



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 07:18 AM UTC

PDB ID : 4P70 / pdb_00004p70
Title : Crystal Structure of Unmodified tRNA Proline (CGG) Bound to Codon CCG on the Ribosome
Authors : Maehigashi, T.; Dunkle, J.A.; Dunham, C.M.
Deposited on : 2014-03-25
Resolution : 3.68 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

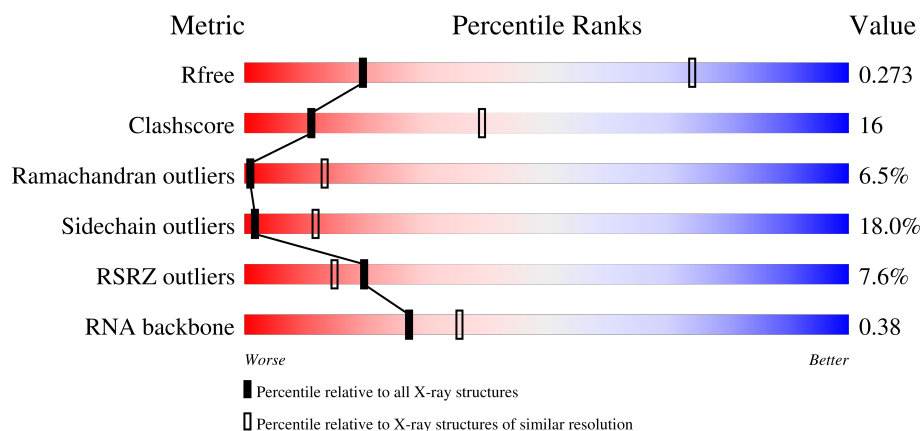
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.68 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}	180053	1263 (3.80-3.56)
Clashscore	190562	1305 (3.80-3.56)
Ramachandran outliers	187476	1259 (3.80-3.56)
Sidechain outliers	187428	1256 (3.80-3.56)
RSRZ outliers	180081	1262 (3.80-3.56)
RNA backbone	3983	1000 (4.26-3.08)

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 of 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	QA	1522	4% 36% 48% 14%
1	XA	1522	4% 35% 50% 14%
2	QB	256	10% 46% 38% 8% 7%
2	XB	256	8% 43% 39% 9% 7%

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Mol	Chain	Length	Quality of chain
3	QC	239	
3	XC	239	
4	QD	209	
4	XD	209	
5	QE	162	
5	XE	162	
6	QF	101	
6	XF	101	
7	QG	156	
7	XG	156	
8	QH	138	
8	XH	138	
9	QI	128	
9	XI	128	
10	QJ	105	
10	XJ	105	
11	QK	129	
11	XK	129	
12	QL	132	
12	XL	132	
13	QM	126	
13	XM	126	
14	QN	61	
14	XN	61	
15	QO	89	

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Mol	Chain	Length	Quality of chain
15	XO	89	
16	QP	88	
16	XP	88	
17	QQ	105	
17	XQ	105	
18	QR	88	
18	XR	88	
19	QS	93	
19	XS	93	
20	QT	106	
20	XT	106	
21	QU	27	
21	XU	27	
22	RA	2916	
22	YA	2916	
23	RB	122	
23	YB	122	
24	RD	276	
24	YD	276	
25	RE	206	
25	YE	206	
26	RF	210	
26	YF	210	
27	RG	182	
27	YG	182	

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Mol	Chain	Length	Quality of chain
28	RH	180	
28	YH	180	
29	RI	148	
29	YI	148	
30	RN	140	
30	YN	140	
31	RO	122	
31	YO	122	
32	RP	150	
32	YP	150	
33	RQ	141	
33	YQ	141	
34	RR	118	
34	YR	118	
35	RS	112	
35	YS	112	
36	RT	146	
36	YT	146	
37	RU	118	
37	YU	118	
38	RV	101	
38	YV	101	
39	RW	113	
39	YW	113	
40	RX	96	

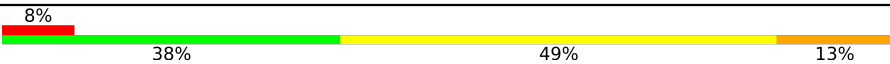
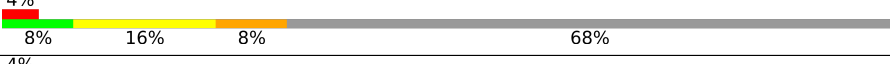
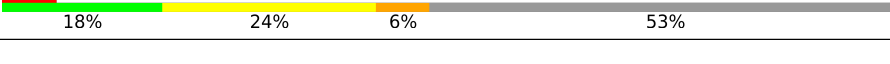
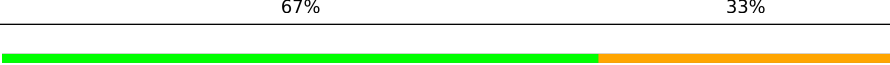
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Mol	Chain	Length	Quality of chain
40	YX	96	
41	RY	110	
41	YY	110	
42	RZ	206	
42	YZ	206	
43	R0	85	
43	Y0	85	
44	R1	98	
44	Y1	98	
45	R2	72	
45	Y2	72	
46	R3	60	
46	Y3	60	
47	R4	71	
47	Y4	71	
48	R5	60	
48	Y5	60	
49	R6	54	
49	Y6	54	
50	R7	49	
50	Y7	49	
51	R8	65	
51	Y8	65	
52	R9	37	
52	Y9	37	

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Mol	Chain	Length	Quality of chain
53	QV	77	
53	XV	77	
54	QX	25	
54	XX	25	
55	QY	17	
55	XY	17	
56	Z6	3	
56	Z8	3	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
58	MG	RA	3009	-	-	-	X
58	MG	RA	3037	-	-	-	X
58	MG	RA	3056	-	-	-	X
58	MG	RA	3067	-	-	-	X
58	MG	RA	3235	-	-	-	X
58	MG	XA	1617	-	-	-	X
58	MG	XA	1643	-	-	-	X
58	MG	Y0	101	-	-	-	X
58	MG	YA	3003	-	-	-	X
58	MG	YA	3014	-	-	-	X
58	MG	YA	3015	-	-	-	X
58	MG	YA	3018	-	-	-	X
58	MG	YA	3041	-	-	-	X
58	MG	YA	3046	-	-	-	X
58	MG	YA	3049	-	-	-	X
58	MG	YA	3080	-	-	-	X
58	MG	YA	3095	-	-	-	X
58	MG	YA	3099	-	-	-	X
58	MG	YA	3205	-	-	-	X
58	MG	YA	3256	-	-	-	X
58	MG	YA	3260	-	-	-	X
58	MG	YD	301	-	-	-	X

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 291730 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 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	QA	1500	Total	C	N	O	P	0	0	0
			32247	14353	5981	10414	1499			
1	XA	1500	Total	C	N	O	P	0	0	0
			32249	14354	5984	10412	1499			

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	QB	237	Total	C	N	O	S	0	0	0
			1924	1228	344	347	5			
2	XB	237	Total	C	N	O	S	0	0	0
			1924	1228	344	347	5			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	QC	205	Total	C	N	O	S	0	0	0
			1605	1011	313	280	1			
3	XC	205	Total	C	N	O	S	0	0	0
			1605	1011	313	280	1			

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	QD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			
4	XD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	QE	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	4			
5	XE	151	Total	C	N	O	S	0	0	0
			1155	729	218	204	4			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	QF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			
6	XF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	QG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			
7	XG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	QH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			
8	XH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	QI	127	Total	C	N	O		0	0	0
			1010	639	197	174				
9	XI	127	Total	C	N	O		0	0	0
			1010	639	197	174				

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	QJ	99	Total	C	N	O	S	0	0	0
			801	504	157	139	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	XJ	99	Total	C	N	O	S	0	0	0
			801	504	157	139	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	QK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			
11	XK	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	QL	125	Total	C	N	O	S	0	0	0
			975	614	196	164	1			
12	XL	125	Total	C	N	O	S	0	0	0
			975	614	196	164	1			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	QM	121	Total	C	N	O	S	0	0	0
			964	597	199	166	2			
13	XM	121	Total	C	N	O	S	0	0	0
			964	597	199	166	2			

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	QN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
14	XN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	QO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			
15	XO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	QP	84	Total	C	N	O	S	0	0	0
			705	446	140	118	1			
16	XP	84	Total	C	N	O	S	0	0	0
			705	446	140	118	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	QQ	100	Total	C	N	O	S	0	0	0
			834	534	155	143	2			
17	XQ	100	Total	C	N	O	S	0	0	0
			834	534	155	143	2			

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	QR	70	Total	C	N	O	0	0	0
			574	367	112	95			
18	XR	70	Total	C	N	O	0	0	0
			574	367	112	95			

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	QS	84	Total	C	N	O	S	0	0	0
			674	430	126	116	2			
19	XS	84	Total	C	N	O	S	0	0	0
			674	430	126	116	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	QT	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			
20	XT	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

- Molecule 21 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	QU	25	Total	C	N	O	0	0	0
			217	134	52	31			
21	XU	25	Total	C	N	O	0	0	0
			217	134	52	31			

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	RA	2882	Total	C	N	O	P	0	0	0
			62071	27627	11611	19952	2881			
22	YA	2883	Total	C	N	O	P	0	0	0
			62091	27636	11613	19960	2882			

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	RB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			
23	YB	120	Total	C	N	O	P	0	0	0
			2573	1146	476	832	119			

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	RD	272	Total	C	N	O	S	0	0	0
			2115	1335	420	357	3			
24	YD	272	Total	C	N	O	S	0	0	0
			2115	1335	420	357	3			

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	RE	205	Total	C	N	O	S	0	0	0
			1568	991	300	271	6			
25	YE	205	Total	C	N	O	S	0	0	0
			1568	991	300	271	6			

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	RF	202	Total	C	N	O	S	0	0	0
			1585	1011	297	275	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	YF	202	Total	C	N	O	S	0	0	0
			1585	1011	297	275	2			

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	RG	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			
27	YG	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	RH	170	Total	C	N	O	S	0	0	0
			1307	829	245	232	1			
28	YH	170	Total	C	N	O	S	0	0	0
			1307	829	245	232	1			

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	RI	146	Total	C	N	O	S	0	0	0
			1136	726	201	208	1			
29	YI	146	Total	C	N	O	S	0	0	0
			1136	726	201	208	1			

- Molecule 30 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	RN	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			
30	YN	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			

- Molecule 31 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	RO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
31	YO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 32 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	RP	150	Total	C	N	O	S	0	0	0
			1145	712	232	198	3			
32	YP	150	Total	C	N	O	S	0	0	0
			1145	712	232	198	3			

- Molecule 33 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	RQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
33	YQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 34 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	RR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			
34	YR	118	Total	C	N	O	S	0	0	0
			968	604	203	160	1			

- Molecule 35 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
35	RS	111	Total	C	N	O	0	0	0
			882	556	176	150			
35	YS	111	Total	C	N	O	0	0	0
			882	556	176	150			

- Molecule 36 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	RT	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			
36	YT	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			

- Molecule 37 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	RU	117	Total	C	N	O	S	0	0	0
			964	610	202	151	1			
37	YU	117	Total	C	N	O	S	0	0	0
			964	610	202	151	1			

- Molecule 38 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	RV	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			
38	YV	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 39 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	RW	113	Total	C	N	O	S	0	0	0
			900	566	177	155	2			
39	YW	113	Total	C	N	O	S	0	0	0
			900	566	177	155	2			

- Molecule 40 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	RX	92	Total	C	N	O	0	0	0
			725	471	131	123			
40	YX	92	Total	C	N	O	0	0	0
			725	471	131	123			

- Molecule 41 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	RY	102	Total	C	N	O	S	0	0	0
			785	505	150	125	5			
41	YY	102	Total	C	N	O	S	0	0	0
			785	505	150	125	5			

- Molecule 42 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	RZ	183	Total	C	N	O	S	0	0	0
			1461	933	260	265	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	YZ	183	Total	C	N	O	S	0	0	0
			1461	933	260	265	3			

- Molecule 43 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	R0	82	Total	C	N	O	S	0	0	0
			648	401	138	108	1			
43	Y0	82	Total	C	N	O	S	0	0	0
			648	401	138	108	1			

- Molecule 44 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	R1	97	Total	C	N	O	S	0	0	0
			763	481	150	131	1			
44	Y1	97	Total	C	N	O	S	0	0	0
			763	481	150	131	1			

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	R2	69	Total	C	N	O	S	0	0	0
			581	358	118	104	1			
45	Y2	69	Total	C	N	O	S	0	0	0
			581	358	118	104	1			

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
46	R3	59	Total	C	N	O	0	0	0
			469	298	90	81			
46	Y3	59	Total	C	N	O	0	0	0
			469	298	90	81			

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	R4	71	Total	C	N	O	S	0	0	0
			581	364	108	104	5			
47	Y4	71	Total	C	N	O	S	0	0	0
			581	364	108	104	5			

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	R5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			
48	Y5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	R6	49	Total	C	N	O	S	0	0	0
			424	264	87	69	4			
49	Y6	49	Total	C	N	O	S	0	0	0
			424	264	87	69	4			

- Molecule 50 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	R7	49	Total	C	N	O	S	0	0	0
			430	263	108	57	2			
50	Y7	49	Total	C	N	O	S	0	0	0
			430	263	108	57	2			

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	R8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			
51	Y8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	R9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
52	Y9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 53 is a RNA chain called P-site tRNA fMET.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	QV	77	Total	C	N	O	P	0	0	0
			1644	732	297	538	77			
53	XV	77	Total	C	N	O	P	0	0	0
			1644	732	297	538	77			

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	QX	8	Total	C	N	O	P	0	0	0
			173	77	33	55	8			
54	XX	8	Total	C	N	O	P	0	0	0
			173	77	33	55	8			

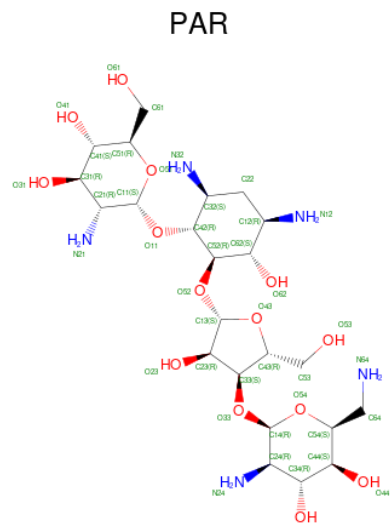
- Molecule 55 is a RNA chain called A site ASL of tRNA-Proline CGG (unmodified).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	QY	8	Total	C	N	O	P	0	0	0
			174	77	33	56	8			
55	XY	8	Total	C	N	O	P	0	0	0
			174	77	33	56	8			

- Molecule 56 is a RNA chain called tRNA acceptor end mimic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	Z6	3	Total	C	N	O	P	0	0	0
			74	40	13	19	2			
56	Z8	3	Total	C	N	O	P	0	0	0
			74	40	13	19	2			

- Molecule 57 is PAROMOMYCIN (CCD ID: PAR) (formula: C₂₃H₄₅N₅O₁₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
57	QA	1	Total 42	C 23	N 5	O 14	0	0
57	XA	1	Total 42	C 23	N 5	O 14	0	0

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	QA	76	Total 76	Mg 76	0	0
58	QF	1	Total 1	Mg 1	0	0
58	QM	1	Total 1	Mg 1	0	0
58	RA	247	Total 247	Mg 247	0	0
58	RB	2	Total 2	Mg 2	0	0
58	RD	1	Total 1	Mg 1	0	0
58	RE	2	Total 2	Mg 2	0	0
58	RF	1	Total 1	Mg 1	0	0
58	RP	2	Total 2	Mg 2	0	0
58	R0	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	R5	1	Total 1	Mg 1	0	0
58	R8	2	Total 2	Mg 2	0	0
58	XA	82	Total 82	Mg 82	0	0
58	XB	1	Total 1	Mg 1	0	0
58	XM	1	Total 1	Mg 1	0	0
58	YA	265	Total 265	Mg 265	0	0
58	YB	3	Total 3	Mg 3	0	0
58	YD	2	Total 2	Mg 2	0	0
58	YP	2	Total 2	Mg 2	0	0
58	YQ	1	Total 1	Mg 1	0	0
58	YX	1	Total 1	Mg 1	0	0
58	Y0	1	Total 1	Mg 1	0	0
58	Y5	1	Total 1	Mg 1	0	0
58	QV	1	Total 1	Mg 1	0	0
58	XV	2	Total 2	Mg 2	0	0

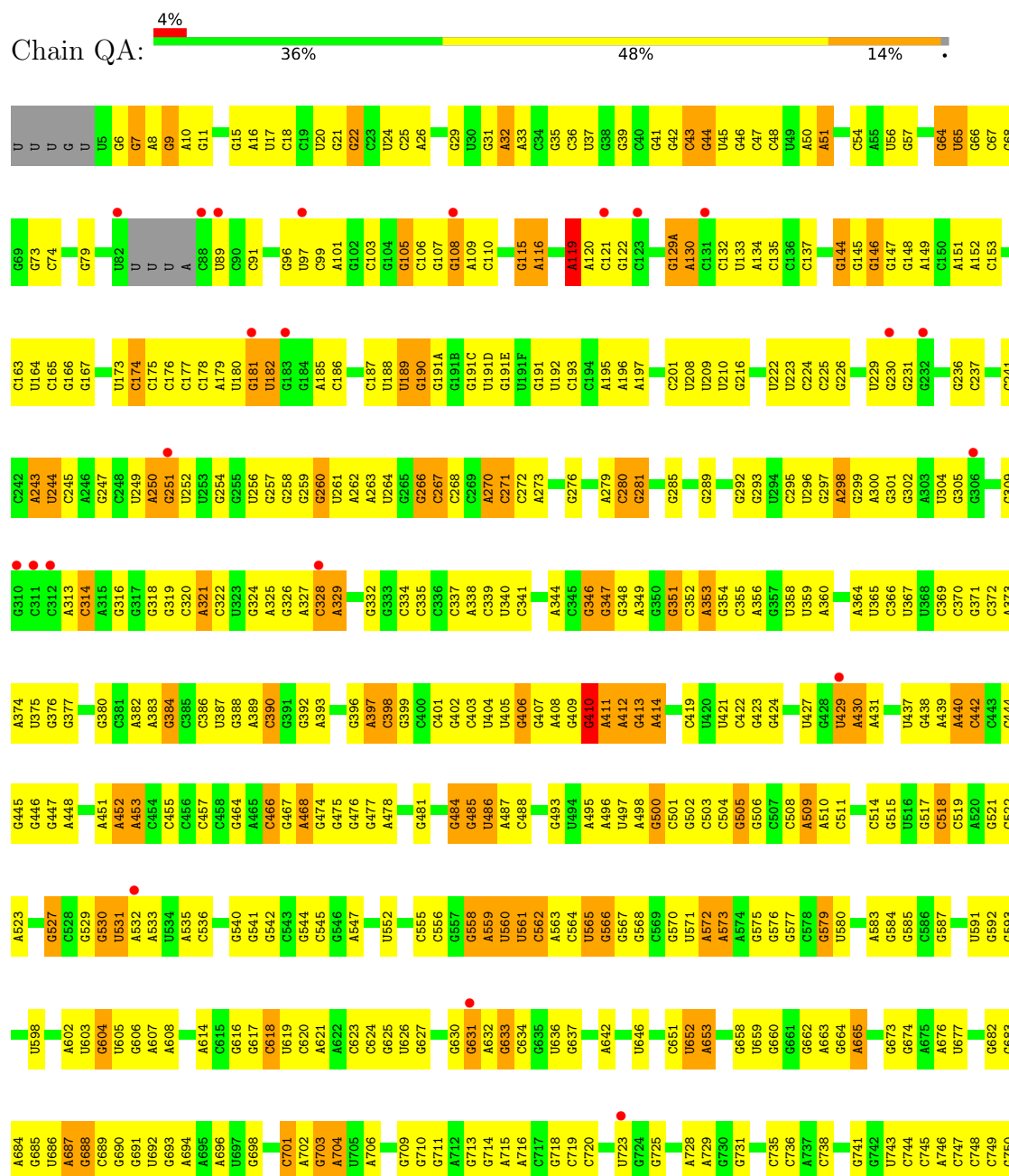
- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

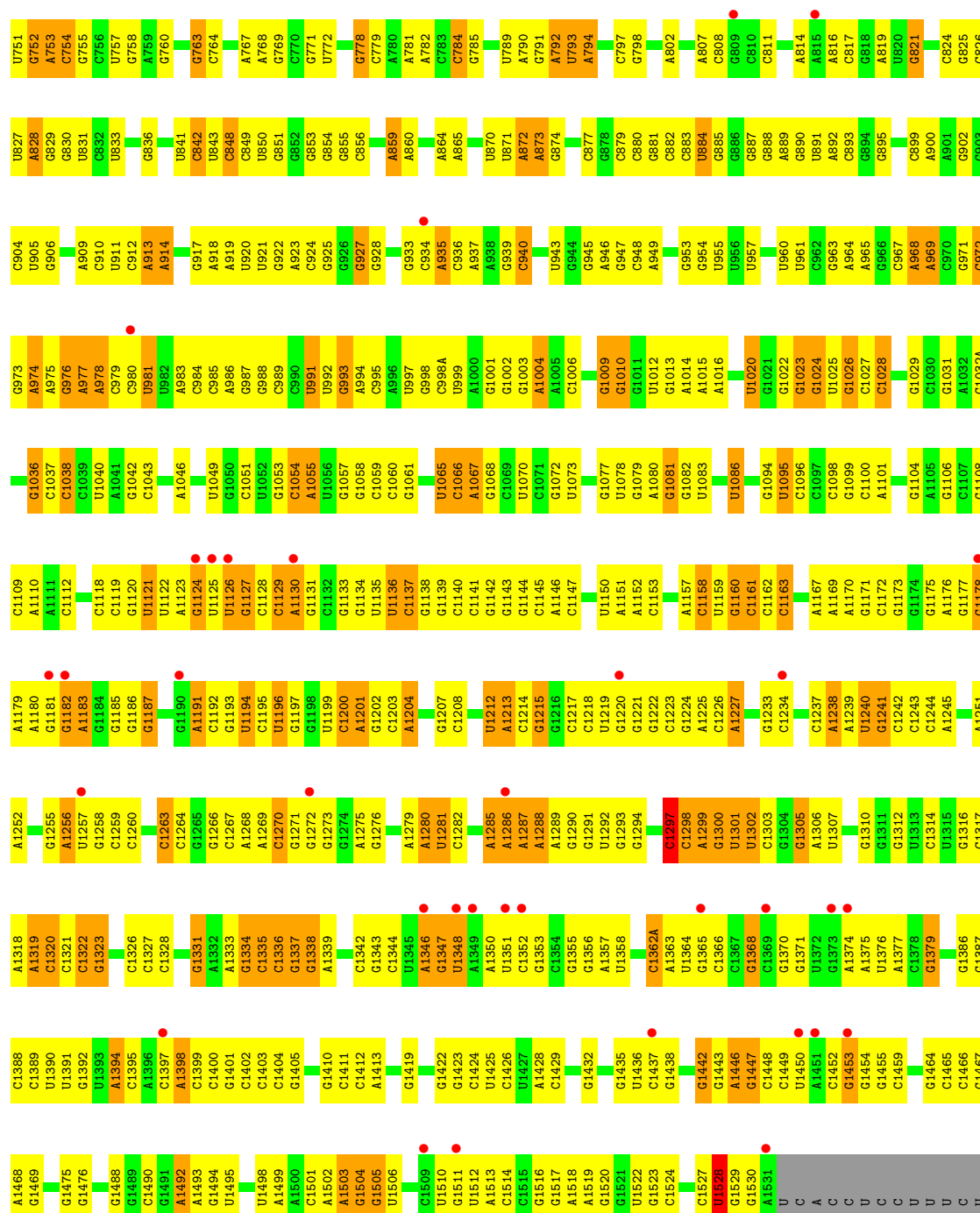
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	QD	1	Total 1	Zn 1	0	0
59	QN	1	Total 1	Zn 1	0	0
59	XD	1	Total 1	Zn 1	0	0
59	XN	1	Total 1	Zn 1	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

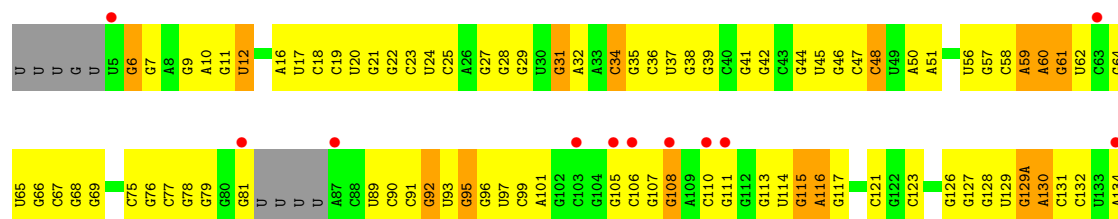
• Molecule 1: 16S rRNA

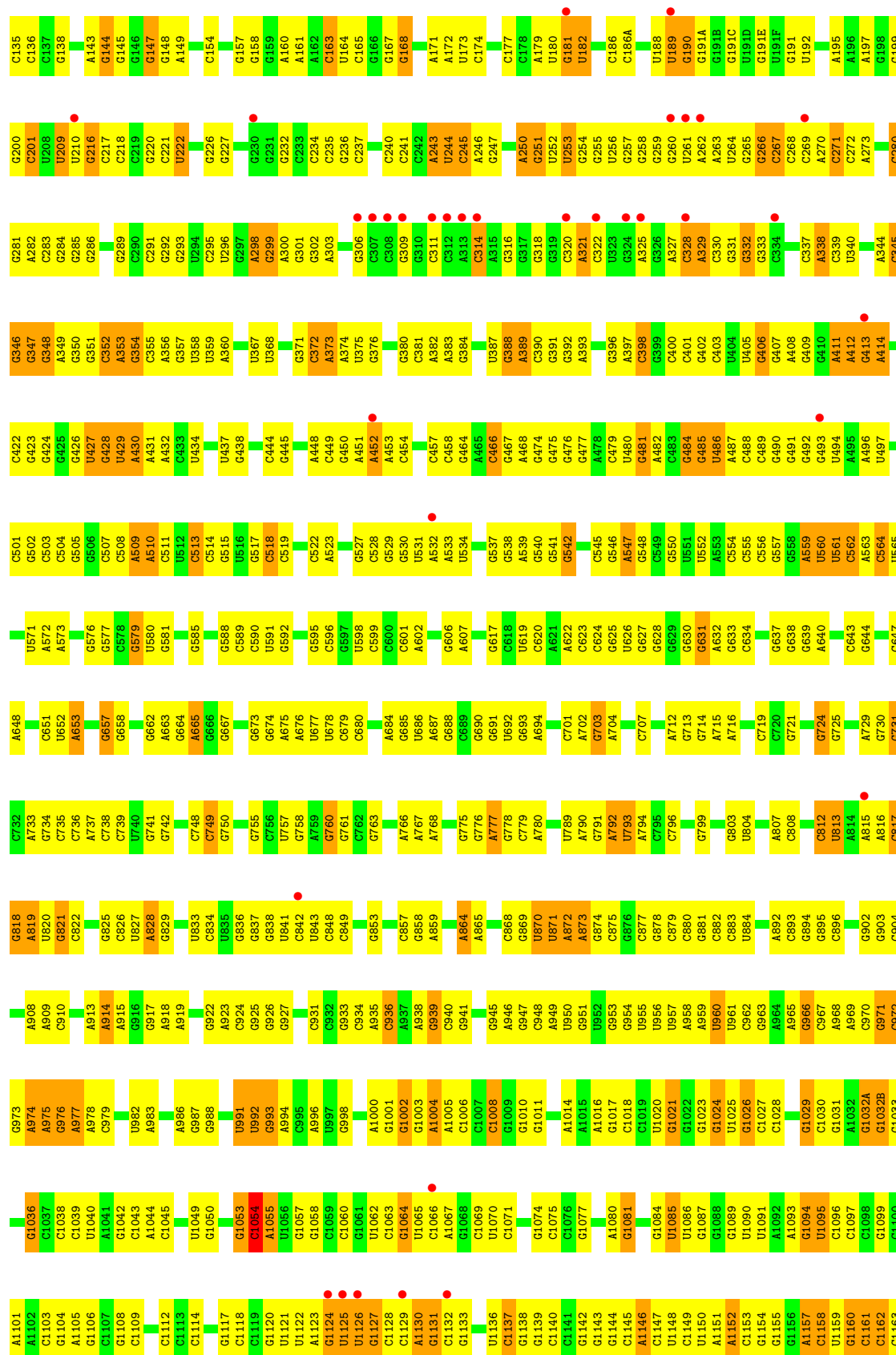


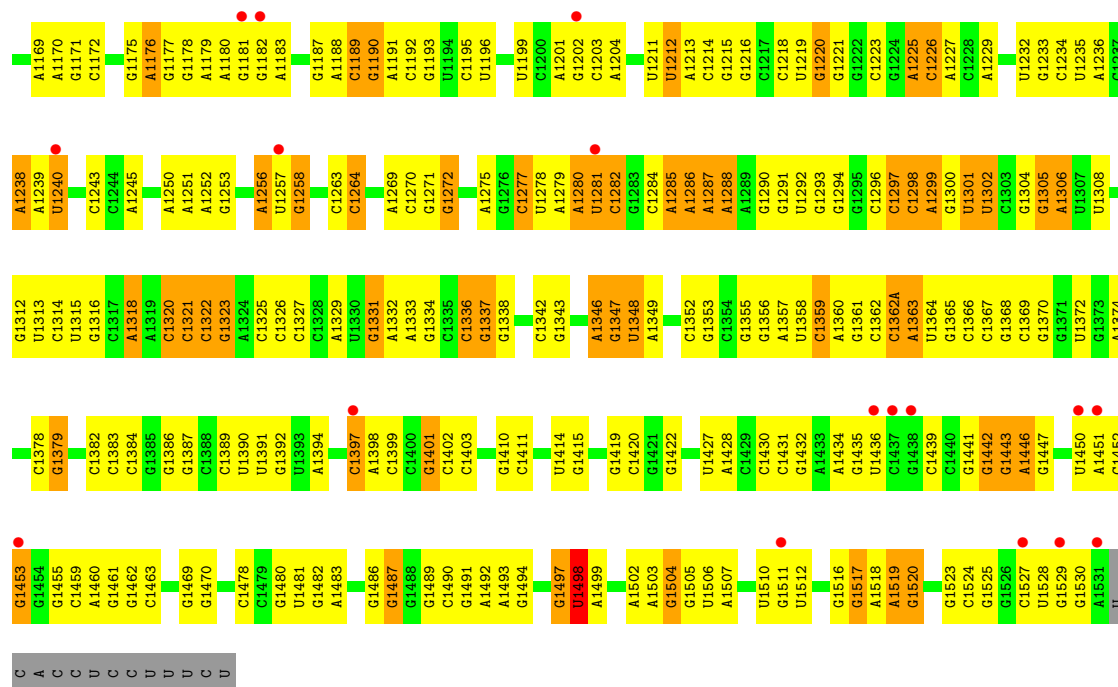


• Molecule 1: 16S rRNA

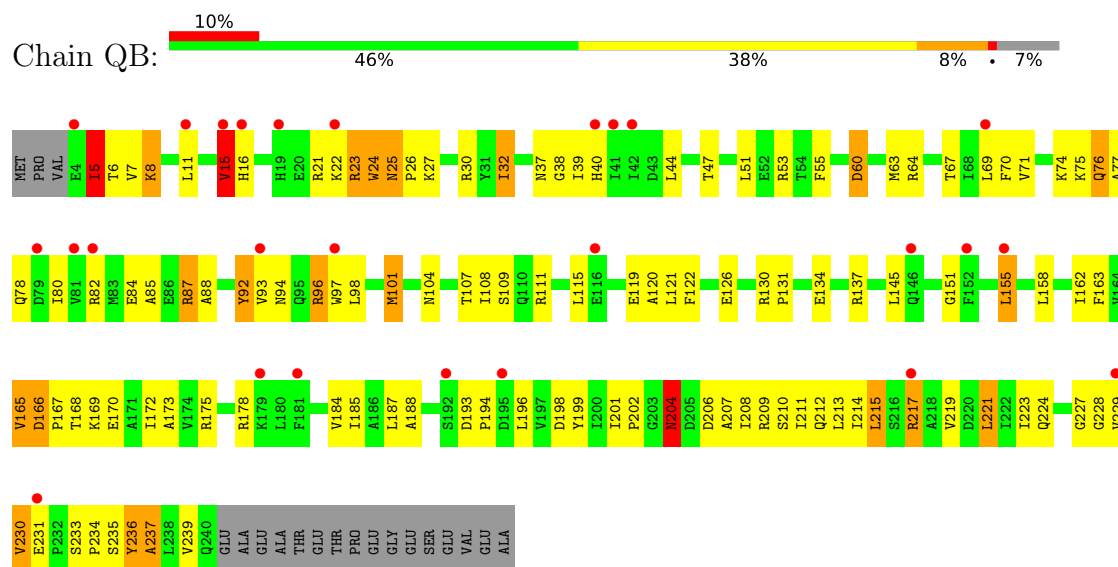
Chain XA: 4% 35% 50% 14%



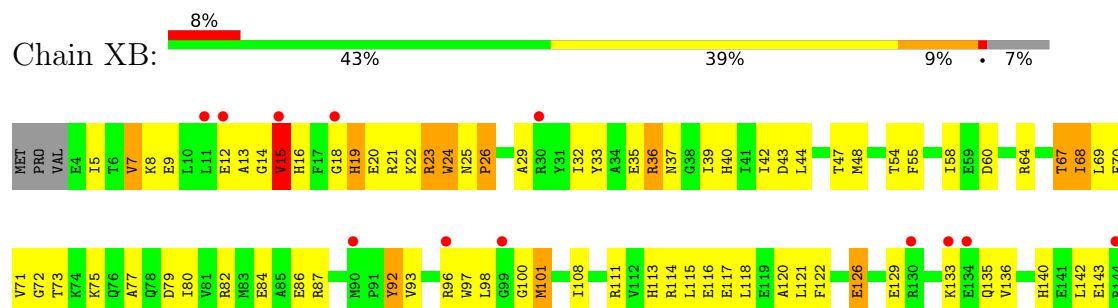


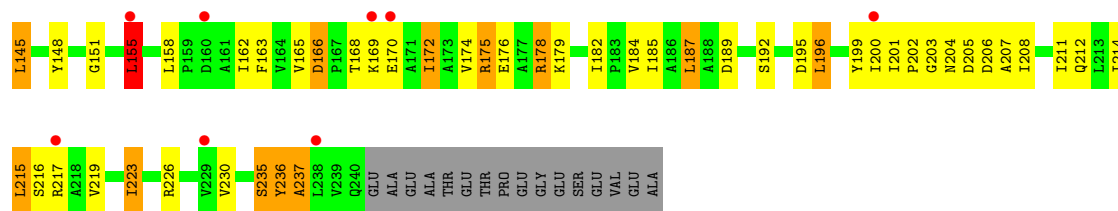


• Molecule 2: 30S ribosomal protein S2

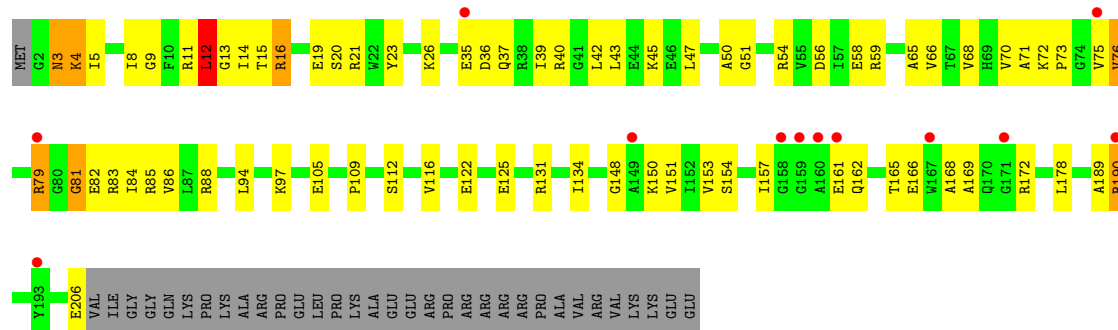


• Molecule 2: 30S ribosomal protein S2

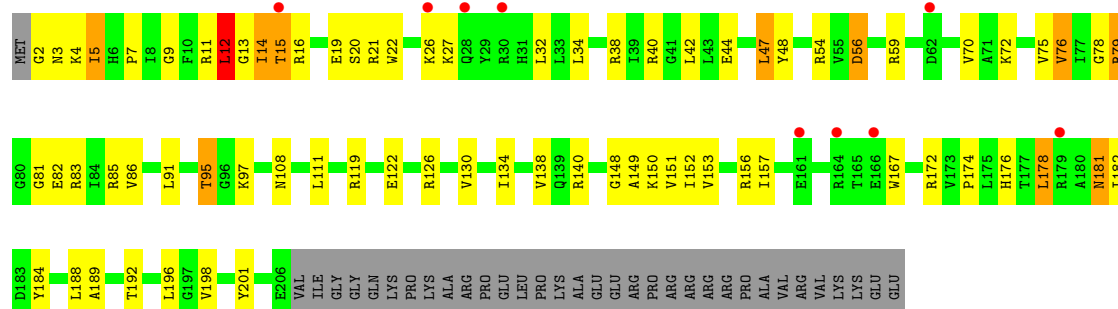




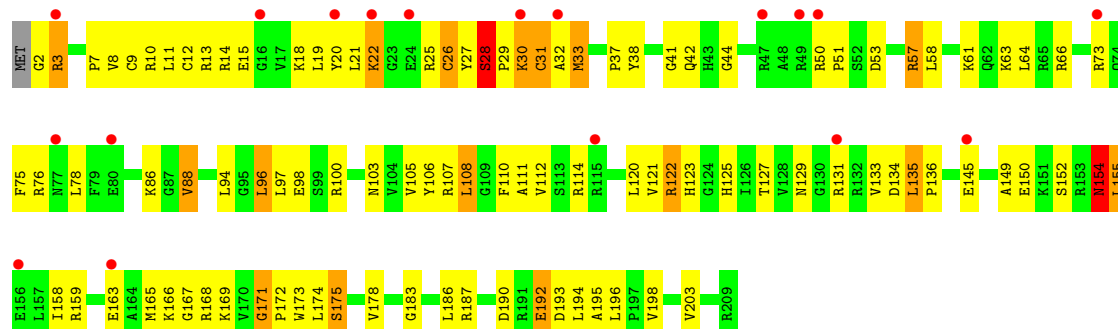
• Molecule 3: 30S ribosomal protein S3



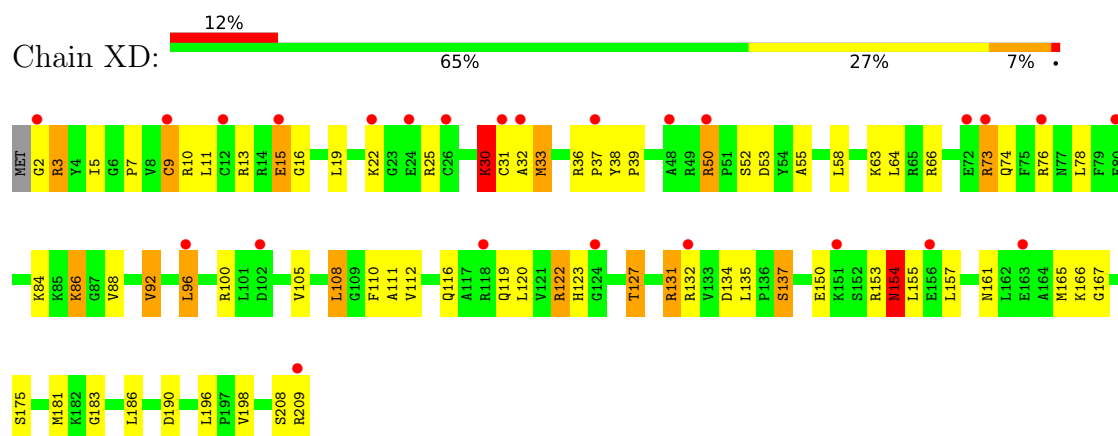
• Molecule 3: 30S ribosomal protein S3



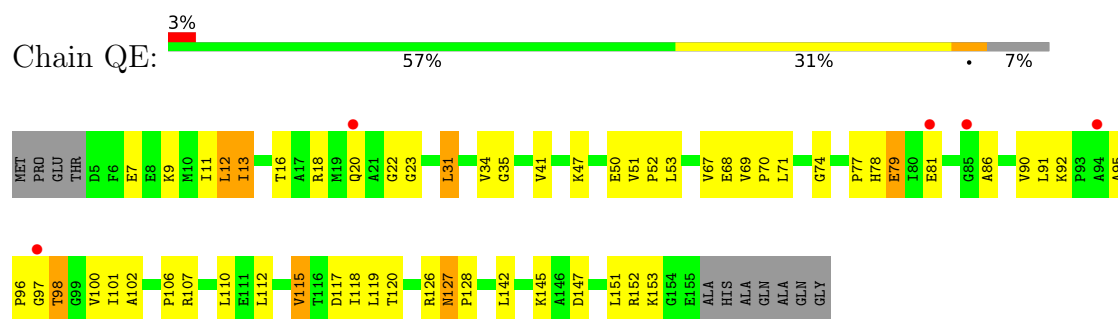
• Molecule 4: 30S ribosomal protein S4



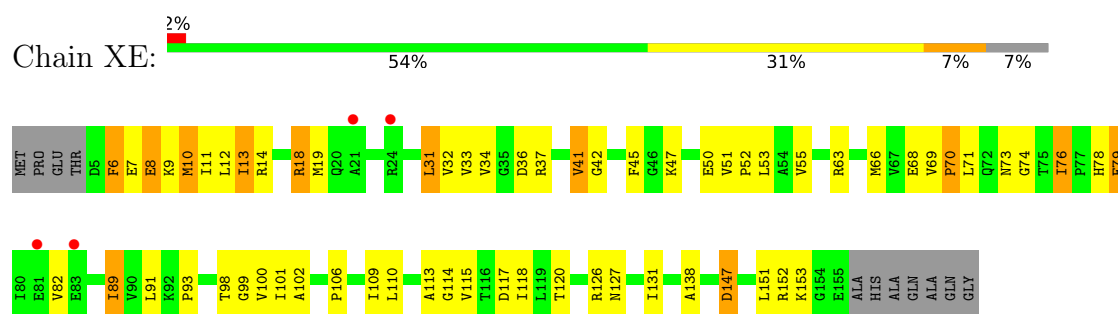
- Molecule 4: 30S ribosomal protein S4



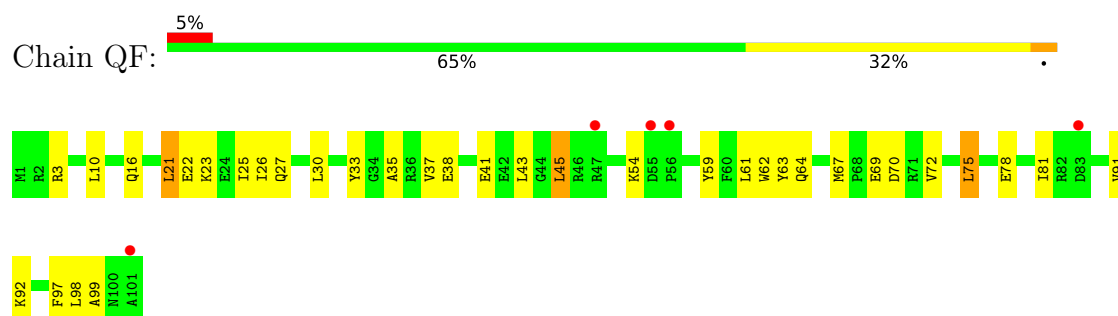
- Molecule 5: 30S ribosomal protein S5



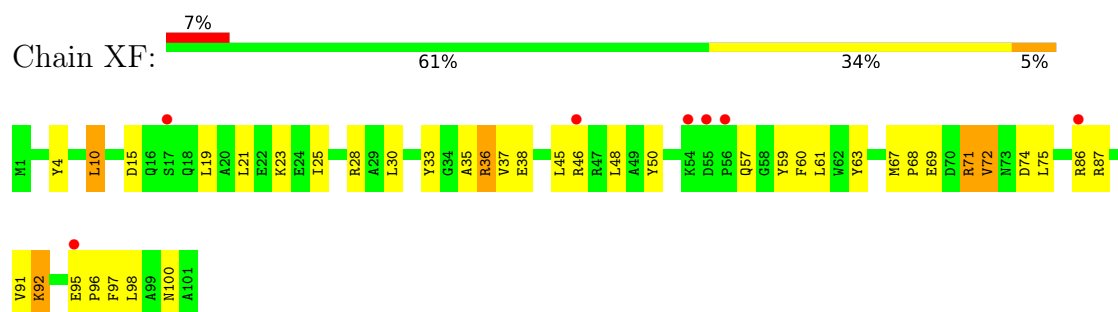
- Molecule 5: 30S ribosomal protein S5



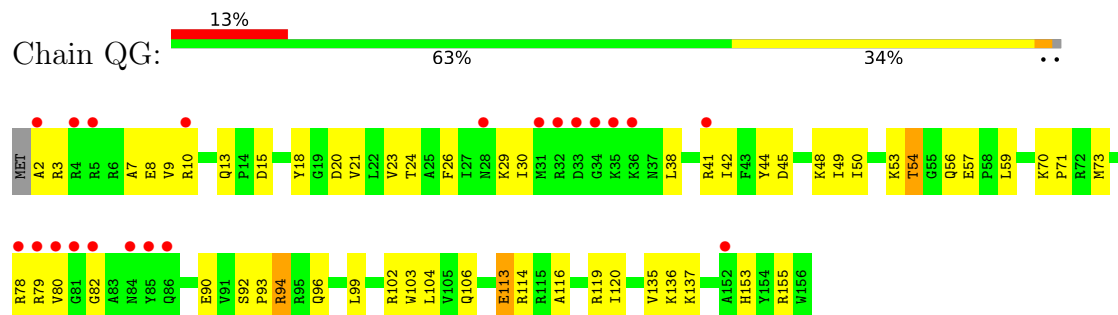
- Molecule 6: 30S ribosomal protein S6



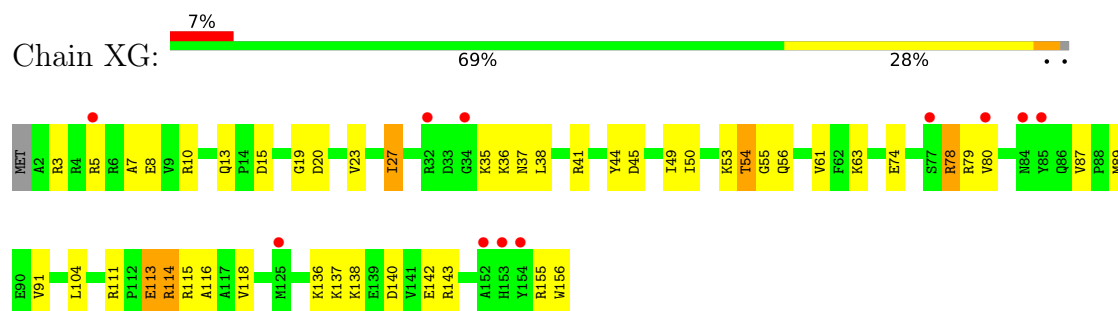
- Molecule 6: 30S ribosomal protein S6



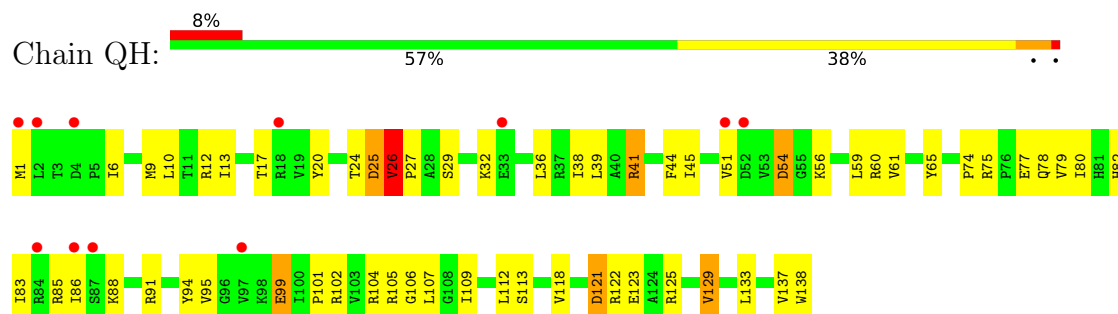
- Molecule 7: 30S ribosomal protein S7



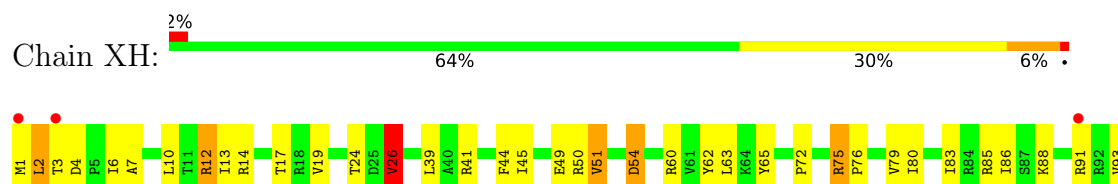
- Molecule 7: 30S ribosomal protein S7

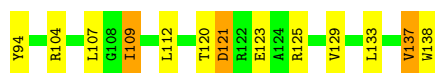


- Molecule 8: 30S ribosomal protein S8

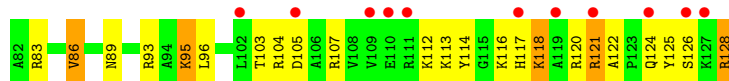
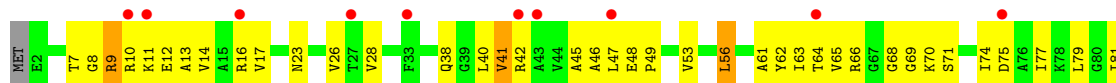


- Molecule 8: 30S ribosomal protein S8

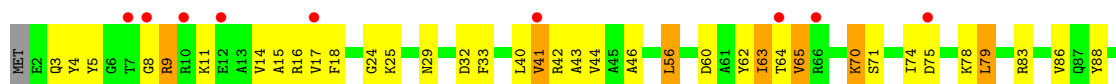




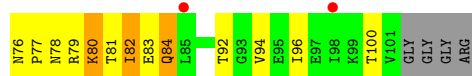
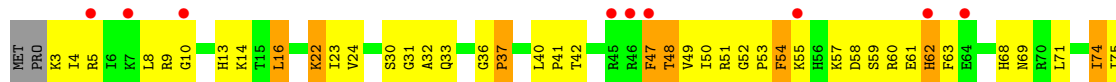
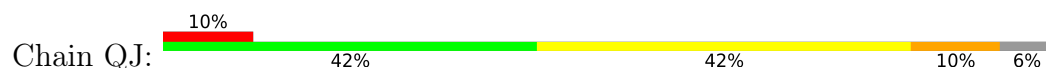
• Molecule 9: 30S ribosomal protein S9



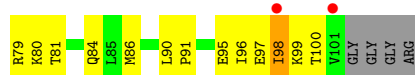
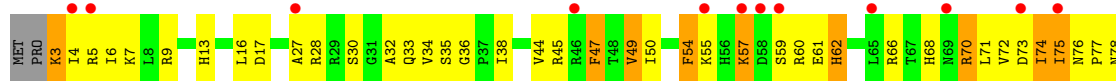
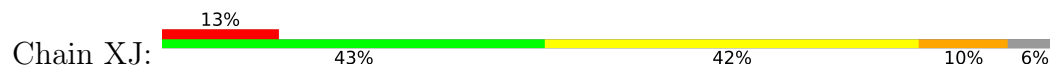
• Molecule 9: 30S ribosomal protein S9



• Molecule 10: 30S ribosomal protein S10

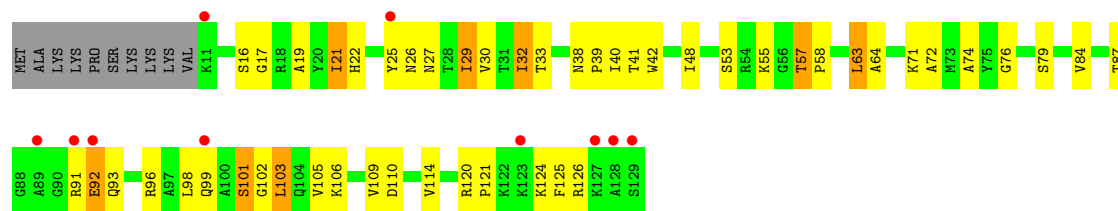


• Molecule 10: 30S ribosomal protein S10

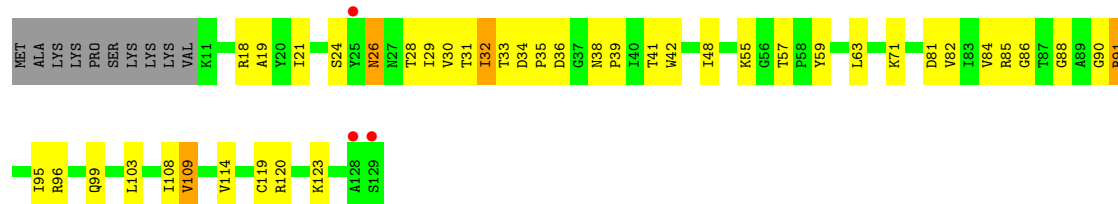


• Molecule 11: 30S ribosomal protein S11

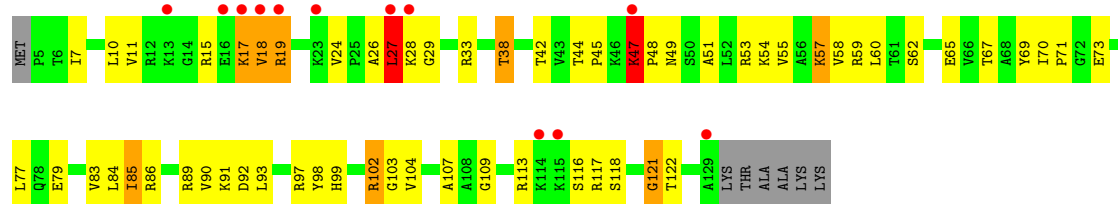




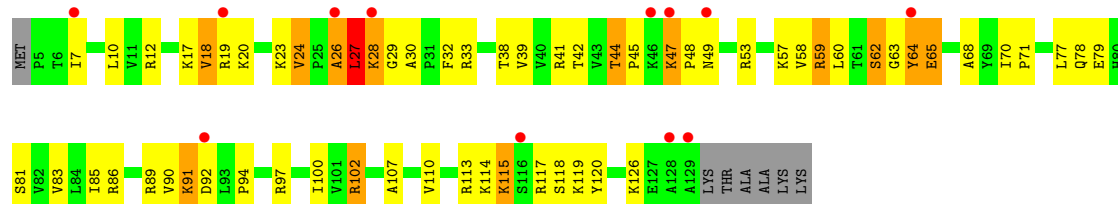
• Molecule 11: 30S ribosomal protein S11



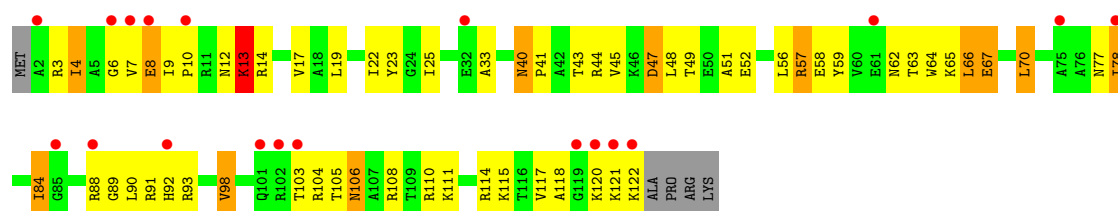
• Molecule 12: 30S ribosomal protein S12



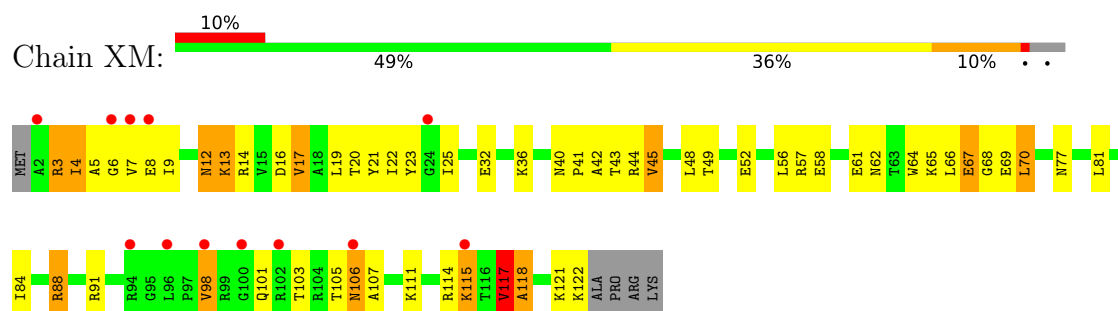
• Molecule 12: 30S ribosomal protein S12



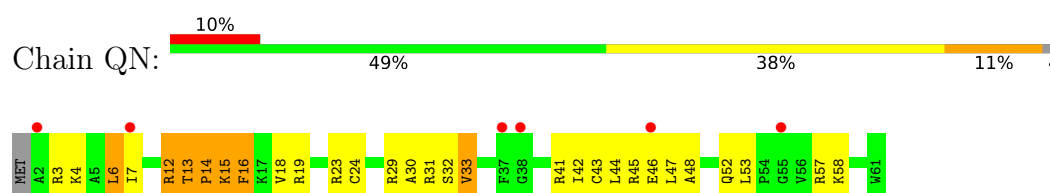
• Molecule 13: 30S ribosomal protein S13



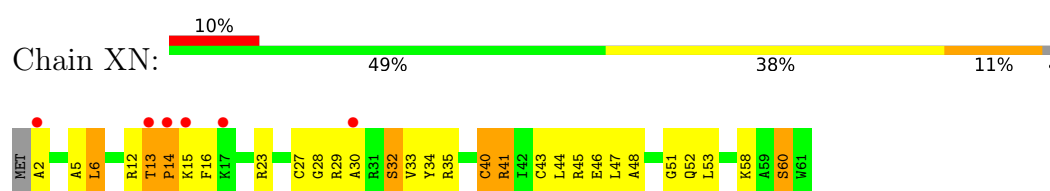
- Molecule 13: 30S ribosomal protein S13



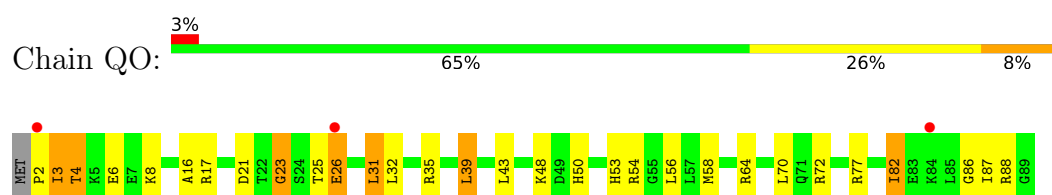
- Molecule 14: 30S ribosomal protein S14 type Z



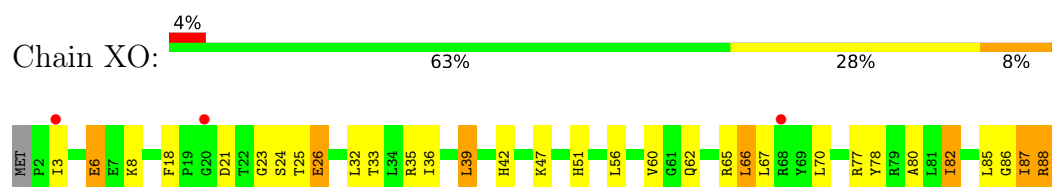
- Molecule 14: 30S ribosomal protein S14 type Z



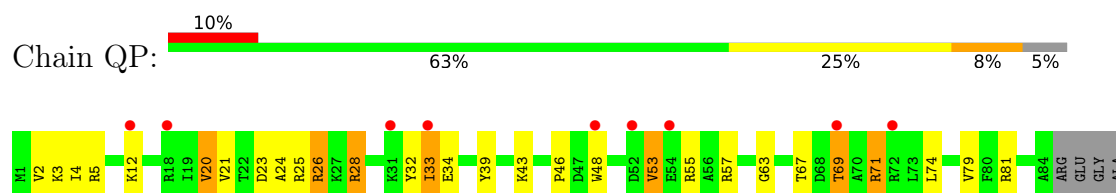
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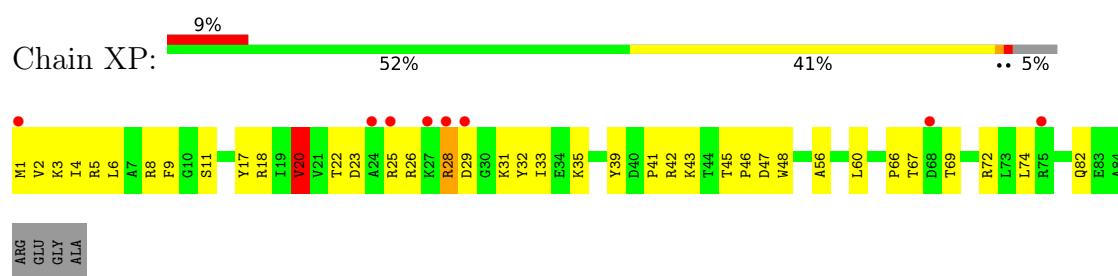
- Molecule 15: 30S ribosomal protein S15



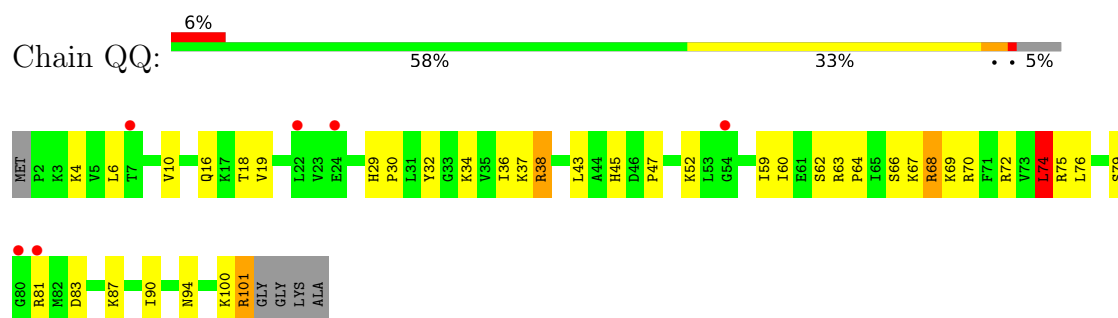
- Molecule 16: 30S ribosomal protein S16



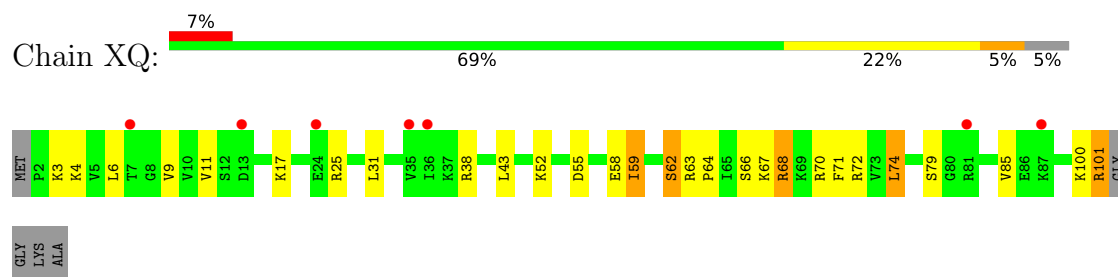
- Molecule 16: 30S ribosomal protein S16



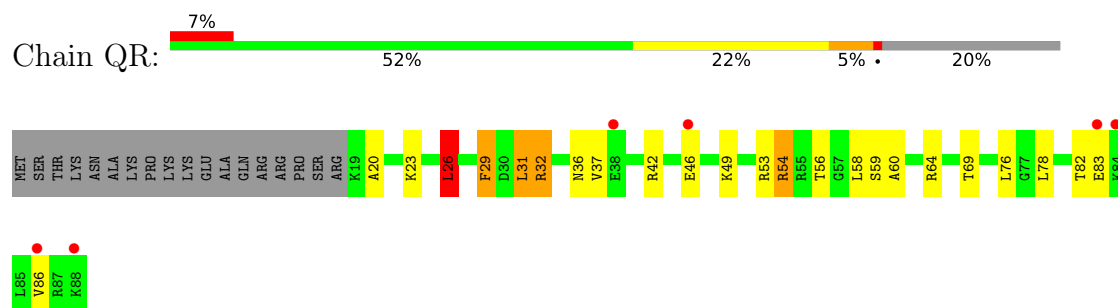
- Molecule 17: 30S ribosomal protein S17



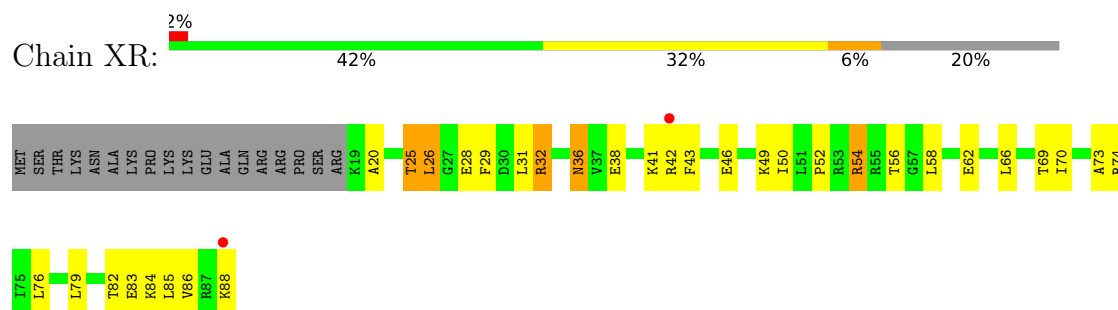
- Molecule 17: 30S ribosomal protein S17



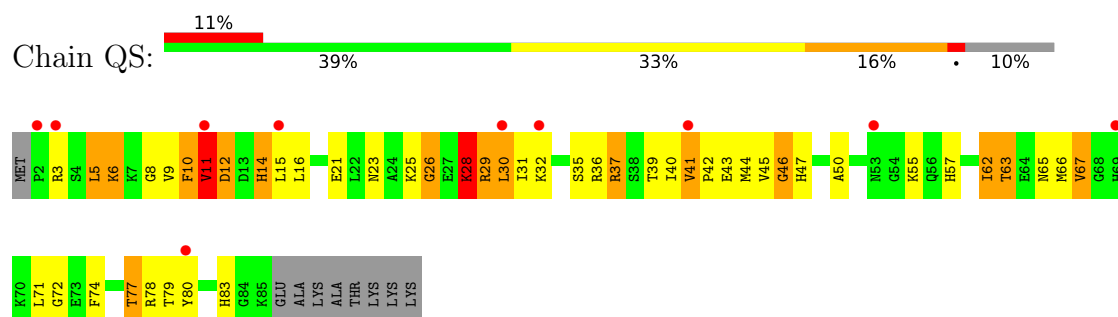
- Molecule 18: 30S ribosomal protein S18



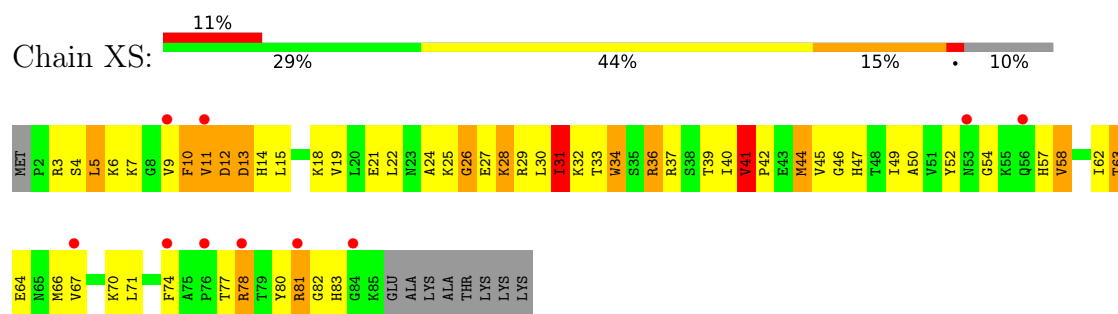
- Molecule 18: 30S ribosomal protein S18



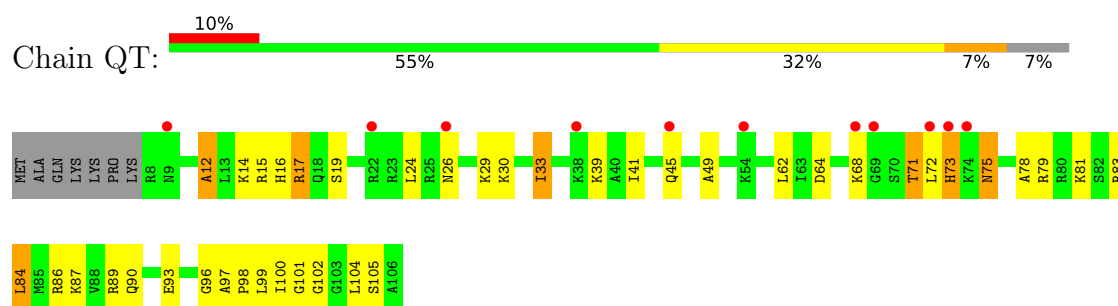
- Molecule 19: 30S ribosomal protein S19



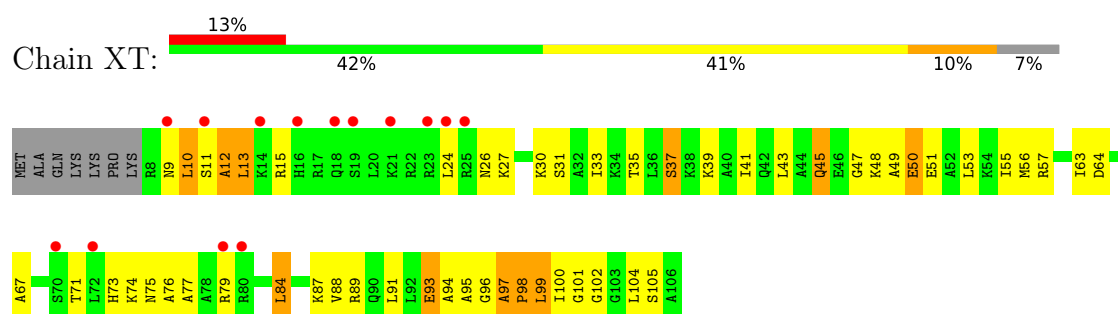
- Molecule 19: 30S ribosomal protein S19



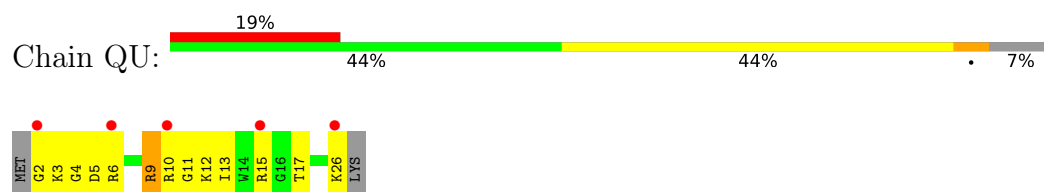
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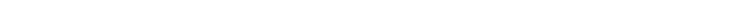


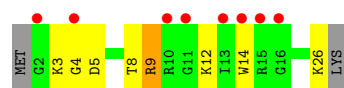
- Molecule 20: 30S ribosomal protein S20

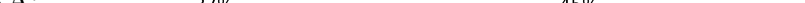


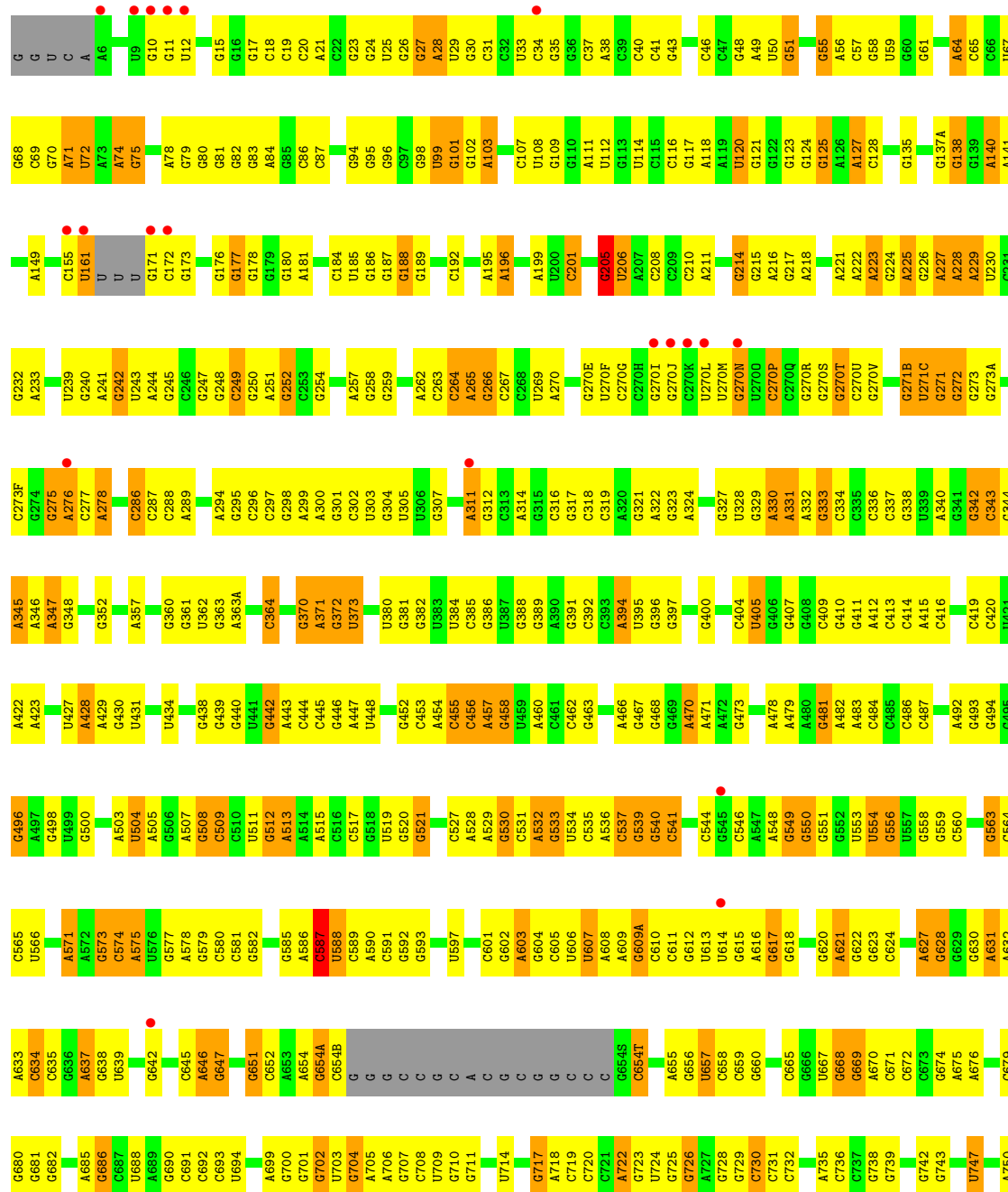
- Molecule 21: 30S ribosomal protein Thx



- Chain XU: 

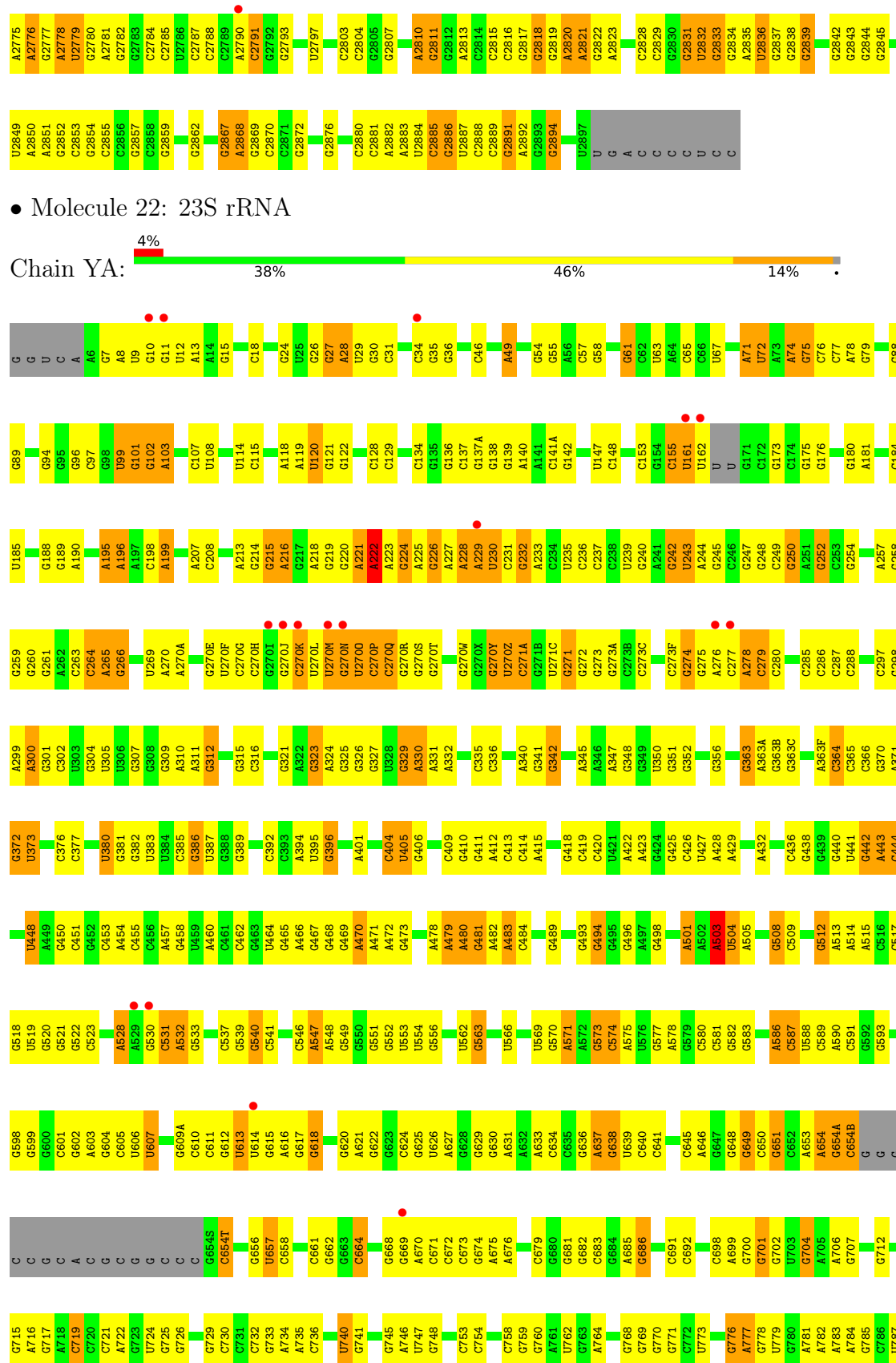


- Chain RA: 



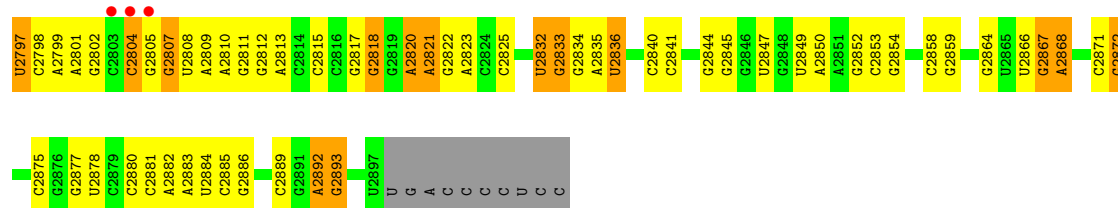


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A2711	U2562	A2488	A2411	A2327	A2247	G2103	G2029		G1855	A1784	U1688
U2712	U2563	G2489		A2328	G2248	G2104	G2030		A1856	A1785	A1689
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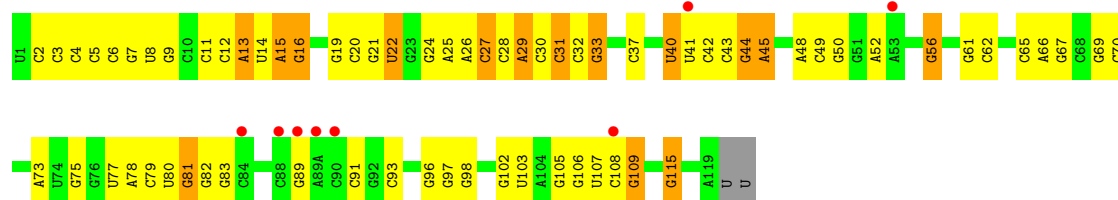


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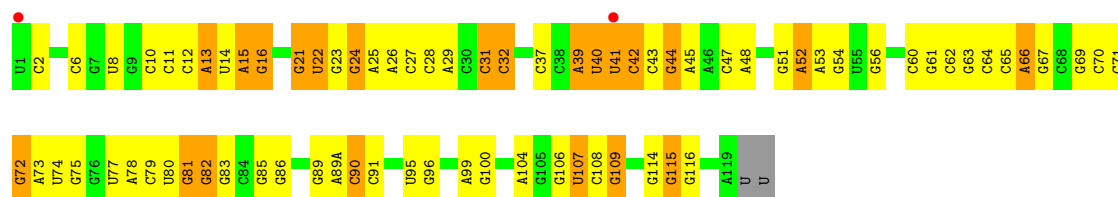
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G1763	U1834	G1933	U2099	C2163	G2242	A2311	G2379	U2449	G2526	G2599	C2666	G2735
G1764	G1835	G1934	C2104	C2165	U2244	C2313	C2380	A2451	C2527	A2602	C2667	
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A1829				G2156	G2234	G2370	C2443				G2729	
G1830	G1929	G2003	G2094	G2157	G2235	G2371	G2444				C2730	
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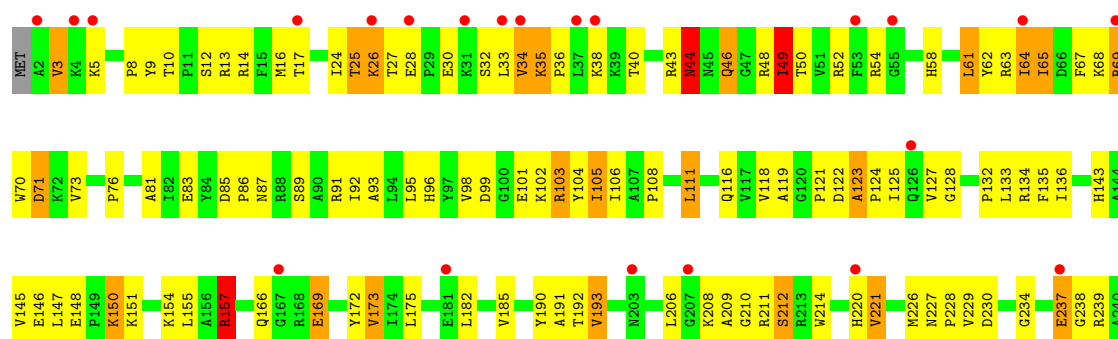
• Molecule 23: 5S rRNA



• Molecule 23: 5S rRNA

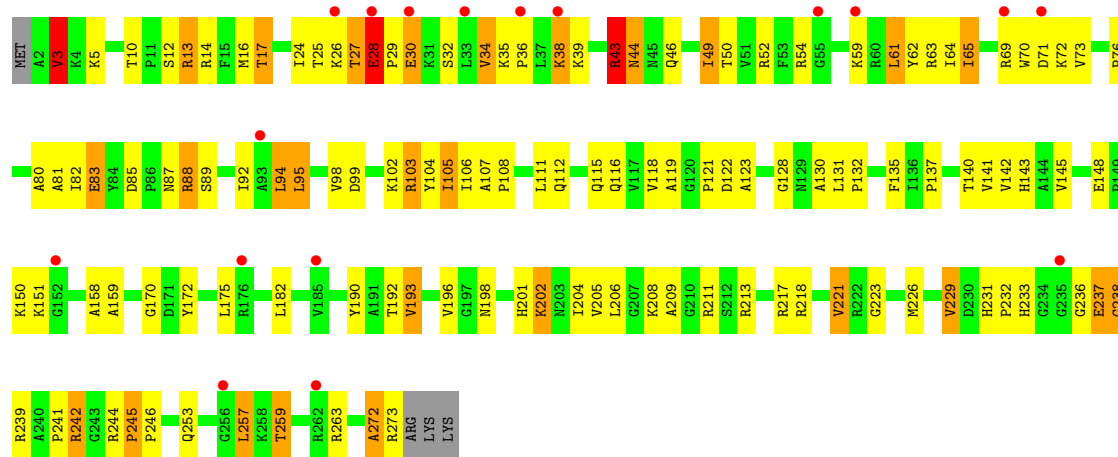


• Molecule 24: 50S ribosomal protein L2

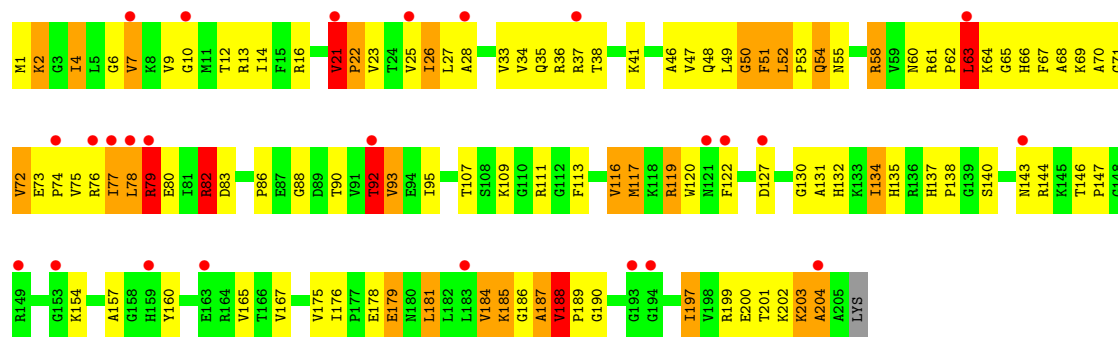


• Molecule 24: 50S ribosomal protein L2

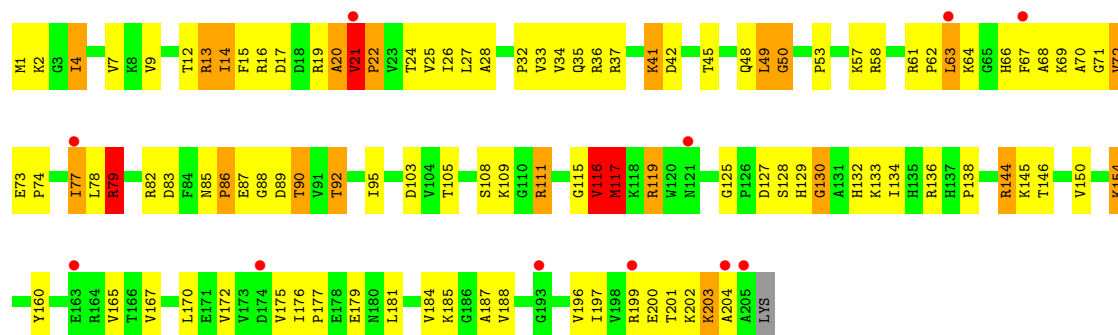




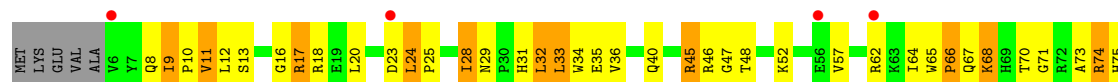
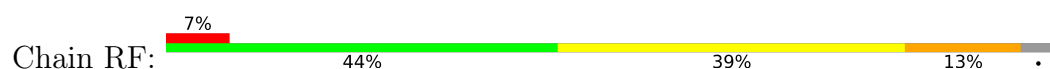
• Molecule 25: 50S ribosomal protein L3

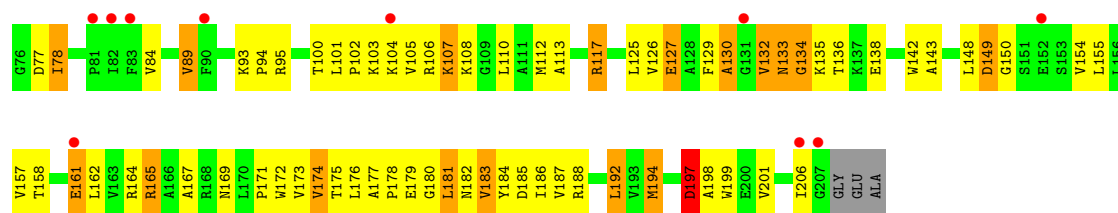


• Molecule 25: 50S ribosomal protein L3

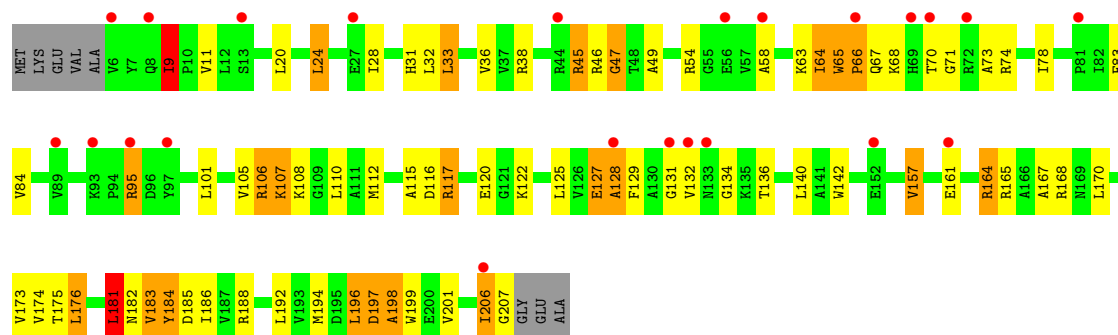


• Molecule 26: 50S ribosomal protein L4

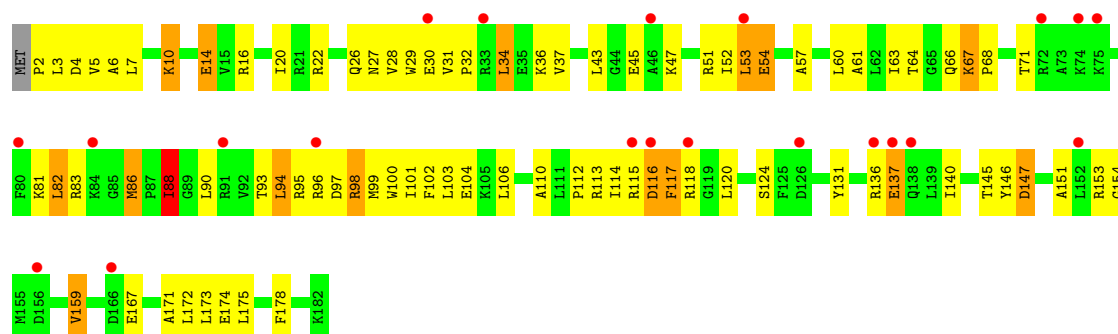




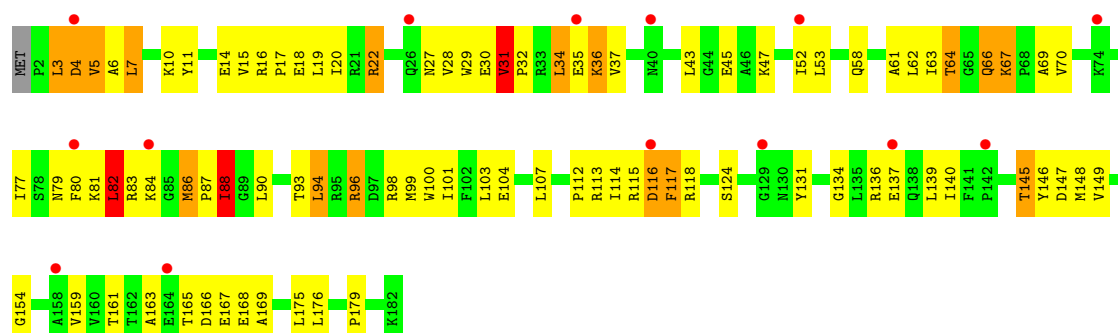
• Molecule 26: 50S ribosomal protein L4



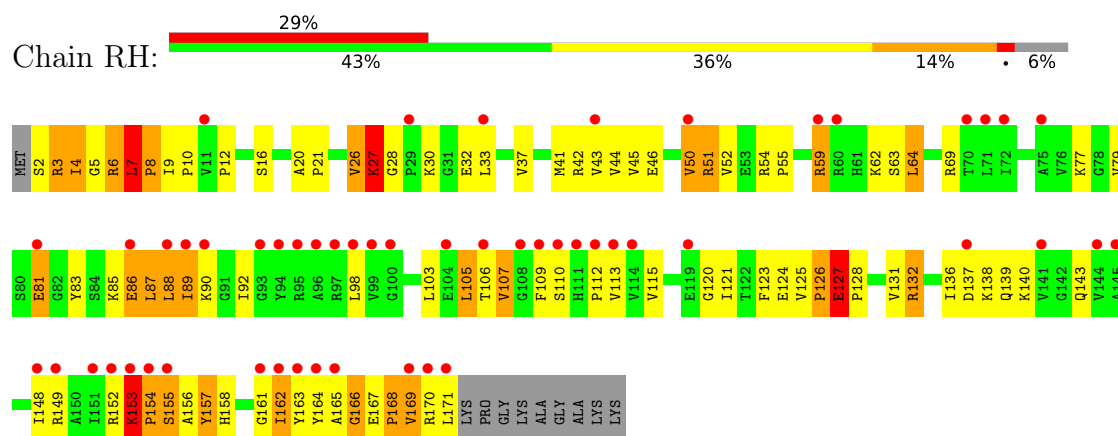
• Molecule 27: 50S ribosomal protein L5



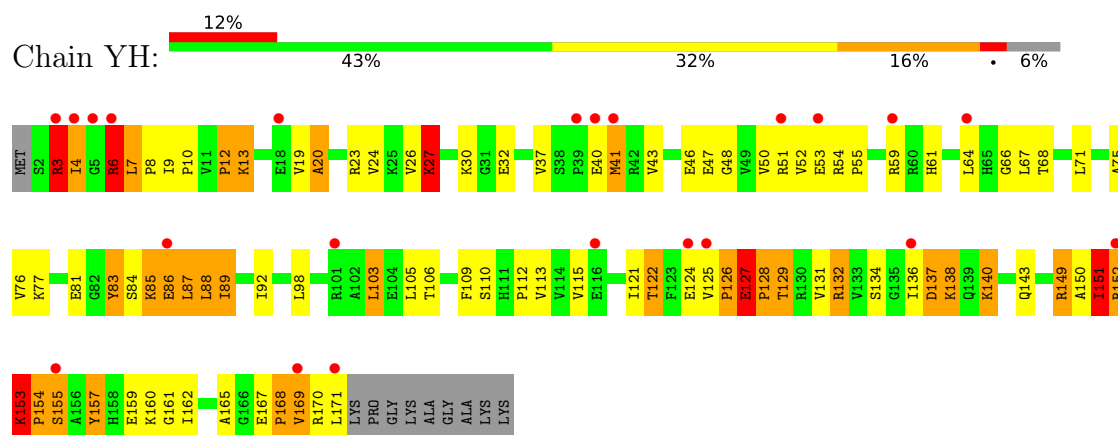
• Molecule 27: 50S ribosomal protein L5



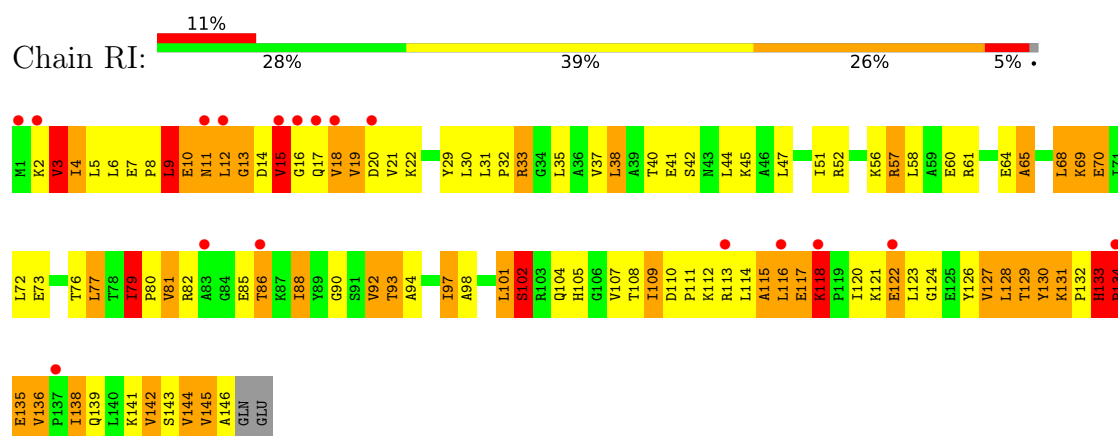
- Molecule 28: 50S ribosomal protein L6



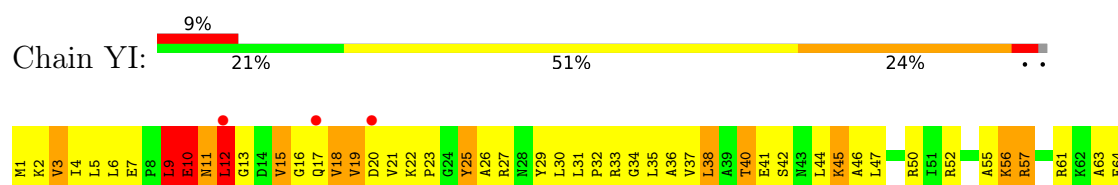
- Molecule 28: 50S ribosomal protein L6

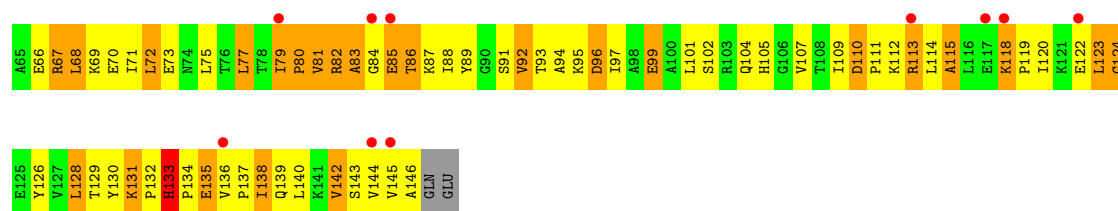


- Molecule 29: 50S ribosomal protein L9

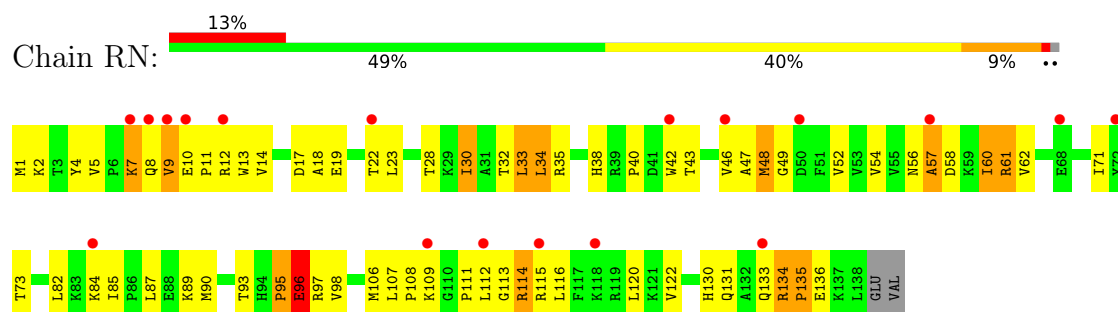


- Molecule 29: 50S ribosomal protein L9

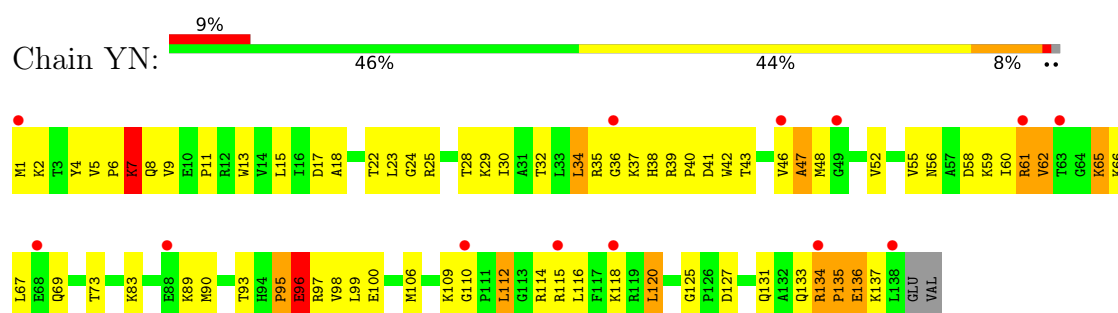




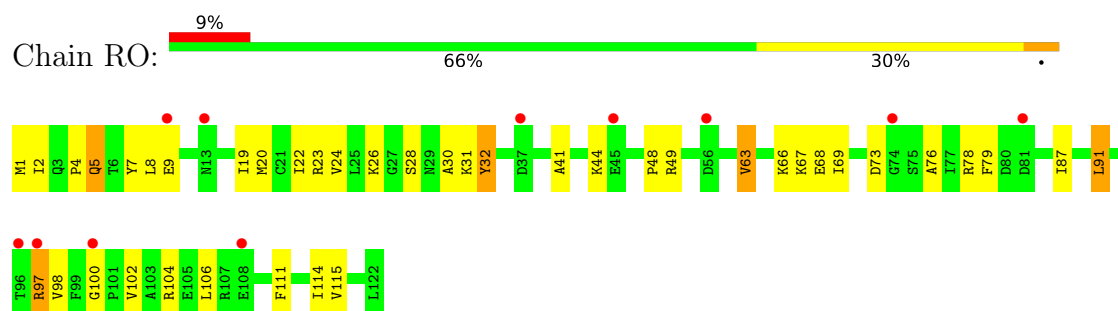
• Molecule 30: 50S ribosomal protein L13



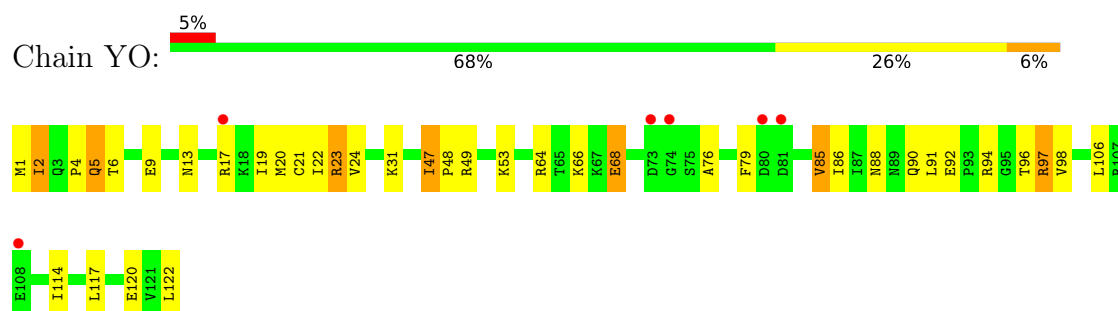
• Molecule 30: 50S ribosomal protein L13



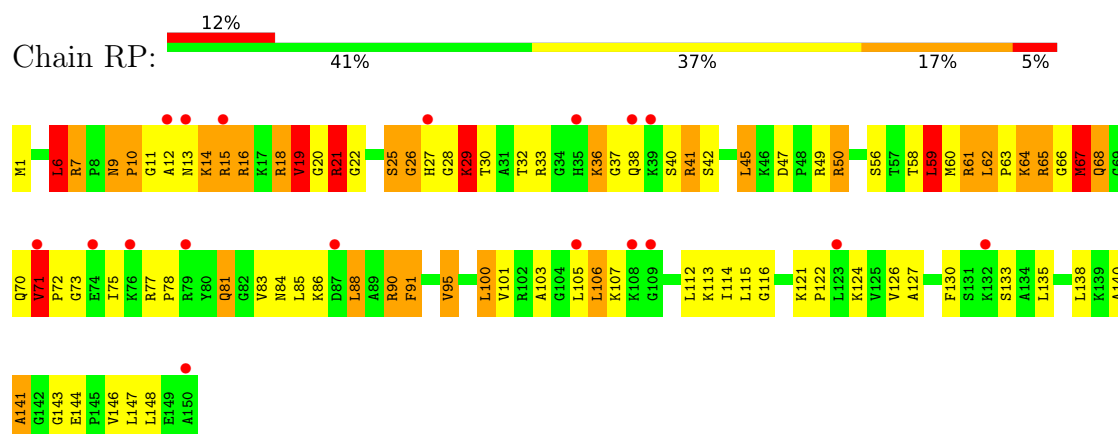
• Molecule 31: 50S ribosomal protein L14



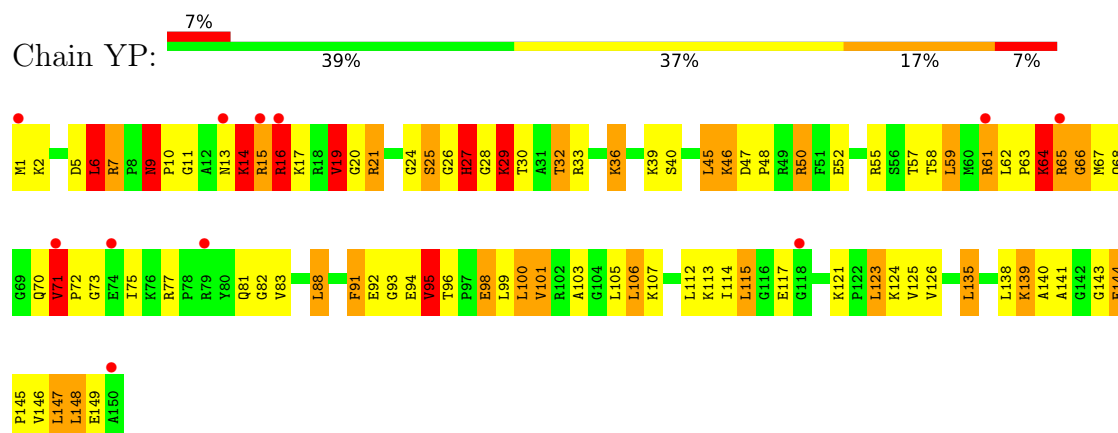
• Molecule 31: 50S ribosomal protein L14



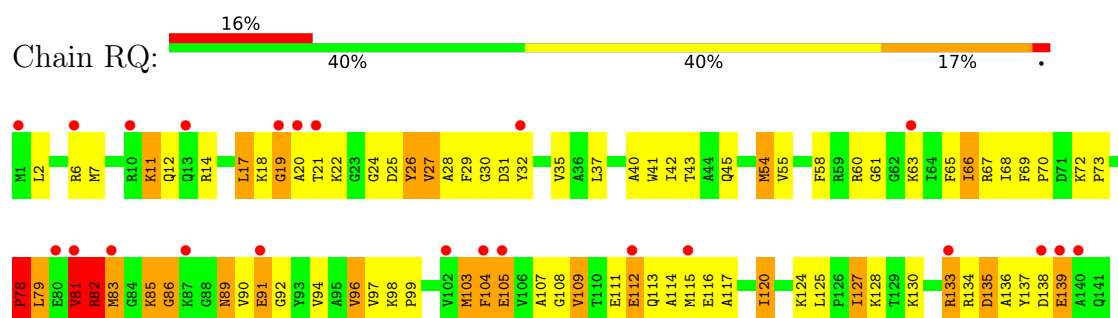
- Molecule 32: 50S ribosomal protein L15



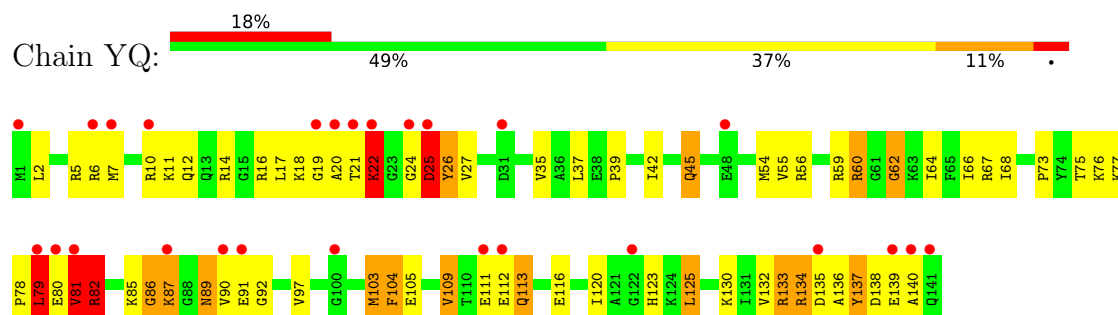
- Molecule 32: 50S ribosomal protein L15



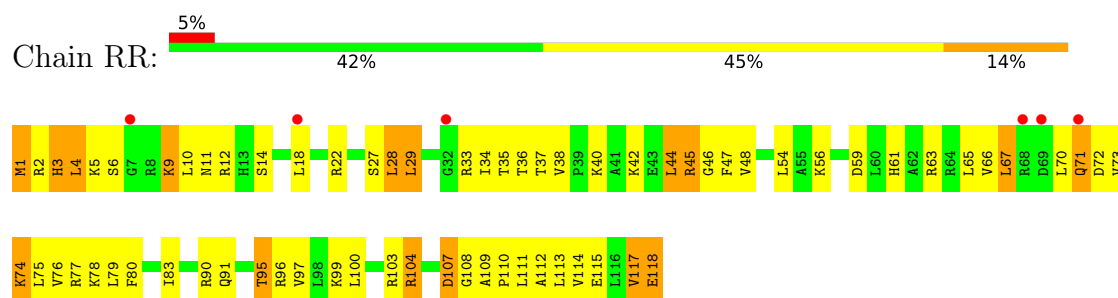
- Molecule 33: 50S ribosomal protein L16



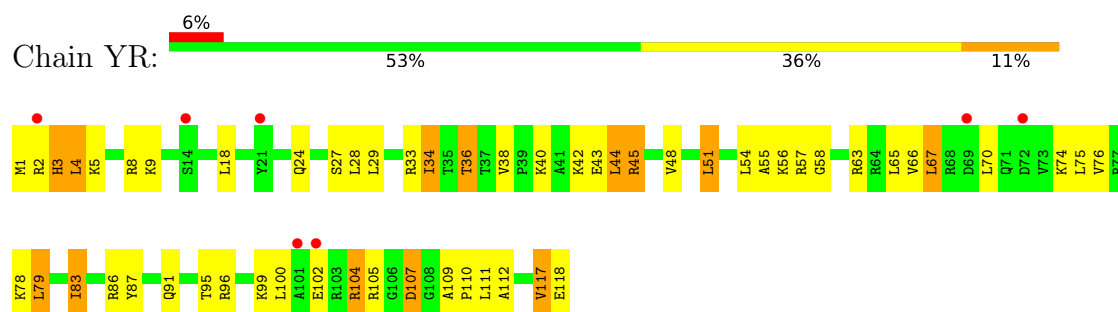
- Molecule 33: 50S ribosomal protein L16



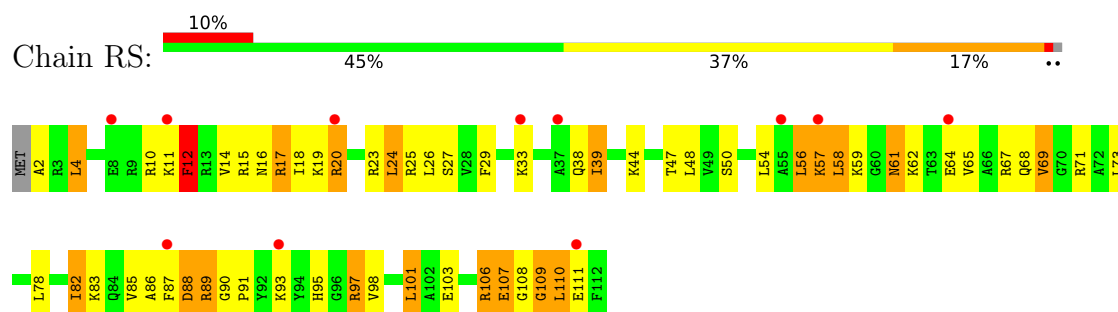
- Molecule 34: 50S ribosomal protein L17



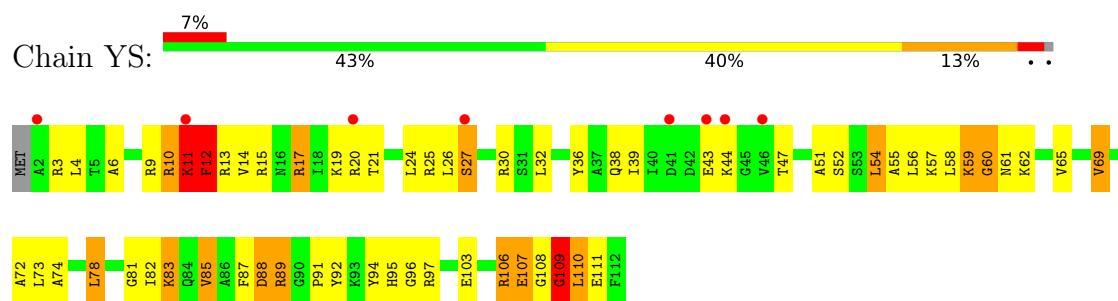
- Molecule 34: 50S ribosomal protein L17



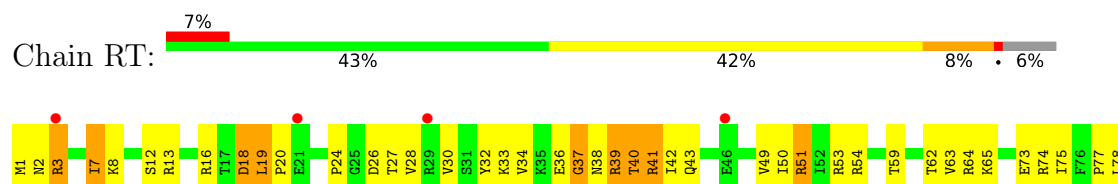
- Molecule 35: 50S ribosomal protein L18

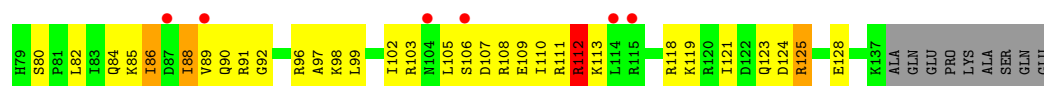


- Molecule 35: 50S ribosomal protein L18

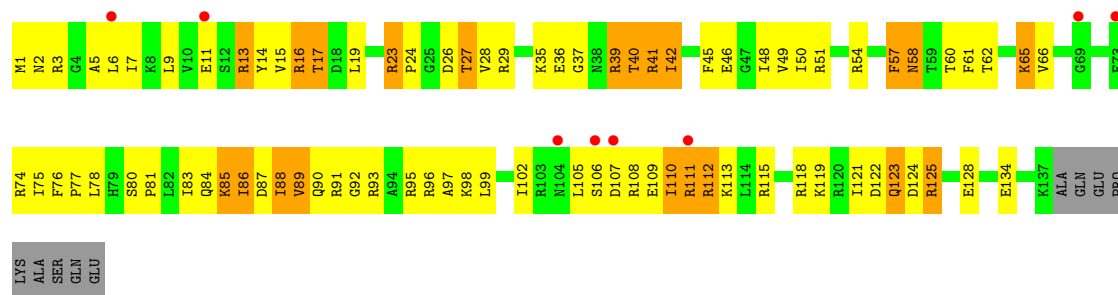


- Molecule 36: 50S ribosomal protein L19

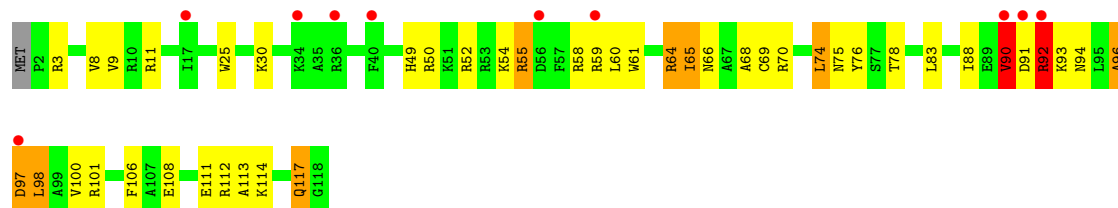




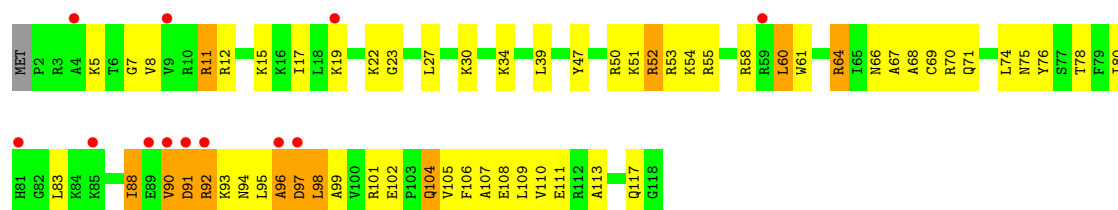
• Molecule 36: 50S ribosomal protein L19



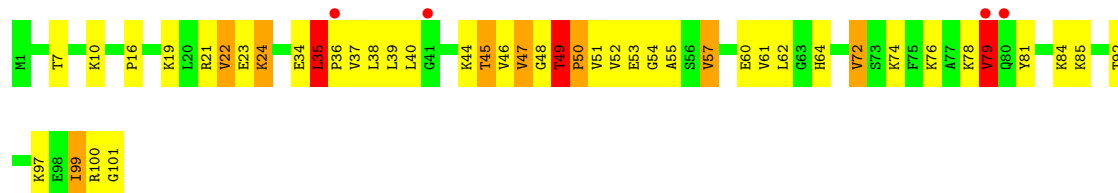
• Molecule 37: 50S ribosomal protein L20



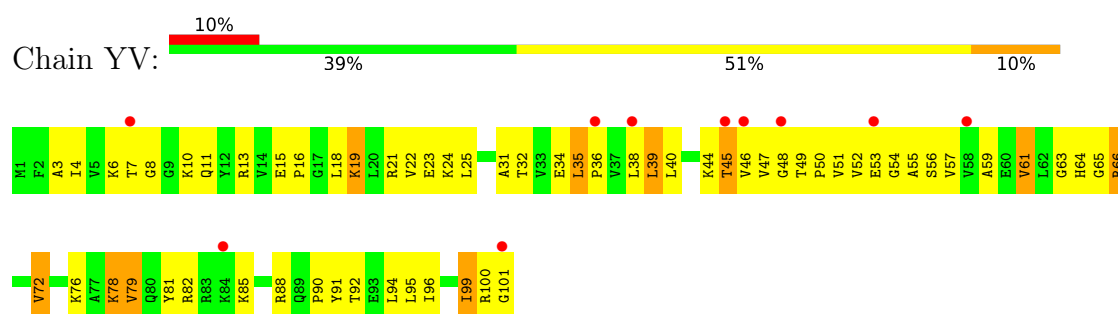
• Molecule 37: 50S ribosomal protein L20



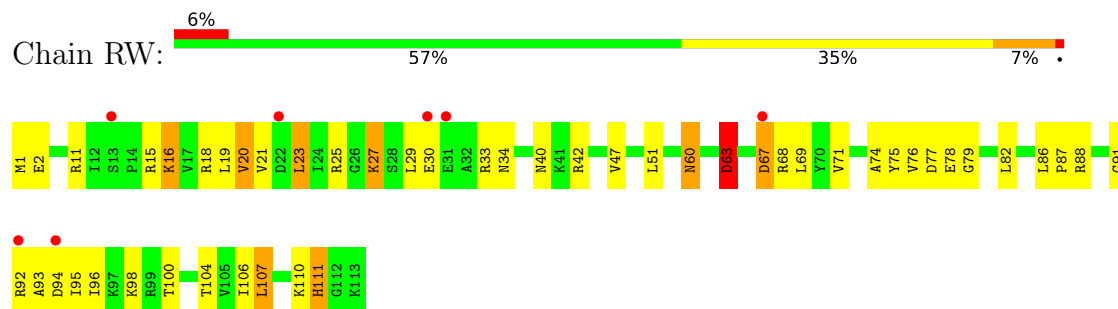
• Molecule 38: 50S ribosomal protein L21



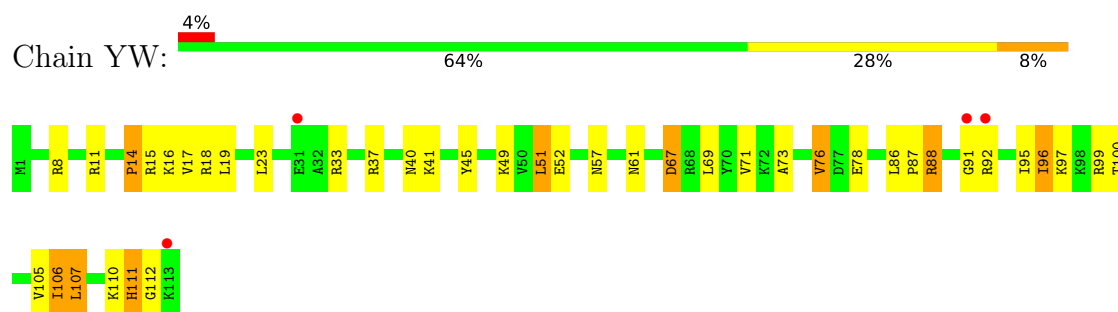
• Molecule 38: 50S ribosomal protein L21



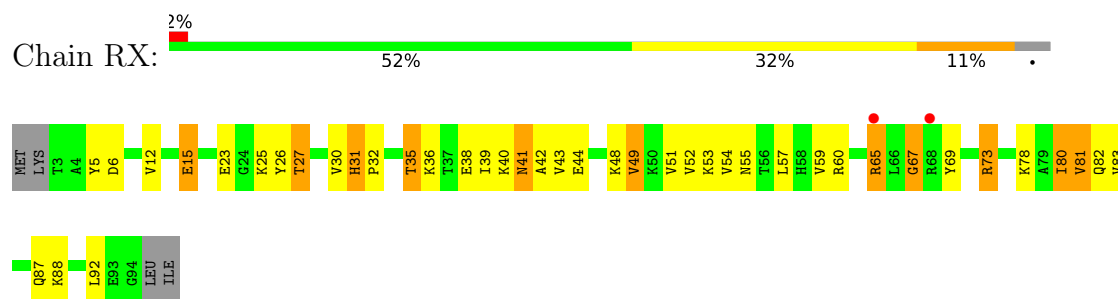
- Molecule 39: 50S ribosomal protein L22



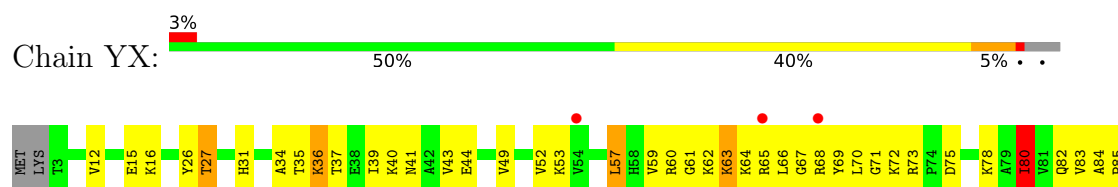
- Molecule 39: 50S ribosomal protein L22

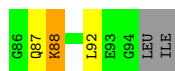


- Molecule 40: 50S ribosomal protein L23

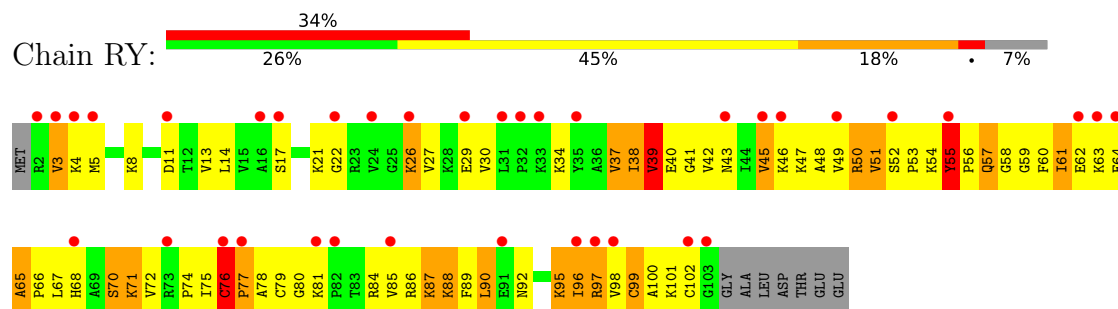


- Molecule 40: 50S ribosomal protein L23

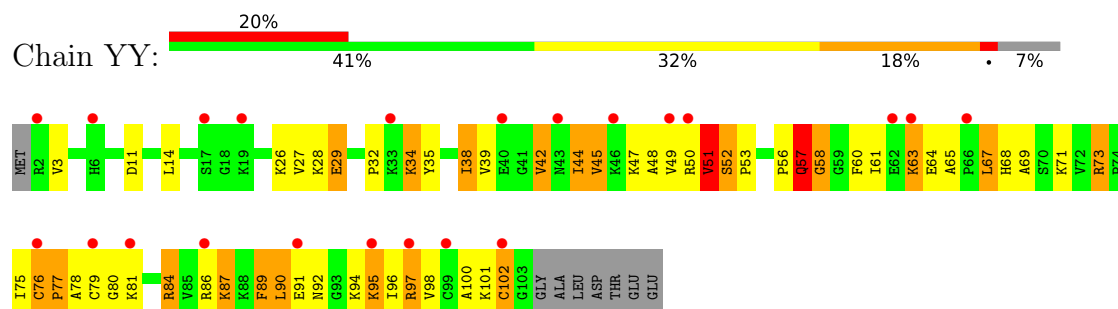




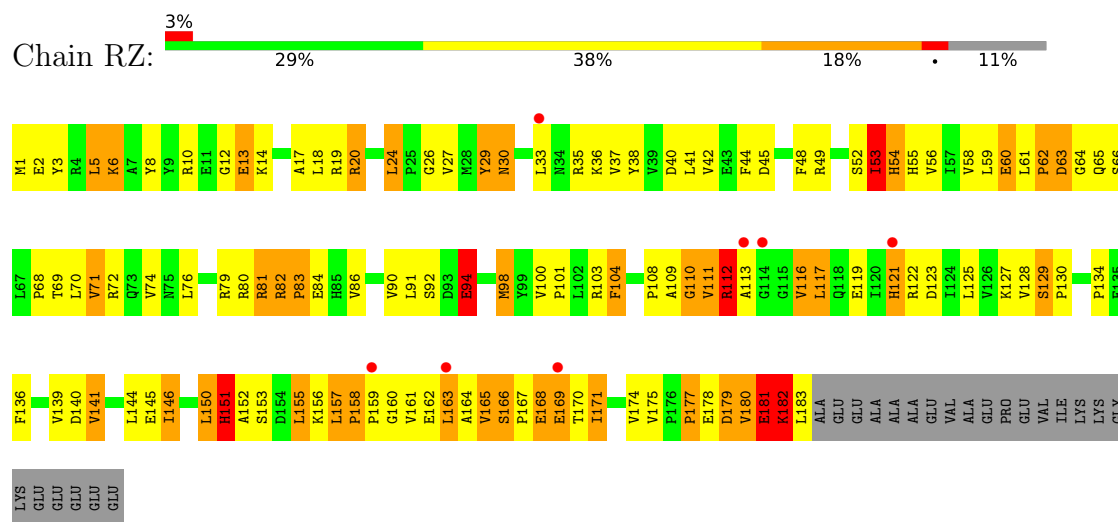
• Molecule 41: 50S ribosomal protein L24



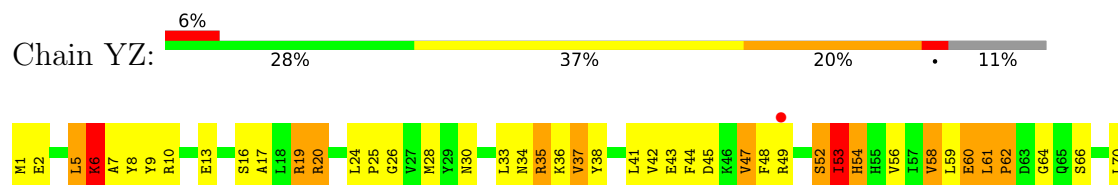
• Molecule 41: 50S ribosomal protein L24



• Molecule 42: 50S ribosomal protein L25



• Molecule 42: 50S ribosomal protein L25

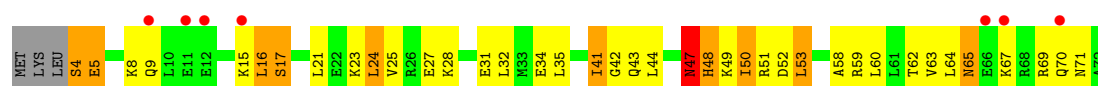
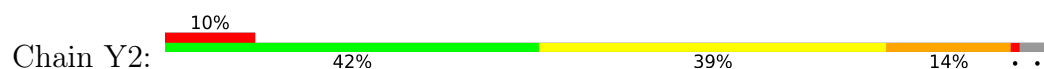




- Molecule 45: 50S ribosomal protein L29



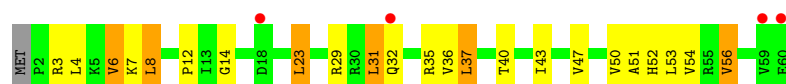
- Molecule 45: 50S ribosomal protein L29



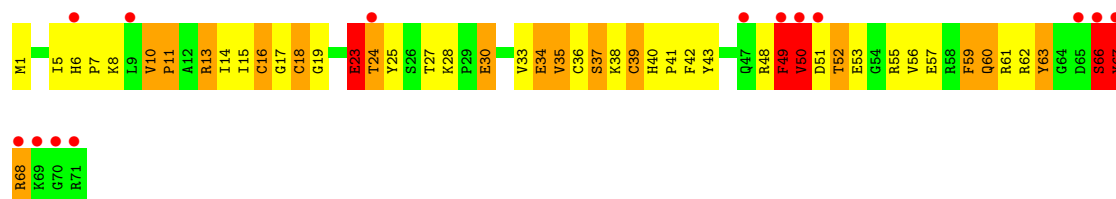
- Molecule 46: 50S ribosomal protein L30



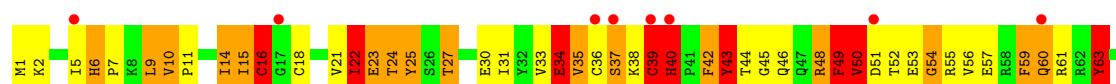
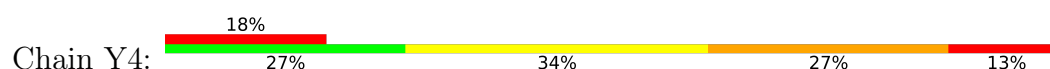
- Molecule 46: 50S ribosomal protein L30

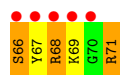


- Molecule 47: 50S ribosomal protein L31

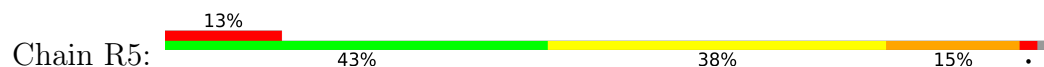


- Molecule 47: 50S ribosomal protein L31

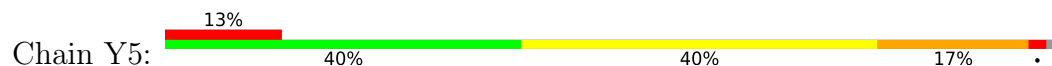




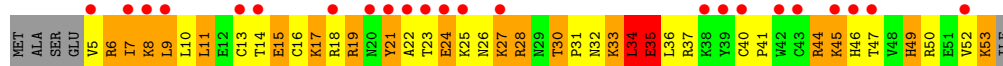
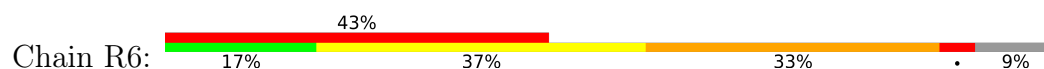
- Molecule 48: 50S ribosomal protein L32



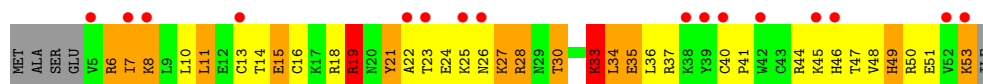
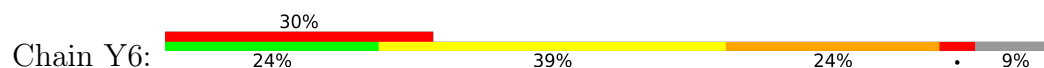
- Molecule 48: 50S ribosomal protein L32



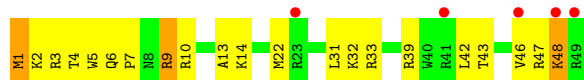
- Molecule 49: 50S ribosomal protein L33



- Molecule 49: 50S ribosomal protein L33



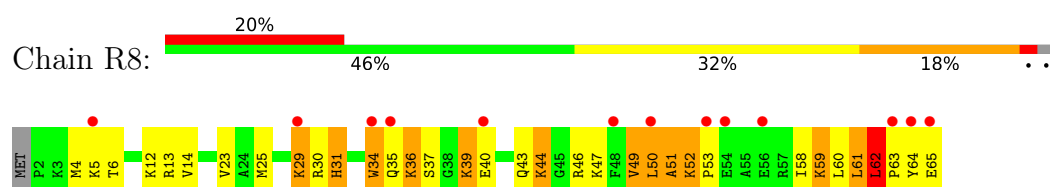
- Molecule 50: 50S ribosomal protein L34



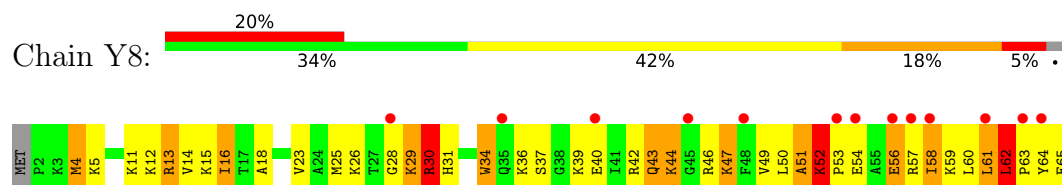
- Molecule 50: 50S ribosomal protein L34



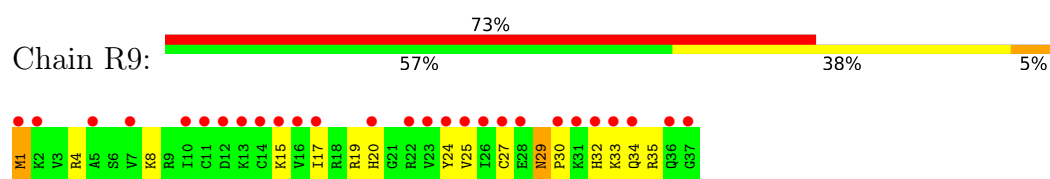
- Molecule 51: 50S ribosomal protein L35



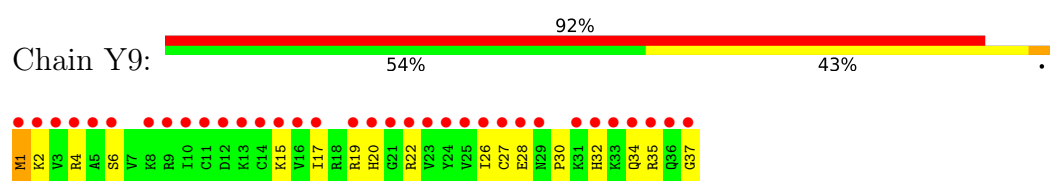
- Molecule 51: 50S ribosomal protein L35



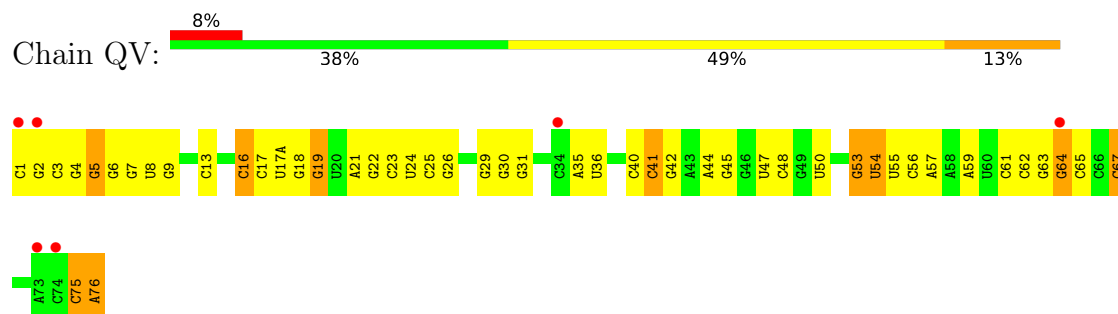
- Molecule 52: 50S ribosomal protein L36



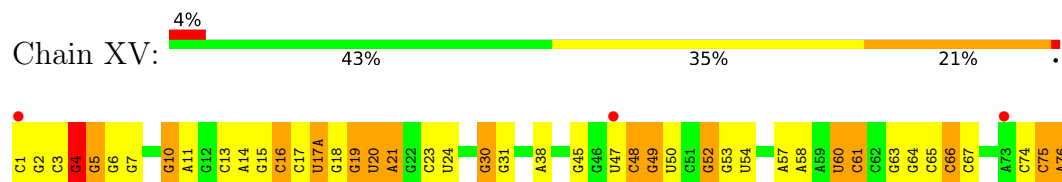
- Molecule 52: 50S ribosomal protein L36



- Molecule 53: P-site tRNA fMET



- Molecule 53: P-site tRNA fMET



- Molecule 54: mRNA





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	209.82Å 447.39Å 619.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	187.58 – 3.68 187.58 – 3.68	Depositor EDS
% Data completeness (in resolution range)	99.1 (187.58-3.68) 99.2 (187.58-3.68)	Depositor EDS
R_{merge}	0.34	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 3.58Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.3_1479)	Depositor
R, R_{free}	0.212 , 0.272 0.215 , 0.273	Depositor DCC
R_{free} test set	31728 reflections (4.55%)	wwPDB-VP
Wilson B-factor (Å ²)	83.8	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 133.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	291730	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.79% 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: MG, ZN, PPU, PAR

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	QA	0.33	0/36098	0.56	6/56341 (0.0%)
1	XA	0.36	0/36101	0.59	3/56346 (0.0%)
2	QB	0.39	0/1959	0.86	4/2642 (0.2%)
2	XB	0.40	0/1959	0.89	4/2642 (0.2%)
3	QC	0.43	0/1629	0.87	0/2195
3	XC	0.48	0/1629	0.85	0/2195
4	QD	0.48	0/1733	0.96	3/2318 (0.1%)
4	XD	0.51	0/1733	0.97	5/2318 (0.2%)
5	QE	0.46	0/1171	0.95	6/1576 (0.4%)
5	XE	0.52	0/1171	0.95	2/1576 (0.1%)
6	QF	0.45	0/856	0.80	0/1154
6	XF	0.51	0/856	0.88	0/1154
7	QG	0.43	0/1276	0.85	0/1709
7	XG	0.46	0/1276	0.86	1/1709 (0.1%)
8	QH	0.43	0/1136	0.93	2/1527 (0.1%)
8	XH	0.47	0/1136	0.93	4/1527 (0.3%)
9	QI	0.41	0/1029	0.90	1/1379 (0.1%)
9	XI	0.42	0/1029	0.89	1/1379 (0.1%)
10	QJ	0.42	0/814	0.90	2/1095 (0.2%)
10	XJ	0.48	0/814	1.00	3/1095 (0.3%)
11	QK	0.48	0/900	0.91	2/1213 (0.2%)
11	XK	0.51	0/900	0.94	0/1213
12	QL	0.48	0/991	0.96	3/1327 (0.2%)
12	XL	0.59	0/991	1.14	9/1327 (0.7%)
13	QM	0.42	0/974	0.98	2/1303 (0.2%)
13	XM	0.47	0/974	0.98	1/1303 (0.1%)
14	QN	0.48	0/501	0.90	0/664
14	XN	0.57	0/501	1.04	3/664 (0.5%)
15	QO	0.45	0/745	0.80	0/992
15	XO	0.49	0/745	0.90	0/992
16	QP	0.47	0/721	0.93	2/970 (0.2%)
16	XP	0.47	0/721	0.89	1/970 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	QQ	0.42	0/847	0.85	0/1131
17	XQ	0.42	0/847	0.83	0/1131
18	QR	0.44	0/579	0.89	0/768
18	XR	0.47	0/579	0.85	1/768 (0.1%)
19	QS	0.45	0/689	0.99	3/926 (0.3%)
19	XS	0.47	0/689	1.01	6/926 (0.6%)
20	QT	0.46	0/765	0.96	2/1007 (0.2%)
20	XT	0.43	0/765	0.97	2/1007 (0.2%)
21	QU	0.37	0/221	0.79	0/288
21	XU	0.38	0/221	0.82	0/288
22	RA	0.39	0/69521	0.61	15/108529 (0.0%)
22	YA	0.42	0/69543	0.64	19/108563 (0.0%)
23	RB	0.32	0/2878	0.55	0/4490
23	YB	0.35	0/2878	0.58	0/4490
24	RD	0.64	0/2165	1.07	8/2919 (0.3%)
24	YD	0.73	0/2165	1.13	13/2919 (0.4%)
25	RE	0.56	0/1601	1.07	5/2160 (0.2%)
25	YE	0.60	0/1601	1.11	10/2160 (0.5%)
26	RF	0.53	0/1620	0.95	4/2194 (0.2%)
26	YF	0.60	0/1620	1.08	9/2194 (0.4%)
27	RG	0.41	0/1499	0.91	2/2016 (0.1%)
27	YG	0.50	0/1499	0.91	2/2016 (0.1%)
28	RH	0.41	0/1332	1.02	9/1802 (0.5%)
28	YH	0.59	0/1332	1.10	7/1802 (0.4%)
29	RI	0.74	2/1151 (0.2%)	1.18	10/1558 (0.6%)
29	YI	0.78	1/1151 (0.1%)	1.13	7/1558 (0.4%)
30	RN	0.52	0/1131	1.01	2/1525 (0.1%)
30	YN	0.56	0/1131	0.94	1/1525 (0.1%)
31	RO	0.55	0/943	0.98	3/1269 (0.2%)
31	YO	0.60	0/943	0.97	0/1269
32	RP	0.61	0/1162	1.20	11/1544 (0.7%)
32	YP	0.67	0/1162	1.27	9/1544 (0.6%)
33	RQ	0.63	0/1143	1.09	4/1527 (0.3%)
33	YQ	0.73	1/1143 (0.1%)	1.13	8/1527 (0.5%)
34	RR	0.54	0/982	0.99	1/1312 (0.1%)
34	YR	0.56	0/982	1.04	3/1312 (0.2%)
35	RS	0.43	0/892	0.88	0/1187
35	YS	0.51	0/892	0.99	1/1187 (0.1%)
36	RT	0.53	0/1155	0.98	3/1542 (0.2%)
36	YT	0.57	0/1155	1.05	7/1542 (0.5%)
37	RU	0.54	0/982	1.04	6/1306 (0.5%)
37	YU	0.62	0/982	1.05	3/1306 (0.2%)
38	RV	0.47	0/790	0.97	4/1057 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	YV	0.58	0/790	1.01	2/1057 (0.2%)
39	RW	0.64	0/911	0.98	0/1220
39	YW	0.60	0/911	1.01	0/1220
40	RX	0.59	0/739	0.96	4/993 (0.4%)
40	YX	0.60	0/739	1.00	1/993 (0.1%)
41	RY	0.54	0/798	1.07	6/1064 (0.6%)
41	YY	0.59	0/798	1.09	5/1064 (0.5%)
42	RZ	0.84	4/1493 (0.3%)	1.17	13/2026 (0.6%)
42	YZ	0.73	1/1493 (0.1%)	1.18	11/2026 (0.5%)
43	R0	0.79	0/657	1.07	3/874 (0.3%)
43	Y0	0.90	0/657	1.20	3/874 (0.3%)
44	R1	0.55	0/770	0.97	0/1022
44	Y1	0.58	0/770	0.96	1/1022 (0.1%)
45	R2	0.46	0/583	1.01	1/771 (0.1%)
45	Y2	0.60	0/583	1.05	1/771 (0.1%)
46	R3	0.46	0/474	0.91	0/635
46	Y3	0.53	0/474	0.86	0/635
47	R4	0.45	0/594	1.18	8/795 (1.0%)
47	Y4	0.49	0/594	1.15	6/795 (0.8%)
48	R5	0.63	0/473	1.22	4/639 (0.6%)
48	Y5	0.64	0/473	1.33	7/639 (1.1%)
49	R6	0.53	0/431	1.01	2/575 (0.3%)
49	Y6	0.56	0/431	1.00	2/575 (0.3%)
50	R7	0.63	0/438	1.04	2/575 (0.3%)
50	Y7	0.70	0/438	1.02	3/575 (0.5%)
51	R8	0.69	0/525	1.17	4/691 (0.6%)
51	Y8	0.75	0/525	1.15	5/691 (0.7%)
52	R9	0.34	0/310	0.81	0/407
52	Y9	0.45	0/310	0.81	0/407
53	QV	0.45	0/1836	0.64	0/2859
53	XV	0.47	0/1836	0.71	1/2859 (0.0%)
54	QX	0.50	0/193	0.81	0/299
54	XX	0.65	0/193	0.80	0/299
55	QY	0.41	0/194	0.60	0/301
55	XY	0.42	0/194	0.62	0/301
56	Z6	0.41	0/40	0.62	0/60
56	Z8	0.62	0/40	0.86	0/60
All	All	0.44	9/316105 (0.0%)	0.74	365/472575 (0.1%)

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
12	QL	0	1
12	XL	0	1
25	RE	0	1
25	YE	0	1
26	YF	0	1
28	RH	0	2
28	YH	0	2
29	RI	0	1
35	YS	0	1
42	YZ	0	2
45	Y2	0	1
47	R4	0	1
51	R8	0	2
51	Y8	0	2
All	All	0	19

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	RZ	54	HIS	CG-ND1	-10.09	1.27	1.38
42	RZ	54	HIS	ND1-CE1	8.37	1.41	1.32
42	RZ	55	HIS	CG-CD2	7.21	1.43	1.35
42	RZ	55	HIS	CD2-NE2	-7.17	1.29	1.37
29	RI	136	VAL	CA-CB	6.15	1.59	1.54

The worst 5 of 365 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	RQ	82	ARG	N-CA-C	11.95	124.51	110.41
48	Y5	4	HIS	CA-C-N	-11.27	108.49	119.76
48	Y5	4	HIS	C-N-CA	-11.27	108.49	119.76
32	YP	59	LEU	N-CA-C	-10.56	99.94	112.92
4	QD	28	SER	CA-C-N	-10.47	108.83	120.45

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	QL	47	LYS	Peptide
25	RE	21	VAL	Peptide
28	RH	127	GLU	Peptide
28	RH	153	LYS	Peptide

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Mol	Chain	Res	Type	Group
29	RI	134	PRO	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	QA	32247	0	16277	779	0
1	XA	32249	0	16279	827	0
2	QB	1924	0	1975	68	0
2	XB	1924	0	1975	89	0
3	QC	1605	0	1668	51	0
3	XC	1605	0	1668	63	0
4	QD	1703	0	1763	70	0
4	XD	1703	0	1764	52	0
5	QE	1155	0	1213	36	0
5	XE	1155	0	1213	44	0
6	QF	843	0	857	20	0
6	XF	843	0	857	23	0
7	QG	1257	0	1296	41	0
7	XG	1257	0	1296	28	0
8	QH	1116	0	1177	41	0
8	XH	1116	0	1177	32	0
9	QI	1010	0	1037	43	0
9	XI	1010	0	1037	60	0
10	QJ	801	0	849	50	0
10	XJ	801	0	849	39	0
11	QK	885	0	904	33	0
11	XK	885	0	904	33	0
12	QL	975	0	1062	45	0
12	XL	975	0	1062	48	0
13	QM	964	0	1034	49	0
13	XM	964	0	1034	63	0
14	QN	492	0	529	26	0
14	XN	492	0	529	22	0
15	QO	734	0	771	25	0
15	XO	734	0	771	22	0
16	QP	705	0	725	21	0
16	XP	705	0	725	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	QQ	834	0	904	26	0
17	XQ	834	0	904	20	0
18	QR	574	0	644	13	0
18	XR	574	0	644	21	0
19	QS	674	0	699	41	0
19	XS	674	0	699	56	0
20	QT	763	0	861	25	0
20	XT	763	0	861	42	0
21	QU	217	0	234	12	0
21	XU	217	0	234	8	0
22	RA	62071	0	31292	1374	0
22	YA	62091	0	31301	1331	1
23	RB	2573	0	1306	60	0
23	YB	2573	0	1306	64	1
24	RD	2115	0	2195	109	0
24	YD	2115	0	2195	110	0
25	RE	1568	0	1634	69	0
25	YE	1568	0	1634	70	0
26	RF	1585	0	1632	80	0
26	YF	1585	0	1632	67	0
27	RG	1474	0	1535	64	0
27	YG	1474	0	1535	73	0
28	RH	1307	0	1382	68	0
28	YH	1307	0	1382	65	0
29	RI	1136	0	1223	86	0
29	YI	1136	0	1223	75	0
30	RN	1104	0	1180	42	0
30	YN	1104	0	1180	53	0
31	RO	933	0	996	27	0
31	YO	933	0	996	25	0
32	RP	1145	0	1227	82	0
32	YP	1145	0	1228	97	0
33	RQ	1122	0	1179	64	0
33	YQ	1122	0	1179	51	0
34	RR	968	0	1033	49	0
34	YR	968	0	1033	37	0
35	RS	882	0	943	44	0
35	YS	882	0	943	44	0
36	RT	1141	0	1202	53	0
36	YT	1141	0	1202	55	0
37	RU	964	0	1022	36	0
37	YU	964	0	1022	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	RV	779	0	852	24	0
38	YV	779	0	852	45	0
39	RW	900	0	964	31	0
39	YW	900	0	964	27	0
40	RX	725	0	778	33	0
40	YX	725	0	778	25	0
41	RY	785	0	878	53	0
41	YY	785	0	878	45	0
42	RZ	1461	0	1493	101	0
42	YZ	1461	0	1493	106	0
43	R0	648	0	671	38	0
43	Y0	648	0	672	42	0
44	R1	763	0	848	32	0
44	Y1	763	0	848	37	0
45	R2	581	0	629	14	0
45	Y2	581	0	629	23	0
46	R3	469	0	518	7	0
46	Y3	469	0	518	15	0
47	R4	581	0	574	33	0
47	Y4	581	0	574	79	0
48	R5	459	0	480	31	0
48	Y5	459	0	480	32	0
49	R6	424	0	450	30	0
49	Y6	424	0	450	28	0
50	R7	430	0	480	19	0
50	Y7	430	0	480	20	0
51	R8	517	0	582	37	0
51	Y8	517	0	582	45	0
52	R9	307	0	338	14	0
52	Y9	307	0	338	19	0
53	QV	1644	0	836	30	0
53	XV	1644	0	836	35	0
54	QX	173	0	88	3	0
54	XX	173	0	88	3	0
55	QY	174	0	88	4	0
55	XY	174	0	88	2	0
56	Z6	74	0	51	0	0
56	Z8	74	0	51	3	0
57	QA	42	0	45	1	0
57	XA	42	0	45	2	0
58	QA	76	0	0	0	0
58	QF	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	QM	1	0	0	0	0
58	QV	1	0	0	0	0
58	R0	1	0	0	0	0
58	R5	1	0	0	0	0
58	R8	2	0	0	0	0
58	RA	247	0	0	0	0
58	RB	2	0	0	0	0
58	RD	1	0	0	0	0
58	RE	2	0	0	0	0
58	RF	1	0	0	0	0
58	RP	2	0	0	0	0
58	XA	82	0	0	0	0
58	XB	1	0	0	0	0
58	XM	1	0	0	0	0
58	XV	2	0	0	0	0
58	Y0	1	0	0	0	0
58	Y5	1	0	0	0	0
58	YA	265	0	0	0	0
58	YB	3	0	0	0	0
58	YD	2	0	0	0	0
58	YP	2	0	0	0	0
58	YQ	1	0	0	0	0
58	YX	1	0	0	0	0
59	QD	1	0	0	0	0
59	QN	1	0	0	0	0
59	XD	1	0	0	0	0
59	XN	1	0	0	0	0
All	All	291730	0	198220	7742	1

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 16.

The worst 5 of 7742 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)
22:RA:2701:C:H3'	22:RA:2702:U:H5''	1.27	1.07
1:XA:963:G:N3	10:XJ:55:LYS:NZ	2.02	1.07
24:YD:43:ARG:NH1	24:YD:44:ASN:OD1	1.86	1.06
22:YA:2701:C:H3'	22:YA:2702:U:H5''	1.38	1.05
22:YA:1138:G:H21	30:YN:106:MET:HE3	1.18	1.03

All (1) 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)
22:YA:1593:G:O2'	23:YB:54:G:OP1[1_655]	2.14	0.06

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	QB	235/256 (92%)	174 (74%)	44 (19%)	17 (7%)	1	11
2	XB	235/256 (92%)	178 (76%)	42 (18%)	15 (6%)	1	13
3	QC	203/239 (85%)	163 (80%)	34 (17%)	6 (3%)	3	25
3	XC	203/239 (85%)	171 (84%)	29 (14%)	3 (2%)	8	35
4	QD	206/209 (99%)	176 (85%)	24 (12%)	6 (3%)	3	25
4	XD	206/209 (99%)	177 (86%)	24 (12%)	5 (2%)	4	28
5	QE	149/162 (92%)	136 (91%)	8 (5%)	5 (3%)	3	23
5	XE	149/162 (92%)	133 (89%)	13 (9%)	3 (2%)	6	31
6	QF	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
6	XF	99/101 (98%)	94 (95%)	5 (5%)	0	100	100
7	QG	153/156 (98%)	135 (88%)	16 (10%)	2 (1%)	9	38
7	XG	153/156 (98%)	138 (90%)	13 (8%)	2 (1%)	9	38
8	QH	136/138 (99%)	121 (89%)	14 (10%)	1 (1%)	18	50
8	XH	136/138 (99%)	120 (88%)	12 (9%)	4 (3%)	3	25
9	QI	125/128 (98%)	103 (82%)	17 (14%)	5 (4%)	2	20
9	XI	125/128 (98%)	97 (78%)	24 (19%)	4 (3%)	3	24
10	QJ	97/105 (92%)	75 (77%)	19 (20%)	3 (3%)	3	24
10	XJ	97/105 (92%)	79 (81%)	13 (13%)	5 (5%)	1	16
11	QK	117/129 (91%)	100 (86%)	14 (12%)	3 (3%)	4	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	XK	117/129 (91%)	101 (86%)	14 (12%)	2 (2%)	7	33
12	QL	123/132 (93%)	98 (80%)	18 (15%)	7 (6%)	1	15
12	XL	123/132 (93%)	98 (80%)	15 (12%)	10 (8%)	1	9
13	QM	119/126 (94%)	95 (80%)	15 (13%)	9 (8%)	1	10
13	XM	119/126 (94%)	94 (79%)	16 (13%)	9 (8%)	1	10
14	QN	58/61 (95%)	48 (83%)	6 (10%)	4 (7%)	1	12
14	XN	58/61 (95%)	46 (79%)	6 (10%)	6 (10%)	0	5
15	QO	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	10	39
15	XO	86/89 (97%)	80 (93%)	4 (5%)	2 (2%)	5	29
16	QP	82/88 (93%)	74 (90%)	7 (8%)	1 (1%)	10	39
16	XP	82/88 (93%)	71 (87%)	10 (12%)	1 (1%)	10	39
17	QQ	98/105 (93%)	91 (93%)	5 (5%)	2 (2%)	6	31
17	XQ	98/105 (93%)	88 (90%)	10 (10%)	0	100	100
18	QR	68/88 (77%)	56 (82%)	9 (13%)	3 (4%)	2	18
18	XR	68/88 (77%)	61 (90%)	6 (9%)	1 (2%)	8	35
19	QS	82/93 (88%)	56 (68%)	15 (18%)	11 (13%)	0	3
19	XS	82/93 (88%)	54 (66%)	17 (21%)	11 (13%)	0	3
20	QT	97/106 (92%)	76 (78%)	15 (16%)	6 (6%)	1	14
20	XT	97/106 (92%)	75 (77%)	16 (16%)	6 (6%)	1	14
21	QU	23/27 (85%)	19 (83%)	3 (13%)	1 (4%)	2	18
21	XU	23/27 (85%)	18 (78%)	4 (17%)	1 (4%)	2	18
24	RD	270/276 (98%)	226 (84%)	32 (12%)	12 (4%)	2	18
24	YD	270/276 (98%)	227 (84%)	34 (13%)	9 (3%)	3	24
25	RE	203/206 (98%)	147 (72%)	36 (18%)	20 (10%)	0	6
25	YE	203/206 (98%)	142 (70%)	41 (20%)	20 (10%)	0	6
26	RF	200/210 (95%)	167 (84%)	20 (10%)	13 (6%)	1	13
26	YF	200/210 (95%)	167 (84%)	25 (12%)	8 (4%)	2	20
27	RG	179/182 (98%)	139 (78%)	26 (14%)	14 (8%)	1	10
27	YG	179/182 (98%)	142 (79%)	25 (14%)	12 (7%)	1	12
28	RH	168/180 (93%)	114 (68%)	33 (20%)	21 (12%)	0	3
28	YH	168/180 (93%)	121 (72%)	23 (14%)	24 (14%)	0	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	RI	144/148 (97%)	94 (65%)	31 (22%)	19 (13%)	0	3
29	YI	144/148 (97%)	100 (69%)	23 (16%)	21 (15%)	0	2
30	RN	136/140 (97%)	104 (76%)	20 (15%)	12 (9%)	0	8
30	YN	136/140 (97%)	106 (78%)	16 (12%)	14 (10%)	0	5
31	RO	120/122 (98%)	109 (91%)	9 (8%)	2 (2%)	7	33
31	YO	120/122 (98%)	108 (90%)	10 (8%)	2 (2%)	7	33
32	RP	148/150 (99%)	107 (72%)	27 (18%)	14 (10%)	0	7
32	YP	148/150 (99%)	108 (73%)	23 (16%)	17 (12%)	0	4
33	RQ	139/141 (99%)	99 (71%)	22 (16%)	18 (13%)	0	3
33	YQ	139/141 (99%)	98 (70%)	22 (16%)	19 (14%)	0	3
34	RR	116/118 (98%)	106 (91%)	5 (4%)	5 (4%)	2	18
34	YR	116/118 (98%)	99 (85%)	11 (10%)	6 (5%)	1	16
35	RS	109/112 (97%)	76 (70%)	22 (20%)	11 (10%)	0	6
35	YS	109/112 (97%)	78 (72%)	18 (16%)	13 (12%)	0	4
36	RT	135/146 (92%)	106 (78%)	17 (13%)	12 (9%)	0	7
36	YT	135/146 (92%)	108 (80%)	17 (13%)	10 (7%)	1	10
37	RU	115/118 (98%)	102 (89%)	9 (8%)	4 (4%)	3	23
37	YU	115/118 (98%)	101 (88%)	10 (9%)	4 (4%)	3	23
38	RV	99/101 (98%)	82 (83%)	11 (11%)	6 (6%)	1	14
38	YV	99/101 (98%)	79 (80%)	12 (12%)	8 (8%)	1	9
39	RW	111/113 (98%)	99 (89%)	8 (7%)	4 (4%)	2	22
39	YW	111/113 (98%)	100 (90%)	9 (8%)	2 (2%)	6	32
40	RX	90/96 (94%)	77 (86%)	11 (12%)	2 (2%)	5	29
40	YX	90/96 (94%)	82 (91%)	6 (7%)	2 (2%)	5	29
41	RY	100/110 (91%)	71 (71%)	13 (13%)	16 (16%)	0	2
41	YY	100/110 (91%)	70 (70%)	18 (18%)	12 (12%)	0	4
42	RZ	181/206 (88%)	118 (65%)	35 (19%)	28 (16%)	0	2
42	YZ	181/206 (88%)	113 (62%)	46 (25%)	22 (12%)	0	4
43	R0	80/85 (94%)	61 (76%)	15 (19%)	4 (5%)	1	16
43	Y0	80/85 (94%)	66 (82%)	13 (16%)	1 (1%)	9	38
44	R1	95/98 (97%)	75 (79%)	11 (12%)	9 (10%)	0	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	Y1	95/98 (97%)	72 (76%)	17 (18%)	6 (6%)	1	13
45	R2	67/72 (93%)	53 (79%)	9 (13%)	5 (8%)	1	10
45	Y2	67/72 (93%)	55 (82%)	6 (9%)	6 (9%)	0	7
46	R3	57/60 (95%)	52 (91%)	3 (5%)	2 (4%)	3	23
46	Y3	57/60 (95%)	52 (91%)	4 (7%)	1 (2%)	6	32
47	R4	69/71 (97%)	35 (51%)	18 (26%)	16 (23%)	0	0
47	Y4	69/71 (97%)	35 (51%)	15 (22%)	19 (28%)	0	0
48	R5	57/60 (95%)	44 (77%)	11 (19%)	2 (4%)	3	23
48	Y5	57/60 (95%)	46 (81%)	9 (16%)	2 (4%)	3	23
49	R6	47/54 (87%)	23 (49%)	13 (28%)	11 (23%)	0	0
49	Y6	47/54 (87%)	22 (47%)	17 (36%)	8 (17%)	0	2
50	R7	47/49 (96%)	45 (96%)	1 (2%)	1 (2%)	5	30
50	Y7	47/49 (96%)	43 (92%)	3 (6%)	1 (2%)	5	30
51	R8	62/65 (95%)	51 (82%)	6 (10%)	5 (8%)	1	9
51	Y8	62/65 (95%)	48 (77%)	10 (16%)	4 (6%)	1	13
52	R9	35/37 (95%)	35 (100%)	0	0	100	100
52	Y9	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
All	All	11470/12128 (95%)	9180 (80%)	1546 (14%)	744 (6%)	1	13

5 of 744 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	QB	236	TYR
3	QC	12	LEU
3	QC	190	ARG
4	QD	28	SER
13	QM	67	GLU

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	QB	205/220 (93%)	169 (82%)	36 (18%)	2	12
2	XB	205/220 (93%)	181 (88%)	24 (12%)	5	24
3	QC	159/188 (85%)	147 (92%)	12 (8%)	12	39
3	XC	159/188 (85%)	145 (91%)	14 (9%)	9	33
4	QD	180/181 (99%)	155 (86%)	25 (14%)	3	18
4	XD	180/181 (99%)	155 (86%)	25 (14%)	3	18
5	QE	116/123 (94%)	102 (88%)	14 (12%)	5	22
5	XE	116/123 (94%)	100 (86%)	16 (14%)	3	18
6	QF	90/90 (100%)	79 (88%)	11 (12%)	5	22
6	XF	90/90 (100%)	78 (87%)	12 (13%)	4	20
7	QG	126/127 (99%)	115 (91%)	11 (9%)	9	33
7	XG	126/127 (99%)	112 (89%)	14 (11%)	6	25
8	QH	119/119 (100%)	105 (88%)	14 (12%)	5	23
8	XH	119/119 (100%)	106 (89%)	13 (11%)	6	26
9	QI	98/99 (99%)	80 (82%)	18 (18%)	1	10
9	XI	98/99 (99%)	77 (79%)	21 (21%)	1	7
10	QJ	89/92 (97%)	75 (84%)	14 (16%)	2	14
10	XJ	89/92 (97%)	74 (83%)	15 (17%)	2	13
11	QK	90/99 (91%)	79 (88%)	11 (12%)	5	22
11	XK	90/99 (91%)	81 (90%)	9 (10%)	7	29
12	QL	104/109 (95%)	91 (88%)	13 (12%)	4	21
12	XL	104/109 (95%)	90 (86%)	14 (14%)	4	19
13	QM	97/101 (96%)	73 (75%)	24 (25%)	1	4
13	XM	97/101 (96%)	79 (81%)	18 (19%)	1	10
14	QN	49/50 (98%)	40 (82%)	9 (18%)	1	10
14	XN	49/50 (98%)	42 (86%)	7 (14%)	3	17
15	QO	79/80 (99%)	72 (91%)	7 (9%)	9	33
15	XO	79/80 (99%)	68 (86%)	11 (14%)	3	18
16	QP	72/74 (97%)	62 (86%)	10 (14%)	3	18
16	XP	72/74 (97%)	65 (90%)	7 (10%)	8	30
17	QQ	95/97 (98%)	86 (90%)	9 (10%)	8	31
17	XQ	95/97 (98%)	88 (93%)	7 (7%)	13	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	QR	61/77 (79%)	50 (82%)	11 (18%)	2	12
18	XR	61/77 (79%)	50 (82%)	11 (18%)	2	12
19	QS	73/80 (91%)	58 (80%)	15 (20%)	1	8
19	XS	73/80 (91%)	56 (77%)	17 (23%)	1	5
20	QT	76/82 (93%)	66 (87%)	10 (13%)	4	20
20	XT	76/82 (93%)	66 (87%)	10 (13%)	4	20
21	QU	20/22 (91%)	20 (100%)	0	100	100
21	XU	20/22 (91%)	20 (100%)	0	100	100
24	RD	214/218 (98%)	170 (79%)	44 (21%)	1	8
24	YD	214/218 (98%)	176 (82%)	38 (18%)	2	12
25	RE	165/166 (99%)	122 (74%)	43 (26%)	0	4
25	YE	165/166 (99%)	134 (81%)	31 (19%)	1	10
26	RF	161/166 (97%)	127 (79%)	34 (21%)	1	7
26	YF	161/166 (97%)	134 (83%)	27 (17%)	2	13
27	RG	155/156 (99%)	135 (87%)	20 (13%)	4	20
27	YG	155/156 (99%)	131 (84%)	24 (16%)	2	15
28	RH	142/148 (96%)	116 (82%)	26 (18%)	2	11
28	YH	142/148 (96%)	112 (79%)	30 (21%)	1	7
29	RI	122/124 (98%)	79 (65%)	43 (35%)	0	1
29	YI	122/124 (98%)	83 (68%)	39 (32%)	0	2
30	RN	117/119 (98%)	94 (80%)	23 (20%)	1	8
30	YN	117/119 (98%)	94 (80%)	23 (20%)	1	8
31	RO	100/100 (100%)	91 (91%)	9 (9%)	9	32
31	YO	100/100 (100%)	85 (85%)	15 (15%)	3	15
32	RP	116/116 (100%)	83 (72%)	33 (28%)	0	3
32	YP	116/116 (100%)	81 (70%)	35 (30%)	0	2
33	RQ	111/111 (100%)	90 (81%)	21 (19%)	1	9
33	YQ	111/111 (100%)	94 (85%)	17 (15%)	3	15
34	RR	101/101 (100%)	81 (80%)	20 (20%)	1	8
34	YR	101/101 (100%)	80 (79%)	21 (21%)	1	7
35	RS	87/88 (99%)	67 (77%)	20 (23%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	YS	87/88 (99%)	65 (75%)	22 (25%)	0	4
36	RT	120/127 (94%)	101 (84%)	19 (16%)	2	14
36	YT	120/127 (94%)	93 (78%)	27 (22%)	1	6
37	RU	93/94 (99%)	79 (85%)	14 (15%)	3	15
37	YU	93/94 (99%)	79 (85%)	14 (15%)	3	15
38	RV	82/82 (100%)	63 (77%)	19 (23%)	1	5
38	YV	82/82 (100%)	66 (80%)	16 (20%)	1	9
39	RW	92/92 (100%)	73 (79%)	19 (21%)	1	7
39	YW	92/92 (100%)	76 (83%)	16 (17%)	2	12
40	RX	74/78 (95%)	61 (82%)	13 (18%)	2	12
40	YX	74/78 (95%)	59 (80%)	15 (20%)	1	8
41	RY	85/91 (93%)	56 (66%)	29 (34%)	0	1
41	YY	85/91 (93%)	62 (73%)	23 (27%)	0	3
42	RZ	162/179 (90%)	131 (81%)	31 (19%)	1	9
42	YZ	162/179 (90%)	111 (68%)	51 (32%)	0	2
43	R0	65/67 (97%)	54 (83%)	11 (17%)	2	13
43	Y0	65/67 (97%)	50 (77%)	15 (23%)	1	6
44	R1	82/83 (99%)	74 (90%)	8 (10%)	7	30
44	Y1	82/83 (99%)	69 (84%)	13 (16%)	2	14
45	R2	64/67 (96%)	49 (77%)	15 (23%)	1	5
45	Y2	64/67 (96%)	48 (75%)	16 (25%)	0	4
46	R3	51/52 (98%)	43 (84%)	8 (16%)	2	14
46	Y3	51/52 (98%)	44 (86%)	7 (14%)	3	19
47	R4	63/63 (100%)	44 (70%)	19 (30%)	0	2
47	Y4	63/63 (100%)	42 (67%)	21 (33%)	0	1
48	R5	51/52 (98%)	35 (69%)	16 (31%)	0	2
48	Y5	51/52 (98%)	37 (72%)	14 (28%)	0	3
49	R6	48/52 (92%)	32 (67%)	16 (33%)	0	1
49	Y6	48/52 (92%)	34 (71%)	14 (29%)	0	2
50	R7	42/42 (100%)	35 (83%)	7 (17%)	2	13
50	Y7	42/42 (100%)	35 (83%)	7 (17%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	R8	54/55 (98%)	43 (80%)	11 (20%)	1	8
51	Y8	54/55 (98%)	37 (68%)	17 (32%)	0	2
52	R9	34/34 (100%)	30 (88%)	4 (12%)	5	23
52	Y9	34/34 (100%)	31 (91%)	3 (9%)	9	33
All	All	9702/10066 (96%)	7957 (82%)	1745 (18%)	2	12

5 of 1745 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	XD	137	SER
24	YD	61	LEU
42	YZ	133	ILE
6	XF	45	LEU
4	XD	131	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
10	XJ	78	ASN
47	Y4	60	GLN
24	YD	96	HIS
33	YQ	57	HIS
29	RI	104	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	QA	1498/1522 (98%)	341 (22%)	49 (3%)
1	XA	1498/1522 (98%)	353 (23%)	40 (2%)
22	RA	2879/2916 (98%)	749 (26%)	65 (2%)
22	YA	2880/2916 (98%)	735 (25%)	57 (1%)
23	RB	119/122 (97%)	29 (24%)	2 (1%)
23	YB	119/122 (97%)	32 (26%)	1 (0%)
53	QV	76/77 (98%)	22 (28%)	1 (1%)
53	XV	76/77 (98%)	27 (35%)	3 (3%)
54	QX	7/25 (28%)	4 (57%)	1 (14%)
54	XX	7/25 (28%)	3 (42%)	1 (14%)
55	QY	7/17 (41%)	3 (42%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
55	XY	7/17 (41%)	2 (28%)	0
56	Z6	1/3 (33%)	0	0
56	Z8	1/3 (33%)	0	0
All	All	9175/9364 (97%)	2300 (25%)	220 (2%)

5 of 2300 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	QA	7	G
1	QA	9	G
1	QA	22	G
1	QA	32	A
1	QA	39	G

5 of 220 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	RB	66	A
1	XA	992	U
54	XX	3	G
22	YA	1955	U
1	XA	89	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
56	PPU	Z6	76	56,22	37,40,41	1.34	5 (13%)	47,57,60	2.43	19 (40%)
56	PPU	Z8	76	56,22	37,40,41	1.35	6 (16%)	47,57,60	2.13	15 (31%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	PPU	Z6	76	56,22	-	3/25/43/44	0/4/4/4
56	PPU	Z8	76	56,22	-	1/25/43/44	0/4/4/4

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	Z6	76	PPU	C5-C4	4.61	1.47	1.39
56	Z8	76	PPU	C5-C4	4.22	1.46	1.39
56	Z8	76	PPU	C4-N9	-2.86	1.31	1.37
56	Z6	76	PPU	C5-C6	2.65	1.48	1.41
56	Z8	76	PPU	C2'-C3'	-2.48	1.49	1.53

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	Z6	76	PPU	C3'-N3'-C	-5.92	114.20	123.20
56	Z6	76	PPU	C5-C4-N3	-5.54	119.09	126.72
56	Z8	76	PPU	C5-C4-N3	-5.28	119.44	126.72
56	Z6	76	PPU	N3-C4-N9	4.48	134.78	127.17
56	Z6	76	PPU	C10-N6-C6	-4.31	109.56	120.52

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	Z6	76	PPU	CE1-CZ-OC-CM
56	Z6	76	PPU	CE2-CZ-OC-CM
56	Z6	76	PPU	C5-C6-N6-C9
56	Z8	76	PPU	C5-C6-N6-C9

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	Z8	76	PPU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 706 ligands modelled in this entry, 704 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	PAR	XA	1601	-	44,45,45	1.32	5 (11%)	63,67,67	1.31	4 (6%)
57	PAR	QA	1601	-	44,45,45	1.27	6 (13%)	63,67,67	1.32	8 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	PAR	XA	1601	-	-	6/18/94/94	0/4/4/4
57	PAR	QA	1601	-	-	8/18/94/94	0/4/4/4

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	QA	1601	PAR	C52-C42	3.19	1.58	1.52
57	XA	1601	PAR	C11-C21	2.86	1.57	1.52
57	XA	1601	PAR	C52-C42	2.86	1.58	1.52
57	QA	1601	PAR	O54-C14	2.84	1.49	1.41
57	XA	1601	PAR	O54-C14	2.82	1.49	1.41

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	XA	1601	PAR	O33-C14-C24	5.07	116.37	108.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	XA	1601	PAR	C14-O54-C54	4.31	122.13	113.72
57	QA	1601	PAR	O33-C14-C24	4.04	114.69	108.08
57	QA	1601	PAR	C14-O54-C54	3.79	121.13	113.72
57	QA	1601	PAR	O11-C42-C32	-3.13	101.71	109.18

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

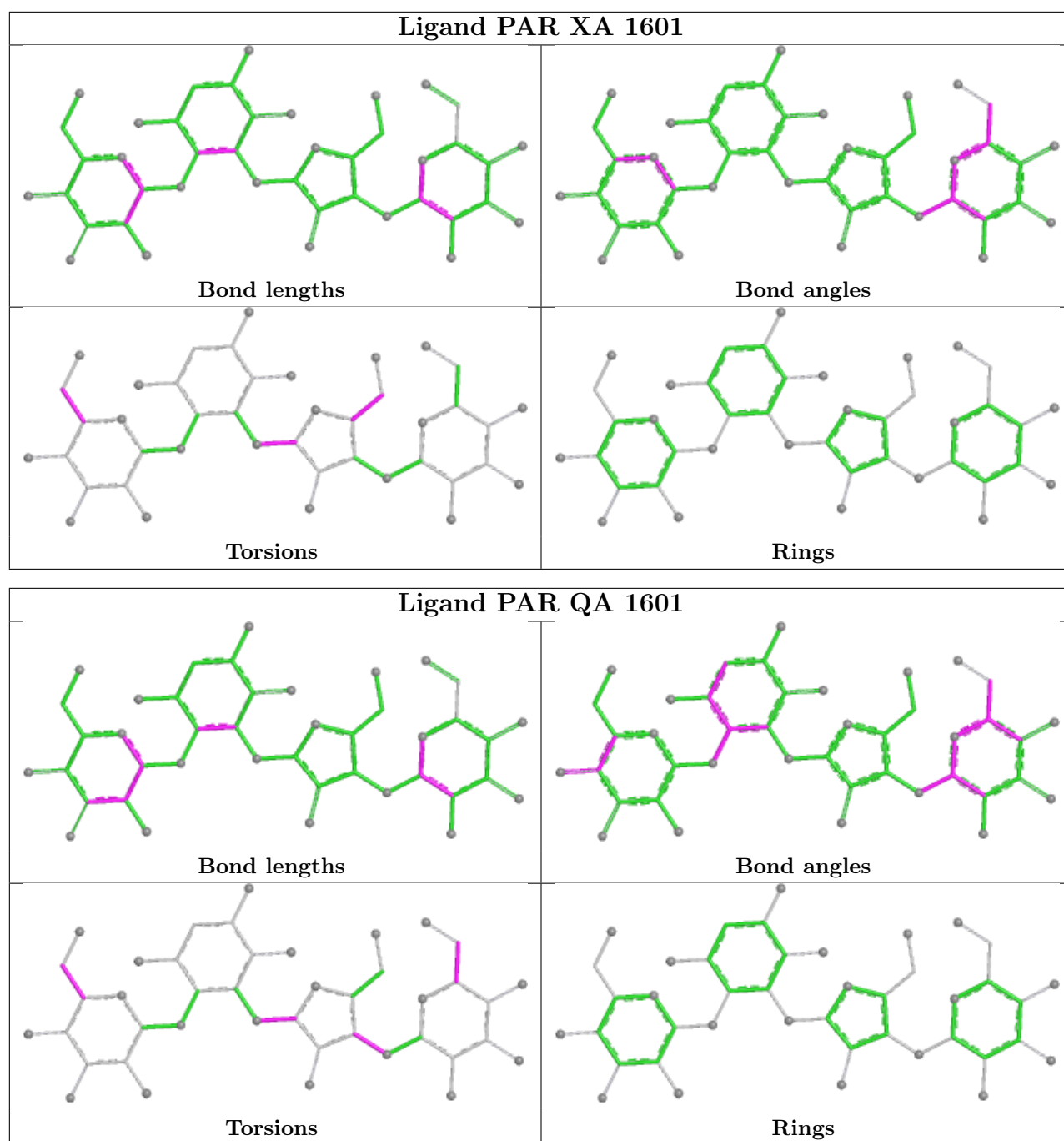
Mol	Chain	Res	Type	Atoms
57	QA	1601	PAR	C44-C54-C64-N64
57	QA	1601	PAR	O54-C54-C64-N64
57	XA	1601	PAR	O51-C51-C61-O61
57	QA	1601	PAR	O51-C51-C61-O61
57	XA	1601	PAR	C41-C51-C61-O61

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	XA	1601	PAR	2	0
57	QA	1601	PAR	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 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	QA	1500/1522 (98%)	0.42	56 (3%)	45	28	28, 70, 146, 264	0
1	XA	1500/1522 (98%)	0.39	62 (4%)	41	26	18, 64, 151, 247	0
2	QB	237/256 (92%)	1.01	26 (10%)	10	11	48, 115, 166, 191	0
2	XB	237/256 (92%)	0.86	20 (8%)	17	13	35, 98, 150, 194	0
3	QC	205/239 (85%)	0.69	12 (5%)	28	19	45, 105, 149, 166	0
3	XC	205/239 (85%)	0.47	9 (4%)	39	24	35, 78, 130, 168	0
4	QD	208/209 (99%)	0.83	18 (8%)	16	13	27, 79, 119, 169	0
4	XD	208/209 (99%)	0.92	25 (12%)	9	10	34, 75, 127, 151	0
5	QE	151/162 (93%)	0.58	5 (3%)	49	30	37, 88, 135, 167	0
5	XE	151/162 (93%)	0.54	4 (2%)	57	35	29, 65, 115, 148	0
6	QF	101/101 (100%)	0.42	5 (4%)	34	22	21, 76, 112, 185	0
6	XF	101/101 (100%)	0.68	7 (6%)	23	16	32, 72, 115, 153	0
7	QG	155/156 (99%)	0.87	21 (13%)	7	8	46, 96, 152, 185	0
7	XG	155/156 (99%)	0.71	11 (7%)	22	16	40, 87, 145, 167	0
8	QH	138/138 (100%)	0.85	11 (7%)	18	14	41, 90, 125, 153	0
8	XH	138/138 (100%)	0.53	3 (2%)	62	39	33, 72, 108, 149	0
9	QI	127/128 (99%)	1.05	21 (16%)	4	6	67, 109, 148, 172	0
9	XI	127/128 (99%)	1.03	15 (11%)	9	10	28, 99, 147, 164	0
10	QJ	99/105 (94%)	0.91	11 (11%)	10	11	59, 114, 165, 205	0
10	XJ	99/105 (94%)	1.06	14 (14%)	6	7	41, 103, 147, 171	0
11	QK	119/129 (92%)	0.75	10 (8%)	17	13	35, 79, 130, 177	0
11	XK	119/129 (92%)	0.44	3 (2%)	58	36	24, 71, 125, 182	0
12	QL	125/132 (94%)	0.80	12 (9%)	13	12	30, 70, 120, 182	0
12	XL	125/132 (94%)	0.72	12 (9%)	13	12	15, 58, 120, 182	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	QM	121/126 (96%)	1.04	19 (15%) 5 6	36, 106, 144, 196	0
13	XM	121/126 (96%)	0.82	12 (9%) 13 12	38, 88, 137, 187	0
14	QN	60/61 (98%)	0.95	6 (10%) 12 12	58, 97, 124, 142	0
14	XN	60/61 (98%)	0.73	6 (10%) 12 12	34, 75, 109, 125	0
15	QO	88/89 (98%)	0.46	3 (3%) 48 29	30, 79, 123, 154	0
15	XO	88/89 (98%)	0.74	4 (4%) 38 24	28, 73, 108, 124	0
16	QP	84/88 (95%)	0.91	9 (10%) 11 11	35, 69, 107, 152	0
16	XP	84/88 (95%)	0.99	8 (9%) 14 12	34, 74, 129, 163	0
17	QQ	100/105 (95%)	0.75	6 (6%) 27 19	24, 83, 122, 140	0
17	XQ	100/105 (95%)	0.71	7 (7%) 22 16	39, 78, 113, 165	0
18	QR	70/88 (79%)	0.75	6 (8%) 16 13	26, 78, 137, 167	0
18	XR	70/88 (79%)	0.51	2 (2%) 53 33	24, 70, 120, 147	0
19	QS	84/93 (90%)	0.93	10 (11%) 9 10	68, 111, 151, 176	0
19	XS	84/93 (90%)	0.92	10 (11%) 9 10	32, 97, 148, 177	0
20	QT	99/106 (93%)	0.76	11 (11%) 10 11	34, 79, 133, 144	0
20	XT	99/106 (93%)	1.04	14 (14%) 6 7	44, 88, 140, 174	0
21	QU	25/27 (92%)	1.42	5 (20%) 3 3	36, 102, 144, 147	0
21	XU	25/27 (92%)	1.64	8 (32%) 1 1	67, 92, 119, 132	0
22	RA	2882/2916 (98%)	0.27	122 (4%) 40 25	14, 51, 198, 261	0
22	YA	2883/2916 (98%)	0.20	105 (3%) 46 29	8, 43, 187, 292	0
23	RB	120/122 (98%)	0.66	8 (6%) 24 17	53, 81, 118, 144	0
23	YB	120/122 (98%)	0.18	2 (1%) 69 43	36, 67, 98, 136	0
24	RD	272/276 (98%)	0.59	23 (8%) 16 13	9, 50, 100, 155	0
24	YD	272/276 (98%)	0.74	17 (6%) 26 18	2, 42, 86, 187	0
25	RE	205/206 (99%)	0.99	25 (12%) 8 9	17, 61, 126, 193	0
25	YE	205/206 (99%)	0.68	11 (5%) 31 21	3, 56, 124, 170	0
26	RF	202/210 (96%)	0.77	14 (6%) 23 16	9, 61, 124, 182	0
26	YF	202/210 (96%)	0.77	23 (11%) 10 10	10, 53, 113, 148	0
27	RG	181/182 (99%)	0.92	21 (11%) 9 10	42, 97, 145, 178	0
27	YG	181/182 (99%)	0.90	14 (7%) 19 15	40, 80, 130, 201	0
28	RH	170/180 (94%)	1.74	53 (31%) 1 1	67, 134, 177, 201	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	YH	170/180 (94%)	0.91	22 (12%) 7 8	24, 76, 126, 177	0
29	RI	146/148 (98%)	0.78	17 (11%) 9 10	24, 87, 130, 181	0
29	YI	146/148 (98%)	0.73	13 (8%) 15 13	19, 86, 127, 152	0
30	RN	138/140 (98%)	0.83	18 (13%) 7 8	29, 68, 121, 174	0
30	YN	138/140 (98%)	0.84	13 (9%) 14 13	13, 56, 111, 173	0
31	RO	122/122 (100%)	0.81	11 (9%) 15 13	11, 55, 102, 158	0
31	YO	122/122 (100%)	0.50	6 (4%) 35 22	9, 51, 88, 123	0
32	RP	150/150 (100%)	1.05	18 (12%) 9 10	13, 69, 133, 176	0
32	YP	150/150 (100%)	0.84	11 (7%) 21 16	12, 61, 122, 182	0
33	RQ	141/141 (100%)	1.03	23 (16%) 4 6	29, 71, 124, 164	0
33	YQ	141/141 (100%)	0.91	26 (18%) 3 4	16, 56, 115, 152	0
34	RR	118/118 (100%)	0.57	6 (5%) 33 22	3, 55, 102, 136	0
34	YR	118/118 (100%)	0.71	7 (5%) 28 19	27, 57, 95, 140	0
35	RS	111/112 (99%)	1.00	11 (9%) 13 12	34, 80, 124, 162	0
35	YS	111/112 (99%)	0.82	8 (7%) 21 16	27, 72, 113, 138	0
36	RT	137/146 (93%)	0.84	10 (7%) 21 16	27, 67, 143, 169	0
36	YT	137/146 (93%)	0.59	8 (5%) 29 19	19, 65, 135, 172	0
37	RU	117/118 (99%)	0.79	10 (8%) 16 13	12, 62, 111, 167	0
37	YU	117/118 (99%)	0.91	12 (10%) 12 12	13, 45, 111, 172	0
38	RV	101/101 (100%)	0.59	4 (3%) 42 26	16, 78, 131, 186	0
38	YV	101/101 (100%)	1.00	10 (9%) 13 12	21, 68, 139, 214	0
39	RW	113/113 (100%)	0.47	7 (6%) 26 18	15, 47, 106, 158	0
39	YW	113/113 (100%)	0.55	4 (3%) 47 29	16, 46, 106, 168	0
40	RX	92/96 (95%)	0.57	2 (2%) 62 39	17, 56, 103, 130	0
40	YX	92/96 (95%)	0.48	3 (3%) 49 30	9, 42, 86, 138	0
41	RY	102/110 (92%)	1.74	37 (36%) 1 1	28, 86, 142, 176	0
41	YY	102/110 (92%)	1.16	22 (21%) 2 3	30, 73, 138, 185	0
42	RZ	183/206 (88%)	0.62	7 (3%) 44 28	45, 92, 141, 160	0
42	YZ	183/206 (88%)	0.44	12 (6%) 24 17	21, 82, 136, 178	0
43	R0	82/85 (96%)	0.12	4 (4%) 35 22	9, 51, 88, 102	0
43	Y0	82/85 (96%)	0.14	2 (2%) 59 36	20, 48, 73, 92	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	R1	97/98 (98%)	1.18	16 (16%) 4 6	13, 60, 144, 182	0
44	Y1	97/98 (98%)	1.27	21 (21%) 2 3	7, 53, 136, 172	0
45	R2	69/72 (95%)	0.83	8 (11%) 9 10	36, 77, 136, 164	0
45	Y2	69/72 (95%)	0.89	7 (10%) 12 12	18, 57, 116, 159	0
46	R3	59/60 (98%)	0.78	3 (5%) 33 22	33, 76, 118, 142	0
46	Y3	59/60 (98%)	0.71	4 (6%) 23 17	19, 57, 109, 169	0
47	R4	71/71 (100%)	1.48	14 (19%) 3 3	61, 142, 196, 236	0
47	Y4	71/71 (100%)	1.27	13 (18%) 3 4	58, 131, 182, 223	0
48	R5	59/60 (98%)	0.96	8 (13%) 7 8	12, 66, 149, 160	0
48	Y5	59/60 (98%)	0.95	8 (13%) 7 8	17, 64, 166, 185	0
49	R6	49/54 (90%)	2.05	23 (46%) 0 1	101, 159, 184, 200	0
49	Y6	49/54 (90%)	1.62	16 (32%) 1 1	95, 152, 182, 209	0
50	R7	49/49 (100%)	0.77	5 (10%) 12 12	11, 41, 95, 153	0
50	Y7	49/49 (100%)	0.52	2 (4%) 41 26	6, 33, 78, 135	0
51	R8	64/65 (98%)	1.22	13 (20%) 3 3	18, 59, 121, 163	0
51	Y8	64/65 (98%)	1.08	13 (20%) 3 3	16, 52, 108, 164	0
52	R9	37/37 (100%)	3.11	27 (72%) 0 0	92, 141, 184, 204	0
52	Y9	37/37 (100%)	3.77	34 (91%) 0 0	102, 132, 168, 182	0
53	QV	77/77 (100%)	0.71	6 (7%) 19 14	35, 82, 137, 160	0
53	XV	77/77 (100%)	0.44	3 (3%) 43 27	11, 71, 111, 159	0
54	QX	8/25 (32%)	1.01	1 (12%) 8 9	44, 56, 107, 137	0
54	XX	8/25 (32%)	0.81	1 (12%) 8 9	37, 46, 104, 148	0
55	QY	8/17 (47%)	0.32	1 (12%) 8 9	62, 74, 124, 144	0
55	XY	8/17 (47%)	0.20	0 100 100	54, 71, 109, 122	0
56	Z6	2/3 (66%)	0.33	0 100 100	45, 45, 45, 52	0
56	Z8	2/3 (66%)	0.41	0 100 100	30, 30, 30, 32	0
All	All	20861/21492 (97%)	0.60	1588 (7%) 20 15	2, 66, 150, 292	0

The worst 5 of 1588 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
47	R4	49	PHE	8.4
29	YI	117	GLU	8.0

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Mol	Chain	Res	Type	RSRZ
50	R7	49	ARG	7.7
18	QR	88	LYS	7.7
22	RA	2159	G	7.5

6.2 Non-standard residues in protein, DNA, RNA chains [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
56	PPU	Z6	76	37/38	0.95	0.12	37,37,37,37	0
56	PPU	Z8	76	37/38	0.96	0.10	30,30,30,30	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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
58	MG	XM	201	1/1	0.19	0.11	98,98,98,98	0
58	MG	YA	3060	1/1	0.37	0.20	8,8,8,8	0
58	MG	RA	3067	1/1	0.44	1.04	74,74,74,74	0
58	MG	QA	1664	1/1	0.46	0.28	56,56,56,56	0
58	MG	YD	301	1/1	0.46	0.74	74,74,74,74	0
58	MG	YA	3041	1/1	0.47	0.75	74,74,74,74	0
58	MG	YA	3018	1/1	0.48	0.69	74,74,74,74	0
58	MG	YA	3205	1/1	0.49	0.48	62,62,62,62	0
58	MG	RA	3227	1/1	0.51	0.27	60,60,60,60	0
58	MG	XA	1617	1/1	0.53	0.80	74,74,74,74	0
58	MG	Y0	101	1/1	0.55	0.59	74,74,74,74	0
58	MG	YA	3099	1/1	0.58	0.66	74,74,74,74	0
58	MG	RA	3235	1/1	0.60	0.56	74,74,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3209	1/1	0.61	0.22	47,47,47,47	0
58	MG	YA	3256	1/1	0.61	0.79	74,74,74,74	0
58	MG	YA	3049	1/1	0.62	0.82	74,74,74,74	0
58	MG	YA	3095	1/1	0.64	0.42	19,19,19,19	0
58	MG	YA	3046	1/1	0.64	0.59	74,74,74,74	0
58	MG	YA	3015	1/1	0.67	0.73	74,74,74,74	0
58	MG	RA	3196	1/1	0.67	0.26	63,63,63,63	0
58	MG	YA	3014	1/1	0.67	0.67	74,74,74,74	0
58	MG	YA	3003	1/1	0.68	0.62	74,74,74,74	0
58	MG	YA	3080	1/1	0.69	0.81	74,74,74,74	0
58	MG	RA	3056	1/1	0.70	0.60	74,74,74,74	0
58	MG	RA	3013	1/1	0.71	0.14	29,29,29,29	0
58	MG	YA	3260	1/1	0.71	0.72	74,74,74,74	0
58	MG	XA	1665	1/1	0.71	0.20	33,33,33,33	0
58	MG	RA	3037	1/1	0.71	0.75	74,74,74,74	0
58	MG	YA	3170	1/1	0.74	0.30	33,33,33,33	0
58	MG	QA	1647	1/1	0.74	0.20	38,38,38,38	0
58	MG	YA	3130	1/1	0.74	0.21	21,21,21,21	0
58	MG	QA	1619	1/1	0.75	0.33	12,12,12,12	0
58	MG	XA	1663	1/1	0.76	0.19	32,32,32,32	0
58	MG	YA	3207	1/1	0.76	0.16	55,55,55,55	0
58	MG	RA	3144	1/1	0.77	0.32	32,32,32,32	0
58	MG	RA	3047	1/1	0.77	0.32	19,19,19,19	0
58	MG	RA	3099	1/1	0.77	0.38	11,11,11,11	0
58	MG	RA	3105	1/1	0.77	0.23	14,14,14,14	0
58	MG	RA	3031	1/1	0.78	0.36	9,9,9,9	0
58	MG	XA	1643	1/1	0.78	0.53	74,74,74,74	0
58	MG	QA	1616	1/1	0.79	0.17	52,52,52,52	0
58	MG	RA	3102	1/1	0.80	0.39	21,21,21,21	0
58	MG	RA	3165	1/1	0.80	0.28	30,30,30,30	0
58	MG	RA	3009	1/1	0.80	0.70	74,74,74,74	0
58	MG	RA	3154	1/1	0.81	0.14	59,59,59,59	0
58	MG	QA	1621	1/1	0.81	0.22	38,38,38,38	0
58	MG	RA	3046	1/1	0.81	0.30	24,24,24,24	0
58	MG	QA	1648	1/1	0.81	0.14	43,43,43,43	0
58	MG	YA	3263	1/1	0.81	0.17	40,40,40,40	0
58	MG	YA	3155	1/1	0.81	0.26	45,45,45,45	0
58	MG	RA	3224	1/1	0.81	0.50	142,142,142,142	0
58	MG	RA	3214	1/1	0.82	0.13	24,24,24,24	0
58	MG	YA	3118	1/1	0.82	0.32	8,8,8,8	0
58	MG	RA	3223	1/1	0.82	0.27	54,54,54,54	0
58	MG	RA	3018	1/1	0.82	0.23	5,5,5,5	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3063	1/1	0.82	0.51	19,19,19,19	0
58	MG	RA	3159	1/1	0.82	0.18	23,23,23,23	0
58	MG	QA	1677	1/1	0.83	0.27	47,47,47,47	0
58	MG	RA	3187	1/1	0.83	0.32	42,42,42,42	0
58	MG	RA	3081	1/1	0.83	0.26	18,18,18,18	0
58	MG	RA	3157	1/1	0.83	0.14	37,37,37,37	0
58	MG	YA	3172	1/1	0.83	0.21	40,40,40,40	0
58	MG	RA	3095	1/1	0.83	0.26	18,18,18,18	0
58	MG	RA	3093	1/1	0.84	0.26	12,12,12,12	0
58	MG	RA	3036	1/1	0.84	0.37	18,18,18,18	0
58	MG	YA	3214	1/1	0.84	0.26	50,50,50,50	0
58	MG	RA	3054	1/1	0.84	0.23	18,18,18,18	0
58	MG	YA	3053	1/1	0.84	0.20	8,8,8,8	0
58	MG	RA	3101	1/1	0.84	0.25	18,18,18,18	0
58	MG	YA	3024	1/1	0.84	0.43	10,10,10,10	0
58	MG	YA	3081	1/1	0.84	0.35	10,10,10,10	0
58	MG	QA	1613	1/1	0.85	0.26	8,8,8,8	0
58	MG	RA	3134	1/1	0.85	0.14	17,17,17,17	0
58	MG	RA	3006	1/1	0.85	0.12	10,10,10,10	0
58	MG	RA	3076	1/1	0.85	0.12	7,7,7,7	0
58	MG	QA	1666	1/1	0.85	0.14	68,68,68,68	0
58	MG	RA	3091	1/1	0.85	0.28	9,9,9,9	0
58	MG	YA	3139	1/1	0.85	0.18	8,8,8,8	0
58	MG	YA	3140	1/1	0.85	0.28	8,8,8,8	0
58	MG	YA	3068	1/1	0.85	0.24	20,20,20,20	0
58	MG	YA	3156	1/1	0.85	0.32	29,29,29,29	0
58	MG	XA	1656	1/1	0.86	0.24	17,17,17,17	0
58	MG	RA	3155	1/1	0.86	0.41	54,54,54,54	0
58	MG	QA	1672	1/1	0.86	0.13	19,19,19,19	0
58	MG	RA	3138	1/1	0.86	0.18	38,38,38,38	0
58	MG	RA	3119	1/1	0.86	0.19	20,20,20,20	0
58	MG	YA	3007	1/1	0.86	0.30	8,8,8,8	0
58	MG	YA	3069	1/1	0.86	0.23	12,12,12,12	0
58	MG	RA	3182	1/1	0.86	0.23	22,22,22,22	0
58	MG	RA	3150	1/1	0.86	0.24	27,27,27,27	0
58	MG	YA	3215	1/1	0.86	0.15	42,42,42,42	0
58	MG	YA	3235	1/1	0.86	0.08	26,26,26,26	0
58	MG	RA	3191	1/1	0.86	0.14	46,46,46,46	0
58	MG	RA	3126	1/1	0.86	0.20	16,16,16,16	0
58	MG	YA	3117	1/1	0.86	0.20	28,28,28,28	0
58	MG	YA	3027	1/1	0.86	0.20	21,21,21,21	0
58	MG	YA	3038	1/1	0.86	0.27	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3027	1/1	0.87	0.41	15,15,15,15	0
58	MG	XA	1619	1/1	0.87	0.28	5,5,5,5	0
58	MG	YA	3012	1/1	0.87	0.27	10,10,10,10	0
58	MG	XA	1622	1/1	0.87	0.30	6,6,6,6	0
58	MG	YA	3161	1/1	0.87	0.16	23,23,23,23	0
58	MG	YA	3164	1/1	0.87	0.24	44,44,44,44	0
58	MG	RA	3029	1/1	0.87	0.22	2,2,2,2	0
58	MG	QF	201	1/1	0.87	0.14	36,36,36,36	0
58	MG	YA	3194	1/1	0.87	0.17	36,36,36,36	0
58	MG	YA	3199	1/1	0.87	0.22	12,12,12,12	0
58	MG	YA	3078	1/1	0.87	0.21	9,9,9,9	0
58	MG	RA	3124	1/1	0.87	0.23	2,2,2,2	0
58	MG	YA	3025	1/1	0.87	0.23	16,16,16,16	0
58	MG	YA	3085	1/1	0.87	0.26	17,17,17,17	0
58	MG	YA	3216	1/1	0.87	0.17	55,55,55,55	0
58	MG	YA	3093	1/1	0.87	0.26	10,10,10,10	0
58	MG	YA	3255	1/1	0.87	0.31	12,12,12,12	0
58	MG	RA	3238	1/1	0.87	0.23	32,32,32,32	0
58	MG	YA	3028	1/1	0.87	0.20	15,15,15,15	0
58	MG	XA	1680	1/1	0.87	0.20	45,45,45,45	0
58	MG	YB	201	1/1	0.87	0.16	33,33,33,33	0
58	MG	YA	3040	1/1	0.87	0.22	19,19,19,19	0
58	MG	RA	3240	1/1	0.87	0.20	5,5,5,5	0
58	MG	RA	3084	1/1	0.88	0.28	14,14,14,14	0
58	MG	YA	3187	1/1	0.88	0.14	41,41,41,41	0
58	MG	RA	3204	1/1	0.88	0.19	50,50,50,50	0
58	MG	QA	1625	1/1	0.88	0.20	29,29,29,29	0
58	MG	QA	1663	1/1	0.88	0.15	19,19,19,19	0
58	MG	YA	3035	1/1	0.88	0.29	12,12,12,12	0
58	MG	QA	1632	1/1	0.88	0.14	42,42,42,42	0
58	MG	RA	3127	1/1	0.88	0.16	22,22,22,22	0
58	MG	RA	3162	1/1	0.88	0.24	18,18,18,18	0
58	MG	RA	3164	1/1	0.88	0.07	45,45,45,45	0
58	MG	YA	3251	1/1	0.88	0.39	10,10,10,10	0
58	MG	YA	3005	1/1	0.88	0.22	26,26,26,26	0
58	MG	RA	3130	1/1	0.88	0.28	15,15,15,15	0
58	MG	QA	1602	1/1	0.88	0.21	6,6,6,6	0
58	MG	XA	1616	1/1	0.88	0.29	5,5,5,5	0
58	MG	RA	3079	1/1	0.88	0.18	25,25,25,25	0
58	MG	QA	1667	1/1	0.88	0.24	35,35,35,35	0
58	MG	YA	3079	1/1	0.88	0.19	22,22,22,22	0
58	MG	RA	3115	1/1	0.89	0.18	21,21,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	YA	3019	1/1	0.89	0.28	13,13,13,13	0
58	MG	RA	3083	1/1	0.89	0.17	32,32,32,32	0
58	MG	XA	1659	1/1	0.89	0.09	36,36,36,36	0
58	MG	RA	3070	1/1	0.89	0.31	4,4,4,4	0
58	MG	RA	3143	1/1	0.89	0.18	5,5,5,5	0
58	MG	RA	3199	1/1	0.89	0.18	63,63,63,63	0
58	MG	RA	3094	1/1	0.89	0.20	16,16,16,16	0
58	MG	XA	1612	1/1	0.89	0.23	10,10,10,10	0
58	MG	YA	3096	1/1	0.89	0.26	6,6,6,6	0
58	MG	RA	3146	1/1	0.89	0.29	25,25,25,25	0
58	MG	YA	3224	1/1	0.89	0.30	18,18,18,18	0
58	MG	YA	3042	1/1	0.89	0.17	15,15,15,15	0
58	MG	YA	3245	1/1	0.89	0.16	33,33,33,33	0
58	MG	RA	3212	1/1	0.89	0.27	73,73,73,73	0
58	MG	YA	3047	1/1	0.89	0.25	3,3,3,3	0
58	MG	RA	3213	1/1	0.89	0.12	9,9,9,9	0
58	MG	RA	3087	1/1	0.89	0.29	10,10,10,10	0
58	MG	YA	3058	1/1	0.89	0.30	20,20,20,20	0
58	MG	XA	1642	1/1	0.89	0.23	47,47,47,47	0
58	MG	YA	3160	1/1	0.89	0.06	16,16,16,16	0
58	MG	YA	3063	1/1	0.89	0.25	12,12,12,12	0
58	MG	YA	3032	1/1	0.90	0.29	1,1,1,1	0
58	MG	RA	3088	1/1	0.90	0.10	7,7,7,7	0
58	MG	YA	3036	1/1	0.90	0.09	11,11,11,11	0
58	MG	QA	1603	1/1	0.90	0.27	11,11,11,11	0
58	MG	RA	3060	1/1	0.90	0.28	15,15,15,15	0
58	MG	YA	3158	1/1	0.90	0.16	21,21,21,21	0
58	MG	QA	1639	1/1	0.90	0.15	33,33,33,33	0
58	MG	RA	3198	1/1	0.90	0.11	26,26,26,26	0
58	MG	YA	3044	1/1	0.90	0.35	2,2,2,2	0
58	MG	XA	1654	1/1	0.90	0.09	54,54,54,54	0
58	MG	QA	1641	1/1	0.90	0.24	43,43,43,43	0
58	MG	YA	3174	1/1	0.90	0.26	10,10,10,10	0
58	MG	YA	3180	1/1	0.90	0.30	19,19,19,19	0
58	MG	YA	3182	1/1	0.90	0.11	3,3,3,3	0
58	MG	QA	1618	1/1	0.90	0.14	17,17,17,17	0
58	MG	QA	1604	1/1	0.90	0.14	5,5,5,5	0
58	MG	YA	3198	1/1	0.90	0.43	18,18,18,18	0
58	MG	RA	3148	1/1	0.90	0.23	47,47,47,47	0
58	MG	YA	3204	1/1	0.90	0.32	42,42,42,42	0
58	MG	RA	3149	1/1	0.90	0.26	4,4,4,4	0
58	MG	YA	3206	1/1	0.90	0.37	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3078	1/1	0.90	0.20	16,16,16,16	0
58	MG	RA	3215	1/1	0.90	0.10	13,13,13,13	0
58	MG	QA	1612	1/1	0.90	0.25	15,15,15,15	0
58	MG	RA	3114	1/1	0.90	0.26	10,10,10,10	0
58	MG	RA	3042	1/1	0.90	0.15	1,1,1,1	0
58	MG	YA	3233	1/1	0.90	0.18	34,34,34,34	0
58	MG	RA	3116	1/1	0.90	0.20	8,8,8,8	0
57	PAR	QA	1601	42/42	0.90	0.14	42,42,42,42	0
58	MG	RA	3011	1/1	0.90	0.19	0,0,0,0	0
58	MG	RA	3243	1/1	0.90	0.19	1,1,1,1	0
58	MG	RA	3247	1/1	0.90	0.17	9,9,9,9	0
58	MG	XA	1609	1/1	0.90	0.17	51,51,51,51	0
58	MG	QA	1665	1/1	0.90	0.11	37,37,37,37	0
58	MG	YA	3116	1/1	0.90	0.11	14,14,14,14	0
58	MG	YB	202	1/1	0.90	0.24	19,19,19,19	0
58	MG	RA	3172	1/1	0.90	0.15	42,42,42,42	0
58	MG	YA	3029	1/1	0.90	0.26	12,12,12,12	0
58	MG	RA	3211	1/1	0.91	0.11	16,16,16,16	0
58	MG	QA	1614	1/1	0.91	0.23	2,2,2,2	0
58	MG	YA	3147	1/1	0.91	0.08	9,9,9,9	0
58	MG	XA	1655	1/1	0.91	0.13	68,68,68,68	0
58	MG	RA	3007	1/1	0.91	0.27	8,8,8,8	0
58	MG	RA	3096	1/1	0.91	0.20	17,17,17,17	0
58	MG	QA	1623	1/1	0.91	0.17	46,46,46,46	0
58	MG	RA	3168	1/1	0.91	0.22	3,3,3,3	0
58	MG	YA	3163	1/1	0.91	0.18	21,21,21,21	0
58	MG	XA	1679	1/1	0.91	0.09	18,18,18,18	0
58	MG	YA	3050	1/1	0.91	0.23	5,5,5,5	0
58	MG	YA	3052	1/1	0.91	0.08	12,12,12,12	0
58	MG	RA	3169	1/1	0.91	0.16	13,13,13,13	0
58	MG	YA	3055	1/1	0.91	0.25	6,6,6,6	0
58	MG	QA	1674	1/1	0.91	0.14	8,8,8,8	0
58	MG	RA	3233	1/1	0.91	0.11	42,42,42,42	0
58	MG	YA	3188	1/1	0.91	0.12	13,13,13,13	0
58	MG	YA	3192	1/1	0.91	0.22	21,21,21,21	0
58	MG	RA	3044	1/1	0.91	0.19	8,8,8,8	0
58	MG	QA	1657	1/1	0.91	0.12	19,19,19,19	0
58	MG	QA	1660	1/1	0.91	0.15	36,36,36,36	0
58	MG	YA	3201	1/1	0.91	0.05	57,57,57,57	0
58	MG	RA	3192	1/1	0.91	0.15	17,17,17,17	0
58	MG	RA	3193	1/1	0.91	0.13	47,47,47,47	0
58	MG	RP	201	1/1	0.91	0.41	118,118,118,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3195	1/1	0.91	0.13	7,7,7,7	0
58	MG	YA	3084	1/1	0.91	0.14	12,12,12,12	0
58	MG	RA	3051	1/1	0.91	0.28	1,1,1,1	0
58	MG	YA	3086	1/1	0.91	0.23	3,3,3,3	0
58	MG	YA	3219	1/1	0.91	0.26	22,22,22,22	0
58	MG	YA	3090	1/1	0.91	0.19	26,26,26,26	0
58	MG	YA	3227	1/1	0.91	0.19	39,39,39,39	0
58	MG	YA	3092	1/1	0.91	0.16	28,28,28,28	0
58	MG	RA	3019	1/1	0.91	0.11	8,8,8,8	0
58	MG	YA	3236	1/1	0.91	0.22	18,18,18,18	0
58	MG	RA	3023	1/1	0.91	0.17	9,9,9,9	0
58	MG	YA	3247	1/1	0.91	0.10	34,34,34,34	0
58	MG	RA	3202	1/1	0.91	0.12	0,0,0,0	0
58	MG	XA	1620	1/1	0.91	0.16	15,15,15,15	0
58	MG	YA	3103	1/1	0.91	0.15	8,8,8,8	0
58	MG	YA	3106	1/1	0.91	0.16	16,16,16,16	0
58	MG	YA	3115	1/1	0.91	0.15	17,17,17,17	0
58	MG	RA	3001	1/1	0.91	0.18	16,16,16,16	0
58	MG	YA	3034	1/1	0.91	0.23	7,7,7,7	0
58	MG	XA	1637	1/1	0.91	0.25	14,14,14,14	0
58	MG	RA	3002	1/1	0.91	0.12	30,30,30,30	0
58	MG	QA	1629	1/1	0.92	0.14	11,11,11,11	0
58	MG	RA	3142	1/1	0.92	0.29	20,20,20,20	0
58	MG	XA	1650	1/1	0.92	0.18	14,14,14,14	0
58	MG	YA	3030	1/1	0.92	0.30	18,18,18,18	0
57	PAR	XA	1601	42/42	0.92	0.13	38,38,38,38	0
58	MG	RA	3234	1/1	0.92	0.70	69,69,69,69	0
58	MG	RA	3049	1/1	0.92	0.30	12,12,12,12	0
58	MG	RA	3120	1/1	0.92	0.18	4,4,4,4	0
58	MG	YA	3094	1/1	0.92	0.16	12,12,12,12	0
58	MG	QA	1645	1/1	0.92	0.13	4,4,4,4	0
58	MG	RA	3171	1/1	0.92	0.06	31,31,31,31	0
58	MG	RA	3205	1/1	0.92	0.23	17,17,17,17	0
58	MG	YA	3100	1/1	0.92	0.24	8,8,8,8	0
58	MG	RA	3010	1/1	0.92	0.22	14,14,14,14	0
58	MG	XB	301	1/1	0.92	0.32	41,41,41,41	0
58	MG	YA	3108	1/1	0.92	0.31	7,7,7,7	0
58	MG	RA	3173	1/1	0.92	0.20	35,35,35,35	0
58	MG	YA	3002	1/1	0.92	0.20	0,0,0,0	0
58	MG	RA	3103	1/1	0.92	0.16	5,5,5,5	0
58	MG	XA	1613	1/1	0.92	0.21	8,8,8,8	0
58	MG	YA	3221	1/1	0.92	0.04	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	YA	3127	1/1	0.92	0.27	23,23,23,23	0
58	MG	RA	3183	1/1	0.92	0.05	11,11,11,11	0
58	MG	YA	3131	1/1	0.92	0.13	16,16,16,16	0
58	MG	YA	3133	1/1	0.92	0.26	32,32,32,32	0
58	MG	YA	3134	1/1	0.92	0.13	19,19,19,19	0
58	MG	YA	3237	1/1	0.92	0.21	36,36,36,36	0
58	MG	YA	3008	1/1	0.92	0.21	8,8,8,8	0
58	MG	RA	3024	1/1	0.92	0.24	11,11,11,11	0
58	MG	RA	3133	1/1	0.92	0.14	7,7,7,7	0
58	MG	YA	3149	1/1	0.92	0.23	16,16,16,16	0
58	MG	RA	3216	1/1	0.92	0.18	2,2,2,2	0
58	MG	YA	3062	1/1	0.92	0.18	4,4,4,4	0
58	MG	RA	3220	1/1	0.92	0.15	13,13,13,13	0
58	MG	XA	1632	1/1	0.92	0.11	9,9,9,9	0
58	MG	YA	3023	1/1	0.92	0.23	18,18,18,18	0
58	MG	XA	1635	1/1	0.92	0.14	26,26,26,26	0
58	MG	RA	3005	1/1	0.92	0.24	24,24,24,24	0
58	MG	RA	3231	1/1	0.93	0.14	16,16,16,16	0
58	MG	YA	3138	1/1	0.93	0.14	6,6,6,6	0
58	MG	RA	3136	1/1	0.93	0.07	5,5,5,5	0
58	MG	RA	3160	1/1	0.93	0.14	19,19,19,19	0
58	MG	YA	3145	1/1	0.93	0.12	20,20,20,20	0
58	MG	YA	3146	1/1	0.93	0.25	40,40,40,40	0
58	MG	RA	3137	1/1	0.93	0.21	14,14,14,14	0
58	MG	RA	3074	1/1	0.93	0.20	6,6,6,6	0
58	MG	RA	3239	1/1	0.93	0.11	0,0,0,0	0
58	MG	XA	1667	1/1	0.93	0.11	34,34,34,34	0
58	MG	XA	1668	1/1	0.93	0.16	0,0,0,0	0
58	MG	XA	1670	1/1	0.93	0.20	27,27,27,27	0
58	MG	XA	1671	1/1	0.93	0.13	33,33,33,33	0
58	MG	YA	3054	1/1	0.93	0.10	14,14,14,14	0
58	MG	XA	1674	1/1	0.93	0.18	4,4,4,4	0
58	MG	XA	1675	1/1	0.93	0.35	14,14,14,14	0
58	MG	RA	3085	1/1	0.93	0.20	7,7,7,7	0
58	MG	RA	3086	1/1	0.93	0.21	22,22,22,22	0
58	MG	YA	3175	1/1	0.93	0.22	14,14,14,14	0
58	MG	XA	1683	1/1	0.93	0.17	10,10,10,10	0
58	MG	RA	3012	1/1	0.93	0.26	31,31,31,31	0
58	MG	YA	3183	1/1	0.93	0.16	19,19,19,19	0
58	MG	QA	1620	1/1	0.93	0.14	3,3,3,3	0
58	MG	YA	3073	1/1	0.93	0.23	4,4,4,4	0
58	MG	YA	3077	1/1	0.93	0.18	6,6,6,6	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RP	202	1/1	0.93	0.16	76,76,76,76	0
58	MG	YA	3196	1/1	0.93	0.09	41,41,41,41	0
58	MG	YA	3197	1/1	0.93	0.20	42,42,42,42	0
58	MG	R5	101	1/1	0.93	0.21	11,11,11,11	0
58	MG	XA	1604	1/1	0.93	0.27	9,9,9,9	0
58	MG	RA	3208	1/1	0.93	0.07	30,30,30,30	0
58	MG	YA	3203	1/1	0.93	0.16	18,18,18,18	0
58	MG	YA	3083	1/1	0.93	0.21	5,5,5,5	0
58	MG	RA	3125	1/1	0.93	0.22	19,19,19,19	0
58	MG	YA	3011	1/1	0.93	0.20	9,9,9,9	0
58	MG	RA	3026	1/1	0.93	0.22	7,7,7,7	0
58	MG	YA	3087	1/1	0.93	0.24	5,5,5,5	0
58	MG	YA	3089	1/1	0.93	0.20	13,13,13,13	0
58	MG	XA	1615	1/1	0.93	0.13	19,19,19,19	0
58	MG	YA	3217	1/1	0.93	0.11	18,18,18,18	0
58	MG	YA	3218	1/1	0.93	0.12	59,59,59,59	0
58	MG	RA	3175	1/1	0.93	0.23	14,14,14,14	0
58	MG	QA	1643	1/1	0.93	0.14	21,21,21,21	0
58	MG	RA	3106	1/1	0.93	0.13	6,6,6,6	0
58	MG	YA	3020	1/1	0.93	0.27	8,8,8,8	0
58	MG	RA	3184	1/1	0.93	0.15	23,23,23,23	0
58	MG	RA	3185	1/1	0.93	0.12	16,16,16,16	0
58	MG	XA	1624	1/1	0.93	0.14	22,22,22,22	0
58	MG	XA	1630	1/1	0.93	0.17	15,15,15,15	0
58	MG	YA	3243	1/1	0.93	0.15	13,13,13,13	0
58	MG	RA	3111	1/1	0.93	0.15	12,12,12,12	0
58	MG	RA	3221	1/1	0.93	0.17	30,30,30,30	0
58	MG	XA	1636	1/1	0.93	0.23	8,8,8,8	0
58	MG	RA	3188	1/1	0.93	0.11	48,48,48,48	0
58	MG	YA	3033	1/1	0.93	0.23	12,12,12,12	0
58	MG	QA	1670	1/1	0.93	0.30	5,5,5,5	0
58	MG	YA	3261	1/1	0.93	0.07	16,16,16,16	0
58	MG	YA	3120	1/1	0.93	0.41	46,46,46,46	0
58	MG	RA	3158	1/1	0.93	0.14	15,15,15,15	0
58	MG	XA	1648	1/1	0.93	0.15	19,19,19,19	0
58	MG	RA	3229	1/1	0.93	0.09	23,23,23,23	0
58	MG	YA	3039	1/1	0.93	0.20	20,20,20,20	0
58	MG	Y5	101	1/1	0.93	0.20	13,13,13,13	0
58	MG	RA	3008	1/1	0.94	0.25	6,6,6,6	0
58	MG	YA	3178	1/1	0.94	0.15	17,17,17,17	0
58	MG	YA	3037	1/1	0.94	0.18	16,16,16,16	0
58	MG	RA	3082	1/1	0.94	0.16	10,10,10,10	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	XA	1672	1/1	0.94	0.13	16,16,16,16	0
58	MG	YA	3185	1/1	0.94	0.12	22,22,22,22	0
58	MG	RA	3025	1/1	0.94	0.21	3,3,3,3	0
58	MG	QA	1624	1/1	0.94	0.10	26,26,26,26	0
58	MG	YA	3190	1/1	0.94	0.13	8,8,8,8	0
58	MG	YA	3191	1/1	0.94	0.15	9,9,9,9	0
58	MG	RA	3228	1/1	0.94	0.07	13,13,13,13	0
58	MG	YA	3101	1/1	0.94	0.21	5,5,5,5	0
58	MG	QA	1607	1/1	0.94	0.16	22,22,22,22	0
58	MG	YA	3105	1/1	0.94	0.17	19,19,19,19	0
58	MG	RA	3230	1/1	0.94	0.12	41,41,41,41	0
58	MG	RA	3201	1/1	0.94	0.16	34,34,34,34	0
58	MG	YA	3200	1/1	0.94	0.07	6,6,6,6	0
58	MG	YA	3113	1/1	0.94	0.24	17,17,17,17	0
58	MG	XA	1625	1/1	0.94	0.18	5,5,5,5	0
58	MG	QA	1635	1/1	0.94	0.09	76,76,76,76	0
58	MG	RA	3203	1/1	0.94	0.13	15,15,15,15	0
58	MG	QA	1671	1/1	0.94	0.20	6,6,6,6	0
58	MG	RA	3237	1/1	0.94	0.24	6,6,6,6	0
58	MG	YA	3213	1/1	0.94	0.13	31,31,31,31	0
58	MG	RA	3004	1/1	0.94	0.27	40,40,40,40	0
58	MG	YA	3129	1/1	0.94	0.19	20,20,20,20	0
58	MG	YA	3056	1/1	0.94	0.09	5,5,5,5	0
58	MG	XA	1640	1/1	0.94	0.16	27,27,27,27	0
58	MG	XA	1641	1/1	0.94	0.29	11,11,11,11	0
58	MG	RA	3206	1/1	0.94	0.05	5,5,5,5	0
58	MG	YA	3137	1/1	0.94	0.14	10,10,10,10	0
58	MG	RA	3117	1/1	0.94	0.17	11,11,11,11	0
58	MG	YA	3017	1/1	0.94	0.10	11,11,11,11	0
58	MG	YA	3230	1/1	0.94	0.24	42,42,42,42	0
58	MG	XA	1645	1/1	0.94	0.13	5,5,5,5	0
58	MG	YA	3142	1/1	0.94	0.11	31,31,31,31	0
58	MG	RA	3014	1/1	0.94	0.14	28,28,28,28	0
58	MG	RA	3246	1/1	0.94	0.29	33,33,33,33	0
58	MG	YA	3239	1/1	0.94	0.12	41,41,41,41	0
58	MG	XA	1651	1/1	0.94	0.24	33,33,33,33	0
58	MG	YA	3244	1/1	0.94	0.21	0,0,0,0	0
58	MG	RA	3092	1/1	0.94	0.24	0,0,0,0	0
58	MG	YA	3151	1/1	0.94	0.20	3,3,3,3	0
58	MG	YA	3153	1/1	0.94	0.15	14,14,14,14	0
58	MG	YA	3253	1/1	0.94	0.15	22,22,22,22	0
58	MG	RA	3071	1/1	0.94	0.18	11,11,11,11	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3072	1/1	0.94	0.12	18,18,18,18	0
58	MG	YA	3259	1/1	0.94	0.16	5,5,5,5	0
58	MG	YA	3082	1/1	0.94	0.11	17,17,17,17	0
58	MG	XA	1657	1/1	0.94	0.06	19,19,19,19	0
58	MG	RA	3015	1/1	0.94	0.21	0,0,0,0	0
58	MG	XA	1662	1/1	0.94	0.29	12,12,12,12	0
58	MG	QA	1638	1/1	0.94	0.10	14,14,14,14	0
58	MG	XA	1605	1/1	0.94	0.46	15,15,15,15	0
58	MG	YD	302	1/1	0.94	0.21	5,5,5,5	0
58	MG	YX	101	1/1	0.94	0.10	47,47,47,47	0
58	MG	QA	1626	1/1	0.94	0.12	17,17,17,17	0
58	MG	QA	1675	1/1	0.94	0.19	32,32,32,32	0
58	MG	QV	101	1/1	0.94	0.15	22,22,22,22	0
58	MG	RA	3218	1/1	0.95	0.05	17,17,17,17	0
58	MG	QA	1605	1/1	0.95	0.20	6,6,6,6	0
58	MG	XA	1628	1/1	0.95	0.14	18,18,18,18	0
58	MG	RA	3178	1/1	0.95	0.13	25,25,25,25	0
58	MG	RA	3038	1/1	0.95	0.29	4,4,4,4	0
58	MG	YA	3088	1/1	0.95	0.12	6,6,6,6	0
58	MG	YA	3184	1/1	0.95	0.07	23,23,23,23	0
58	MG	RA	3040	1/1	0.95	0.15	13,13,13,13	0
58	MG	YA	3186	1/1	0.95	0.10	25,25,25,25	0
58	MG	RA	3225	1/1	0.95	0.13	33,33,33,33	0
58	MG	YA	3091	1/1	0.95	0.16	29,29,29,29	0
58	MG	RA	3021	1/1	0.95	0.20	18,18,18,18	0
58	MG	RA	3140	1/1	0.95	0.10	34,34,34,34	0
58	MG	RA	3186	1/1	0.95	0.10	17,17,17,17	0
58	MG	RA	3075	1/1	0.95	0.16	9,9,9,9	0
58	MG	RA	3043	1/1	0.95	0.21	10,10,10,10	0
58	MG	RA	3189	1/1	0.95	0.10	14,14,14,14	0
58	MG	XA	1646	1/1	0.95	0.15	21,21,21,21	0
58	MG	RA	3190	1/1	0.95	0.11	40,40,40,40	0
58	MG	RA	3104	1/1	0.95	0.14	11,11,11,11	0
58	MG	QA	1633	1/1	0.95	0.06	15,15,15,15	0
58	MG	QA	1649	1/1	0.95	0.14	32,32,32,32	0
58	MG	RA	3108	1/1	0.95	0.07	6,6,6,6	0
58	MG	QA	1615	1/1	0.95	0.18	9,9,9,9	0
58	MG	RA	3113	1/1	0.95	0.08	1,1,1,1	0
58	MG	QA	1658	1/1	0.95	0.18	39,39,39,39	0
58	MG	QA	1668	1/1	0.95	0.11	0,0,0,0	0
58	MG	RA	3052	1/1	0.95	0.18	1,1,1,1	0
58	MG	YA	3119	1/1	0.95	0.20	9,9,9,9	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3028	1/1	0.95	0.16	17,17,17,17	0
58	MG	XA	1666	1/1	0.95	0.17	85,85,85,85	0
58	MG	YA	3128	1/1	0.95	0.23	6,6,6,6	0
58	MG	YA	3045	1/1	0.95	0.15	5,5,5,5	0
58	MG	RA	3016	1/1	0.95	0.15	8,8,8,8	0
58	MG	R8	101	1/1	0.95	0.12	6,6,6,6	0
58	MG	R8	102	1/1	0.95	0.12	2,2,2,2	0
58	MG	YA	3228	1/1	0.95	0.06	9,9,9,9	0
58	MG	XA	1602	1/1	0.95	0.26	15,15,15,15	0
58	MG	YA	3231	1/1	0.95	0.11	34,34,34,34	0
58	MG	RA	3161	1/1	0.95	0.16	10,10,10,10	0
58	MG	YA	3234	1/1	0.95	0.16	17,17,17,17	0
58	MG	XA	1673	1/1	0.95	0.13	6,6,6,6	0
58	MG	RA	3057	1/1	0.95	0.15	4,4,4,4	0
58	MG	XA	1608	1/1	0.95	0.09	1,1,1,1	0
58	MG	XA	1676	1/1	0.95	0.16	19,19,19,19	0
58	MG	YA	3241	1/1	0.95	0.15	18,18,18,18	0
58	MG	YA	3242	1/1	0.95	0.11	9,9,9,9	0
58	MG	RA	3121	1/1	0.95	0.14	36,36,36,36	0
58	MG	XA	1610	1/1	0.95	0.16	6,6,6,6	0
58	MG	XA	1681	1/1	0.95	0.22	31,31,31,31	0
58	MG	XA	1682	1/1	0.95	0.21	35,35,35,35	0
58	MG	YA	3248	1/1	0.95	0.11	8,8,8,8	0
58	MG	YA	3150	1/1	0.95	0.15	16,16,16,16	0
58	MG	YA	3065	1/1	0.95	0.10	31,31,31,31	0
58	MG	YA	3254	1/1	0.95	0.20	16,16,16,16	0
58	MG	YA	3152	1/1	0.95	0.18	27,27,27,27	0
58	MG	RA	3017	1/1	0.95	0.24	18,18,18,18	0
58	MG	YA	3258	1/1	0.95	0.16	4,4,4,4	0
58	MG	YA	3154	1/1	0.95	0.11	11,11,11,11	0
58	MG	RA	3210	1/1	0.95	0.23	8,8,8,8	0
58	MG	RA	3090	1/1	0.95	0.22	6,6,6,6	0
58	MG	YA	3076	1/1	0.95	0.27	10,10,10,10	0
58	MG	RA	3034	1/1	0.95	0.21	6,6,6,6	0
58	MG	RA	3064	1/1	0.95	0.21	4,4,4,4	0
58	MG	YA	3162	1/1	0.95	0.07	11,11,11,11	0
58	MG	XA	1618	1/1	0.95	0.17	0,0,0,0	0
58	MG	RA	3066	1/1	0.95	0.08	7,7,7,7	0
58	MG	YA	3169	1/1	0.95	0.12	16,16,16,16	0
58	MG	QA	1610	1/1	0.95	0.04	21,21,21,21	0
58	MG	RA	3174	1/1	0.95	0.08	17,17,17,17	0
58	MG	YA	3181	1/1	0.96	0.12	0,0,0,0	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3163	1/1	0.96	0.05	34,34,34,34	0
58	MG	QA	1617	1/1	0.96	0.11	46,46,46,46	0
58	MG	RA	3222	1/1	0.96	0.04	2,2,2,2	0
58	MG	XA	1658	1/1	0.96	0.14	3,3,3,3	0
58	MG	RA	3194	1/1	0.96	0.16	0,0,0,0	0
58	MG	YA	3098	1/1	0.96	0.23	8,8,8,8	0
58	MG	QA	1644	1/1	0.96	0.07	26,26,26,26	0
58	MG	RA	3089	1/1	0.96	0.14	6,6,6,6	0
58	MG	XA	1611	1/1	0.96	0.14	11,11,11,11	0
58	MG	RA	3226	1/1	0.96	0.09	1,1,1,1	0
58	MG	RA	3197	1/1	0.96	0.20	81,81,81,81	0
58	MG	YA	3195	1/1	0.96	0.12	5,5,5,5	0
58	MG	RA	3059	1/1	0.96	0.19	8,8,8,8	0
58	MG	YA	3107	1/1	0.96	0.15	9,9,9,9	0
58	MG	XA	1669	1/1	0.96	0.10	55,55,55,55	0
58	MG	QA	1656	1/1	0.96	0.07	44,44,44,44	0
58	MG	RA	3147	1/1	0.96	0.07	32,32,32,32	0
58	MG	YA	3043	1/1	0.96	0.23	5,5,5,5	0
58	MG	RA	3107	1/1	0.96	0.05	2,2,2,2	0
58	MG	RA	3232	1/1	0.96	0.05	15,15,15,15	0
58	MG	RA	3045	1/1	0.96	0.14	2,2,2,2	0
58	MG	XA	1621	1/1	0.96	0.17	19,19,19,19	0
58	MG	YA	3121	1/1	0.96	0.06	6,6,6,6	0
58	MG	YA	3210	1/1	0.96	0.09	17,17,17,17	0
58	MG	YA	3212	1/1	0.96	0.06	10,10,10,10	0
58	MG	YA	3124	1/1	0.96	0.21	6,6,6,6	0
58	MG	RA	3129	1/1	0.96	0.13	21,21,21,21	0
58	MG	XA	1678	1/1	0.96	0.09	2,2,2,2	0
58	MG	XA	1623	1/1	0.96	0.05	28,28,28,28	0
58	MG	RA	3177	1/1	0.96	0.17	15,15,15,15	0
58	MG	RA	3151	1/1	0.96	0.05	3,3,3,3	0
58	MG	RA	3153	1/1	0.96	0.09	0,0,0,0	0
58	MG	RA	3033	1/1	0.96	0.19	6,6,6,6	0
58	MG	YA	3223	1/1	0.96	0.04	34,34,34,34	0
58	MG	YA	3057	1/1	0.96	0.31	11,11,11,11	0
58	MG	YA	3226	1/1	0.96	0.11	11,11,11,11	0
58	MG	RA	3131	1/1	0.96	0.16	7,7,7,7	0
58	MG	YA	3059	1/1	0.96	0.12	11,11,11,11	0
58	MG	YA	3229	1/1	0.96	0.11	14,14,14,14	0
58	MG	XA	1633	1/1	0.96	0.12	7,7,7,7	0
58	MG	YA	3141	1/1	0.96	0.09	19,19,19,19	0
58	MG	XA	1634	1/1	0.96	0.17	7,7,7,7	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3241	1/1	0.96	0.12	8,8,8,8	0
58	MG	RA	3242	1/1	0.96	0.23	13,13,13,13	0
58	MG	YA	3067	1/1	0.96	0.16	17,17,17,17	0
58	MG	YA	3006	1/1	0.96	0.16	26,26,26,26	0
58	MG	RA	3156	1/1	0.96	0.15	9,9,9,9	0
58	MG	YA	3240	1/1	0.96	0.23	12,12,12,12	0
58	MG	YA	3071	1/1	0.96	0.04	1,1,1,1	0
58	MG	YA	3072	1/1	0.96	0.17	22,22,22,22	0
58	MG	XA	1639	1/1	0.96	0.07	45,45,45,45	0
58	MG	YA	3009	1/1	0.96	0.19	15,15,15,15	0
58	MG	YA	3010	1/1	0.96	0.24	15,15,15,15	0
58	MG	YA	3246	1/1	0.96	0.08	0,0,0,0	0
58	MG	QA	1609	1/1	0.96	0.08	32,32,32,32	0
58	MG	QA	1646	1/1	0.96	0.07	28,28,28,28	0
58	MG	YA	3249	1/1	0.96	0.16	20,20,20,20	0
58	MG	YA	3250	1/1	0.96	0.15	15,15,15,15	0
58	MG	YA	3159	1/1	0.96	0.09	12,12,12,12	0
58	MG	YA	3252	1/1	0.96	0.24	1,1,1,1	0
58	MG	YA	3013	1/1	0.96	0.23	3,3,3,3	0
58	MG	RB	202	1/1	0.96	0.14	29,29,29,29	0
58	MG	RE	301	1/1	0.96	0.08	9,9,9,9	0
58	MG	XA	1644	1/1	0.96	0.08	4,4,4,4	0
58	MG	RA	3135	1/1	0.96	0.07	12,12,12,12	0
58	MG	YA	3165	1/1	0.96	0.17	1,1,1,1	0
58	MG	QA	1631	1/1	0.96	0.09	50,50,50,50	0
58	MG	XA	1647	1/1	0.96	0.07	22,22,22,22	0
58	MG	YA	3171	1/1	0.96	0.07	22,22,22,22	0
58	MG	YA	3022	1/1	0.96	0.21	7,7,7,7	0
58	MG	YA	3173	1/1	0.96	0.06	15,15,15,15	0
58	MG	R0	101	1/1	0.96	0.13	2,2,2,2	0
58	MG	QA	1669	1/1	0.96	0.24	18,18,18,18	0
58	MG	YP	201	1/1	0.96	0.22	54,54,54,54	0
58	MG	YP	202	1/1	0.96	0.08	1,1,1,1	0
58	MG	YQ	201	1/1	0.96	0.09	90,90,90,90	0
58	MG	YA	3176	1/1	0.96	0.05	45,45,45,45	0
58	MG	QM	201	1/1	0.96	0.09	51,51,51,51	0
58	MG	YA	3179	1/1	0.96	0.13	26,26,26,26	0
58	MG	RA	3219	1/1	0.96	0.16	8,8,8,8	0
58	MG	RA	3097	1/1	0.97	0.18	5,5,5,5	0
58	MG	RA	3152	1/1	0.97	0.16	14,14,14,14	0
58	MG	QA	1661	1/1	0.97	0.14	50,50,50,50	0
58	MG	QA	1676	1/1	0.97	0.08	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	YA	3220	1/1	0.97	0.11	1,1,1,1	0
58	MG	XA	1660	1/1	0.97	0.04	22,22,22,22	0
58	MG	RA	3080	1/1	0.97	0.15	10,10,10,10	0
58	MG	YA	3016	1/1	0.97	0.09	7,7,7,7	0
58	MG	YA	3109	1/1	0.97	0.10	10,10,10,10	0
58	MG	YA	3110	1/1	0.97	0.13	4,4,4,4	0
58	MG	YA	3111	1/1	0.97	0.05	26,26,26,26	0
58	MG	YA	3112	1/1	0.97	0.09	13,13,13,13	0
58	MG	RA	3245	1/1	0.97	0.28	7,7,7,7	0
58	MG	YA	3114	1/1	0.97	0.18	6,6,6,6	0
58	MG	XA	1664	1/1	0.97	0.08	22,22,22,22	0
58	MG	YA	3064	1/1	0.97	0.12	4,4,4,4	0
58	MG	RA	3058	1/1	0.97	0.07	5,5,5,5	0
58	MG	YA	3177	1/1	0.97	0.06	4,4,4,4	0
58	MG	RA	3020	1/1	0.97	0.13	4,4,4,4	0
58	MG	XA	1627	1/1	0.97	0.11	12,12,12,12	0
58	MG	QA	1640	1/1	0.97	0.05	13,13,13,13	0
58	MG	RA	3032	1/1	0.97	0.11	14,14,14,14	0
58	MG	YA	3122	1/1	0.97	0.07	9,9,9,9	0
58	MG	XA	1631	1/1	0.97	0.12	4,4,4,4	0
58	MG	RE	302	1/1	0.97	0.12	15,15,15,15	0
58	MG	RA	3022	1/1	0.97	0.18	24,24,24,24	0
58	MG	QA	1627	1/1	0.97	0.07	30,30,30,30	0
58	MG	RA	3048	1/1	0.97	0.14	2,2,2,2	0
58	MG	RA	3069	1/1	0.97	0.13	19,19,19,19	0
58	MG	RA	3139	1/1	0.97	0.13	12,12,12,12	0
58	MG	XA	1677	1/1	0.97	0.12	2,2,2,2	0
58	MG	XA	1638	1/1	0.97	0.15	4,4,4,4	0
58	MG	YA	3193	1/1	0.97	0.10	14,14,14,14	0
58	MG	QA	1630	1/1	0.97	0.08	7,7,7,7	0
58	MG	RA	3141	1/1	0.97	0.12	40,40,40,40	0
58	MG	RA	3050	1/1	0.97	0.12	9,9,9,9	0
58	MG	RA	3170	1/1	0.97	0.05	9,9,9,9	0
58	MG	YA	3257	1/1	0.97	0.23	14,14,14,14	0
58	MG	XA	1606	1/1	0.97	0.22	3,3,3,3	0
58	MG	YA	3143	1/1	0.97	0.06	0,0,0,0	0
58	MG	YA	3144	1/1	0.97	0.05	6,6,6,6	0
58	MG	RA	3200	1/1	0.97	0.07	9,9,9,9	0
58	MG	QA	1659	1/1	0.97	0.06	42,42,42,42	0
58	MG	YA	3264	1/1	0.97	0.30	5,5,5,5	0
58	MG	YA	3265	1/1	0.97	0.13	24,24,24,24	0
58	MG	YA	3001	1/1	0.97	0.20	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3073	1/1	0.97	0.09	10,10,10,10	0
58	MG	RA	3118	1/1	0.97	0.18	16,16,16,16	0
58	MG	YA	3004	1/1	0.97	0.12	11,11,11,11	0
58	MG	YA	3208	1/1	0.97	0.11	35,35,35,35	0
58	MG	YA	3209	1/1	0.97	0.10	7,7,7,7	0
58	MG	QA	1650	1/1	0.97	0.07	53,53,53,53	0
58	MG	RA	3053	1/1	0.97	0.07	2,2,2,2	0
58	MG	RA	3039	1/1	0.97	0.17	7,7,7,7	0
58	MG	RA	3077	1/1	0.97	0.17	6,6,6,6	0
58	MG	RA	3180	1/1	0.97	0.06	17,17,17,17	0
58	MG	XV	101	1/1	0.97	0.09	3,3,3,3	0
58	MG	XV	102	1/1	0.97	0.14	2,2,2,2	0
58	MG	QA	1634	1/1	0.98	0.10	23,23,23,23	0
58	MG	YA	3225	1/1	0.98	0.13	12,12,12,12	0
58	MG	RA	3176	1/1	0.98	0.04	21,21,21,21	0
58	MG	RA	3100	1/1	0.98	0.05	0,0,0,0	0
58	MG	YA	3123	1/1	0.98	0.14	1,1,1,1	0
58	MG	RA	3061	1/1	0.98	0.08	0,0,0,0	0
58	MG	YA	3125	1/1	0.98	0.07	11,11,11,11	0
58	MG	YA	3126	1/1	0.98	0.04	0,0,0,0	0
58	MG	RA	3207	1/1	0.98	0.18	7,7,7,7	0
58	MG	QA	1642	1/1	0.98	0.04	38,38,38,38	0
58	MG	XA	1652	1/1	0.98	0.03	32,32,32,32	0
58	MG	XA	1653	1/1	0.98	0.09	42,42,42,42	0
58	MG	RA	3181	1/1	0.98	0.12	21,21,21,21	0
58	MG	RA	3128	1/1	0.98	0.09	9,9,9,9	0
58	MG	QA	1652	1/1	0.98	0.05	13,13,13,13	0
58	MG	YA	3135	1/1	0.98	0.04	6,6,6,6	0
58	MG	QA	1653	1/1	0.98	0.10	0,0,0,0	0
58	MG	RA	3030	1/1	0.98	0.07	8,8,8,8	0
58	MG	YA	3189	1/1	0.98	0.06	30,30,30,30	0
58	MG	YA	3048	1/1	0.98	0.13	4,4,4,4	0
58	MG	RA	3244	1/1	0.98	0.06	0,0,0,0	0
58	MG	RA	3068	1/1	0.98	0.35	13,13,13,13	0
58	MG	QA	1654	1/1	0.98	0.07	12,12,12,12	0
58	MG	RA	3003	1/1	0.98	0.12	4,4,4,4	0
58	MG	RB	201	1/1	0.98	0.11	16,16,16,16	0
58	MG	YA	3097	1/1	0.98	0.04	11,11,11,11	0
58	MG	RA	3109	1/1	0.98	0.09	0,0,0,0	0
58	MG	RD	301	1/1	0.98	0.07	12,12,12,12	0
58	MG	YA	3148	1/1	0.98	0.05	15,15,15,15	0
58	MG	QA	1655	1/1	0.98	0.07	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3112	1/1	0.98	0.08	7,7,7,7	0
58	MG	YA	3202	1/1	0.98	0.08	38,38,38,38	0
58	MG	RF	301	1/1	0.98	0.07	13,13,13,13	0
58	MG	YA	3104	1/1	0.98	0.06	0,0,0,0	0
58	MG	QA	1608	1/1	0.98	0.08	4,4,4,4	0
58	MG	YA	3061	1/1	0.98	0.09	15,15,15,15	0
58	MG	YA	3262	1/1	0.98	0.19	26,26,26,26	0
58	MG	YA	3021	1/1	0.98	0.15	8,8,8,8	0
58	MG	QA	1636	1/1	0.98	0.21	1,1,1,1	0
58	MG	YA	3157	1/1	0.98	0.05	0,0,0,0	0
58	MG	QA	1637	1/1	0.98	0.06	17,17,17,17	0
58	MG	RA	3166	1/1	0.98	0.05	5,5,5,5	0
58	MG	QA	1611	1/1	0.98	0.05	1,1,1,1	0
58	MG	QA	1628	1/1	0.98	0.04	10,10,10,10	0
58	MG	QA	1606	1/1	0.98	0.30	10,10,10,10	0
58	MG	RA	3145	1/1	0.98	0.10	3,3,3,3	0
58	MG	RA	3041	1/1	0.98	0.20	9,9,9,9	0
58	MG	QA	1662	1/1	0.98	0.06	0,0,0,0	0
58	MG	YA	3168	1/1	0.98	0.06	3,3,3,3	0
58	MG	YA	3075	1/1	0.98	0.06	12,12,12,12	0
58	MG	XA	1607	1/1	0.98	0.24	7,7,7,7	0
58	MG	YA	3222	1/1	0.98	0.09	13,13,13,13	0
58	MG	RA	3098	1/1	0.98	0.09	10,10,10,10	0
58	MG	RA	3110	1/1	0.99	0.04	19,19,19,19	0
58	MG	RA	3035	1/1	0.99	0.07	2,2,2,2	0
58	MG	YA	3136	1/1	0.99	0.03	0,0,0,0	0
58	MG	RA	3062	1/1	0.99	0.09	21,21,21,21	0
58	MG	YA	3026	1/1	0.99	0.32	5,5,5,5	0
58	MG	YA	3066	1/1	0.99	0.26	6,6,6,6	0
58	MG	YA	3166	1/1	0.99	0.03	11,11,11,11	0
58	MG	YA	3167	1/1	0.99	0.08	15,15,15,15	0
58	MG	XA	1626	1/1	0.99	0.06	15,15,15,15	0
58	MG	RA	3167	1/1	0.99	0.10	1,1,1,1	0
58	MG	QA	1622	1/1	0.99	0.07	12,12,12,12	0
58	MG	YA	3070	1/1	0.99	0.05	1,1,1,1	0
58	MG	XA	1629	1/1	0.99	0.04	4,4,4,4	0
58	MG	YA	3031	1/1	0.99	0.04	5,5,5,5	0
58	MG	YA	3051	1/1	0.99	0.16	13,13,13,13	0
58	MG	YA	3232	1/1	0.99	0.04	35,35,35,35	0
58	MG	YA	3074	1/1	0.99	0.03	1,1,1,1	0
58	MG	XA	1614	1/1	0.99	0.09	21,21,21,21	0
58	MG	RA	3179	1/1	0.99	0.04	4,4,4,4	0

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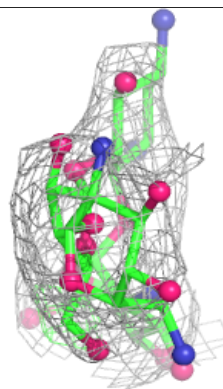
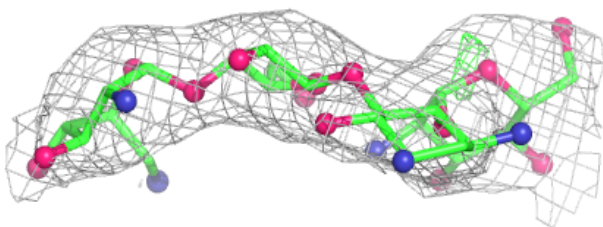
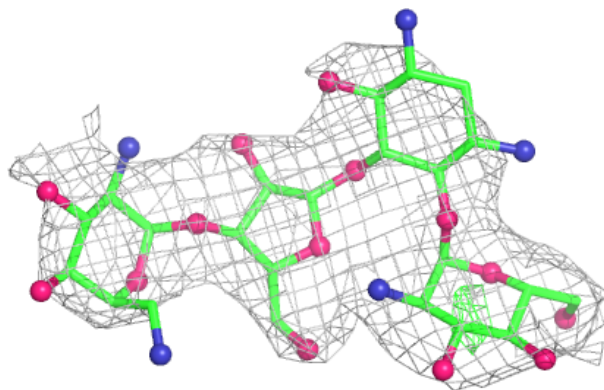
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
58	MG	RA	3236	1/1	0.99	0.27	13,13,13,13	0
58	MG	YB	203	1/1	0.99	0.03	4,4,4,4	0
58	MG	XA	1649	1/1	0.99	0.04	17,17,17,17	0
58	MG	YA	3238	1/1	0.99	0.07	76,76,76,76	0
58	MG	YA	3102	1/1	0.99	0.03	8,8,8,8	0
58	MG	XA	1603	1/1	0.99	0.09	1,1,1,1	0
58	MG	RA	3132	1/1	0.99	0.05	9,9,9,9	0
58	MG	YA	3211	1/1	0.99	0.15	55,55,55,55	0
58	MG	QA	1673	1/1	0.99	0.10	9,9,9,9	0
58	MG	RA	3065	1/1	0.99	0.10	0,0,0,0	0
58	MG	QA	1651	1/1	0.99	0.03	5,5,5,5	0
58	MG	YA	3132	1/1	0.99	0.03	7,7,7,7	0
58	MG	RA	3055	1/1	0.99	0.04	10,10,10,10	0
59	ZN	QN	101	1/1	0.99	0.04	86,86,86,86	0
59	ZN	XD	301	1/1	0.99	0.13	10,10,10,10	0
58	MG	RA	3123	1/1	1.00	0.02	10,10,10,10	0
58	MG	RA	3122	1/1	1.00	0.02	5,5,5,5	0
59	ZN	QD	301	1/1	1.00	0.09	27,27,27,27	0
58	MG	XA	1661	1/1	1.00	0.04	2,2,2,2	0
58	MG	RA	3217	1/1	1.00	0.03	8,8,8,8	0
59	ZN	XN	101	1/1	1.00	0.02	70,70,70,70	0

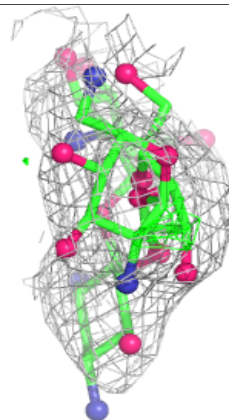
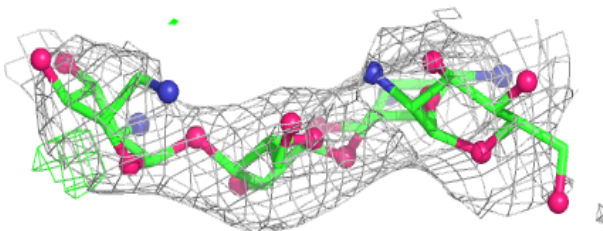
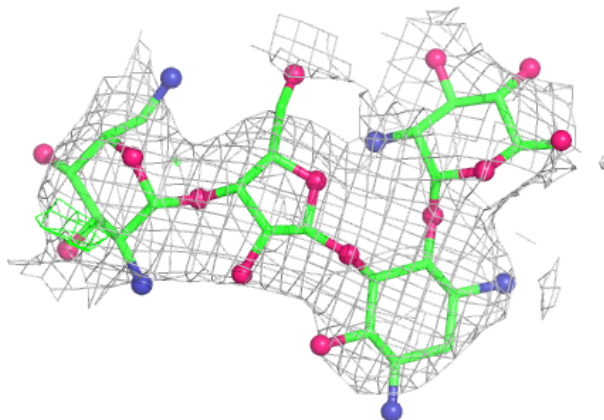
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around PAR QA 1601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around PAR XA 1601:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.