



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 25, 2024 – 04:38 AM EST

PDB ID : 4ZSN  
Title : 70S-wild-type HigB toxin complex bound to a AAA lysine codon  
Authors : Schureck, M.A.; Dunham, C.M.  
Deposited on : 2015-05-13  
Resolution : 3.60 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](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

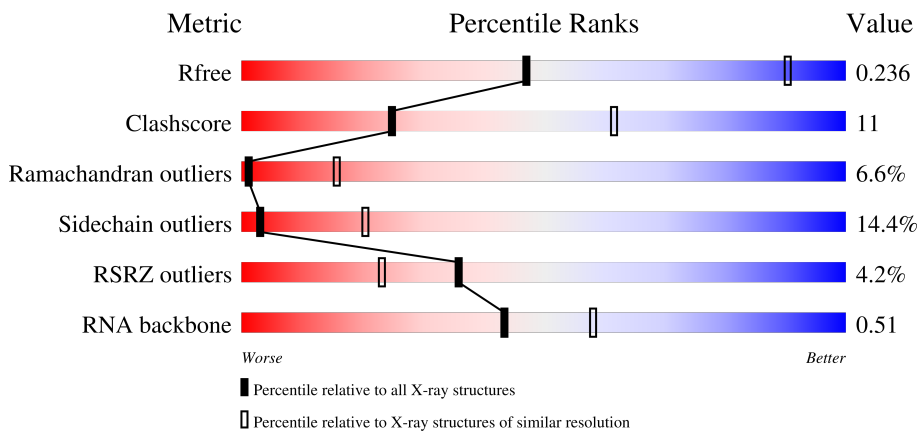
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.60 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)
RNA backbone	3102	1017 (4.20-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	 2% 56% 34% 9%
1	XA	1522	 2% 57% 33% 8%
2	QB	256	 4% 52% 31% 8% 8%
2	XB	256	 50% 34% 8% 8%

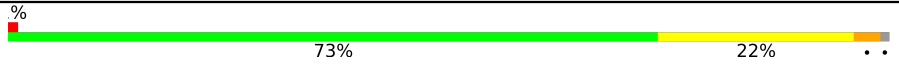
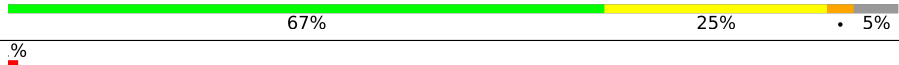
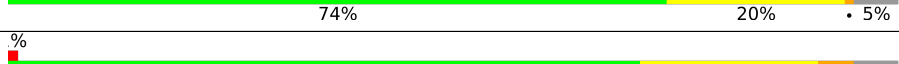
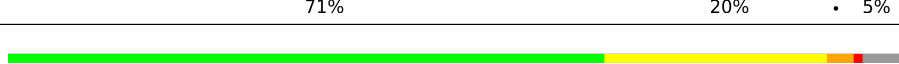
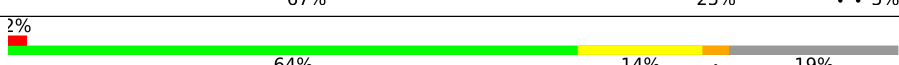

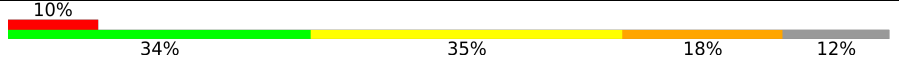
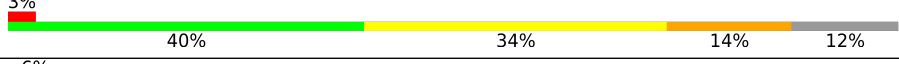
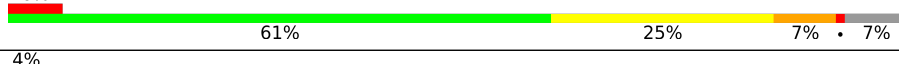


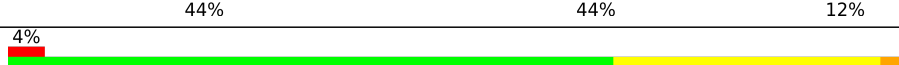
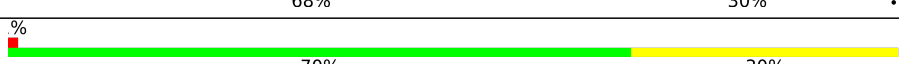
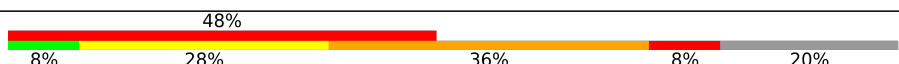
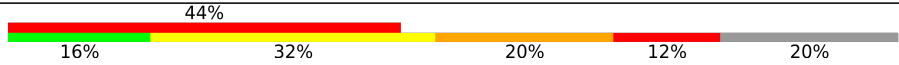
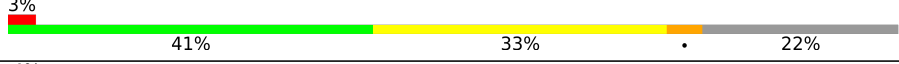





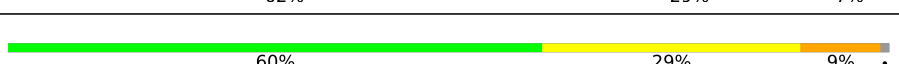



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Mol	Chain	Length	Quality of chain
3	QC	239	
3	XC	239	
4	QD	209	
4	XD	209	
5	QE	162	
5	XE	162	
6	QF	101	
6	XF	101	
7	QG	156	
7	XG	156	
8	QH	138	
8	XH	138	
9	QI	128	
9	XI	128	
10	QJ	105	
10	XJ	105	
11	QK	129	
11	XK	129	
12	QL	132	
12	XL	132	
13	QM	126	
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	 73% 22% 5%
16	QP	88	 67% 25% 5%
16	XP	88	 74% 20% 5%
17	QQ	105	 71% 20% 5%
17	XQ	105	 67% 25% 5%
18	QR	88	 64% 14% 19% 2%
18	XR	88	 47% 30% 5% 19%
19	QS	93	 34% 35% 18% 12% 10%
19	XS	93	 40% 34% 14% 12% 3%
20	QT	106	 61% 25% 7% 7% 6%
20	XT	106	 55% 32% 6% 7% 4%
21	QU	25	 48% 44% 8%
21	XU	25	 44% 44% 12%
22	QV	77	 68% 30%
22	XV	77	 70% 30%
23	QX	25	 28% 36% 8% 20% 8%
23	XX	25	 16% 32% 20% 12% 20%
24	QY	118	 41% 33% 22% 3%
24	XY	118	 35% 41% 22% 4%
25	RA	2916	 58% 32% 9%
25	YA	2916	 58% 32% 8%
26	RB	124	 61% 29% 8%
26	YB	124	 59% 28% 11%
27	RD	276	 62% 29% 7%
27	YD	276	 60% 29% 9%

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Mol	Chain	Length	Quality of chain
28	RE	206	3% 49% 36% 12%
28	YE	206	3% 49% 39% 9%
29	RF	210	3% 60% 31% 8%
29	YF	210	3% 54% 35% 10%
30	RG	182	% 60% 35%
30	YG	182	2% 57% 36% 7%
31	RH	180	13% 44% 37% 12% 6%
31	YH	180	11% 38% 40% 14% 6%
32	RI	148	% 59% 27% 11%
32	YI	148	2% 58% 29% 11%
33	RN	140	% 74% 21%
33	YN	140	% 68% 26%
34	RO	122	% 65% 30%
34	YO	122	% 71% 25%
35	RP	150	2% 41% 38% 15% 7%
35	YP	150	3% 44% 36% 13% 7%
36	RQ	141	% 63% 28%
36	YQ	141	% 58% 30% 9%
37	RR	118	% 69% 24%
37	YR	118	% 69% 25%
38	RS	112	6% 58% 35%
38	YS	112	2% 52% 38%
39	RT	146	% 51% 38%
39	YT	146	4% 55% 31% 8% 6%
40	RU	118	2% 67% 29%







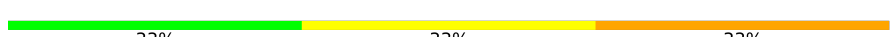
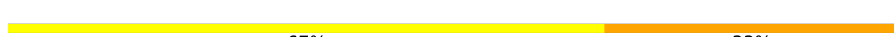
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Mol	Chain	Length	Quality of chain
40	YU	118	68% 27% . . .
41	RV	101	2% 40% 45% 12% .
41	YV	101	2% 43% 43% 12% .
42	RW	113	66% 29% .
42	YW	113	2% 65% 26% 9%
43	RX	96	72% 21% . .
43	YX	96	64% 30% . .
44	RY	110	10% 35% 38% 14% 6% 7%
44	YY	110	6% 34% 40% 17% . 7%
45	RZ	206	3% 40% 31% 14% 15%
45	YZ	206	3% 48% 30% 10% . 11%
46	R0	85	2% 64% 31% . .
46	Y0	85	58% 35% 5% .
47	R1	98	6% 49% 38% 10% . .
47	Y1	98	5% 59% 35% . . .
48	R2	72	6% 53% 31% 10% . .
48	Y2	72	62% 24% 7% . .
49	R3	60	5% 70% 22% 7% .
49	Y3	60	68% 27% . .
50	R4	71	14% 44% 37% 18% .
50	Y4	71	14% 32% 45% 18% . .
51	R5	60	7% 70% 25% . . .
51	Y5	60	2% 57% 32% 5% . 5%
52	R6	54	78% 24% 37% 28% 11%
52	Y6	54	74% 22% 31% 30% 6% 11%

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Mol	Chain	Length	Quality of chain
53	R7	49	
53	Y7	49	
54	R8	65	
54	Y8	65	
55	R9	37	
55	Y9	37	
56	Z6	3	
56	Z7	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
57	MG	QA	1613	-	-	-	X
57	MG	QA	1629	-	-	-	X
57	MG	QA	1637	-	-	-	X
57	MG	QA	1658	-	-	-	X
57	MG	QA	1663	-	-	-	X
57	MG	QA	1671	-	-	-	X
57	MG	QA	1672	-	-	-	X
57	MG	QA	1683	-	-	-	X
57	MG	QA	1696	-	-	-	X
57	MG	QA	1707	-	-	-	X
57	MG	QA	1710	-	-	-	X
57	MG	QA	1711	-	-	-	X
57	MG	QA	1716	-	-	-	X
57	MG	QA	1718	-	-	-	X
57	MG	QA	1719	-	-	-	X
57	MG	QA	1740	-	-	-	X
57	MG	QA	1742	-	-	-	X
57	MG	QA	1744	-	-	-	X
57	MG	QA	1747	-	-	-	X
57	MG	QD	302	-	-	-	X
57	MG	R0	102	-	-	-	X
57	MG	RA	3001	-	-	-	X
57	MG	RA	3048	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	RA	3089	-	-	-	X
57	MG	RA	3102	-	-	-	X
57	MG	RA	3142	-	-	-	X
57	MG	RA	3173	-	-	-	X
57	MG	RA	3176	-	-	-	X
57	MG	RA	3177	-	-	-	X
57	MG	RA	3182	-	-	-	X
57	MG	RA	3186	-	-	-	X
57	MG	RA	3187	-	-	-	X
57	MG	RA	3204	-	-	-	X
57	MG	RA	3221	-	-	-	X
57	MG	RA	3234	-	-	-	X
57	MG	RA	3262	-	-	-	X
57	MG	RA	3266	-	-	-	X
57	MG	RA	3269	-	-	-	X
57	MG	RA	3270	-	-	-	X
57	MG	RA	3275	-	-	-	X
57	MG	RA	3278	-	-	-	X
57	MG	RA	3284	-	-	-	X
57	MG	RA	3292	-	-	-	X
57	MG	RA	3298	-	-	-	X
57	MG	RA	3300	-	-	-	X
57	MG	RA	3302	-	-	-	X
57	MG	RA	3311	-	-	-	X
57	MG	RA	3316	-	-	-	X
57	MG	RA	3325	-	-	-	X
57	MG	RA	3326	-	-	-	X
57	MG	RA	3327	-	-	-	X
57	MG	RA	3333	-	-	-	X
57	MG	RA	3334	-	-	-	X
57	MG	RA	3335	-	-	-	X
57	MG	RA	3338	-	-	-	X
57	MG	RA	3340	-	-	-	X
57	MG	RA	3342	-	-	-	X
57	MG	RA	3347	-	-	-	X
57	MG	RA	3370	-	-	-	X
57	MG	RA	3372	-	-	-	X
57	MG	RA	3394	-	-	-	X
57	MG	RA	3400	-	-	-	X
57	MG	RA	3421	-	-	-	X
57	MG	RA	3425	-	-	-	X
57	MG	RA	3428	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	RA	3431	-	-	-	X
57	MG	RD	301	-	-	-	X
57	MG	RY	202	-	-	-	X
57	MG	XA	1630	-	-	-	X
57	MG	XA	1652	-	-	-	X
57	MG	XA	1676	-	-	-	X
57	MG	XA	1686	-	-	-	X
57	MG	XA	1688	-	-	-	X
57	MG	XA	1689	-	-	-	X
57	MG	XA	1700	-	-	-	X
57	MG	XA	1709	-	-	-	X
57	MG	XA	1710	-	-	-	X
57	MG	XA	1714	-	-	-	X
57	MG	XA	1718	-	-	-	X
57	MG	XA	1720	-	-	-	X
57	MG	XA	1722	-	-	-	X
57	MG	XA	1725	-	-	-	X
57	MG	XA	1729	-	-	-	X
57	MG	XA	1735	-	-	-	X
57	MG	XA	1742	-	-	-	X
57	MG	XA	1755	-	-	-	X
57	MG	XA	1756	-	-	-	X
57	MG	XV	103	-	-	-	X
57	MG	Y5	103	-	-	-	X
57	MG	YA	3113	-	-	-	X
57	MG	YA	3135	-	-	-	X
57	MG	YA	3146	-	-	-	X
57	MG	YA	3167	-	-	-	X
57	MG	YA	3168	-	-	-	X
57	MG	YA	3169	-	-	-	X
57	MG	YA	3179	-	-	-	X
57	MG	YA	3184	-	-	-	X
57	MG	YA	3191	-	-	-	X
57	MG	YA	3202	-	-	-	X
57	MG	YA	3222	-	-	-	X
57	MG	YA	3226	-	-	-	X
57	MG	YA	3228	-	-	-	X
57	MG	YA	3237	-	-	-	X
57	MG	YA	3264	-	-	-	X
57	MG	YA	3265	-	-	-	X
57	MG	YA	3278	-	-	-	X
57	MG	YA	3286	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	YA	3301	-	-	-	X
57	MG	YA	3303	-	-	-	X
57	MG	YA	3306	-	-	-	X
57	MG	YA	3309	-	-	-	X
57	MG	YA	3316	-	-	-	X
57	MG	YA	3318	-	-	-	X
57	MG	YA	3322	-	-	-	X
57	MG	YA	3325	-	-	-	X
57	MG	YA	3333	-	-	-	X
57	MG	YA	3338	-	-	-	X
57	MG	YA	3342	-	-	-	X
57	MG	YA	3343	-	-	-	X
57	MG	YA	3349	-	-	-	X
57	MG	YA	3351	-	-	-	X
57	MG	YA	3352	-	-	-	X
57	MG	YA	3353	-	-	-	X
57	MG	YA	3354	-	-	-	X
57	MG	YA	3357	-	-	-	X
57	MG	YA	3368	-	-	-	X
57	MG	YA	3372	-	-	-	X
57	MG	YA	3373	-	-	-	X
57	MG	YA	3377	-	-	-	X
57	MG	YA	3399	-	-	-	X
57	MG	YA	3400	-	-	-	X
57	MG	YA	3405	-	-	-	X
57	MG	YA	3409	-	-	-	X
57	MG	YA	3423	-	-	-	X
57	MG	YA	3425	-	-	-	X
57	MG	YA	3451	-	-	-	X
57	MG	YA	3459	-	-	-	X
57	MG	YA	3461	-	-	-	X
57	MG	YA	3471	-	-	-	X
57	MG	YD	301	-	-	-	X
57	MG	YQ	202	-	-	-	X
57	MG	YU	201	-	-	-	X

## 2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 294410 atoms, of which 18 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
			Total	C	N	O	P			
1	QA	1511	Total 32472	C 14453	N 6011	O 10497	P 1511	0	0	0
1	XA	1508	Total 32409	C 14425	N 6001	O 10475	P 1508	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	QB	236	Total 1915	C 1223	N 343	O 344	S 5	0	0	0
2	XB	236	Total 1915	C 1223	N 343	O 344	S 5	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	QC	206	Total 1612	C 1016	N 314	O 281	S 1	0	0	0
3	XC	206	Total 1612	C 1016	N 314	O 281	S 1	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	QE	154	Total	C	N	O	S	0	0	0
			1178	743	221	210	4			
5	XE	154	Total	C	N	O	S	0	0	0
			1178	743	221	210	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	128	Total	C	N	O	S	0	0	0
			1018	644	198	175	1			
9	XI	128	Total	C	N	O	S	0	0	0
			1018	644	198	175	1			

- 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
			Total	C	N	O	S			
10	XJ	99	801	504	157	139	1	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
11	QK	121	901	560	171	167	3	0	0	0
11	XK	121	901	560	171	167	3	0	0	0

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
13	QM	118	937	579	193	163	2	0	0	0
13	XM	118	937	579	193	163	2	0	0	0

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

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

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

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

- 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	71	Total	C	N	O	0	0	0
			585	373	116	96			
18	XR	71	Total	C	N	O	0	0	0
			585	373	116	96			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	QS	82	Total	C	N	O	S	0	0	0
			656	419	121	114	2			
19	XS	82	Total	C	N	O	S	0	0	0
			656	419	121	114	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 P-site tRNA-fMet.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	QV	77	Total	C	N	O	P	0	0	0
			1640	732	297	535	76			
22	XV	77	Total	C	N	O	P	0	0	0
			1640	732	297	535	76			

- Molecule 23 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
23	QX	20	Total	C	H	N	O	P	0	0	0
			449	199	9	89	132	20			
23	XX	20	Total	C	H	N	O	P	0	0	0
			449	199	9	89	132	20			

- Molecule 24 is a protein called Killer protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
24	QY	92	Total	C	N	O	0	0	0
			756	484	134	138			
24	XY	92	Total	C	N	O	0	0	0
			756	484	134	138			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
QY	0	MET	-	initiating methionine	UNP Q7A225
QY	1	GLY	-	expression tag	UNP Q7A225
QY	93	LYS	-	expression tag	UNP Q7A225
QY	94	LEU	-	expression tag	UNP Q7A225
QY	95	GLY	-	expression tag	UNP Q7A225
QY	96	PRO	-	expression tag	UNP Q7A225
QY	97	GLU	-	expression tag	UNP Q7A225
QY	98	GLN	-	expression tag	UNP Q7A225
QY	99	LYS	-	expression tag	UNP Q7A225
QY	100	LEU	-	expression tag	UNP Q7A225
QY	101	ILE	-	expression tag	UNP Q7A225

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Chain	Residue	Modelled	Actual	Comment	Reference
QY	102	SER	-	expression tag	UNP Q7A225
QY	103	GLU	-	expression tag	UNP Q7A225
QY	104	GLU	-	expression tag	UNP Q7A225
QY	105	ASP	-	expression tag	UNP Q7A225
QY	106	LEU	-	expression tag	UNP Q7A225
QY	107	ASN	-	expression tag	UNP Q7A225
QY	108	SER	-	expression tag	UNP Q7A225
QY	109	ALA	-	expression tag	UNP Q7A225
QY	110	VAL	-	expression tag	UNP Q7A225
QY	111	ASP	-	expression tag	UNP Q7A225
QY	112	HIS	-	expression tag	UNP Q7A225
QY	113	HIS	-	expression tag	UNP Q7A225
QY	114	HIS	-	expression tag	UNP Q7A225
QY	115	HIS	-	expression tag	UNP Q7A225
QY	116	HIS	-	expression tag	UNP Q7A225
QY	117	HIS	-	expression tag	UNP Q7A225
XY	0	MET	-	initiating methionine	UNP Q7A225
XY	1	GLY	-	expression tag	UNP Q7A225
XY	93	LYS	-	expression tag	UNP Q7A225
XY	94	LEU	-	expression tag	UNP Q7A225
XY	95	GLY	-	expression tag	UNP Q7A225
XY	96	PRO	-	expression tag	UNP Q7A225
XY	97	GLU	-	expression tag	UNP Q7A225
XY	98	GLN	-	expression tag	UNP Q7A225
XY	99	LYS	-	expression tag	UNP Q7A225
XY	100	LEU	-	expression tag	UNP Q7A225
XY	101	ILE	-	expression tag	UNP Q7A225
XY	102	SER	-	expression tag	UNP Q7A225
XY	103	GLU	-	expression tag	UNP Q7A225
XY	104	GLU	-	expression tag	UNP Q7A225
XY	105	ASP	-	expression tag	UNP Q7A225
XY	106	LEU	-	expression tag	UNP Q7A225
XY	107	ASN	-	expression tag	UNP Q7A225
XY	108	SER	-	expression tag	UNP Q7A225
XY	109	ALA	-	expression tag	UNP Q7A225
XY	110	VAL	-	expression tag	UNP Q7A225
XY	111	ASP	-	expression tag	UNP Q7A225
XY	112	HIS	-	expression tag	UNP Q7A225
XY	113	HIS	-	expression tag	UNP Q7A225
XY	114	HIS	-	expression tag	UNP Q7A225
XY	115	HIS	-	expression tag	UNP Q7A225
XY	116	HIS	-	expression tag	UNP Q7A225

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Chain	Residue	Modelled	Actual	Comment	Reference
XY	117	HIS	-	expression tag	UNP Q7A225

- Molecule 25 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	RA	2891	Total	C	N	O	P	0	0	0
			62269	27713	11649	20016	2891			
25	YA	2875	Total	C	N	O	P	0	0	0
			61924	27560	11583	19906	2875			

- Molecule 26 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	RB	122	Total	C	N	O	P	0	0	0
			2617	1166	486	844	121			
26	YB	122	Total	C	N	O	P	0	0	0
			2617	1166	486	844	121			

- Molecule 27 is a protein called 50S ribosomal protein L2.

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

- Molecule 28 is a protein called 50S ribosomal protein L3.

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

- Molecule 29 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	RF	208	Total	C	N	O	S	0	0	0
			1627	1037	304	283	3			
29	YF	208	Total	C	N	O	S	0	0	0
			1627	1037	304	283	3			

- Molecule 30 is a protein called 50S ribosomal protein L5.

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

- Molecule 31 is a protein called 50S ribosomal protein L6.

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

- Molecule 32 is a protein called 50S ribosomal protein L9.

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

- Molecule 33 is a protein called 50S ribosomal protein L13.

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

- Molecule 34 is a protein called 50S ribosomal protein L14.

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

- Molecule 35 is a protein called 50S ribosomal protein L15.

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

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	RQ	140	Total	C	N	O	S	0	0	0
			1112	710	210	185	7			
36	YQ	139	Total	C	N	O	S	0	0	0
			1107	707	209	184	7			

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
37	RR	117	Total	C	N	O	0	0	0
			960	599	202	159			
37	YR	117	Total	C	N	O	0	0	0
			960	599	202	159			

- Molecule 38 is a protein called 50S ribosomal protein L18.

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

- Molecule 39 is a protein called 50S ribosomal protein L19.

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

- Molecule 40 is a protein called 50S ribosomal protein L20.

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

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

- Molecule 41 is a protein called 50S ribosomal protein L21.

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

- Molecule 42 is a protein called 50S ribosomal protein L22.

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

- Molecule 43 is a protein called 50S ribosomal protein L23.

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

- Molecule 44 is a protein called 50S ribosomal protein L24.

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

- Molecule 45 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
45	RZ	176	1404	897	252	252	3	0	0	0
45	YZ	183	1461	933	260	265	3	0	0	0

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	R0	83	Total	C	N	O	S	0	0	0
			657	407	139	110	1			
46	Y0	83	Total	C	N	O	S	0	0	0
			657	407	139	110	1			

- Molecule 47 is a protein called 50S ribosomal protein L28.

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

- Molecule 48 is a protein called 50S ribosomal protein L29.

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

- Molecule 49 is a protein called 50S ribosomal protein L30.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	R4	70	Total	C	N	O	S	0	0	0
			573	359	107	103	4			
50	Y4	70	Total	C	N	O	S	0	0	0
			573	359	107	103	4			

- Molecule 51 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	R5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			
51	Y5	57	Total	C	N	O	S	0	0	0
			442	278	88	71	5			

- Molecule 52 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	R6	48	Total	C	N	O	S	0	0	0
			417	259	86	68	4			
52	Y6	48	Total	C	N	O	S	0	0	0
			417	259	86	68	4			

- Molecule 53 is a protein called 50S ribosomal protein L34.

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

- Molecule 54 is a protein called 50S ribosomal protein L35.

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

- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	R9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			
55	Y9	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			

- Molecule 56 is a RNA chain called CC-puromycin.

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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
56	Z7	3	74	40	13	19	2	0	0	0

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	QA	147	Total 147	Mg 147	0	0
57	QD	1	Total 1	Mg 1	0	0
57	QE	1	Total 1	Mg 1	0	0
57	QL	1	Total 1	Mg 1	0	0
57	QV	5	Total 5	Mg 5	0	0
57	RA	431	Total 431	Mg 431	0	0
57	RB	5	Total 5	Mg 5	0	0
57	RD	2	Total 2	Mg 2	0	0
57	RE	2	Total 2	Mg 2	0	0
57	RF	1	Total 1	Mg 1	0	0
57	RP	2	Total 2	Mg 2	0	0
57	RQ	2	Total 2	Mg 2	0	0
57	RR	1	Total 1	Mg 1	0	0
57	RY	2	Total 2	Mg 2	0	0
57	R0	3	Total 3	Mg 3	0	0
57	R2	1	Total 1	Mg 1	0	0
57	R5	3	Total 3	Mg 3	0	0
57	XA	161	Total 161	Mg 161	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
57	XD	1	Total Mg 1 1	0	0
57	XF	1	Total Mg 1 1	0	0
57	XL	1	Total Mg 1 1	0	0
57	XN	1	Total Mg 1 1	0	0
57	XV	4	Total Mg 4 4	0	0
57	YA	473	Total Mg 473 473	0	0
57	YB	6	Total Mg 6 6	0	0
57	YD	1	Total Mg 1 1	0	0
57	YE	1	Total Mg 1 1	0	0
57	YF	1	Total Mg 1 1	0	0
57	YG	1	Total Mg 1 1	0	0
57	YH	2	Total Mg 2 2	0	0
57	YN	1	Total Mg 1 1	0	0
57	YP	2	Total Mg 2 2	0	0
57	YQ	2	Total Mg 2 2	0	0
57	YR	1	Total Mg 1 1	0	0
57	YU	1	Total Mg 1 1	0	0
57	YV	1	Total Mg 1 1	0	0
57	YY	1	Total Mg 1 1	0	0
57	Y0	3	Total Mg 3 3	0	0
57	Y1	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	Y5	3	Total 3	Mg 3	0	0
57	Y7	1	Total 1	Mg 1	0	0

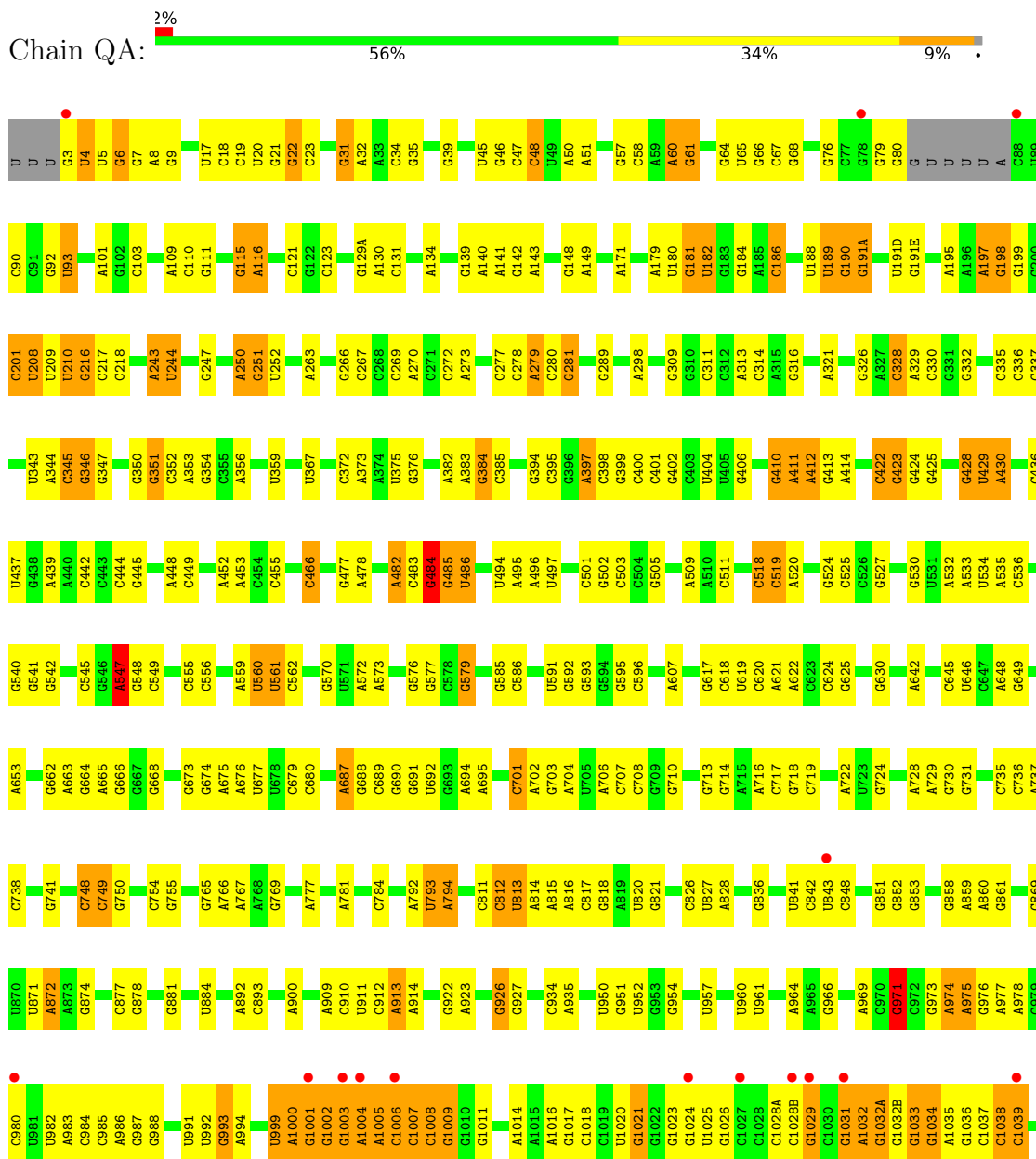
- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

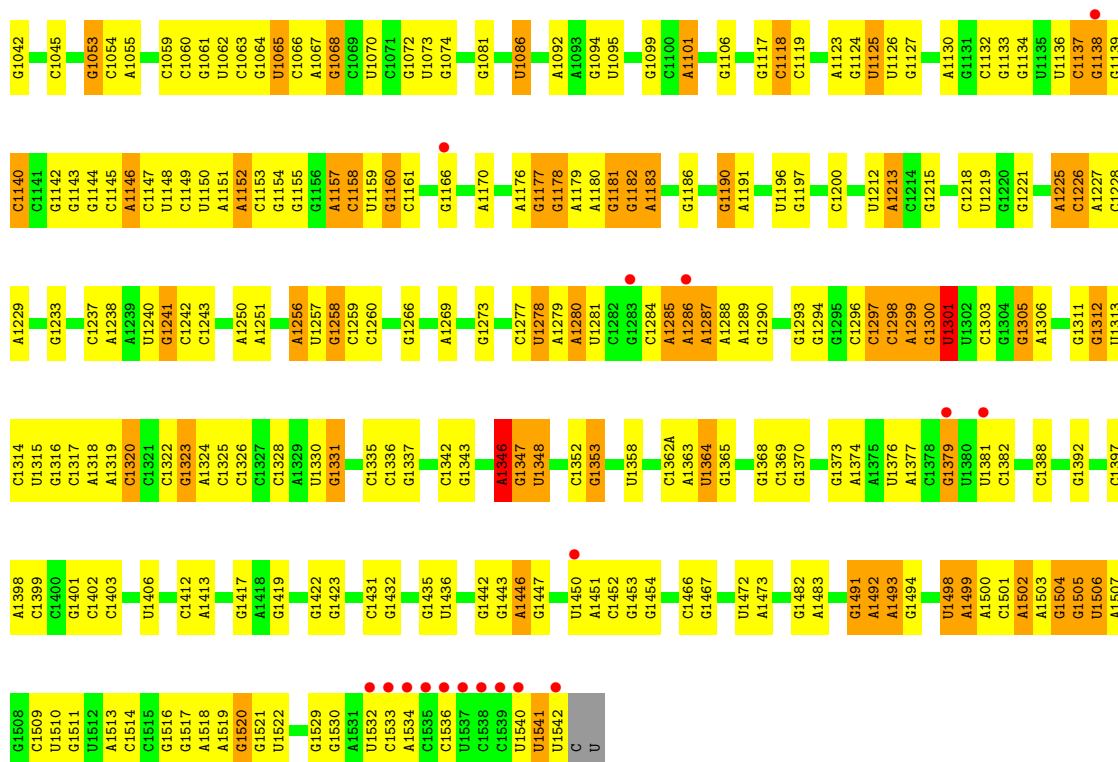
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	QD	1	Total 1	Zn 1	0	0
58	QN	1	Total 1	Zn 1	0	0
58	XD	1	Total 1	Zn 1	0	0
58	XN	1	Total 1	Zn 1	0	0

### 3 Residue-property plots i

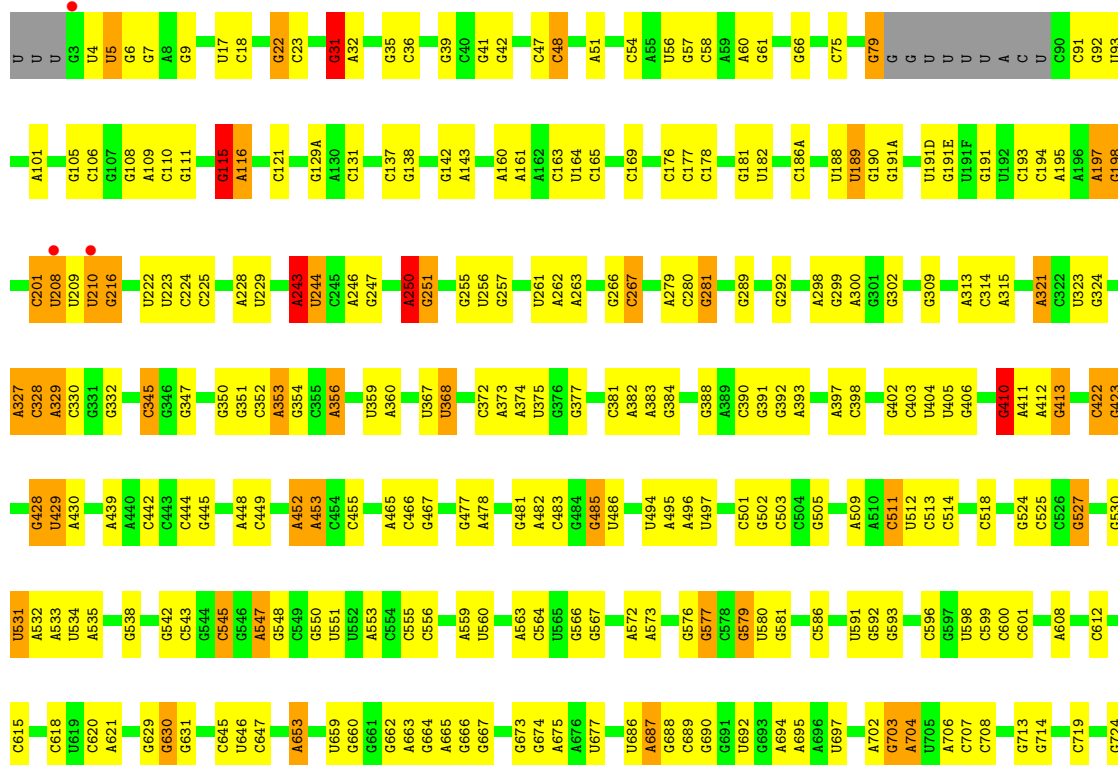
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

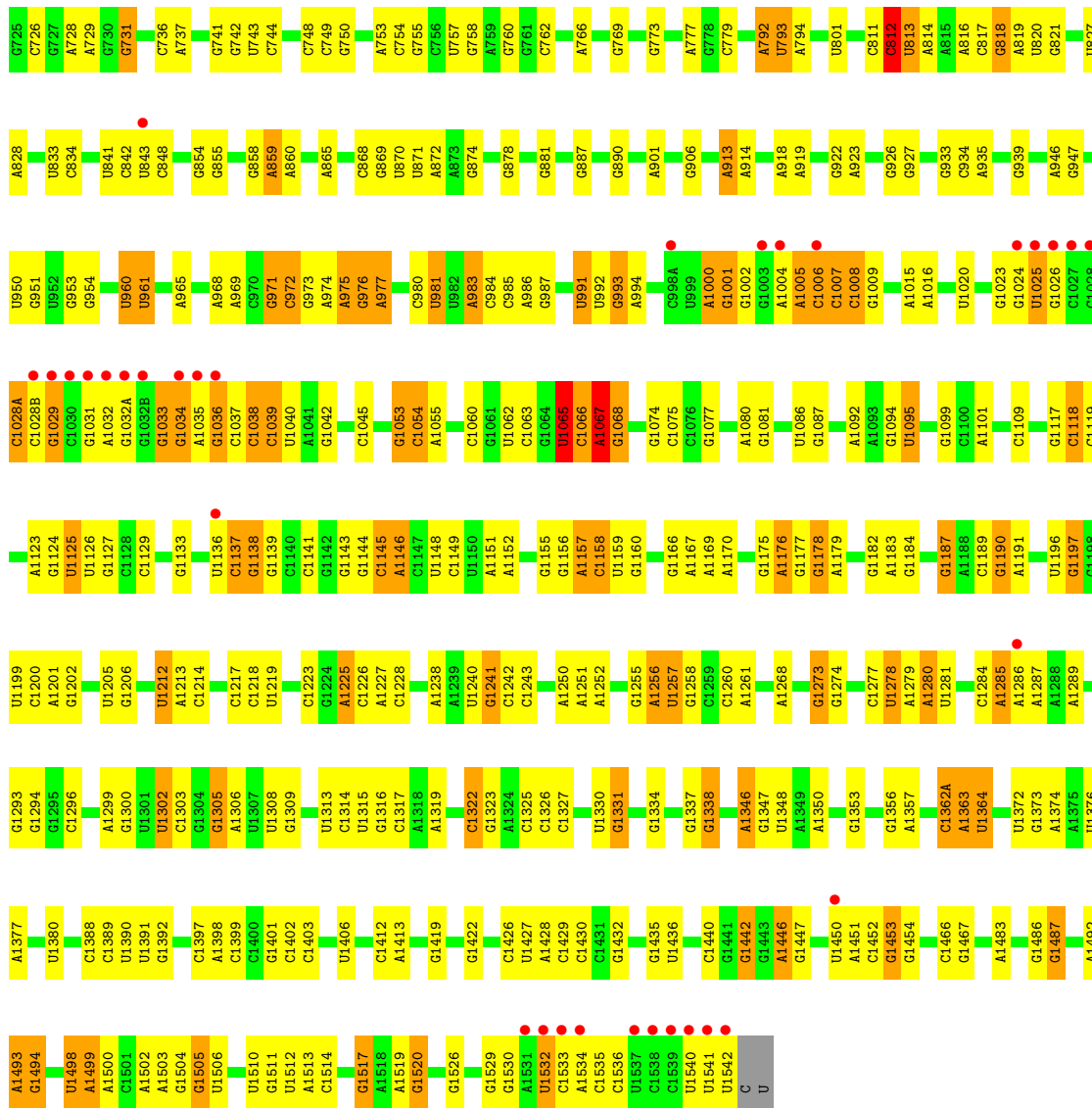
- Molecule 1: 16S rRNA



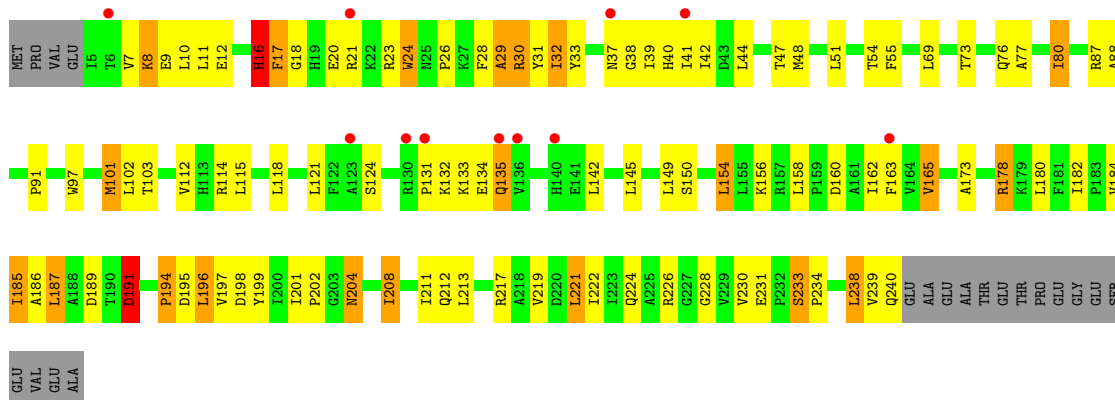


● Molecule 1: 16S rRNA



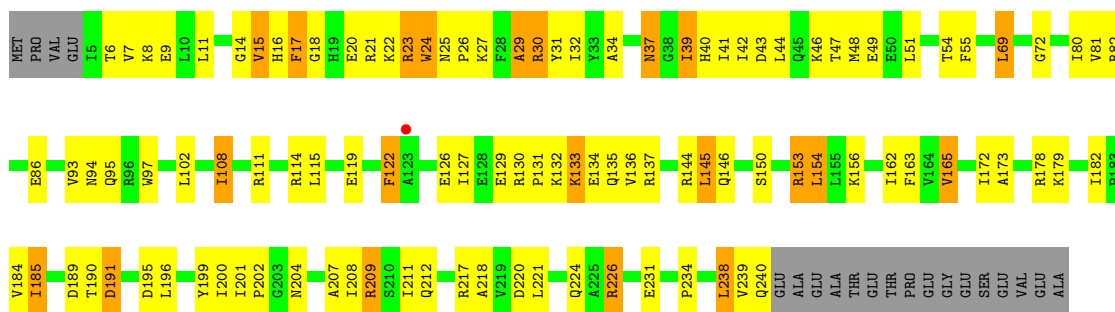


• Molecule 2: 30S ribosomal protein S2



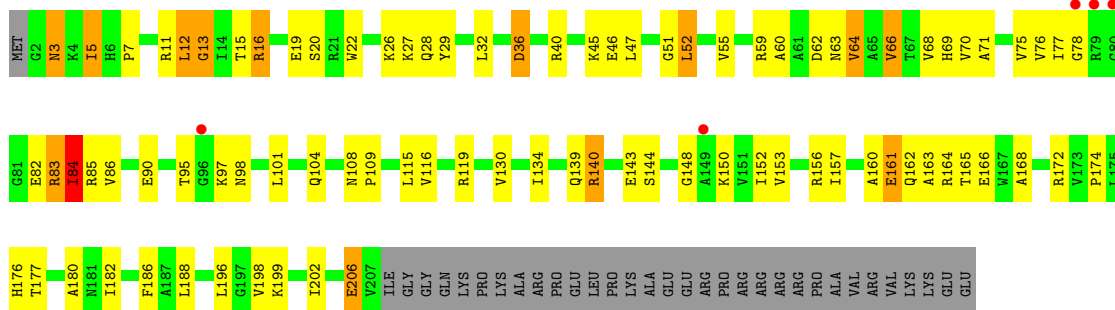
- Molecule 2: 30S ribosomal protein S2

Chain XB: 



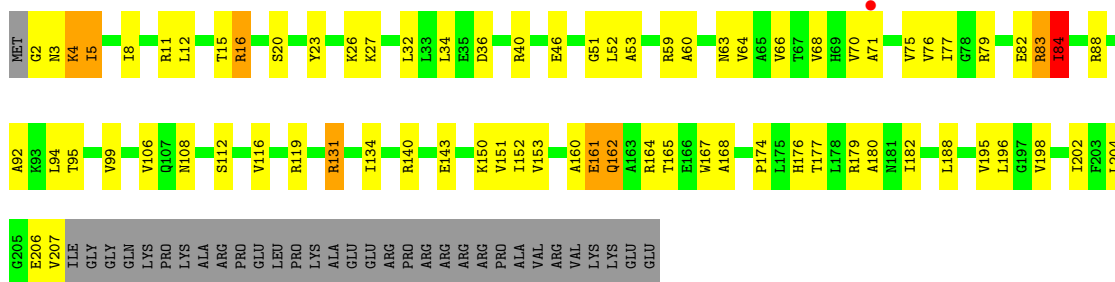
- Molecule 3: 30S ribosomal protein S3

Chain QC: 



- Molecule 3: 30S ribosomal protein S3

Chain XC: 



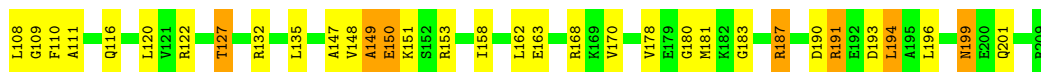
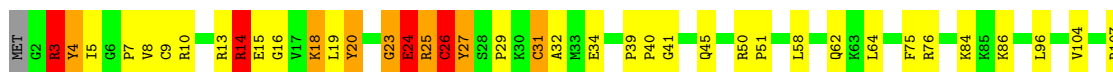
- Molecule 4: 30S ribosomal protein S4

Chain QD: 





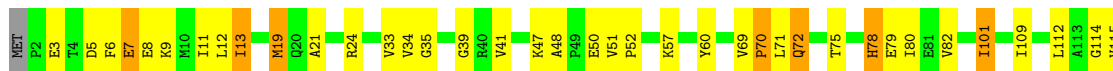
- Molecule 4: 30S ribosomal protein S4



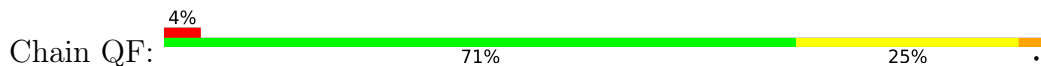
- Molecule 5: 30S ribosomal protein S5



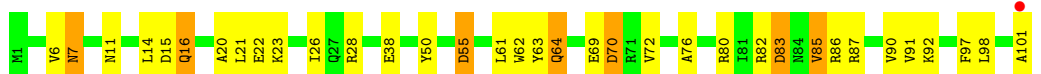
- Molecule 5: 30S ribosomal protein S5




- Molecule 6: 30S ribosomal protein S6



- Molecule 6: 30S ribosomal protein S6



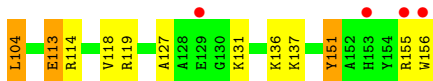
- Molecule 7: 30S ribosomal protein S7

Chain QG: 



- Molecule 7: 30S ribosomal protein S7

Chain XG: 



- Molecule 8: 30S ribosomal protein S8

Chain QH: 



- Molecule 8: 30S ribosomal protein S8

Chain XH: 



- Molecule 9: 30S ribosomal protein S9

Chain QI: 

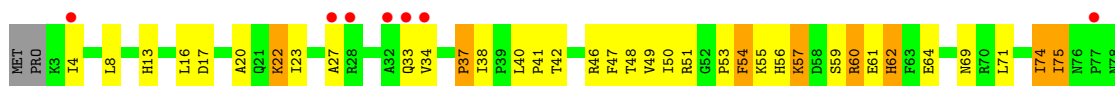




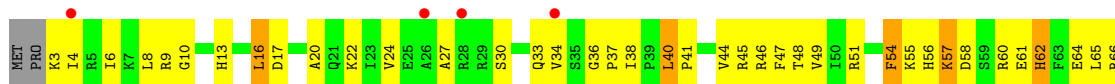
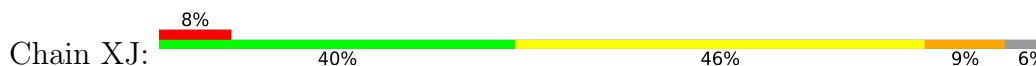
- Molecule 9: 30S ribosomal protein S9



- Molecule 10: 30S ribosomal protein S10



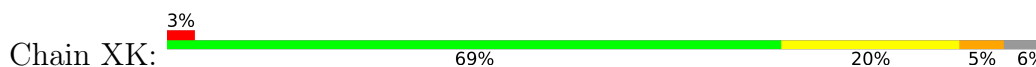
- Molecule 10: 30S ribosomal protein S10



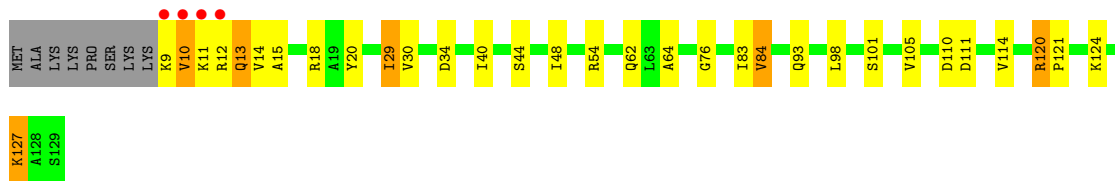
- Molecule 11: 30S ribosomal protein S11



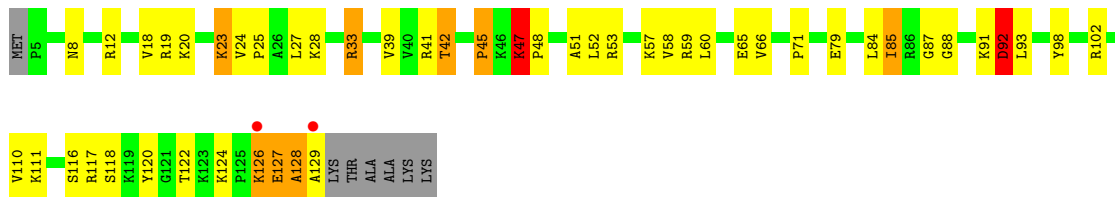
- Molecule 11: 30S ribosomal protein S11



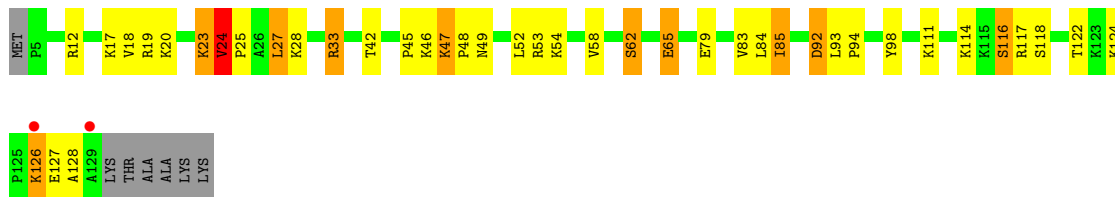




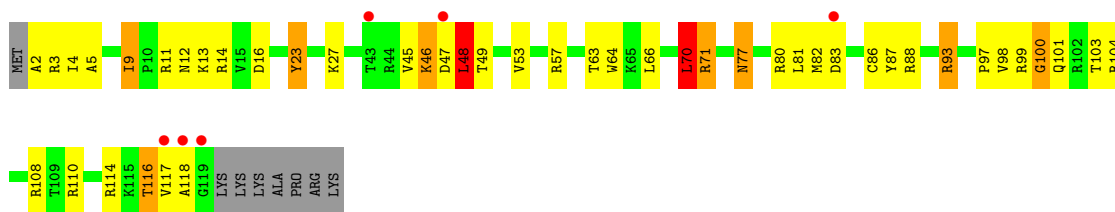
• Molecule 12: 30S ribosomal protein S12



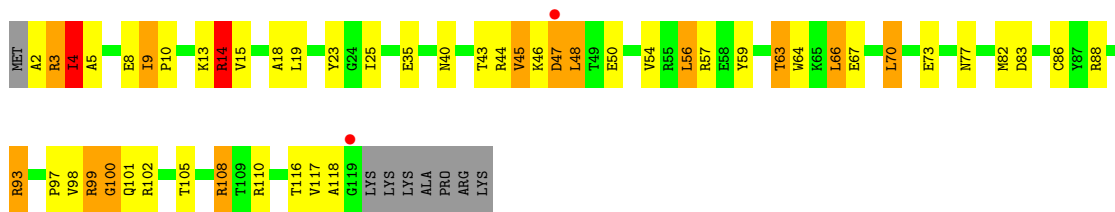
• Molecule 12: 30S ribosomal protein S12



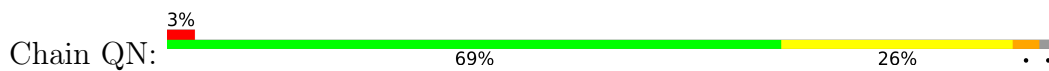
• Molecule 13: 30S ribosomal protein S13



• Molecule 13: 30S ribosomal protein S13



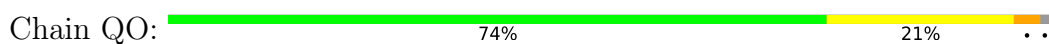
• Molecule 14: 30S ribosomal protein S14 type Z



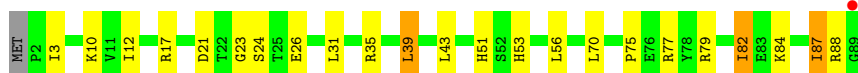
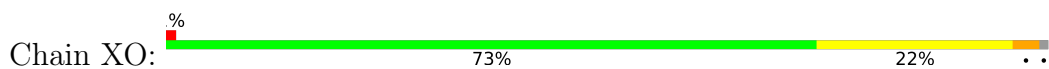
- Molecule 14: 30S ribosomal protein S14 type Z



- Molecule 15: 30S ribosomal protein S15



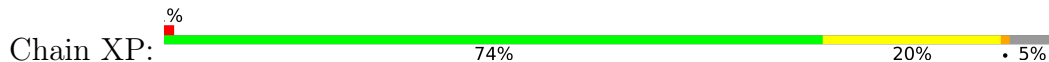
- Molecule 15: 30S ribosomal protein S15



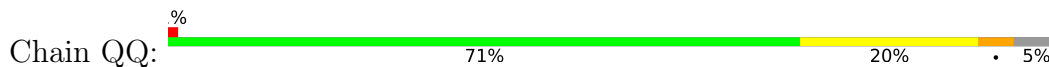
- Molecule 16: 30S ribosomal protein S16



- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17



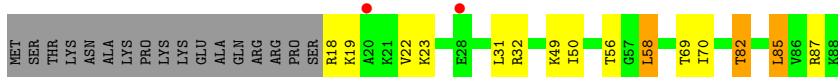
- Molecule 17: 30S ribosomal protein S17

Chain XQ:  67% 25% 5%



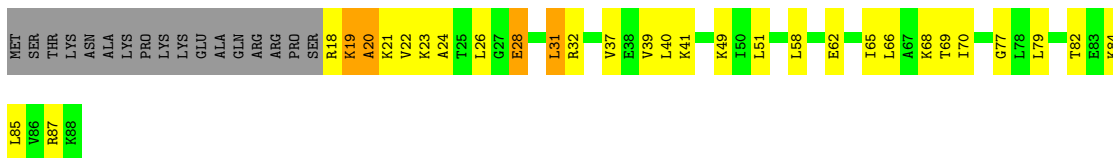
- Molecule 18: 30S ribosomal protein S18

Chain QR:  2% 64% 14% 19%



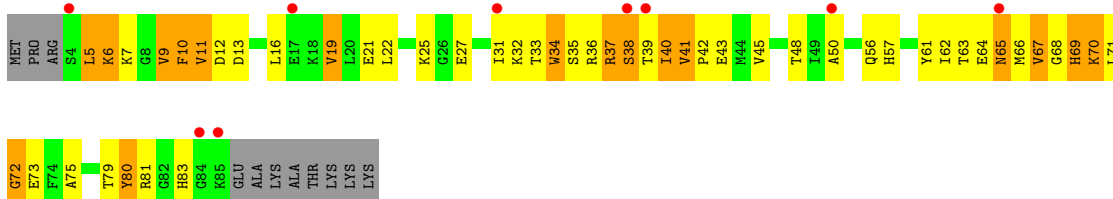
- Molecule 18: 30S ribosomal protein S18

Chain XR:  47% 30% 5% 19%



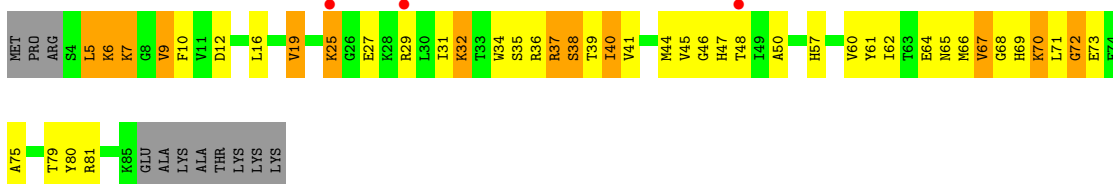
- Molecule 19: 30S ribosomal protein S19

Chain QS:  10% 34% 35% 18% 12%



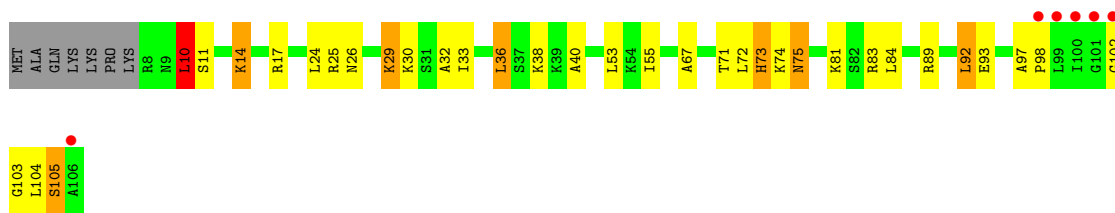
- Molecule 19: 30S ribosomal protein S19

Chain XS:  3% 40% 34% 14% 12%

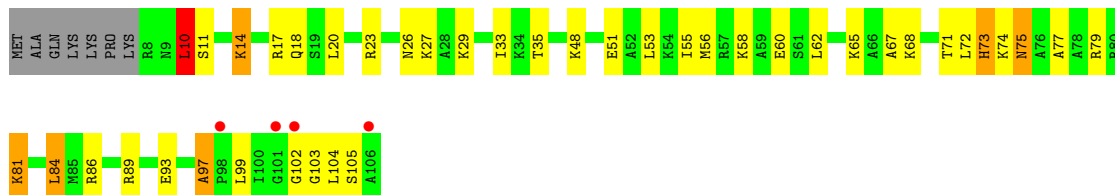


- Molecule 20: 30S ribosomal protein S20

Chain QT:  6% 61% 25% 7% 7%



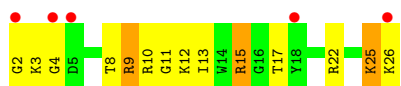
• Molecule 20: 30S ribosomal protein S20



• Molecule 21: 30S ribosomal protein Thx



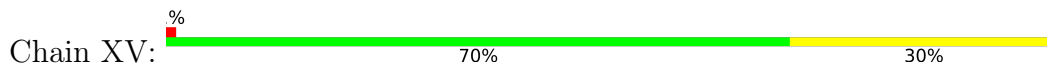
• Molecule 21: 30S ribosomal protein Thx



• Molecule 22: P-site tRNA-fMet

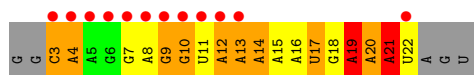


• Molecule 22: P-site tRNA-fMet



• Molecule 23: messenger RNA

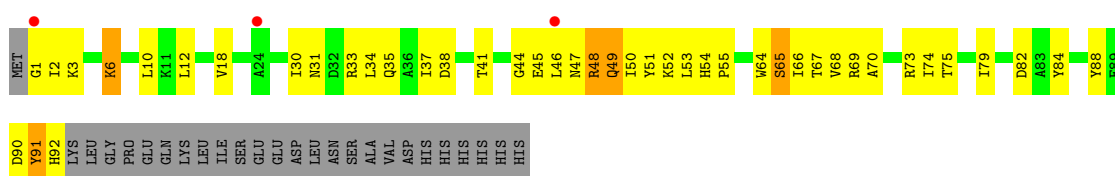




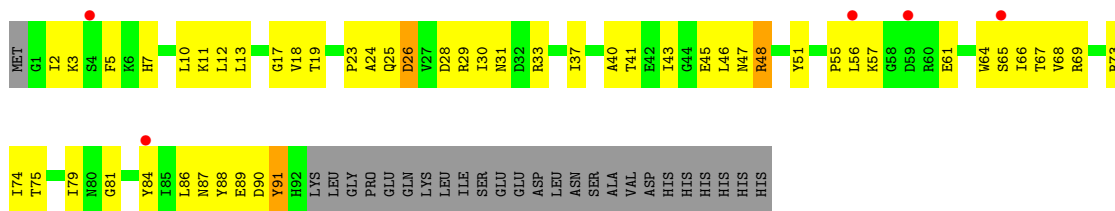
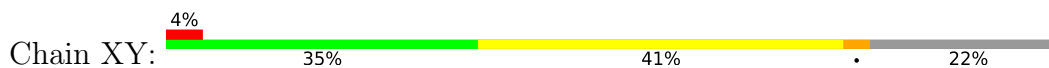
• Molecule 23: messenger RNA



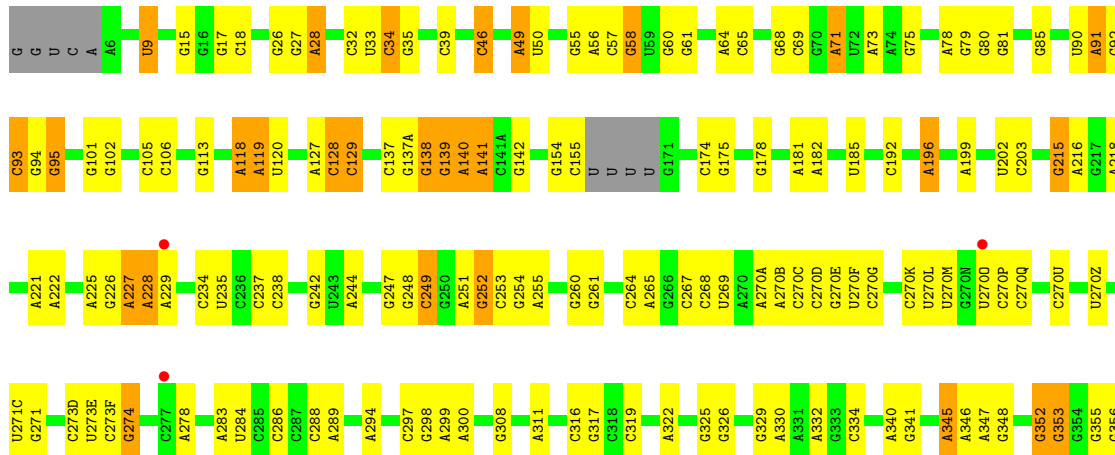
• Molecule 24: Killer protein



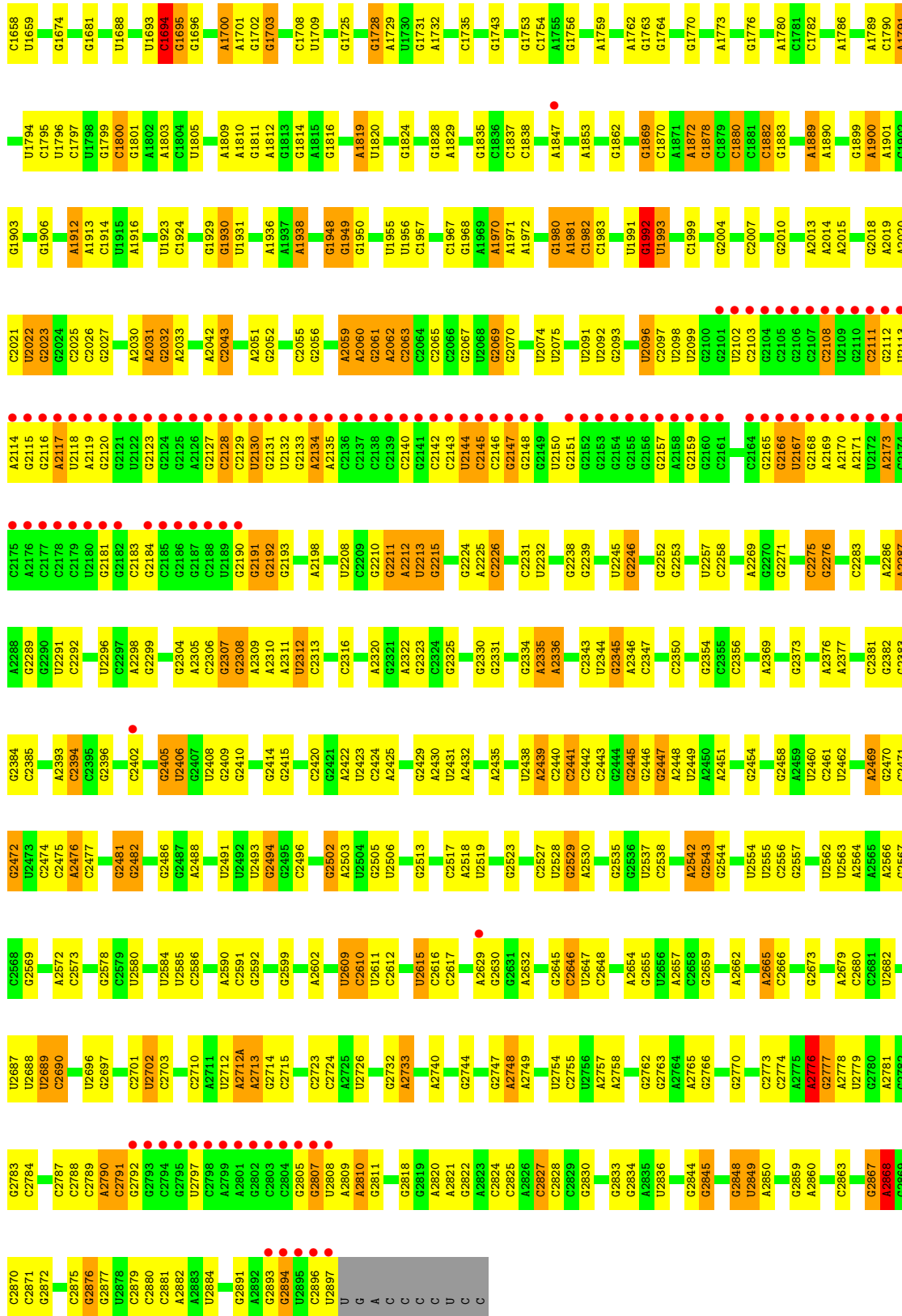
• Molecule 24: Killer protein



• Molecule 25: 23S rRNA

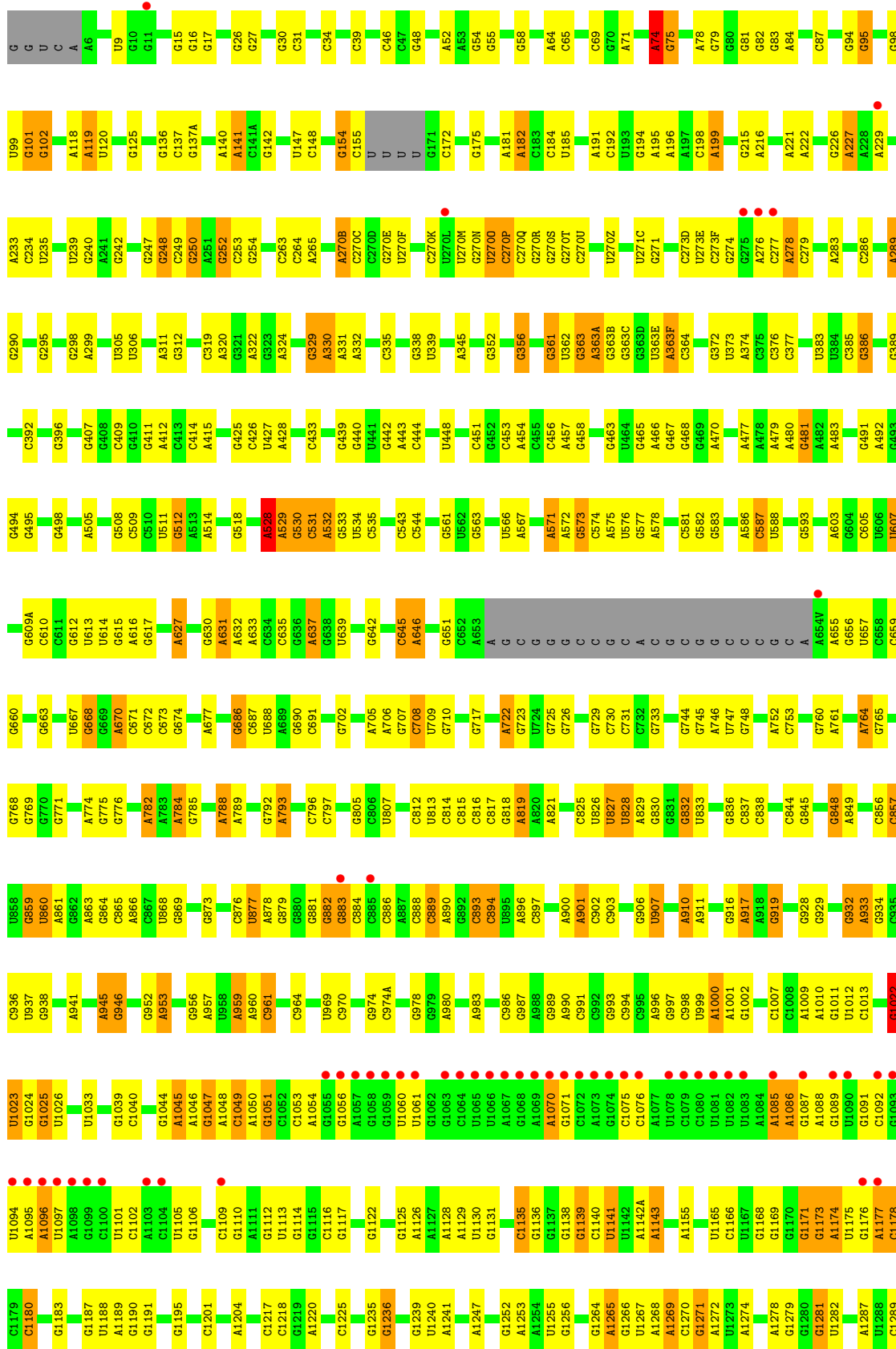






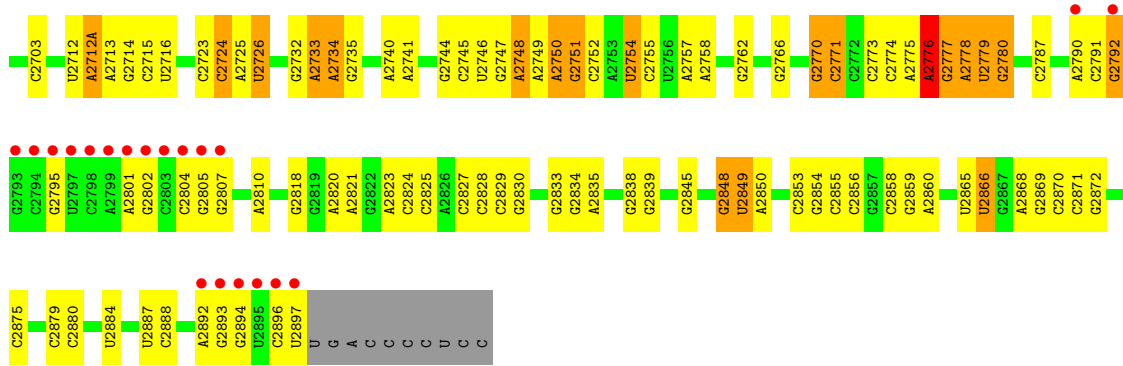
• Molecule 25: 23S rRNA



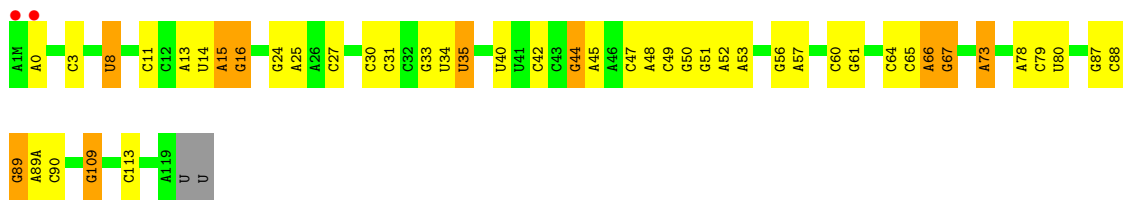




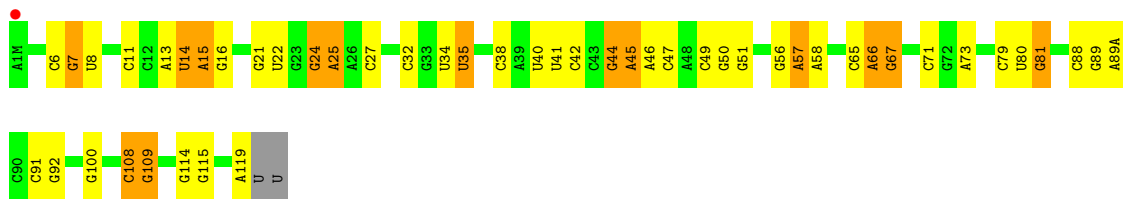




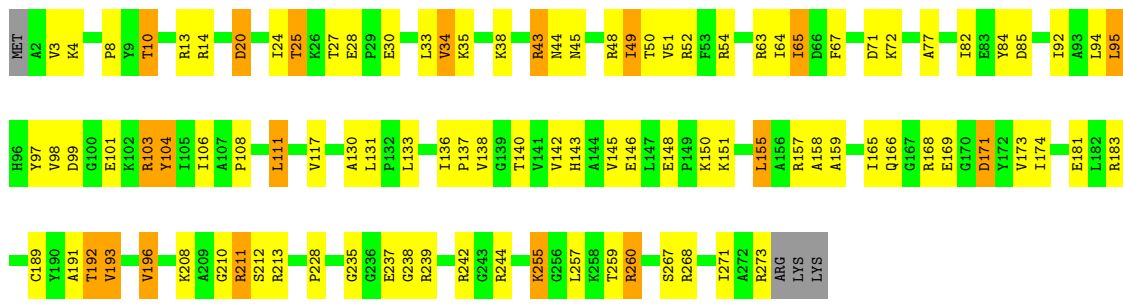
• Molecule 26: 5S rRNA



• Molecule 26: 5S rRNA

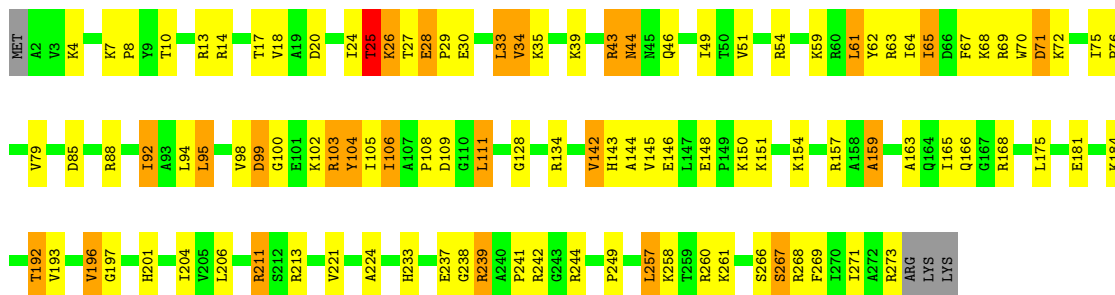


• Molecule 27: 50S ribosomal protein L2

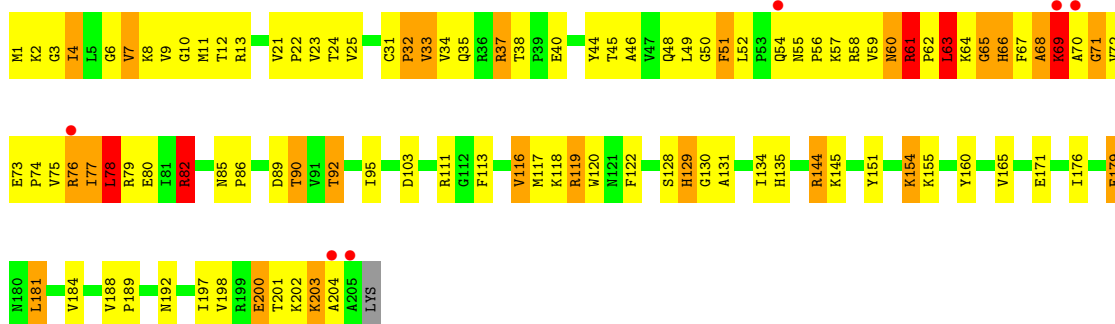


• Molecule 27: 50S ribosomal protein L2

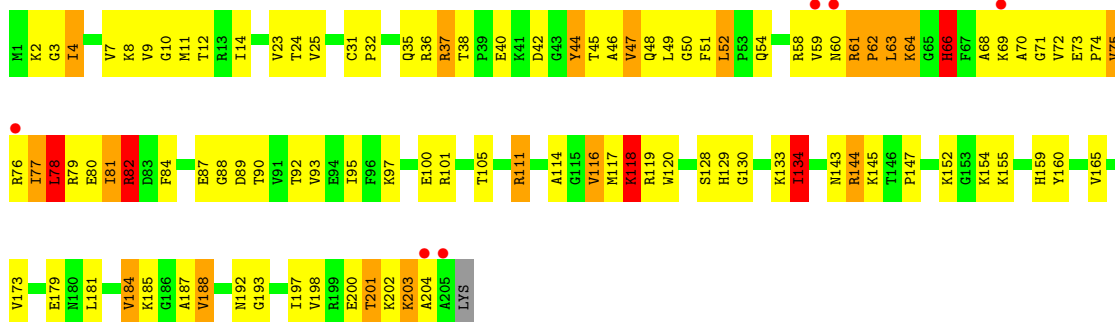




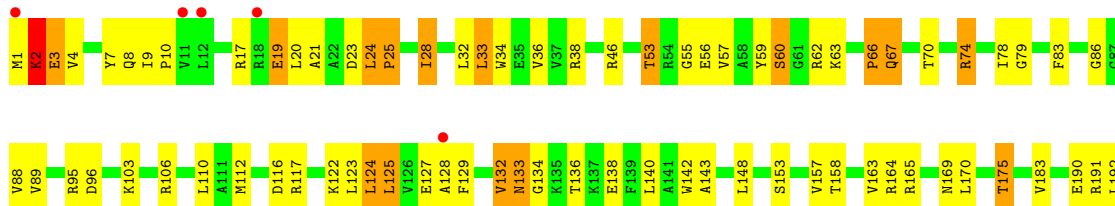
- Molecule 28: 50S ribosomal protein L3



- Molecule 28: 50S ribosomal protein L3

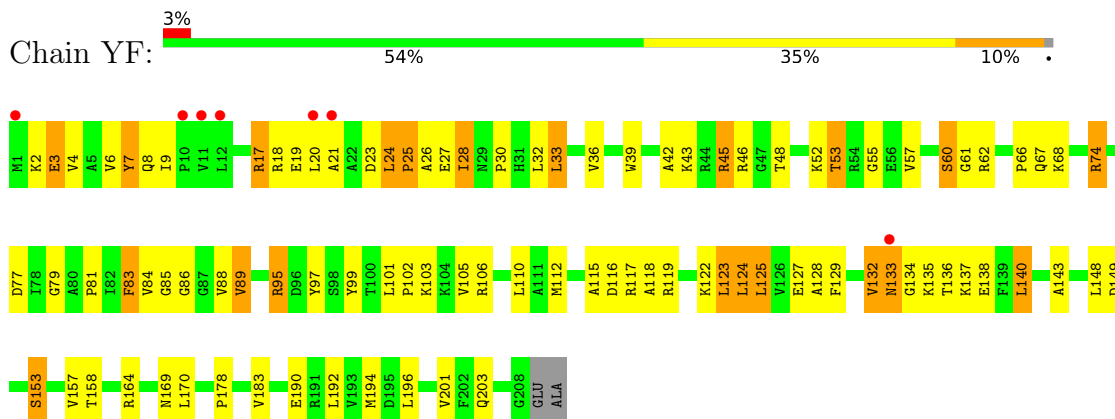


- Molecule 29: 50S ribosomal protein L4

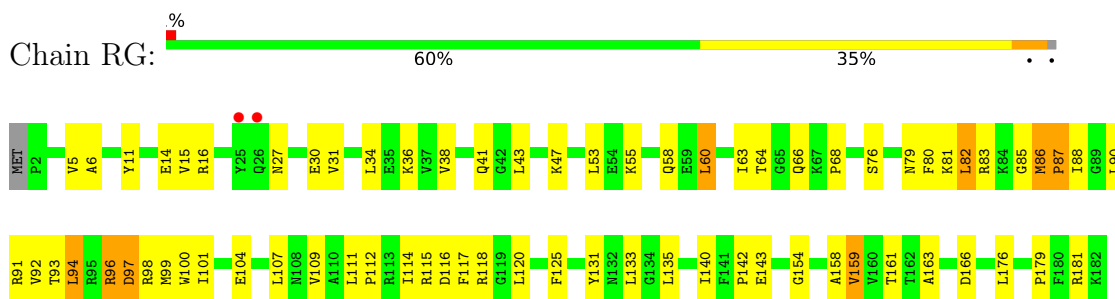




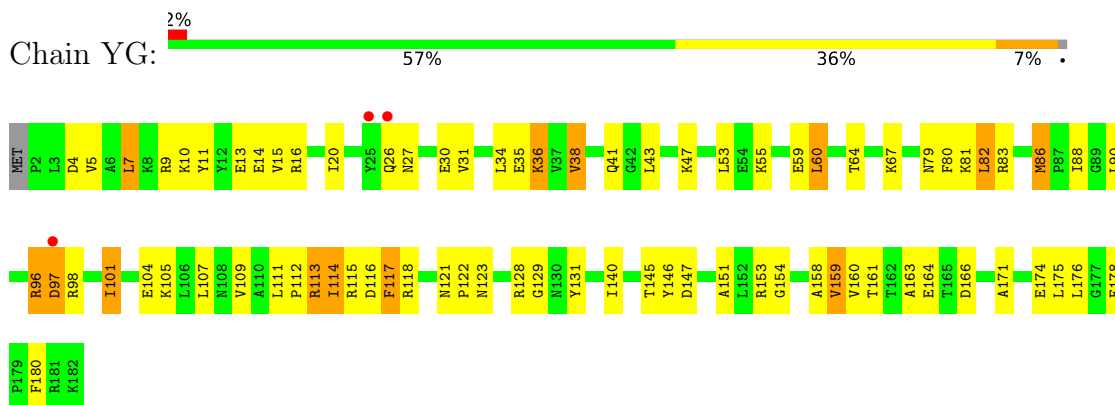
- Molecule 29: 50S ribosomal protein L4



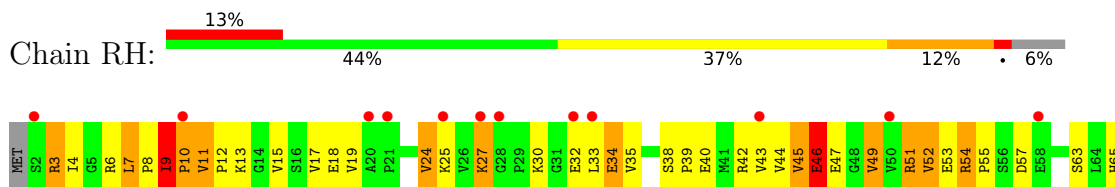
- Molecule 30: 50S ribosomal protein L5

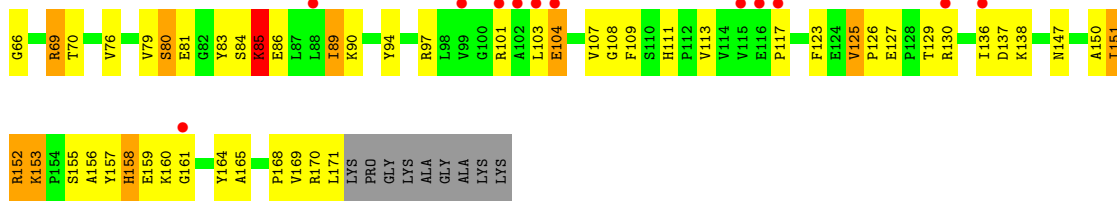


- Molecule 30: 50S ribosomal protein L5

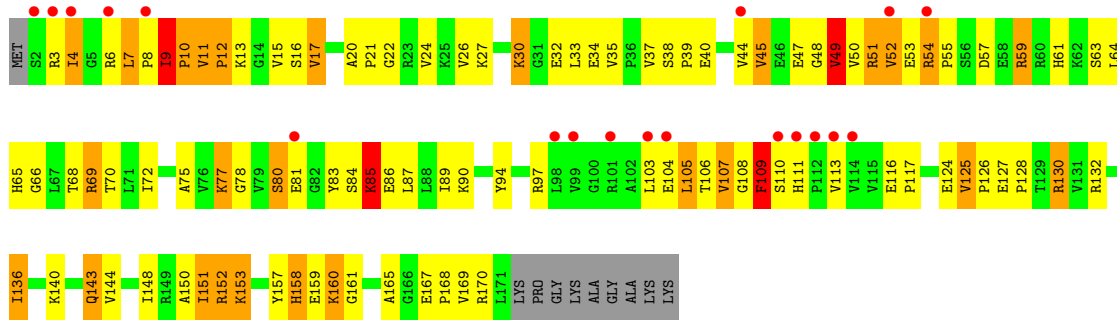


- Molecule 31: 50S ribosomal protein L6

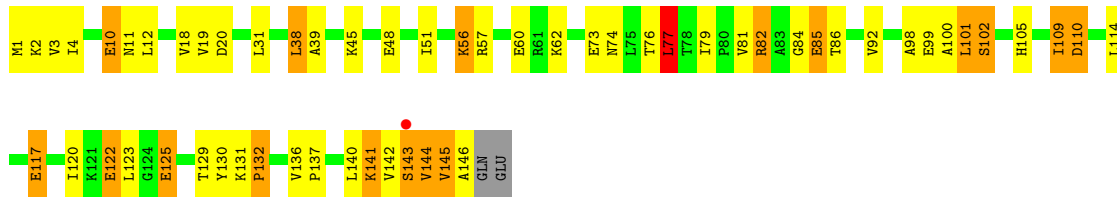




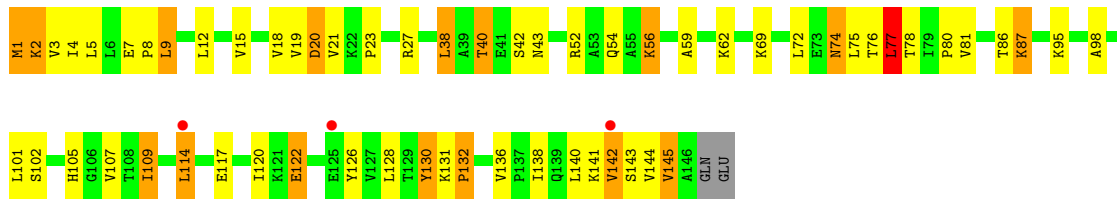
• Molecule 31: 50S ribosomal protein L6



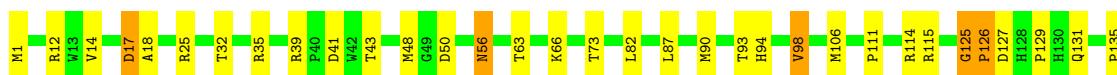
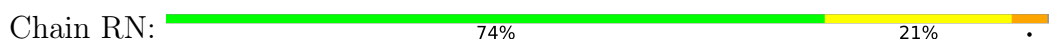
• Molecule 32: 50S ribosomal protein L9



• Molecule 32: 50S ribosomal protein L9



• Molecule 33: 50S ribosomal protein L13



E136  
K137  
L138  
GLU  
VAL

- Molecule 33: 50S ribosomal protein L13

Chain YN: 68% 26%

M1 Q8 V9 R12 R13 V14 D17 A18 L23 L26 L30 L34 R35 R36 K37 R38 R39 P40 D41 W42 T43 V46 V47 M48 G49 D50 N56 T63 R66 L67 L87 E88 T93 H94 P95 Y98 L99 M106 R119 L120 G125 P126 D127

H128 P129 H130 Q131 A132 Q133 R134 P135 E136 L138 GLU VAL

- Molecule 34: 50S ribosomal protein L14

Chain RO: 65% 30% 5%

M1 I2 Q3 P4 Q5 L8 E9 V10 R17 K18 I19 R23 V24 L25 S28 N29 Y32 A33 T34 V35 V38 I47 P48 R49 V63 R64 E68 A76 I77 R78 F79 D80 A83 I86 I87 L91 E92 F93 R94 R97 V98 F99 A103 R104 E105

L106 R107 E108 K113 I114 V115 S116 L117 E120 V121 L122

- Molecule 34: 50S ribosomal protein L14

Chain YO: 71% 25%

M1 P4 Q5 L8 G15 I19 I22 L25 S28 N29 V35 V38 I47 P48 R49 E68 R71 F72 D73 G74 S75 R78 F79 D80 I87 N88 L91 E92 R97 V98 A103 R104 E105 E108 K113 L117 A118 V121 L122

- Molecule 35: 50S ribosomal protein L15

Chain RP: 41% 38% 15% 7%

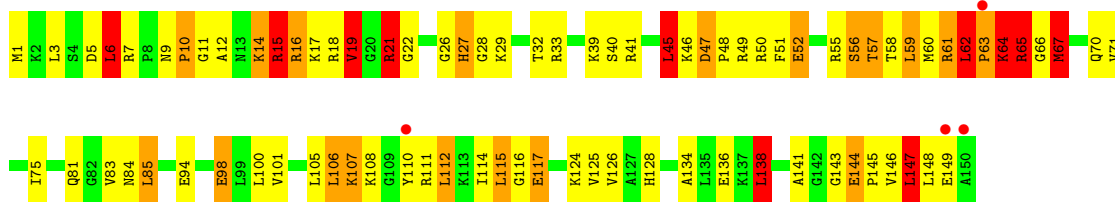
M1 K2 L3 S4 D5 L6 R7 P8 N9 P10 G11 A12 N13 K14 R15 R16 V19 G20 R21 G22 P23 G24 S25 G26 H27 G28 K29 T30 A31 T32 R33 K36 G37 Y110 Q38 R111 K39 S40 R41 S42 G43 G44 L45 K46 D47 R50 F51 E52 G53 G54 R55 S56 T57 T58 L59 M60 R61 L62 P63

K64 R65 G66 M67 Q68 G69 Q70 V71 P72 I75 R79 Y80 Q81 G82 V83 K86 E94 P97 E98 L99 L100 V101 A103 L106 K107 K108 G109 Y110 R111 L112 L113 L114 L115 G116 E117 P122 L123 K124 V125 V126 L135 E136 K137 L138 A141 E144 P145 V146 L147

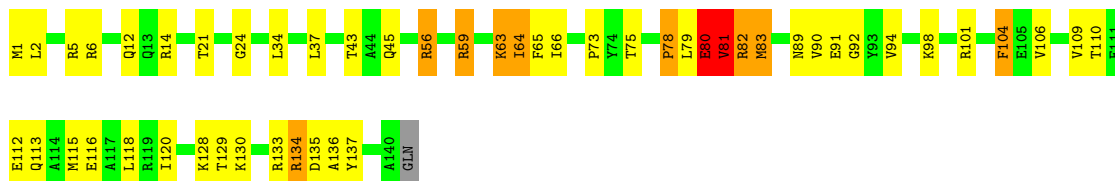
L148 E149 A150

- Molecule 35: 50S ribosomal protein L15

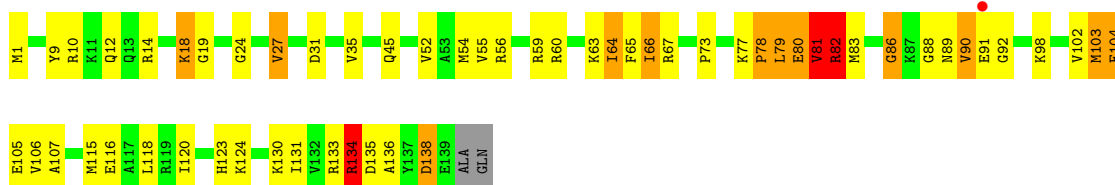
Chain YP: 44% 36% 13% 7%



- Molecule 36: 50S ribosomal protein L16



- Molecule 36: 50S ribosomal protein L16



- Molecule 37: 50S ribosomal protein L17



- Molecule 37: 50S ribosomal protein L17

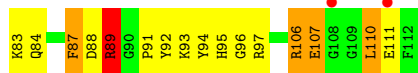


- Molecule 38: 50S ribosomal protein L18

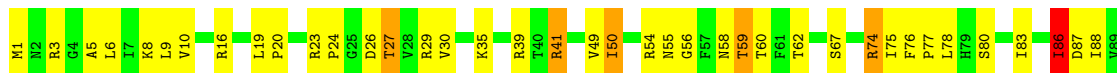




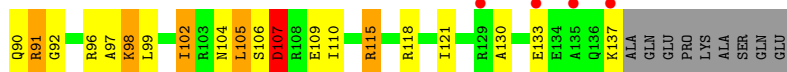
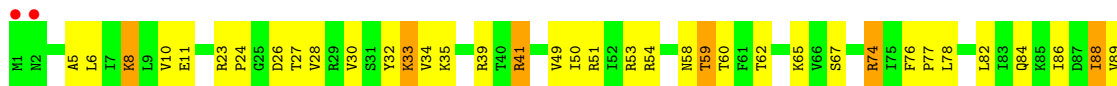
• Molecule 38: 50S ribosomal protein L18



• Molecule 39: 50S ribosomal protein L19



• Molecule 39: 50S ribosomal protein L19



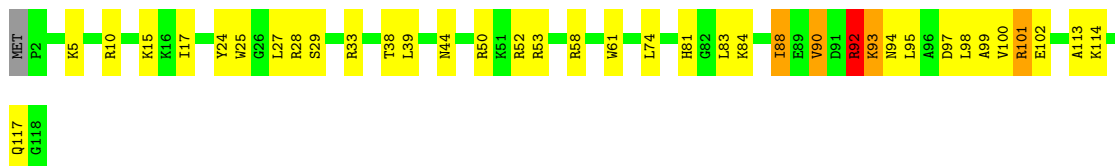
• Molecule 40: 50S ribosomal protein L20



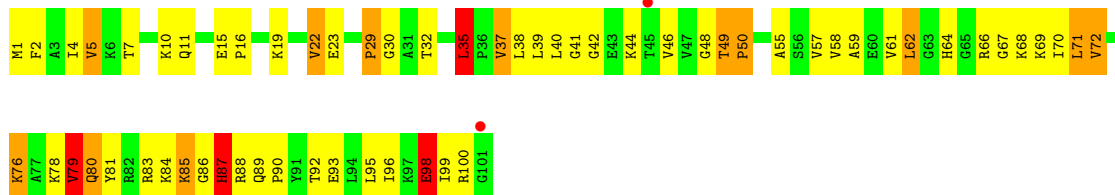
• Molecule 40: 50S ribosomal protein L20



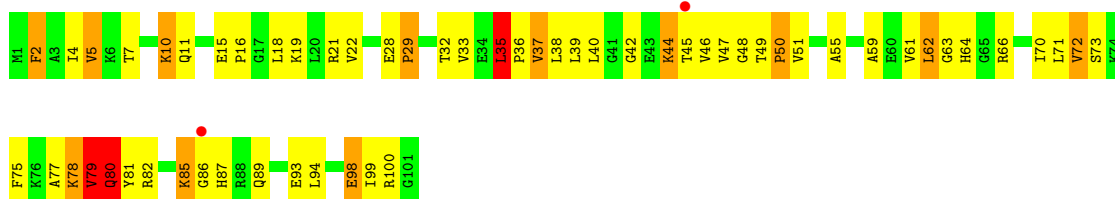
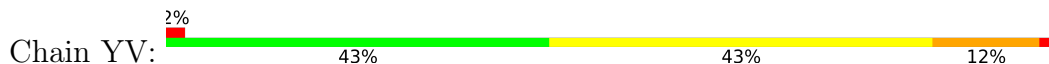




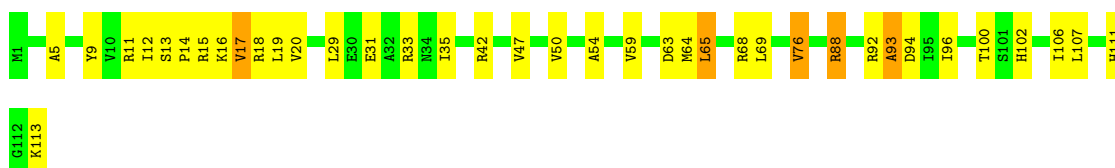
- Molecule 41: 50S ribosomal protein L21



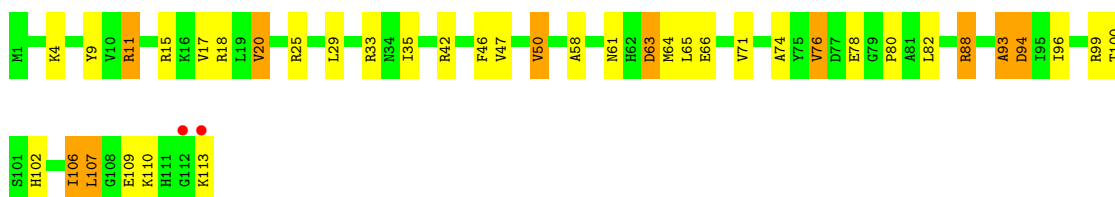
- Molecule 41: 50S ribosomal protein L21



- Molecule 42: 50S ribosomal protein L22



- Molecule 42: 50S ribosomal protein L22

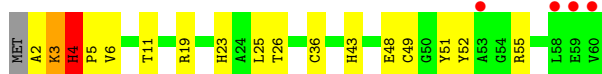


- Molecule 43: 50S ribosomal protein L23





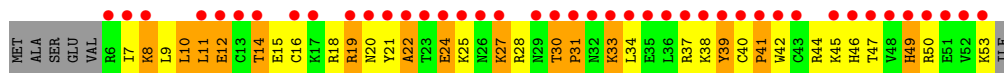
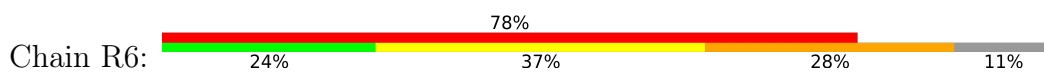




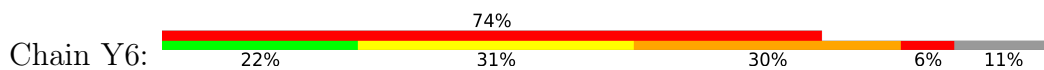
- Molecule 51: 50S ribosomal protein L32



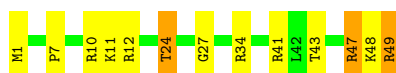
- Molecule 52: 50S ribosomal protein L33



- Molecule 52: 50S ribosomal protein L33



- Molecule 53: 50S ribosomal protein L34



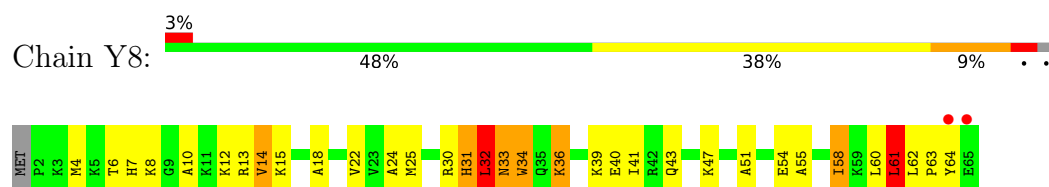
- Molecule 53: 50S ribosomal protein L34



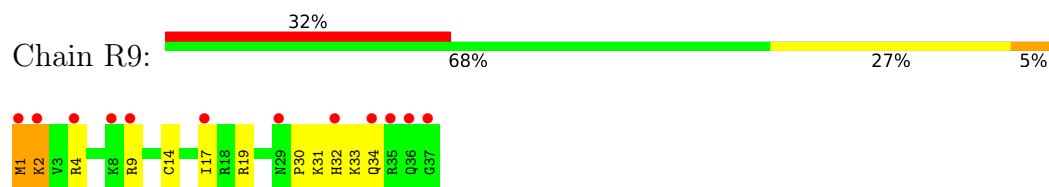
- Molecule 54: 50S ribosomal protein L35



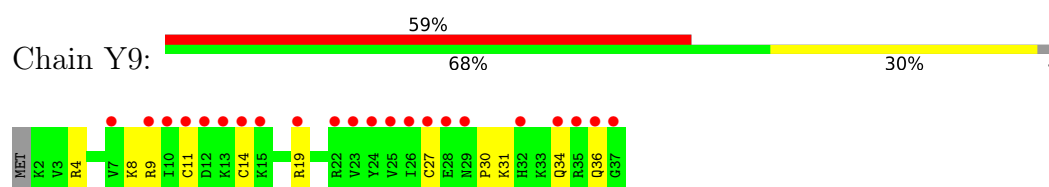
- Molecule 54: 50S ribosomal protein L35



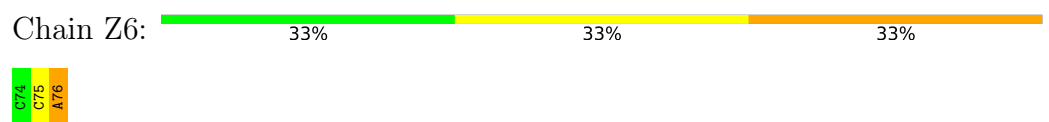
- Molecule 55: 50S ribosomal protein L36



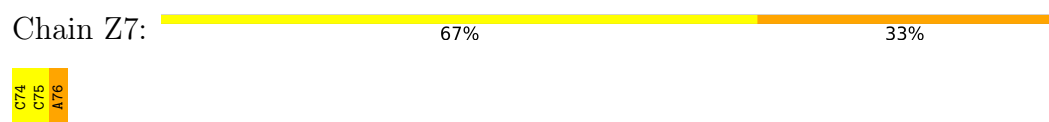
- Molecule 55: 50S ribosomal protein L36



- Molecule 56: CC-puromycin



- Molecule 56: CC-puromycin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	213.45Å 452.92Å 608.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.92 – 3.60 49.92 – 3.60	Depositor EDS
% Data completeness (in resolution range)	98.7 (49.92-3.60) 98.7 (49.92-3.60)	Depositor EDS
$R_{merge}$	0.22	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.77 (at 3.57Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.198 , 0.234 0.201 , 0.236	Depositor DCC
$R_{free}$ test set	30161 reflections (4.53%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	86.5	Xtrriage
Anisotropy	0.089	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 93.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	294410	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	95.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.58% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PPU, ZN, A2M

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	1/36346 (0.0%)	0.82	16/56724 (0.0%)
1	XA	0.35	0/36276	0.83	15/56615 (0.0%)
2	QB	0.25	0/1950	0.49	0/2630
2	XB	0.26	0/1950	0.49	1/2630 (0.0%)
3	QC	0.24	0/1636	0.47	0/2205
3	XC	0.27	0/1636	0.48	0/2205
4	QD	0.28	0/1733	0.50	0/2318
4	XD	0.28	0/1733	0.50	0/2318
5	QE	0.28	0/1195	0.48	0/1609
5	XE	0.29	0/1195	0.48	0/1609
6	QF	0.25	0/856	0.44	0/1154
6	XF	0.28	0/856	0.45	0/1154
7	QG	0.24	0/1276	0.45	0/1709
7	XG	0.27	0/1276	0.46	0/1709
8	QH	0.25	0/1136	0.47	0/1527
8	XH	0.27	0/1136	0.45	0/1527
9	QI	0.24	0/1037	0.48	0/1389
9	XI	0.26	0/1037	0.48	0/1389
10	QJ	0.24	0/814	0.45	0/1095
10	XJ	0.24	0/814	0.46	0/1095
11	QK	0.24	0/916	0.44	0/1234
11	XK	0.28	0/916	0.48	0/1234
12	QL	0.31	0/991	0.52	1/1327 (0.1%)
12	XL	0.36	0/991	0.56	1/1327 (0.1%)
13	QM	0.26	0/947	0.53	1/1270 (0.1%)
13	XM	0.25	0/947	0.53	0/1270
14	QN	0.25	0/501	0.47	0/664
14	XN	0.29	0/501	0.49	0/664
15	QO	0.24	0/745	0.39	0/992
15	XO	0.27	0/745	0.43	0/992
16	QP	0.26	0/721	0.46	0/970
16	XP	0.25	0/721	0.45	0/970



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
17	QQ	0.26	0/847	0.46	0/1131
17	XQ	0.30	0/847	0.47	0/1131
18	QR	0.25	0/590	0.48	0/782
18	XR	0.26	0/590	0.52	0/782
19	QS	0.27	0/670	0.53	0/901
19	XS	0.29	0/670	0.52	0/901
20	QT	0.25	0/765	0.49	1/1007 (0.1%)
20	XT	0.25	0/765	0.48	0/1007
21	QU	0.23	0/221	0.47	0/288
21	XU	0.24	0/221	0.45	0/288
22	QV	0.34	0/1832	0.83	0/2855
22	XV	0.35	0/1832	0.81	0/2855
23	QX	0.70	0/417	1.26	3/649 (0.5%)
23	XX	0.62	0/417	1.24	0/649
24	QY	0.26	0/773	0.40	0/1043
24	XY	0.26	0/773	0.41	0/1043
25	RA	0.41	0/69742	0.89	17/108874 (0.0%)
25	YA	0.44	1/69356 (0.0%)	0.91	31/108271 (0.0%)
26	RB	0.31	0/2928	0.82	0/4568
26	YB	0.34	0/2928	0.85	0/4568
27	RD	0.34	0/2165	0.56	0/2919
27	YD	0.37	0/2165	0.60	0/2919
28	RE	0.30	0/1601	0.55	0/2160
28	YE	0.34	0/1601	0.58	0/2160
29	RF	0.35	0/1662	0.58	0/2249
29	YF	0.31	0/1662	0.57	0/2249
30	RG	0.25	0/1499	0.47	0/2016
30	YG	0.26	0/1499	0.46	0/2016
31	RH	0.25	0/1332	0.60	1/1802 (0.1%)
31	YH	0.27	0/1332	0.61	1/1802 (0.1%)
32	RI	0.24	0/1151	0.54	0/1558
32	YI	0.28	0/1151	0.58	0/1558
33	RN	0.28	0/1131	0.50	0/1525
33	YN	0.29	0/1131	0.50	0/1525
34	RO	0.32	0/943	0.51	0/1269
34	YO	0.33	0/943	0.53	0/1269
35	RP	0.34	0/1162	0.66	0/1544
35	YP	0.35	0/1162	0.68	2/1544 (0.1%)
36	RQ	0.36	0/1133	0.58	0/1515
36	YQ	0.35	0/1128	0.58	1/1508 (0.1%)
37	RR	0.27	0/974	0.51	0/1302
37	YR	0.30	0/974	0.53	0/1302
38	RS	0.25	0/892	0.49	0/1187

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
38	YS	0.29	0/892	0.54	0/1187
39	RT	0.27	0/1155	0.46	0/1542
39	YT	0.30	0/1155	0.47	0/1542
40	RU	0.32	0/982	0.53	0/1306
40	YU	0.33	0/982	0.52	0/1306
41	RV	0.38	0/790	0.69	1/1057 (0.1%)
41	YV	0.35	0/790	0.67	1/1057 (0.1%)
42	RW	0.30	0/911	0.51	0/1220
42	YW	0.30	0/911	0.52	0/1220
43	RX	0.32	0/739	0.51	0/993
43	YX	0.35	0/739	0.52	0/993
44	RY	0.33	0/798	0.59	0/1064
44	YY	0.32	0/798	0.59	0/1064
45	RZ	0.29	0/1435	0.57	0/1947
45	YZ	0.30	0/1493	0.60	0/2026
46	R0	0.32	0/666	0.52	0/885
46	Y0	0.32	0/666	0.58	0/885
47	R1	0.31	0/770	0.57	0/1022
47	Y1	0.36	0/770	0.59	0/1022
48	R2	0.28	0/583	0.57	0/771
48	Y2	0.33	0/583	0.59	1/771 (0.1%)
49	R3	0.29	0/474	0.44	0/635
49	Y3	0.28	0/474	0.47	0/635
50	R4	0.24	0/586	0.46	0/785
50	Y4	0.30	0/586	0.51	0/785
51	R5	0.30	0/473	0.58	1/639 (0.2%)
51	Y5	0.50	1/456 (0.2%)	0.71	2/617 (0.3%)
52	R6	0.29	0/424	0.67	0/565
52	Y6	0.44	0/424	0.82	0/565
53	R7	0.33	0/438	0.49	0/575
53	Y7	0.34	0/438	0.53	0/575
54	R8	0.42	0/525	0.75	0/691
54	Y8	0.38	0/525	0.66	0/691
55	R9	0.26	0/310	0.42	0/407
55	Y9	0.24	0/302	0.42	0/397
56	Z6	0.54	0/40	0.56	0/60
56	Z7	0.31	0/40	0.59	0/60
All	All	0.37	3/318230 (0.0%)	0.79	98/475578 (0.0%)

All (3) bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	QA	1336	C	C3'-C2'	5.34	1.58	1.52
25	YA	1762	A	O3'-P	-5.30	1.54	1.61
51	Y5	7	PRO	N-CD	5.29	1.55	1.47

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	XL	24	VAL	C-N-CD	6.00	140.99	128.40
51	Y5	4	HIS	C-N-CD	6.00	140.99	128.40
25	YA	2655	G	O4'-C1'-N9	5.98	112.98	108.20
25	YA	1313	U	C2-N1-C1'	5.98	124.87	117.70
1	QA	328	C	P-O3'-C3'	5.94	126.83	119.70

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	QA	32472	0	16393	434	0
1	XA	32409	0	16361	385	0
2	QB	1915	0	1969	55	0
2	XB	1915	0	1969	60	0
3	QC	1612	0	1677	51	0
3	XC	1612	0	1677	40	0
4	QD	1703	0	1765	43	0
4	XD	1703	0	1765	36	0
5	QE	1178	0	1233	31	0
5	XE	1178	0	1234	22	0
6	QF	843	0	857	19	0
6	XF	843	0	857	21	0
7	QG	1257	0	1296	22	0
7	XG	1257	0	1296	31	0
8	QH	1116	0	1177	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	XH	1116	0	1177	26	0
9	QI	1018	0	1049	55	0
9	XI	1018	0	1049	41	0
10	QJ	801	0	849	36	0
10	XJ	801	0	849	44	0
11	QK	901	0	926	26	0
11	XK	901	0	926	20	0
12	QL	975	0	1062	28	0
12	XL	975	0	1062	21	0
13	QM	937	0	994	37	0
13	XM	937	0	994	56	0
14	QN	492	0	530	17	0
14	XN	492	0	528	12	0
15	QO	734	0	771	14	0
15	XO	734	0	771	14	0
16	QP	705	0	725	15	0
16	XP	705	0	725	9	0
17	QQ	834	0	904	13	0
17	XQ	834	0	904	18	0
18	QR	585	0	657	10	0
18	XR	585	0	657	19	0
19	QS	656	0	678	44	0
19	XS	656	0	678	36	0
20	QT	763	0	861	21	0
20	XT	763	0	861	27	0
21	QU	217	0	234	11	0
21	XU	217	0	234	15	0
22	QV	1640	0	837	8	0
22	XV	1640	0	837	6	0
23	QX	440	9	224	25	0
23	XX	440	9	224	18	0
24	QY	756	0	749	46	0
24	XY	756	0	749	39	0
25	RA	62269	0	31392	699	0
25	YA	61924	0	31215	651	0
26	RB	2617	0	1328	27	0
26	YB	2617	0	1328	34	0
27	RD	2115	0	2195	65	0
27	YD	2115	0	2195	78	0
28	RE	1568	0	1634	101	0
28	YE	1568	0	1634	77	0
29	RF	1627	0	1680	62	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	YF	1627	0	1680	65	0
30	RG	1474	0	1535	44	0
30	YG	1474	0	1535	47	0
31	RH	1307	0	1382	91	0
31	YH	1307	0	1381	83	0
32	RI	1136	0	1223	53	0
32	YI	1136	0	1223	71	0
33	RN	1104	0	1180	14	0
33	YN	1104	0	1180	22	0
34	RO	933	0	996	29	0
34	YO	933	0	996	24	0
35	RP	1145	0	1228	127	0
35	YP	1145	0	1228	125	0
36	RQ	1112	0	1170	35	0
36	YQ	1107	0	1166	37	0
37	RR	960	0	1021	15	0
37	YR	960	0	1021	21	0
38	RS	882	0	943	29	0
38	YS	882	0	943	35	0
39	RT	1141	0	1202	43	0
39	YT	1141	0	1202	38	0
40	RU	964	0	1022	38	0
40	YU	964	0	1022	34	0
41	RV	779	0	852	60	0
41	YV	779	0	852	54	0
42	RW	900	0	964	22	0
42	YW	900	0	964	23	0
43	RX	725	0	778	16	0
43	YX	725	0	778	19	0
44	RY	785	0	877	67	0
44	YY	785	0	878	47	0
45	RZ	1404	0	1437	92	0
45	YZ	1461	0	1493	47	0
46	R0	657	0	683	23	0
46	Y0	657	0	683	25	0
47	R1	763	0	848	32	0
47	Y1	763	0	848	22	0
48	R2	581	0	629	17	0
48	Y2	581	0	629	15	0
49	R3	469	0	518	9	0
49	Y3	469	0	518	8	0
50	R4	573	0	565	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	Y4	573	0	565	40	0
51	R5	459	0	480	9	0
51	Y5	442	0	465	16	0
52	R6	417	0	441	25	0
52	Y6	417	0	441	51	0
53	R7	430	0	480	7	0
53	Y7	430	0	480	12	0
54	R8	517	0	582	50	0
54	Y8	517	0	582	68	0
55	R9	307	0	338	10	0
55	Y9	299	0	326	7	0
56	Z6	74	0	51	6	0
56	Z7	74	0	51	23	0
57	QA	147	0	0	0	0
57	QD	1	0	0	0	0
57	QE	1	0	0	0	0
57	QL	1	0	0	0	0
57	QV	5	0	0	0	0
57	R0	3	0	0	0	0
57	R2	1	0	0	0	0
57	R5	3	0	0	0	0
57	RA	431	0	0	0	0
57	RB	5	0	0	0	0
57	RD	2	0	0	0	0
57	RE	2	0	0	0	0
57	RF	1	0	0	0	0
57	RP	2	0	0	0	0
57	RQ	2	0	0	0	0
57	RR	1	0	0	0	0
57	RY	2	0	0	0	0
57	XA	161	0	0	0	0
57	XD	1	0	0	0	0
57	XF	1	0	0	0	0
57	XL	1	0	0	0	0
57	XN	1	0	0	0	0
57	XV	4	0	0	0	0
57	Y0	3	0	0	0	0
57	Y1	1	0	0	0	0
57	Y5	3	0	0	0	0
57	Y7	1	0	0	0	0
57	YA	473	0	0	0	0
57	YB	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	YD	1	0	0	0	0
57	YE	1	0	0	0	0
57	YF	1	0	0	0	0
57	YG	1	0	0	0	0
57	YH	2	0	0	0	0
57	YN	1	0	0	0	0
57	YP	2	0	0	0	0
57	YQ	2	0	0	0	0
57	YR	1	0	0	0	0
57	YU	1	0	0	0	0
57	YV	1	0	0	0	0
57	YY	1	0	0	0	0
58	QD	1	0	0	0	0
58	QN	1	0	0	0	0
58	XD	1	0	0	0	0
58	XN	1	0	0	0	0
All	All	294392	18	199957	5185	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 5185 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)
41:YV:49:THR:CG2	41:YV:50:PRO:HD3	1.35	1.52
31:RH:9:ILE:CG2	31:RH:10:PRO:HA	1.36	1.51
31:YH:9:ILE:CG2	31:YH:10:PRO:HA	1.39	1.47
50:Y4:6:HIS:HB2	50:Y4:7:PRO:CD	1.43	1.47
41:RV:49:THR:CG2	41:RV:50:PRO:HD3	1.48	1.42

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	234/256 (91%)	186 (80%)	29 (12%)	19 (8%)	1	11
2	XB	234/256 (91%)	189 (81%)	27 (12%)	18 (8%)	1	12
3	QC	204/239 (85%)	161 (79%)	27 (13%)	16 (8%)	1	11
3	XC	204/239 (85%)	160 (78%)	32 (16%)	12 (6%)	1	18
4	QD	206/209 (99%)	169 (82%)	26 (13%)	11 (5%)	2	19
4	XD	206/209 (99%)	168 (82%)	22 (11%)	16 (8%)	1	11
5	QE	152/162 (94%)	135 (89%)	12 (8%)	5 (3%)	4	31
5	XE	152/162 (94%)	137 (90%)	9 (6%)	6 (4%)	3	27
6	QF	99/101 (98%)	89 (90%)	10 (10%)	0	100	100
6	XF	99/101 (98%)	95 (96%)	4 (4%)	0	100	100
7	QG	153/156 (98%)	136 (89%)	13 (8%)	4 (3%)	5	35
7	XG	153/156 (98%)	134 (88%)	15 (10%)	4 (3%)	5	35
8	QH	136/138 (99%)	126 (93%)	7 (5%)	3 (2%)	6	39
8	XH	136/138 (99%)	123 (90%)	10 (7%)	3 (2%)	6	39
9	QI	126/128 (98%)	94 (75%)	24 (19%)	8 (6%)	1	17
9	XI	126/128 (98%)	96 (76%)	23 (18%)	7 (6%)	2	19
10	QJ	97/105 (92%)	80 (82%)	13 (13%)	4 (4%)	3	26
10	XJ	97/105 (92%)	81 (84%)	11 (11%)	5 (5%)	2	20
11	QK	119/129 (92%)	102 (86%)	13 (11%)	4 (3%)	3	31
11	XK	119/129 (92%)	105 (88%)	10 (8%)	4 (3%)	3	31
12	QL	123/132 (93%)	99 (80%)	16 (13%)	8 (6%)	1	16
12	XL	123/132 (93%)	97 (79%)	18 (15%)	8 (6%)	1	16
13	QM	116/126 (92%)	88 (76%)	17 (15%)	11 (10%)	0	8
13	XM	116/126 (92%)	88 (76%)	17 (15%)	11 (10%)	0	8
14	QN	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	2	20
14	XN	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	2	20
15	QO	86/89 (97%)	81 (94%)	5 (6%)	0	100	100
15	XO	86/89 (97%)	79 (92%)	7 (8%)	0	100	100
16	QP	82/88 (93%)	72 (88%)	10 (12%)	0	100	100
16	XP	82/88 (93%)	76 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	QQ	98/105 (93%)	90 (92%)	7 (7%)	1 (1%)	15	55
17	XQ	98/105 (93%)	89 (91%)	7 (7%)	2 (2%)	7	41
18	QR	69/88 (78%)	61 (88%)	8 (12%)	0	100	100
18	XR	69/88 (78%)	62 (90%)	6 (9%)	1 (1%)	11	48
19	QS	80/93 (86%)	52 (65%)	18 (22%)	10 (12%)	0	5
19	XS	80/93 (86%)	52 (65%)	18 (22%)	10 (12%)	0	5
20	QT	97/106 (92%)	79 (81%)	15 (16%)	3 (3%)	4	32
20	XT	97/106 (92%)	80 (82%)	14 (14%)	3 (3%)	4	32
21	QU	23/25 (92%)	16 (70%)	6 (26%)	1 (4%)	2	24
21	XU	23/25 (92%)	18 (78%)	3 (13%)	2 (9%)	1	9
24	QY	90/118 (76%)	84 (93%)	5 (6%)	1 (1%)	14	53
24	XY	90/118 (76%)	80 (89%)	8 (9%)	2 (2%)	6	39
27	RD	270/276 (98%)	224 (83%)	38 (14%)	8 (3%)	4	33
27	YD	270/276 (98%)	228 (84%)	32 (12%)	10 (4%)	3	28
28	RE	203/206 (98%)	137 (68%)	38 (19%)	28 (14%)	0	4
28	YE	203/206 (98%)	133 (66%)	40 (20%)	30 (15%)	0	3
29	RF	206/210 (98%)	167 (81%)	26 (13%)	13 (6%)	1	17
29	YF	206/210 (98%)	168 (82%)	22 (11%)	16 (8%)	1	11
30	RG	179/182 (98%)	141 (79%)	26 (14%)	12 (7%)	1	15
30	YG	179/182 (98%)	146 (82%)	22 (12%)	11 (6%)	1	17
31	RH	168/180 (93%)	104 (62%)	37 (22%)	27 (16%)	0	3
31	YH	168/180 (93%)	98 (58%)	42 (25%)	28 (17%)	0	3
32	RI	144/148 (97%)	109 (76%)	28 (19%)	7 (5%)	2	21
32	YI	144/148 (97%)	116 (81%)	24 (17%)	4 (3%)	5	34
33	RN	136/140 (97%)	116 (85%)	13 (10%)	7 (5%)	2	20
33	YN	136/140 (97%)	110 (81%)	19 (14%)	7 (5%)	2	20
34	RO	120/122 (98%)	111 (92%)	8 (7%)	1 (1%)	19	59
34	YO	120/122 (98%)	109 (91%)	10 (8%)	1 (1%)	19	59
35	RP	148/150 (99%)	97 (66%)	23 (16%)	28 (19%)	0	2
35	YP	148/150 (99%)	102 (69%)	22 (15%)	24 (16%)	0	3
36	RQ	138/141 (98%)	110 (80%)	17 (12%)	11 (8%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	YQ	137/141 (97%)	111 (81%)	15 (11%)	11 (8%)	1	11
37	RR	115/118 (98%)	107 (93%)	4 (4%)	4 (4%)	3	30
37	YR	115/118 (98%)	109 (95%)	3 (3%)	3 (3%)	5	35
38	RS	109/112 (97%)	84 (77%)	17 (16%)	8 (7%)	1	13
38	YS	109/112 (97%)	85 (78%)	13 (12%)	11 (10%)	0	7
39	RT	135/146 (92%)	109 (81%)	24 (18%)	2 (2%)	10	47
39	YT	135/146 (92%)	113 (84%)	17 (13%)	5 (4%)	3	28
40	RU	115/118 (98%)	107 (93%)	6 (5%)	2 (2%)	9	45
40	YU	115/118 (98%)	103 (90%)	9 (8%)	3 (3%)	5	35
41	RV	99/101 (98%)	72 (73%)	12 (12%)	15 (15%)	0	3
41	YV	99/101 (98%)	71 (72%)	15 (15%)	13 (13%)	0	4
42	RW	111/113 (98%)	107 (96%)	1 (1%)	3 (3%)	5	35
42	YW	111/113 (98%)	104 (94%)	3 (3%)	4 (4%)	3	29
43	RX	90/96 (94%)	76 (84%)	12 (13%)	2 (2%)	6	39
43	YX	90/96 (94%)	77 (86%)	11 (12%)	2 (2%)	6	39
44	RY	100/110 (91%)	56 (56%)	28 (28%)	16 (16%)	0	3
44	YY	100/110 (91%)	57 (57%)	27 (27%)	16 (16%)	0	3
45	RZ	174/206 (84%)	116 (67%)	33 (19%)	25 (14%)	0	4
45	YZ	181/206 (88%)	122 (67%)	42 (23%)	17 (9%)	0	8
46	R0	81/85 (95%)	73 (90%)	5 (6%)	3 (4%)	3	28
46	Y0	81/85 (95%)	67 (83%)	11 (14%)	3 (4%)	3	28
47	R1	95/98 (97%)	71 (75%)	12 (13%)	12 (13%)	0	5
47	Y1	95/98 (97%)	76 (80%)	13 (14%)	6 (6%)	1	17
48	R2	67/72 (93%)	54 (81%)	8 (12%)	5 (8%)	1	12
48	Y2	67/72 (93%)	56 (84%)	5 (8%)	6 (9%)	1	9
49	R3	57/60 (95%)	51 (90%)	6 (10%)	0	100	100
49	Y3	57/60 (95%)	51 (90%)	6 (10%)	0	100	100
50	R4	68/71 (96%)	43 (63%)	12 (18%)	13 (19%)	0	2
50	Y4	68/71 (96%)	38 (56%)	15 (22%)	15 (22%)	0	1
51	R5	57/60 (95%)	46 (81%)	9 (16%)	2 (4%)	3	30
51	Y5	55/60 (92%)	48 (87%)	4 (7%)	3 (6%)	2	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	R6	46/54 (85%)	22 (48%)	15 (33%)	9 (20%)	0	2
52	Y6	46/54 (85%)	16 (35%)	16 (35%)	14 (30%)	0	0
53	R7	47/49 (96%)	47 (100%)	0	0	100	100
53	Y7	47/49 (96%)	44 (94%)	3 (6%)	0	100	100
54	R8	62/65 (95%)	48 (77%)	7 (11%)	7 (11%)	0	6
54	Y8	62/65 (95%)	49 (79%)	6 (10%)	7 (11%)	0	6
55	R9	35/37 (95%)	34 (97%)	0	1 (3%)	4	33
55	Y9	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
All	All	11649/12360 (94%)	9390 (81%)	1489 (13%)	770 (7%)	1	16

5 of 770 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	QB	29	ALA
2	QB	165	VAL
2	QB	195	ASP
2	QB	238	LEU
3	QC	64	VAL

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	204/220 (93%)	173 (85%)	31 (15%)	3	19
2	XB	204/220 (93%)	176 (86%)	28 (14%)	3	22
3	QC	160/188 (85%)	142 (89%)	18 (11%)	6	30
3	XC	160/188 (85%)	141 (88%)	19 (12%)	5	27
4	QD	180/181 (99%)	157 (87%)	23 (13%)	4	24
4	XD	180/181 (99%)	156 (87%)	24 (13%)	4	23
5	QE	119/123 (97%)	101 (85%)	18 (15%)	3	19
5	XE	119/123 (97%)	106 (89%)	13 (11%)	6	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	QF	90/90 (100%)	85 (94%)	5 (6%)	21	56
6	XF	90/90 (100%)	77 (86%)	13 (14%)	3	20
7	QG	126/127 (99%)	112 (89%)	14 (11%)	6	31
7	XG	126/127 (99%)	109 (86%)	17 (14%)	4	23
8	QH	119/119 (100%)	109 (92%)	10 (8%)	11	42
8	XH	119/119 (100%)	106 (89%)	13 (11%)	6	32
9	QI	99/99 (100%)	79 (80%)	20 (20%)	1	8
9	XI	99/99 (100%)	80 (81%)	19 (19%)	1	9
10	QJ	89/92 (97%)	77 (86%)	12 (14%)	4	23
10	XJ	89/92 (97%)	75 (84%)	14 (16%)	2	17
11	QK	92/99 (93%)	82 (89%)	10 (11%)	6	32
11	XK	92/99 (93%)	83 (90%)	9 (10%)	8	36
12	QL	104/109 (95%)	89 (86%)	15 (14%)	3	20
12	XL	104/109 (95%)	87 (84%)	17 (16%)	2	15
13	QM	94/101 (93%)	80 (85%)	14 (15%)	3	19
13	XM	94/101 (93%)	82 (87%)	12 (13%)	4	24
14	QN	49/50 (98%)	48 (98%)	1 (2%)	55	79
14	XN	49/50 (98%)	44 (90%)	5 (10%)	7	34
15	QO	79/80 (99%)	74 (94%)	5 (6%)	18	53
15	XO	79/80 (99%)	74 (94%)	5 (6%)	18	53
16	QP	72/74 (97%)	64 (89%)	8 (11%)	6	31
16	XP	72/74 (97%)	64 (89%)	8 (11%)	6	31
17	QQ	95/97 (98%)	90 (95%)	5 (5%)	22	58
17	XQ	95/97 (98%)	88 (93%)	7 (7%)	13	46
18	QR	62/77 (80%)	56 (90%)	6 (10%)	8	36
18	XR	62/77 (80%)	54 (87%)	8 (13%)	4	24
19	QS	71/80 (89%)	54 (76%)	17 (24%)	0	4
19	XS	71/80 (89%)	58 (82%)	13 (18%)	1	10
20	QT	76/82 (93%)	62 (82%)	14 (18%)	1	10
20	XT	76/82 (93%)	66 (87%)	10 (13%)	4	23
21	QU	20/20 (100%)	18 (90%)	2 (10%)	7	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	XU	20/20 (100%)	18 (90%)	2 (10%)	7	35
24	QY	79/103 (77%)	73 (92%)	6 (8%)	13	45
24	XY	79/103 (77%)	74 (94%)	5 (6%)	18	53
27	RD	214/218 (98%)	178 (83%)	36 (17%)	2	14
27	YD	214/218 (98%)	179 (84%)	35 (16%)	2	15
28	RE	165/166 (99%)	137 (83%)	28 (17%)	2	14
28	YE	165/166 (99%)	138 (84%)	27 (16%)	2	15
29	RF	165/166 (99%)	139 (84%)	26 (16%)	2	17
29	YF	165/166 (99%)	141 (86%)	24 (14%)	3	20
30	RG	155/156 (99%)	147 (95%)	8 (5%)	23	58
30	YG	155/156 (99%)	138 (89%)	17 (11%)	6	31
31	RH	142/148 (96%)	123 (87%)	19 (13%)	4	23
31	YH	142/148 (96%)	115 (81%)	27 (19%)	1	9
32	RI	122/124 (98%)	98 (80%)	24 (20%)	1	8
32	YI	122/124 (98%)	99 (81%)	23 (19%)	1	9
33	RN	117/119 (98%)	107 (92%)	10 (8%)	10	41
33	YN	117/119 (98%)	104 (89%)	13 (11%)	6	31
34	RO	100/100 (100%)	91 (91%)	9 (9%)	9	39
34	YO	100/100 (100%)	90 (90%)	10 (10%)	7	35
35	RP	116/116 (100%)	80 (69%)	36 (31%)	0	2
35	YP	116/116 (100%)	84 (72%)	32 (28%)	0	3
36	RQ	110/111 (99%)	93 (84%)	17 (16%)	2	18
36	YQ	110/111 (99%)	93 (84%)	17 (16%)	2	18
37	RR	100/101 (99%)	82 (82%)	18 (18%)	1	11
37	YR	100/101 (99%)	87 (87%)	13 (13%)	4	24
38	RS	87/88 (99%)	80 (92%)	7 (8%)	12	43
38	YS	87/88 (99%)	73 (84%)	14 (16%)	2	16
39	RT	120/127 (94%)	100 (83%)	20 (17%)	2	14
39	YT	120/127 (94%)	98 (82%)	22 (18%)	1	10
40	RU	93/94 (99%)	85 (91%)	8 (9%)	10	41
40	YU	93/94 (99%)	85 (91%)	8 (9%)	10	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	RV	82/82 (100%)	66 (80%)	16 (20%)	1	9
41	YV	82/82 (100%)	63 (77%)	19 (23%)	1	5
42	RW	92/92 (100%)	82 (89%)	10 (11%)	6	32
42	YW	92/92 (100%)	79 (86%)	13 (14%)	3	21
43	RX	74/78 (95%)	65 (88%)	9 (12%)	5	26
43	YX	74/78 (95%)	68 (92%)	6 (8%)	11	43
44	RY	85/91 (93%)	63 (74%)	22 (26%)	0	4
44	YY	85/91 (93%)	61 (72%)	24 (28%)	0	3
45	RZ	155/179 (87%)	129 (83%)	26 (17%)	2	14
45	YZ	162/179 (90%)	134 (83%)	28 (17%)	2	12
46	R0	66/67 (98%)	62 (94%)	4 (6%)	18	53
46	Y0	66/67 (98%)	58 (88%)	8 (12%)	5	26
47	R1	82/83 (99%)	68 (83%)	14 (17%)	2	13
47	Y1	82/83 (99%)	72 (88%)	10 (12%)	5	26
48	R2	64/67 (96%)	52 (81%)	12 (19%)	1	9
48	Y2	64/67 (96%)	57 (89%)	7 (11%)	6	32
49	R3	51/52 (98%)	44 (86%)	7 (14%)	3	22
49	Y3	51/52 (98%)	47 (92%)	4 (8%)	12	44
50	R4	62/63 (98%)	47 (76%)	15 (24%)	0	4
50	Y4	62/63 (98%)	44 (71%)	18 (29%)	0	2
51	R5	51/52 (98%)	41 (80%)	10 (20%)	1	8
51	Y5	49/52 (94%)	42 (86%)	7 (14%)	3	21
52	R6	47/52 (90%)	32 (68%)	15 (32%)	0	2
52	Y6	47/52 (90%)	30 (64%)	17 (36%)	0	1
53	R7	42/42 (100%)	35 (83%)	7 (17%)	2	14
53	Y7	42/42 (100%)	35 (83%)	7 (17%)	2	14
54	R8	54/55 (98%)	43 (80%)	11 (20%)	1	8
54	Y8	54/55 (98%)	44 (82%)	10 (18%)	1	10
55	R9	34/34 (100%)	32 (94%)	2 (6%)	19	55
55	Y9	33/34 (97%)	33 (100%)	0	100	100
All	All	9856/10268 (96%)	8435 (86%)	1421 (14%)	3	20

5 of 1421 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	XR	37	VAL
35	YP	56	SER
20	XT	93	GLU
18	XR	31	LEU
29	YF	136	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
37	YR	3	HIS
40	YU	81	HIS
40	YU	117	GLN
40	RU	81	HIS
45	RZ	118	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	QA	1509/1522 (99%)	286 (18%)	44 (2%)
1	XA	1506/1522 (98%)	290 (19%)	35 (2%)
22	QV	76/77 (98%)	15 (19%)	0
22	XV	76/77 (98%)	13 (17%)	1 (1%)
23	QX	19/25 (76%)	13 (68%)	2 (10%)
23	XX	19/25 (76%)	8 (42%)	2 (10%)
25	RA	2888/2916 (99%)	575 (19%)	45 (1%)
25	YA	2872/2916 (98%)	560 (19%)	39 (1%)
26	RB	121/124 (97%)	21 (17%)	1 (0%)
26	YB	121/124 (97%)	20 (16%)	2 (1%)
56	Z6	1/3 (33%)	0	0
56	Z7	1/3 (33%)	0	0
All	All	9209/9334 (98%)	1801 (19%)	171 (1%)

5 of 1801 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	QA	4	U
1	QA	5	U
1	QA	6	G
1	QA	9	G
1	QA	22	G

5 of 171 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	XA	818	G
25	YA	1085	A
1	XA	1004	A
25	YA	74	A
25	YA	1762	A

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

8 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
23	A2M	XX	20	23	18,25,26	0.99	1 (5%)	18,36,39	1.49	3 (16%)
23	A2M	QX	21	1,23	18,25,26	1.16	1 (5%)	18,36,39	1.39	4 (22%)
23	A2M	XX	21	23	18,25,26	1.08	2 (11%)	18,36,39	1.41	2 (11%)
23	A2M	QX	19	23	18,25,26	1.03	1 (5%)	18,36,39	1.41	3 (16%)
56	PPU	Z6	76	56,25	32,40,41	0.90	1 (3%)	33,57,60	1.73	7 (21%)
56	PPU	Z7	76	56,25	32,40,41	0.90	1 (3%)	33,57,60	1.36	6 (18%)
23	A2M	XX	19	23	18,25,26	0.98	1 (5%)	18,36,39	1.85	5 (27%)
23	A2M	QX	20	23	18,25,26	1.20	2 (11%)	18,36,39	1.40	2 (11%)

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
23	A2M	XX	20	23	-	0/5/27/28	0/3/3/3
23	A2M	QX	21	1,23	-	5/5/27/28	0/3/3/3
23	A2M	XX	21	23	-	4/5/27/28	0/3/3/3
23	A2M	QX	19	23	-	0/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	PPU	Z6	76	56,25	-	1/21/43/44	0/4/4/4
56	PPU	Z7	76	56,25	-	7/21/43/44	0/4/4/4
23	A2M	XX	19	23	-	2/5/27/28	0/3/3/3
23	A2M	QX	20	23	-	0/5/27/28	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	QX	20	A2M	C5-C4	3.07	1.49	1.40
23	QX	21	A2M	C5-C4	2.75	1.48	1.40
23	QX	19	A2M	C5-C4	2.52	1.47	1.40
23	XX	21	A2M	O4'-C1'	2.47	1.44	1.41
23	XX	19	A2M	C5-C4	2.39	1.47	1.40

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	Z6	76	PPU	N1-C6-N6	6.36	123.75	117.06
23	XX	19	A2M	N3-C2-N1	-3.97	122.47	128.68
23	QX	19	A2M	N3-C2-N1	-3.70	122.89	128.68
56	Z6	76	PPU	C9-N6-C6	-3.57	108.69	119.51
23	XX	19	A2M	C1'-N9-C4	-3.47	120.54	126.64

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	QX	21	A2M	C1'-C2'-O2'-CM'
23	XX	21	A2M	O4'-C4'-C5'-O5'
23	XX	21	A2M	C3'-C4'-C5'-O5'
23	XX	21	A2M	C1'-C2'-O2'-CM'
56	Z7	76	PPU	C-CA-CB-CG

There are no ring outliers.

7 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	XX	20	A2M	1	0
23	QX	21	A2M	3	0
23	XX	21	A2M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	QX	19	A2M	1	0
56	Z6	76	PPU	5	0
56	Z7	76	PPU	12	0
23	XX	19	A2M	2	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 1285 ligands modelled in this entry, 1285 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data i

### 6.1 Protein, DNA and RNA chains i

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	QA	1511/1522 (99%)	0.09	32 (2%) 63 48	52, 94, 194, 353	0
1	XA	1508/1522 (99%)	0.03	36 (2%) 59 42	41, 84, 179, 401	0
2	QB	236/256 (92%)	0.22	11 (4%) 31 19	76, 141, 220, 278	0
2	XB	236/256 (92%)	-0.03	1 (0%) 92 86	56, 119, 205, 243	0
3	QC	206/239 (86%)	0.30	5 (2%) 59 42	81, 126, 222, 383	0
3	XC	206/239 (86%)	0.08	1 (0%) 91 83	58, 106, 171, 346	0
4	QD	208/209 (99%)	-0.25	0 100 100	53, 85, 131, 188	0
4	XD	208/209 (99%)	-0.18	0 100 100	56, 87, 139, 181	0
5	QE	154/162 (95%)	-0.05	0 100 100	45, 86, 147, 236	0
5	XE	154/162 (95%)	-0.09	0 100 100	41, 77, 151, 303	0
6	QF	101/101 (100%)	0.15	4 (3%) 38 25	75, 119, 160, 179	0
6	XF	101/101 (100%)	-0.35	1 (0%) 82 70	49, 83, 120, 199	0
7	QG	155/156 (99%)	0.40	13 (8%) 11 7	83, 138, 199, 270	0
7	XG	155/156 (99%)	0.20	9 (5%) 23 13	70, 111, 186, 242	0
8	QH	138/138 (100%)	-0.10	0 100 100	52, 93, 131, 193	0
8	XH	138/138 (100%)	-0.06	0 100 100	55, 83, 120, 154	0
9	QI	128/128 (100%)	0.85	18 (14%) 2 2	87, 160, 242, 319	0
9	XI	128/128 (100%)	0.09	2 (1%) 72 57	66, 119, 199, 272	0
10	QJ	99/105 (94%)	0.67	8 (8%) 12 7	94, 155, 255, 330	0
10	XJ	99/105 (94%)	0.57	8 (8%) 12 7	73, 136, 199, 337	0
11	QK	121/129 (93%)	0.36	7 (5%) 23 13	65, 110, 191, 294	0
11	XK	121/129 (93%)	-0.05	4 (3%) 46 31	50, 85, 156, 284	0
12	QL	125/132 (94%)	0.01	2 (1%) 72 57	52, 78, 121, 306	0
12	XL	125/132 (94%)	-0.08	2 (1%) 72 57	46, 73, 119, 225	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
13	QM	118/126 (93%)	0.31	6 (5%) 28 17	92, 139, 223, 308	0
13	XM	118/126 (93%)	0.18	2 (1%) 70 55	61, 120, 172, 350	0
14	QN	60/61 (98%)	0.08	2 (3%) 46 31	82, 124, 170, 221	0
14	XN	60/61 (98%)	-0.17	0 100 100	72, 100, 128, 193	0
15	QO	88/89 (98%)	0.01	0 100 100	58, 94, 138, 168	0
15	XO	88/89 (98%)	-0.20	1 (1%) 80 68	45, 78, 134, 146	0
16	QP	84/88 (95%)	0.14	0 100 100	56, 81, 121, 206	0
16	XP	84/88 (95%)	0.35	1 (1%) 79 66	58, 90, 134, 294	0
17	QQ	100/105 (95%)	-0.07	1 (1%) 82 70	51, 91, 126, 136	0
17	XQ	100/105 (95%)	-0.05	0 100 100	51, 83, 119, 217	0
18	QR	71/88 (80%)	0.29	2 (2%) 53 37	77, 119, 180, 288	0
18	XR	71/88 (80%)	-0.11	0 100 100	50, 81, 183, 271	0
19	QS	82/93 (88%)	0.71	9 (10%) 5 3	96, 150, 245, 348	0
19	XS	82/93 (88%)	0.46	3 (3%) 41 27	72, 128, 212, 281	0
20	QT	99/106 (93%)	0.23	6 (6%) 21 12	55, 97, 153, 209	0
20	XT	99/106 (93%)	0.35	4 (4%) 38 25	63, 106, 171, 235	0
21	QU	25/25 (100%)	1.22	4 (16%) 1 1	104, 142, 192, 230	0
21	XU	25/25 (100%)	1.02	5 (20%) 1 0	91, 117, 148, 176	0
22	QV	77/77 (100%)	0.18	3 (3%) 39 25	45, 95, 141, 191	0
22	XV	77/77 (100%)	0.03	1 (1%) 77 63	41, 86, 120, 188	0
23	QX	17/25 (68%)	3.24	12 (70%) 0 0	73, 229, 280, 291	0
23	XX	17/25 (68%)	3.47	11 (64%) 0 0	58, 223, 329, 349	0
24	QY	92/118 (77%)	0.88	3 (3%) 46 31	58, 116, 149, 189	0
24	XY	92/118 (77%)	0.81	5 (5%) 25 16	72, 113, 143, 177	0
25	RA	2891/2916 (99%)	0.26	163 (5%) 24 14	36, 68, 244, 472	0
25	YA	2875/2916 (98%)	0.29	162 (5%) 24 14	32, 61, 254, 518	0
26	RB	122/124 (98%)	-0.06	2 (1%) 72 57	72, 115, 150, 204	0
26	YB	122/124 (98%)	-0.05	1 (0%) 86 75	72, 95, 141, 236	0
27	RD	272/276 (98%)	-0.21	0 100 100	29, 66, 111, 221	0
27	YD	272/276 (98%)	-0.27	0 100 100	19, 51, 94, 175	0
28	RE	205/206 (99%)	0.09	6 (2%) 51 35	42, 84, 156, 368	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
28	YE	205/206 (99%)	0.13	6 (2%) 51 35	31, 73, 154, 409	0
29	RF	208/210 (99%)	-0.26	6 (2%) 51 35	27, 58, 160, 285	0
29	YF	208/210 (99%)	-0.12	7 (3%) 45 30	32, 69, 206, 333	0
30	RG	181/182 (99%)	0.07	2 (1%) 80 68	68, 120, 176, 225	0
30	YG	181/182 (99%)	-0.01	3 (1%) 70 55	65, 105, 154, 215	0
31	RH	170/180 (94%)	0.94	24 (14%) 2 2	82, 161, 292, 396	0
31	YH	170/180 (94%)	0.69	19 (11%) 5 3	66, 132, 250, 421	0
32	RI	146/148 (98%)	0.33	1 (0%) 87 78	64, 112, 168, 286	0
32	YI	146/148 (98%)	0.11	3 (2%) 63 48	47, 99, 175, 333	0
33	RN	138/140 (98%)	-0.07	0 100 100	54, 87, 135, 192	0
33	YN	138/140 (98%)	-0.07	1 (0%) 87 78	47, 79, 134, 185	0
34	RO	122/122 (100%)	-0.34	0 100 100	37, 72, 107, 153	0
34	YO	122/122 (100%)	-0.28	0 100 100	31, 64, 98, 132	0
35	RP	150/150 (100%)	0.11	3 (2%) 65 49	29, 79, 147, 252	0
35	YP	150/150 (100%)	0.11	4 (2%) 54 38	37, 73, 131, 253	0
36	RQ	140/141 (99%)	-0.11	0 100 100	41, 85, 142, 208	0
36	YQ	139/141 (98%)	-0.14	1 (0%) 87 78	39, 74, 127, 231	0
37	RR	117/118 (99%)	-0.05	1 (0%) 84 73	41, 75, 114, 165	0
37	YR	117/118 (99%)	-0.20	0 100 100	39, 65, 100, 157	0
38	RS	111/112 (99%)	0.44	7 (6%) 20 11	65, 117, 178, 256	0
38	YS	111/112 (99%)	0.03	2 (1%) 68 53	58, 94, 154, 253	0
39	RT	137/146 (93%)	-0.04	0 100 100	52, 88, 171, 361	0
39	YT	137/146 (93%)	-0.03	6 (4%) 34 21	45, 74, 201, 347	0
40	RU	117/118 (99%)	-0.23	2 (1%) 70 55	30, 66, 135, 205	0
40	YU	117/118 (99%)	-0.30	0 100 100	38, 69, 133, 179	0
41	RV	101/101 (100%)	0.02	2 (1%) 65 49	37, 84, 144, 284	0
41	YV	101/101 (100%)	-0.08	2 (1%) 65 49	43, 92, 135, 361	0
42	RW	113/113 (100%)	-0.19	0 100 100	40, 64, 130, 201	0
42	YW	113/113 (100%)	0.00	2 (1%) 68 53	33, 62, 110, 192	0
43	RX	92/96 (95%)	-0.00	0 100 100	48, 80, 118, 155	0
43	YX	92/96 (95%)	-0.27	0 100 100	32, 65, 113, 139	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
44	RY	102/110 (92%)	0.75	11 (10%) 5 3	50, 84, 222, 392	0
44	YY	102/110 (92%)	0.56	7 (6%) 16 10	52, 94, 210, 487	0
45	RZ	176/206 (85%)	0.33	7 (3%) 38 25	63, 117, 216, 401	0
45	YZ	183/206 (88%)	0.19	6 (3%) 46 31	64, 113, 192, 282	0
46	R0	83/85 (97%)	0.06	2 (2%) 59 42	50, 75, 111, 253	0
46	Y0	83/85 (97%)	0.11	1 (1%) 79 66	39, 69, 98, 204	0
47	R1	97/98 (98%)	0.30	6 (6%) 20 12	41, 76, 203, 321	0
47	Y1	97/98 (98%)	0.18	5 (5%) 27 17	30, 61, 190, 315	0
48	R2	69/72 (95%)	0.01	4 (5%) 23 13	49, 99, 191, 258	0
48	Y2	69/72 (95%)	-0.22	1 (1%) 75 61	41, 78, 123, 222	0
49	R3	59/60 (98%)	0.64	3 (5%) 28 17	42, 72, 131, 159	0
49	Y3	59/60 (98%)	0.18	0 100 100	47, 81, 131, 164	0
50	R4	70/71 (98%)	0.79	10 (14%) 2 2	99, 196, 456, 558	0
50	Y4	70/71 (98%)	0.71	10 (14%) 2 2	94, 171, 356, 481	0
51	R5	59/60 (98%)	0.06	4 (6%) 17 10	40, 75, 185, 238	0
51	Y5	57/60 (95%)	-0.13	1 (1%) 68 53	24, 70, 159, 234	0
52	R6	48/54 (88%)	3.90	42 (87%) 0 0	126, 181, 242, 300	0
52	Y6	48/54 (88%)	3.85	40 (83%) 0 0	119, 172, 254, 281	0
53	R7	49/49 (100%)	-0.10	0 100 100	33, 54, 146, 188	0
53	Y7	49/49 (100%)	-0.08	0 100 100	20, 45, 117, 224	0
54	R8	64/65 (98%)	0.00	0 100 100	34, 66, 138, 223	0
54	Y8	64/65 (98%)	-0.02	2 (3%) 49 33	31, 62, 118, 203	0
55	R9	37/37 (100%)	1.50	12 (32%) 0 0	76, 134, 192, 230	0
55	Y9	36/37 (97%)	2.53	22 (61%) 0 0	102, 141, 190, 242	0
56	Z6	2/3 (66%)	-0.01	0 100 100	42, 42, 42, 55	0
56	Z7	2/3 (66%)	0.68	0 100 100	62, 62, 62, 63	0
All	All	21070/21694 (97%)	0.17	879 (4%) 36 23	19, 85, 199, 558	0

The worst 5 of 879 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
25	YA	2114	A	20.8
25	YA	2110	G	16.2

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Mol	Chain	Res	Type	RSRZ
25	RA	2139	C	15.4
25	YA	2138	C	14.7
25	YA	2165	G	14.2

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
23	A2M	XX	21	23/24	0.76	0.37	111,165,165,165	0
23	A2M	QX	21	23/24	0.79	0.40	111,168,168,168	0
23	A2M	QX	20	23/24	0.90	0.28	111,117,117,117	0
23	A2M	XX	19	23/24	0.91	0.27	96,96,111,111	0
23	A2M	XX	20	23/24	0.91	0.31	105,105,111,111	0
23	A2M	QX	19	23/24	0.93	0.26	111,115,115,115	0
56	PPU	Z7	76	37/38	0.93	0.31	61,61,61,61	0
56	PPU	Z6	76	37/38	0.96	0.24	41,47,54,58	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
57	MG	YA	3286	1/1	0.07	0.46	47,47,47,47	0
57	MG	QD	302	1/1	0.37	1.32	78,78,78,78	0
57	MG	YA	3222	1/1	0.38	0.49	78,78,78,78	0
57	MG	YG	201	1/1	0.40	0.23	85,85,85,85	0
57	MG	YA	3226	1/1	0.41	0.48	55,55,55,55	0
57	MG	RA	3292	1/1	0.43	0.54	52,52,52,52	0
57	MG	RA	3400	1/1	0.44	0.50	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XV	103	1/1	0.44	0.41	62,62,62,62	0
57	MG	RA	3300	1/1	0.44	0.73	44,44,44,44	0
57	MG	QA	1658	1/1	0.46	0.58	34,34,34,34	0
57	MG	QA	1747	1/1	0.48	0.41	111,111,111,111	0
57	MG	YA	3410	1/1	0.48	0.34	43,43,43,43	0
57	MG	YA	3169	1/1	0.48	0.80	61,61,61,61	0
57	MG	YA	3399	1/1	0.49	0.66	73,73,73,73	0
57	MG	RA	3221	1/1	0.50	1.18	46,46,46,46	0
57	MG	QA	1711	1/1	0.50	0.63	70,70,70,70	0
57	MG	YA	3468	1/1	0.51	0.36	44,44,44,44	0
57	MG	QA	1693	1/1	0.51	0.16	47,47,47,47	0
57	MG	QA	1647	1/1	0.52	0.23	72,72,72,72	0
57	MG	YA	3181	1/1	0.53	0.30	58,58,58,58	0
57	MG	QA	1731	1/1	0.53	0.35	54,54,54,54	0
57	MG	QA	1671	1/1	0.54	0.62	38,38,38,38	0
57	MG	QA	1668	1/1	0.54	0.39	50,50,50,50	0
57	MG	XA	1742	1/1	0.54	0.85	62,62,62,62	0
57	MG	YA	3352	1/1	0.54	0.50	65,65,65,65	0
57	MG	RA	3278	1/1	0.55	0.43	68,68,68,68	0
57	MG	YA	3446	1/1	0.55	0.34	49,49,49,49	0
57	MG	YA	3353	1/1	0.56	0.48	34,34,34,34	0
57	MG	RA	3110	1/1	0.56	0.31	38,38,38,38	0
57	MG	YA	3377	1/1	0.57	0.52	85,85,85,85	0
57	MG	RA	3298	1/1	0.57	0.75	79,79,79,79	0
57	MG	XA	1760	1/1	0.57	0.24	71,71,71,71	0
57	MG	YA	3301	1/1	0.58	0.85	65,65,65,65	0
57	MG	YA	3333	1/1	0.59	0.81	47,47,47,47	0
57	MG	RA	3318	1/1	0.59	0.36	38,38,38,38	0
57	MG	RA	3335	1/1	0.59	1.11	44,44,44,44	0
57	MG	QA	1719	1/1	0.60	0.82	68,68,68,68	0
57	MG	RA	3342	1/1	0.60	0.49	109,109,109,109	0
57	MG	YA	3423	1/1	0.60	0.51	50,50,50,50	0
57	MG	YA	3355	1/1	0.60	0.32	39,39,39,39	0
57	MG	YA	3265	1/1	0.60	0.69	56,56,56,56	0
57	MG	YA	3392	1/1	0.60	0.31	52,52,52,52	0
57	MG	XA	1749	1/1	0.61	0.40	81,81,81,81	0
57	MG	RA	3206	1/1	0.61	0.23	30,30,30,30	0
57	MG	XA	1714	1/1	0.62	0.83	54,54,54,54	0
57	MG	RD	301	1/1	0.62	0.54	35,35,35,35	0
57	MG	XA	1688	1/1	0.62	0.51	37,37,37,37	0
57	MG	XA	1689	1/1	0.62	1.16	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YQ	202	1/1	0.62	0.60	39,39,39,39	0
57	MG	Y5	103	1/1	0.62	0.62	50,50,50,50	0
57	MG	YA	3182	1/1	0.63	0.40	51,51,51,51	0
57	MG	RA	3365	1/1	0.63	0.27	58,58,58,58	0
57	MG	RA	3048	1/1	0.63	0.62	27,27,27,27	0
57	MG	QA	1703	1/1	0.63	0.30	57,57,57,57	0
57	MG	RA	3134	1/1	0.63	0.38	39,39,39,39	0
57	MG	RA	3394	1/1	0.64	0.53	39,39,39,39	0
57	MG	YA	3368	1/1	0.64	0.51	36,36,36,36	0
57	MG	XA	1722	1/1	0.64	1.08	74,74,74,74	0
57	MG	YA	3471	1/1	0.64	0.56	85,85,85,85	0
57	MG	XA	1752	1/1	0.64	0.37	62,62,62,62	0
57	MG	YA	3242	1/1	0.64	0.37	54,54,54,54	0
57	MG	XA	1755	1/1	0.64	0.45	61,61,61,61	0
57	MG	YA	3459	1/1	0.65	0.54	42,42,42,42	0
57	MG	QA	1663	1/1	0.65	1.31	64,64,64,64	0
57	MG	YA	3146	1/1	0.65	0.48	63,63,63,63	0
57	MG	RA	3173	1/1	0.65	0.48	50,50,50,50	0
57	MG	RA	3370	1/1	0.65	0.71	101,101,101,101	0
57	MG	YA	3348	1/1	0.65	0.25	45,45,45,45	0
57	MG	RA	3326	1/1	0.66	0.55	65,65,65,65	0
57	MG	YA	3325	1/1	0.66	0.94	53,53,53,53	0
57	MG	RA	3330	1/1	0.66	0.20	64,64,64,64	0
57	MG	RA	3275	1/1	0.66	0.64	79,79,79,79	0
57	MG	RA	3248	1/1	0.66	0.30	23,23,23,23	0
57	MG	YA	3376	1/1	0.67	0.37	82,82,82,82	0
57	MG	QA	1696	1/1	0.67	1.04	64,64,64,64	0
57	MG	RA	3327	1/1	0.67	0.41	71,71,71,71	0
57	MG	QA	1695	1/1	0.67	0.34	48,48,48,48	0
57	MG	YB	206	1/1	0.67	0.23	50,50,50,50	0
57	MG	YA	3405	1/1	0.67	0.43	33,33,33,33	0
57	MG	XA	1700	1/1	0.67	0.59	36,36,36,36	0
57	MG	XA	1709	1/1	0.67	1.07	63,63,63,63	0
57	MG	RA	3040	1/1	0.68	0.18	19,19,19,19	0
57	MG	YA	3349	1/1	0.68	0.42	63,63,63,63	0
57	MG	RA	3167	1/1	0.68	0.36	25,25,25,25	0
57	MG	YA	3443	1/1	0.68	0.29	65,65,65,65	0
57	MG	QA	1724	1/1	0.68	0.27	60,60,60,60	0
57	MG	XA	1656	1/1	0.68	0.09	50,50,50,50	0
57	MG	XA	1676	1/1	0.68	0.48	44,44,44,44	0
57	MG	YA	3372	1/1	0.68	0.49	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3182	1/1	0.68	0.41	56,56,56,56	0
57	MG	YF	301	1/1	0.68	0.33	38,38,38,38	0
57	MG	QA	1710	1/1	0.68	0.51	59,59,59,59	0
57	MG	YA	3184	1/1	0.68	0.42	49,49,49,49	0
57	MG	YA	3338	1/1	0.68	0.58	57,57,57,57	0
57	MG	YA	3172	1/1	0.69	0.36	43,43,43,43	0
57	MG	RA	3334	1/1	0.69	0.67	40,40,40,40	0
57	MG	YA	3394	1/1	0.69	0.26	61,61,61,61	0
57	MG	RA	3203	1/1	0.69	0.22	29,29,29,29	0
57	MG	RA	3339	1/1	0.69	0.17	69,69,69,69	0
57	MG	XA	1736	1/1	0.69	0.16	45,45,45,45	0
57	MG	R0	102	1/1	0.69	0.46	47,47,47,47	0
57	MG	YA	3426	1/1	0.69	0.19	45,45,45,45	0
57	MG	XA	1630	1/1	0.69	0.53	46,46,46,46	0
57	MG	RA	3102	1/1	0.70	0.52	56,56,56,56	0
57	MG	YA	3356	1/1	0.70	0.20	55,55,55,55	0
57	MG	YA	3303	1/1	0.70	0.44	47,47,47,47	0
57	MG	YA	3096	1/1	0.70	0.29	36,36,36,36	0
57	MG	YA	3109	1/1	0.70	0.34	31,31,31,31	0
57	MG	RA	3340	1/1	0.70	0.47	56,56,56,56	0
57	MG	YA	3388	1/1	0.70	0.39	55,55,55,55	0
57	MG	YA	3150	1/1	0.70	0.37	44,44,44,44	0
57	MG	QA	1742	1/1	0.70	0.57	57,57,57,57	0
57	MG	YA	3351	1/1	0.70	0.45	48,48,48,48	0
57	MG	QE	201	1/1	0.70	0.26	62,62,62,62	0
57	MG	YA	3179	1/1	0.70	0.46	64,64,64,64	0
57	MG	YA	3318	1/1	0.71	0.81	48,48,48,48	0
57	MG	YA	3390	1/1	0.71	0.26	54,54,54,54	0
57	MG	RA	3416	1/1	0.71	0.29	61,61,61,61	0
57	MG	QA	1744	1/1	0.71	0.72	44,44,44,44	0
57	MG	XA	1720	1/1	0.71	0.83	62,62,62,62	0
57	MG	QA	1672	1/1	0.71	0.73	71,71,71,71	0
57	MG	YA	3461	1/1	0.71	0.43	57,57,57,57	0
57	MG	YA	3425	1/1	0.72	0.45	61,61,61,61	0
57	MG	RA	3187	1/1	0.72	0.40	42,42,42,42	0
57	MG	YA	3431	1/1	0.72	0.36	65,65,65,65	0
57	MG	YA	3217	1/1	0.72	0.25	46,46,46,46	0
57	MG	RA	3431	1/1	0.72	0.52	34,34,34,34	0
57	MG	QA	1718	1/1	0.72	0.49	66,66,66,66	0
57	MG	RA	3372	1/1	0.72	0.43	44,44,44,44	0
57	MG	RA	3333	1/1	0.72	0.47	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	YA	3268	1/1	0.72	0.38	51,51,51,51	0
57	MG	QA	1743	1/1	0.72	0.34	71,71,71,71	0
57	MG	RA	3403	1/1	0.72	0.33	59,59,59,59	0
57	MG	XA	1729	1/1	0.72	1.08	48,48,48,48	0
57	MG	YA	3306	1/1	0.72	0.67	54,54,54,54	0
57	MG	YA	3367	1/1	0.72	0.30	57,57,57,57	0
57	MG	RA	3324	1/1	0.73	0.27	62,62,62,62	0
57	MG	XA	1702	1/1	0.73	0.35	38,38,38,38	0
57	MG	XA	1730	1/1	0.73	0.29	55,55,55,55	0
57	MG	RA	3001	1/1	0.73	0.71	60,60,60,60	0
57	MG	R2	101	1/1	0.73	0.38	80,80,80,80	0
57	MG	YA	3419	1/1	0.73	0.17	54,54,54,54	0
57	MG	QA	1637	1/1	0.73	0.48	61,61,61,61	0
57	MG	RA	3262	1/1	0.74	0.46	62,62,62,62	0
57	MG	XA	1739	1/1	0.74	0.24	49,49,49,49	0
57	MG	YA	3183	1/1	0.74	0.32	28,28,28,28	0
57	MG	RA	3269	1/1	0.74	0.49	50,50,50,50	0
57	MG	YA	3113	1/1	0.74	0.42	37,37,37,37	0
57	MG	YA	3141	1/1	0.74	0.27	31,31,31,31	0
57	MG	RA	3219	1/1	0.74	0.31	31,31,31,31	0
57	MG	YA	3342	1/1	0.74	0.79	43,43,43,43	0
57	MG	RA	3390	1/1	0.74	0.20	53,53,53,53	0
57	MG	YA	3260	1/1	0.74	0.40	48,48,48,48	0
57	MG	YA	3264	1/1	0.74	0.52	60,60,60,60	0
57	MG	RA	3417	1/1	0.74	0.20	45,45,45,45	0
57	MG	YA	3409	1/1	0.74	0.69	54,54,54,54	0
57	MG	XA	1756	1/1	0.74	0.54	59,59,59,59	0
57	MG	XA	1631	1/1	0.74	0.29	74,74,74,74	0
57	MG	QA	1734	1/1	0.75	0.34	53,53,53,53	0
57	MG	RA	3421	1/1	0.75	0.43	43,43,43,43	0
57	MG	YA	3167	1/1	0.75	0.96	49,49,49,49	0
57	MG	YA	3438	1/1	0.75	0.19	54,54,54,54	0
57	MG	YA	3237	1/1	0.75	0.43	26,26,26,26	0
57	MG	YA	3168	1/1	0.75	0.48	34,34,34,34	0
57	MG	XL	201	1/1	0.75	0.17	43,43,43,43	0
57	MG	RA	3430	1/1	0.75	0.27	38,38,38,38	0
57	MG	RA	3294	1/1	0.75	0.24	48,48,48,48	0
57	MG	QA	1707	1/1	0.75	0.61	64,64,64,64	0
57	MG	RP	202	1/1	0.75	0.36	34,34,34,34	0
57	MG	RA	3362	1/1	0.75	0.33	45,45,45,45	0
57	MG	YA	3145	1/1	0.75	0.23	32,32,32,32	0
57	MG	YA	3357	1/1	0.75	0.50	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	YA	3191	1/1	0.75	0.59	28,28,28,28	0
57	MG	RA	3255	1/1	0.76	0.09	40,40,40,40	0
57	MG	YA	3228	1/1	0.76	1.27	51,51,51,51	0
57	MG	RY	202	1/1	0.76	0.56	66,66,66,66	0
57	MG	RA	3204	1/1	0.76	0.68	34,34,34,34	0
57	MG	YA	3152	1/1	0.76	0.27	34,34,34,34	0
57	MG	RA	3265	1/1	0.76	0.18	33,33,33,33	0
57	MG	XA	1710	1/1	0.76	0.50	57,57,57,57	0
57	MG	XA	1757	1/1	0.76	0.39	66,66,66,66	0
57	MG	XA	1759	1/1	0.76	0.12	36,36,36,36	0
57	MG	RA	3176	1/1	0.76	0.42	51,51,51,51	0
57	MG	YA	3451	1/1	0.76	0.46	63,63,63,63	0
57	MG	XD	302	1/1	0.76	0.10	77,77,77,77	0
57	MG	RA	3428	1/1	0.76	0.46	41,41,41,41	0
57	MG	YA	3309	1/1	0.76	0.85	56,56,56,56	0
57	MG	YA	3315	1/1	0.76	0.22	55,55,55,55	0
57	MG	XA	1635	1/1	0.76	0.21	44,44,44,44	0
57	MG	XA	1652	1/1	0.76	0.92	41,41,41,41	0
57	MG	RA	3142	1/1	0.76	0.40	48,48,48,48	0
57	MG	RA	3089	1/1	0.76	0.50	33,33,33,33	0
57	MG	QA	1733	1/1	0.76	0.35	57,57,57,57	0
57	MG	XA	1697	1/1	0.77	0.33	52,52,52,52	0
57	MG	RA	3380	1/1	0.77	0.33	45,45,45,45	0
57	MG	RA	3266	1/1	0.77	0.74	48,48,48,48	0
57	MG	RA	3251	1/1	0.77	0.39	58,58,58,58	0
57	MG	YA	3202	1/1	0.77	0.54	22,22,22,22	0
57	MG	YA	3210	1/1	0.77	0.16	29,29,29,29	0
57	MG	RA	3198	1/1	0.77	0.29	49,49,49,49	0
57	MG	RA	3311	1/1	0.77	0.79	61,61,61,61	0
57	MG	QA	1740	1/1	0.77	0.59	69,69,69,69	0
57	MG	RA	3210	1/1	0.77	0.37	29,29,29,29	0
57	MG	YD	301	1/1	0.77	0.53	21,21,21,21	0
57	MG	YA	3316	1/1	0.77	0.65	53,53,53,53	0
57	MG	YA	3127	1/1	0.77	0.13	48,48,48,48	0
57	MG	YA	3322	1/1	0.77	0.68	42,42,42,42	0
57	MG	RA	3338	1/1	0.77	0.43	52,52,52,52	0
57	MG	YA	3354	1/1	0.78	0.43	67,67,67,67	0
57	MG	RA	3100	1/1	0.78	0.18	14,14,14,14	0
57	MG	YA	3195	1/1	0.78	0.29	30,30,30,30	0
57	MG	XA	1751	1/1	0.78	0.34	59,59,59,59	0
57	MG	QA	1678	1/1	0.78	0.24	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3439	1/1	0.78	0.34	53,53,53,53	0
57	MG	YA	3440	1/1	0.78	0.29	75,75,75,75	0
57	MG	XA	1753	1/1	0.78	0.32	67,67,67,67	0
57	MG	RA	3284	1/1	0.78	0.67	41,41,41,41	0
57	MG	YA	3447	1/1	0.78	0.25	38,38,38,38	0
57	MG	QA	1629	1/1	0.78	0.45	46,46,46,46	0
57	MG	RA	3425	1/1	0.78	0.49	46,46,46,46	0
57	MG	QA	1613	1/1	0.78	0.43	50,50,50,50	0
57	MG	YA	3466	1/1	0.78	0.35	58,58,58,58	0
57	MG	RA	3212	1/1	0.78	0.31	19,19,19,19	0
57	MG	XA	1725	1/1	0.78	0.45	64,64,64,64	0
57	MG	YA	3343	1/1	0.78	0.45	25,25,25,25	0
57	MG	RA	3140	1/1	0.78	0.17	59,59,59,59	0
57	MG	XA	1686	1/1	0.78	0.47	47,47,47,47	0
57	MG	RA	3302	1/1	0.78	0.55	36,36,36,36	0
57	MG	QL	201	1/1	0.78	0.23	49,49,49,49	0
57	MG	RA	3316	1/1	0.78	0.58	52,52,52,52	0
57	MG	XA	1718	1/1	0.79	0.71	51,51,51,51	0
57	MG	YA	3313	1/1	0.79	0.18	65,65,65,65	0
57	MG	QA	1677	1/1	0.79	0.19	86,86,86,86	0
57	MG	XA	1721	1/1	0.79	0.23	57,57,57,57	0
57	MG	RB	203	1/1	0.79	0.36	31,31,31,31	0
57	MG	YA	3373	1/1	0.79	0.60	42,42,42,42	0
57	MG	YA	3156	1/1	0.79	0.22	40,40,40,40	0
57	MG	RA	3218	1/1	0.79	0.18	39,39,39,39	0
57	MG	XA	1726	1/1	0.79	0.39	56,56,56,56	0
57	MG	RA	3325	1/1	0.79	0.52	67,67,67,67	0
57	MG	QA	1716	1/1	0.79	0.97	35,35,35,35	0
57	MG	YA	3261	1/1	0.79	0.39	54,54,54,54	0
57	MG	RA	3353	1/1	0.79	0.39	43,43,43,43	0
57	MG	YA	3400	1/1	0.79	0.42	80,80,80,80	0
57	MG	YA	3094	1/1	0.79	0.37	75,75,75,75	0
57	MG	RA	3177	1/1	0.79	0.49	45,45,45,45	0
57	MG	RA	3234	1/1	0.79	0.50	36,36,36,36	0
57	MG	RA	3270	1/1	0.79	0.56	35,35,35,35	0
57	MG	RA	3151	1/1	0.79	0.34	35,35,35,35	0
57	MG	YU	201	1/1	0.79	0.43	60,60,60,60	0
57	MG	QA	1640	1/1	0.79	0.36	58,58,58,58	0
57	MG	YA	3347	1/1	0.80	0.39	44,44,44,44	0
57	MG	YA	3300	1/1	0.80	0.61	35,35,35,35	0
57	MG	RA	3186	1/1	0.80	0.54	40,40,40,40	0
57	MG	RA	3090	1/1	0.80	0.33	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RB	205	1/1	0.80	0.39	58,58,58,58	0
57	MG	YA	3452	1/1	0.80	0.56	58,58,58,58	0
57	MG	XA	1646	1/1	0.80	0.21	57,57,57,57	0
57	MG	YA	3135	1/1	0.80	0.76	39,39,39,39	0
57	MG	QA	1683	1/1	0.80	0.87	42,42,42,42	0
57	MG	XA	1735	1/1	0.80	0.43	18,18,18,18	0
57	MG	YA	3412	1/1	0.80	0.34	49,49,49,49	0
57	MG	RA	3343	1/1	0.80	0.14	48,48,48,48	0
57	MG	XA	1666	1/1	0.80	0.48	46,46,46,46	0
57	MG	RA	3347	1/1	0.80	0.96	65,65,65,65	0
57	MG	RA	3163	1/1	0.80	0.52	61,61,61,61	0
57	MG	YA	3278	1/1	0.80	0.99	33,33,33,33	0
57	MG	QA	1746	1/1	0.80	0.09	44,44,44,44	0
57	MG	YA	3293	1/1	0.80	0.15	33,33,33,33	0
57	MG	YA	3381	1/1	0.81	0.27	35,35,35,35	0
57	MG	YA	3384	1/1	0.81	0.99	53,53,53,53	0
57	MG	QA	1690	1/1	0.81	0.49	27,27,27,27	0
57	MG	QA	1745	1/1	0.81	0.19	72,72,72,72	0
57	MG	RA	3091	1/1	0.81	0.22	29,29,29,29	0
57	MG	XA	1723	1/1	0.81	0.36	35,35,35,35	0
57	MG	YA	3101	1/1	0.81	0.35	22,22,22,22	0
57	MG	YA	3230	1/1	0.81	0.61	53,53,53,53	0
57	MG	YA	3404	1/1	0.81	0.83	54,54,54,54	0
57	MG	YA	3232	1/1	0.81	0.13	27,27,27,27	0
57	MG	RA	3223	1/1	0.81	0.74	36,36,36,36	0
57	MG	QA	1630	1/1	0.81	0.24	55,55,55,55	0
57	MG	QA	1705	1/1	0.81	0.46	47,47,47,47	0
57	MG	YA	3130	1/1	0.81	0.20	28,28,28,28	0
57	MG	R5	102	1/1	0.81	0.44	33,33,33,33	0
57	MG	XA	1758	1/1	0.81	0.68	58,58,58,58	0
57	MG	XA	1681	1/1	0.81	1.09	49,49,49,49	0
57	MG	XA	1717	1/1	0.81	0.28	31,31,31,31	0
57	MG	Y0	101	1/1	0.81	0.29	12,12,12,12	0
57	MG	QA	1621	1/1	0.81	0.19	49,49,49,49	0
57	MG	RA	3345	1/1	0.82	0.39	36,36,36,36	0
57	MG	QV	105	1/1	0.82	0.22	34,34,34,34	0
57	MG	RA	3309	1/1	0.82	0.22	49,49,49,49	0
57	MG	RA	3249	1/1	0.82	0.68	41,41,41,41	0
57	MG	YA	3310	1/1	0.82	0.74	50,50,50,50	0
57	MG	YA	3457	1/1	0.82	0.18	63,63,63,63	0
57	MG	YA	3250	1/1	0.82	0.54	67,67,67,67	0
57	MG	RA	3059	1/1	0.82	0.18	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3423	1/1	0.82	0.44	48,48,48,48	0
57	MG	QA	1728	1/1	0.82	0.17	36,36,36,36	0
57	MG	YA	3469	1/1	0.82	0.35	70,70,70,70	0
57	MG	XA	1612	1/1	0.82	0.32	49,49,49,49	0
57	MG	RA	3147	1/1	0.82	0.19	65,65,65,65	0
57	MG	QA	1698	1/1	0.82	0.34	69,69,69,69	0
57	MG	YA	3374	1/1	0.82	0.23	38,38,38,38	0
57	MG	YA	3279	1/1	0.82	0.17	71,71,71,71	0
57	MG	YA	3284	1/1	0.82	0.35	57,57,57,57	0
57	MG	YA	3225	1/1	0.82	0.30	43,43,43,43	0
57	MG	YY	201	1/1	0.82	0.30	33,33,33,33	0
57	MG	RA	3119	1/1	0.82	0.45	67,67,67,67	0
57	MG	RA	3237	1/1	0.82	0.39	54,54,54,54	0
57	MG	QA	1737	1/1	0.83	0.25	47,47,47,47	0
57	MG	YA	3164	1/1	0.83	0.75	48,48,48,48	0
57	MG	YA	3383	1/1	0.83	0.23	47,47,47,47	0
57	MG	YA	3088	1/1	0.83	0.56	21,21,21,21	0
57	MG	RA	3412	1/1	0.83	0.42	57,57,57,57	0
57	MG	YA	3450	1/1	0.83	0.39	49,49,49,49	0
57	MG	RE	302	1/1	0.83	0.31	53,53,53,53	0
57	MG	QA	1612	1/1	0.83	0.80	37,37,37,37	0
57	MG	RR	201	1/1	0.83	0.44	21,21,21,21	0
57	MG	RA	3366	1/1	0.83	0.18	58,58,58,58	0
57	MG	QA	1709	1/1	0.83	0.59	45,45,45,45	0
57	MG	YA	3465	1/1	0.83	0.43	47,47,47,47	0
57	MG	QA	1628	1/1	0.83	0.16	61,61,61,61	0
57	MG	RA	3154	1/1	0.83	0.41	48,48,48,48	0
57	MG	XA	1692	1/1	0.83	0.18	71,71,71,71	0
57	MG	YA	3360	1/1	0.83	0.43	41,41,41,41	0
57	MG	YA	3365	1/1	0.83	0.65	24,24,24,24	0
57	MG	RA	3263	1/1	0.83	0.29	50,50,50,50	0
57	MG	YA	3267	1/1	0.83	0.86	49,49,49,49	0
57	MG	RA	3392	1/1	0.83	0.27	43,43,43,43	0
57	MG	YA	3328	1/1	0.83	0.42	55,55,55,55	0
57	MG	YA	3430	1/1	0.83	0.16	43,43,43,43	0
57	MG	RA	3285	1/1	0.83	0.47	35,35,35,35	0
57	MG	YA	3436	1/1	0.83	0.26	22,22,22,22	0
57	MG	RA	3242	1/1	0.83	0.41	28,28,28,28	0
57	MG	Y7	101	1/1	0.83	0.41	43,43,43,43	0
57	MG	QA	1625	1/1	0.84	0.22	59,59,59,59	0
57	MG	YA	3236	1/1	0.84	0.13	23,23,23,23	0
57	MG	XA	1672	1/1	0.84	0.28	60,60,60,60	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3013	1/1	0.84	0.47	32,32,32,32	0
57	MG	RA	3427	1/1	0.84	0.28	56,56,56,56	0
57	MG	YA	3255	1/1	0.84	0.41	41,41,41,41	0
57	MG	YA	3382	1/1	0.84	0.26	37,37,37,37	0
57	MG	RA	3408	1/1	0.84	0.12	62,62,62,62	0
57	MG	RA	3022	1/1	0.84	0.35	52,52,52,52	0
57	MG	RA	3414	1/1	0.84	0.44	45,45,45,45	0
57	MG	XA	1625	1/1	0.84	0.20	75,75,75,75	0
57	MG	RA	3415	1/1	0.84	0.30	50,50,50,50	0
57	MG	RB	204	1/1	0.84	0.12	41,41,41,41	0
57	MG	YA	3398	1/1	0.84	0.20	36,36,36,36	0
57	MG	XA	1633	1/1	0.84	0.25	49,49,49,49	0
57	MG	XA	1703	1/1	0.84	0.38	48,48,48,48	0
57	MG	YA	3283	1/1	0.84	0.60	66,66,66,66	0
57	MG	XA	1743	1/1	0.84	0.34	50,50,50,50	0
57	MG	XA	1704	1/1	0.84	0.28	55,55,55,55	0
57	MG	YA	3292	1/1	0.84	0.50	33,33,33,33	0
57	MG	YA	3134	1/1	0.84	0.37	37,37,37,37	0
57	MG	XA	1706	1/1	0.84	0.36	41,41,41,41	0
57	MG	YH	202	1/1	0.84	0.21	59,59,59,59	0
57	MG	YQ	201	1/1	0.84	0.18	52,52,52,52	0
57	MG	YA	3422	1/1	0.84	0.52	27,27,27,27	0
57	MG	RA	3341	1/1	0.84	0.28	46,46,46,46	0
57	MG	RA	3092	1/1	0.84	0.57	36,36,36,36	0
57	MG	RA	3419	1/1	0.84	0.27	47,47,47,47	0
57	MG	XA	1654	1/1	0.84	0.57	26,26,26,26	0
57	MG	RA	3313	1/1	0.84	0.36	50,50,50,50	0
57	MG	YA	3294	1/1	0.85	0.53	37,37,37,37	0
57	MG	YA	3432	1/1	0.85	0.44	31,31,31,31	0
57	MG	YA	3295	1/1	0.85	0.38	46,46,46,46	0
57	MG	RA	3407	1/1	0.85	0.39	56,56,56,56	0
57	MG	RA	3360	1/1	0.85	0.33	64,64,64,64	0
57	MG	XA	1639	1/1	0.85	0.39	58,58,58,58	0
57	MG	QA	1659	1/1	0.85	0.39	31,31,31,31	0
57	MG	YA	3307	1/1	0.85	0.23	43,43,43,43	0
57	MG	XA	1754	1/1	0.85	0.16	84,84,84,84	0
57	MG	XA	1647	1/1	0.85	0.23	83,83,83,83	0
57	MG	QA	1706	1/1	0.85	0.27	48,48,48,48	0
57	MG	RD	302	1/1	0.85	0.50	29,29,29,29	0
57	MG	YA	3240	1/1	0.85	0.22	43,43,43,43	0
57	MG	RA	3276	1/1	0.85	1.05	65,65,65,65	0
57	MG	YA	3460	1/1	0.85	0.37	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XA	1663	1/1	0.85	0.42	30,30,30,30	0
57	MG	RA	3254	1/1	0.85	0.41	50,50,50,50	0
57	MG	RA	3233	1/1	0.85	0.36	37,37,37,37	0
57	MG	YA	3467	1/1	0.85	0.39	48,48,48,48	0
57	MG	RA	3256	1/1	0.85	0.36	47,47,47,47	0
57	MG	XA	1677	1/1	0.85	0.15	39,39,39,39	0
57	MG	QA	1735	1/1	0.85	0.14	40,40,40,40	0
57	MG	YA	3091	1/1	0.85	0.68	26,26,26,26	0
57	MG	YA	3346	1/1	0.85	0.66	45,45,45,45	0
57	MG	QA	1682	1/1	0.85	0.95	39,39,39,39	0
57	MG	YA	3276	1/1	0.85	0.38	53,53,53,53	0
57	MG	RA	3241	1/1	0.85	0.34	38,38,38,38	0
57	MG	RA	3397	1/1	0.85	0.39	34,34,34,34	0
57	MG	YA	3280	1/1	0.85	0.35	70,70,70,70	0
57	MG	QV	104	1/1	0.85	0.34	52,52,52,52	0
57	MG	XA	1629	1/1	0.85	0.15	53,53,53,53	0
57	MG	RA	3402	1/1	0.85	0.17	32,32,32,32	0
57	MG	QA	1609	1/1	0.85	0.32	57,57,57,57	0
57	MG	YA	3220	1/1	0.85	0.57	39,39,39,39	0
57	MG	XA	1695	1/1	0.86	0.18	71,71,71,71	0
57	MG	RA	3413	1/1	0.86	0.35	35,35,35,35	0
57	MG	RA	3348	1/1	0.86	0.36	68,68,68,68	0
57	MG	YA	3401	1/1	0.86	0.25	56,56,56,56	0
57	MG	QA	1639	1/1	0.86	0.20	49,49,49,49	0
57	MG	RA	3358	1/1	0.86	1.04	57,57,57,57	0
57	MG	YA	3312	1/1	0.86	0.86	40,40,40,40	0
57	MG	RA	3181	1/1	0.86	0.52	62,62,62,62	0
57	MG	YA	3411	1/1	0.86	0.43	35,35,35,35	0
57	MG	RA	3146	1/1	0.86	0.20	25,25,25,25	0
57	MG	RA	3279	1/1	0.86	0.40	40,40,40,40	0
57	MG	RA	3422	1/1	0.86	0.48	45,45,45,45	0
57	MG	RA	3283	1/1	0.86	0.33	37,37,37,37	0
57	MG	XA	1636	1/1	0.86	0.63	43,43,43,43	0
57	MG	YA	3231	1/1	0.86	0.27	44,44,44,44	0
57	MG	YA	3332	1/1	0.86	0.66	36,36,36,36	0
57	MG	QA	1608	1/1	0.86	0.30	25,25,25,25	0
57	MG	XA	1719	1/1	0.86	0.61	71,71,71,71	0
57	MG	RA	3222	1/1	0.86	0.46	30,30,30,30	0
57	MG	YA	3238	1/1	0.86	0.44	48,48,48,48	0
57	MG	YA	3239	1/1	0.86	0.31	29,29,29,29	0
57	MG	QA	1662	1/1	0.86	0.21	56,56,56,56	0
57	MG	XA	1651	1/1	0.86	0.42	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3246	1/1	0.86	0.39	43,43,43,43	0
57	MG	RA	3388	1/1	0.86	0.52	18,18,18,18	0
57	MG	YA	3251	1/1	0.86	0.59	48,48,48,48	0
57	MG	YA	3253	1/1	0.86	0.59	25,25,25,25	0
57	MG	XA	1724	1/1	0.86	0.35	48,48,48,48	0
57	MG	YA	3455	1/1	0.86	0.27	36,36,36,36	0
57	MG	YA	3258	1/1	0.86	0.29	48,48,48,48	0
57	MG	RA	3260	1/1	0.86	0.59	65,65,65,65	0
57	MG	RB	201	1/1	0.86	0.37	30,30,30,30	0
57	MG	RA	3337	1/1	0.86	0.23	58,58,58,58	0
57	MG	QA	1620	1/1	0.86	0.57	30,30,30,30	0
57	MG	XA	1670	1/1	0.86	0.20	30,30,30,30	0
57	MG	YA	3155	1/1	0.86	0.18	27,27,27,27	0
57	MG	RA	3064	1/1	0.86	0.58	15,15,15,15	0
57	MG	RA	3068	1/1	0.86	0.32	14,14,14,14	0
57	MG	QA	1729	1/1	0.86	0.16	54,54,54,54	0
57	MG	RA	3268	1/1	0.86	0.44	35,35,35,35	0
57	MG	XA	1683	1/1	0.86	0.51	45,45,45,45	0
57	MG	YA	3170	1/1	0.86	0.54	7,7,7,7	0
57	MG	XA	1684	1/1	0.86	0.32	41,41,41,41	0
57	MG	RA	3406	1/1	0.86	0.34	49,49,49,49	0
57	MG	QA	1666	1/1	0.86	0.45	51,51,51,51	0
57	MG	RA	3314	1/1	0.86	1.19	47,47,47,47	0
57	MG	RA	3244	1/1	0.86	0.20	45,45,45,45	0
57	MG	XA	1693	1/1	0.86	0.15	25,25,25,25	0
57	MG	YA	3393	1/1	0.86	0.14	39,39,39,39	0
57	MG	YA	3187	1/1	0.86	0.48	35,35,35,35	0
57	MG	YA	3396	1/1	0.86	0.35	59,59,59,59	0
57	MG	YA	3142	1/1	0.87	0.51	50,50,50,50	0
57	MG	YA	3249	1/1	0.87	0.33	46,46,46,46	0
57	MG	YA	3350	1/1	0.87	0.25	28,28,28,28	0
57	MG	QA	1638	1/1	0.87	0.23	67,67,67,67	0
57	MG	XA	1712	1/1	0.87	0.18	53,53,53,53	0
57	MG	RA	3132	1/1	0.87	0.54	35,35,35,35	0
57	MG	RA	3228	1/1	0.87	0.25	47,47,47,47	0
57	MG	YA	3215	1/1	0.87	0.26	15,15,15,15	0
57	MG	RA	3230	1/1	0.87	0.21	73,73,73,73	0
57	MG	XA	1745	1/1	0.87	0.12	47,47,47,47	0
57	MG	YA	3358	1/1	0.87	0.67	25,25,25,25	0
57	MG	YA	3158	1/1	0.87	0.26	43,43,43,43	0
57	MG	YA	3160	1/1	0.87	0.37	42,42,42,42	0
57	MG	YA	3366	1/1	0.87	0.47	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	XA	1668	1/1	0.87	0.36	29,29,29,29	0
57	MG	RA	3049	1/1	0.87	0.29	1,1,1,1	0
57	MG	YA	3369	1/1	0.87	0.26	58,58,58,58	0
57	MG	RA	3050	1/1	0.87	0.51	23,23,23,23	0
57	MG	YA	3105	1/1	0.87	0.57	45,45,45,45	0
57	MG	QA	1717	1/1	0.87	0.43	55,55,55,55	0
57	MG	YA	3235	1/1	0.87	0.46	19,19,19,19	0
57	MG	RA	3095	1/1	0.87	0.77	47,47,47,47	0
57	MG	XA	1678	1/1	0.87	0.70	65,65,65,65	0
57	MG	QA	1627	1/1	0.87	0.40	52,52,52,52	0
57	MG	XA	1705	1/1	0.87	0.62	30,30,30,30	0
57	MG	QA	1648	1/1	0.87	0.12	74,74,74,74	0
57	MG	YA	3387	1/1	0.87	0.21	49,49,49,49	0
57	MG	RA	3081	1/1	0.87	0.12	20,20,20,20	0
57	MG	XA	1741	1/1	0.88	0.16	44,44,44,44	0
57	MG	YA	3327	1/1	0.88	0.40	30,30,30,30	0
57	MG	YA	3407	1/1	0.88	0.49	7,7,7,7	0
57	MG	RA	3211	1/1	0.88	0.10	26,26,26,26	0
57	MG	XA	1694	1/1	0.88	0.19	43,43,43,43	0
57	MG	QA	1721	1/1	0.88	1.37	46,46,46,46	0
57	MG	YA	3151	1/1	0.88	0.54	15,15,15,15	0
57	MG	YA	3418	1/1	0.88	0.17	19,19,19,19	0
57	MG	XA	1748	1/1	0.88	1.16	55,55,55,55	0
57	MG	RA	3367	1/1	0.88	0.44	43,43,43,43	0
57	MG	RA	3215	1/1	0.88	0.32	29,29,29,29	0
57	MG	RA	3328	1/1	0.88	0.45	37,37,37,37	0
57	MG	YA	3252	1/1	0.88	0.46	47,47,47,47	0
57	MG	QA	1738	1/1	0.88	0.11	42,42,42,42	0
57	MG	RA	3179	1/1	0.88	0.32	43,43,43,43	0
57	MG	RA	3180	1/1	0.88	0.47	18,18,18,18	0
57	MG	RA	3286	1/1	0.88	0.38	34,34,34,34	0
57	MG	QA	1674	1/1	0.88	0.42	57,57,57,57	0
57	MG	RA	3259	1/1	0.88	0.34	39,39,39,39	0
57	MG	XA	1661	1/1	0.88	0.44	28,28,28,28	0
57	MG	YA	3266	1/1	0.88	0.89	43,43,43,43	0
57	MG	YA	3175	1/1	0.88	0.18	34,34,34,34	0
57	MG	QA	1697	1/1	0.88	0.43	34,34,34,34	0
57	MG	RA	3401	1/1	0.88	0.63	60,60,60,60	0
57	MG	QA	1689	1/1	0.88	0.37	30,30,30,30	0
57	MG	RA	3152	1/1	0.88	0.84	33,33,33,33	0
57	MG	YA	3060	1/1	0.88	0.35	11,11,11,11	0
57	MG	YA	3282	1/1	0.88	0.21	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3067	1/1	0.88	0.22	6,6,6,6	0
57	MG	YA	3073	1/1	0.88	0.57	24,24,24,24	0
57	MG	RA	3308	1/1	0.88	0.62	63,63,63,63	0
57	MG	YA	3291	1/1	0.88	0.88	34,34,34,34	0
57	MG	YA	3200	1/1	0.88	0.39	32,32,32,32	0
57	MG	YA	3089	1/1	0.88	0.26	44,44,44,44	0
57	MG	RQ	202	1/1	0.88	0.25	74,74,74,74	0
57	MG	YA	3211	1/1	0.88	0.10	67,67,67,67	0
57	MG	RA	3264	1/1	0.88	0.72	39,39,39,39	0
57	MG	RA	3231	1/1	0.88	0.61	30,30,30,30	0
57	MG	YA	3099	1/1	0.88	0.17	10,10,10,10	0
57	MG	RA	3153	1/1	0.88	0.17	13,13,13,13	0
57	MG	YA	3224	1/1	0.88	0.25	15,15,15,15	0
57	MG	XA	1682	1/1	0.88	0.18	51,51,51,51	0
57	MG	YP	202	1/1	0.88	0.39	38,38,38,38	0
57	MG	QA	1618	1/1	0.88	0.44	32,32,32,32	0
57	MG	QA	1692	1/1	0.88	0.46	47,47,47,47	0
57	MG	QA	1636	1/1	0.88	0.67	47,47,47,47	0
57	MG	RA	3323	1/1	0.88	0.12	37,37,37,37	0
57	MG	QA	1661	1/1	0.88	0.26	57,57,57,57	0
57	MG	XA	1737	1/1	0.88	0.20	40,40,40,40	0
57	MG	RA	3363	1/1	0.88	0.45	46,46,46,46	0
57	MG	YA	3417	1/1	0.89	0.27	78,78,78,78	0
57	MG	YA	3198	1/1	0.89	0.37	25,25,25,25	0
57	MG	XA	1626	1/1	0.89	0.42	28,28,28,28	0
57	MG	RA	3158	1/1	0.89	0.32	59,59,59,59	0
57	MG	YA	3209	1/1	0.89	0.51	19,19,19,19	0
57	MG	RA	3160	1/1	0.89	0.36	58,58,58,58	0
57	MG	RA	3288	1/1	0.89	0.45	56,56,56,56	0
57	MG	YA	3427	1/1	0.89	0.22	27,27,27,27	0
57	MG	RA	3196	1/1	0.89	0.66	39,39,39,39	0
57	MG	YA	3216	1/1	0.89	0.27	24,24,24,24	0
57	MG	RA	3331	1/1	0.89	0.33	59,59,59,59	0
57	MG	QA	1741	1/1	0.89	0.52	45,45,45,45	0
57	MG	YA	3221	1/1	0.89	0.25	28,28,28,28	0
57	MG	YA	3139	1/1	0.89	0.12	38,38,38,38	0
57	MG	RA	3296	1/1	0.89	0.36	46,46,46,46	0
57	MG	RA	3166	1/1	0.89	0.59	30,30,30,30	0
57	MG	RA	3389	1/1	0.89	0.40	9,9,9,9	0
57	MG	YA	3371	1/1	0.89	0.45	57,57,57,57	0
57	MG	XA	1648	1/1	0.89	0.20	39,39,39,39	0
57	MG	QV	102	1/1	0.89	0.22	15,15,15,15	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3302	1/1	0.89	0.42	57,57,57,57	0
57	MG	XA	1707	1/1	0.89	0.40	35,35,35,35	0
57	MG	RA	3205	1/1	0.89	0.19	34,34,34,34	0
57	MG	RA	3306	1/1	0.89	0.55	43,43,43,43	0
57	MG	RA	3172	1/1	0.89	0.44	50,50,50,50	0
57	MG	RA	3399	1/1	0.89	0.23	46,46,46,46	0
57	MG	RA	3240	1/1	0.89	0.44	56,56,56,56	0
57	MG	RA	3106	1/1	0.89	0.31	32,32,32,32	0
57	MG	QV	103	1/1	0.89	0.43	8,8,8,8	0
57	MG	RP	201	1/1	0.89	0.21	35,35,35,35	0
57	MG	YA	3244	1/1	0.89	0.74	34,34,34,34	0
57	MG	YA	3001	1/1	0.89	0.80	28,28,28,28	0
57	MG	YA	3472	1/1	0.89	0.36	45,45,45,45	0
57	MG	YB	203	1/1	0.89	0.35	16,16,16,16	0
57	MG	YA	3022	1/1	0.89	0.52	54,54,54,54	0
57	MG	RA	3061	1/1	0.89	0.42	28,28,28,28	0
57	MG	RQ	201	1/1	0.89	0.43	37,37,37,37	0
57	MG	RA	3213	1/1	0.89	0.32	30,30,30,30	0
57	MG	YA	3180	1/1	0.89	0.33	38,38,38,38	0
57	MG	QA	1633	1/1	0.89	0.32	39,39,39,39	0
57	MG	RA	3320	1/1	0.89	0.46	58,58,58,58	0
57	MG	RA	3354	1/1	0.89	0.55	82,82,82,82	0
57	MG	YR	201	1/1	0.89	0.39	12,12,12,12	0
57	MG	YA	3344	1/1	0.89	0.23	71,71,71,71	0
57	MG	RA	3355	1/1	0.89	0.10	51,51,51,51	0
57	MG	RA	3133	1/1	0.89	0.59	39,39,39,39	0
57	MG	Y0	103	1/1	0.89	0.28	18,18,18,18	0
57	MG	Y5	102	1/1	0.89	0.41	16,16,16,16	0
57	MG	QA	1646	1/1	0.89	0.52	70,70,70,70	0
57	MG	RA	3157	1/1	0.89	0.20	79,79,79,79	0
57	MG	RA	3282	1/1	0.90	0.13	47,47,47,47	0
57	MG	XA	1632	1/1	0.90	0.48	20,20,20,20	0
57	MG	YA	3117	1/1	0.90	0.40	34,34,34,34	0
57	MG	YA	3375	1/1	0.90	0.28	30,30,30,30	0
57	MG	QA	1665	1/1	0.90	0.50	52,52,52,52	0
57	MG	RA	3135	1/1	0.90	0.98	49,49,49,49	0
57	MG	QA	1704	1/1	0.90	0.54	35,35,35,35	0
57	MG	QA	1601	1/1	0.90	0.40	11,11,11,11	0
57	MG	YA	3204	1/1	0.90	0.29	34,34,34,34	0
57	MG	YA	3263	1/1	0.90	0.47	50,50,50,50	0
57	MG	YA	3386	1/1	0.90	0.31	58,58,58,58	0
57	MG	YA	3454	1/1	0.90	0.20	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	XA	1642	1/1	0.90	0.13	43,43,43,43	0
57	MG	RA	3321	1/1	0.90	0.39	37,37,37,37	0
57	MG	QA	1723	1/1	0.90	0.19	50,50,50,50	0
57	MG	RA	3042	1/1	0.90	0.32	9,9,9,9	0
57	MG	RA	3087	1/1	0.90	0.20	36,36,36,36	0
57	MG	QA	1712	1/1	0.90	0.33	38,38,38,38	0
57	MG	RA	3127	1/1	0.90	0.17	33,33,33,33	0
57	MG	XA	1655	1/1	0.90	0.47	41,41,41,41	0
57	MG	XA	1698	1/1	0.90	0.48	112,112,112,112	0
57	MG	YA	3005	1/1	0.90	0.22	9,9,9,9	0
57	MG	XA	1699	1/1	0.90	0.25	31,31,31,31	0
57	MG	YA	3057	1/1	0.90	0.22	59,59,59,59	0
57	MG	QA	1614	1/1	0.90	0.30	44,44,44,44	0
57	MG	RA	3253	1/1	0.90	0.32	21,21,21,21	0
57	MG	XA	1738	1/1	0.90	0.45	35,35,35,35	0
57	MG	YA	3083	1/1	0.90	0.12	21,21,21,21	0
57	MG	R5	103	1/1	0.90	0.07	34,34,34,34	0
57	MG	RA	3208	1/1	0.90	0.48	52,52,52,52	0
57	MG	YN	201	1/1	0.90	0.25	44,44,44,44	0
57	MG	RA	3307	1/1	0.90	0.43	43,43,43,43	0
57	MG	YA	3177	1/1	0.90	0.32	26,26,26,26	0
57	MG	YA	3362	1/1	0.90	0.85	31,31,31,31	0
57	MG	YA	3178	1/1	0.90	0.18	47,47,47,47	0
57	MG	QA	1675	1/1	0.90	0.18	36,36,36,36	0
57	MG	XA	1744	1/1	0.90	0.28	36,36,36,36	0
57	MG	RA	3232	1/1	0.90	0.31	39,39,39,39	0
57	MG	XA	1746	1/1	0.90	0.21	63,63,63,63	0
57	MG	YA	3428	1/1	0.90	0.27	39,39,39,39	0
57	MG	YA	3370	1/1	0.90	0.49	39,39,39,39	0
57	MG	RA	3281	1/1	0.90	0.15	40,40,40,40	0
58	ZN	XN	101	1/1	0.90	0.15	78,78,78,78	0
57	MG	YA	3336	1/1	0.91	0.27	32,32,32,32	0
57	MG	YA	3248	1/1	0.91	0.35	15,15,15,15	0
57	MG	YA	3035	1/1	0.91	0.26	26,26,26,26	0
57	MG	QA	1650	1/1	0.91	0.38	31,31,31,31	0
57	MG	RA	3374	1/1	0.91	0.35	18,18,18,18	0
57	MG	XA	1621	1/1	0.91	0.44	39,39,39,39	0
57	MG	YA	3069	1/1	0.91	0.41	18,18,18,18	0
57	MG	QA	1631	1/1	0.91	0.51	41,41,41,41	0
57	MG	YA	3257	1/1	0.91	0.32	51,51,51,51	0
57	MG	XA	1732	1/1	0.91	0.09	52,52,52,52	0
57	MG	RA	3384	1/1	0.91	0.27	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3387	1/1	0.91	0.41	24,24,24,24	0
57	MG	RA	3424	1/1	0.91	0.21	45,45,45,45	0
57	MG	RA	3200	1/1	0.91	0.36	20,20,20,20	0
57	MG	YA	3434	1/1	0.91	0.27	21,21,21,21	0
57	MG	YA	3095	1/1	0.91	0.77	16,16,16,16	0
57	MG	YA	3185	1/1	0.91	0.58	9,9,9,9	0
57	MG	RA	3426	1/1	0.91	0.25	24,24,24,24	0
57	MG	YA	3097	1/1	0.91	0.33	22,22,22,22	0
57	MG	YA	3359	1/1	0.91	0.39	52,52,52,52	0
57	MG	YA	3269	1/1	0.91	0.18	35,35,35,35	0
57	MG	YA	3194	1/1	0.91	0.17	56,56,56,56	0
57	MG	YA	3098	1/1	0.91	0.45	69,69,69,69	0
57	MG	RA	3165	1/1	0.91	0.18	71,71,71,71	0
57	MG	QA	1702	1/1	0.91	0.14	99,99,99,99	0
57	MG	YA	3453	1/1	0.91	0.21	33,33,33,33	0
57	MG	RA	3344	1/1	0.91	0.23	39,39,39,39	0
57	MG	YA	3108	1/1	0.91	0.40	22,22,22,22	0
57	MG	QA	1670	1/1	0.91	0.43	53,53,53,53	0
57	MG	YA	3458	1/1	0.91	0.14	49,49,49,49	0
57	MG	YA	3285	1/1	0.91	0.30	42,42,42,42	0
57	MG	RA	3395	1/1	0.91	0.54	46,46,46,46	0
57	MG	YA	3290	1/1	0.91	0.31	22,22,22,22	0
57	MG	YA	3114	1/1	0.91	0.42	36,36,36,36	0
57	MG	RA	3396	1/1	0.91	0.15	43,43,43,43	0
57	MG	YA	3120	1/1	0.91	0.16	37,37,37,37	0
57	MG	RA	3168	1/1	0.91	0.31	43,43,43,43	0
57	MG	YA	3379	1/1	0.91	0.20	44,44,44,44	0
57	MG	RA	3293	1/1	0.91	0.60	21,21,21,21	0
57	MG	YA	3299	1/1	0.91	0.28	70,70,70,70	0
57	MG	QA	1606	1/1	0.91	0.24	12,12,12,12	0
57	MG	RA	3105	1/1	0.91	0.16	38,38,38,38	0
57	MG	RA	3028	1/1	0.91	0.34	34,34,34,34	0
57	MG	RA	3035	1/1	0.91	0.29	59,59,59,59	0
57	MG	RA	3301	1/1	0.91	0.32	34,34,34,34	0
57	MG	RA	3113	1/1	0.91	0.25	33,33,33,33	0
57	MG	QA	1679	1/1	0.91	0.22	39,39,39,39	0
57	MG	YA	3147	1/1	0.91	0.44	20,20,20,20	0
57	MG	RA	3364	1/1	0.91	0.20	67,67,67,67	0
57	MG	YA	3233	1/1	0.91	0.44	35,35,35,35	0
57	MG	XA	1667	1/1	0.91	0.81	27,27,27,27	0
57	MG	RY	201	1/1	0.91	0.20	24,24,24,24	0
57	MG	QA	1680	1/1	0.91	0.23	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3155	1/1	0.91	0.20	27,27,27,27	0
57	MG	XA	1675	1/1	0.91	0.77	29,29,29,29	0
57	MG	RA	3129	1/1	0.91	0.34	19,19,19,19	0
57	MG	R5	101	1/1	0.91	0.20	25,25,25,25	0
57	MG	YA	3007	1/1	0.91	0.50	13,13,13,13	0
58	ZN	QN	100	1/1	0.91	0.14	90,90,90,90	0
57	MG	QA	1660	1/1	0.91	0.41	20,20,20,20	0
57	MG	YA	3048	1/1	0.92	0.21	32,32,32,32	0
57	MG	YA	3243	1/1	0.92	0.19	56,56,56,56	0
57	MG	QA	1643	1/1	0.92	0.30	59,59,59,59	0
57	MG	RA	3322	1/1	0.92	0.28	30,30,30,30	0
57	MG	YA	3065	1/1	0.92	0.23	16,16,16,16	0
57	MG	YA	3340	1/1	0.92	0.52	52,52,52,52	0
57	MG	YA	3341	1/1	0.92	0.23	56,56,56,56	0
57	MG	YA	3171	1/1	0.92	0.11	35,35,35,35	0
57	MG	YA	3424	1/1	0.92	0.18	28,28,28,28	0
57	MG	RA	3084	1/1	0.92	0.31	28,28,28,28	0
57	MG	RA	3359	1/1	0.92	0.36	42,42,42,42	0
57	MG	RA	3044	1/1	0.92	0.42	2,2,2,2	0
57	MG	RA	3111	1/1	0.92	0.20	38,38,38,38	0
57	MG	YA	3254	1/1	0.92	0.18	41,41,41,41	0
57	MG	YA	3084	1/1	0.92	0.39	29,29,29,29	0
57	MG	R0	101	1/1	0.92	0.29	14,14,14,14	0
57	MG	QA	1685	1/1	0.92	0.09	25,25,25,25	0
57	MG	YA	3090	1/1	0.92	0.32	34,34,34,34	0
57	MG	YA	3437	1/1	0.92	0.26	74,74,74,74	0
57	MG	RA	3226	1/1	0.92	0.31	49,49,49,49	0
57	MG	RA	3201	1/1	0.92	0.46	27,27,27,27	0
57	MG	RA	3171	1/1	0.92	0.80	38,38,38,38	0
57	MG	YA	3442	1/1	0.92	0.20	49,49,49,49	0
57	MG	YA	3186	1/1	0.92	0.41	27,27,27,27	0
57	MG	QA	1617	1/1	0.92	0.38	37,37,37,37	0
57	MG	XA	1608	1/1	0.92	0.26	27,27,27,27	0
57	MG	YA	3193	1/1	0.92	0.73	27,27,27,27	0
57	MG	XA	1611	1/1	0.92	0.69	36,36,36,36	0
57	MG	YA	3274	1/1	0.92	0.34	33,33,33,33	0
57	MG	YA	3363	1/1	0.92	0.58	29,29,29,29	0
57	MG	RA	3418	1/1	0.92	0.24	39,39,39,39	0
57	MG	YA	3197	1/1	0.92	0.27	23,23,23,23	0
57	MG	QA	1736	1/1	0.92	0.56	49,49,49,49	0
57	MG	QA	1603	1/1	0.92	0.19	53,53,53,53	0
57	MG	YA	3281	1/1	0.92	0.07	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	YA	3201	1/1	0.92	0.32	30,30,30,30	0
57	MG	RA	3093	1/1	0.92	0.28	21,21,21,21	0
57	MG	XA	1628	1/1	0.92	0.37	33,33,33,33	0
57	MG	RA	3378	1/1	0.92	0.14	112,112,112,112	0
57	MG	RA	3336	1/1	0.92	0.11	32,32,32,32	0
57	MG	RA	3305	1/1	0.92	0.17	24,24,24,24	0
57	MG	RA	3209	1/1	0.92	0.50	34,34,34,34	0
57	MG	YA	3122	1/1	0.92	0.35	44,44,44,44	0
57	MG	RA	3156	1/1	0.92	0.10	36,36,36,36	0
57	MG	YA	3218	1/1	0.92	0.35	23,23,23,23	0
57	MG	YB	204	1/1	0.92	0.14	54,54,54,54	0
57	MG	YA	3219	1/1	0.92	0.40	27,27,27,27	0
57	MG	XA	1634	1/1	0.92	0.30	17,17,17,17	0
57	MG	RA	3271	1/1	0.92	0.53	14,14,14,14	0
57	MG	QA	1623	1/1	0.92	0.61	37,37,37,37	0
57	MG	RA	3310	1/1	0.92	0.44	69,69,69,69	0
57	MG	RA	3039	1/1	0.92	0.49	7,7,7,7	0
57	MG	QA	1739	1/1	0.92	0.15	57,57,57,57	0
57	MG	RA	3246	1/1	0.92	0.23	22,22,22,22	0
57	MG	RA	3214	1/1	0.92	0.39	63,63,63,63	0
57	MG	RA	3398	1/1	0.92	0.10	38,38,38,38	0
57	MG	RA	3185	1/1	0.92	0.11	31,31,31,31	0
57	MG	RE	301	1/1	0.92	0.29	8,8,8,8	0
57	MG	XA	1716	1/1	0.92	0.64	39,39,39,39	0
57	MG	RA	3350	1/1	0.92	0.22	53,53,53,53	0
57	MG	Y1	101	1/1	0.92	0.30	17,17,17,17	0
57	MG	YA	3317	1/1	0.92	0.19	35,35,35,35	0
57	MG	RF	301	1/1	0.92	0.10	27,27,27,27	0
57	MG	YA	3019	1/1	0.92	0.36	14,14,14,14	0
57	MG	RA	3217	1/1	0.92	0.18	16,16,16,16	0
57	MG	XA	1662	1/1	0.92	0.35	13,13,13,13	0
57	MG	QA	1708	1/1	0.93	0.43	19,19,19,19	0
57	MG	QA	1722	1/1	0.93	0.27	49,49,49,49	0
57	MG	YA	3262	1/1	0.93	0.39	14,14,14,14	0
57	MG	RA	3287	1/1	0.93	0.16	33,33,33,33	0
57	MG	RA	3037	1/1	0.93	0.19	1,1,1,1	0
57	MG	XA	1620	1/1	0.93	0.21	30,30,30,30	0
57	MG	RA	3083	1/1	0.93	0.09	19,19,19,19	0
57	MG	YA	3100	1/1	0.93	0.39	23,23,23,23	0
57	MG	RA	3329	1/1	0.93	0.25	47,47,47,47	0
57	MG	RA	3369	1/1	0.93	0.70	46,46,46,46	0
57	MG	YA	3273	1/1	0.93	0.30	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	QA	1699	1/1	0.93	0.26	72,72,72,72	0
57	MG	QA	1700	1/1	0.93	0.83	35,35,35,35	0
57	MG	RA	3120	1/1	0.93	0.29	67,67,67,67	0
57	MG	RA	3123	1/1	0.93	0.40	33,33,33,33	0
57	MG	RA	3299	1/1	0.93	0.20	76,76,76,76	0
57	MG	RA	3381	1/1	0.93	0.70	11,11,11,11	0
57	MG	YA	3214	1/1	0.93	0.23	34,34,34,34	0
57	MG	RA	3224	1/1	0.93	0.48	37,37,37,37	0
57	MG	YA	3449	1/1	0.93	0.35	39,39,39,39	0
57	MG	RA	3385	1/1	0.93	0.38	3,3,3,3	0
57	MG	RA	3126	1/1	0.93	0.56	67,67,67,67	0
57	MG	RA	3199	1/1	0.93	0.32	5,5,5,5	0
57	MG	RA	3162	1/1	0.93	0.16	23,23,23,23	0
57	MG	QA	1602	1/1	0.93	0.61	20,20,20,20	0
57	MG	QA	1694	1/1	0.93	0.18	31,31,31,31	0
57	MG	XA	1761	1/1	0.93	0.10	68,68,68,68	0
57	MG	RA	3393	1/1	0.93	0.15	29,29,29,29	0
57	MG	XA	1650	1/1	0.93	0.51	20,20,20,20	0
57	MG	QA	1669	1/1	0.93	0.10	48,48,48,48	0
57	MG	YA	3148	1/1	0.93	0.78	9,9,9,9	0
57	MG	XV	104	1/1	0.93	0.15	16,16,16,16	0
57	MG	XA	1711	1/1	0.93	0.59	24,24,24,24	0
57	MG	QA	1732	1/1	0.93	0.42	60,60,60,60	0
57	MG	XA	1653	1/1	0.93	0.18	29,29,29,29	0
57	MG	QA	1615	1/1	0.93	0.20	59,59,59,59	0
57	MG	YA	3020	1/1	0.93	0.28	19,19,19,19	0
57	MG	RA	3238	1/1	0.93	0.25	9,9,9,9	0
57	MG	RA	3169	1/1	0.93	0.85	39,39,39,39	0
57	MG	YA	3042	1/1	0.93	0.29	4,4,4,4	0
57	MG	XA	1658	1/1	0.93	0.21	25,25,25,25	0
57	MG	XA	1660	1/1	0.93	0.20	27,27,27,27	0
57	MG	YA	3058	1/1	0.93	0.20	39,39,39,39	0
57	MG	RA	3277	1/1	0.93	0.36	51,51,51,51	0
57	MG	YA	3245	1/1	0.93	0.38	33,33,33,33	0
57	MG	RA	3058	1/1	0.93	0.21	31,31,31,31	0
57	MG	RA	3352	1/1	0.93	0.83	39,39,39,39	0
57	MG	RA	3317	1/1	0.93	0.52	36,36,36,36	0
57	MG	YA	3329	1/1	0.93	0.24	34,34,34,34	0
57	MG	RA	3099	1/1	0.93	0.43	32,32,32,32	0
57	MG	YA	3076	1/1	0.93	0.42	24,24,24,24	0
57	MG	YV	201	1/1	0.93	0.33	11,11,11,11	0
57	MG	QA	1681	1/1	0.93	0.23	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	RA	3357	1/1	0.93	0.33	45,45,45,45	0
57	MG	YA	3339	1/1	0.93	0.37	31,31,31,31	0
57	MG	RA	3245	1/1	0.93	0.50	30,30,30,30	0
57	MG	YA	3413	1/1	0.93	0.19	36,36,36,36	0
57	MG	RA	3409	1/1	0.93	0.35	0,0,0,0	0
57	MG	QA	1634	1/1	0.93	0.32	65,65,65,65	0
57	MG	RA	3104	1/1	0.93	0.17	34,34,34,34	0
57	MG	YA	3259	1/1	0.93	0.22	43,43,43,43	0
57	MG	XV	102	1/1	0.94	0.29	0,0,0,0	0
57	MG	RA	3202	1/1	0.94	0.10	40,40,40,40	0
57	MG	YA	3402	1/1	0.94	0.48	14,14,14,14	0
57	MG	QA	1673	1/1	0.94	0.26	72,72,72,72	0
57	MG	RA	3086	1/1	0.94	0.20	20,20,20,20	0
57	MG	RA	3303	1/1	0.94	0.15	44,44,44,44	0
57	MG	YA	3314	1/1	0.94	0.28	43,43,43,43	0
57	MG	XA	1665	1/1	0.94	0.21	19,19,19,19	0
57	MG	RA	3052	1/1	0.94	0.21	38,38,38,38	0
57	MG	XA	1607	1/1	0.94	0.31	32,32,32,32	0
57	MG	RA	3053	1/1	0.94	0.55	26,26,26,26	0
57	MG	YA	3321	1/1	0.94	0.22	36,36,36,36	0
57	MG	XA	1610	1/1	0.94	0.38	22,22,22,22	0
57	MG	YA	3040	1/1	0.94	0.19	5,5,5,5	0
57	MG	RA	3149	1/1	0.94	0.63	1,1,1,1	0
57	MG	YA	3043	1/1	0.94	0.44	7,7,7,7	0
57	MG	RA	3056	1/1	0.94	0.84	32,32,32,32	0
57	MG	YA	3330	1/1	0.94	0.47	24,24,24,24	0
57	MG	YA	3159	1/1	0.94	0.39	26,26,26,26	0
57	MG	XA	1614	1/1	0.94	0.16	40,40,40,40	0
57	MG	YA	3163	1/1	0.94	0.23	21,21,21,21	0
57	MG	YA	3429	1/1	0.94	0.19	81,81,81,81	0
57	MG	YA	3337	1/1	0.94	0.41	4,4,4,4	0
57	MG	XA	1728	1/1	0.94	0.39	46,46,46,46	0
57	MG	YA	3247	1/1	0.94	0.46	30,30,30,30	0
57	MG	QA	1720	1/1	0.94	0.19	35,35,35,35	0
57	MG	YA	3061	1/1	0.94	0.22	10,10,10,10	0
57	MG	QA	1713	1/1	0.94	0.36	32,32,32,32	0
57	MG	XA	1622	1/1	0.94	0.78	35,35,35,35	0
57	MG	XA	1734	1/1	0.94	0.19	15,15,15,15	0
57	MG	YA	3345	1/1	0.94	0.27	29,29,29,29	0
57	MG	RA	3386	1/1	0.94	0.19	36,36,36,36	0
57	MG	YA	3173	1/1	0.94	0.22	43,43,43,43	0
57	MG	YA	3444	1/1	0.94	0.16	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	QA	1684	1/1	0.94	0.26	42,42,42,42	0
57	MG	YA	3081	1/1	0.94	0.20	26,26,26,26	0
57	MG	YA	3082	1/1	0.94	0.29	20,20,20,20	0
57	MG	RA	3124	1/1	0.94	0.21	45,45,45,45	0
57	MG	RA	3094	1/1	0.94	0.21	47,47,47,47	0
57	MG	YA	3087	1/1	0.94	0.24	18,18,18,18	0
57	MG	RA	3346	1/1	0.94	0.68	53,53,53,53	0
57	MG	RA	3019	1/1	0.94	0.30	16,16,16,16	0
57	MG	RA	3216	1/1	0.94	0.28	20,20,20,20	0
57	MG	RB	202	1/1	0.94	0.39	27,27,27,27	0
57	MG	YA	3093	1/1	0.94	0.11	41,41,41,41	0
57	MG	RA	3247	1/1	0.94	0.30	35,35,35,35	0
57	MG	RA	3351	1/1	0.94	0.22	70,70,70,70	0
57	MG	RA	3319	1/1	0.94	0.14	95,95,95,95	0
57	MG	YA	3270	1/1	0.94	0.85	37,37,37,37	0
57	MG	RA	3096	1/1	0.94	0.73	29,29,29,29	0
57	MG	QA	1657	1/1	0.94	0.36	21,21,21,21	0
57	MG	RA	3192	1/1	0.94	0.26	22,22,22,22	0
57	MG	YA	3277	1/1	0.94	0.14	83,83,83,83	0
57	MG	RA	3356	1/1	0.94	0.13	56,56,56,56	0
57	MG	YA	3199	1/1	0.94	0.25	11,11,11,11	0
57	MG	YB	202	1/1	0.94	0.56	31,31,31,31	0
57	MG	RA	3220	1/1	0.94	0.23	34,34,34,34	0
57	MG	YA	3103	1/1	0.94	0.13	42,42,42,42	0
57	MG	RA	3078	1/1	0.94	0.29	12,12,12,12	0
57	MG	YA	3106	1/1	0.94	0.49	12,12,12,12	0
57	MG	YA	3205	1/1	0.94	0.24	32,32,32,32	0
57	MG	YA	3206	1/1	0.94	0.22	27,27,27,27	0
57	MG	RA	3023	1/1	0.94	0.54	3,3,3,3	0
57	MG	QA	1654	1/1	0.94	0.49	34,34,34,34	0
57	MG	YA	3111	1/1	0.94	0.25	21,21,21,21	0
57	MG	RA	3257	1/1	0.94	0.54	48,48,48,48	0
57	MG	XA	1708	1/1	0.94	0.26	54,54,54,54	0
57	MG	RA	3136	1/1	0.94	0.35	61,61,61,61	0
57	MG	YA	3385	1/1	0.94	0.27	40,40,40,40	0
57	MG	YA	3119	1/1	0.94	0.55	40,40,40,40	0
57	MG	YA	3298	1/1	0.94	0.68	41,41,41,41	0
57	MG	RA	3138	1/1	0.94	0.30	49,49,49,49	0
57	MG	Y0	102	1/1	0.94	0.10	24,24,24,24	0
57	MG	RA	3261	1/1	0.94	0.52	30,30,30,30	0
57	MG	YA	3124	1/1	0.94	0.18	16,16,16,16	0
57	MG	RA	3227	1/1	0.94	0.51	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XA	1713	1/1	0.94	0.20	31,31,31,31	0
57	MG	YA	3304	1/1	0.94	0.46	27,27,27,27	0
57	MG	YA	3305	1/1	0.94	0.47	38,38,38,38	0
57	MG	XN	102	1/1	0.94	0.22	54,54,54,54	0
57	MG	RA	3030	1/1	0.95	0.30	16,16,16,16	0
57	MG	YA	3414	1/1	0.95	0.11	127,127,127,127	0
57	MG	RA	3183	1/1	0.95	0.50	67,67,67,67	0
57	MG	XA	1604	1/1	0.95	0.34	19,19,19,19	0
57	MG	YA	3256	1/1	0.95	0.17	15,15,15,15	0
57	MG	YA	3421	1/1	0.95	0.25	33,33,33,33	0
57	MG	RA	3383	1/1	0.95	0.34	26,26,26,26	0
57	MG	RA	3128	1/1	0.95	0.13	37,37,37,37	0
57	MG	QA	1619	1/1	0.95	0.48	10,10,10,10	0
57	MG	QA	1655	1/1	0.95	0.29	29,29,29,29	0
57	MG	RA	3038	1/1	0.95	0.44	39,39,39,39	0
57	MG	RA	3195	1/1	0.95	0.21	20,20,20,20	0
57	MG	YA	3189	1/1	0.95	0.35	25,25,25,25	0
57	MG	RA	3349	1/1	0.95	0.48	49,49,49,49	0
57	MG	YA	3104	1/1	0.95	0.14	50,50,50,50	0
57	MG	RA	3252	1/1	0.95	0.12	62,62,62,62	0
57	MG	RA	3391	1/1	0.95	0.23	32,32,32,32	0
57	MG	QA	1725	1/1	0.95	0.29	41,41,41,41	0
57	MG	RA	3071	1/1	0.95	0.35	41,41,41,41	0
57	MG	QA	1604	1/1	0.95	0.14	31,31,31,31	0
57	MG	YA	3112	1/1	0.95	0.26	29,29,29,29	0
57	MG	RA	3137	1/1	0.95	0.32	22,22,22,22	0
57	MG	YA	3015	1/1	0.95	0.28	17,17,17,17	0
57	MG	YA	3016	1/1	0.95	0.12	17,17,17,17	0
57	MG	YA	3018	1/1	0.95	0.38	11,11,11,11	0
57	MG	XA	1680	1/1	0.95	0.23	25,25,25,25	0
57	MG	YA	3445	1/1	0.95	0.25	25,25,25,25	0
57	MG	RA	3002	1/1	0.95	0.32	24,24,24,24	0
57	MG	YA	3361	1/1	0.95	0.34	37,37,37,37	0
57	MG	RA	3043	1/1	0.95	0.48	7,7,7,7	0
57	MG	YA	3126	1/1	0.95	0.25	41,41,41,41	0
57	MG	YA	3212	1/1	0.95	0.66	25,25,25,25	0
57	MG	YA	3213	1/1	0.95	0.63	30,30,30,30	0
57	MG	YA	3031	1/1	0.95	0.33	26,26,26,26	0
57	MG	RA	3295	1/1	0.95	0.21	41,41,41,41	0
57	MG	YA	3131	1/1	0.95	0.17	27,27,27,27	0
57	MG	YA	3456	1/1	0.95	0.33	125,125,125,125	0
57	MG	YA	3133	1/1	0.95	0.60	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3037	1/1	0.95	0.18	11,11,11,11	0
57	MG	YA	3039	1/1	0.95	0.48	9,9,9,9	0
57	MG	RA	3141	1/1	0.95	0.18	41,41,41,41	0
57	MG	XA	1685	1/1	0.95	0.15	17,17,17,17	0
57	MG	YA	3463	1/1	0.95	0.22	48,48,48,48	0
57	MG	QA	1688	1/1	0.95	0.29	32,32,32,32	0
57	MG	YA	3045	1/1	0.95	0.41	8,8,8,8	0
57	MG	YA	3046	1/1	0.95	0.16	23,23,23,23	0
57	MG	RA	3045	1/1	0.95	0.32	11,11,11,11	0
57	MG	YA	3380	1/1	0.95	0.58	38,38,38,38	0
57	MG	YA	3227	1/1	0.95	0.16	44,44,44,44	0
57	MG	YA	3050	1/1	0.95	0.30	7,7,7,7	0
57	MG	YA	3149	1/1	0.95	0.38	37,37,37,37	0
57	MG	YA	3051	1/1	0.95	0.44	4,4,4,4	0
57	MG	RA	3014	1/1	0.95	0.23	1,1,1,1	0
57	MG	XA	1690	1/1	0.95	0.39	29,29,29,29	0
57	MG	YA	3308	1/1	0.95	0.30	26,26,26,26	0
57	MG	YA	3234	1/1	0.95	0.51	31,31,31,31	0
57	MG	XA	1691	1/1	0.95	0.19	27,27,27,27	0
57	MG	YA	3391	1/1	0.95	0.71	44,44,44,44	0
57	MG	RA	3332	1/1	0.95	0.35	40,40,40,40	0
57	MG	YP	201	1/1	0.95	0.18	8,8,8,8	0
57	MG	YA	3062	1/1	0.95	0.45	32,32,32,32	0
57	MG	RA	3207	1/1	0.95	0.49	20,20,20,20	0
57	MG	YA	3395	1/1	0.95	0.56	55,55,55,55	0
57	MG	XA	1740	1/1	0.95	0.44	69,69,69,69	0
57	MG	XA	1645	1/1	0.95	0.53	41,41,41,41	0
57	MG	RA	3175	1/1	0.95	0.10	45,45,45,45	0
57	MG	RA	3236	1/1	0.95	0.35	23,23,23,23	0
57	MG	RA	3017	1/1	0.95	0.42	5,5,5,5	0
57	MG	XA	1649	1/1	0.95	0.22	13,13,13,13	0
57	MG	QA	1730	1/1	0.95	0.17	40,40,40,40	0
57	MG	XA	1701	1/1	0.95	0.37	30,30,30,30	0
57	MG	QA	1626	1/1	0.95	0.12	40,40,40,40	0
57	MG	QA	1607	1/1	0.95	0.51	26,26,26,26	0
57	MG	QA	1691	1/1	0.95	0.37	26,26,26,26	0
57	MG	RA	3376	1/1	0.95	0.33	25,25,25,25	0
57	MG	RA	3243	1/1	0.95	0.11	37,37,37,37	0
57	MG	RA	3097	1/1	0.96	0.22	17,17,17,17	0
57	MG	RA	3150	1/1	0.96	0.42	42,42,42,42	0
57	MG	YA	3378	1/1	0.96	0.70	40,40,40,40	0
57	MG	RA	3382	1/1	0.96	0.25	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	QA	1611	1/1	0.96	0.33	33,33,33,33	0
57	MG	QA	1632	1/1	0.96	0.28	46,46,46,46	0
57	MG	XA	1687	1/1	0.96	0.98	53,53,53,53	0
57	MG	QA	1624	1/1	0.96	0.12	41,41,41,41	0
57	MG	YA	3006	1/1	0.96	0.36	18,18,18,18	0
57	MG	YA	3153	1/1	0.96	0.49	36,36,36,36	0
57	MG	RA	3103	1/1	0.96	0.34	36,36,36,36	0
57	MG	YA	3013	1/1	0.96	0.36	2,2,2,2	0
57	MG	YA	3157	1/1	0.96	0.32	19,19,19,19	0
57	MG	QA	1649	1/1	0.96	0.30	22,22,22,22	0
57	MG	QA	1701	1/1	0.96	0.13	48,48,48,48	0
57	MG	RA	3024	1/1	0.96	0.38	42,42,42,42	0
57	MG	XA	1602	1/1	0.96	0.50	6,6,6,6	0
57	MG	YA	3275	1/1	0.96	0.29	40,40,40,40	0
57	MG	RA	3108	1/1	0.96	0.29	25,25,25,25	0
57	MG	YA	3165	1/1	0.96	0.27	37,37,37,37	0
57	MG	YA	3166	1/1	0.96	0.48	10,10,10,10	0
57	MG	XA	1605	1/1	0.96	0.37	23,23,23,23	0
57	MG	YA	3023	1/1	0.96	0.40	2,2,2,2	0
57	MG	YA	3025	1/1	0.96	0.55	25,25,25,25	0
57	MG	YA	3027	1/1	0.96	0.44	15,15,15,15	0
57	MG	YA	3403	1/1	0.96	0.26	27,27,27,27	0
57	MG	XA	1696	1/1	0.96	0.33	20,20,20,20	0
57	MG	YA	3034	1/1	0.96	0.24	24,24,24,24	0
57	MG	XA	1606	1/1	0.96	0.42	10,10,10,10	0
57	MG	YA	3174	1/1	0.96	0.31	24,24,24,24	0
57	MG	YA	3287	1/1	0.96	0.17	34,34,34,34	0
57	MG	YA	3288	1/1	0.96	0.25	50,50,50,50	0
57	MG	RA	3109	1/1	0.96	0.43	11,11,11,11	0
57	MG	RA	3267	1/1	0.96	0.35	51,51,51,51	0
57	MG	QA	1667	1/1	0.96	0.17	39,39,39,39	0
57	MG	YA	3415	1/1	0.96	0.51	24,24,24,24	0
57	MG	YA	3416	1/1	0.96	0.21	46,46,46,46	0
57	MG	RA	3066	1/1	0.96	0.30	17,17,17,17	0
57	MG	RA	3164	1/1	0.96	0.25	34,34,34,34	0
57	MG	XA	1613	1/1	0.96	0.12	18,18,18,18	0
57	MG	QA	1605	1/1	0.96	0.28	35,35,35,35	0
57	MG	XA	1619	1/1	0.96	0.34	13,13,13,13	0
57	MG	RA	3273	1/1	0.96	0.09	53,53,53,53	0
57	MG	RA	3274	1/1	0.96	0.28	41,41,41,41	0
57	MG	YA	3053	1/1	0.96	0.68	5,5,5,5	0
57	MG	RA	3114	1/1	0.96	0.25	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XA	1623	1/1	0.96	0.09	33,33,33,33	0
57	MG	YA	3190	1/1	0.96	0.50	19,19,19,19	0
57	MG	XA	1624	1/1	0.96	0.09	51,51,51,51	0
57	MG	YA	3192	1/1	0.96	0.07	32,32,32,32	0
57	MG	RA	3117	1/1	0.96	0.56	28,28,28,28	0
57	MG	RA	3069	1/1	0.96	0.36	23,23,23,23	0
57	MG	RA	3031	1/1	0.96	0.26	16,16,16,16	0
57	MG	RA	3170	1/1	0.96	0.49	64,64,64,64	0
57	MG	RA	3405	1/1	0.96	0.50	52,52,52,52	0
57	MG	YA	3070	1/1	0.96	0.23	47,47,47,47	0
57	MG	YA	3071	1/1	0.96	0.30	11,11,11,11	0
57	MG	RA	3122	1/1	0.96	0.24	21,21,21,21	0
57	MG	RA	3073	1/1	0.96	0.33	32,32,32,32	0
57	MG	RA	3225	1/1	0.96	0.18	23,23,23,23	0
57	MG	YA	3319	1/1	0.96	0.29	41,41,41,41	0
57	MG	RA	3074	1/1	0.96	0.34	16,16,16,16	0
57	MG	RA	3410	1/1	0.96	0.15	49,49,49,49	0
57	MG	RA	3174	1/1	0.96	0.54	1,1,1,1	0
57	MG	YA	3448	1/1	0.96	0.20	20,20,20,20	0
57	MG	XA	1637	1/1	0.96	0.23	49,49,49,49	0
57	MG	RA	3076	1/1	0.96	0.29	13,13,13,13	0
57	MG	XA	1641	1/1	0.96	0.11	38,38,38,38	0
57	MG	RA	3034	1/1	0.96	0.24	41,41,41,41	0
57	MG	YA	3331	1/1	0.96	0.48	19,19,19,19	0
57	MG	XA	1727	1/1	0.96	0.18	31,31,31,31	0
57	MG	YA	3092	1/1	0.96	0.25	12,12,12,12	0
57	MG	QA	1726	1/1	0.96	0.15	48,48,48,48	0
57	MG	RA	3290	1/1	0.96	0.13	49,49,49,49	0
57	MG	RA	3291	1/1	0.96	0.32	39,39,39,39	0
57	MG	XA	1731	1/1	0.96	0.26	27,27,27,27	0
57	MG	RA	3178	1/1	0.96	0.27	45,45,45,45	0
57	MG	QA	1727	1/1	0.96	0.25	77,77,77,77	0
57	MG	RA	3420	1/1	0.96	0.27	74,74,74,74	0
57	MG	RA	3130	1/1	0.96	0.11	34,34,34,34	0
57	MG	QA	1715	1/1	0.96	0.14	46,46,46,46	0
57	MG	QA	1676	1/1	0.96	0.32	40,40,40,40	0
57	MG	QA	1622	1/1	0.96	0.19	20,20,20,20	0
57	MG	RA	3184	1/1	0.96	0.36	28,28,28,28	0
57	MG	RA	3088	1/1	0.96	0.45	15,15,15,15	0
57	MG	XA	1657	1/1	0.96	0.50	34,34,34,34	0
57	MG	YB	201	1/1	0.96	0.43	28,28,28,28	0
57	MG	RA	3005	1/1	0.96	0.14	9,9,9,9	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	XA	1659	1/1	0.96	0.69	22,22,22,22	0
57	MG	RA	3007	1/1	0.96	0.43	13,13,13,13	0
57	MG	RA	3188	1/1	0.96	0.46	38,38,38,38	0
57	MG	XA	1747	1/1	0.96	0.27	55,55,55,55	0
57	MG	YE	301	1/1	0.96	0.29	4,4,4,4	0
57	MG	YA	3116	1/1	0.96	0.55	17,17,17,17	0
57	MG	RA	3361	1/1	0.96	0.26	35,35,35,35	0
57	MG	YH	201	1/1	0.96	0.20	80,80,80,80	0
57	MG	YA	3118	1/1	0.96	0.28	23,23,23,23	0
57	MG	RA	3304	1/1	0.96	0.28	36,36,36,36	0
57	MG	YA	3241	1/1	0.96	0.27	19,19,19,19	0
57	MG	RA	3009	1/1	0.96	0.60	16,16,16,16	0
57	MG	RA	3010	1/1	0.96	0.20	16,16,16,16	0
57	MG	RA	3047	1/1	0.96	0.55	5,5,5,5	0
57	MG	RA	3197	1/1	0.96	0.32	17,17,17,17	0
57	MG	YA	3364	1/1	0.96	0.50	52,52,52,52	0
57	MG	RA	3011	1/1	0.96	0.54	8,8,8,8	0
57	MG	RA	3250	1/1	0.96	0.31	31,31,31,31	0
57	MG	RA	3143	1/1	0.96	0.29	4,4,4,4	0
57	MG	RA	3012	1/1	0.96	0.24	4,4,4,4	0
57	MG	RA	3373	1/1	0.96	0.14	52,52,52,52	0
57	MG	QA	1687	1/1	0.96	0.29	50,50,50,50	0
57	MG	Y5	101	1/1	0.96	0.13	7,7,7,7	0
57	MG	YA	3138	1/1	0.96	0.24	17,17,17,17	0
57	MG	RA	3315	1/1	0.96	0.44	25,25,25,25	0
57	MG	YA	3140	1/1	0.96	0.19	30,30,30,30	0
57	MG	RA	3148	1/1	0.96	0.32	10,10,10,10	0
58	ZN	XD	301	1/1	0.96	0.34	66,66,66,66	0
57	MG	XF	201	1/1	0.96	0.38	41,41,41,41	0
57	MG	QA	1652	1/1	0.97	0.19	20,20,20,20	0
57	MG	XA	1627	1/1	0.97	0.11	73,73,73,73	0
57	MG	RA	3297	1/1	0.97	0.31	49,49,49,49	0
57	MG	RA	3125	1/1	0.97	0.22	29,29,29,29	0
57	MG	RA	3098	1/1	0.97	0.38	11,11,11,11	0
57	MG	YA	3003	1/1	0.97	0.35	10,10,10,10	0
57	MG	RA	3075	1/1	0.97	0.22	14,14,14,14	0
57	MG	YA	3335	1/1	0.97	0.36	31,31,31,31	0
57	MG	QA	1653	1/1	0.97	0.34	25,25,25,25	0
57	MG	RA	3032	1/1	0.97	0.40	26,26,26,26	0
57	MG	YA	3009	1/1	0.97	0.46	10,10,10,10	0
57	MG	YA	3010	1/1	0.97	0.20	1,1,1,1	0
57	MG	YA	3012	1/1	0.97	0.24	12,12,12,12	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	QA	1635	1/1	0.97	0.23	30,30,30,30	0
57	MG	YA	3014	1/1	0.97	0.29	18,18,18,18	0
57	MG	RA	3368	1/1	0.97	0.29	59,59,59,59	0
57	MG	RA	3272	1/1	0.97	0.12	35,35,35,35	0
57	MG	YA	3017	1/1	0.97	0.38	2,2,2,2	0
57	MG	YA	3433	1/1	0.97	0.22	33,33,33,33	0
57	MG	RA	3082	1/1	0.97	0.43	22,22,22,22	0
57	MG	YA	3435	1/1	0.97	0.16	35,35,35,35	0
57	MG	RA	3371	1/1	0.97	0.21	33,33,33,33	0
57	MG	QA	1686	1/1	0.97	0.11	31,31,31,31	0
57	MG	RA	3159	1/1	0.97	0.34	19,19,19,19	0
57	MG	XA	1644	1/1	0.97	0.28	24,24,24,24	0
57	MG	YA	3188	1/1	0.97	0.28	43,43,43,43	0
57	MG	RA	3036	1/1	0.97	0.37	4,4,4,4	0
57	MG	RA	3375	1/1	0.97	0.28	10,10,10,10	0
57	MG	YA	3028	1/1	0.97	0.20	14,14,14,14	0
57	MG	YA	3110	1/1	0.97	0.30	27,27,27,27	0
57	MG	YA	3029	1/1	0.97	0.23	18,18,18,18	0
57	MG	YA	3271	1/1	0.97	0.30	25,25,25,25	0
57	MG	YA	3272	1/1	0.97	0.36	49,49,49,49	0
57	MG	RA	3161	1/1	0.97	0.18	44,44,44,44	0
57	MG	QA	1714	1/1	0.97	0.32	66,66,66,66	0
57	MG	RA	3379	1/1	0.97	0.18	44,44,44,44	0
57	MG	RA	3016	1/1	0.97	0.08	7,7,7,7	0
57	MG	YA	3038	1/1	0.97	0.32	38,38,38,38	0
57	MG	RA	3312	1/1	0.97	0.30	1,1,1,1	0
57	MG	RA	3280	1/1	0.97	0.16	20,20,20,20	0
57	MG	RA	3190	1/1	0.97	0.46	10,10,10,10	0
57	MG	YA	3203	1/1	0.97	0.11	18,18,18,18	0
57	MG	RA	3191	1/1	0.97	0.17	10,10,10,10	0
57	MG	YA	3044	1/1	0.97	0.44	2,2,2,2	0
57	MG	RA	3060	1/1	0.97	0.25	18,18,18,18	0
57	MG	YA	3208	1/1	0.97	0.31	7,7,7,7	0
57	MG	YA	3462	1/1	0.97	0.54	39,39,39,39	0
57	MG	XA	1609	1/1	0.97	0.08	53,53,53,53	0
57	MG	YA	3464	1/1	0.97	0.14	46,46,46,46	0
57	MG	YA	3129	1/1	0.97	0.39	20,20,20,20	0
57	MG	YA	3047	1/1	0.97	0.59	32,32,32,32	0
57	MG	YA	3289	1/1	0.97	0.30	31,31,31,31	0
57	MG	RA	3193	1/1	0.97	0.69	17,17,17,17	0
57	MG	YA	3132	1/1	0.97	0.38	59,59,59,59	0
57	MG	YA	3470	1/1	0.97	0.20	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	XA	1750	1/1	0.97	0.21	46,46,46,46	0
57	MG	QA	1610	1/1	0.97	0.09	48,48,48,48	0
57	MG	YA	3052	1/1	0.97	0.61	26,26,26,26	0
57	MG	YA	3136	1/1	0.97	0.34	28,28,28,28	0
57	MG	YA	3296	1/1	0.97	0.50	34,34,34,34	0
57	MG	YA	3297	1/1	0.97	0.45	31,31,31,31	0
57	MG	YB	205	1/1	0.97	0.11	58,58,58,58	0
57	MG	QA	1656	1/1	0.97	0.28	16,16,16,16	0
57	MG	YA	3054	1/1	0.97	0.21	0,0,0,0	0
57	MG	YA	3056	1/1	0.97	0.22	4,4,4,4	0
57	MG	RA	3021	1/1	0.97	0.47	25,25,25,25	0
57	MG	RA	3115	1/1	0.97	0.37	13,13,13,13	0
57	MG	XA	1617	1/1	0.97	0.56	36,36,36,36	0
57	MG	XA	1618	1/1	0.97	0.62	23,23,23,23	0
57	MG	RA	3429	1/1	0.97	0.15	19,19,19,19	0
57	MG	YA	3063	1/1	0.97	0.51	4,4,4,4	0
57	MG	QA	1664	1/1	0.97	0.23	23,23,23,23	0
57	MG	YA	3229	1/1	0.97	0.29	54,54,54,54	0
57	MG	YA	3066	1/1	0.97	0.33	29,29,29,29	0
57	MG	RA	3145	1/1	0.97	0.25	20,20,20,20	0
57	MG	YA	3068	1/1	0.97	0.28	35,35,35,35	0
57	MG	XA	1715	1/1	0.97	0.36	27,27,27,27	0
57	MG	RA	3006	1/1	0.97	0.29	3,3,3,3	0
57	MG	QA	1642	1/1	0.97	0.20	51,51,51,51	0
57	MG	YA	3072	1/1	0.97	0.32	12,12,12,12	0
57	MG	RA	3072	1/1	0.97	0.35	4,4,4,4	0
57	MG	YA	3074	1/1	0.97	0.43	13,13,13,13	0
57	MG	YA	3406	1/1	0.97	0.35	8,8,8,8	0
57	MG	QA	1651	1/1	0.97	0.25	31,31,31,31	0
57	MG	YA	3320	1/1	0.97	0.21	56,56,56,56	0
57	MG	YA	3162	1/1	0.97	0.18	38,38,38,38	0
57	MG	YA	3077	1/1	0.97	0.49	8,8,8,8	0
57	MG	YA	3080	1/1	0.97	0.51	2,2,2,2	0
57	MG	YA	3326	1/1	0.97	0.19	64,64,64,64	0
57	MG	YA	3107	1/1	0.98	0.14	2,2,2,2	0
57	MG	RA	3144	1/1	0.98	0.37	11,11,11,11	0
57	MG	RA	3229	1/1	0.98	0.30	16,16,16,16	0
57	MG	XA	1615	1/1	0.98	0.55	46,46,46,46	0
57	MG	RA	3046	1/1	0.98	0.16	17,17,17,17	0
57	MG	RA	3118	1/1	0.98	0.20	5,5,5,5	0
57	MG	RA	3027	1/1	0.98	0.31	8,8,8,8	0
57	MG	RA	3077	1/1	0.98	0.49	5,5,5,5	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3115	1/1	0.98	0.16	3,3,3,3	0
57	MG	YA	3049	1/1	0.98	0.43	4,4,4,4	0
57	MG	RA	3018	1/1	0.98	0.34	17,17,17,17	0
57	MG	XA	1664	1/1	0.98	0.31	14,14,14,14	0
57	MG	RA	3235	1/1	0.98	0.10	20,20,20,20	0
57	MG	YA	3196	1/1	0.98	0.40	22,22,22,22	0
57	MG	RA	3079	1/1	0.98	0.34	5,5,5,5	0
57	MG	YA	3121	1/1	0.98	0.36	11,11,11,11	0
57	MG	RA	3080	1/1	0.98	0.44	4,4,4,4	0
57	MG	YA	3123	1/1	0.98	0.32	5,5,5,5	0
57	MG	YA	3055	1/1	0.98	0.46	5,5,5,5	0
57	MG	RA	3063	1/1	0.98	0.29	23,23,23,23	0
57	MG	YA	3441	1/1	0.98	0.40	9,9,9,9	0
57	MG	XA	1669	1/1	0.98	0.27	25,25,25,25	0
57	MG	RA	3404	1/1	0.98	0.19	51,51,51,51	0
57	MG	YA	3059	1/1	0.98	0.22	7,7,7,7	0
57	MG	XA	1671	1/1	0.98	0.11	6,6,6,6	0
57	MG	YA	3207	1/1	0.98	0.61	13,13,13,13	0
57	MG	RA	3239	1/1	0.98	0.21	20,20,20,20	0
57	MG	XA	1673	1/1	0.98	0.21	45,45,45,45	0
57	MG	XA	1674	1/1	0.98	0.09	18,18,18,18	0
57	MG	YA	3002	1/1	0.98	0.20	5,5,5,5	0
57	MG	RA	3101	1/1	0.98	0.28	37,37,37,37	0
57	MG	YA	3137	1/1	0.98	0.26	5,5,5,5	0
57	MG	YA	3004	1/1	0.98	0.30	4,4,4,4	0
57	MG	RA	3003	1/1	0.98	0.38	16,16,16,16	0
57	MG	RA	3065	1/1	0.98	0.18	32,32,32,32	0
57	MG	QA	1644	1/1	0.98	0.25	19,19,19,19	0
57	MG	YA	3008	1/1	0.98	0.15	20,20,20,20	0
57	MG	YA	3143	1/1	0.98	0.39	28,28,28,28	0
57	MG	YA	3144	1/1	0.98	0.46	41,41,41,41	0
57	MG	XA	1679	1/1	0.98	0.30	41,41,41,41	0
57	MG	RA	3085	1/1	0.98	0.17	26,26,26,26	0
57	MG	RA	3411	1/1	0.98	0.40	44,44,44,44	0
57	MG	YA	3075	1/1	0.98	0.20	19,19,19,19	0
57	MG	RA	3131	1/1	0.98	0.13	20,20,20,20	0
57	MG	RA	3377	1/1	0.98	0.42	10,10,10,10	0
57	MG	YA	3078	1/1	0.98	0.29	28,28,28,28	0
57	MG	YA	3079	1/1	0.98	0.44	7,7,7,7	0
57	MG	RA	3067	1/1	0.98	0.48	20,20,20,20	0
57	MG	YA	3154	1/1	0.98	0.21	17,17,17,17	0
57	MG	RA	3107	1/1	0.98	0.36	5,5,5,5	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
57	MG	XA	1638	1/1	0.98	0.34	57,57,57,57	0
57	MG	RA	3015	1/1	0.98	0.36	10,10,10,10	0
57	MG	YA	3473	1/1	0.98	0.40	8,8,8,8	0
57	MG	YA	3389	1/1	0.98	0.14	55,55,55,55	0
57	MG	XA	1640	1/1	0.98	0.46	23,23,23,23	0
57	MG	YA	3311	1/1	0.98	0.14	60,60,60,60	0
57	MG	YA	3085	1/1	0.98	0.17	7,7,7,7	0
57	MG	YA	3086	1/1	0.98	0.23	38,38,38,38	0
57	MG	RA	3189	1/1	0.98	0.51	21,21,21,21	0
57	MG	YA	3021	1/1	0.98	0.44	11,11,11,11	0
57	MG	QA	1616	1/1	0.98	0.20	52,52,52,52	0
57	MG	YA	3397	1/1	0.98	0.06	41,41,41,41	0
57	MG	XA	1601	1/1	0.98	0.36	7,7,7,7	0
57	MG	YA	3024	1/1	0.98	0.44	12,12,12,12	0
57	MG	RA	3070	1/1	0.98	0.41	18,18,18,18	0
57	MG	YA	3026	1/1	0.98	0.23	8,8,8,8	0
57	MG	XA	1603	1/1	0.98	0.15	19,19,19,19	0
57	MG	RA	3054	1/1	0.98	0.39	0,0,0,0	0
57	MG	YA	3323	1/1	0.98	0.29	1,1,1,1	0
57	MG	YA	3324	1/1	0.98	0.57	4,4,4,4	0
57	MG	RA	3112	1/1	0.98	0.16	36,36,36,36	0
57	MG	YA	3030	1/1	0.98	0.48	6,6,6,6	0
57	MG	YA	3408	1/1	0.98	0.07	46,46,46,46	0
57	MG	RA	3139	1/1	0.98	0.19	15,15,15,15	0
57	MG	YA	3033	1/1	0.98	0.23	10,10,10,10	0
57	MG	QV	101	1/1	0.98	0.23	19,19,19,19	0
57	MG	YA	3176	1/1	0.98	0.35	3,3,3,3	0
57	MG	RA	3057	1/1	0.98	0.28	5,5,5,5	0
57	MG	YA	3102	1/1	0.98	0.31	18,18,18,18	0
57	MG	RA	3289	1/1	0.98	0.12	14,14,14,14	0
57	MG	YA	3334	1/1	0.98	0.60	24,24,24,24	0
57	MG	RA	3026	1/1	0.98	0.25	5,5,5,5	0
57	MG	RA	3258	1/1	0.98	0.26	32,32,32,32	0
57	MG	RA	3116	1/1	0.98	0.46	30,30,30,30	0
57	MG	YA	3420	1/1	0.98	0.19	33,33,33,33	0
57	MG	XA	1616	1/1	0.99	0.29	11,11,11,11	0
57	MG	RA	3051	1/1	0.99	0.36	11,11,11,11	0
57	MG	RA	3033	1/1	0.99	0.28	12,12,12,12	0
57	MG	RA	3020	1/1	0.99	0.37	9,9,9,9	0
57	MG	RA	3008	1/1	0.99	0.14	35,35,35,35	0
57	MG	RA	3055	1/1	0.99	0.24	17,17,17,17	0
57	MG	RA	3194	1/1	0.99	0.38	2,2,2,2	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
57	MG	YA	3125	1/1	0.99	0.28	13,13,13,13	0
57	MG	QA	1645	1/1	0.99	0.17	52,52,52,52	0
57	MG	YA	3011	1/1	0.99	0.62	3,3,3,3	0
57	MG	YA	3128	1/1	0.99	0.08	27,27,27,27	0
57	MG	YA	3032	1/1	0.99	0.27	7,7,7,7	0
57	MG	RA	3029	1/1	0.99	0.19	14,14,14,14	0
57	MG	QA	1641	1/1	0.99	0.32	28,28,28,28	0
57	MG	RA	3004	1/1	0.99	0.56	3,3,3,3	0
57	MG	YA	3036	1/1	0.99	0.44	7,7,7,7	0
57	MG	XA	1643	1/1	0.99	0.29	29,29,29,29	0
57	MG	YA	3161	1/1	0.99	0.22	10,10,10,10	0
57	MG	R0	103	1/1	0.99	0.29	22,22,22,22	0
57	MG	XV	101	1/1	0.99	0.19	7,7,7,7	0
57	MG	RA	3025	1/1	0.99	0.28	10,10,10,10	0
57	MG	YA	3064	1/1	0.99	0.15	11,11,11,11	0
57	MG	YA	3041	1/1	0.99	0.31	23,23,23,23	0
57	MG	RA	3121	1/1	0.99	0.21	5,5,5,5	0
57	MG	RA	3041	1/1	0.99	0.33	7,7,7,7	0
58	ZN	QD	301	1/1	0.99	0.32	44,44,44,44	0
57	MG	YA	3223	1/1	0.99	0.29	25,25,25,25	0
57	MG	XA	1733	1/1	0.99	0.38	8,8,8,8	0
57	MG	RA	3062	1/1	0.99	0.35	2,2,2,2	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.