0.28	150,150,150,150	0
48	MG	H1	3415	1/1	0.66	0.13	133,133,133,133	0
48	MG	H1	3511	1/1	0.66	0.27	140,140,140,140	0
48	MG	F1	3469	1/1	0.66	0.16	112,112,112,112	0
48	MG	D1	3605	1/1	0.66	0.13	108,108,108,108	0
48	MG	D1	3446	1/1	0.66	0.83	176,176,176,176	0
48	MG	A1	3436	1/1	0.66	0.23	110,110,110,110	0
48	MG	B2	207	1/1	0.66	0.38	149,149,149,149	0
48	MG	BQ	201	1/1	0.66	0.21	122,122,122,122	0
48	MG	H1	3402	1/1	0.66	0.23	118,118,118,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	A1	3593	1/1	0.66	0.72	158,158,158,158	0
48	MG	D1	3497	1/1	0.67	0.53	151,151,151,151	0
48	MG	F1	3493	1/1	0.67	0.51	145,145,145,145	0
48	MG	A1	3515	1/1	0.67	0.25	111,111,111,111	0
48	MG	F1	3570	1/1	0.67	0.27	113,113,113,113	0
48	MG	G2	206	1/1	0.67	0.90	174,174,174,174	0
48	MG	EN	201	1/1	0.67	0.17	111,111,111,111	0
48	MG	H1	3550	1/1	0.68	0.44	152,152,152,152	0
48	MG	F1	3566	1/1	0.68	1.27	146,146,146,146	0
48	MG	A1	3592	1/1	0.68	0.30	134,134,134,134	0
48	MG	F1	3577	1/1	0.68	0.26	152,152,152,152	0
48	MG	D1	3548	1/1	0.68	0.96	183,183,183,183	0
48	MG	H1	3532	1/1	0.68	0.39	162,162,162,162	0
48	MG	B3	203	1/1	0.68	0.23	160,160,160,160	0
48	MG	A1	3580	1/1	0.68	0.21	130,130,130,130	0
48	MG	H1	3477	1/1	0.68	0.30	103,103,103,103	0
48	MG	E2	202	1/1	0.69	0.18	89,89,89,89	0
48	MG	F1	3583	1/1	0.69	0.18	104,104,104,104	0
48	MG	H1	3542	1/1	0.69	0.36	137,137,137,137	0
48	MG	C3	207	1/1	0.69	0.62	160,160,160,160	0
48	MG	H1	3420	1/1	0.69	0.26	113,113,113,113	0
48	MG	D1	3597	1/1	0.70	0.83	158,158,158,158	0
48	MG	F1	3555	1/1	0.70	0.27	168,168,168,168	0
48	MG	A1	3507	1/1	0.70	0.20	129,129,129,129	0
48	MG	H1	3531	1/1	0.70	0.59	157,157,157,157	0
48	MG	D1	3547	1/1	0.71	0.28	109,109,109,109	0
48	MG	A1	3451	1/1	0.71	0.16	146,146,146,146	0
48	MG	D1	3550	1/1	0.71	0.59	136,136,136,136	0
48	MG	A1	3435	1/1	0.71	0.54	151,151,151,151	0
48	MG	D1	3603	1/1	0.72	0.44	125,125,125,125	0
48	MG	A1	3401	1/1	0.72	0.12	108,108,108,108	0
48	MG	A1	3483	1/1	0.72	0.14	83,83,83,83	0
48	MG	F1	3489	1/1	0.72	0.10	85,85,85,85	0
48	MG	F1	3574	1/1	0.72	0.70	161,161,161,161	0
48	MG	D1	3418	1/1	0.72	0.16	114,114,114,114	0
48	MG	D1	3576	1/1	0.72	0.54	150,150,150,150	0
48	MG	D1	3579	1/1	0.72	0.10	97,97,97,97	0
48	MG	D1	3467	1/1	0.72	0.18	123,123,123,123	0
48	MG	F1	3488	1/1	0.73	0.37	110,110,110,110	0
48	MG	A1	3595	1/1	0.73	1.09	151,151,151,151	0
48	MG	D1	3541	1/1	0.73	0.34	114,114,114,114	0
48	MG	F1	3563	1/1	0.73	0.18	124,124,124,124	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	B2	201	1/1	0.73	0.20	119,119,119,119	0
48	MG	H1	3410	1/1	0.73	0.44	192,192,192,192	0
48	MG	D1	3600	1/1	0.73	0.40	123,123,123,123	0
48	MG	A1	3454	1/1	0.73	0.18	101,101,101,101	0
48	MG	D1	3596	1/1	0.73	0.66	165,165,165,165	0
48	MG	H1	3524	1/1	0.74	0.57	139,139,139,139	0
48	MG	F1	3462	1/1	0.74	0.15	118,118,118,118	0
48	MG	D1	3424	1/1	0.74	0.43	150,150,150,150	0
48	MG	H1	3526	1/1	0.74	0.22	94,94,94,94	0
48	MG	A1	3416	1/1	0.74	0.23	140,140,140,140	0
48	MG	A1	3491	1/1	0.74	0.24	125,125,125,125	0
48	MG	E3	206	1/1	0.74	0.35	132,132,132,132	0
48	MG	H1	3521	1/1	0.74	0.29	123,123,123,123	0
48	MG	H1	3418	1/1	0.74	0.21	141,141,141,141	0
48	MG	D1	3429	1/1	0.74	0.23	113,113,113,113	0
48	MG	A1	3420	1/1	0.75	0.30	155,155,155,155	0
48	MG	A1	3587	1/1	0.75	1.09	182,182,182,182	0
48	MG	A1	3582	1/1	0.75	0.19	110,110,110,110	0
48	MG	GA	301	1/1	0.75	0.24	142,142,142,142	0
48	MG	F1	3560	1/1	0.75	0.47	169,169,169,169	0
48	MG	C3	205	1/1	0.75	1.45	175,175,175,175	0
48	MG	H1	3408	1/1	0.75	0.30	111,111,111,111	0
48	MG	EW	202	1/1	0.75	0.20	121,121,121,121	0
48	MG	A1	3437	1/1	0.75	0.48	141,141,141,141	0
48	MG	D1	3625	1/1	0.75	0.39	164,164,164,164	0
48	MG	A1	3449	1/1	0.75	0.23	115,115,115,115	0
48	MG	D1	3434	1/1	0.75	0.63	144,144,144,144	0
48	MG	A1	3408	1/1	0.76	0.27	122,122,122,122	0
48	MG	A1	3567	1/1	0.76	0.30	144,144,144,144	0
48	MG	F1	3451	1/1	0.76	0.49	122,122,122,122	0
48	MG	A1	3547	1/1	0.76	0.16	81,81,81,81	0
48	MG	D1	3593	1/1	0.76	0.36	180,180,180,180	0
48	MG	D1	3551	1/1	0.76	0.18	142,142,142,142	0
48	MG	H1	3539	1/1	0.76	0.34	128,128,128,128	0
48	MG	F1	3564	1/1	0.76	0.38	143,143,143,143	0
48	MG	H1	3537	1/1	0.76	0.18	152,152,152,152	0
48	MG	A1	3414	1/1	0.76	0.19	142,142,142,142	0
48	MG	F1	3554	1/1	0.76	0.18	131,131,131,131	0
48	MG	D1	3583	1/1	0.76	0.32	139,139,139,139	0
48	MG	A1	3576	1/1	0.76	0.40	122,122,122,122	0
48	MG	E3	205	1/1	0.76	0.17	127,127,127,127	0
48	MG	A1	3579	1/1	0.76	0.52	94,94,94,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	F1	3580	1/1	0.76	0.21	147,147,147,147	0
48	MG	DJ	301	1/1	0.77	0.45	150,150,150,150	0
48	MG	F1	3511	1/1	0.77	0.71	154,154,154,154	0
48	MG	F1	3576	1/1	0.77	0.46	142,142,142,142	0
48	MG	D1	3514	1/1	0.77	0.20	128,128,128,128	0
48	MG	A1	3503	1/1	0.77	0.16	95,95,95,95	0
48	MG	F1	3468	1/1	0.77	0.16	103,103,103,103	0
48	MG	H1	3446	1/1	0.77	0.34	120,120,120,120	0
48	MG	D1	3571	1/1	0.77	0.43	130,130,130,130	0
48	MG	D1	3588	1/1	0.77	0.18	156,156,156,156	0
48	MG	F1	3519	1/1	0.77	0.16	65,65,65,65	0
48	MG	B2	202	1/1	0.78	0.12	103,103,103,103	0
48	MG	D1	3448	1/1	0.78	0.22	125,125,125,125	0
48	MG	H1	3478	1/1	0.78	0.10	114,114,114,114	0
48	MG	H1	3413	1/1	0.78	0.20	117,117,117,117	0
48	MG	A1	3577	1/1	0.78	0.14	104,104,104,104	0
48	MG	H1	3473	1/1	0.78	0.19	123,123,123,123	0
48	MG	A1	3530	1/1	0.78	0.48	149,149,149,149	0
48	MG	A1	3431	1/1	0.78	0.12	90,90,90,90	0
48	MG	H1	3492	1/1	0.78	0.13	96,96,96,96	0
48	MG	F1	3503	1/1	0.78	0.18	129,129,129,129	0
48	MG	D1	3442	1/1	0.79	0.35	126,126,126,126	0
48	MG	F1	3550	1/1	0.79	0.21	154,154,154,154	0
48	MG	GP	201	1/1	0.79	0.47	109,109,109,109	0
48	MG	F1	3448	1/1	0.79	0.15	126,126,126,126	0
48	MG	A1	3433	1/1	0.79	0.10	84,84,84,84	0
48	MG	A1	3555	1/1	0.79	0.58	128,128,128,128	0
48	MG	F1	3572	1/1	0.79	0.36	155,155,155,155	0
48	MG	GP	202	1/1	0.79	0.24	137,137,137,137	0
48	MG	F1	3483	1/1	0.79	0.32	129,129,129,129	0
48	MG	FT	101	1/1	0.79	0.11	124,124,124,124	0
48	MG	D1	3427	1/1	0.79	0.26	153,153,153,153	0
48	MG	C3	202	1/1	0.80	0.15	135,135,135,135	0
48	MG	A1	3419	1/1	0.80	0.14	100,100,100,100	0
48	MG	F1	3565	1/1	0.80	0.86	168,168,168,168	0
48	MG	H1	3486	1/1	0.80	0.15	105,105,105,105	0
48	MG	B3	202	1/1	0.80	0.15	113,113,113,113	0
48	MG	A1	3472	1/1	0.80	0.63	149,149,149,149	0
48	MG	A1	3591	1/1	0.80	0.27	121,121,121,121	0
48	MG	A1	3551	1/1	0.80	0.33	123,123,123,123	0
48	MG	D1	3516	1/1	0.80	0.36	82,82,82,82	0
48	MG	H1	3549	1/1	0.80	0.47	124,124,124,124	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	D1	3417	1/1	0.80	0.20	132,132,132,132	0
48	MG	D1	3604	1/1	0.81	0.44	141,141,141,141	0
48	MG	H1	3503	1/1	0.81	0.26	91,91,91,91	0
48	MG	H1	3434	1/1	0.81	0.18	93,93,93,93	0
48	MG	CD	201	1/1	0.81	0.16	93,93,93,93	0
48	MG	A1	3586	1/1	0.81	0.72	177,177,177,177	0
48	MG	H1	3433	1/1	0.81	0.19	132,132,132,132	0
48	MG	D1	3627	1/1	0.81	0.08	119,119,119,119	0
48	MG	D1	3586	1/1	0.81	0.16	109,109,109,109	0
48	MG	A1	3425	1/1	0.81	0.16	107,107,107,107	0
48	MG	D1	3626	1/1	0.81	0.20	137,137,137,137	0
48	MG	C2	206	1/1	0.81	0.31	123,123,123,123	0
48	MG	F1	3501	1/1	0.81	0.16	116,116,116,116	0
48	MG	H1	3553	1/1	0.81	0.39	146,146,146,146	0
48	MG	HT	101	1/1	0.81	0.35	174,174,174,174	0
48	MG	F1	3548	1/1	0.81	0.12	106,106,106,106	0
48	MG	A1	3589	1/1	0.81	0.13	113,113,113,113	0
48	MG	H1	3443	1/1	0.82	0.42	157,157,157,157	0
48	MG	H1	3411	1/1	0.82	0.32	120,120,120,120	0
48	MG	D1	3565	1/1	0.82	0.33	114,114,114,114	0
48	MG	H1	3448	1/1	0.82	0.15	98,98,98,98	0
48	MG	H1	3530	1/1	0.82	0.34	154,154,154,154	0
48	MG	H1	3436	1/1	0.82	0.43	146,146,146,146	0
48	MG	D1	3557	1/1	0.82	0.13	116,116,116,116	0
48	MG	F1	3447	1/1	0.82	0.30	156,156,156,156	0
48	MG	F1	3425	1/1	0.82	0.33	115,115,115,115	0
48	MG	F1	3422	1/1	0.82	0.29	149,149,149,149	0
48	MG	A1	3499	1/1	0.82	0.16	117,117,117,117	0
48	MG	F1	3428	1/1	0.82	0.30	111,111,111,111	0
48	MG	F1	3506	1/1	0.82	0.32	114,114,114,114	0
48	MG	D1	3594	1/1	0.82	0.23	106,106,106,106	0
48	MG	A1	3461	1/1	0.82	0.14	67,67,67,67	0
48	MG	F1	3567	1/1	0.82	0.42	128,128,128,128	0
48	MG	F1	3498	1/1	0.82	0.22	141,141,141,141	0
48	MG	A1	3444	1/1	0.83	0.13	126,126,126,126	0
48	MG	F1	3482	1/1	0.83	0.21	130,130,130,130	0
48	MG	H1	3482	1/1	0.83	0.61	162,162,162,162	0
48	MG	H1	3509	1/1	0.83	0.18	143,143,143,143	0
48	MG	H1	3422	1/1	0.83	0.46	151,151,151,151	0
48	MG	D1	3435	1/1	0.83	0.14	108,108,108,108	0
48	MG	D1	3615	1/1	0.83	0.24	132,132,132,132	0
48	MG	D1	3574	1/1	0.83	0.12	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	E2	201	1/1	0.83	0.34	156,156,156,156	0
48	MG	F1	3549	1/1	0.83	0.20	125,125,125,125	0
48	MG	G3	204	1/1	0.83	0.36	143,143,143,143	0
48	MG	D1	3609	1/1	0.83	0.67	120,120,120,120	0
48	MG	D1	3540	1/1	0.83	0.20	139,139,139,139	0
48	MG	A1	3453	1/1	0.83	0.72	184,184,184,184	0
48	MG	D1	3613	1/1	0.83	0.23	120,120,120,120	0
48	MG	F1	3453	1/1	0.83	0.23	131,131,131,131	0
48	MG	F1	3461	1/1	0.83	0.49	106,106,106,106	0
48	MG	D1	3425	1/1	0.83	0.59	123,123,123,123	0
48	MG	D1	3485	1/1	0.83	0.17	120,120,120,120	0
48	MG	D1	3484	1/1	0.83	0.31	96,96,96,96	0
48	MG	H1	3552	1/1	0.83	0.18	131,131,131,131	0
48	MG	H1	3438	1/1	0.83	0.29	120,120,120,120	0
48	MG	D1	3433	1/1	0.83	0.14	149,149,149,149	0
48	MG	F1	3573	1/1	0.83	0.08	84,84,84,84	0
48	MG	BN	201	1/1	0.84	0.22	147,147,147,147	0
48	MG	A1	3565	1/1	0.84	0.13	132,132,132,132	0
48	MG	GO	201	1/1	0.84	0.44	141,141,141,141	0
48	MG	D1	3582	1/1	0.84	0.19	93,93,93,93	0
48	MG	D1	3614	1/1	0.84	0.19	129,129,129,129	0
48	MG	H1	3490	1/1	0.84	0.55	122,122,122,122	0
48	MG	A1	3409	1/1	0.84	0.14	87,87,87,87	0
48	MG	H1	3441	1/1	0.84	0.15	102,102,102,102	0
48	MG	A1	3412	1/1	0.84	0.33	117,117,117,117	0
48	MG	A1	3553	1/1	0.84	0.16	108,108,108,108	0
48	MG	F1	3424	1/1	0.84	0.31	114,114,114,114	0
48	MG	F1	3464	1/1	0.84	0.23	120,120,120,120	0
48	MG	H1	3465	1/1	0.84	0.42	143,143,143,143	0
48	MG	E3	203	1/1	0.84	0.17	104,104,104,104	0
48	MG	H1	3462	1/1	0.84	0.36	131,131,131,131	0
48	MG	D1	3607	1/1	0.84	0.30	89,89,89,89	0
48	MG	H1	3417	1/1	0.84	0.11	114,114,114,114	0
48	MG	H1	3426	1/1	0.84	0.15	105,105,105,105	0
48	MG	B2	208	1/1	0.84	0.42	138,138,138,138	0
48	MG	F1	3558	1/1	0.84	0.17	144,144,144,144	0
48	MG	A1	3513	1/1	0.84	0.33	133,133,133,133	0
48	MG	C2	205	1/1	0.84	0.19	127,127,127,127	0
48	MG	D1	3530	1/1	0.84	0.16	94,94,94,94	0
48	MG	H1	3528	1/1	0.84	0.23	119,119,119,119	0
48	MG	D1	3542	1/1	0.85	0.13	71,71,71,71	0
48	MG	F1	3413	1/1	0.85	0.38	110,110,110,110	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	D1	3580	1/1	0.85	0.11	95,95,95,95	0
48	MG	H1	3487	1/1	0.85	0.19	122,122,122,122	0
48	MG	A1	3571	1/1	0.85	0.24	100,100,100,100	0
48	MG	D1	3534	1/1	0.85	0.20	98,98,98,98	0
48	MG	G2	201	1/1	0.85	0.14	141,141,141,141	0
48	MG	A1	3594	1/1	0.85	0.28	150,150,150,150	0
48	MG	F1	3403	1/1	0.85	0.11	96,96,96,96	0
48	MG	A1	3569	1/1	0.85	0.09	91,91,91,91	0
48	MG	D1	3513	1/1	0.85	0.16	89,89,89,89	0
48	MG	H1	3546	1/1	0.85	0.27	120,120,120,120	0
48	MG	A1	3528	1/1	0.85	0.37	120,120,120,120	0
48	MG	D1	3499	1/1	0.85	0.14	118,118,118,118	0
48	MG	F1	3545	1/1	0.85	0.21	137,137,137,137	0
48	MG	EN	202	1/1	0.85	1.14	238,238,238,238	0
48	MG	D1	3631	1/1	0.85	0.08	78,78,78,78	0
48	MG	D1	3482	1/1	0.85	0.15	106,106,106,106	0
48	MG	A1	3450	1/1	0.85	0.20	133,133,133,133	0
48	MG	F1	3433	1/1	0.85	0.64	95,95,95,95	0
48	MG	D1	3426	1/1	0.85	0.38	143,143,143,143	0
48	MG	H1	3512	1/1	0.86	0.31	121,121,121,121	0
48	MG	D1	3561	1/1	0.86	0.19	57,57,57,57	0
48	MG	F1	3529	1/1	0.86	0.71	140,140,140,140	0
48	MG	F1	3477	1/1	0.86	0.68	146,146,146,146	0
48	MG	F1	3569	1/1	0.86	0.40	130,130,130,130	0
48	MG	F1	3408	1/1	0.86	0.14	82,82,82,82	0
48	MG	D1	3504	1/1	0.86	0.27	98,98,98,98	0
48	MG	CQ	201	1/1	0.86	0.18	127,127,127,127	0
48	MG	A1	3552	1/1	0.86	0.10	97,97,97,97	0
48	MG	F1	3495	1/1	0.86	0.12	83,83,83,83	0
48	MG	D1	3622	1/1	0.86	0.30	133,133,133,133	0
48	MG	H1	3484	1/1	0.86	0.24	166,166,166,166	0
48	MG	D1	3421	1/1	0.86	0.22	126,126,126,126	0
48	MG	DQ	201	1/1	0.86	0.32	118,118,118,118	0
48	MG	F1	3542	1/1	0.86	0.13	107,107,107,107	0
48	MG	F1	3463	1/1	0.86	0.19	100,100,100,100	0
48	MG	D1	3444	1/1	0.86	0.22	139,139,139,139	0
48	MG	A1	3584	1/1	0.86	0.23	125,125,125,125	0
48	MG	D1	3522	1/1	0.86	0.64	162,162,162,162	0
48	MG	GQ	201	1/1	0.86	0.30	102,102,102,102	0
48	MG	F1	3544	1/1	0.86	0.13	97,97,97,97	0
48	MG	D1	3515	1/1	0.86	0.15	106,106,106,106	0
48	MG	F1	3527	1/1	0.87	0.30	105,105,105,105	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	D1	3422	1/1	0.87	0.22	150,150,150,150	0
48	MG	A1	3574	1/1	0.87	0.15	119,119,119,119	0
48	MG	F1	3491	1/1	0.87	0.18	96,96,96,96	0
48	MG	F1	3538	1/1	0.87	0.36	113,113,113,113	0
48	MG	H1	3545	1/1	0.87	0.19	156,156,156,156	0
48	MG	D1	3623	1/1	0.87	0.26	151,151,151,151	0
48	MG	D1	3525	1/1	0.87	0.34	113,113,113,113	0
48	MG	D1	3618	1/1	0.87	0.09	95,95,95,95	0
48	MG	F1	3473	1/1	0.87	0.42	156,156,156,156	0
48	MG	A1	3474	1/1	0.87	0.13	88,88,88,88	0
48	MG	F1	3434	1/1	0.87	0.13	83,83,83,83	0
48	MG	A1	3531	1/1	0.87	0.28	128,128,128,128	0
48	MG	D1	3532	1/1	0.87	0.14	119,119,119,119	0
48	MG	D1	3575	1/1	0.87	0.13	124,124,124,124	0
48	MG	A1	3497	1/1	0.87	0.12	116,116,116,116	0
48	MG	D1	3439	1/1	0.87	0.38	146,146,146,146	0
48	MG	D1	3563	1/1	0.87	0.12	93,93,93,93	0
48	MG	A1	3566	1/1	0.87	0.11	75,75,75,75	0
48	MG	D1	3595	1/1	0.87	0.23	94,94,94,94	0
48	MG	D1	3475	1/1	0.87	0.51	120,120,120,120	0
48	MG	F1	3532	1/1	0.87	0.19	87,87,87,87	0
48	MG	DA	102	1/1	0.87	0.20	115,115,115,115	0
48	MG	F1	3401	1/1	0.87	0.35	101,101,101,101	0
48	MG	F1	3492	1/1	0.87	0.20	78,78,78,78	0
48	MG	H1	3459	1/1	0.87	0.10	97,97,97,97	0
48	MG	D1	3445	1/1	0.87	0.19	126,126,126,126	0
48	MG	F1	3423	1/1	0.87	0.08	56,56,56,56	0
48	MG	A1	3455	1/1	0.87	0.13	111,111,111,111	0
48	MG	D1	3621	1/1	0.87	0.15	110,110,110,110	0
48	MG	F1	3500	1/1	0.88	0.17	105,105,105,105	0
48	MG	H1	3504	1/1	0.88	0.11	111,111,111,111	0
48	MG	A1	3415	1/1	0.88	0.20	120,120,120,120	0
48	MG	B2	206	1/1	0.88	0.45	139,139,139,139	0
48	MG	A1	3542	1/1	0.88	0.22	96,96,96,96	0
48	MG	H1	3472	1/1	0.88	0.32	104,104,104,104	0
48	MG	A1	3424	1/1	0.88	0.37	150,150,150,150	0
48	MG	BP	200	1/1	0.88	0.10	123,123,123,123	0
48	MG	D1	3498	1/1	0.88	0.47	99,99,99,99	0
48	MG	A1	3512	1/1	0.88	0.10	90,90,90,90	0
48	MG	F1	3485	1/1	0.88	0.16	117,117,117,117	0
48	MG	A1	3536	1/1	0.88	0.14	104,104,104,104	0
48	MG	D1	3505	1/1	0.88	0.16	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	H1	3425	1/1	0.88	0.31	108,108,108,108	0
48	MG	D1	3496	1/1	0.88	0.16	78,78,78,78	0
48	MG	A1	3554	1/1	0.88	0.14	76,76,76,76	0
48	MG	F1	3516	1/1	0.88	0.30	121,121,121,121	0
48	MG	CW	201	1/1	0.88	0.29	90,90,90,90	0
48	MG	H1	3485	1/1	0.88	0.12	104,104,104,104	0
48	MG	A1	3404	1/1	0.88	0.12	94,94,94,94	0
48	MG	D1	3602	1/1	0.88	0.19	118,118,118,118	0
48	MG	D1	3599	1/1	0.88	0.27	126,126,126,126	0
48	MG	F1	3556	1/1	0.88	0.08	90,90,90,90	0
48	MG	A1	3516	1/1	0.88	0.23	88,88,88,88	0
48	MG	D1	3620	1/1	0.88	0.15	106,106,106,106	0
48	MG	H1	3510	1/1	0.88	0.24	120,120,120,120	0
48	MG	H1	3407	1/1	0.88	0.20	105,105,105,105	0
48	MG	G3	201	1/1	0.88	0.12	119,119,119,119	0
48	MG	H1	3452	1/1	0.88	0.10	108,108,108,108	0
48	MG	A1	3532	1/1	0.89	0.07	74,74,74,74	0
48	MG	F1	3484	1/1	0.89	0.17	78,78,78,78	0
48	MG	A1	3423	1/1	0.89	0.21	115,115,115,115	0
48	MG	A1	3479	1/1	0.89	0.22	120,120,120,120	0
48	MG	H1	3404	1/1	0.89	0.11	132,132,132,132	0
48	MG	A1	3590	1/1	0.89	0.26	142,142,142,142	0
48	MG	F1	3431	1/1	0.89	0.17	103,103,103,103	0
48	MG	A1	3438	1/1	0.89	0.23	148,148,148,148	0
48	MG	H1	3501	1/1	0.89	0.30	110,110,110,110	0
48	MG	A1	3563	1/1	0.89	0.13	100,100,100,100	0
48	MG	A1	3492	1/1	0.89	0.28	127,127,127,127	0
48	MG	H1	3555	1/1	0.89	0.15	123,123,123,123	0
48	MG	H1	3496	1/1	0.89	0.44	141,141,141,141	0
48	MG	F1	3559	1/1	0.89	0.10	133,133,133,133	0
48	MG	D1	3577	1/1	0.89	0.22	121,121,121,121	0
48	MG	F1	3456	1/1	0.89	0.07	62,62,62,62	0
48	MG	H1	3468	1/1	0.89	0.23	121,121,121,121	0
48	MG	D1	3523	1/1	0.89	0.10	105,105,105,105	0
48	MG	A1	3500	1/1	0.89	0.30	89,89,89,89	0
48	MG	C2	201	1/1	0.89	0.15	121,121,121,121	0
48	MG	H1	3499	1/1	0.89	0.11	75,75,75,75	0
48	MG	F1	3502	1/1	0.89	0.26	108,108,108,108	0
48	MG	D1	3440	1/1	0.89	0.12	99,99,99,99	0
48	MG	A1	3470	1/1	0.89	0.32	164,164,164,164	0
48	MG	H1	3464	1/1	0.89	0.15	108,108,108,108	0
48	MG	F1	3446	1/1	0.89	0.20	130,130,130,130	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	D1	3468	1/1	0.89	0.13	75,75,75,75	0
48	MG	D1	3549	1/1	0.90	0.13	99,99,99,99	0
48	MG	F1	3541	1/1	0.90	0.23	112,112,112,112	0
48	MG	H1	3442	1/1	0.90	0.09	79,79,79,79	0
48	MG	F1	3439	1/1	0.90	0.09	62,62,62,62	0
48	MG	D1	3511	1/1	0.90	0.24	118,118,118,118	0
48	MG	D1	3481	1/1	0.90	0.39	114,114,114,114	0
48	MG	F1	3475	1/1	0.90	0.17	93,93,93,93	0
48	MG	H1	3435	1/1	0.90	0.17	116,116,116,116	0
48	MG	F1	3440	1/1	0.90	0.11	82,82,82,82	0
48	MG	H1	3488	1/1	0.90	0.19	108,108,108,108	0
48	MG	H1	3449	1/1	0.90	0.62	118,118,118,118	0
48	MG	F1	3457	1/1	0.90	0.27	91,91,91,91	0
48	MG	A1	3443	1/1	0.90	0.14	90,90,90,90	0
48	MG	E2	207	1/1	0.90	0.41	147,147,147,147	0
49	ZN	HC	201	1/1	0.90	0.04	168,168,168,168	0
48	MG	F1	3535	1/1	0.90	0.11	58,58,58,58	0
48	MG	D1	3535	1/1	0.90	0.17	86,86,86,86	0
48	MG	F1	3581	1/1	0.90	0.38	144,144,144,144	0
48	MG	A1	3529	1/1	0.90	0.10	96,96,96,96	0
48	MG	C3	203	1/1	0.90	0.08	69,69,69,69	0
48	MG	H1	3430	1/1	0.90	0.20	82,82,82,82	0
48	MG	C2	202	1/1	0.90	0.23	112,112,112,112	0
48	MG	H1	3523	1/1	0.90	0.12	167,167,167,167	0
48	MG	CL	301	1/1	0.90	0.15	109,109,109,109	0
48	MG	H1	3518	1/1	0.90	0.15	110,110,110,110	0
48	MG	D1	3472	1/1	0.90	0.10	82,82,82,82	0
48	MG	A1	3575	1/1	0.90	0.62	143,143,143,143	0
48	MG	A1	3596	1/1	0.90	0.30	163,163,163,163	0
48	MG	F1	3553	1/1	0.90	0.09	68,68,68,68	0
48	MG	A1	3471	1/1	0.90	0.31	88,88,88,88	0
48	MG	H1	3457	1/1	0.90	0.56	147,147,147,147	0
48	MG	A1	3600	1/1	0.90	0.11	111,111,111,111	0
48	MG	EL	302	1/1	0.90	0.09	68,68,68,68	0
48	MG	F1	3579	1/1	0.90	0.12	166,166,166,166	0
48	MG	F1	3472	1/1	0.90	0.15	111,111,111,111	0
48	MG	F1	3537	1/1	0.90	0.21	136,136,136,136	0
48	MG	F1	3513	1/1	0.90	0.17	79,79,79,79	0
48	MG	D1	3538	1/1	0.90	0.10	119,119,119,119	0
48	MG	F1	3534	1/1	0.90	0.08	79,79,79,79	0
48	MG	A1	3510	1/1	0.90	0.21	109,109,109,109	0
48	MG	D1	3628	1/1	0.90	0.07	107,107,107,107	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	F1	3520	1/1	0.91	0.19	85,85,85,85	0
48	MG	F1	3568	1/1	0.91	0.13	98,98,98,98	0
48	MG	A1	3447	1/1	0.91	0.13	58,58,58,58	0
48	MG	A1	3519	1/1	0.91	0.10	113,113,113,113	0
48	MG	E3	202	1/1	0.91	0.20	122,122,122,122	0
48	MG	D1	3512	1/1	0.91	0.14	101,101,101,101	0
48	MG	H1	3455	1/1	0.91	0.14	113,113,113,113	0
48	MG	A1	3572	1/1	0.91	0.23	121,121,121,121	0
48	MG	D1	3506	1/1	0.91	0.30	132,132,132,132	0
48	MG	A1	3403	1/1	0.91	0.13	96,96,96,96	0
48	MG	D1	3545	1/1	0.91	0.15	88,88,88,88	0
48	MG	D1	3572	1/1	0.91	0.23	69,69,69,69	0
48	MG	CY	201	1/1	0.91	0.20	99,99,99,99	0
48	MG	F1	3571	1/1	0.91	0.29	132,132,132,132	0
48	MG	FK	201	1/1	0.91	0.50	168,168,168,168	0
48	MG	D1	3568	1/1	0.91	0.17	105,105,105,105	0
48	MG	D1	3416	1/1	0.91	0.24	110,110,110,110	0
48	MG	H1	3432	1/1	0.91	0.09	91,91,91,91	0
48	MG	F1	3497	1/1	0.91	0.12	93,93,93,93	0
48	MG	G2	202	1/1	0.91	0.34	122,122,122,122	0
48	MG	FA	101	1/1	0.91	0.11	97,97,97,97	0
48	MG	F1	3466	1/1	0.91	0.34	140,140,140,140	0
48	MG	D1	3507	1/1	0.91	0.10	75,75,75,75	0
48	MG	D1	3441	1/1	0.91	0.15	75,75,75,75	0
48	MG	A1	3467	1/1	0.91	0.19	106,106,106,106	0
48	MG	D1	3573	1/1	0.91	0.14	126,126,126,126	0
48	MG	D1	3409	1/1	0.91	0.13	57,57,57,57	0
48	MG	D1	3447	1/1	0.91	0.23	101,101,101,101	0
48	MG	D1	3406	1/1	0.91	0.14	67,67,67,67	0
48	MG	F1	3429	1/1	0.91	0.17	73,73,73,73	0
48	MG	H1	3429	1/1	0.91	0.14	87,87,87,87	0
48	MG	D1	3543	1/1	0.91	0.27	127,127,127,127	0
48	MG	GW	201	1/1	0.91	0.22	114,114,114,114	0
48	MG	H1	3416	1/1	0.91	0.66	113,113,113,113	0
48	MG	A1	3496	1/1	0.91	0.24	137,137,137,137	0
48	MG	A1	3498	1/1	0.91	0.11	116,116,116,116	0
48	MG	D1	3476	1/1	0.91	0.08	43,43,43,43	0
48	MG	H1	3456	1/1	0.91	0.76	145,145,145,145	0
48	MG	H1	3505	1/1	0.92	0.11	95,95,95,95	0
48	MG	F1	3517	1/1	0.92	0.11	62,62,62,62	0
48	MG	A1	3509	1/1	0.92	0.12	128,128,128,128	0
48	MG	H1	3447	1/1	0.92	0.25	110,110,110,110	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	F1	3562	1/1	0.92	0.40	140,140,140,140	0
48	MG	D1	3451	1/1	0.92	0.42	115,115,115,115	0
48	MG	AK	202	1/1	0.92	0.72	179,179,179,179	0
48	MG	H1	3431	1/1	0.92	0.25	94,94,94,94	0
48	MG	D1	3452	1/1	0.92	0.15	106,106,106,106	0
48	MG	D1	3443	1/1	0.92	0.48	112,112,112,112	0
48	MG	D1	3403	1/1	0.92	0.07	89,89,89,89	0
48	MG	D1	3552	1/1	0.92	0.06	55,55,55,55	0
48	MG	D1	3562	1/1	0.92	0.22	93,93,93,93	0
48	MG	D1	3491	1/1	0.92	0.15	97,97,97,97	0
48	MG	F1	3442	1/1	0.92	0.27	109,109,109,109	0
48	MG	H1	3474	1/1	0.92	0.09	123,123,123,123	0
48	MG	A1	3548	1/1	0.92	0.17	124,124,124,124	0
48	MG	B2	204	1/1	0.92	0.08	85,85,85,85	0
48	MG	A1	3521	1/1	0.92	0.12	105,105,105,105	0
48	MG	D1	3537	1/1	0.92	0.28	121,121,121,121	0
48	MG	H1	3480	1/1	0.92	0.14	81,81,81,81	0
48	MG	A1	3490	1/1	0.92	0.21	105,105,105,105	0
48	MG	F1	3402	1/1	0.92	0.09	83,83,83,83	0
48	MG	A1	3501	1/1	0.92	0.22	102,102,102,102	0
48	MG	A1	3429	1/1	0.92	0.11	122,122,122,122	0
48	MG	G3	203	1/1	0.92	0.13	86,86,86,86	0
48	MG	D1	3407	1/1	0.92	0.09	70,70,70,70	0
48	MG	A1	3518	1/1	0.92	0.24	109,109,109,109	0
48	MG	H1	3424	1/1	0.92	0.08	96,96,96,96	0
48	MG	A1	3468	1/1	0.92	0.18	109,109,109,109	0
48	MG	D1	3610	1/1	0.92	0.21	66,66,66,66	0
48	MG	H1	3508	1/1	0.92	0.16	80,80,80,80	0
48	MG	D1	3517	1/1	0.92	0.31	127,127,127,127	0
48	MG	F1	3470	1/1	0.92	0.09	49,49,49,49	0
48	MG	H1	3467	1/1	0.92	0.11	95,95,95,95	0
48	MG	D1	3581	1/1	0.92	0.08	68,68,68,68	0
48	MG	H1	3403	1/1	0.92	0.14	111,111,111,111	0
48	MG	A1	3511	1/1	0.92	0.08	90,90,90,90	0
48	MG	EL	301	1/1	0.92	0.12	119,119,119,119	0
48	MG	F1	3407	1/1	0.92	0.10	111,111,111,111	0
48	MG	F1	3543	1/1	0.92	0.09	71,71,71,71	0
48	MG	A1	3581	1/1	0.92	0.32	126,126,126,126	0
48	MG	A1	3464	1/1	0.92	0.06	64,64,64,64	0
48	MG	F1	3444	1/1	0.92	0.42	155,155,155,155	0
48	MG	D1	3432	1/1	0.92	0.17	118,118,118,118	0
48	MG	H1	3405	1/1	0.93	0.25	101,101,101,101	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	A1	3559	1/1	0.93	0.06	89,89,89,89	0
48	MG	A1	3562	1/1	0.93	0.20	91,91,91,91	0
48	MG	H1	3451	1/1	0.93	0.13	78,78,78,78	0
48	MG	F1	3479	1/1	0.93	0.29	81,81,81,81	0
48	MG	H1	3495	1/1	0.93	0.06	65,65,65,65	0
48	MG	D1	3412	1/1	0.93	0.35	95,95,95,95	0
48	MG	F1	3405	1/1	0.93	0.13	79,79,79,79	0
48	MG	A1	3439	1/1	0.93	0.08	106,106,106,106	0
48	MG	D1	3527	1/1	0.93	0.28	106,106,106,106	0
48	MG	A1	3488	1/1	0.93	0.17	91,91,91,91	0
48	MG	A1	3493	1/1	0.93	0.21	113,113,113,113	0
48	MG	D1	3585	1/1	0.93	0.08	108,108,108,108	0
48	MG	H1	3419	1/1	0.93	0.17	62,62,62,62	0
48	MG	A1	3441	1/1	0.93	0.50	127,127,127,127	0
48	MG	C3	204	1/1	0.93	0.11	85,85,85,85	0
48	MG	A1	3564	1/1	0.93	0.07	141,141,141,141	0
48	MG	F1	3551	1/1	0.93	0.24	91,91,91,91	0
48	MG	A1	3599	1/1	0.93	0.12	103,103,103,103	0
48	MG	A1	3475	1/1	0.93	0.22	80,80,80,80	0
48	MG	F1	3420	1/1	0.93	0.09	88,88,88,88	0
48	MG	D1	3458	1/1	0.93	0.06	51,51,51,51	0
48	MG	F1	3436	1/1	0.93	0.10	70,70,70,70	0
48	MG	F1	3458	1/1	0.93	0.09	95,95,95,95	0
48	MG	D1	3414	1/1	0.93	0.15	96,96,96,96	0
48	MG	H1	3527	1/1	0.93	0.14	99,99,99,99	0
48	MG	A1	3570	1/1	0.93	0.08	70,70,70,70	0
48	MG	F1	3455	1/1	0.93	0.09	65,65,65,65	0
48	MG	H1	3461	1/1	0.93	0.15	134,134,134,134	0
48	MG	D1	3487	1/1	0.93	0.09	65,65,65,65	0
48	MG	H1	3520	1/1	0.93	0.17	114,114,114,114	0
48	MG	D1	3494	1/1	0.93	0.13	78,78,78,78	0
48	MG	D1	3531	1/1	0.93	0.08	87,87,87,87	0
48	MG	BL	301	1/1	0.93	0.09	71,71,71,71	0
48	MG	H1	3517	1/1	0.93	0.16	79,79,79,79	0
48	MG	A1	3541	1/1	0.93	0.35	86,86,86,86	0
48	MG	F1	3494	1/1	0.93	0.12	97,97,97,97	0
48	MG	D1	3520	1/1	0.93	0.11	93,93,93,93	0
48	MG	F1	3406	1/1	0.93	0.08	83,83,83,83	0
48	MG	FA	102	1/1	0.93	0.10	84,84,84,84	0
48	MG	D1	3454	1/1	0.93	0.14	64,64,64,64	0
48	MG	A1	3560	1/1	0.93	0.45	138,138,138,138	0
48	MG	H1	3522	1/1	0.93	0.16	107,107,107,107	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	H1	3513	1/1	0.93	0.11	87,87,87,87	0
48	MG	A1	3549	1/1	0.93	0.13	54,54,54,54	0
48	MG	F1	3478	1/1	0.94	0.12	73,73,73,73	0
48	MG	E2	203	1/1	0.94	0.07	77,77,77,77	0
48	MG	F1	3507	1/1	0.94	0.17	87,87,87,87	0
48	MG	F1	3530	1/1	0.94	0.15	107,107,107,107	0
48	MG	A1	3469	1/1	0.94	0.17	113,113,113,113	0
48	MG	H1	3471	1/1	0.94	0.21	124,124,124,124	0
48	MG	F1	3437	1/1	0.94	0.17	100,100,100,100	0
48	MG	H1	3469	1/1	0.94	0.34	119,119,119,119	0
48	MG	F1	3536	1/1	0.94	0.20	67,67,67,67	0
48	MG	AA	102	1/1	0.94	0.08	98,98,98,98	0
48	MG	H1	3440	1/1	0.94	0.08	73,73,73,73	0
48	MG	F1	3471	1/1	0.94	0.17	90,90,90,90	0
48	MG	F1	3531	1/1	0.94	0.09	95,95,95,95	0
48	MG	A1	3405	1/1	0.94	0.08	65,65,65,65	0
48	MG	C3	201	1/1	0.94	0.34	123,123,123,123	0
48	MG	EJ	201	1/1	0.94	0.12	69,69,69,69	0
48	MG	BJ	201	1/1	0.94	0.17	66,66,66,66	0
48	MG	A1	3504	1/1	0.94	0.49	138,138,138,138	0
48	MG	F1	3480	1/1	0.94	0.12	59,59,59,59	0
48	MG	D1	3589	1/1	0.94	0.26	107,107,107,107	0
48	MG	A1	3533	1/1	0.94	0.22	73,73,73,73	0
48	MG	H1	3428	1/1	0.94	0.12	77,77,77,77	0
48	MG	D1	3508	1/1	0.94	0.05	86,86,86,86	0
48	MG	D1	3423	1/1	0.94	0.17	67,67,67,67	0
48	MG	D1	3478	1/1	0.94	0.12	81,81,81,81	0
48	MG	F1	3533	1/1	0.94	0.18	101,101,101,101	0
48	MG	D1	3413	1/1	0.94	0.09	51,51,51,51	0
48	MG	H1	3475	1/1	0.94	0.10	70,70,70,70	0
48	MG	A1	3505	1/1	0.94	0.12	137,137,137,137	0
48	MG	A1	3481	1/1	0.94	0.16	88,88,88,88	0
48	MG	F1	3557	1/1	0.94	0.15	84,84,84,84	0
48	MG	F1	3418	1/1	0.94	0.12	126,126,126,126	0
48	MG	D1	3431	1/1	0.94	0.19	95,95,95,95	0
48	MG	A1	3407	1/1	0.94	0.11	83,83,83,83	0
48	MG	A1	3494	1/1	0.94	0.07	98,98,98,98	0
48	MG	H1	3454	1/1	0.94	0.12	111,111,111,111	0
48	MG	D1	3601	1/1	0.94	0.22	124,124,124,124	0
48	MG	DA	101	1/1	0.94	0.07	82,82,82,82	0
48	MG	D1	3558	1/1	0.94	0.07	56,56,56,56	0
48	MG	F1	3417	1/1	0.94	0.17	110,110,110,110	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	D1	3492	1/1	0.94	0.34	125,125,125,125	0
48	MG	AA	103	1/1	0.94	0.08	56,56,56,56	0
48	MG	A1	3448	1/1	0.94	0.14	78,78,78,78	0
48	MG	F1	3443	1/1	0.94	0.06	104,104,104,104	0
48	MG	B2	205	1/1	0.94	0.09	81,81,81,81	0
48	MG	H1	3427	1/1	0.94	0.14	83,83,83,83	0
48	MG	D1	3584	1/1	0.94	0.13	101,101,101,101	0
48	MG	D1	3612	1/1	0.94	0.23	123,123,123,123	0
48	MG	D1	3564	1/1	0.94	0.21	92,92,92,92	0
48	MG	F1	3410	1/1	0.94	0.17	42,42,42,42	0
48	MG	D1	3455	1/1	0.94	0.09	80,80,80,80	0
48	MG	A1	3558	1/1	0.94	0.10	91,91,91,91	0
48	MG	D1	3617	1/1	0.94	0.34	113,113,113,113	0
48	MG	D1	3553	1/1	0.94	0.07	90,90,90,90	0
48	MG	A1	3485	1/1	0.95	0.15	137,137,137,137	0
48	MG	A1	3482	1/1	0.95	0.06	62,62,62,62	0
48	MG	H1	3476	1/1	0.95	0.08	52,52,52,52	0
48	MG	D1	3591	1/1	0.95	0.10	55,55,55,55	0
48	MG	A1	3487	1/1	0.95	0.23	121,121,121,121	0
48	MG	F1	3524	1/1	0.95	0.14	56,56,56,56	0
48	MG	D1	3524	1/1	0.95	0.06	69,69,69,69	0
48	MG	D1	3449	1/1	0.95	0.09	68,68,68,68	0
48	MG	D1	3566	1/1	0.95	0.14	80,80,80,80	0
48	MG	D1	3477	1/1	0.95	0.09	60,60,60,60	0
48	MG	F1	3452	1/1	0.95	0.10	50,50,50,50	0
48	MG	A1	3506	1/1	0.95	0.12	77,77,77,77	0
48	MG	CN	201	1/1	0.95	0.29	175,175,175,175	0
48	MG	GJ	201	1/1	0.95	0.13	69,69,69,69	0
48	MG	F1	3552	1/1	0.95	0.15	139,139,139,139	0
48	MG	D1	3590	1/1	0.95	0.20	89,89,89,89	0
48	MG	D1	3474	1/1	0.95	0.10	58,58,58,58	0
48	MG	A1	3508	1/1	0.95	0.12	89,89,89,89	0
48	MG	H1	3507	1/1	0.95	0.07	64,64,64,64	0
48	MG	H1	3463	1/1	0.95	0.11	78,78,78,78	0
48	MG	H1	3491	1/1	0.95	0.13	111,111,111,111	0
48	MG	A1	3411	1/1	0.95	0.17	83,83,83,83	0
48	MG	F1	3412	1/1	0.95	0.11	60,60,60,60	0
48	MG	A1	3535	1/1	0.95	0.09	99,99,99,99	0
48	MG	A1	3480	1/1	0.95	0.31	120,120,120,120	0
48	MG	D1	3483	1/1	0.95	0.09	88,88,88,88	0
48	MG	A1	3459	1/1	0.95	0.20	90,90,90,90	0
48	MG	A1	3418	1/1	0.95	0.10	117,117,117,117	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	A1	3434	1/1	0.95	0.16	74,74,74,74	0
48	MG	H1	3483	1/1	0.95	0.14	108,108,108,108	0
48	MG	D1	3419	1/1	0.95	0.10	92,92,92,92	0
48	MG	F1	3504	1/1	0.95	0.13	84,84,84,84	0
48	MG	D1	3488	1/1	0.95	0.18	97,97,97,97	0
48	MG	D1	3402	1/1	0.95	0.08	52,52,52,52	0
48	MG	A1	3550	1/1	0.95	0.04	69,69,69,69	0
48	MG	E3	201	1/1	0.95	0.09	90,90,90,90	0
48	MG	H1	3423	1/1	0.95	0.11	98,98,98,98	0
48	MG	F1	3481	1/1	0.95	0.13	45,45,45,45	0
48	MG	F1	3584	1/1	0.95	0.16	97,97,97,97	0
48	MG	D1	3510	1/1	0.95	0.19	81,81,81,81	0
48	MG	A1	3544	1/1	0.95	0.48	135,135,135,135	0
48	MG	F1	3416	1/1	0.95	0.45	116,116,116,116	0
48	MG	D1	3408	1/1	0.95	0.30	106,106,106,106	0
48	MG	A1	3484	1/1	0.95	0.13	108,108,108,108	0
48	MG	A1	3445	1/1	0.95	0.18	88,88,88,88	0
48	MG	H1	3460	1/1	0.95	0.13	69,69,69,69	0
48	MG	H1	3500	1/1	0.95	0.16	82,82,82,82	0
48	MG	A1	3406	1/1	0.95	0.10	75,75,75,75	0
48	MG	D1	3567	1/1	0.95	0.26	60,60,60,60	0
48	MG	D1	3555	1/1	0.95	0.39	119,119,119,119	0
48	MG	D1	3450	1/1	0.95	0.07	49,49,49,49	0
48	MG	GL	301	1/1	0.95	0.11	113,113,113,113	0
48	MG	A1	3477	1/1	0.95	0.13	62,62,62,62	0
48	MG	A1	3545	1/1	0.95	0.30	71,71,71,71	0
48	MG	D1	3457	1/1	0.95	0.12	34,34,34,34	0
48	MG	F1	3582	1/1	0.95	0.20	77,77,77,77	0
48	MG	H1	3466	1/1	0.95	0.08	107,107,107,107	0
48	MG	D1	3415	1/1	0.95	0.11	117,117,117,117	0
48	MG	A1	3478	1/1	0.95	0.08	79,79,79,79	0
48	MG	DK	201	1/1	0.95	0.29	101,101,101,101	0
48	MG	D1	3629	1/1	0.95	0.11	121,121,121,121	0
48	MG	A1	3486	1/1	0.95	0.15	93,93,93,93	0
48	MG	D1	3529	1/1	0.96	0.10	80,80,80,80	0
48	MG	A1	3463	1/1	0.96	0.10	59,59,59,59	0
48	MG	F1	3512	1/1	0.96	0.11	94,94,94,94	0
48	MG	D1	3438	1/1	0.96	0.08	39,39,39,39	0
48	MG	A1	3523	1/1	0.96	0.12	91,91,91,91	0
48	MG	H1	3453	1/1	0.96	0.11	66,66,66,66	0
48	MG	A1	3520	1/1	0.96	0.16	70,70,70,70	0
48	MG	H1	3514	1/1	0.96	0.07	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	H1	3445	1/1	0.96	0.14	68,68,68,68	0
48	MG	D1	3578	1/1	0.96	0.07	88,88,88,88	0
48	MG	H1	3502	1/1	0.96	0.07	82,82,82,82	0
48	MG	F1	3476	1/1	0.96	0.16	99,99,99,99	0
48	MG	D1	3526	1/1	0.96	0.05	54,54,54,54	0
48	MG	F1	3521	1/1	0.96	0.09	65,65,65,65	0
48	MG	D1	3465	1/1	0.96	0.09	65,65,65,65	0
48	MG	D1	3459	1/1	0.96	0.07	63,63,63,63	0
48	MG	D1	3519	1/1	0.96	0.08	72,72,72,72	0
49	ZN	AC	201	1/1	0.96	0.08	143,143,143,143	0
48	MG	D1	3473	1/1	0.96	0.11	63,63,63,63	0
48	MG	A1	3557	1/1	0.96	0.20	104,104,104,104	0
48	MG	A1	3462	1/1	0.96	0.10	46,46,46,46	0
48	MG	D1	3539	1/1	0.96	0.14	57,57,57,57	0
48	MG	F1	3465	1/1	0.96	0.26	101,101,101,101	0
48	MG	A1	3537	1/1	0.96	0.12	54,54,54,54	0
48	MG	A1	3442	1/1	0.96	0.10	52,52,52,52	0
48	MG	D1	3518	1/1	0.96	0.21	92,92,92,92	0
48	MG	D1	3466	1/1	0.96	0.22	132,132,132,132	0
49	ZN	FL	201	1/1	0.96	0.09	86,86,86,86	0
48	MG	G2	203	1/1	0.96	0.10	112,112,112,112	0
48	MG	CJ	201	1/1	0.96	0.14	64,64,64,64	0
48	MG	F1	3487	1/1	0.96	0.09	60,60,60,60	0
48	MG	F1	3445	1/1	0.96	0.16	78,78,78,78	0
48	MG	F1	3526	1/1	0.96	0.14	72,72,72,72	0
48	MG	D1	3493	1/1	0.96	0.33	128,128,128,128	0
48	MG	D1	3495	1/1	0.96	0.07	88,88,88,88	0
48	MG	H1	3498	1/1	0.96	0.07	60,60,60,60	0
48	MG	F1	3508	1/1	0.96	0.24	127,127,127,127	0
48	MG	D1	3461	1/1	0.96	0.10	86,86,86,86	0
48	MG	D1	3619	1/1	0.96	0.07	101,101,101,101	0
48	MG	F1	3409	1/1	0.96	0.16	60,60,60,60	0
48	MG	EQ	201	1/1	0.96	0.18	88,88,88,88	0
48	MG	D1	3404	1/1	0.96	0.11	55,55,55,55	0
48	MG	D1	3544	1/1	0.96	0.09	50,50,50,50	0
48	MG	A1	3546	1/1	0.96	0.23	51,51,51,51	0
48	MG	A1	3514	1/1	0.96	0.14	59,59,59,59	0
48	MG	F1	3514	1/1	0.96	0.13	70,70,70,70	0
48	MG	H1	3494	1/1	0.96	0.14	56,56,56,56	0
48	MG	F1	3486	1/1	0.96	0.11	90,90,90,90	0
48	MG	C3	206	1/1	0.96	0.15	120,120,120,120	0
48	MG	F1	3518	1/1	0.96	0.13	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	A1	3465	1/1	0.96	0.08	54,54,54,54	0
48	MG	D1	3460	1/1	0.96	0.09	85,85,85,85	0
48	MG	F1	3547	1/1	0.96	0.10	112,112,112,112	0
48	MG	D1	3500	1/1	0.96	0.09	44,44,44,44	0
48	MG	A1	3539	1/1	0.96	0.08	46,46,46,46	0
48	MG	D1	3436	1/1	0.96	0.16	78,78,78,78	0
48	MG	A1	3597	1/1	0.97	0.38	133,133,133,133	0
48	MG	D1	3503	1/1	0.97	0.14	82,82,82,82	0
48	MG	D1	3420	1/1	0.97	0.08	105,105,105,105	0
48	MG	H1	3437	1/1	0.97	0.11	93,93,93,93	0
48	MG	A1	3466	1/1	0.97	0.12	40,40,40,40	0
48	MG	F1	3441	1/1	0.97	0.19	111,111,111,111	0
48	MG	CL	302	1/1	0.97	0.10	68,68,68,68	0
48	MG	A1	3540	1/1	0.97	0.15	66,66,66,66	0
48	MG	A1	3452	1/1	0.97	0.10	90,90,90,90	0
48	MG	F1	3525	1/1	0.97	0.09	73,73,73,73	0
48	MG	H1	3444	1/1	0.97	0.06	65,65,65,65	0
48	MG	CQ	202	1/1	0.97	0.06	62,62,62,62	0
48	MG	D1	3479	1/1	0.97	0.04	50,50,50,50	0
48	MG	A1	3538	1/1	0.97	0.08	49,49,49,49	0
48	MG	D1	3464	1/1	0.97	0.08	44,44,44,44	0
48	MG	D1	3509	1/1	0.97	0.09	41,41,41,41	0
48	MG	C2	204	1/1	0.97	0.07	75,75,75,75	0
48	MG	D1	3632	1/1	0.97	0.12	83,83,83,83	0
48	MG	D1	3456	1/1	0.97	0.11	70,70,70,70	0
48	MG	D1	3453	1/1	0.97	0.11	54,54,54,54	0
48	MG	F1	3432	1/1	0.97	0.08	68,68,68,68	0
48	MG	D1	3490	1/1	0.97	0.16	92,92,92,92	0
48	MG	A1	3457	1/1	0.97	0.35	94,94,94,94	0
48	MG	D1	3570	1/1	0.97	0.20	54,54,54,54	0
48	MG	D1	3501	1/1	0.97	0.13	51,51,51,51	0
48	MG	A1	3526	1/1	0.97	0.10	48,48,48,48	0
48	MG	D1	3462	1/1	0.97	0.19	116,116,116,116	0
48	MG	D1	3559	1/1	0.97	0.08	55,55,55,55	0
48	MG	D1	3536	1/1	0.97	0.10	73,73,73,73	0
48	MG	A1	3598	1/1	0.97	0.21	111,111,111,111	0
48	MG	D1	3546	1/1	0.97	0.10	49,49,49,49	0
48	MG	F1	3449	1/1	0.97	0.10	90,90,90,90	0
48	MG	F1	3459	1/1	0.97	0.07	79,79,79,79	0
48	MG	C2	203	1/1	0.97	0.06	63,63,63,63	0
48	MG	F1	3427	1/1	0.97	0.16	51,51,51,51	0
48	MG	H1	3493	1/1	0.97	0.12	79,79,79,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
48	MG	B2	203	1/1	0.97	0.06	81,81,81,81	0
48	MG	D1	3630	1/1	0.97	0.14	71,71,71,71	0
48	MG	A1	3458	1/1	0.97	0.10	59,59,59,59	0
48	MG	A1	3517	1/1	0.97	0.08	74,74,74,74	0
48	MG	A1	3446	1/1	0.97	0.19	64,64,64,64	0
48	MG	BW	201	1/1	0.97	0.09	67,67,67,67	0
48	MG	H1	3439	1/1	0.97	0.12	75,75,75,75	0
48	MG	F1	3426	1/1	0.97	0.24	110,110,110,110	0
48	MG	BQ	202	1/1	0.97	0.07	53,53,53,53	0
48	MG	H1	3506	1/1	0.97	0.12	75,75,75,75	0
48	MG	H1	3515	1/1	0.97	0.09	73,73,73,73	0
48	MG	F1	3510	1/1	0.97	0.10	95,95,95,95	0
48	MG	D1	3560	1/1	0.97	0.10	64,64,64,64	0
48	MG	A1	3426	1/1	0.97	0.09	73,73,73,73	0
48	MG	D1	3587	1/1	0.97	0.14	93,93,93,93	0
48	MG	E2	204	1/1	0.97	0.06	75,75,75,75	0
48	MG	A1	3495	1/1	0.97	0.06	70,70,70,70	0
48	MG	F1	3404	1/1	0.97	0.10	75,75,75,75	0
48	MG	D1	3486	1/1	0.97	0.13	47,47,47,47	0
48	MG	F1	3474	1/1	0.97	0.13	64,64,64,64	0
48	MG	A1	3456	1/1	0.97	0.12	49,49,49,49	0
48	MG	F1	3454	1/1	0.98	0.15	56,56,56,56	0
48	MG	F1	3460	1/1	0.98	0.14	36,36,36,36	0
48	MG	F1	3528	1/1	0.98	0.06	75,75,75,75	0
48	MG	A1	3524	1/1	0.98	0.12	63,63,63,63	0
48	MG	A1	3432	1/1	0.98	0.07	45,45,45,45	0
48	MG	H1	3458	1/1	0.98	0.06	90,90,90,90	0
49	ZN	DC	201	1/1	0.98	0.07	89,89,89,89	0
48	MG	A1	3421	1/1	0.98	0.06	71,71,71,71	0
49	ZN	GY	201	1/1	0.98	0.10	116,116,116,116	0
48	MG	D1	3430	1/1	0.98	0.08	59,59,59,59	0
48	MG	F1	3499	1/1	0.98	0.04	57,57,57,57	0
48	MG	A1	3440	1/1	0.98	0.04	78,78,78,78	0
48	MG	F1	3523	1/1	0.98	0.09	55,55,55,55	0
48	MG	D1	3480	1/1	0.98	0.09	32,32,32,32	0
48	MG	D1	3411	1/1	0.98	0.11	44,44,44,44	0
48	MG	F1	3450	1/1	0.98	0.09	59,59,59,59	0
48	MG	D1	3489	1/1	0.98	0.07	44,44,44,44	0
48	MG	D1	3405	1/1	0.98	0.10	59,59,59,59	0
48	MG	D1	3569	1/1	0.98	0.09	48,48,48,48	0
48	MG	F1	3546	1/1	0.98	0.07	59,59,59,59	0
48	MG	D1	3469	1/1	0.98	0.10	64,64,64,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
49	ZN	DL	201	1/1	0.98	0.17	86,86,86,86	0
48	MG	A1	3476	1/1	0.98	0.07	59,59,59,59	0
48	MG	F1	3505	1/1	0.98	0.10	83,83,83,83	0
48	MG	A1	3543	1/1	0.98	0.08	96,96,96,96	0
48	MG	A1	3561	1/1	0.98	0.14	60,60,60,60	0
49	ZN	HA	101	1/1	0.98	0.14	112,112,112,112	0
48	MG	H1	3421	1/1	0.98	0.13	97,97,97,97	0
49	ZN	BY	201	1/1	0.98	0.10	59,59,59,59	0
49	ZN	FC	201	1/1	0.98	0.04	108,108,108,108	0
49	ZN	HL	201	1/1	0.98	0.08	118,118,118,118	0
49	ZN	AK	201	1/1	0.98	0.10	89,89,89,89	0
48	MG	D1	3428	1/1	0.98	0.06	106,106,106,106	0
48	MG	A1	3525	1/1	0.98	0.08	51,51,51,51	0
48	MG	D1	3556	1/1	0.98	0.07	76,76,76,76	0
49	ZN	EY	201	1/1	0.98	0.10	77,77,77,77	0
48	MG	A1	3410	1/1	0.98	0.21	62,62,62,62	0
49	ZN	AA	101	1/1	0.98	0.14	64,64,64,64	0
48	MG	A1	3460	1/1	0.99	0.13	61,61,61,61	0
48	MG	D1	3502	1/1	0.99	0.07	38,38,38,38	0
48	MG	D1	3471	1/1	0.99	0.20	40,40,40,40	0
49	ZN	AL	201	1/1	0.99	0.09	70,70,70,70	0
48	MG	A1	3473	1/1	0.99	0.08	55,55,55,55	0
48	MG	D1	3410	1/1	0.99	0.12	39,39,39,39	0
48	MG	F1	3467	1/1	0.99	0.10	57,57,57,57	0
49	ZN	CY	202	1/1	0.99	0.08	70,70,70,70	0
48	MG	F1	3438	1/1	0.99	0.14	58,58,58,58	0
49	ZN	FA	103	1/1	0.99	0.12	80,80,80,80	0
48	MG	H1	3497	1/1	0.99	0.13	50,50,50,50	0
49	ZN	HK	201	1/1	0.99	0.11	70,70,70,70	0
48	MG	D1	3554	1/1	0.99	0.12	59,59,59,59	0
49	ZN	DK	202	1/1	0.99	0.11	68,68,68,68	0
49	ZN	DA	103	1/1	0.99	0.14	69,69,69,69	0
48	MG	D1	3533	1/1	0.99	0.07	41,41,41,41	0
48	MG	F1	3435	1/1	0.99	0.11	44,44,44,44	0
48	MG	A1	3502	1/1	0.99	0.10	80,80,80,80	0
48	MG	A1	3534	1/1	0.99	0.13	62,62,62,62	0
49	ZN	FK	202	1/1	0.99	0.12	74,74,74,74	0
48	MG	A1	3413	1/1	0.99	0.18	136,136,136,136	0
48	MG	A1	3489	1/1	0.99	0.07	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.