



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 26, 2016 – 10:15 PM EDT

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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027939
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027939

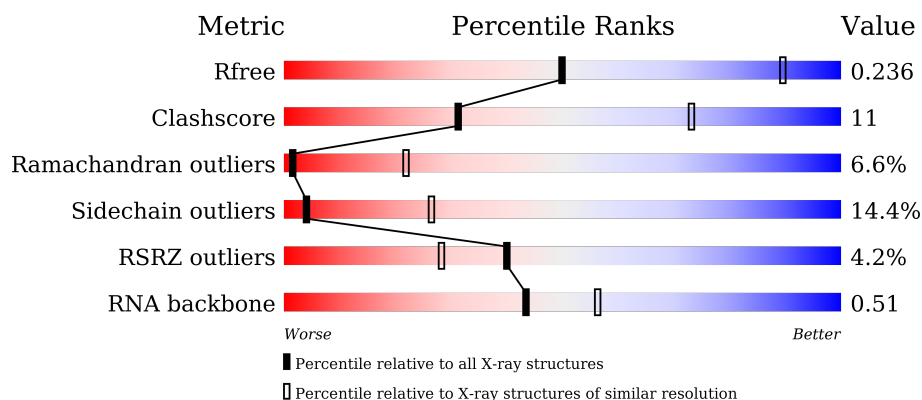
1 Overall quality at a glance

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}	91344	1408 (3.80-3.40)
Clashscore	102246	1010 (3.74-3.46)
Ramachandran outliers	100387	1007 (3.76-3.44)
Sidechain outliers	100360	1007 (3.76-3.44)
RSRZ outliers	91569	1003 (3.78-3.42)
RNA backbone	2183	1058 (4.40-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>2%</div> <div>56% 34% 9%</div> </div>
1	XA	1522	<div> <div>2%</div> <div>57% 33% 8%</div> </div>
2	QB	256	<div> <div>4%</div> <div>52% 31% 8% 8%</div> </div>
2	XB	256	<div> <div></div> <div>50% 34% 8% 8%</div> </div>

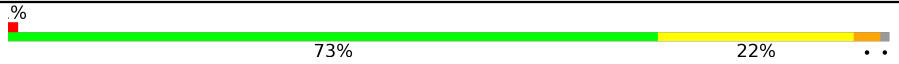

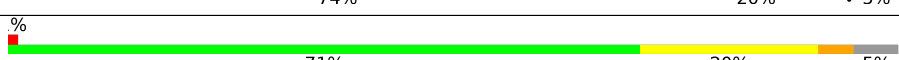
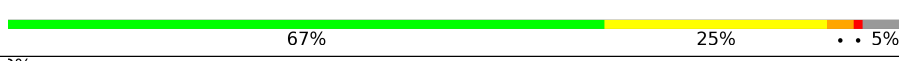
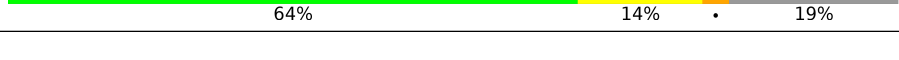
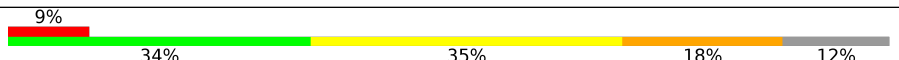
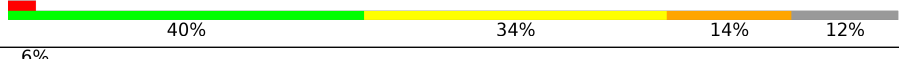
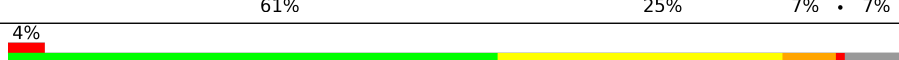

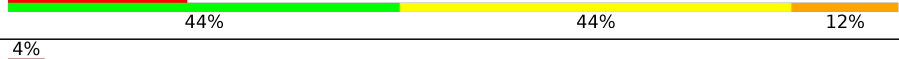

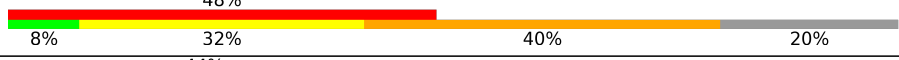

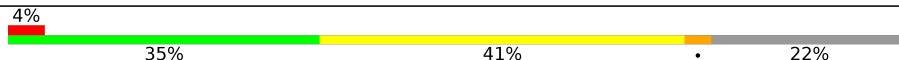
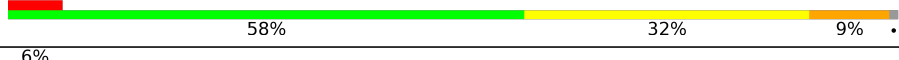
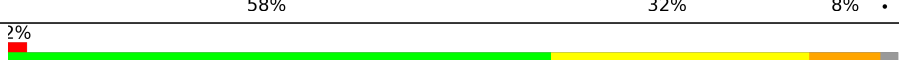





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Mol	Chain	Length	Quality of chain
3	QC	239	
3	XC	239	
4	QD	209	
4	XD	209	
5	QE	162	
5	XE	162	
6	QF	101	
6	XF	101	
7	QG	156	
7	XG	156	
8	QH	138	
8	XH	138	
9	QI	128	
9	XI	128	
10	QJ	105	
10	XJ	105	
11	QK	129	
11	XK	129	
12	QL	132	
12	XL	132	
13	QM	126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

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Mol	Chain	Length	Quality of chain
15	XO	89	
16	QP	88	
16	XP	88	
17	QQ	105	
17	XQ	105	
18	QR	88	
18	XR	88	
19	QS	93	
19	XS	93	
20	QT	106	
20	XT	106	
21	QU	25	
21	XU	25	
22	QV	77	
22	XV	77	
23	QX	25	
23	XX	25	
24	QY	118	
24	XY	118	
25	RA	2916	
25	YA	2916	
26	RB	124	
26	YB	124	
27	RD	276	
27	YD	276	








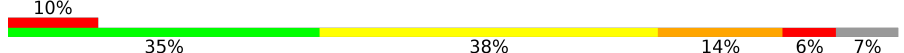
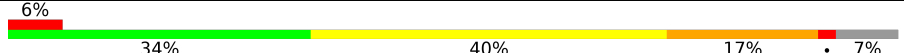
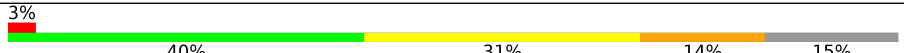
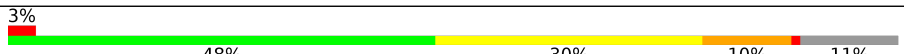

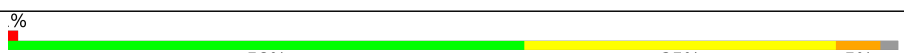


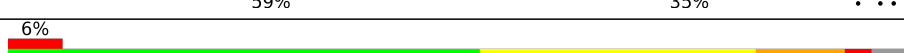


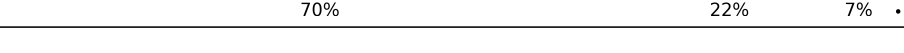


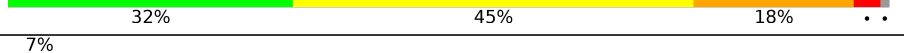



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Mol	Chain	Length	Quality of chain
28	RE	206	
28	YE	206	
29	RF	210	
29	YF	210	
30	RG	182	
30	YG	182	
31	RH	180	
31	YH	180	
32	RI	148	
32	YI	148	
33	RN	140	
33	YN	140	
34	RO	122	
34	YO	122	
35	RP	150	
35	YP	150	
36	RQ	141	
36	YQ	141	
37	RR	118	
37	YR	118	
38	RS	112	
38	YS	112	
39	RT	146	
39	YT	146	
40	RU	118	

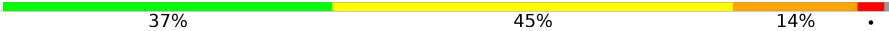



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Mol	Chain	Length	Quality of chain
40	YU	118	
41	RV	101	
41	YV	101	
42	RW	113	
42	YW	113	
43	RX	96	
43	YX	96	
44	RY	110	
44	YY	110	
45	RZ	206	
45	YZ	206	
46	R0	85	
46	Y0	85	
47	R1	98	
47	Y1	98	
48	R2	72	
48	Y2	72	
49	R3	60	
49	Y3	60	
50	R4	71	
50	Y4	71	
51	R5	60	
51	Y5	60	
52	R6	54	
52	Y6	54	

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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	1601	-	-	-	X
57	MG	QA	1605	-	-	-	X
57	MG	QA	1612	-	-	-	X
57	MG	QA	1614	-	-	-	X
57	MG	QA	1619	-	-	-	X
57	MG	QA	1632	-	-	-	X
57	MG	QA	1636	-	-	-	X
57	MG	QA	1640	-	-	-	X
57	MG	QA	1641	-	-	-	X
57	MG	QA	1643	-	-	-	X
57	MG	QA	1644	-	-	-	X
57	MG	QA	1651	-	-	-	X
57	MG	QA	1654	-	-	-	X
57	MG	QA	1656	-	-	-	X
57	MG	QA	1666	-	-	-	X
57	MG	QA	1668	-	-	-	X
57	MG	QA	1670	-	-	-	X
57	MG	QA	1682	-	-	-	X
57	MG	QA	1683	-	-	-	X
57	MG	QA	1684	-	-	-	X
57	MG	QA	1687	-	-	-	X
57	MG	QA	1688	-	-	-	X
57	MG	QA	1699	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	QA	1718	-	-	-	X
57	MG	QA	1722	-	-	-	X
57	MG	QA	1725	-	-	-	X
57	MG	QA	1737	-	-	-	X
57	MG	QV	101	-	-	-	X
57	MG	RA	3003	-	-	-	X
57	MG	RA	3006	-	-	-	X
57	MG	RA	3011	-	-	-	X
57	MG	RA	3012	-	-	-	X
57	MG	RA	3013	-	-	-	X
57	MG	RA	3017	-	-	-	X
57	MG	RA	3018	-	-	-	X
57	MG	RA	3021	-	-	-	X
57	MG	RA	3025	-	-	-	X
57	MG	RA	3026	-	-	-	X
57	MG	RA	3027	-	-	-	X
57	MG	RA	3031	-	-	-	X
57	MG	RA	3032	-	-	-	X
57	MG	RA	3033	-	-	-	X
57	MG	RA	3038	-	-	-	X
57	MG	RA	3042	-	-	-	X
57	MG	RA	3044	-	-	-	X
57	MG	RA	3047	-	-	-	X
57	MG	RA	3049	-	-	-	X
57	MG	RA	3054	-	-	-	X
57	MG	RA	3055	-	-	-	X
57	MG	RA	3056	-	-	-	X
57	MG	RA	3059	-	-	-	X
57	MG	RA	3060	-	-	-	X
57	MG	RA	3062	-	-	-	X
57	MG	RA	3064	-	-	-	X
57	MG	RA	3066	-	-	-	X
57	MG	RA	3069	-	-	-	X
57	MG	RA	3070	-	-	-	X
57	MG	RA	3071	-	-	-	X
57	MG	RA	3072	-	-	-	X
57	MG	RA	3073	-	-	-	X
57	MG	RA	3077	-	-	-	X
57	MG	RA	3078	-	-	-	X
57	MG	RA	3079	-	-	-	X
57	MG	RA	3080	-	-	-	X
57	MG	RA	3092	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	RA	3093	-	-	-	X
57	MG	RA	3098	-	-	-	X
57	MG	RA	3101	-	-	-	X
57	MG	RA	3102	-	-	-	X
57	MG	RA	3103	-	-	-	X
57	MG	RA	3106	-	-	-	X
57	MG	RA	3109	-	-	-	X
57	MG	RA	3120	-	-	-	X
57	MG	RA	3134	-	-	-	X
57	MG	RA	3148	-	-	-	X
57	MG	RA	3149	-	-	-	X
57	MG	RA	3157	-	-	-	X
57	MG	RA	3159	-	-	-	X
57	MG	RA	3163	-	-	-	X
57	MG	RA	3166	-	-	-	X
57	MG	RA	3167	-	-	-	X
57	MG	RA	3171	-	-	-	X
57	MG	RA	3173	-	-	-	X
57	MG	RA	3174	-	-	-	X
57	MG	RA	3189	-	-	-	X
57	MG	RA	3190	-	-	-	X
57	MG	RA	3194	-	-	-	X
57	MG	RA	3198	-	-	-	X
57	MG	RA	3199	-	-	-	X
57	MG	RA	3203	-	-	-	X
57	MG	RA	3206	-	-	-	X
57	MG	RA	3209	-	-	-	X
57	MG	RA	3213	-	-	-	X
57	MG	RA	3214	-	-	-	X
57	MG	RA	3223	-	-	-	X
57	MG	RA	3229	-	-	-	X
57	MG	RA	3234	-	-	-	X
57	MG	RA	3236	-	-	-	X
57	MG	RA	3240	-	-	-	X
57	MG	RA	3241	-	-	-	X
57	MG	RA	3245	-	-	-	X
57	MG	RA	3247	-	-	-	X
57	MG	RA	3260	-	-	-	X
57	MG	RA	3276	-	-	-	X
57	MG	RA	3283	-	-	-	X
57	MG	RA	3296	-	-	-	X
57	MG	RA	3297	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	RA	3301	-	-	-	X
57	MG	RA	3308	-	-	-	X
57	MG	RA	3318	-	-	-	X
57	MG	RA	3331	-	-	-	X
57	MG	RA	3345	-	-	-	X
57	MG	RA	3348	-	-	-	X
57	MG	RA	3354	-	-	-	X
57	MG	RA	3361	-	-	-	X
57	MG	RA	3363	-	-	-	X
57	MG	RA	3368	-	-	-	X
57	MG	RA	3369	-	-	-	X
57	MG	RA	3375	-	-	-	X
57	MG	RA	3376	-	-	-	X
57	MG	RA	3382	-	-	-	X
57	MG	RA	3384	-	-	-	X
57	MG	RA	3385	-	-	-	X
57	MG	RA	3389	-	-	-	X
57	MG	RA	3395	-	-	-	X
57	MG	RA	3406	-	-	-	X
57	MG	RA	3409	-	-	-	X
57	MG	RA	3411	-	-	-	X
57	MG	RA	3428	-	-	-	X
57	MG	RA	3431	-	-	-	X
57	MG	RD	301	-	-	-	X
57	MG	RD	302	-	-	-	X
57	MG	RY	202	-	-	-	X
57	MG	XA	1601	-	-	-	X
57	MG	XA	1604	-	-	-	X
57	MG	XA	1605	-	-	-	X
57	MG	XA	1607	-	-	-	X
57	MG	XA	1611	-	-	-	X
57	MG	XA	1618	-	-	-	X
57	MG	XA	1636	-	-	-	X
57	MG	XA	1638	-	-	-	X
57	MG	XA	1640	-	-	-	X
57	MG	XA	1643	-	-	-	X
57	MG	XA	1644	-	-	-	X
57	MG	XA	1652	-	-	-	X
57	MG	XA	1659	-	-	-	X
57	MG	XA	1664	-	-	-	X
57	MG	XA	1667	-	-	-	X
57	MG	XA	1672	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	XA	1679	-	-	-	X
57	MG	XA	1682	-	-	-	X
57	MG	XA	1696	-	-	-	X
57	MG	XA	1731	-	-	-	X
57	MG	XA	1740	-	-	-	X
57	MG	XA	1743	-	-	-	X
57	MG	XA	1746	-	-	-	X
57	MG	XA	1753	-	-	-	X
57	MG	YA	3003	-	-	-	X
57	MG	YA	3006	-	-	-	X
57	MG	YA	3011	-	-	-	X
57	MG	YA	3012	-	-	-	X
57	MG	YA	3013	-	-	-	X
57	MG	YA	3014	-	-	-	X
57	MG	YA	3017	-	-	-	X
57	MG	YA	3018	-	-	-	X
57	MG	YA	3021	-	-	-	X
57	MG	YA	3022	-	-	-	X
57	MG	YA	3025	-	-	-	X
57	MG	YA	3027	-	-	-	X
57	MG	YA	3029	-	-	-	X
57	MG	YA	3031	-	-	-	X
57	MG	YA	3033	-	-	-	X
57	MG	YA	3038	-	-	-	X
57	MG	YA	3042	-	-	-	X
57	MG	YA	3044	-	-	-	X
57	MG	YA	3047	-	-	-	X
57	MG	YA	3053	-	-	-	X
57	MG	YA	3054	-	-	-	X
57	MG	YA	3055	-	-	-	X
57	MG	YA	3063	-	-	-	X
57	MG	YA	3065	-	-	-	X
57	MG	YA	3068	-	-	-	X
57	MG	YA	3069	-	-	-	X
57	MG	YA	3071	-	-	-	X
57	MG	YA	3072	-	-	-	X
57	MG	YA	3077	-	-	-	X
57	MG	YA	3078	-	-	-	X
57	MG	YA	3079	-	-	-	X
57	MG	YA	3080	-	-	-	X
57	MG	YA	3087	-	-	-	X
57	MG	YA	3089	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	YA	3091	-	-	-	X
57	MG	YA	3092	-	-	-	X
57	MG	YA	3096	-	-	-	X
57	MG	YA	3097	-	-	-	X
57	MG	YA	3102	-	-	-	X
57	MG	YA	3105	-	-	-	X
57	MG	YA	3108	-	-	-	X
57	MG	YA	3110	-	-	-	X
57	MG	YA	3119	-	-	-	X
57	MG	YA	3134	-	-	-	X
57	MG	YA	3136	-	-	-	X
57	MG	YA	3138	-	-	-	X
57	MG	YA	3147	-	-	-	X
57	MG	YA	3148	-	-	-	X
57	MG	YA	3152	-	-	-	X
57	MG	YA	3156	-	-	-	X
57	MG	YA	3164	-	-	-	X
57	MG	YA	3167	-	-	-	X
57	MG	YA	3170	-	-	-	X
57	MG	YA	3189	-	-	-	X
57	MG	YA	3190	-	-	-	X
57	MG	YA	3191	-	-	-	X
57	MG	YA	3205	-	-	-	X
57	MG	YA	3208	-	-	-	X
57	MG	YA	3209	-	-	-	X
57	MG	YA	3217	-	-	-	X
57	MG	YA	3219	-	-	-	X
57	MG	YA	3220	-	-	-	X
57	MG	YA	3223	-	-	-	X
57	MG	YA	3225	-	-	-	X
57	MG	YA	3226	-	-	-	X
57	MG	YA	3231	-	-	-	X
57	MG	YA	3233	-	-	-	X
57	MG	YA	3237	-	-	-	X
57	MG	YA	3239	-	-	-	X
57	MG	YA	3246	-	-	-	X
57	MG	YA	3249	-	-	-	X
57	MG	YA	3253	-	-	-	X
57	MG	YA	3274	-	-	-	X
57	MG	YA	3278	-	-	-	X
57	MG	YA	3285	-	-	-	X
57	MG	YA	3294	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
57	MG	YA	3297	-	-	-	X
57	MG	YA	3304	-	-	-	X
57	MG	YA	3306	-	-	-	X
57	MG	YA	3334	-	-	-	X
57	MG	YA	3335	-	-	-	X
57	MG	YA	3337	-	-	-	X
57	MG	YA	3338	-	-	-	X
57	MG	YA	3352	-	-	-	X
57	MG	YA	3358	-	-	-	X
57	MG	YA	3360	-	-	-	X
57	MG	YA	3371	-	-	-	X
57	MG	YA	3386	-	-	-	X
57	MG	YA	3399	-	-	-	X
57	MG	YA	3404	-	-	-	X
57	MG	YA	3406	-	-	-	X
57	MG	YA	3416	-	-	-	X
57	MG	YA	3421	-	-	-	X
57	MG	YA	3423	-	-	-	X
57	MG	YA	3425	-	-	-	X
57	MG	YA	3426	-	-	-	X
57	MG	YA	3428	-	-	-	X
57	MG	YA	3441	-	-	-	X
57	MG	YA	3449	-	-	-	X
57	MG	YA	3450	-	-	-	X
57	MG	YA	3456	-	-	-	X
57	MG	YA	3461	-	-	-	X
57	MG	YA	3469	-	-	-	X
57	MG	YA	3471	-	-	-	X
57	MG	YD	301	-	-	-	X
57	MG	YF	301	-	-	-	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
1	QA	1511	Total	C	N	O	P	0	0	0
			32472	14453	6011	10497	1511			
1	XA	1508	Total	C	N	O	P	0	0	0
			32409	14425	6001	10475	1508			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
56	Z7	3	Total	C	N	O	P	0	0	0
			74	40	13	19	2			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	QA	147	Total	Mg	0	0
			147	147		
57	YV	1	Total	Mg	0	0
			1	1		
57	RP	2	Total	Mg	0	0
			2	2		
57	YA	473	Total	Mg	0	0
			473	473		
57	Y5	3	Total	Mg	0	0
			3	3		
57	YH	2	Total	Mg	0	0
			2	2		
57	YR	1	Total	Mg	0	0
			1	1		
57	QD	1	Total	Mg	0	0
			1	1		
57	Y1	1	Total	Mg	0	0
			1	1		
57	YD	1	Total	Mg	0	0
			1	1		
57	QV	5	Total	Mg	0	0
			5	5		
57	XA	161	Total	Mg	0	0
			161	161		
57	YY	1	Total	Mg	0	0
			1	1		
57	RQ	2	Total	Mg	0	0
			2	2		
57	XN	1	Total	Mg	0	0
			1	1		
57	QL	1	Total	Mg	0	0
			1	1		
57	YU	1	Total	Mg	0	0
			1	1		
57	Y0	3	Total	Mg	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	YG	1	Total 1	Mg 1	0	0
57	YQ	2	Total 2	Mg 2	0	0
57	RY	2	Total 2	Mg 2	0	0
57	YN	1	Total 1	Mg 1	0	0
57	XF	1	Total 1	Mg 1	0	0
57	RR	1	Total 1	Mg 1	0	0
57	RD	2	Total 2	Mg 2	0	0
57	XL	1	Total 1	Mg 1	0	0
57	Y7	1	Total 1	Mg 1	0	0
57	R5	3	Total 3	Mg 3	0	0
57	RA	431	Total 431	Mg 431	0	0
57	YF	1	Total 1	Mg 1	0	0
57	YP	2	Total 2	Mg 2	0	0
57	RE	2	Total 2	Mg 2	0	0
57	R2	1	Total 1	Mg 1	0	0
57	YB	6	Total 6	Mg 6	0	0
57	R0	3	Total 3	Mg 3	0	0
57	XV	4	Total 4	Mg 4	0	0
57	RB	5	Total 5	Mg 5	0	0
57	QE	1	Total 1	Mg 1	0	0
57	XD	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
57	RF	1	Total 1	Mg 1	0	0
57	YE	1	Total 1	Mg 1	0	0

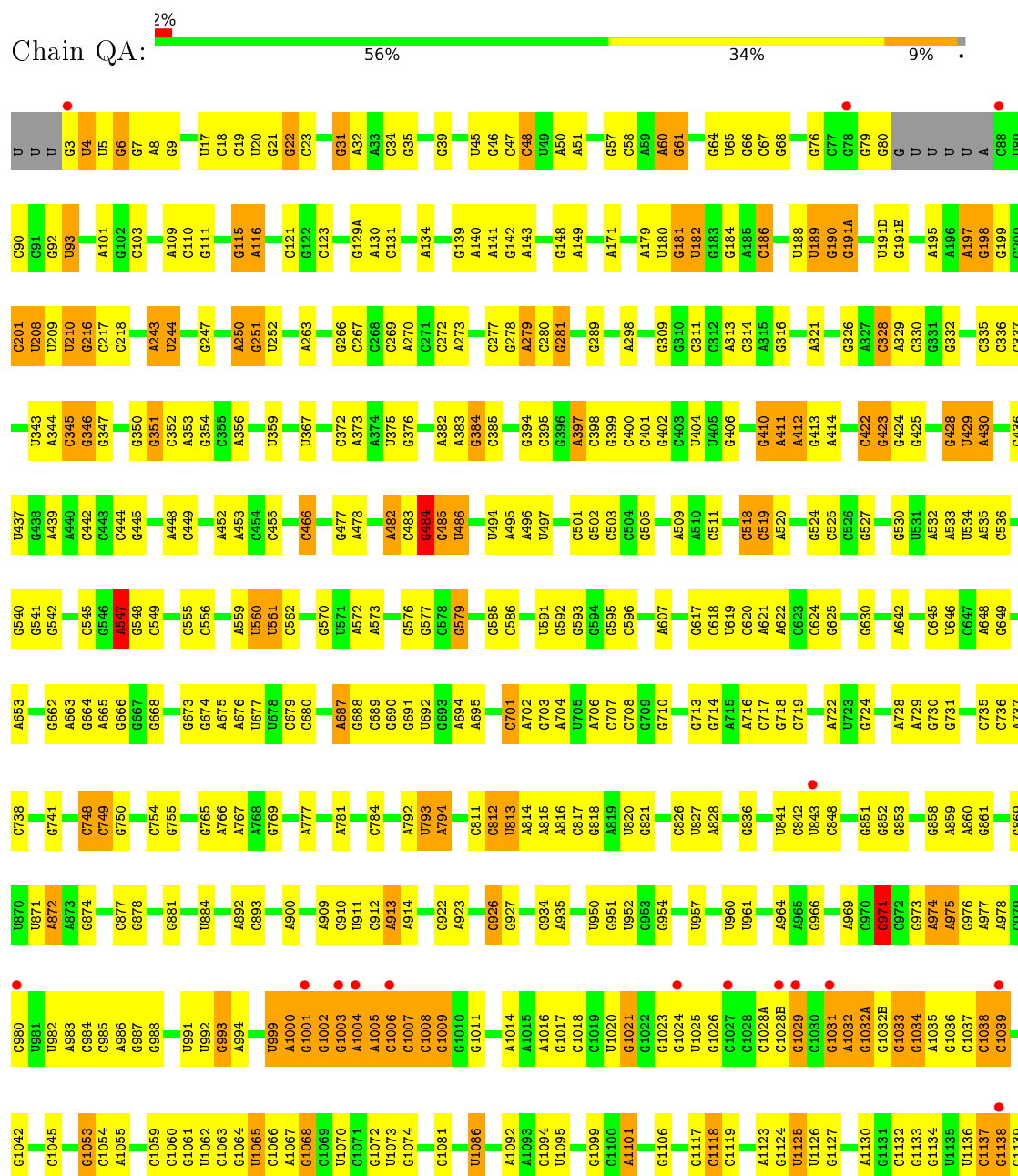
- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

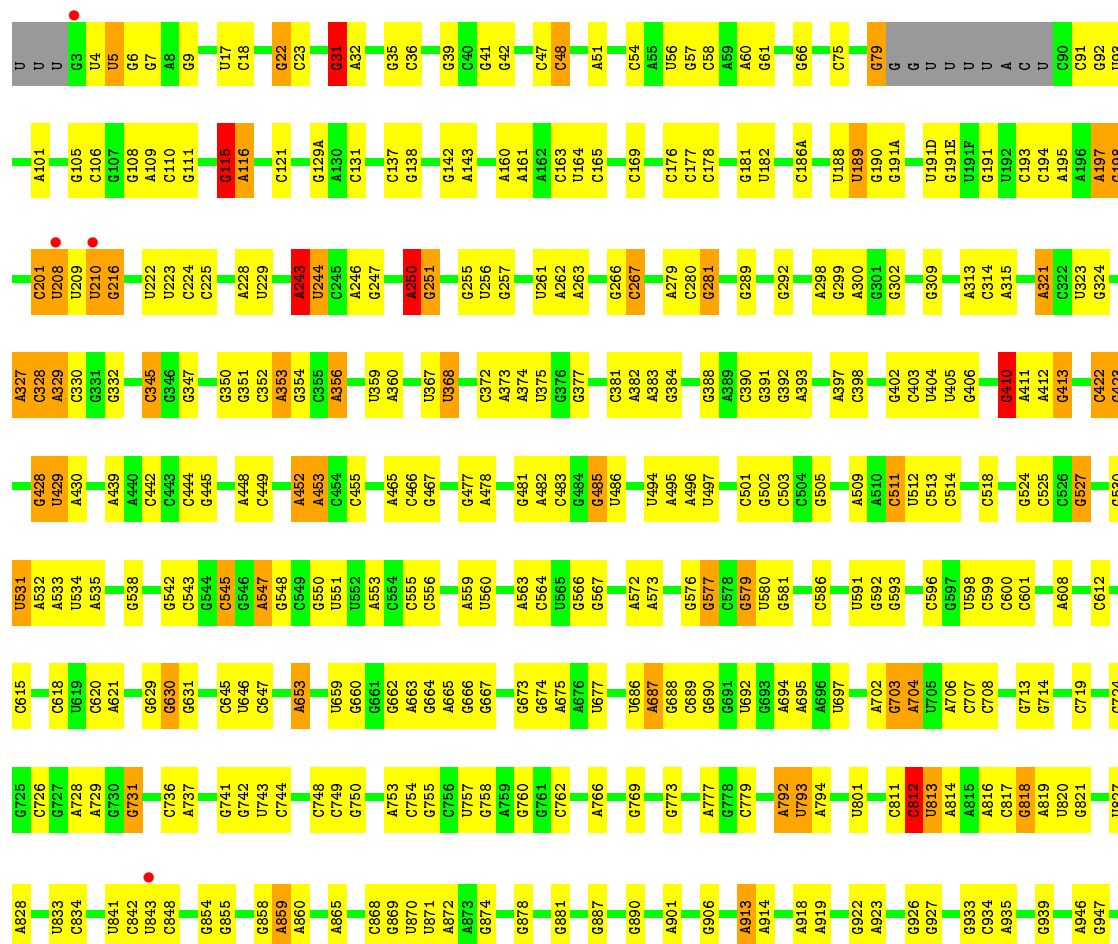
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
58	XD	1	Total 1	Zn 1	0	0
58	QD	1	Total 1	Zn 1	0	0
58	QN	1	Total 1	Zn 1	0	0
58	XN	1	Total 1	Zn 1	0	0

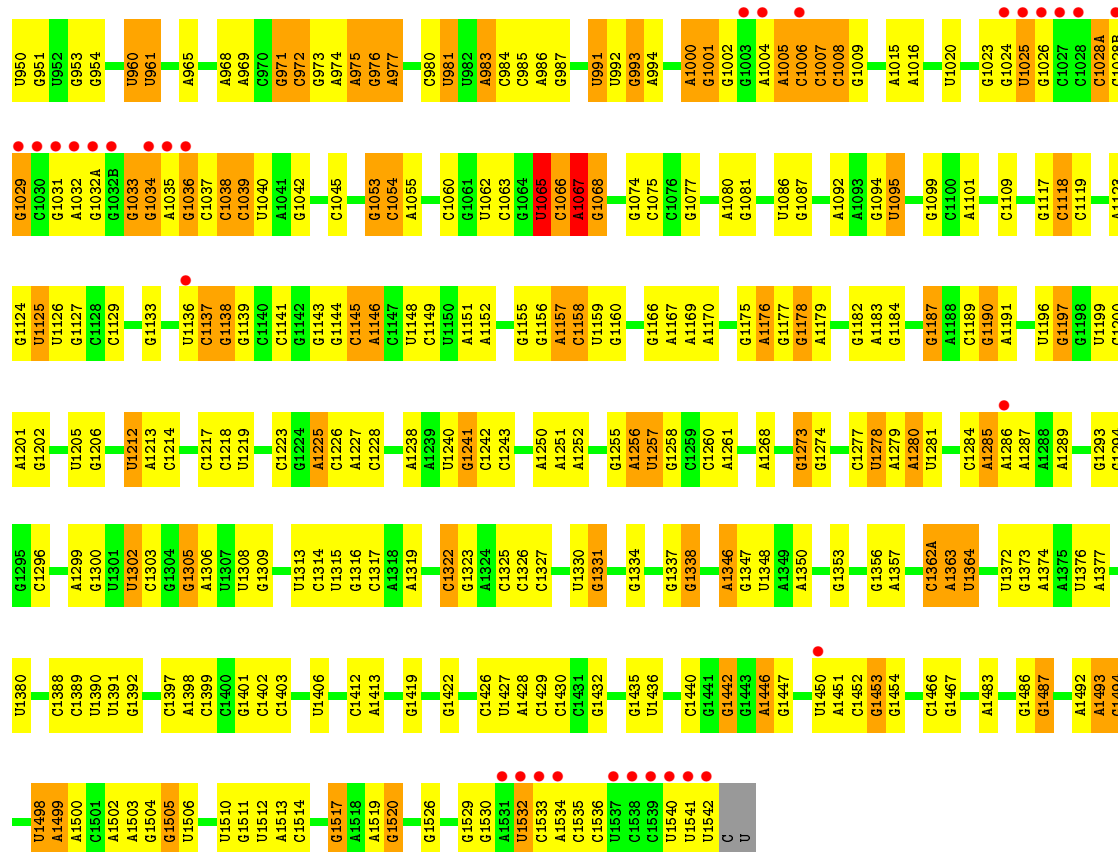
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

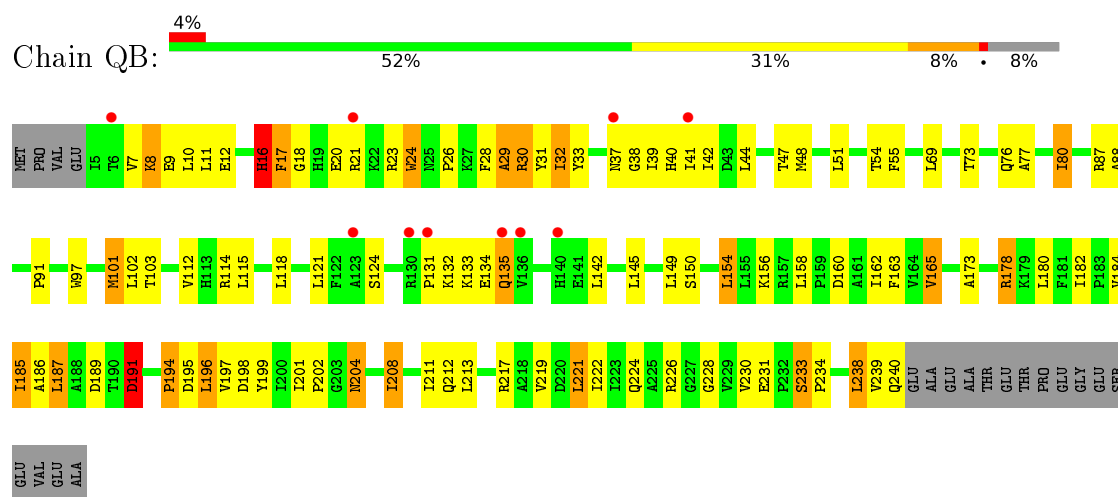
• Molecule 1: 16S rRNA



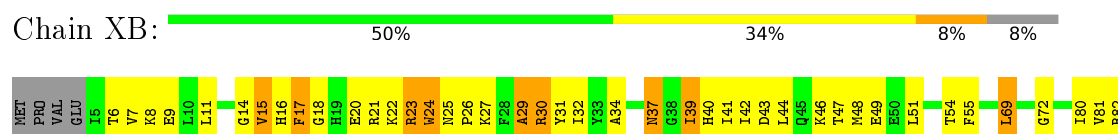


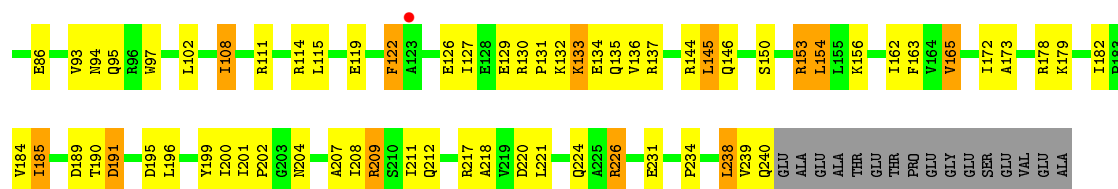


• Molecule 2: 30S ribosomal protein S2

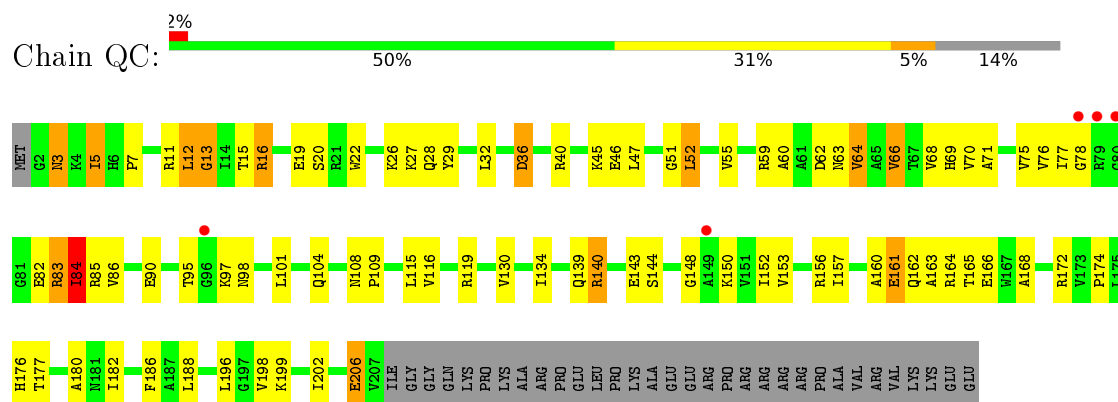


• Molecule 2: 30S ribosomal protein S2

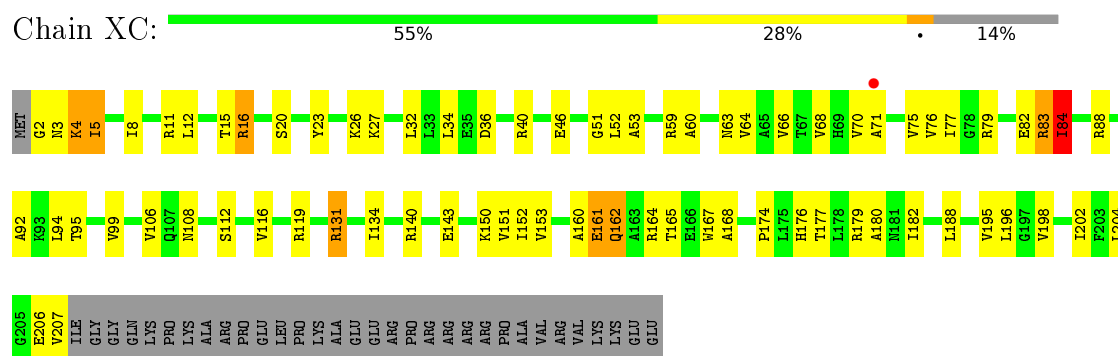




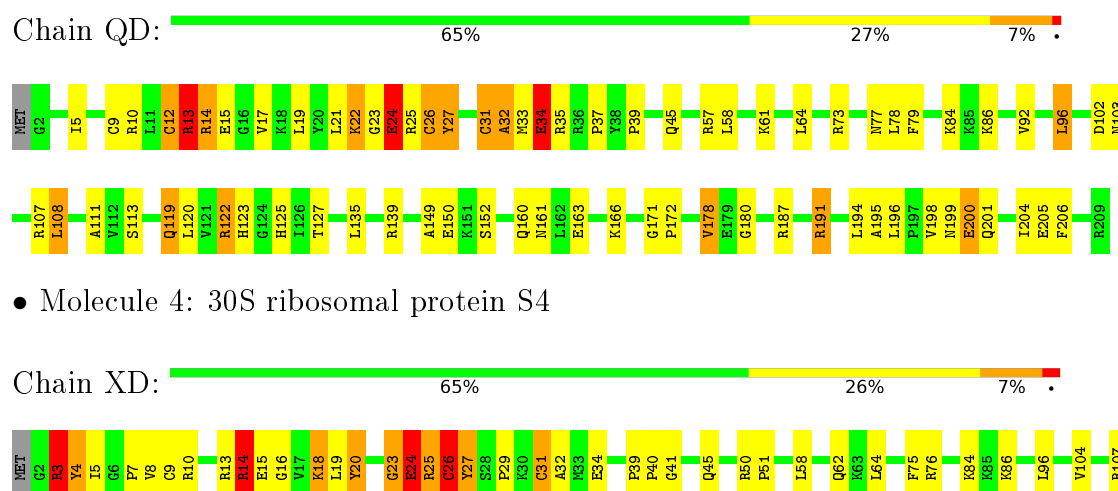
• Molecule 3: 30S ribosomal protein S3



• Molecule 3: 30S ribosomal protein S3



• Molecule 4: 30S ribosomal protein S4

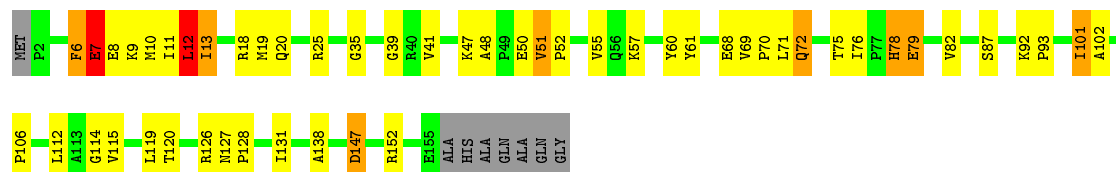


• Molecule 4: 30S ribosomal protein S4



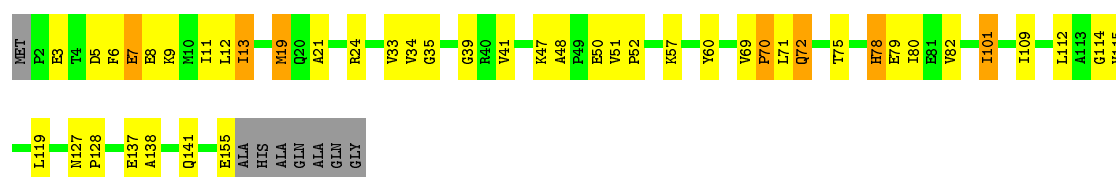
- Molecule 5: 30S ribosomal protein S5

Chain QE: 63% 26% 5% • 5%



- Molecule 5: 30S ribosomal protein S5

Chain XE: 67% 23% • 5%



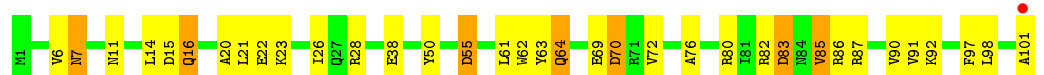
- Molecule 6: 30S ribosomal protein S6

Chain QF: 4% 71% 25% •



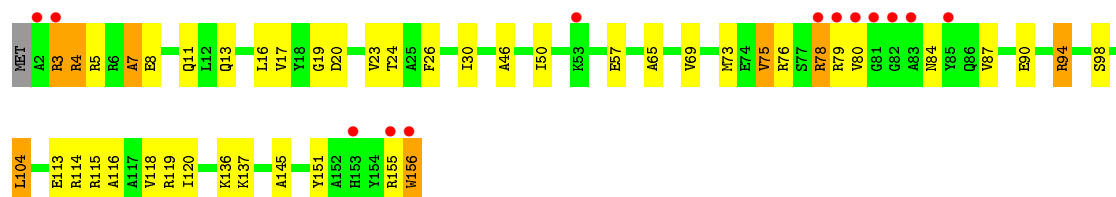
- Molecule 6: 30S ribosomal protein S6

Chain XF: % 65% 28% 7%

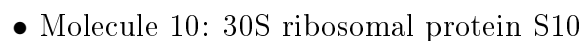


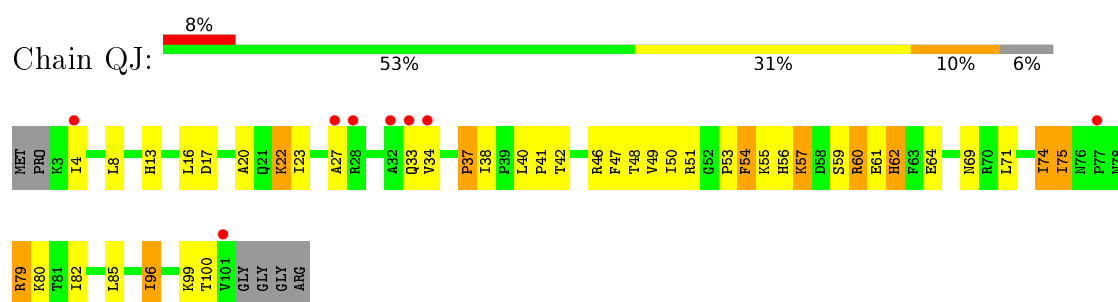
- Molecule 7: 30S ribosomal protein S7

Chain QG: 8% 71% 24% 5% •

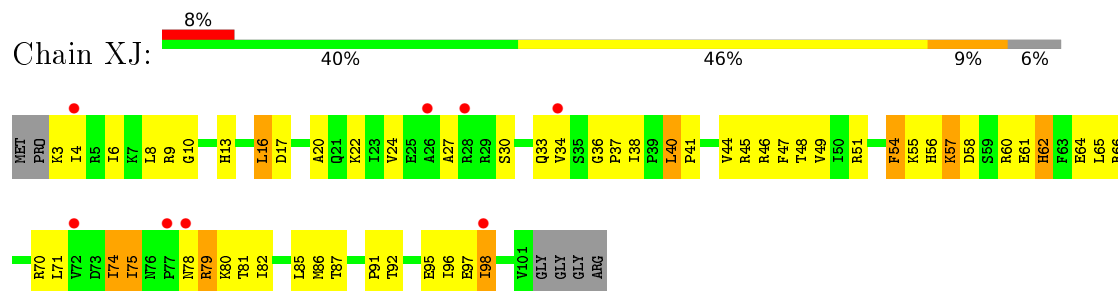


- Molecule 7: 30S ribosomal protein S7

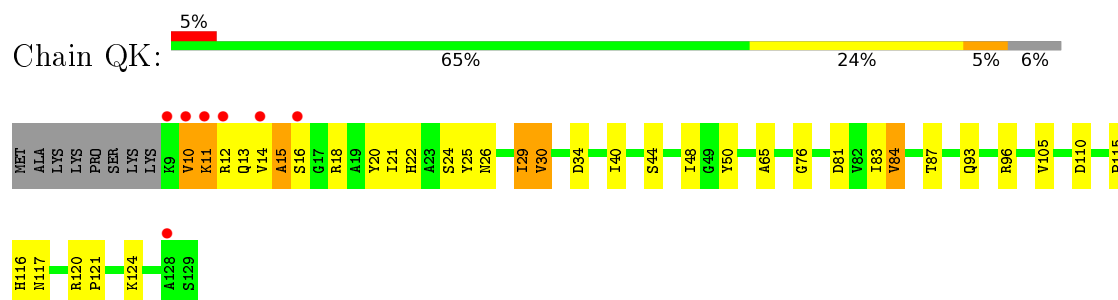




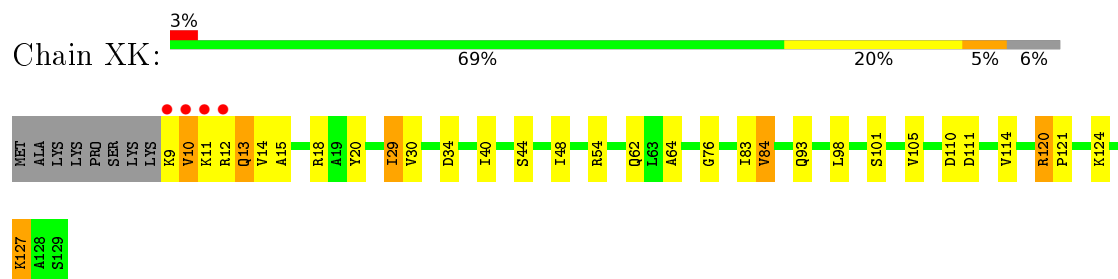
- Molecule 10: 30S ribosomal protein S10



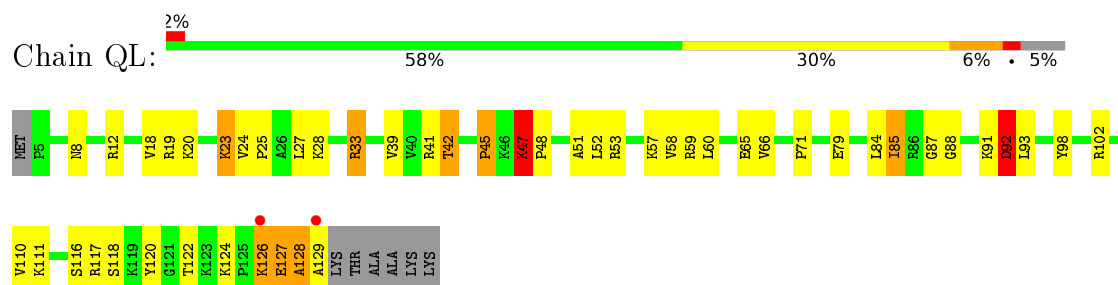
- Molecule 11: 30S ribosomal protein S11



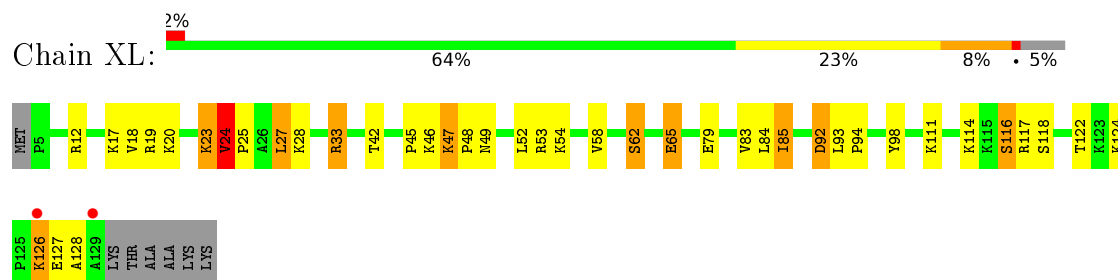
- Molecule 11: 30S ribosomal protein S11



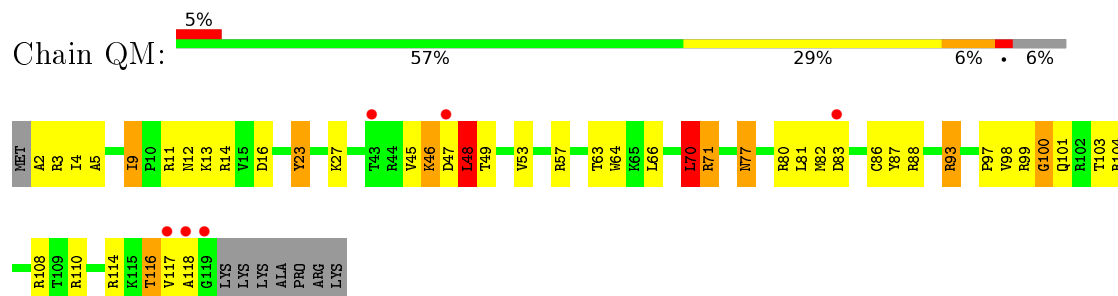
- Molecule 12: 30S ribosomal protein S12



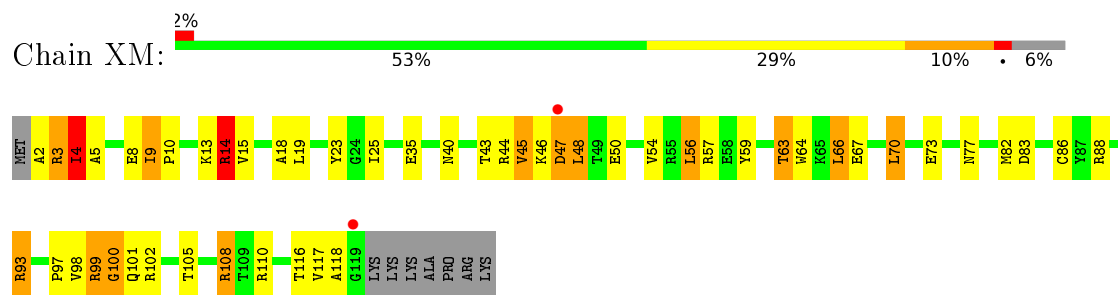
- Molecule 12: 30S ribosomal protein S12



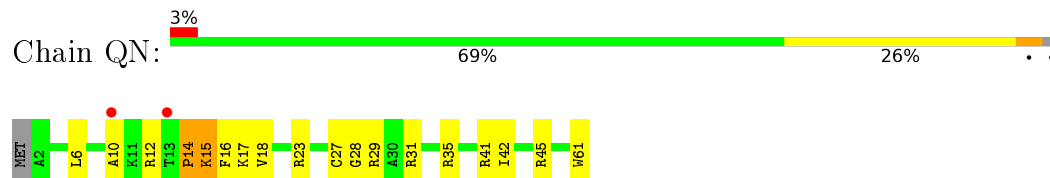
- Molecule 13: 30S ribosomal protein S13



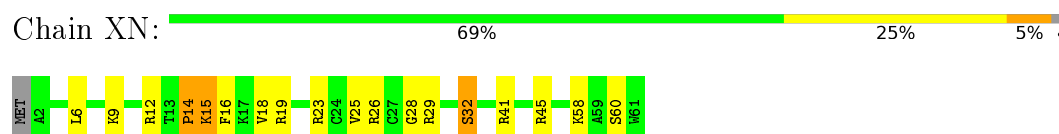
- Molecule 13: 30S ribosomal protein S13



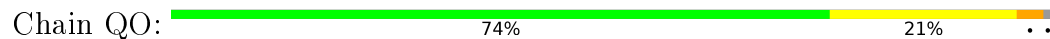
- Molecule 14: 30S ribosomal protein S14 type Z



- Molecule 14: 30S ribosomal protein S14 type Z

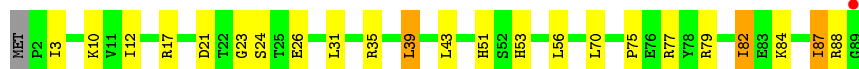
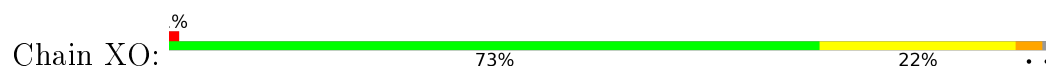


- Molecule 15: 30S ribosomal protein S15





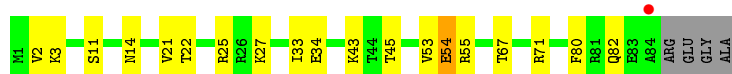
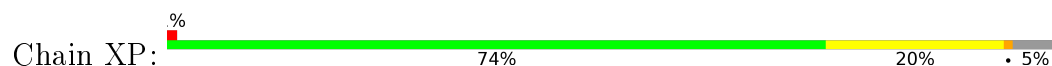
- Molecule 15: 30S ribosomal protein S15



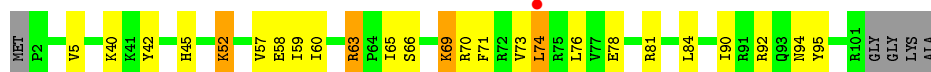
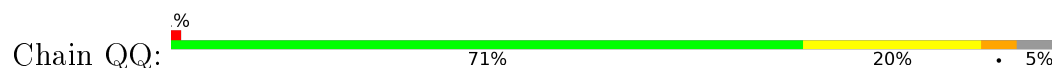
- Molecule 16: 30S ribosomal protein S16



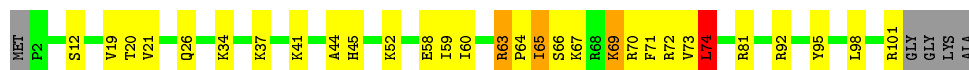
- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17



- Molecule 17: 30S ribosomal protein S17

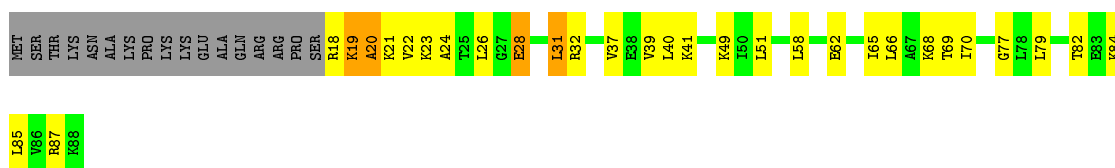


- Molecule 18: 30S ribosomal protein S18

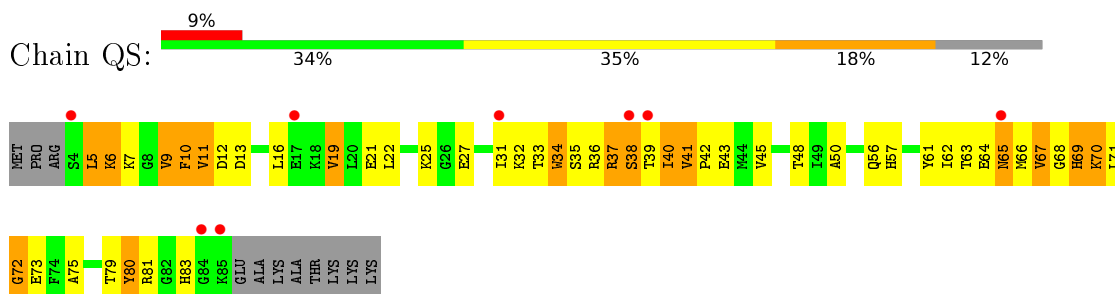


- Molecule 18: 30S ribosomal protein S18

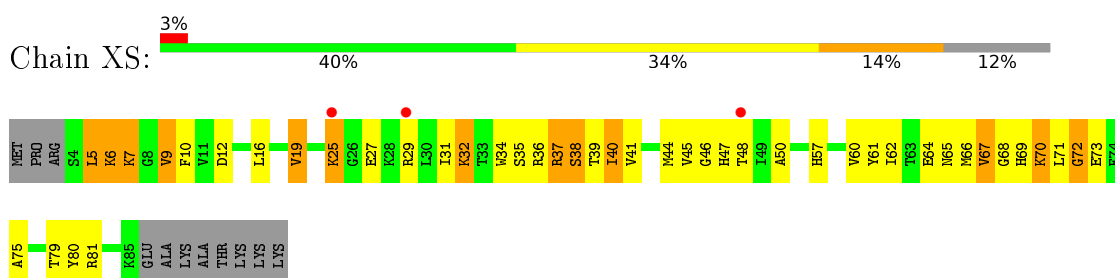




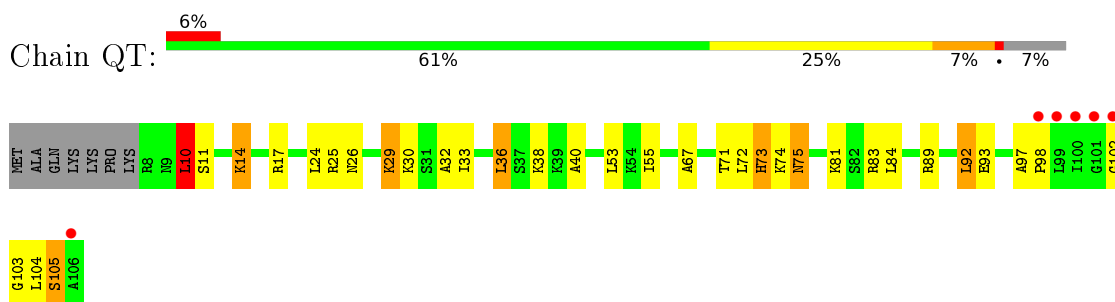
- Molecule 19: 30S ribosomal protein S19



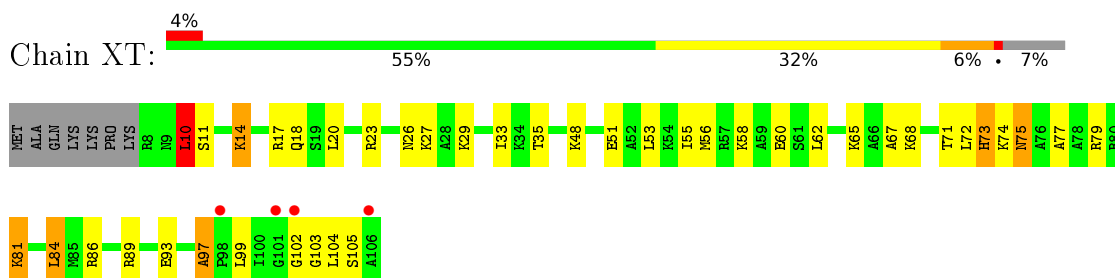
- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20



- Molecule 20: 30S ribosomal protein S20



- Molecule 21: 30S ribosomal protein Thx

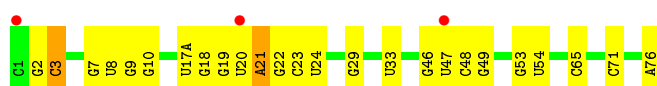




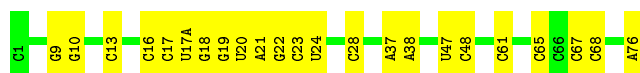
- Molecule 21: 30S ribosomal protein Thx



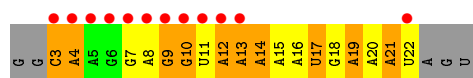
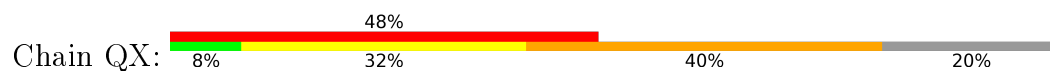
- Molecule 22: P-site tRNA-fMet



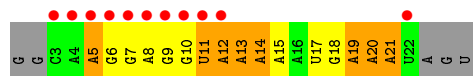
- Molecule 22: P-site tRNA-fMet



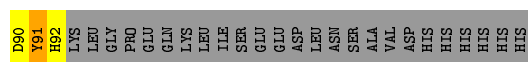
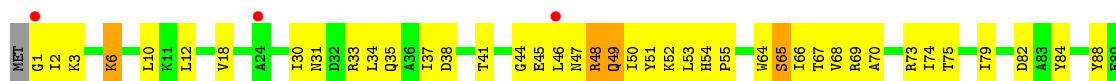
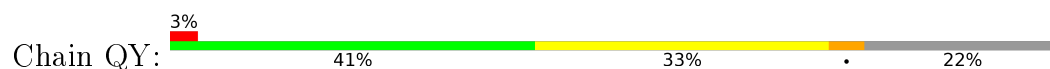
- Molecule 23: messenger RNA



- Molecule 23: messenger RNA



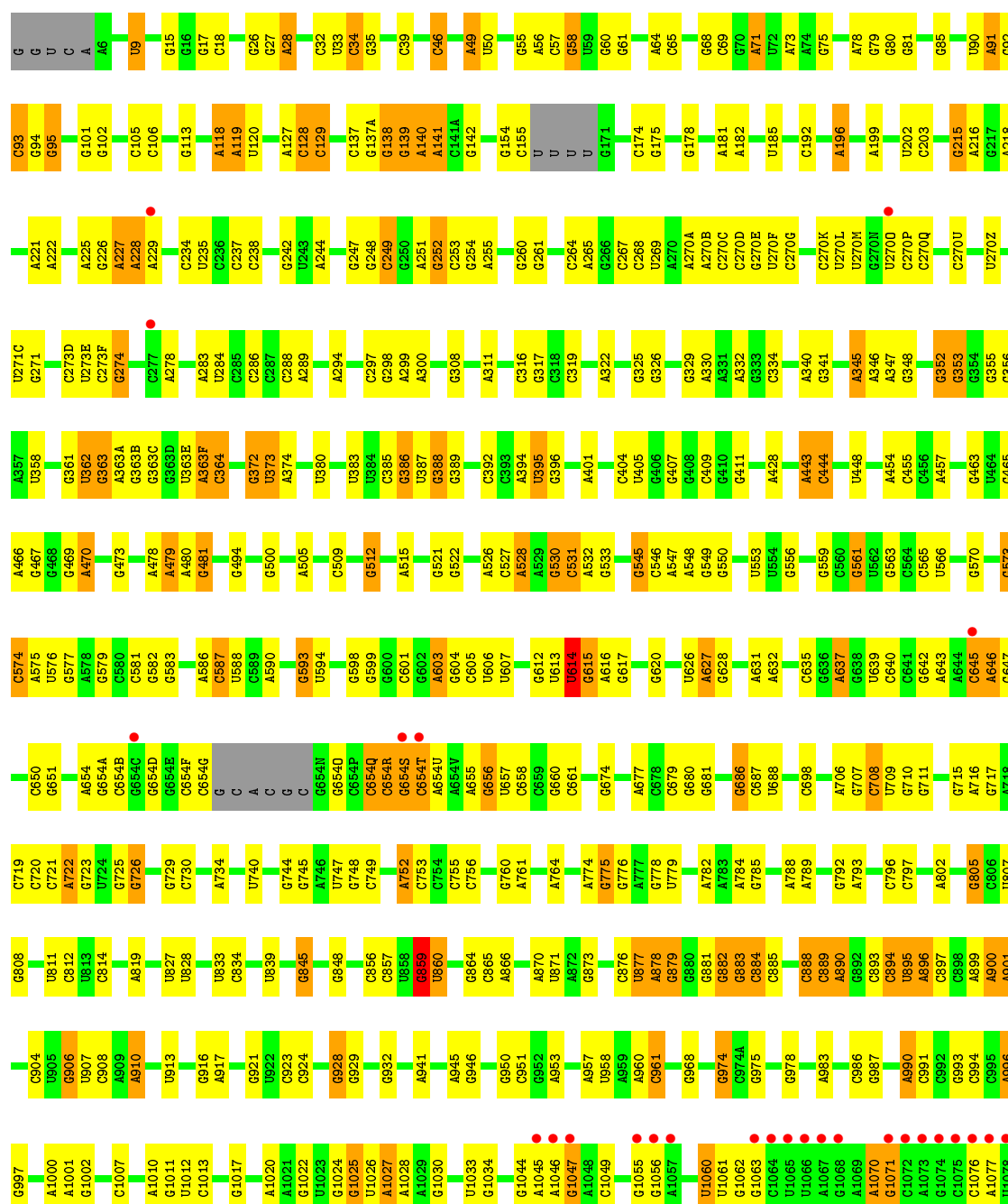
- Molecule 24: Killer protein



- Molecule 24: Killer protein

Protein	Residue	Score	Category
Protein A	I74	0.85	High
	T75	0.75	High
	I79	0.95	High
	W80	0.90	High
	G81	0.80	High
	I84	0.70	High
	I85	0.88	High
	L86	0.82	High
	N87	0.78	High
	Y88	0.85	High
Protein B	E89	0.72	High
	D90	0.68	High
	Y91	0.92	High
	H92	0.88	High
	L93	0.75	High
	LEU	0.70	High
	GLY	0.82	High
	PRQ	0.78	High
	GLN	0.85	High
	GLU	0.72	High
Protein C	LYS	0.80	High
	LEU	0.75	High
	ILE	0.82	High
	SER	0.78	High
	GLU	0.85	High
	GLU	0.72	High
	ASP	0.80	High
	LEU	0.75	High
	ASN	0.82	High
	SER	0.78	High
Protein D	ALA	0.85	High
	VAL	0.75	High
	ASP	0.88	High
	HIS	0.72	High
	HIS	0.82	High
	HIS	0.78	High
	HIS	0.85	High
	HIS	0.72	High
	HIS	0.80	High
	HIS	0.75	High
Protein E	I74	0.85	High
	T75	0.75	High
	I79	0.95	High
	W80	0.90	High
	G81	0.80	High
	I84	0.70	High
	I85	0.88	High
	L86	0.82	High
	N87	0.78	High
	Y88	0.85	High
Protein F	E89	0.72	High
	D90	0.68	High
	Y91	0.92	High
	H92	0.88	High
	L93	0.75	High
	LEU	0.70	High
	GLY	0.82	High
	PRQ	0.78	High
	GLN	0.85	High
	GLU	0.72	High
Protein G	LYS	0.80	High
	LEU	0.75	High
	ILE	0.82	High
	SER	0.78	High
	GLU	0.85	High
	GLU	0.72	High
	ASP	0.80	High
	LEU	0.75	High
	ASN	0.82	High
	SER	0.78	High
Protein H	ALA	0.85	High
	VAL	0.75	High
	ASP	0.88	High
	HIS	0.72	High
	HIS	0.82	High
	HIS	0.78	High
	HIS	0.85	High
	HIS	0.72	High
	HIS	0.80	High
	HIS	0.75	High
Protein I	I74	0.85	High
	T75	0.75	High
	I79	0.95	High
	W80	0.90	High
	G81	0.80	High
	I84	0.70	High
	I85	0.88	High
	L86	0.82	High
	N87	0.78	High
	Y88	0.85	High
Protein J	E89	0.72	High
	D90	0.68	High
	Y91	0.92	High
	H92	0.88	High
	L93	0.75	High
	LEU	0.70	High
	GLY	0.82	High
	PRQ	0.78	High
	GLN	0.85	High
	GLU	0.72	High
Protein K	LYS	0.80	High
	LEU	0.75	High
	ILE	0.82	High
	SER	0.78	High
	GLU	0.85	High
	GLU	0.72	High
	ASP	0.80	High
	LEU	0.75	High
	ASN	0.82	High
	SER	0.78	High
Protein L	ALA	0.85	High
	VAL	0.75	High
	ASP	0.88	High
	HIS	0.72	High
	HIS	0.82	High
	HIS	0.78	High
	HIS	0.85	High
	HIS	0.72	High
	HIS	0.80	High
	HIS	0.75	High
Protein M	I74	0.85	High
	T75	0.75	High
	I79	0.95	High
	W80	0.90	High
	G81	0.80	High
	I84	0.70	High
	I85	0.88	High
	L86	0.82	High
	N87	0.78	High
	Y88	0.85	High
Protein N	E89	0.72	High
	D90	0.68	High
	Y91	0.92	High
	H92	0.88	High
	L93	0.75	High
	LEU	0.70	High
	GLY	0.82	High
	PRQ	0.78	High
	GLN	0.85	High
	GLU	0.72	High
Protein O	LYS	0.80	High
	LEU	0.75	High
	ILE	0.82	High
	SER	0.78	High
	GLU	0.8	

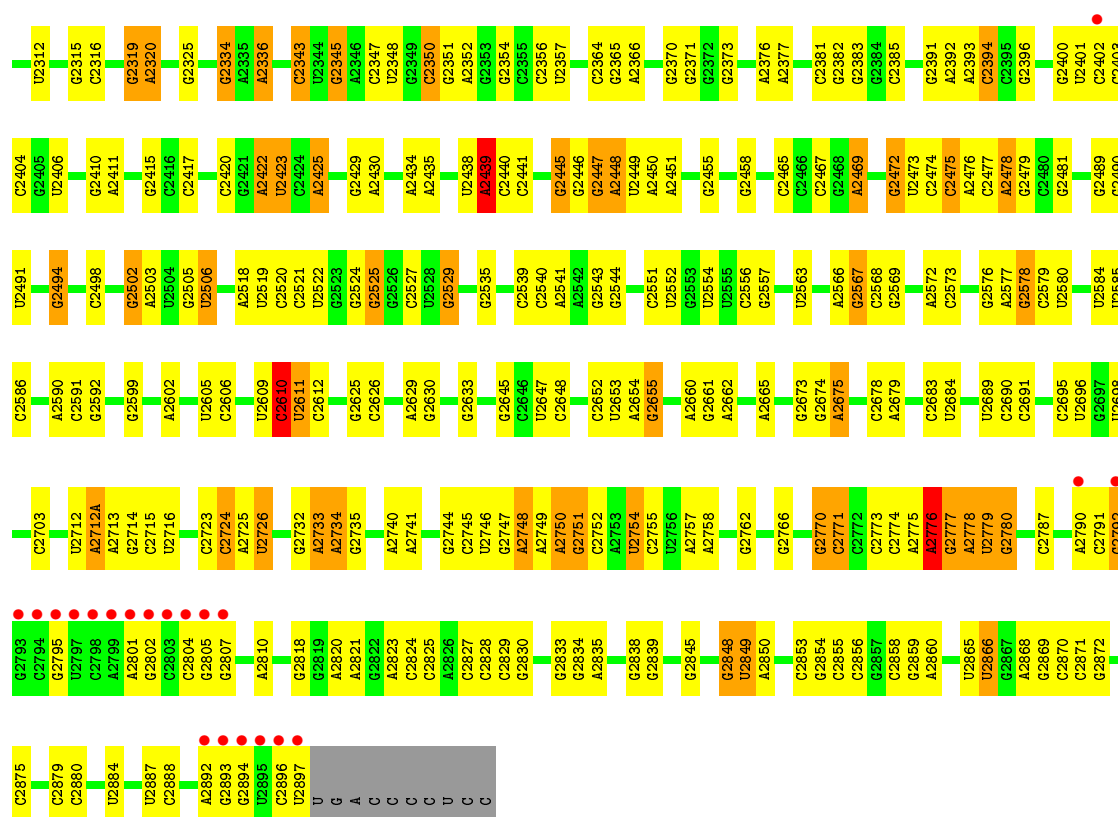
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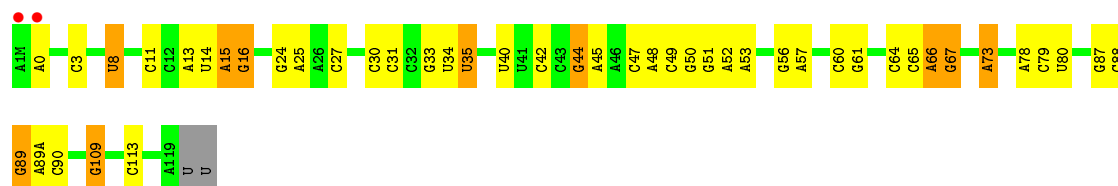




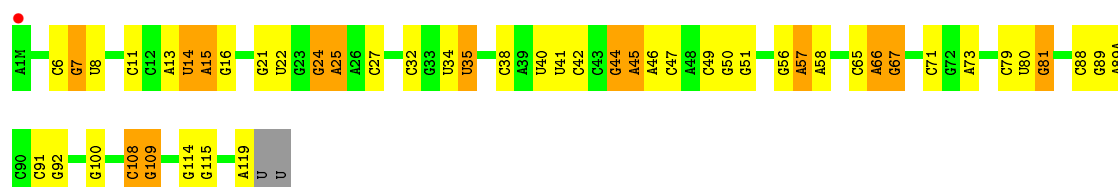
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G2190	C2040	G1935	C1836	A1729	G1592	G1501	G1416	C1180	A1095	G1024	U937	G859
G2191	A1936	G1936	C1837	G1730	A1597	C1501	G1417	G1183	A1096	G1025	G938	U860
G2192		A1937	C1838	G1731	G1595	C1505	G1418	G1187	U1097	U1026	A941	A861
G2193	A2051	A1938	G1845	G1732	C1598	C1506	A1419	G1188	A1098	U1033	A944	G862
A2198		G1948	G1846	G1733	A1598	A1507	A1419	G1187	G1099	U1033	A944	A863
U2208	C2055	A1952	G1847	G1735	C1599	A1508	G1420	A1188	C1100	G1039	A945	G864
C2209	C2056	A1952	G1847	G1735	C1599	A1508	G1421	A1189	U1101	G1039	A946	C865
G2210		A1952	G1847	G1735	C1599	A1508	G1422	G1190	C1040	C1040	A866	A866
G2211	A2059	U1955	G1858	G1743	A1608	A1510	A1427	G1191	A1103		G952	G867
A2212	A2060	U1963	G1859	G1750	A1609	A1514	C1428	G1195	A1104	G1044	A953	U868
G2213	G2061	U1963	G1860	G1750	A1610	C1515	C1428	G1195	U1105	A1045	A953	U868
G2215	G2062	G1964	G1862	G1753	A1614	C1515	A1434	C1201	G1106	A1046	G956	G869
C2143	C2063	G1964	G1862	G1754	A1615	G1519	A1434	C1201	C1047	A1046	A957	G873
U2144	C2064	G1967	U1864	A1755	A1755	G1519	C1437	A1204	A1048	C1049	A959	C876
A2225		G1968	G1869	G1756	C1617	G1522	C1437	A1204	A1110	C1049	A960	U877
A2226	G2067	A1969	C1870	G1761	A1617	G1522	A1444	C1217	A1111	G1051	C961	A878
A2227	U2068	A1970	G1871	G1762	A1618	G1525	A1444	C1217	G1112	C1052	C961	A878
G2228	G2069	A1971	A1872	A1762	A1618	G1525	C1445	C1218	U1113	C1053	C964	G880
A2229	G2070	A1972	G1878	G1763	A1634	A1528	C1446	G1219	G1114	C1053	C964	G880
C2231	A2071	A1972	G1878	G1764	C1638	A1528	G1447	A1220	G1115	A1054	C964	G881
G2238	G2072	G1981	C1881	G1772	U1639	G1534	G1448	C1225	G1116	G1055	U969	G882
G2239		A1981	C1882	A1773	C1840	U1535	G1449	C1225	G1117	G1056	C970	G883
U2243	G2080	C1982	G1883	A1773	A1536	C1537	C1450	G1235	G1122	A1057	G974	G884
U2244	G2087	A1986	A1884	U1778	C1648	C1537	A1451	G1236	G1058	A1059	C974A	C886
U2245		G1987	A1885	U1779	A1652	U1541	A1453	A1239	U1060	U1060	A877	A877
U2246	G2093	G1987	C1886	A1780	G1653	G1542	U1454	U1240	A1126	G1062	G978	C888
G2246		U1991	G1888	A1784	C1657	A1543	G1455	A1241	A1128	G1062	G979	C889
A2247	U2099	G1992	A1889	A1785	C1658	C1544	A1457	G1358	A1129	G1064	A980	A890
C2261	G2100	U1993	G1899	A1786	A1669	A1545	G1458	A1359	U1085	C1064	A983	G892
C2262	U2101	G1999	G1899	A1787	A1669	A1554	G1459	A1360	G1131	U1066	A983	C894
A2267	C2103	C2006	G1903	C1788	A1665	C1547	G1460	G1262	U1067	A1067	C986	C986
A2268	G2105	C2007	G1904	C1789	G1667	C1548	G1461	A1253	G1068	G1068	G987	A896
A2269	C2106	G2007	G1905	A1789	A1668	C1549	G1461	A1254	A1069	A1069	G988	C987
A2273	U2107	G2010	G1906	G1792	A1669	A1554	C1467	G1256	A1070	A1070	A988	C987
A2274	C2108	U2011	A1912	U1796	G1674	A1558	A1471	G1264	G1071	C1071	A900	A900
C2275	U2109	A2013	A1913	C1797	C1675	G1559	C1474	A1265	A1073	C1073	C902	C902
G2276	G2110	A2014	A1914	C1797	C1675	G1559	G1474	A1265	G1074	G1074	C903	C903
G2277	C2111	A2015	U1915	G1798	U1688	A1566	G1475	G1266	U1142	C1075	C994	C906
C2283	U2113	U2016	A1916	G1799	U1688	A1566	G1476	A1267	C995	A1077	A996	U907
A2286	A2114	U2016	U1917	G1801	C1694	A1569	G1479	A1269	U1078	U1078	G997	C997
A2287	C2115	C2021	A1918	G1801	G1695	A1569	G1480	A1269	C1079	C1079	C998	A910
A2288	G2116	C2021	A1919	G1801	G1696	A1569	G1481	G1271	C1080	C1080	U999	A911
G2289	A2117	U2022	A1920	G1815	G1696	A1569	U1482	A1272	U1081	U1081	A1000	G916
U2180	G2118	G2023	G1921	G1816	A1700	C1574	G1483	A1273	U1082	U1082	G1002	A917
G2181	G2119	A2119	G1922	G1817	A1701	G1576	G1484	A1274	U1083	U1083	G1002	A917
G2182	U2120	C2025	U1923	G1818	G1702	U1576	G1485	U1390	A1084	A1084	C1007	G919
G2183	G2121	C2026	U1923	G1819	G1703	U1577	G1488	U1391	A1085	A1085	C1007	G919
G2184	U2122	G2027	A1927	U1820	G1703	U1578	A1489	U1391	A1086	A1086	C1008	G928
G2185	C2123	A1928	G1928	A1821	C1710	A1579	A1490	U1396	G1087	G1087	A1009	G929
G2186	G2124	G1929	G1929	A1821	C1711	A1580		U1396	A1088	A1088	A1010	G929
G2187	G2125	A2031	G1930	A1825	C1712	G1581	C1493	C1403	G1089	G1089	G1011	G932
G2188	A2126	G2032	U1931	A1829	C1725	C1585	A1494	U1405	U1090	U1090	U1012	G932
G2189	G2127	A2033	C1932	A1829	G1725	A1586	A1495	A1406	G1091	G1091	C1013	G934
	G2128	C1932	C1932	A1829	G1725	A1587	U1407	C1407	C1092	C1092	C1013	G934



• Molecule 26: 5S rRNA

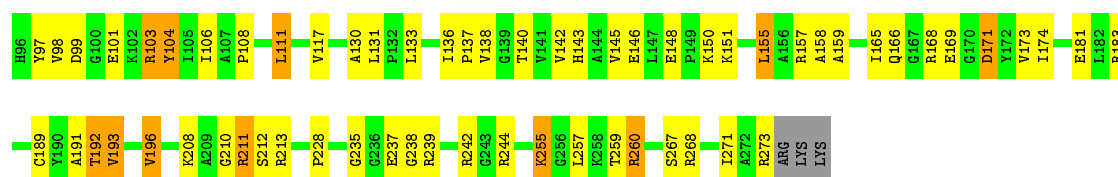


• Molecule 26: 5S rRNA



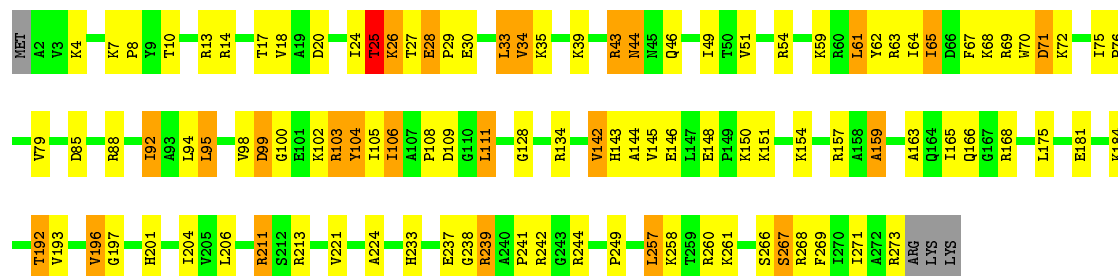
• Molecule 27: 50S ribosomal protein L2





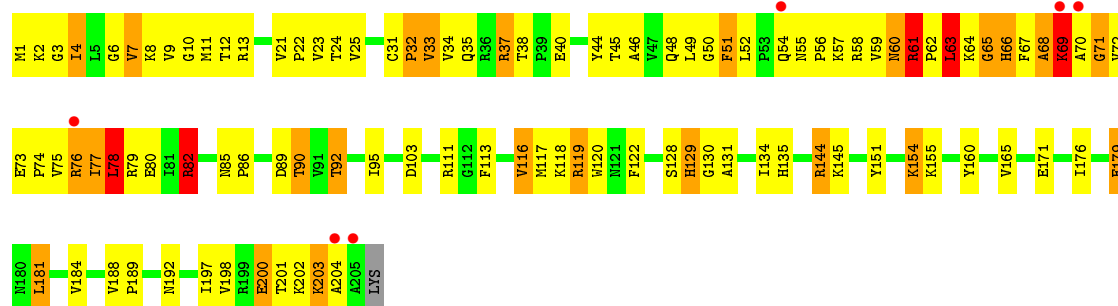
• Molecule 27: 50S ribosomal protein L2

Chain YD:



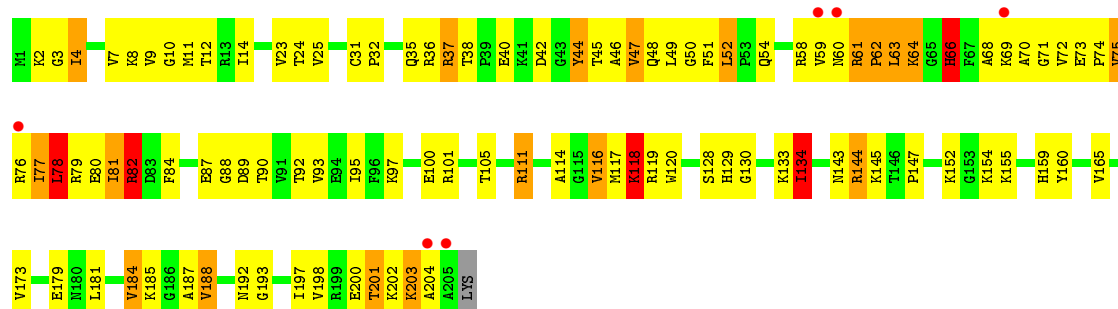
• Molecule 28: 50S ribosomal protein L3

Chain RE:



• Molecule 28: 50S ribosomal protein L3

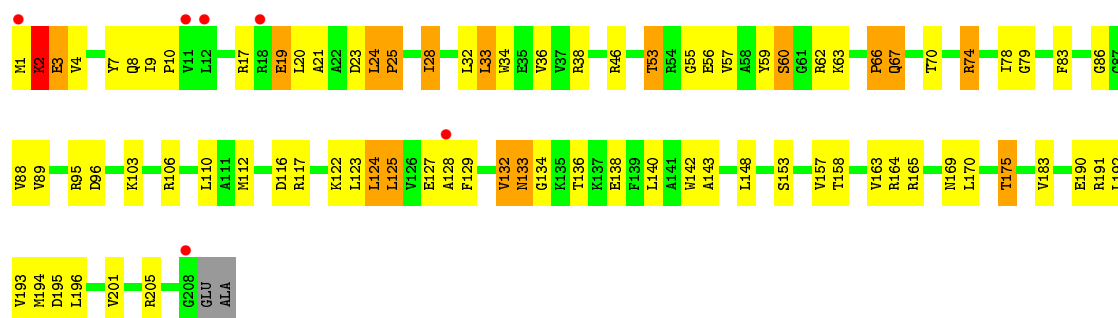
Chain YE:



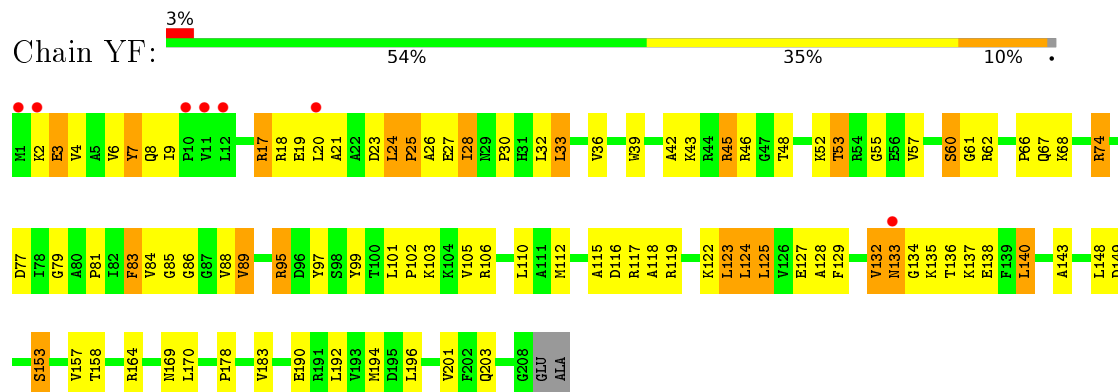
• Molecule 29: 50S ribosomal protein L4

Chain RF:

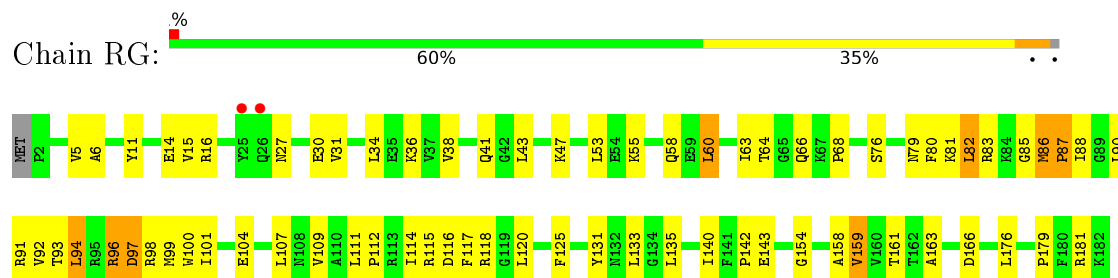




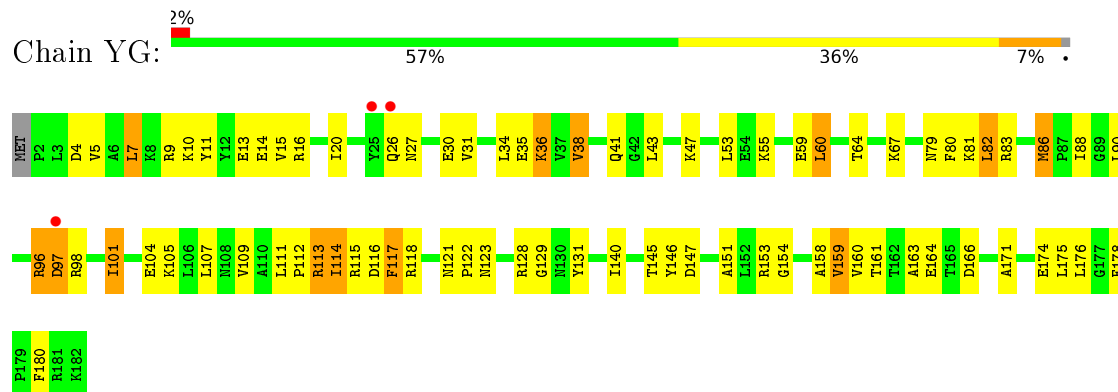
- Molecule 29: 50S ribosomal protein L4



- Molecule 30: 50S ribosomal protein L5

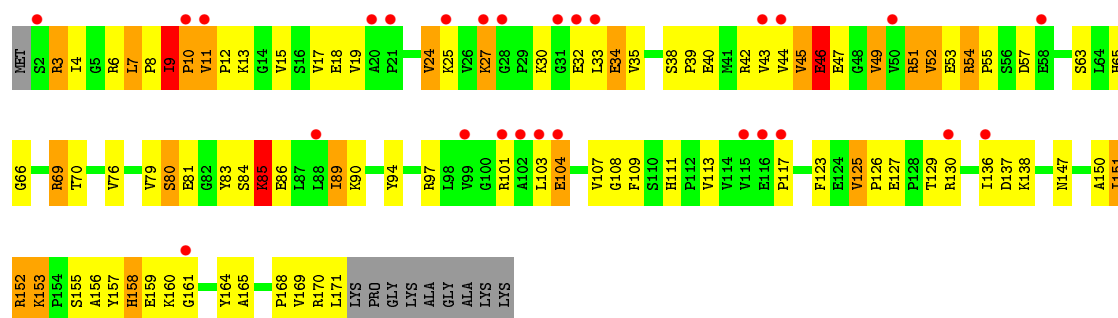


- Molecule 30: 50S ribosomal protein L5

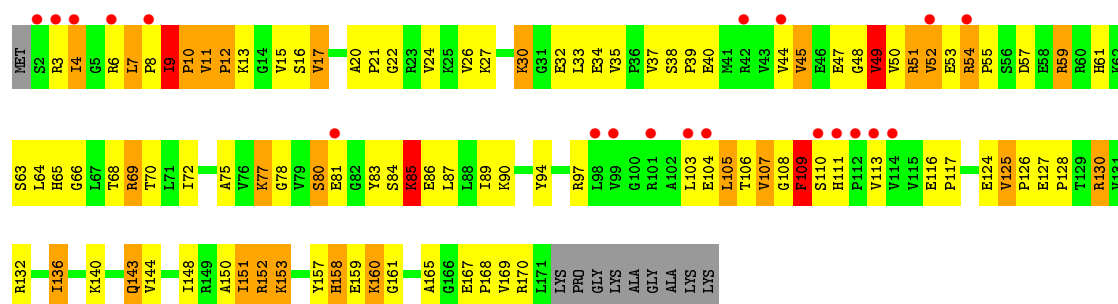


- Molecule 31: 50S ribosomal protein L6

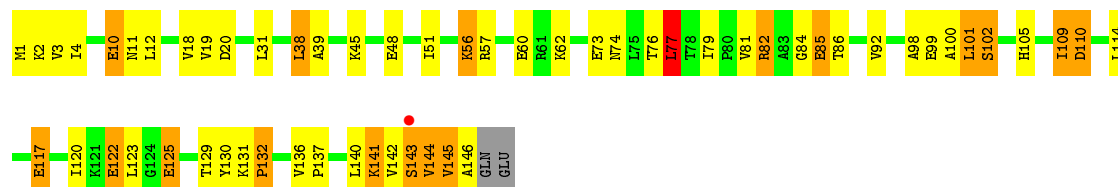




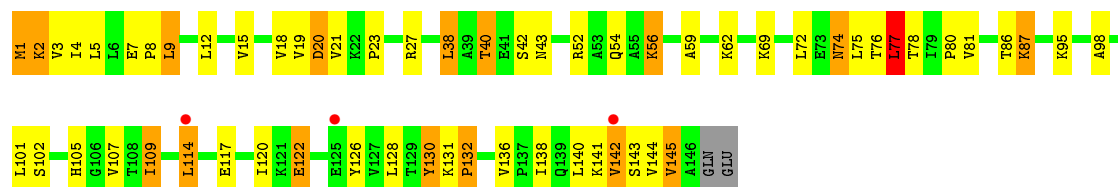
• Molecule 31: 50S ribosomal protein L6



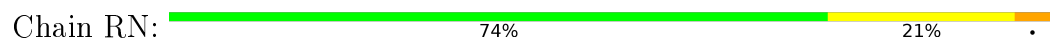
• Molecule 32: 50S ribosomal protein L9



• Molecule 32: 50S ribosomal protein L9



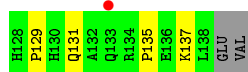
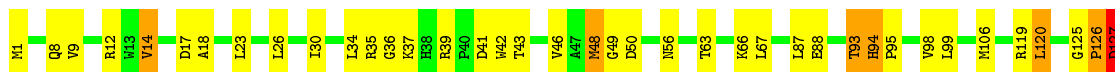
• Molecule 33: 50S ribosomal protein L13





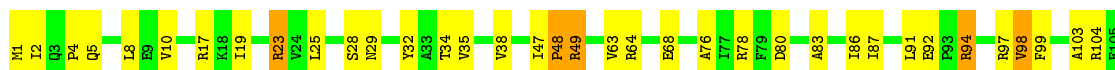
- Molecule 33: 50S ribosomal protein L13

Chain YN: 68% 26%



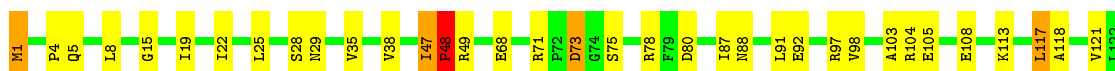
- Molecule 34: 50S ribosomal protein L14

Chain RO: 65% 30% 5%



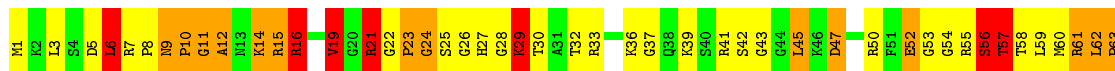
- Molecule 34: 50S ribosomal protein L14

Chain YO: 71% 25%



- Molecule 35: 50S ribosomal protein L15

Chain RP: 41% 38% 15% 7%



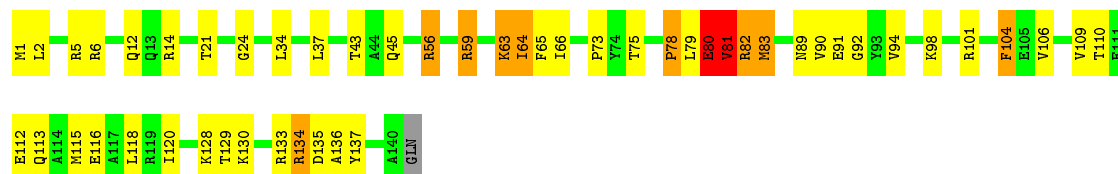
- Molecule 35: 50S ribosomal protein L15

Chain YP: 44% 36% 13% 7%

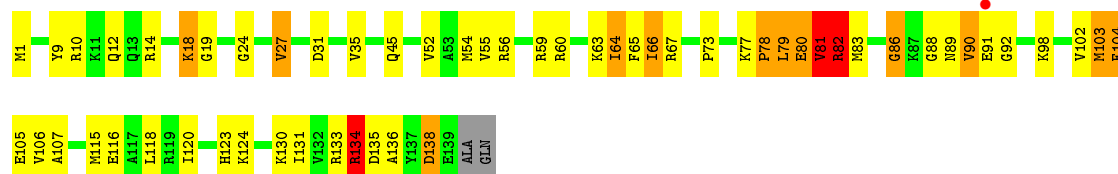




- Molecule 36: 50S ribosomal protein L16



- Molecule 36: 50S ribosomal protein L16



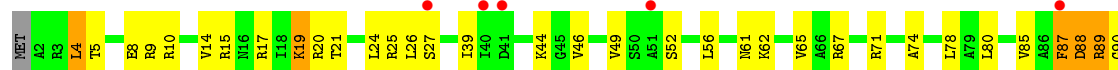
- Molecule 37: 50S ribosomal protein L17



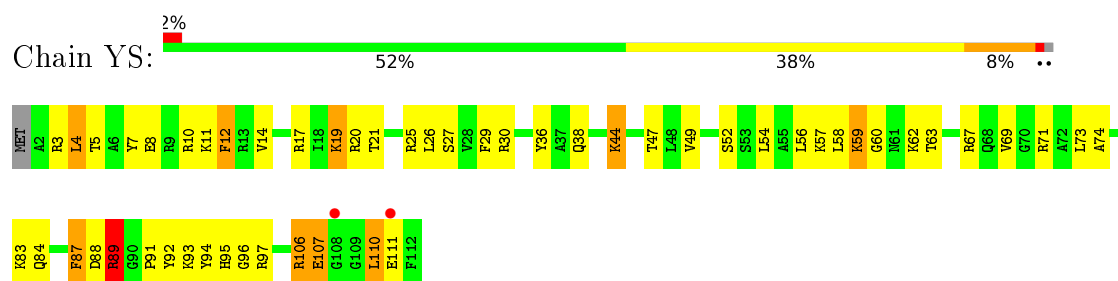
- Molecule 37: 50S ribosomal protein L17



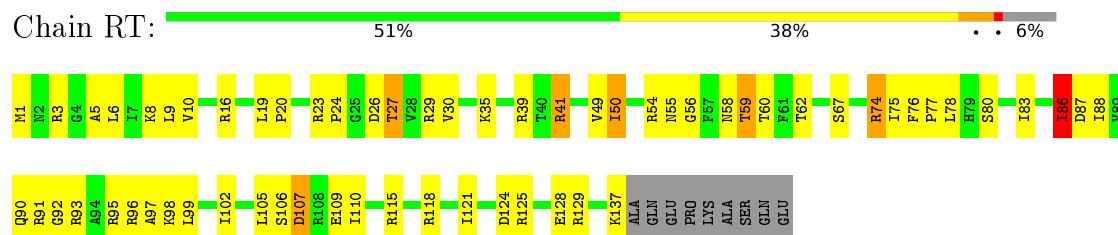
- Molecule 38: 50S ribosomal protein L18



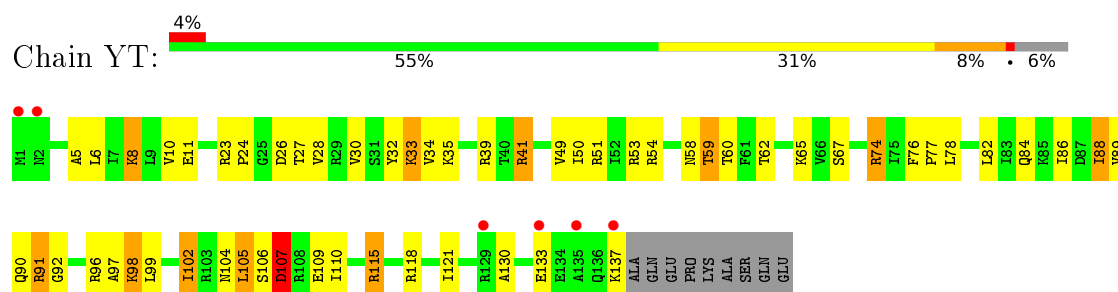
- Molecule 38: 50S ribosomal protein L18



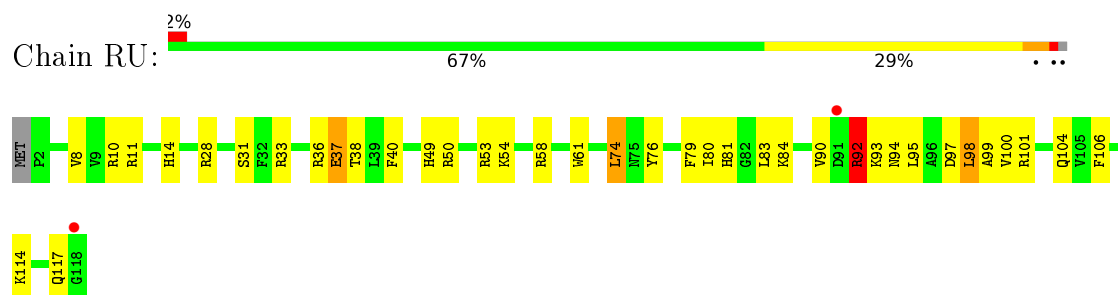
- Molecule 39: 50S ribosomal protein L19



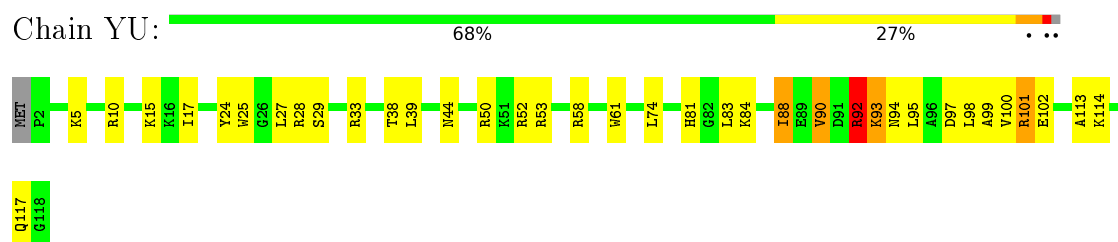
- Molecule 39: 50S ribosomal protein L19



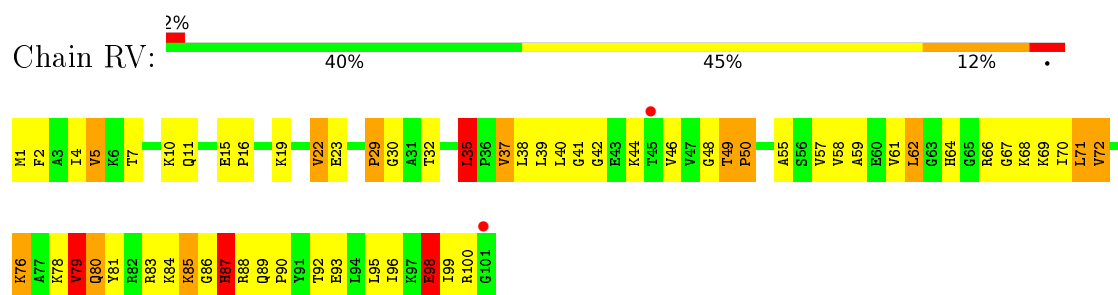
- Molecule 40: 50S ribosomal protein L20



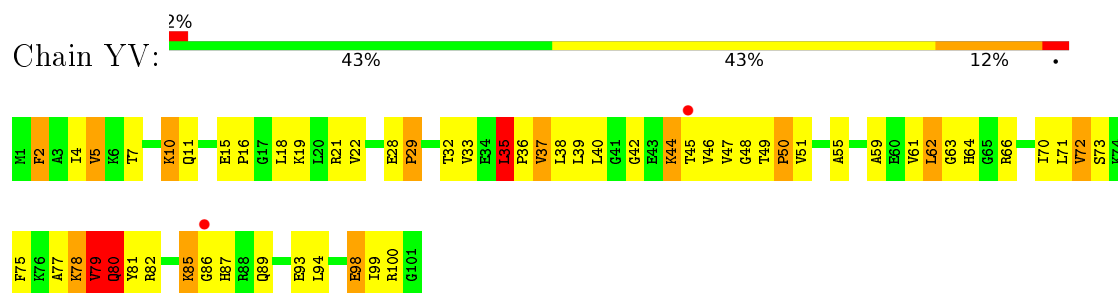
- Molecule 40: 50S ribosomal protein L20



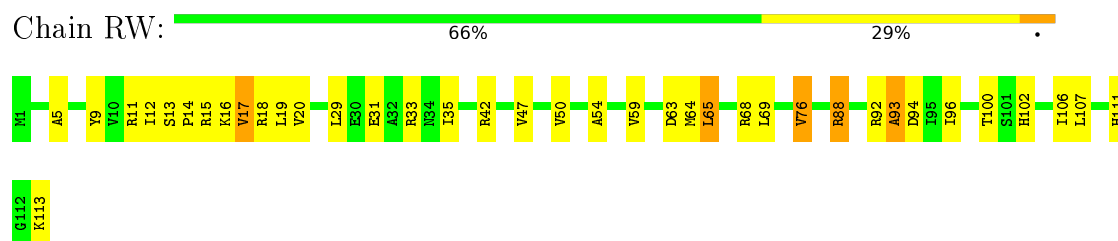
- Molecule 41: 50S ribosomal protein L21



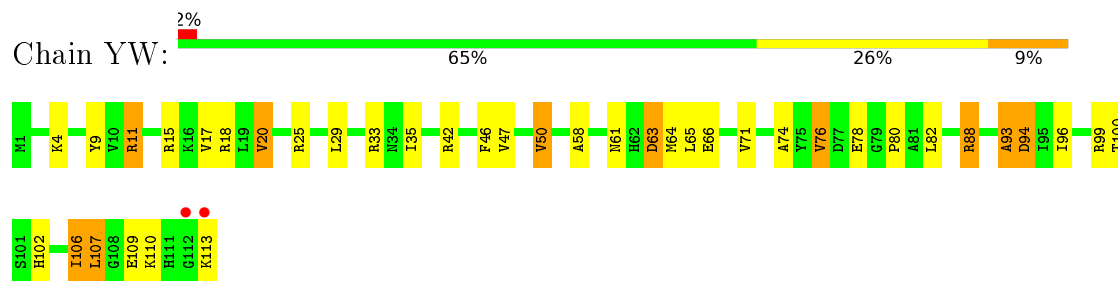
- Molecule 41: 50S ribosomal protein L21



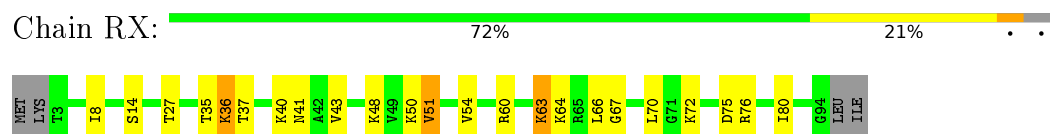
- Molecule 42: 50S ribosomal protein L22



- Molecule 42: 50S ribosomal protein L22

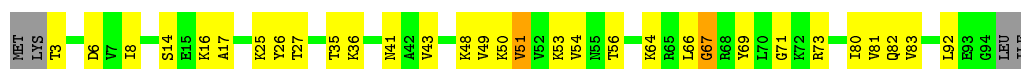


- Molecule 43: 50S ribosomal protein L23

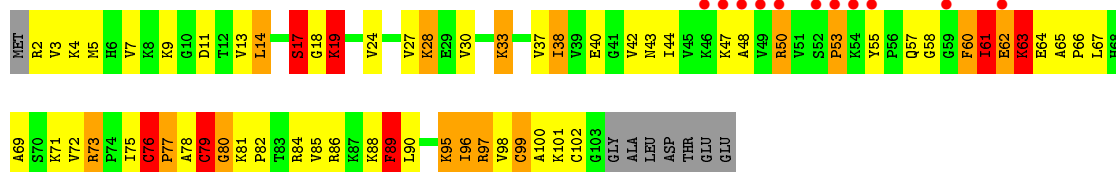


- Molecule 43: 50S ribosomal protein L23

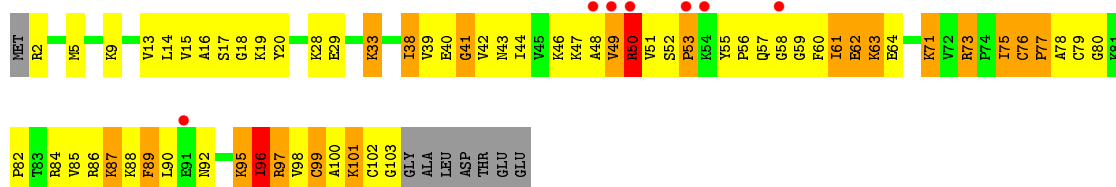




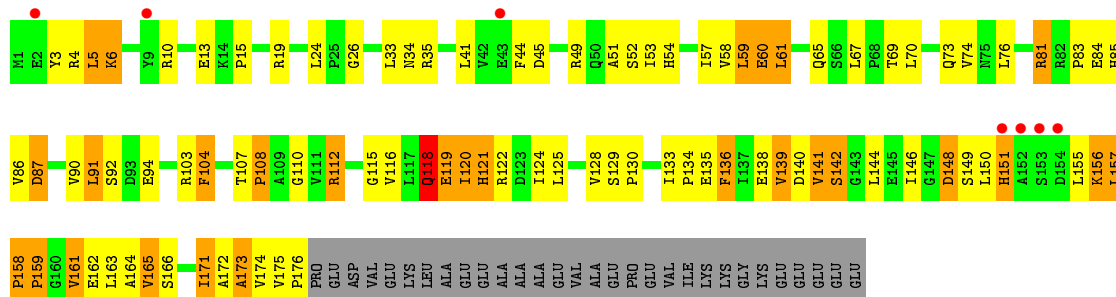
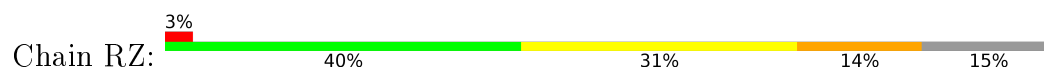
• Molecule 44: 50S ribosomal protein L24



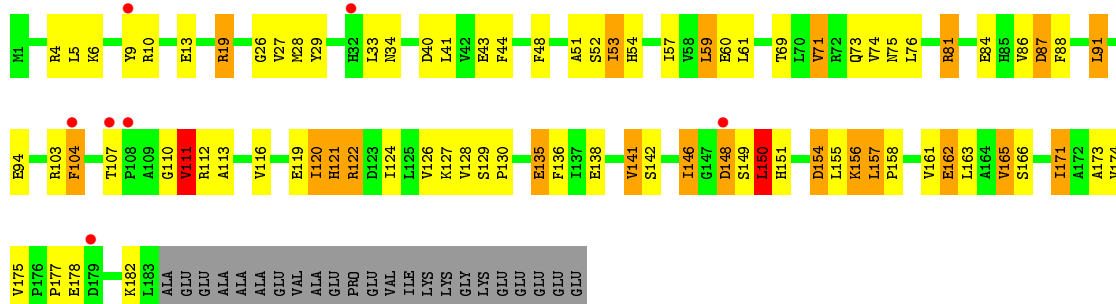
• Molecule 44: 50S ribosomal protein L24



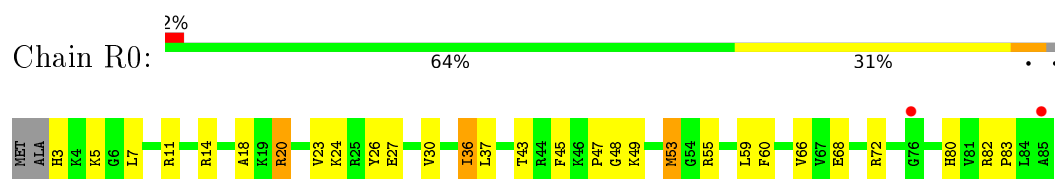
• Molecule 45: 50S ribosomal protein L25



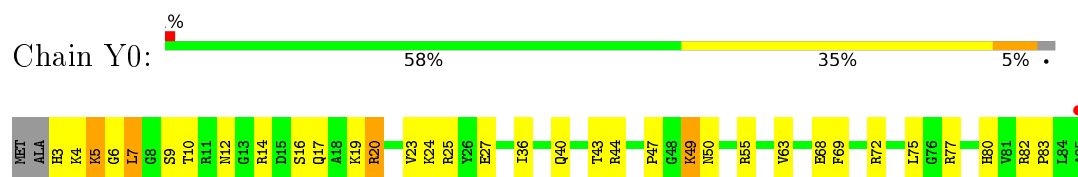
• Molecule 45: 50S ribosomal protein L25



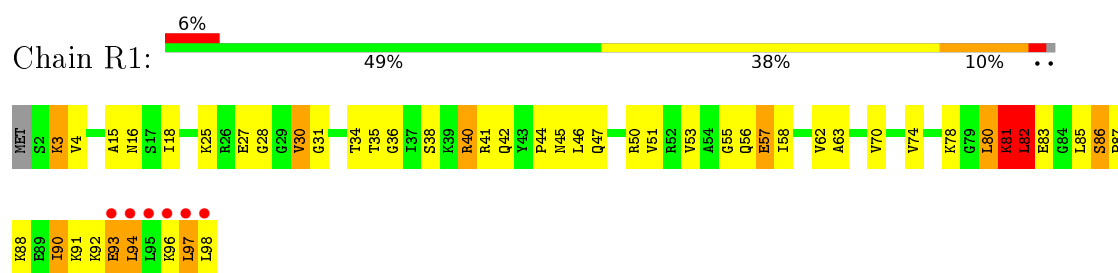
- Molecule 46: 50S ribosomal protein L27



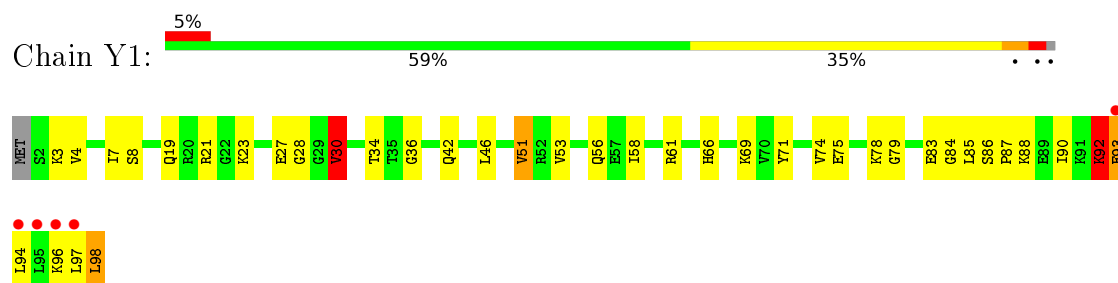
- Molecule 46: 50S ribosomal protein L27



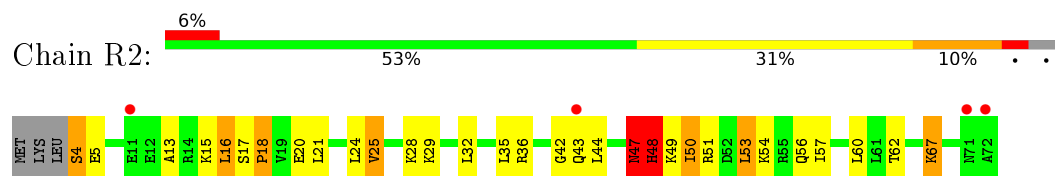
- Molecule 47: 50S ribosomal protein L28



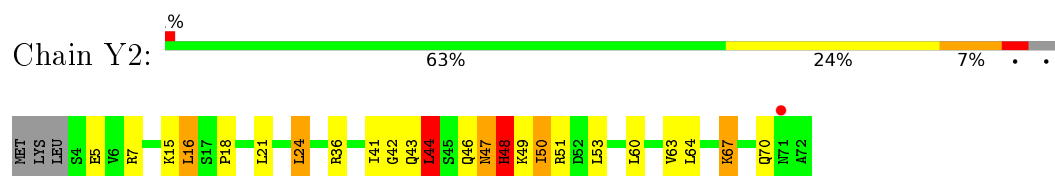
- Molecule 47: 50S ribosomal protein L28



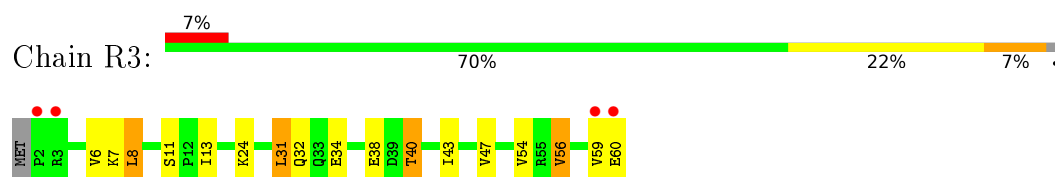
- Molecule 48: 50S ribosomal protein L29



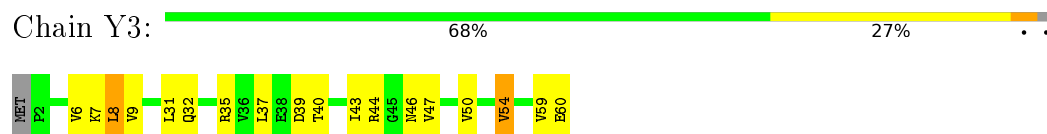
- Molecule 48: 50S ribosomal protein L29



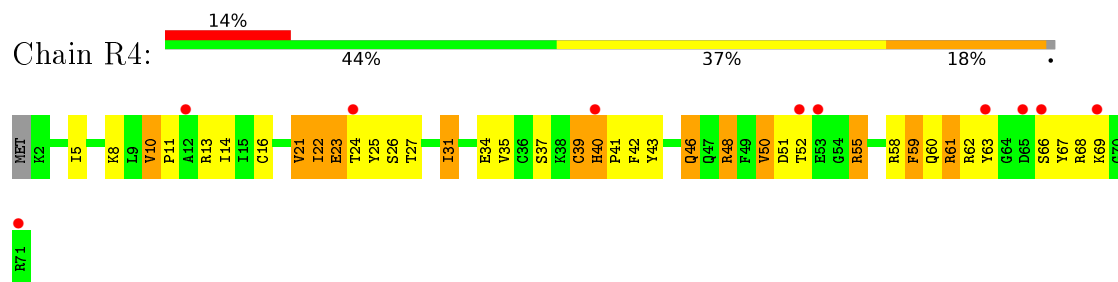
- Molecule 49: 50S ribosomal protein L30



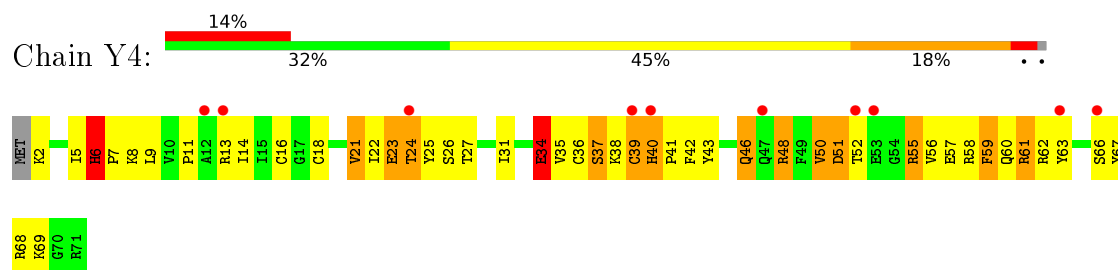
- Molecule 49: 50S ribosomal protein L30



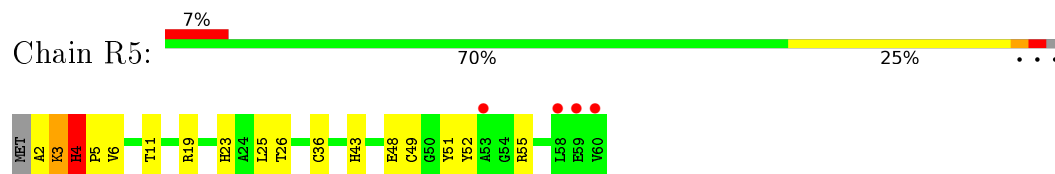
- Molecule 50: 50S ribosomal protein L31



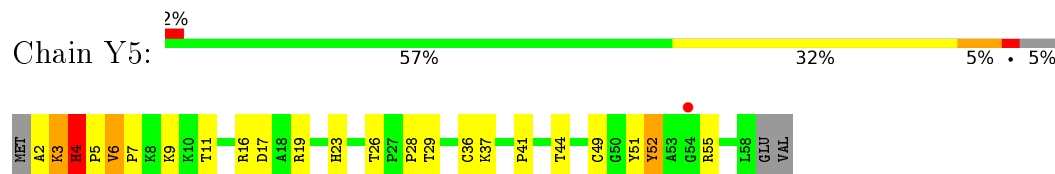
- Molecule 50: 50S ribosomal protein L31



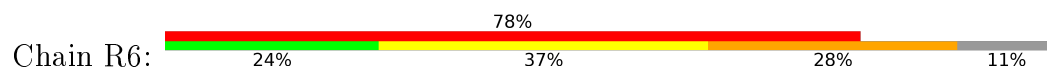
- Molecule 51: 50S ribosomal protein L32



- Molecule 51: 50S ribosomal protein L32

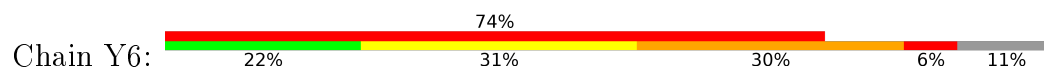


- Molecule 52: 50S ribosomal protein L33

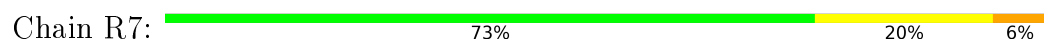




- Molecule 52: 50S ribosomal protein L33



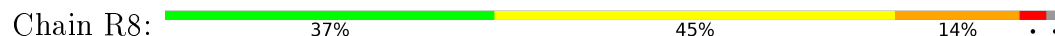
- Molecule 53: 50S ribosomal protein L34



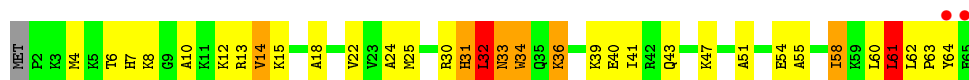
- Molecule 53: 50S ribosomal protein L34



- Molecule 54: 50S ribosomal protein L35



- Molecule 54: 50S ribosomal protein L35



- Molecule 55: 50S ribosomal protein L36



- Molecule 55: 50S ribosomal protein L36

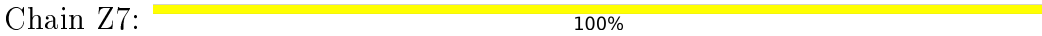




- Molecule 56: CC-puromycin



- Molecule 56: CC-puromycin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 3.57Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.198 , 0.234 0.200 , 0.236	Depositor DCC
R_{free} test set	30184 reflections (4.53%)	DCC
Wilson B-factor (Å ²)	86.5	Xtriage
Anisotropy	0.089	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 94.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	294410	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage'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.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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
50:Y4:6:HIS:HB2	50:Y4:7:PRO:CD	1.43	1.47
31:YH:9:ILE:CG2	31:YH:10:PRO:HA	1.39	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	15
2	XB	234/256 (91%)	189 (81%)	27 (12%)	18 (8%)	1	16
3	QC	204/239 (85%)	161 (79%)	27 (13%)	16 (8%)	1	16
3	XC	204/239 (85%)	160 (78%)	32 (16%)	12 (6%)	2	24
4	QD	206/209 (99%)	169 (82%)	26 (13%)	11 (5%)	2	27
4	XD	206/209 (99%)	168 (82%)	22 (11%)	16 (8%)	1	16
5	QE	152/162 (94%)	135 (89%)	12 (8%)	5 (3%)	5	41
5	XE	152/162 (94%)	137 (90%)	9 (6%)	6 (4%)	4	36
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%)	7	46
7	XG	153/156 (98%)	134 (88%)	15 (10%)	4 (3%)	7	46
8	QH	136/138 (99%)	126 (93%)	7 (5%)	3 (2%)	8	51
8	XH	136/138 (99%)	123 (90%)	10 (7%)	3 (2%)	8	51
9	QI	126/128 (98%)	94 (75%)	24 (19%)	8 (6%)	2	23
9	XI	126/128 (98%)	96 (76%)	23 (18%)	7 (6%)	2	26
10	QJ	97/105 (92%)	80 (82%)	13 (13%)	4 (4%)	3	34
10	XJ	97/105 (92%)	81 (84%)	11 (11%)	5 (5%)	2	27
11	QK	119/129 (92%)	102 (86%)	13 (11%)	4 (3%)	5	41
11	XK	119/129 (92%)	105 (88%)	10 (8%)	4 (3%)	5	41
12	QL	123/132 (93%)	99 (80%)	16 (13%)	8 (6%)	1	22
12	XL	123/132 (93%)	97 (79%)	18 (15%)	8 (6%)	1	22
13	QM	116/126 (92%)	88 (76%)	17 (15%)	11 (10%)	1	12
13	XM	116/126 (92%)	88 (76%)	17 (15%)	11 (10%)	1	12
14	QN	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	2	27
14	XN	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	2	27
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%)	19	66
17	XQ	98/105 (93%)	89 (91%)	7 (7%)	2 (2%)	9	53
18	QR	69/88 (78%)	61 (88%)	8 (12%)	0	100	100
18	XR	69/88 (78%)	62 (90%)	6 (9%)	1 (1%)	14	59
19	QS	80/93 (86%)	52 (65%)	18 (22%)	10 (12%)	0	8
19	XS	80/93 (86%)	52 (65%)	18 (22%)	10 (12%)	0	8
20	QT	97/106 (92%)	79 (81%)	15 (16%)	3 (3%)	5	43
20	XT	97/106 (92%)	80 (82%)	14 (14%)	3 (3%)	5	43
21	QU	23/25 (92%)	16 (70%)	6 (26%)	1 (4%)	3	33
21	XU	23/25 (92%)	18 (78%)	3 (13%)	2 (9%)	1	14
24	QY	90/118 (76%)	84 (93%)	5 (6%)	1 (1%)	17	64
24	XY	90/118 (76%)	80 (89%)	8 (9%)	2 (2%)	8	51
27	RD	270/276 (98%)	224 (83%)	38 (14%)	8 (3%)	5	44
27	YD	270/276 (98%)	228 (84%)	32 (12%)	10 (4%)	4	38
28	RE	203/206 (98%)	137 (68%)	38 (19%)	28 (14%)	0	6
28	YE	203/206 (98%)	133 (66%)	40 (20%)	30 (15%)	0	5
29	RF	206/210 (98%)	167 (81%)	26 (13%)	13 (6%)	2	23
29	YF	206/210 (98%)	168 (82%)	22 (11%)	16 (8%)	1	16
30	RG	179/182 (98%)	141 (79%)	26 (14%)	12 (7%)	1	21
30	YG	179/182 (98%)	146 (82%)	22 (12%)	11 (6%)	2	24
31	RH	168/180 (93%)	104 (62%)	37 (22%)	27 (16%)	0	4
31	YH	168/180 (93%)	98 (58%)	42 (25%)	28 (17%)	0	4
32	RI	144/148 (97%)	109 (76%)	28 (19%)	7 (5%)	3	29
32	YI	144/148 (97%)	116 (81%)	24 (17%)	4 (3%)	6	45
33	RN	136/140 (97%)	116 (85%)	13 (10%)	7 (5%)	2	28
33	YN	136/140 (97%)	110 (81%)	19 (14%)	7 (5%)	2	28
34	RO	120/122 (98%)	111 (92%)	8 (7%)	1 (1%)	24	69
34	YO	120/122 (98%)	109 (91%)	10 (8%)	1 (1%)	24	69
35	RP	148/150 (99%)	97 (66%)	23 (16%)	28 (19%)	0	3
35	YP	148/150 (99%)	102 (69%)	22 (15%)	24 (16%)	0	4
36	RQ	138/141 (98%)	110 (80%)	17 (12%)	11 (8%)	1	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	YQ	137/141 (97%)	111 (81%)	15 (11%)	11 (8%)	1	16
37	RR	115/118 (98%)	107 (93%)	4 (4%)	4 (4%)	4	40
37	YR	115/118 (98%)	109 (95%)	3 (3%)	3 (3%)	7	46
38	RS	109/112 (97%)	84 (77%)	17 (16%)	8 (7%)	1	18
38	YS	109/112 (97%)	85 (78%)	13 (12%)	11 (10%)	1	11
39	RT	135/146 (92%)	109 (81%)	24 (18%)	2 (2%)	13	57
39	YT	135/146 (92%)	113 (84%)	17 (13%)	5 (4%)	4	38
40	RU	115/118 (98%)	107 (93%)	6 (5%)	2 (2%)	11	55
40	YU	115/118 (98%)	103 (90%)	9 (8%)	3 (3%)	7	46
41	RV	99/101 (98%)	72 (73%)	12 (12%)	15 (15%)	0	5
41	YV	99/101 (98%)	71 (72%)	15 (15%)	13 (13%)	0	7
42	RW	111/113 (98%)	107 (96%)	1 (1%)	3 (3%)	6	46
42	YW	111/113 (98%)	104 (94%)	3 (3%)	4 (4%)	4	39
43	RX	90/96 (94%)	76 (84%)	12 (13%)	2 (2%)	8	51
43	YX	90/96 (94%)	77 (86%)	11 (12%)	2 (2%)	8	51
44	RY	100/110 (91%)	56 (56%)	28 (28%)	16 (16%)	0	4
44	YY	100/110 (91%)	57 (57%)	27 (27%)	16 (16%)	0	4
45	RZ	174/206 (84%)	116 (67%)	33 (19%)	25 (14%)	0	5
45	YZ	181/206 (88%)	122 (67%)	42 (23%)	17 (9%)	1	12
46	R0	81/85 (95%)	73 (90%)	5 (6%)	3 (4%)	4	38
46	Y0	81/85 (95%)	67 (83%)	11 (14%)	3 (4%)	4	38
47	R1	95/98 (97%)	71 (75%)	12 (13%)	12 (13%)	0	7
47	Y1	95/98 (97%)	76 (80%)	13 (14%)	6 (6%)	2	23
48	R2	67/72 (93%)	54 (81%)	8 (12%)	5 (8%)	1	17
48	Y2	67/72 (93%)	56 (84%)	5 (8%)	6 (9%)	1	13
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%)	4	40
51	Y5	55/60 (92%)	48 (87%)	4 (7%)	3 (6%)	2	26

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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	9
54	Y8	62/65 (95%)	49 (79%)	6 (10%)	7 (11%)	0	9
55	R9	35/37 (95%)	34 (97%)	0	1 (3%)	6	44
55	Y9	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
All	All	11649/12360 (94%)	9390 (81%)	1489 (13%)	770 (7%)	1	22

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 ⓘ

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	24
2	XB	204/220 (93%)	176 (86%)	28 (14%)	4	28
3	QC	160/188 (85%)	142 (89%)	18 (11%)	7	37
3	XC	160/188 (85%)	141 (88%)	19 (12%)	6	34
4	QD	180/181 (99%)	157 (87%)	23 (13%)	5	31
4	XD	180/181 (99%)	156 (87%)	24 (13%)	5	30
5	QE	119/123 (97%)	101 (85%)	18 (15%)	3	24
5	XE	119/123 (97%)	106 (89%)	13 (11%)	8	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	QF	90/90 (100%)	85 (94%)	5 (6%)	26	68
6	XF	90/90 (100%)	77 (86%)	13 (14%)	4	26
7	QG	126/127 (99%)	112 (89%)	14 (11%)	8	38
7	XG	126/127 (99%)	109 (86%)	17 (14%)	5	29
8	QH	119/119 (100%)	109 (92%)	10 (8%)	14	52
8	XH	119/119 (100%)	106 (89%)	13 (11%)	8	39
9	QI	99/99 (100%)	79 (80%)	20 (20%)	1	11
9	XI	99/99 (100%)	80 (81%)	19 (19%)	2	12
10	QJ	89/92 (97%)	77 (86%)	12 (14%)	5	29
10	XJ	89/92 (97%)	75 (84%)	14 (16%)	3	22
11	QK	92/99 (93%)	82 (89%)	10 (11%)	8	39
11	XK	92/99 (93%)	83 (90%)	9 (10%)	10	44
12	QL	104/109 (95%)	89 (86%)	15 (14%)	4	26
12	XL	104/109 (95%)	87 (84%)	17 (16%)	3	20
13	QM	94/101 (93%)	80 (85%)	14 (15%)	4	25
13	XM	94/101 (93%)	82 (87%)	12 (13%)	5	31
14	QN	49/50 (98%)	48 (98%)	1 (2%)	63	87
14	XN	49/50 (98%)	44 (90%)	5 (10%)	9	42
15	QO	79/80 (99%)	74 (94%)	5 (6%)	22	64
15	XO	79/80 (99%)	74 (94%)	5 (6%)	22	64
16	QP	72/74 (97%)	64 (89%)	8 (11%)	8	38
16	XP	72/74 (97%)	64 (89%)	8 (11%)	8	38
17	QQ	95/97 (98%)	90 (95%)	5 (5%)	28	69
17	XQ	95/97 (98%)	88 (93%)	7 (7%)	17	57
18	QR	62/77 (80%)	56 (90%)	6 (10%)	10	45
18	XR	62/77 (80%)	54 (87%)	8 (13%)	5	31
19	QS	71/80 (89%)	54 (76%)	17 (24%)	1	6
19	XS	71/80 (89%)	58 (82%)	13 (18%)	2	14
20	QT	76/82 (93%)	62 (82%)	14 (18%)	2	14
20	XT	76/82 (93%)	66 (87%)	10 (13%)	5	30
21	QU	20/20 (100%)	18 (90%)	2 (10%)	9	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	XU	20/20 (100%)	18 (90%)	2 (10%)	9	43
24	QY	79/103 (77%)	73 (92%)	6 (8%)	16	56
24	XY	79/103 (77%)	74 (94%)	5 (6%)	22	64
27	RD	214/218 (98%)	178 (83%)	36 (17%)	2	18
27	YD	214/218 (98%)	179 (84%)	35 (16%)	3	20
28	RE	165/166 (99%)	137 (83%)	28 (17%)	2	18
28	YE	165/166 (99%)	138 (84%)	27 (16%)	3	20
29	RF	165/166 (99%)	139 (84%)	26 (16%)	3	22
29	YF	165/166 (99%)	141 (86%)	24 (14%)	4	26
30	RG	155/156 (99%)	147 (95%)	8 (5%)	29	69
30	YG	155/156 (99%)	138 (89%)	17 (11%)	8	39
31	RH	142/148 (96%)	123 (87%)	19 (13%)	5	29
31	YH	142/148 (96%)	115 (81%)	27 (19%)	2	12
32	RI	122/124 (98%)	98 (80%)	24 (20%)	1	12
32	YI	122/124 (98%)	99 (81%)	23 (19%)	2	13
33	RN	117/119 (98%)	107 (92%)	10 (8%)	13	52
33	YN	117/119 (98%)	104 (89%)	13 (11%)	8	38
34	RO	100/100 (100%)	91 (91%)	9 (9%)	12	49
34	YO	100/100 (100%)	90 (90%)	10 (10%)	9	43
35	RP	116/116 (100%)	80 (69%)	36 (31%)	0	3
35	YP	116/116 (100%)	84 (72%)	32 (28%)	0	4
36	RQ	110/111 (99%)	93 (84%)	17 (16%)	3	23
36	YQ	110/111 (99%)	93 (84%)	17 (16%)	3	23
37	RR	100/101 (99%)	82 (82%)	18 (18%)	2	15
37	YR	100/101 (99%)	87 (87%)	13 (13%)	5	30
38	RS	87/88 (99%)	80 (92%)	7 (8%)	15	54
38	YS	87/88 (99%)	73 (84%)	14 (16%)	3	21
39	RT	120/127 (94%)	100 (83%)	20 (17%)	3	19
39	YT	120/127 (94%)	98 (82%)	22 (18%)	2	14
40	RU	93/94 (99%)	85 (91%)	8 (9%)	13	51
40	YU	93/94 (99%)	85 (91%)	8 (9%)	13	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	RV	82/82 (100%)	66 (80%)	16 (20%)	2	12
41	YV	82/82 (100%)	63 (77%)	19 (23%)	1	7
42	RW	92/92 (100%)	82 (89%)	10 (11%)	8	39
42	YW	92/92 (100%)	79 (86%)	13 (14%)	4	28
43	RX	74/78 (95%)	65 (88%)	9 (12%)	6	32
43	YX	74/78 (95%)	68 (92%)	6 (8%)	15	54
44	RY	85/91 (93%)	63 (74%)	22 (26%)	0	5
44	YY	85/91 (93%)	61 (72%)	24 (28%)	0	4
45	RZ	155/179 (87%)	129 (83%)	26 (17%)	2	18
45	YZ	162/179 (90%)	134 (83%)	28 (17%)	2	17
46	R0	66/67 (98%)	62 (94%)	4 (6%)	23	65
46	Y0	66/67 (98%)	58 (88%)	8 (12%)	6	33
47	R1	82/83 (99%)	68 (83%)	14 (17%)	2	18
47	Y1	82/83 (99%)	72 (88%)	10 (12%)	6	32
48	R2	64/67 (96%)	52 (81%)	12 (19%)	2	13
48	Y2	64/67 (96%)	57 (89%)	7 (11%)	8	39
49	R3	51/52 (98%)	44 (86%)	7 (14%)	4	28
49	Y3	51/52 (98%)	47 (92%)	4 (8%)	16	55
50	R4	62/63 (98%)	47 (76%)	15 (24%)	1	6
50	Y4	62/63 (98%)	44 (71%)	18 (29%)	0	4
51	R5	51/52 (98%)	41 (80%)	10 (20%)	1	12
51	Y5	49/52 (94%)	42 (86%)	7 (14%)	4	27
52	R6	47/52 (90%)	32 (68%)	15 (32%)	0	3
52	Y6	47/52 (90%)	30 (64%)	17 (36%)	0	1
53	R7	42/42 (100%)	35 (83%)	7 (17%)	3	19
53	Y7	42/42 (100%)	35 (83%)	7 (17%)	3	19
54	R8	54/55 (98%)	43 (80%)	11 (20%)	1	11
54	Y8	54/55 (98%)	44 (82%)	10 (18%)	2	13
55	R9	34/34 (100%)	32 (94%)	2 (6%)	24	66
55	Y9	33/34 (97%)	33 (100%)	0	100	100
All	All	9856/10268 (96%)	8435 (86%)	1421 (14%)	4	26

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

Mol	Chain	Res	Type
50	R4	16	CYS
6	XF	85	VAL
45	YZ	71	VAL
51	R5	36	CYS
2	XB	185	ILE

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

Mol	Chain	Res	Type
45	RZ	118	GLN
3	XC	108	ASN
37	YR	3	HIS
40	RU	81	HIS
7	XG	97	GLN

5.3.3 RNA ⓘ

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
25	RA	2211	G
1	XA	92	G
25	YA	2211	G
25	RA	2405	G
25	RA	2776	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	QX	19	23	18,25,26	1.05	1 (5%)	18,36,39	2.14	3 (16%)
23	A2M	QX	20	23	18,25,26	1.23	1 (5%)	18,36,39	1.65	1 (5%)
23	A2M	QX	21	1,23	18,25,26	1.20	1 (5%)	18,36,39	2.04	5 (27%)
23	A2M	XX	19	23	18,25,26	1.00	1 (5%)	18,36,39	2.73	7 (38%)
23	A2M	XX	20	23	18,25,26	1.00	1 (5%)	18,36,39	1.77	1 (5%)
23	A2M	XX	21	23	18,25,26	1.09	2 (11%)	18,36,39	2.14	5 (27%)
56	PPU	Z6	76	25,56	31,40,41	0.86	1 (3%)	32,57,60	1.64	4 (12%)
56	PPU	Z7	76	25,56	31,40,41	0.88	1 (3%)	32,57,60	1.61	4 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	A2M	QX	19	23	-	0/5/27/28	0/3/3/3
23	A2M	QX	20	23	-	0/5/27/28	0/3/3/3
23	A2M	QX	21	1,23	-	0/5/27/28	0/3/3/3
23	A2M	XX	19	23	-	0/5/27/28	0/3/3/3
23	A2M	XX	20	23	-	0/5/27/28	0/3/3/3

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

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	XX	21	A2M	O4'-C1'	2.30	1.44	1.41
56	Z6	76	PPU	C5-C4	2.57	1.46	1.40
56	Z7	76	PPU	C5-C4	2.76	1.46	1.40
23	XX	20	A2M	C5-C4	2.87	1.47	1.40
23	XX	21	A2M	C5-C4	2.95	1.47	1.40

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	XX	19	A2M	N3-C2-N1	-8.15	122.47	128.87
23	QX	19	A2M	N3-C2-N1	-7.61	122.89	128.87
23	XX	21	A2M	N3-C2-N1	-6.80	123.53	128.87
23	QX	21	A2M	N3-C2-N1	-6.50	123.77	128.87
56	Z6	76	PPU	N3-C2-N1	-6.48	123.78	128.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	QX	19	A2M	1	0
23	QX	21	A2M	3	0
23	XX	19	A2M	2	0
23	XX	20	A2M	1	0
23	XX	21	A2M	1	0
56	Z6	76	PPU	5	0
56	Z7	76	PPU	12	0

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	QA	1511/1522 (99%)	0.09	31 (2%) 67 52	52, 94, 194, 353	0
1	XA	1508/1522 (99%)	0.03	35 (2%) 64 48	41, 84, 179, 401	0
2	QB	236/256 (92%)	0.21	10 (4%) 40 28	76, 141, 220, 278	0
2	XB	236/256 (92%)	-0.03	1 (0%) 93 88	56, 119, 205, 243	0
3	QC	206/239 (86%)	0.30	5 (2%) 62 47	81, 126, 222, 383	0
3	XC	206/239 (86%)	0.08	1 (0%) 91 86	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%) 42 29	75, 119, 160, 179	0
6	XF	101/101 (100%)	-0.35	1 (0%) 84 73	49, 83, 120, 199	0
7	QG	155/156 (99%)	0.40	13 (8%) 14 10	83, 138, 199, 270	0
7	XG	155/156 (99%)	0.20	10 (6%) 22 14	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%)	0.84	18 (14%) 4 3	87, 160, 242, 319	0
9	XI	128/128 (100%)	0.09	2 (1%) 74 61	66, 119, 199, 272	0
10	QJ	99/105 (94%)	0.67	8 (8%) 15 10	94, 155, 255, 330	0
10	XJ	99/105 (94%)	0.56	8 (8%) 15 10	73, 136, 199, 337	0
11	QK	121/129 (93%)	0.36	7 (5%) 26 18	65, 110, 191, 294	0
11	XK	121/129 (93%)	-0.05	4 (3%) 50 36	50, 85, 156, 284	0
12	QL	125/132 (94%)	0.01	2 (1%) 74 61	52, 78, 121, 306	0
12	XL	125/132 (94%)	-0.08	2 (1%) 74 61	46, 73, 119, 225	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	QM	118/126 (93%)	0.31	6 (5%) 32 22	92, 139, 223, 308	0
13	XM	118/126 (93%)	0.18	2 (1%) 73 59	61, 120, 172, 350	0
14	QN	60/61 (98%)	0.08	2 (3%) 50 36	82, 124, 170, 221	0
14	XN	60/61 (98%)	-0.18	0 100 100	72, 101, 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%) 82 70	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%)	0.34	1 (1%) 81 69	58, 90, 134, 294	0
17	QQ	100/105 (95%)	-0.08	1 (1%) 84 73	51, 91, 126, 136	0
17	XQ	100/105 (95%)	-0.06	0 100 100	51, 83, 119, 217	0
18	QR	71/88 (80%)	0.28	2 (2%) 56 42	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	8 (9%) 10 7	96, 150, 245, 348	0
19	XS	82/93 (88%)	0.46	3 (3%) 45 32	72, 128, 212, 281	0
20	QT	99/106 (93%)	0.23	6 (6%) 25 16	55, 97, 153, 209	0
20	XT	99/106 (93%)	0.35	4 (4%) 42 29	63, 106, 171, 235	0
21	QU	25/25 (100%)	1.21	4 (16%) 3 2	104, 143, 192, 230	0
21	XU	25/25 (100%)	1.02	5 (20%) 1 1	91, 117, 148, 176	0
22	QV	77/77 (100%)	0.18	3 (3%) 43 31	45, 95, 141, 191	0
22	XV	77/77 (100%)	0.03	0 100 100	41, 86, 120, 188	0
23	QX	17/25 (68%)	3.26	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%) 50 36	59, 116, 149, 189	0
24	XY	92/118 (77%)	0.81	5 (5%) 29 20	72, 113, 143, 177	0
25	RA	2891/2916 (99%)	0.26	163 (5%) 28 19	36, 68, 244, 472	0
25	YA	2875/2916 (98%)	0.29	161 (5%) 28 19	32, 61, 254, 518	0
26	RB	122/124 (98%)	-0.06	2 (1%) 74 61	72, 115, 150, 204	0
26	YB	122/124 (98%)	-0.05	1 (0%) 87 78	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%)	0.08	6 (2%) 55 40	42, 84, 157, 368	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	YE	205/206 (99%)	0.13	6 (2%) 55 40	31, 73, 154, 409	0
29	RF	208/210 (99%)	-0.26	6 (2%) 55 40	27, 58, 160, 285	0
29	YF	208/210 (99%)	-0.13	7 (3%) 49 35	32, 69, 206, 333	0
30	RG	181/182 (99%)	0.07	2 (1%) 82 70	68, 120, 176, 225	0
30	YG	181/182 (99%)	-0.01	3 (1%) 73 59	65, 105, 154, 215	0
31	RH	170/180 (94%)	0.94	27 (15%) 3 2	82, 161, 292, 396	0
31	YH	170/180 (94%)	0.69	20 (11%) 6 5	66, 132, 250, 421	0
32	RI	146/148 (98%)	0.32	1 (0%) 89 81	64, 112, 168, 286	0
32	YI	146/148 (98%)	0.11	3 (2%) 67 52	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%) 89 81	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%)	0.10	3 (2%) 68 54	29, 79, 147, 252	0
35	YP	150/150 (100%)	0.11	4 (2%) 58 43	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%) 89 81	39, 74, 127, 231	0
37	RR	117/118 (99%)	-0.05	1 (0%) 85 75	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%) 23 15	65, 117, 178, 256	0
38	YS	111/112 (99%)	0.03	2 (1%) 71 58	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%) 38 27	45, 74, 201, 347	0
40	RU	117/118 (99%)	-0.23	2 (1%) 73 59	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%) 68 54	37, 84, 144, 284	0
41	YV	101/101 (100%)	-0.08	2 (1%) 68 54	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%) 71 58	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%)	-0.28	0 100 100	32, 65, 113, 139	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
44	RY	102/110 (92%)	0.75	11 (10%) 8 6	50, 84, 222, 392	0
44	YY	102/110 (92%)	0.56	7 (6%) 20 13	52, 94, 210, 487	0
45	RZ	176/206 (85%)	0.33	7 (3%) 42 29	63, 117, 216, 401	0
45	YZ	183/206 (88%)	0.19	7 (3%) 44 32	64, 113, 192, 282	0
46	R0	83/85 (97%)	0.06	2 (2%) 62 47	50, 75, 111, 253	0
46	Y0	83/85 (97%)	0.11	1 (1%) 81 69	39, 69, 98, 204	0
47	R1	97/98 (98%)	0.30	6 (6%) 24 16	41, 76, 203, 321	0
47	Y1	97/98 (98%)	0.18	5 (5%) 31 22	30, 61, 190, 315	0
48	R2	69/72 (95%)	0.01	4 (5%) 26 18	49, 99, 191, 258	0
48	Y2	69/72 (95%)	-0.22	1 (1%) 78 65	41, 78, 123, 222	0
49	R3	59/60 (98%)	0.65	4 (6%) 20 13	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%) 4 3	99, 196, 456, 558	0
50	Y4	70/71 (98%)	0.71	10 (14%) 4 3	94, 171, 356, 481	0
51	R5	59/60 (98%)	0.06	4 (6%) 20 13	40, 75, 185, 238	0
51	Y5	57/60 (95%)	-0.13	1 (1%) 71 58	24, 70, 159, 234	0
52	R6	48/54 (88%)	3.89	42 (87%) 0 0	126, 181, 242, 300	0
52	Y6	48/54 (88%)	3.84	40 (83%) 0 0	119, 172, 254, 281	0
53	R7	49/49 (100%)	-0.11	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%)	-0.03	2 (3%) 52 38	31, 62, 118, 203	0
55	R9	37/37 (100%)	1.50	12 (32%) 1 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%)	0.65	0 100 100	62, 62, 62, 63	0
All	All	21070/21694 (97%)	0.17	880 (4%) 40 28	19, 85, 199, 558	0

The worst 5 of 880 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
25	YA	2114	A	20.7
25	YA	2110	G	16.1

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Mol	Chain	Res	Type	RSRZ
25	RA	2139	C	15.5
25	YA	2138	C	14.5
25	YA	2165	G	14.4

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
23	A2M	QX	19	23/24	0.93	0.26	-	111,115,115,115	0
23	A2M	XX	20	23/24	0.91	0.31	-	105,105,111,111	0
23	A2M	XX	21	23/24	0.76	0.38	-	111,165,165,165	0
23	A2M	XX	19	23/24	0.91	0.27	-	96,96,111,111	0
56	PPU	Z7	76	37/38	0.93	0.31	-	61,61,61,61	0
23	A2M	QX	21	23/24	0.79	0.40	-	111,168,168,168	0
56	PPU	Z6	76	37/38	0.96	0.24	-	41,47,54,58	0
23	A2M	QX	20	23/24	0.90	0.28	-	111,117,117,117	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
57	MG	YA	3278	1/1	0.80	1.00	68.50	33,33,33,33	0
57	MG	QA	1682	1/1	0.85	0.94	55.38	39,39,39,39	0
57	MG	YA	3399	1/1	0.50	0.65	50.45	73,73,73,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	XA	1667	1/1	0.91	0.81	47.10	27,27,27,27	0
57	MG	YA	3237	1/1	0.75	0.43	45.66	26,26,26,26	0
57	MG	YA	3167	1/1	0.75	0.96	45.39	49,49,49,49	0
57	MG	RA	3171	1/1	0.92	0.79	44.14	38,38,38,38	0
57	MG	QA	1612	1/1	0.83	0.80	38.88	37,37,37,37	0
57	MG	XA	1652	1/1	0.76	0.91	36.49	41,41,41,41	0
57	MG	YA	3334	1/1	0.98	0.60	34.77	24,24,24,24	0
57	MG	RA	3276	1/1	0.84	1.05	33.21	65,65,65,65	0
57	MG	YA	3080	1/1	0.97	0.50	32.65	2,2,2,2	0
57	MG	YA	3209	1/1	0.89	0.51	32.38	19,19,19,19	0
57	MG	YA	3091	1/1	0.85	0.68	32.35	26,26,26,26	0
57	MG	YA	3360	1/1	0.83	0.43	29.03	41,41,41,41	0
57	MG	YA	3077	1/1	0.97	0.49	28.51	8,8,8,8	0
57	MG	YA	3134	1/1	0.84	0.37	27.65	37,37,37,37	0
57	MG	RA	3149	1/1	0.94	0.62	25.76	1,1,1,1	0
57	MG	YA	3053	1/1	0.97	0.68	25.49	5,5,5,5	0
57	MG	RA	3080	1/1	0.98	0.44	24.99	4,4,4,4	0
57	MG	RA	3245	1/1	0.93	0.50	24.97	30,30,30,30	0
57	MG	YA	3306	1/1	0.72	0.67	24.89	54,54,54,54	0
57	MG	YA	3105	1/1	0.87	0.57	24.58	45,45,45,45	0
57	MG	YA	3226	1/1	0.41	0.47	24.01	55,55,55,55	0
57	MG	YA	3170	1/1	0.86	0.54	23.97	7,7,7,7	0
57	MG	RA	3369	1/1	0.93	0.70	23.64	46,46,46,46	0
57	MG	YA	3148	1/1	0.93	0.77	23.56	9,9,9,9	0
57	MG	YA	3044	1/1	0.97	0.44	22.90	2,2,2,2	0
57	MG	YA	3219	1/1	0.92	0.40	22.88	27,27,27,27	0
57	MG	XA	1618	1/1	0.97	0.62	22.61	23,23,23,23	0
57	MG	XA	1659	1/1	0.96	0.69	22.18	22,22,22,22	0
57	MG	RA	3167	1/1	0.69	0.36	22.04	25,25,25,25	0
57	MG	YA	3047	1/1	0.97	0.59	21.89	32,32,32,32	0
57	MG	RA	3102	1/1	0.70	0.52	21.74	56,56,56,56	0
57	MG	RA	3428	1/1	0.76	0.46	20.90	41,41,41,41	0
57	MG	YA	3025	1/1	0.96	0.55	20.15	25,25,25,25	0
57	MG	YA	3371	1/1	0.89	0.46	20.02	57,57,57,57	0
57	MG	QA	1636	1/1	0.88	0.67	19.67	47,47,47,47	0
57	MG	RA	3209	1/1	0.92	0.50	19.26	34,34,34,34	0
57	MG	YA	3191	1/1	0.75	0.59	18.99	28,28,28,28	0
57	MG	YA	3404	1/1	0.81	0.82	18.59	54,54,54,54	0
57	MG	RA	3240	1/1	0.89	0.43	18.53	56,56,56,56	0
57	MG	RA	3331	1/1	0.90	0.34	18.47	59,59,59,59	0
57	MG	YA	3337	1/1	0.94	0.41	18.40	4,4,4,4	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	XA	1611	1/1	0.92	0.69	18.24	36,36,36,36	0
57	MG	QA	1683	1/1	0.80	0.86	18.00	42,42,42,42	0
57	MG	YA	3220	1/1	0.85	0.57	17.94	39,39,39,39	0
57	MG	RA	3173	1/1	0.65	0.47	17.65	50,50,50,50	0
57	MG	RA	3234	1/1	0.79	0.50	17.49	36,36,36,36	0
57	MG	YA	3294	1/1	0.85	0.52	17.25	37,37,37,37	0
57	MG	RA	3223	1/1	0.81	0.74	17.13	36,36,36,36	0
57	MG	RA	3395	1/1	0.91	0.54	16.80	46,46,46,46	0
57	MG	YA	3304	1/1	0.94	0.46	16.77	27,27,27,27	0
57	MG	YA	3358	1/1	0.87	0.67	16.68	25,25,25,25	0
57	MG	YA	3022	1/1	0.90	0.52	16.63	54,54,54,54	0
57	MG	RA	3174	1/1	0.96	0.54	16.53	1,1,1,1	0
57	MG	YA	3011	1/1	0.99	0.61	16.30	3,3,3,3	0
57	MG	RA	3021	1/1	0.97	0.47	16.23	25,25,25,25	0
57	MG	YA	3253	1/1	0.86	0.59	15.95	25,25,25,25	0
57	MG	QA	1670	1/1	0.91	0.43	15.93	53,53,53,53	0
57	MG	RA	3011	1/1	0.96	0.54	15.92	8,8,8,8	0
57	MG	YA	3164	1/1	0.83	0.76	15.82	48,48,48,48	0
57	MG	RA	3354	1/1	0.89	0.55	15.54	82,82,82,82	0
57	MG	RA	3064	1/1	0.86	0.58	15.51	15,15,15,15	0
57	MG	RA	3375	1/1	0.97	0.29	15.29	10,10,10,10	0
57	MG	YA	3338	1/1	0.68	0.58	15.18	57,57,57,57	0
57	MG	RA	3038	1/1	0.95	0.45	14.95	39,39,39,39	0
57	MG	RA	3047	1/1	0.96	0.55	14.93	5,5,5,5	0
57	MG	YA	3027	1/1	0.96	0.44	14.82	15,15,15,15	0
57	MG	RA	3260	1/1	0.86	0.58	14.75	65,65,65,65	0
57	MG	RA	3056	1/1	0.94	0.84	14.70	32,32,32,32	0
57	MG	RA	3190	1/1	0.97	0.46	14.68	10,10,10,10	0
57	MG	QA	1718	1/1	0.72	0.49	13.82	66,66,66,66	0
57	MG	YA	3079	1/1	0.98	0.44	13.65	7,7,7,7	0
57	MG	YA	3018	1/1	0.95	0.38	13.64	11,11,11,11	0
57	MG	RA	3044	1/1	0.92	0.42	13.56	2,2,2,2	0
57	MG	RA	3077	1/1	0.98	0.49	13.45	5,5,5,5	0
57	MG	RA	3345	1/1	0.82	0.38	13.44	36,36,36,36	0
57	MG	YA	3352	1/1	0.54	0.50	13.35	65,65,65,65	0
57	MG	YA	3031	1/1	0.95	0.32	13.29	26,26,26,26	0
57	MG	RA	3070	1/1	0.98	0.41	13.26	18,18,18,18	0
57	MG	YA	3063	1/1	0.97	0.51	13.24	4,4,4,4	0
57	MG	RA	3054	1/1	0.98	0.39	13.03	0,0,0,0	0
57	MG	YA	3190	1/1	0.96	0.50	12.77	19,19,19,19	0
57	MG	YA	3423	1/1	0.60	0.51	12.55	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3092	1/1	0.85	0.57	12.43	36,36,36,36	0
57	MG	YA	3013	1/1	0.96	0.36	12.28	2,2,2,2	0
57	MG	YA	3147	1/1	0.91	0.43	12.20	20,20,20,20	0
57	MG	YA	3096	1/1	0.70	0.29	12.11	36,36,36,36	0
57	MG	YA	3097	1/1	0.91	0.33	11.95	22,22,22,22	0
57	MG	RA	3406	1/1	0.86	0.34	11.93	49,49,49,49	0
57	MG	YA	3233	1/1	0.91	0.43	11.91	35,35,35,35	0
57	MG	RA	3194	1/1	0.99	0.38	11.70	2,2,2,2	0
57	MG	RA	3079	1/1	0.99	0.34	11.47	5,5,5,5	0
57	MG	RA	3363	1/1	0.88	0.46	11.36	46,46,46,46	0
57	MG	RA	3214	1/1	0.92	0.39	11.19	63,63,63,63	0
57	MG	YA	3297	1/1	0.97	0.45	11.16	31,31,31,31	0
57	MG	RA	3385	1/1	0.93	0.38	11.04	3,3,3,3	0
57	MG	YA	3471	1/1	0.64	0.56	10.83	85,85,85,85	0
57	MG	YA	3441	1/1	0.98	0.40	10.72	9,9,9,9	0
57	MG	XA	1753	1/1	0.77	0.32	10.59	67,67,67,67	0
57	MG	YA	3006	1/1	0.96	0.36	10.52	18,18,18,18	0
57	MG	XA	1636	1/1	0.86	0.63	10.48	43,43,43,43	0
57	MG	RA	3134	1/1	0.64	0.38	10.46	39,39,39,39	0
57	MG	RA	3013	1/1	0.84	0.46	10.36	32,32,32,32	0
57	MG	XA	1743	1/1	0.84	0.34	10.35	50,50,50,50	0
57	MG	RA	3318	1/1	0.59	0.35	10.02	38,38,38,38	0
57	MG	RA	3189	1/1	0.98	0.51	9.98	21,21,21,21	0
57	MG	YA	3469	1/1	0.82	0.34	9.88	70,70,70,70	0
57	MG	RA	3384	1/1	0.91	0.27	9.84	20,20,20,20	0
57	MG	RA	3411	1/1	0.98	0.40	9.81	44,44,44,44	0
57	MG	RA	3296	1/1	0.89	0.36	9.77	46,46,46,46	0
57	MG	RA	3283	1/1	0.86	0.33	9.72	37,37,37,37	0
57	MG	YA	3003	1/1	0.97	0.35	9.67	10,10,10,10	0
57	MG	YA	3021	1/1	0.98	0.44	9.62	11,11,11,11	0
57	MG	QA	1668	1/1	0.54	0.39	9.55	50,50,50,50	0
57	MG	YA	3189	1/1	0.95	0.35	9.44	25,25,25,25	0
57	MG	RA	3072	1/1	0.97	0.35	9.43	4,4,4,4	0
57	MG	XA	1638	1/1	0.98	0.34	9.41	57,57,57,57	0
57	MG	RA	3109	1/1	0.97	0.42	9.40	11,11,11,11	0
57	MG	RA	3062	1/1	0.99	0.35	9.35	2,2,2,2	0
57	MG	RA	3032	1/1	0.97	0.40	9.25	26,26,26,26	0
57	MG	XA	1740	1/1	0.95	0.43	9.23	69,69,69,69	0
57	MG	RA	3098	1/1	0.97	0.38	9.21	11,11,11,11	0
57	MG	RA	3166	1/1	0.89	0.59	9.08	30,30,30,30	0
57	MG	YA	3069	1/1	0.91	0.41	9.05	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3071	1/1	0.96	0.30	8.79	11,11,11,11	0
57	MG	QA	1619	1/1	0.95	0.48	8.67	10,10,10,10	0
57	MG	YA	3249	1/1	0.87	0.33	8.64	46,46,46,46	0
57	MG	RA	3409	1/1	0.93	0.35	8.52	0,0,0,0	0
57	MG	QA	1640	1/1	0.79	0.35	8.49	58,58,58,58	0
57	MG	RA	3148	1/1	0.96	0.31	8.45	10,10,10,10	0
57	MG	RA	3033	1/1	0.99	0.28	8.39	12,12,12,12	0
57	MG	YA	3335	1/1	0.97	0.36	8.37	31,31,31,31	0
57	MG	YA	3406	1/1	0.97	0.35	8.30	8,8,8,8	0
57	MG	YA	3239	1/1	0.86	0.31	8.30	29,29,29,29	0
57	MG	YA	3386	1/1	0.90	0.31	8.30	58,58,58,58	0
57	MG	YA	3055	1/1	0.98	0.46	8.27	5,5,5,5	0
57	MG	RA	3103	1/1	0.96	0.34	8.25	36,36,36,36	0
57	MG	RD	302	1/1	0.86	0.49	8.25	29,29,29,29	0
57	MG	XA	1601	1/1	0.98	0.36	8.19	7,7,7,7	0
57	MG	RA	3017	1/1	0.95	0.42	8.18	5,5,5,5	0
57	MG	RA	3093	1/1	0.92	0.28	8.09	21,21,21,21	0
57	MG	XA	1640	1/1	0.98	0.46	8.02	23,23,23,23	0
57	MG	QA	1725	1/1	0.95	0.29	7.83	41,41,41,41	0
57	MG	YA	3246	1/1	0.86	0.39	7.73	43,43,43,43	0
57	MG	YA	3449	1/1	0.93	0.35	7.71	39,39,39,39	0
57	MG	RA	3308	1/1	0.88	0.61	7.58	63,63,63,63	0
57	MG	YU	201	1/1	0.80	0.42	7.42	60,60,60,60	0
57	MG	XA	1605	1/1	0.96	0.38	7.39	23,23,23,23	0
57	MG	RA	3348	1/1	0.86	0.37	7.26	68,68,68,68	0
57	MG	RA	3199	1/1	0.93	0.32	7.25	5,5,5,5	0
57	MG	YA	3461	1/1	0.71	0.43	7.23	57,57,57,57	0
57	MG	RA	3361	1/1	0.96	0.25	7.13	35,35,35,35	0
57	MG	RA	3106	1/1	0.89	0.31	7.06	32,32,32,32	0
57	MG	RA	3241	1/1	0.85	0.34	7.00	38,38,38,38	0
57	MG	XA	1604	1/1	0.95	0.34	6.86	19,19,19,19	0
57	MG	YA	3223	1/1	0.99	0.29	6.79	25,25,25,25	0
57	MG	YA	3102	1/1	0.98	0.31	6.63	18,18,18,18	0
57	MG	RD	301	1/1	0.62	0.54	6.55	35,35,35,35	0
57	MG	RA	3236	1/1	0.95	0.36	6.44	23,23,23,23	0
57	MG	RA	3297	1/1	0.97	0.30	6.41	49,49,49,49	0
57	MG	YA	3208	1/1	0.97	0.31	6.40	7,7,7,7	0
57	MG	QA	1651	1/1	0.97	0.25	6.39	31,31,31,31	0
57	MG	YA	3225	1/1	0.82	0.30	6.29	43,43,43,43	0
57	MG	YA	3017	1/1	0.97	0.38	6.28	2,2,2,2	0
57	MG	RA	3069	1/1	0.96	0.36	6.22	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	QA	1614	1/1	0.90	0.30	6.19	44,44,44,44	0
57	MG	XA	1643	1/1	0.99	0.29	6.18	29,29,29,29	0
57	MG	RA	3159	1/1	0.97	0.34	6.08	19,19,19,19	0
57	MG	QA	1654	1/1	0.94	0.49	5.98	34,34,34,34	0
57	MG	XA	1644	1/1	0.97	0.28	5.95	24,24,24,24	0
57	MG	XA	1664	1/1	0.98	0.31	5.89	14,14,14,14	0
57	MG	YA	3456	1/1	0.95	0.33	5.86	125,125,125,125	0
57	MG	YA	3274	1/1	0.92	0.34	5.80	33,33,33,33	0
57	MG	YD	301	1/1	0.78	0.53	5.79	21,21,21,21	0
57	MG	QA	1688	1/1	0.95	0.29	5.76	32,32,32,32	0
57	MG	QA	1643	1/1	0.92	0.30	5.75	59,59,59,59	0
57	MG	XA	1607	1/1	0.94	0.31	5.63	32,32,32,32	0
57	MG	RA	3027	1/1	0.98	0.30	5.55	8,8,8,8	0
57	MG	RA	3247	1/1	0.94	0.29	5.51	35,35,35,35	0
57	MG	RA	3229	1/1	0.98	0.30	5.39	16,16,16,16	0
57	MG	YA	3425	1/1	0.72	0.45	5.37	61,61,61,61	0
57	MG	YA	3285	1/1	0.91	0.30	5.36	42,42,42,42	0
57	MG	RA	3073	1/1	0.96	0.33	5.35	32,32,32,32	0
57	MG	RA	3055	1/1	0.99	0.24	5.31	17,17,17,17	0
57	MG	XA	1679	1/1	0.98	0.30	5.21	41,41,41,41	0
57	MG	RA	3071	1/1	0.95	0.35	5.20	41,41,41,41	0
57	MG	QA	1641	1/1	0.99	0.33	5.19	28,28,28,28	0
57	MG	YA	3110	1/1	0.97	0.30	5.17	27,27,27,27	0
57	MG	RA	3376	1/1	0.95	0.33	5.16	25,25,25,25	0
57	MG	RA	3213	1/1	0.89	0.32	5.16	30,30,30,30	0
57	MG	RA	3203	1/1	0.69	0.22	5.14	29,29,29,29	0
57	MG	RA	3025	1/1	0.99	0.28	4.98	10,10,10,10	0
57	MG	YA	3042	1/1	0.93	0.29	4.98	4,4,4,4	0
57	MG	RY	202	1/1	0.76	0.56	4.88	66,66,66,66	0
57	MG	RA	3003	1/1	0.98	0.38	4.85	16,16,16,16	0
57	MG	YA	3152	1/1	0.76	0.27	4.82	34,34,34,34	0
57	MG	RA	3018	1/1	0.98	0.34	4.78	17,17,17,17	0
57	MG	RA	3301	1/1	0.91	0.32	4.77	34,34,34,34	0
57	MG	QA	1687	1/1	0.96	0.29	4.77	50,50,50,50	0
57	MG	QA	1605	1/1	0.96	0.27	4.75	35,35,35,35	0
57	MG	QA	1601	1/1	0.90	0.40	4.70	11,11,11,11	0
57	MG	YA	3072	1/1	0.97	0.32	4.66	12,12,12,12	0
57	MG	XA	1696	1/1	0.96	0.33	4.58	20,20,20,20	0
57	MG	YA	3014	1/1	0.97	0.29	4.48	18,18,18,18	0
57	MG	YA	3108	1/1	0.91	0.40	4.46	22,22,22,22	0
57	MG	RA	3101	1/1	0.98	0.28	4.43	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	QV	101	1/1	0.98	0.23	4.43	19,19,19,19	0
57	MG	YA	3038	1/1	0.97	0.32	4.35	38,38,38,38	0
57	MG	RA	3060	1/1	0.97	0.25	4.34	18,18,18,18	0
57	MG	YA	3231	1/1	0.86	0.27	4.30	44,44,44,44	0
57	MG	RA	3382	1/1	0.96	0.25	4.23	66,66,66,66	0
57	MG	YA	3078	1/1	0.98	0.29	4.17	28,28,28,28	0
57	MG	RA	3198	1/1	0.77	0.29	4.02	49,49,49,49	0
57	MG	YA	3450	1/1	0.83	0.39	3.99	49,49,49,49	0
57	MG	RA	3049	1/1	0.87	0.29	3.94	1,1,1,1	0
57	MG	RA	3006	1/1	0.97	0.29	3.94	3,3,3,3	0
57	MG	RA	3120	1/1	0.94	0.29	3.93	67,67,67,67	0
57	MG	QA	1737	1/1	0.83	0.25	3.92	47,47,47,47	0
57	MG	YA	3136	1/1	0.97	0.34	3.89	28,28,28,28	0
57	MG	YA	3138	1/1	0.96	0.24	3.81	17,17,17,17	0
57	MG	QA	1656	1/1	0.97	0.28	3.78	16,16,16,16	0
57	MG	RA	3066	1/1	0.96	0.30	3.59	17,17,17,17	0
57	MG	XA	1746	1/1	0.90	0.21	3.55	63,63,63,63	0
57	MG	XA	1672	1/1	0.84	0.28	3.47	60,60,60,60	0
57	MG	RA	3431	1/1	0.72	0.51	3.47	34,34,34,34	0
57	MG	QA	1666	1/1	0.86	0.44	3.44	51,51,51,51	0
57	MG	YA	3428	1/1	0.90	0.26	3.36	39,39,39,39	0
57	MG	XA	1731	1/1	0.96	0.25	3.35	27,27,27,27	0
57	MG	QA	1699	1/1	0.93	0.26	3.31	72,72,72,72	0
57	MG	RA	3012	1/1	0.96	0.24	3.23	4,4,4,4	0
57	MG	YA	3065	1/1	0.92	0.23	3.23	16,16,16,16	0
57	MG	YA	3089	1/1	0.88	0.26	3.06	44,44,44,44	0
57	MG	RA	3368	1/1	0.97	0.29	3.04	59,59,59,59	0
57	MG	RA	3157	1/1	0.88	0.20	2.95	79,79,79,79	0
57	MG	QA	1722	1/1	0.93	0.27	2.94	49,49,49,49	0
57	MG	RA	3206	1/1	0.61	0.23	2.89	30,30,30,30	0
57	MG	RA	3078	1/1	0.94	0.29	2.84	12,12,12,12	0
57	MG	YA	3217	1/1	0.72	0.25	2.81	46,46,46,46	0
57	MG	YA	3092	1/1	0.96	0.25	2.74	12,12,12,12	0
57	MG	YA	3156	1/1	0.79	0.22	2.72	40,40,40,40	0
57	MG	YA	3033	1/1	0.99	0.23	2.69	10,10,10,10	0
57	MG	YA	3029	1/1	0.97	0.23	2.67	18,18,18,18	0
57	MG	RA	3059	1/1	0.82	0.18	2.61	25,25,25,25	0
57	MG	RA	3389	1/1	0.89	0.39	2.58	9,9,9,9	0
57	MG	YA	3054	1/1	0.97	0.21	2.57	0,0,0,0	0
57	MG	QA	1632	1/1	0.96	0.28	2.56	46,46,46,46	0
57	MG	YA	3416	1/1	0.96	0.21	2.47	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3426	1/1	0.69	0.19	2.39	45,45,45,45	0
57	MG	YA	3421	1/1	0.95	0.24	2.39	33,33,33,33	0
57	MG	XA	1682	1/1	0.88	0.18	2.37	51,51,51,51	0
57	MG	YA	3205	1/1	0.94	0.24	2.37	32,32,32,32	0
57	MG	RA	3031	1/1	0.96	0.26	2.35	16,16,16,16	0
57	MG	QA	1644	1/1	0.98	0.25	2.30	19,19,19,19	0
57	MG	RA	3026	1/1	0.98	0.25	2.28	5,5,5,5	0
57	MG	QA	1684	1/1	0.94	0.26	2.24	42,42,42,42	0
57	MG	YF	301	1/1	0.68	0.33	2.20	38,38,38,38	0
57	MG	YA	3012	1/1	0.97	0.24	2.15	12,12,12,12	0
57	MG	YA	3068	1/1	0.97	0.28	2.12	35,35,35,35	0
57	MG	RA	3042	1/1	0.90	0.32	2.06	9,9,9,9	0
57	MG	YA	3087	1/1	0.94	0.23	2.06	18,18,18,18	0
57	MG	RA	3052	1/1	0.94	0.21	1.98	38,38,38,38	0
57	MG	YA	3070	1/1	0.96	0.23	1.98	47,47,47,47	0
57	MG	YA	3086	1/1	0.98	0.23	1.97	38,38,38,38	0
57	MG	RA	3108	1/1	0.96	0.29	1.97	25,25,25,25	0
57	MG	YA	3119	1/1	0.94	0.54	1.97	40,40,40,40	0
57	MG	YA	3157	1/1	0.96	0.31	1.95	19,19,19,19	0
57	MG	YA	3061	1/1	0.94	0.22	1.93	10,10,10,10	0
57	MG	YA	3403	1/1	0.96	0.25	1.85	27,27,27,27	0
57	MG	QA	1662	1/1	0.86	0.21	1.77	56,56,56,56	0
57	MG	QA	1678	1/1	0.78	0.23	1.71	48,48,48,48	0
57	MG	RA	3230	1/1	0.87	0.21	1.68	73,73,73,73	0
57	MG	YA	3433	1/1	0.97	0.21	1.63	33,33,33,33	0
57	MG	YA	3032	1/1	0.99	0.27	1.57	7,7,7,7	0
57	MG	YA	3199	1/1	0.94	0.25	1.53	11,11,11,11	0
57	MG	RA	3097	1/1	0.96	0.22	1.38	17,17,17,17	0
57	MG	XA	1739	1/1	0.74	0.24	1.35	49,49,49,49	0
57	MG	YA	3472	1/1	0.89	0.35	1.29	45,45,45,45	0
57	MG	RA	3140	1/1	0.78	0.17	1.27	59,59,59,59	0
57	MG	YA	3427	1/1	0.89	0.22	1.24	27,27,27,27	0
57	MG	QA	1625	1/1	0.84	0.22	1.21	59,59,59,59	0
57	MG	XA	1708	1/1	0.94	0.26	1.20	54,54,54,54	0
57	MG	RA	3430	1/1	0.76	0.27	1.17	38,38,38,38	0
57	MG	RA	3127	1/1	0.91	0.17	1.12	33,33,33,33	0
57	MG	RA	3010	1/1	0.96	0.20	1.10	16,16,16,16	0
57	MG	RA	3239	1/1	0.98	0.21	1.04	20,20,20,20	0
57	MG	RA	3419	1/1	0.84	0.27	1.04	47,47,47,47	0
57	MG	YA	3454	1/1	0.90	0.20	1.04	54,54,54,54	0
57	MG	RA	3163	1/1	0.80	0.52	1.01	61,61,61,61	0
57	MG	YA	3154	1/1	0.98	0.21	0.97	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3057	1/1	0.90	0.22	0.96	59,59,59,59	0
57	MG	RA	3299	1/1	0.93	0.20	0.94	76,76,76,76	0
57	MG	XA	1625	1/1	0.84	0.20	0.90	75,75,75,75	0
57	MG	YA	3323	1/1	0.98	0.29	0.88	1,1,1,1	0
57	MG	YA	3161	1/1	0.99	0.22	0.87	10,10,10,10	0
57	MG	YA	3420	1/1	0.98	0.19	0.86	33,33,33,33	0
57	MG	YA	3026	1/1	0.98	0.23	0.84	8,8,8,8	0
57	MG	RA	3058	1/1	0.93	0.21	0.81	31,31,31,31	0
57	MG	QA	1606	1/1	0.91	0.24	0.79	12,12,12,12	0
57	MG	Y1	101	1/1	0.92	0.30	0.68	17,17,17,17	0
57	MG	RA	3124	1/1	0.94	0.21	0.66	45,45,45,45	0
57	MG	YA	3282	1/1	0.88	0.21	0.63	25,25,25,25	0
57	MG	RQ	202	1/1	0.88	0.25	0.63	74,74,74,74	0
57	MG	YA	3059	1/1	0.98	0.22	0.61	7,7,7,7	0
57	MG	YA	3010	1/1	0.97	0.20	0.57	1,1,1,1	0
57	MG	QA	1681	1/1	0.93	0.23	0.54	83,83,83,83	0
58	ZN	QD	301	1/1	0.99	0.32	0.50	44,44,44,44	0
57	MG	YA	3058	1/1	0.93	0.20	0.48	39,39,39,39	0
57	MG	YA	3005	1/1	0.91	0.22	0.44	9,9,9,9	0
58	ZN	XD	301	1/1	0.96	0.34	0.43	66,66,66,66	0
57	MG	RA	3146	1/1	0.86	0.20	0.42	25,25,25,25	0
57	MG	RA	3205	1/1	0.89	0.19	0.41	34,34,34,34	0
57	MG	RP	202	1/1	0.75	0.36	0.40	34,34,34,34	0
57	MG	XA	1684	1/1	0.86	0.32	0.37	41,41,41,41	0
57	MG	YA	3130	1/1	0.81	0.20	0.35	28,28,28,28	0
57	MG	QA	1727	1/1	0.96	0.25	0.34	77,77,77,77	0
57	MG	XA	1653	1/1	0.93	0.18	0.29	29,29,29,29	0
57	MG	YA	3243	1/1	0.92	0.19	0.25	56,56,56,56	0
57	MG	YA	3081	1/1	0.95	0.20	0.19	26,26,26,26	0
57	MG	RA	3086	1/1	0.94	0.19	0.17	20,20,20,20	0
57	MG	YA	3470	1/1	0.97	0.20	0.04	24,24,24,24	0
57	MG	QA	1723	1/1	0.90	0.18	0.01	50,50,50,50	0
57	MG	RA	3339	1/1	0.69	0.17	-0.01	69,69,69,69	0
57	MG	RA	3139	1/1	0.98	0.19	-0.10	15,15,15,15	0
57	MG	QA	1639	1/1	0.86	0.20	-0.14	49,49,49,49	0
57	MG	RA	3087	1/1	0.90	0.20	-0.17	36,36,36,36	0
57	MG	YA	3317	1/1	0.92	0.19	-0.22	35,35,35,35	0
57	MG	XN	102	1/1	0.94	0.22	-0.22	54,54,54,54	0
57	MG	RA	3265	1/1	0.76	0.18	-0.22	33,33,33,33	0
57	MG	XV	101	1/1	0.99	0.19	-0.30	7,7,7,7	0
57	MG	QA	1645	1/1	0.99	0.17	-0.32	52,52,52,52	0
57	MG	QA	1673	1/1	0.94	0.26	-0.39	72,72,72,72	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RP	201	1/1	0.89	0.21	-0.41	35,35,35,35	0
57	MG	XA	1750	1/1	0.97	0.21	-0.42	46,46,46,46	0
57	MG	YA	3120	1/1	0.91	0.16	-0.43	37,37,37,37	0
57	MG	YA	3418	1/1	0.88	0.17	-0.43	19,19,19,19	0
57	MG	XA	1635	1/1	0.76	0.21	-0.49	44,44,44,44	0
57	MG	YA	3326	1/1	0.96	0.19	-0.49	64,64,64,64	0
57	MG	YQ	201	1/1	0.84	0.18	-0.58	52,52,52,52	0
57	MG	YA	3127	1/1	0.77	0.13	-0.59	48,48,48,48	0
57	MG	YA	3419	1/1	0.73	0.17	-0.60	54,54,54,54	0
57	MG	YH	201	1/1	0.96	0.21	-0.64	80,80,80,80	0
57	MG	RA	3343	1/1	0.80	0.14	-0.69	48,48,48,48	0
57	MG	RA	3244	1/1	0.86	0.20	-0.72	45,45,45,45	0
57	MG	YA	3131	1/1	0.95	0.17	-0.76	27,27,27,27	0
57	MG	YG	201	1/1	0.41	0.23	-0.80	85,85,85,85	0
57	MG	RA	3065	1/1	0.98	0.17	-0.84	32,32,32,32	0
57	MG	RA	3029	1/1	0.99	0.20	-0.87	14,14,14,14	0
57	MG	YA	3124	1/1	0.94	0.18	-0.89	16,16,16,16	0
57	MG	RA	3386	1/1	0.94	0.19	-0.92	36,36,36,36	0
57	MG	QA	1745	1/1	0.81	0.19	-0.94	72,72,72,72	0
57	MG	RA	3165	1/1	0.91	0.18	-1.01	71,71,71,71	0
57	MG	RA	3217	1/1	0.92	0.18	-1.02	16,16,16,16	0
57	MG	YA	3293	1/1	0.80	0.15	-1.02	33,33,33,33	0
57	MG	YA	3107	1/1	0.98	0.14	-1.13	2,2,2,2	0
57	MG	XA	1614	1/1	0.94	0.16	-1.15	40,40,40,40	0
57	MG	YA	3227	1/1	0.95	0.16	-1.16	44,44,44,44	0
57	MG	YN	201	1/1	0.90	0.25	-1.19	44,44,44,44	0
57	MG	YA	3236	1/1	0.84	0.13	-1.20	23,23,23,23	0
57	MG	QA	1739	1/1	0.92	0.15	-1.25	57,57,57,57	0
57	MG	RA	3281	1/1	0.90	0.15	-1.30	40,40,40,40	0
57	MG	RA	3287	1/1	0.93	0.16	-1.32	33,33,33,33	0
57	MG	XD	302	1/1	0.76	0.10	-1.34	77,77,77,77	0
57	MG	RA	3429	1/1	0.97	0.15	-1.35	19,19,19,19	0
57	MG	YA	3046	1/1	0.95	0.15	-1.46	23,23,23,23	0
57	MG	RB	204	1/1	0.84	0.12	-1.49	41,41,41,41	0
57	MG	RA	3410	1/1	0.96	0.15	-1.53	49,49,49,49	0
58	ZN	QN	100	1/1	0.91	0.14	-1.53	90,90,90,90	0
57	MG	YP	201	1/1	0.95	0.18	-1.57	8,8,8,8	0
57	MG	QA	1693	1/1	0.51	0.16	-1.60	47,47,47,47	0
57	MG	QA	1626	1/1	0.95	0.12	-1.64	40,40,40,40	0
57	MG	XA	1642	1/1	0.90	0.13	-1.65	43,43,43,43	0
57	MG	XA	1761	1/1	0.94	0.10	-1.66	68,68,68,68	0
57	MG	XA	1759	1/1	0.76	0.12	-1.71	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	R5	103	1/1	0.91	0.07	-1.77	34,34,34,34	0
57	MG	YA	3083	1/1	0.90	0.12	-1.93	21,21,21,21	0
58	ZN	XN	101	1/1	0.90	0.15	-1.95	78,78,78,78	0
57	MG	QA	1746	1/1	0.81	0.09	-2.08	44,44,44,44	0
57	MG	RA	3252	1/1	0.95	0.12	-2.16	62,62,62,62	0
57	MG	YA	3103	1/1	0.94	0.13	-2.28	42,42,42,42	0
57	MG	XA	1627	1/1	0.97	0.11	-2.33	73,73,73,73	0
57	MG	XA	1741	1/1	0.88	0.16	-2.34	44,44,44,44	0
57	MG	RA	3046	1/1	0.98	0.16	-2.35	17,17,17,17	0
57	MG	XA	1732	1/1	0.91	0.09	-2.35	52,52,52,52	0
57	MG	YA	3162	1/1	0.97	0.18	-2.37	38,38,38,38	0
57	MG	QA	1730	1/1	0.95	0.17	-2.46	40,40,40,40	0
57	MG	RA	3185	1/1	0.92	0.11	-2.56	31,31,31,31	0
57	MG	YA	3139	1/1	0.89	0.12	-2.71	38,38,38,38	0
57	MG	RA	3255	1/1	0.77	0.10	-2.83	40,40,40,40	0
57	MG	RA	3130	1/1	0.96	0.11	-2.87	34,34,34,34	0
57	MG	RA	3153	1/1	0.88	0.17	-2.88	13,13,13,13	0
57	MG	YA	3232	1/1	0.81	0.12	-2.96	27,27,27,27	0
57	MG	YA	3008	1/1	0.98	0.15	-3.06	20,20,20,20	0
57	MG	XA	1656	1/1	0.68	0.08	-3.10	50,50,50,50	0
57	MG	XA	1734	1/1	0.94	0.19	-3.12	15,15,15,15	0
57	MG	YA	3171	1/1	0.92	0.11	-3.23	35,35,35,35	0
57	MG	QA	1685	1/1	0.92	0.09	-3.33	25,25,25,25	0
57	MG	YH	202	1/1	0.84	0.21	-3.44	59,59,59,59	0
57	MG	QA	1726	1/1	0.96	0.14	-3.58	48,48,48,48	0
57	MG	YA	3203	1/1	0.97	0.11	-3.60	18,18,18,18	0
57	MG	YB	205	1/1	0.97	0.11	-3.62	58,58,58,58	0
57	MG	RA	3005	1/1	0.96	0.14	-3.68	9,9,9,9	0
57	MG	RA	3175	1/1	0.96	0.10	-3.71	45,45,45,45	0
57	MG	RA	3083	1/1	0.93	0.09	-3.79	19,19,19,19	0
57	MG	QA	1610	1/1	0.97	0.09	-3.93	48,48,48,48	0
57	MG	XA	1623	1/1	0.96	0.09	-3.96	33,33,33,33	0
57	MG	YA	3211	1/1	0.88	0.10	-4.02	67,67,67,67	0
57	MG	QA	1604	1/1	0.95	0.14	-4.23	31,31,31,31	0
57	MG	RA	3131	1/1	0.98	0.13	-4.36	20,20,20,20	0
57	MG	XA	1624	1/1	0.96	0.09	-4.43	51,51,51,51	0
57	MG	RF	301	1/1	0.92	0.10	-4.44	27,27,27,27	0
57	MG	RA	3081	1/1	0.87	0.12	-4.49	20,20,20,20	0
57	MG	YA	3016	1/1	0.95	0.12	-4.61	17,17,17,17	0
57	MG	XA	1613	1/1	0.96	0.12	-4.64	18,18,18,18	0
57	MG	XA	1603	1/1	0.98	0.15	-4.87	19,19,19,19	0
57	MG	RA	3272	1/1	0.97	0.12	-4.89	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3128	1/1	0.99	0.08	-5.01	27,27,27,27	0
57	MG	QA	1624	1/1	0.96	0.12	-5.10	41,41,41,41	0
57	MG	RA	3128	1/1	0.95	0.12	-5.25	37,37,37,37	0
57	MG	QA	1686	1/1	0.97	0.11	-5.28	31,31,31,31	0
57	MG	XA	1609	1/1	0.97	0.08	-7.24	53,53,53,53	0
57	MG	RA	3008	1/1	0.99	0.14	-7.40	35,35,35,35	0
57	MG	RA	3398	1/1	0.92	0.10	-8.68	38,38,38,38	0
57	MG	RA	3143	1/1	0.96	0.29	-	4,4,4,4	0
57	MG	XA	1608	1/1	0.92	0.25	-	27,27,27,27	0
57	MG	XA	1632	1/1	0.90	0.48	-	20,20,20,20	0
57	MG	YA	3168	1/1	0.75	0.48	-	34,34,34,34	0
57	MG	YA	3132	1/1	0.97	0.38	-	59,59,59,59	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	XA	1710	1/1	0.76	0.50	-	57,57,57,57	0
57	MG	YA	3201	1/1	0.92	0.32	-	30,30,30,30	0
57	MG	YA	3434	1/1	0.91	0.27	-	21,21,21,21	0
57	MG	RA	3393	1/1	0.93	0.15	-	29,29,29,29	0
57	MG	QA	1648	1/1	0.87	0.12	-	74,74,74,74	0
57	MG	RA	3323	1/1	0.88	0.12	-	37,37,37,37	0
57	MG	RA	3145	1/1	0.97	0.25	-	20,20,20,20	0
57	MG	RA	3420	1/1	0.96	0.26	-	74,74,74,74	0
57	MG	YA	3341	1/1	0.92	0.23	-	56,56,56,56	0
57	MG	RA	3286	1/1	0.88	0.38	-	34,34,34,34	0
57	MG	YA	3230	1/1	0.81	0.61	-	53,53,53,53	0
57	MG	RA	3015	1/1	0.98	0.36	-	10,10,10,10	0
57	MG	RA	3310	1/1	0.92	0.43	-	69,69,69,69	0
57	MG	RA	3342	1/1	0.61	0.49	-	109,109,109,109	0
57	MG	YA	3275	1/1	0.96	0.29	-	40,40,40,40	0
57	MG	QA	1689	1/1	0.88	0.37	-	30,30,30,30	0
57	MG	YA	3186	1/1	0.92	0.41	-	27,27,27,27	0
57	MG	RA	3168	1/1	0.91	0.30	-	43,43,43,43	0
57	MG	RA	3184	1/1	0.96	0.36	-	28,28,28,28	0
57	MG	RA	3180	1/1	0.88	0.46	-	18,18,18,18	0
57	MG	YA	3346	1/1	0.85	0.66	-	45,45,45,45	0
57	MG	XA	1670	1/1	0.86	0.20	-	30,30,30,30	0
57	MG	RA	3392	1/1	0.83	0.27	-	43,43,43,43	0
57	MG	RA	3170	1/1	0.96	0.49	-	64,64,64,64	0
57	MG	XA	1707	1/1	0.89	0.40	-	35,35,35,35	0
57	MG	YA	3270	1/1	0.94	0.84	-	37,37,37,37	0
57	MG	YA	3407	1/1	0.88	0.49	-	7,7,7,7	0
57	MG	XA	1688	1/1	0.62	0.51	-	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3264	1/1	0.88	0.72	-	39,39,39,39	0
57	MG	YA	3109	1/1	0.70	0.34	-	31,31,31,31	0
57	MG	RA	3314	1/1	0.86	1.19	-	47,47,47,47	0
57	MG	RA	3121	1/1	0.99	0.20	-	5,5,5,5	0
57	MG	QA	1747	1/1	0.47	0.41	-	111,111,111,111	0
57	MG	YA	3251	1/1	0.86	0.59	-	48,48,48,48	0
57	MG	YA	3455	1/1	0.86	0.27	-	36,36,36,36	0
57	MG	RA	3179	1/1	0.88	0.32	-	43,43,43,43	0
57	MG	YA	3331	1/1	0.96	0.48	-	19,19,19,19	0
57	MG	RA	3292	1/1	0.43	0.54	-	52,52,52,52	0
57	MG	RA	3326	1/1	0.66	0.55	-	65,65,65,65	0
57	MG	YA	3113	1/1	0.74	0.42	-	37,37,37,37	0
57	MG	XA	1703	1/1	0.84	0.38	-	48,48,48,48	0
57	MG	YA	3248	1/1	0.91	0.34	-	15,15,15,15	0
57	MG	XA	1655	1/1	0.90	0.47	-	41,41,41,41	0
57	MG	RE	301	1/1	0.92	0.29	-	8,8,8,8	0
57	MG	YA	3437	1/1	0.92	0.25	-	74,74,74,74	0
57	MG	RA	3327	1/1	0.67	0.41	-	71,71,71,71	0
57	MG	XA	1630	1/1	0.69	0.53	-	46,46,46,46	0
57	MG	YA	3287	1/1	0.96	0.17	-	34,34,34,34	0
57	MG	QA	1655	1/1	0.95	0.29	-	29,29,29,29	0
57	MG	RB	202	1/1	0.94	0.39	-	27,27,27,27	0
57	MG	RA	3329	1/1	0.93	0.25	-	47,47,47,47	0
57	MG	YA	3150	1/1	0.70	0.37	-	44,44,44,44	0
57	MG	QA	1691	1/1	0.95	0.37	-	26,26,26,26	0
57	MG	RA	3288	1/1	0.89	0.45	-	56,56,56,56	0
57	MG	QA	1692	1/1	0.88	0.46	-	47,47,47,47	0
57	MG	RA	3147	1/1	0.82	0.19	-	65,65,65,65	0
57	MG	XA	1650	1/1	0.93	0.51	-	20,20,20,20	0
57	MG	RA	3254	1/1	0.85	0.41	-	50,50,50,50	0
57	MG	XA	1669	1/1	0.98	0.26	-	25,25,25,25	0
57	MG	YA	3265	1/1	0.61	0.69	-	56,56,56,56	0
57	MG	YA	3467	1/1	0.85	0.39	-	48,48,48,48	0
57	MG	YA	3075	1/1	0.98	0.19	-	19,19,19,19	0
57	MG	XF	201	1/1	0.96	0.38	-	41,41,41,41	0
57	MG	XA	1716	1/1	0.92	0.64	-	39,39,39,39	0
57	MG	YB	201	1/1	0.96	0.43	-	28,28,28,28	0
57	MG	RA	3084	1/1	0.92	0.31	-	28,28,28,28	0
57	MG	YA	3259	1/1	0.93	0.22	-	43,43,43,43	0
57	MG	YA	3375	1/1	0.90	0.27	-	30,30,30,30	0
57	MG	YA	3309	1/1	0.76	0.85	-	56,56,56,56	0
57	MG	RA	3291	1/1	0.96	0.32	-	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3320	1/1	0.89	0.46	-	58,58,58,58	0
57	MG	XA	1662	1/1	0.92	0.34	-	13,13,13,13	0
57	MG	XA	1637	1/1	0.96	0.23	-	49,49,49,49	0
57	MG	YA	3213	1/1	0.95	0.63	-	30,30,30,30	0
57	MG	YA	3242	1/1	0.64	0.37	-	54,54,54,54	0
57	MG	YA	3343	1/1	0.78	0.45	-	25,25,25,25	0
57	MG	YA	3178	1/1	0.90	0.17	-	47,47,47,47	0
57	MG	RA	3294	1/1	0.75	0.24	-	48,48,48,48	0
57	MG	RA	3116	1/1	0.98	0.46	-	30,30,30,30	0
57	MG	RA	3193	1/1	0.97	0.69	-	17,17,17,17	0
57	MG	RA	3129	1/1	0.91	0.34	-	19,19,19,19	0
57	MG	RA	3290	1/1	0.96	0.13	-	49,49,49,49	0
57	MG	XA	1721	1/1	0.79	0.23	-	57,57,57,57	0
57	MG	YA	3348	1/1	0.66	0.25	-	45,45,45,45	0
57	MG	RA	3366	1/1	0.83	0.18	-	58,58,58,58	0
57	MG	QA	1697	1/1	0.88	0.43	-	34,34,34,34	0
57	MG	YA	3234	1/1	0.95	0.51	-	31,31,31,31	0
57	MG	RA	3232	1/1	0.90	0.31	-	39,39,39,39	0
57	MG	XA	1645	1/1	0.95	0.52	-	41,41,41,41	0
57	MG	YA	3443	1/1	0.68	0.30	-	65,65,65,65	0
57	MG	RA	3208	1/1	0.90	0.47	-	52,52,52,52	0
57	MG	RA	3068	1/1	0.86	0.32	-	14,14,14,14	0
57	MG	RA	3122	1/1	0.96	0.24	-	21,21,21,21	0
57	MG	XA	1712	1/1	0.87	0.18	-	53,53,53,53	0
57	MG	YA	3126	1/1	0.95	0.25	-	41,41,41,41	0
57	MG	YA	3397	1/1	0.98	0.06	-	41,41,41,41	0
57	MG	XA	1602	1/1	0.96	0.50	-	6,6,6,6	0
57	MG	YA	3145	1/1	0.76	0.23	-	32,32,32,32	0
57	MG	RA	3007	1/1	0.96	0.43	-	13,13,13,13	0
57	MG	RA	3001	1/1	0.73	0.71	-	60,60,60,60	0
57	MG	RA	3280	1/1	0.97	0.16	-	20,20,20,20	0
57	MG	YA	3378	1/1	0.96	0.70	-	40,40,40,40	0
57	MG	YA	3182	1/1	0.63	0.40	-	51,51,51,51	0
57	MG	RA	3248	1/1	0.66	0.30	-	23,23,23,23	0
57	MG	XA	1639	1/1	0.85	0.39	-	58,58,58,58	0
57	MG	RA	3259	1/1	0.88	0.34	-	39,39,39,39	0
57	MG	YA	3093	1/1	0.94	0.11	-	41,41,41,41	0
57	MG	QA	1701	1/1	0.96	0.13	-	48,48,48,48	0
57	MG	YA	3238	1/1	0.86	0.44	-	48,48,48,48	0
57	MG	YA	3221	1/1	0.89	0.25	-	28,28,28,28	0
57	MG	RA	3282	1/1	0.90	0.13	-	47,47,47,47	0
57	MG	YA	3112	1/1	0.95	0.26	-	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3335	1/1	0.59	1.10	-	44,44,44,44	0
57	MG	YA	3424	1/1	0.92	0.18	-	28,28,28,28	0
57	MG	XA	1702	1/1	0.73	0.35	-	38,38,38,38	0
57	MG	RA	3074	1/1	0.96	0.34	-	16,16,16,16	0
57	MG	QA	1741	1/1	0.89	0.51	-	45,45,45,45	0
57	MG	R5	101	1/1	0.91	0.20	-	25,25,25,25	0
57	MG	RA	3251	1/1	0.77	0.39	-	58,58,58,58	0
57	MG	RA	3394	1/1	0.64	0.53	-	39,39,39,39	0
57	MG	XA	1646	1/1	0.80	0.21	-	57,57,57,57	0
57	MG	RA	3063	1/1	0.98	0.29	-	23,23,23,23	0
57	MG	RA	3332	1/1	0.95	0.35	-	40,40,40,40	0
57	MG	RA	3396	1/1	0.91	0.15	-	43,43,43,43	0
57	MG	QA	1637	1/1	0.73	0.47	-	61,61,61,61	0
57	MG	QA	1734	1/1	0.75	0.34	-	53,53,53,53	0
57	MG	XA	1668	1/1	0.87	0.36	-	29,29,29,29	0
57	MG	RA	3142	1/1	0.76	0.40	-	48,48,48,48	0
57	MG	RA	3306	1/1	0.89	0.54	-	43,43,43,43	0
57	MG	YA	3155	1/1	0.86	0.18	-	27,27,27,27	0
57	MG	RA	3094	1/1	0.94	0.21	-	47,47,47,47	0
57	MG	XA	1692	1/1	0.83	0.18	-	71,71,71,71	0
57	MG	RA	3158	1/1	0.89	0.32	-	59,59,59,59	0
57	MG	QV	103	1/1	0.89	0.43	-	8,8,8,8	0
57	MG	QA	1704	1/1	0.90	0.54	-	35,35,35,35	0
57	MG	RA	3337	1/1	0.86	0.23	-	58,58,58,58	0
57	MG	YA	3099	1/1	0.88	0.17	-	10,10,10,10	0
57	MG	RA	3422	1/1	0.86	0.48	-	45,45,45,45	0
57	MG	RA	3119	1/1	0.82	0.45	-	67,67,67,67	0
57	MG	YA	3188	1/1	0.97	0.28	-	43,43,43,43	0
57	MG	RA	3238	1/1	0.93	0.25	-	9,9,9,9	0
57	MG	QA	1719	1/1	0.60	0.81	-	68,68,68,68	0
57	MG	QA	1659	1/1	0.85	0.39	-	31,31,31,31	0
57	MG	RA	3082	1/1	0.97	0.43	-	22,22,22,22	0
57	MG	YA	3411	1/1	0.86	0.43	-	35,35,35,35	0
57	MG	QA	1680	1/1	0.91	0.23	-	35,35,35,35	0
57	MG	YA	3324	1/1	0.98	0.56	-	4,4,4,4	0
57	MG	YA	3422	1/1	0.84	0.52	-	27,27,27,27	0
57	MG	XA	1742	1/1	0.54	0.84	-	62,62,62,62	0
57	MG	YA	3050	1/1	0.95	0.30	-	7,7,7,7	0
57	MG	RA	3317	1/1	0.93	0.51	-	36,36,36,36	0
57	MG	YA	3393	1/1	0.86	0.14	-	39,39,39,39	0
57	MG	RA	3216	1/1	0.94	0.28	-	20,20,20,20	0
57	MG	RA	3417	1/1	0.74	0.20	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3395	1/1	0.95	0.56	-	55,55,55,55	0
57	MG	YA	3451	1/1	0.76	0.45	-	63,63,63,63	0
57	MG	RA	3277	1/1	0.93	0.36	-	51,51,51,51	0
57	MG	YA	3101	1/1	0.81	0.35	-	22,22,22,22	0
57	MG	XA	1717	1/1	0.81	0.28	-	31,31,31,31	0
57	MG	YA	3202	1/1	0.77	0.54	-	22,22,22,22	0
57	MG	YA	3198	1/1	0.89	0.37	-	25,25,25,25	0
57	MG	RA	3110	1/1	0.56	0.31	-	38,38,38,38	0
57	MG	QA	1660	1/1	0.91	0.40	-	20,20,20,20	0
57	MG	YA	3040	1/1	0.94	0.18	-	5,5,5,5	0
57	MG	YA	3429	1/1	0.94	0.19	-	81,81,81,81	0
57	MG	YA	3222	1/1	0.39	0.49	-	78,78,78,78	0
57	MG	RA	3221	1/1	0.50	1.18	-	46,46,46,46	0
57	MG	XA	1745	1/1	0.87	0.12	-	47,47,47,47	0
57	MG	YA	3329	1/1	0.93	0.24	-	34,34,34,34	0
57	MG	RA	3036	1/1	0.97	0.36	-	4,4,4,4	0
57	MG	RA	3067	1/1	0.98	0.48	-	20,20,20,20	0
57	MG	RA	3051	1/1	0.99	0.36	-	11,11,11,11	0
57	MG	YA	3396	1/1	0.86	0.35	-	59,59,59,59	0
57	MG	YA	3459	1/1	0.65	0.54	-	42,42,42,42	0
57	MG	RA	3311	1/1	0.77	0.79	-	61,61,61,61	0
57	MG	XA	1699	1/1	0.90	0.25	-	31,31,31,31	0
57	MG	YA	3169	1/1	0.48	0.80	-	61,61,61,61	0
57	MG	QA	1618	1/1	0.88	0.44	-	32,32,32,32	0
57	MG	YA	3405	1/1	0.67	0.43	-	33,33,33,33	0
57	MG	RA	3227	1/1	0.94	0.50	-	36,36,36,36	0
57	MG	YA	3140	1/1	0.96	0.19	-	30,30,30,30	0
57	MG	YA	3464	1/1	0.97	0.14	-	46,46,46,46	0
57	MG	RA	3362	1/1	0.75	0.33	-	45,45,45,45	0
57	MG	YA	3466	1/1	0.78	0.35	-	58,58,58,58	0
57	MG	XA	1622	1/1	0.94	0.78	-	35,35,35,35	0
57	MG	RA	3195	1/1	0.95	0.21	-	20,20,20,20	0
57	MG	XA	1728	1/1	0.94	0.39	-	46,46,46,46	0
57	MG	XA	1715	1/1	0.97	0.36	-	27,27,27,27	0
57	MG	RA	3150	1/1	0.96	0.42	-	42,42,42,42	0
57	MG	RA	3155	1/1	0.91	0.20	-	27,27,27,27	0
57	MG	XA	1647	1/1	0.85	0.24	-	83,83,83,83	0
57	MG	YA	3175	1/1	0.88	0.18	-	34,34,34,34	0
57	MG	RA	3135	1/1	0.90	0.98	-	49,49,49,49	0
57	MG	YA	3160	1/1	0.87	0.37	-	42,42,42,42	0
57	MG	YA	3417	1/1	0.89	0.27	-	78,78,78,78	0
57	MG	RA	3176	1/1	0.76	0.41	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	XA	1620	1/1	0.93	0.21	-	30,30,30,30	0
57	MG	QA	1706	1/1	0.86	0.27	-	48,48,48,48	0
57	MG	QA	1663	1/1	0.65	1.30	-	64,64,64,64	0
57	MG	RA	3378	1/1	0.92	0.14	-	112,112,112,112	0
57	MG	YA	3020	1/1	0.93	0.28	-	19,19,19,19	0
57	MG	YA	3398	1/1	0.84	0.20	-	36,36,36,36	0
57	MG	XA	1736	1/1	0.69	0.16	-	45,45,45,45	0
57	MG	RA	3367	1/1	0.88	0.43	-	43,43,43,43	0
57	MG	YA	3299	1/1	0.92	0.28	-	70,70,70,70	0
57	MG	RA	3125	1/1	0.97	0.21	-	29,29,29,29	0
57	MG	YA	3183	1/1	0.74	0.31	-	28,28,28,28	0
57	MG	RA	3423	1/1	0.82	0.43	-	48,48,48,48	0
57	MG	RA	3138	1/1	0.94	0.30	-	49,49,49,49	0
57	MG	RA	3360	1/1	0.85	0.32	-	64,64,64,64	0
57	MG	YA	3336	1/1	0.91	0.27	-	32,32,32,32	0
57	MG	RA	3380	1/1	0.77	0.33	-	45,45,45,45	0
57	MG	RA	3041	1/1	0.99	0.33	-	7,7,7,7	0
57	MG	YA	3258	1/1	0.86	0.29	-	48,48,48,48	0
57	MG	RA	3045	1/1	0.95	0.32	-	11,11,11,11	0
57	MG	YA	3153	1/1	0.96	0.49	-	36,36,36,36	0
57	MG	XA	1615	1/1	0.98	0.55	-	46,46,46,46	0
57	MG	YA	3312	1/1	0.86	0.86	-	40,40,40,40	0
57	MG	RA	3371	1/1	0.97	0.20	-	33,33,33,33	0
57	MG	XA	1724	1/1	0.86	0.35	-	48,48,48,48	0
57	MG	XA	1730	1/1	0.73	0.29	-	55,55,55,55	0
57	MG	RA	3415	1/1	0.84	0.30	-	50,50,50,50	0
57	MG	YA	3302	1/1	0.89	0.42	-	57,57,57,57	0
57	MG	XA	1711	1/1	0.93	0.59	-	24,24,24,24	0
57	MG	RA	3095	1/1	0.87	0.76	-	47,47,47,47	0
57	MG	QA	1671	1/1	0.54	0.62	-	38,38,38,38	0
57	MG	YA	3401	1/1	0.85	0.25	-	56,56,56,56	0
57	MG	XA	1665	1/1	0.94	0.21	-	19,19,19,19	0
57	MG	YA	3117	1/1	0.90	0.39	-	34,34,34,34	0
57	MG	QA	1696	1/1	0.67	1.04	-	64,64,64,64	0
57	MG	R2	101	1/1	0.73	0.38	-	80,80,80,80	0
57	MG	XA	1660	1/1	0.93	0.20	-	27,27,27,27	0
57	MG	XA	1671	1/1	0.98	0.11	-	6,6,6,6	0
57	MG	RA	3289	1/1	0.98	0.12	-	14,14,14,14	0
57	MG	QA	1652	1/1	0.97	0.19	-	20,20,20,20	0
57	MG	XA	1737	1/1	0.88	0.20	-	40,40,40,40	0
57	MG	RA	3312	1/1	0.97	0.30	-	1,1,1,1	0
57	MG	RA	3388	1/1	0.85	0.52	-	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3090	1/1	0.92	0.32	-	34,34,34,34	0
57	MG	YA	3146	1/1	0.65	0.48	-	63,63,63,63	0
57	MG	RA	3030	1/1	0.95	0.30	-	16,16,16,16	0
57	MG	RA	3271	1/1	0.92	0.53	-	14,14,14,14	0
57	MG	YA	3409	1/1	0.74	0.68	-	54,54,54,54	0
57	MG	YA	3452	1/1	0.80	0.55	-	58,58,58,58	0
57	MG	YA	3254	1/1	0.92	0.18	-	41,41,41,41	0
57	MG	YA	3106	1/1	0.94	0.49	-	12,12,12,12	0
57	MG	QA	1715	1/1	0.96	0.15	-	46,46,46,46	0
57	MG	RA	3204	1/1	0.76	0.68	-	34,34,34,34	0
57	MG	YA	3206	1/1	0.94	0.21	-	27,27,27,27	0
57	MG	YA	3340	1/1	0.92	0.52	-	52,52,52,52	0
57	MG	RA	3172	1/1	0.89	0.43	-	50,50,50,50	0
57	MG	QA	1712	1/1	0.90	0.32	-	38,38,38,38	0
57	MG	Y0	103	1/1	0.89	0.27	-	18,18,18,18	0
57	MG	RA	3391	1/1	0.95	0.23	-	32,32,32,32	0
57	MG	RA	3330	1/1	0.67	0.20	-	64,64,64,64	0
57	MG	RA	3133	1/1	0.89	0.59	-	39,39,39,39	0
57	MG	YA	3052	1/1	0.97	0.60	-	26,26,26,26	0
57	MG	QA	1711	1/1	0.50	0.63	-	70,70,70,70	0
57	MG	YA	3266	1/1	0.88	0.89	-	43,43,43,43	0
57	MG	YA	3015	1/1	0.95	0.28	-	17,17,17,17	0
57	MG	RA	3076	1/1	0.97	0.29	-	13,13,13,13	0
57	MG	R5	102	1/1	0.81	0.44	-	33,33,33,33	0
57	MG	XA	1621	1/1	0.91	0.44	-	39,39,39,39	0
57	MG	YA	3142	1/1	0.87	0.51	-	50,50,50,50	0
57	MG	XA	1678	1/1	0.87	0.70	-	65,65,65,65	0
57	MG	XA	1755	1/1	0.64	0.45	-	61,61,61,61	0
57	MG	RA	3261	1/1	0.94	0.53	-	30,30,30,30	0
57	MG	YA	3300	1/1	0.80	0.61	-	35,35,35,35	0
57	MG	RA	3278	1/1	0.55	0.43	-	68,68,68,68	0
57	MG	RA	3356	1/1	0.95	0.13	-	56,56,56,56	0
57	MG	YA	3062	1/1	0.95	0.45	-	32,32,32,32	0
57	MG	RA	3161	1/1	0.97	0.18	-	44,44,44,44	0
57	MG	YA	3094	1/1	0.79	0.37	-	75,75,75,75	0
57	MG	XA	1654	1/1	0.84	0.57	-	26,26,26,26	0
57	MG	RA	3325	1/1	0.79	0.52	-	67,67,67,67	0
57	MG	XA	1722	1/1	0.64	1.08	-	74,74,74,74	0
57	MG	RA	3118	1/1	0.98	0.20	-	5,5,5,5	0
57	MG	RA	3336	1/1	0.92	0.10	-	32,32,32,32	0
57	MG	RA	3132	1/1	0.87	0.54	-	35,35,35,35	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	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3374	1/1	0.82	0.23	-	38,38,38,38	0
57	MG	RA	3040	1/1	0.68	0.18	-	19,19,19,19	0
57	MG	YA	3316	1/1	0.78	0.64	-	53,53,53,53	0
57	MG	RA	3191	1/1	0.97	0.17	-	10,10,10,10	0
57	MG	QA	1735	1/1	0.85	0.14	-	40,40,40,40	0
57	MG	RA	3346	1/1	0.94	0.69	-	53,53,53,53	0
57	MG	QV	102	1/1	0.89	0.22	-	15,15,15,15	0
57	MG	XA	1718	1/1	0.79	0.71	-	51,51,51,51	0
57	MG	YA	3350	1/1	0.87	0.25	-	28,28,28,28	0
57	MG	YA	3373	1/1	0.79	0.59	-	42,42,42,42	0
57	MG	YA	3277	1/1	0.94	0.14	-	83,83,83,83	0
57	MG	XA	1681	1/1	0.82	1.08	-	49,49,49,49	0
57	MG	RA	3355	1/1	0.89	0.10	-	51,51,51,51	0
57	MG	QA	1679	1/1	0.91	0.22	-	39,39,39,39	0
57	MG	RA	3357	1/1	0.93	0.33	-	45,45,45,45	0
57	MG	YA	3064	1/1	0.99	0.15	-	11,11,11,11	0
57	MG	YA	3333	1/1	0.59	0.80	-	47,47,47,47	0
57	MG	YA	3328	1/1	0.83	0.41	-	55,55,55,55	0
57	MG	YA	3241	1/1	0.96	0.27	-	19,19,19,19	0
57	MG	YA	3036	1/1	0.99	0.44	-	7,7,7,7	0
57	MG	YA	3388	1/1	0.70	0.39	-	55,55,55,55	0
57	MG	XV	103	1/1	0.44	0.41	-	62,62,62,62	0
57	MG	RA	3186	1/1	0.80	0.54	-	40,40,40,40	0
57	MG	QA	1635	1/1	0.97	0.23	-	30,30,30,30	0
57	MG	QA	1672	1/1	0.71	0.73	-	71,71,71,71	0
57	MG	YA	3363	1/1	0.92	0.58	-	29,29,29,29	0
57	MG	XA	1685	1/1	0.95	0.14	-	17,17,17,17	0
57	MG	XA	1751	1/1	0.78	0.34	-	59,59,59,59	0
57	MG	YA	3043	1/1	0.94	0.43	-	7,7,7,7	0
57	MG	YA	3377	1/1	0.57	0.51	-	85,85,85,85	0
57	MG	RA	3085	1/1	0.98	0.17	-	26,26,26,26	0
57	MG	YA	3129	1/1	0.97	0.39	-	20,20,20,20	0
57	MG	RA	3075	1/1	0.97	0.22	-	14,14,14,14	0
57	MG	YA	3149	1/1	0.95	0.38	-	37,37,37,37	0
57	MG	YA	3369	1/1	0.87	0.26	-	58,58,58,58	0
57	MG	QA	1707	1/1	0.75	0.60	-	64,64,64,64	0
57	MG	QA	1674	1/1	0.88	0.42	-	57,57,57,57	0
57	MG	XA	1610	1/1	0.94	0.38	-	22,22,22,22	0
57	MG	RA	3114	1/1	0.96	0.25	-	29,29,29,29	0
57	MG	RA	3347	1/1	0.80	0.95	-	65,65,65,65	0
57	MG	QA	1743	1/1	0.72	0.33	-	71,71,71,71	0
57	MG	YA	3041	1/1	0.99	0.31	-	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3240	1/1	0.85	0.22	-	43,43,43,43	0
57	MG	RA	3295	1/1	0.95	0.21	-	41,41,41,41	0
57	MG	XA	1666	1/1	0.80	0.48	-	46,46,46,46	0
57	MG	XA	1628	1/1	0.92	0.37	-	33,33,33,33	0
57	MG	XA	1749	1/1	0.61	0.40	-	81,81,81,81	0
57	MG	YA	3289	1/1	0.97	0.30	-	31,31,31,31	0
57	MG	RA	3144	1/1	0.98	0.37	-	11,11,11,11	0
57	MG	XA	1697	1/1	0.77	0.33	-	52,52,52,52	0
57	MG	YA	3313	1/1	0.80	0.18	-	65,65,65,65	0
57	MG	RA	3220	1/1	0.94	0.24	-	34,34,34,34	0
57	MG	Y0	101	1/1	0.81	0.29	-	12,12,12,12	0
57	MG	XA	1694	1/1	0.88	0.19	-	43,43,43,43	0
57	MG	QA	1629	1/1	0.78	0.45	-	46,46,46,46	0
57	MG	YA	3362	1/1	0.90	0.84	-	31,31,31,31	0
57	MG	RA	3256	1/1	0.85	0.36	-	47,47,47,47	0
57	MG	YA	3355	1/1	0.60	0.33	-	39,39,39,39	0
57	MG	YA	3435	1/1	0.97	0.17	-	35,35,35,35	0
57	MG	QA	1705	1/1	0.81	0.45	-	47,47,47,47	0
57	MG	XA	1657	1/1	0.96	0.50	-	34,34,34,34	0
57	MG	YA	3193	1/1	0.92	0.72	-	27,27,27,27	0
57	MG	YA	3311	1/1	0.98	0.14	-	60,60,60,60	0
57	MG	YA	3414	1/1	0.95	0.11	-	127,127,127,127	0
57	MG	RA	3377	1/1	0.98	0.42	-	10,10,10,10	0
57	MG	XA	1760	1/1	0.57	0.24	-	71,71,71,71	0
57	MG	XA	1677	1/1	0.85	0.15	-	39,39,39,39	0
57	MG	XA	1606	1/1	0.96	0.42	-	10,10,10,10	0
57	MG	YA	3004	1/1	0.98	0.30	-	4,4,4,4	0
57	MG	YA	3039	1/1	0.95	0.47	-	9,9,9,9	0
57	MG	YA	3176	1/1	0.98	0.35	-	3,3,3,3	0
57	MG	YA	3314	1/1	0.94	0.28	-	43,43,43,43	0
57	MG	QA	1708	1/1	0.93	0.43	-	19,19,19,19	0
57	MG	XA	1616	1/1	0.99	0.29	-	11,11,11,11	0
57	MG	QA	1740	1/1	0.77	0.59	-	69,69,69,69	0
57	MG	XA	1704	1/1	0.84	0.28	-	55,55,55,55	0
57	MG	RA	3156	1/1	0.92	0.10	-	36,36,36,36	0
57	MG	QA	1613	1/1	0.78	0.43	-	50,50,50,50	0
57	MG	RA	3253	1/1	0.90	0.32	-	21,21,21,21	0
57	MG	XA	1706	1/1	0.84	0.36	-	41,41,41,41	0
57	MG	YA	3030	1/1	0.98	0.48	-	6,6,6,6	0
57	MG	YA	3019	1/1	0.92	0.36	-	14,14,14,14	0
57	MG	RA	3279	1/1	0.87	0.40	-	40,40,40,40	0
57	MG	RA	3178	1/1	0.96	0.27	-	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3382	1/1	0.84	0.25	-	37,37,37,37	0
57	MG	RA	3126	1/1	0.93	0.56	-	67,67,67,67	0
57	MG	XA	1675	1/1	0.91	0.77	-	29,29,29,29	0
57	MG	YA	3051	1/1	0.95	0.44	-	4,4,4,4	0
57	MG	YA	3391	1/1	0.94	0.70	-	44,44,44,44	0
57	MG	RA	3197	1/1	0.96	0.32	-	17,17,17,17	0
57	MG	RA	3338	1/1	0.77	0.43	-	52,52,52,52	0
57	MG	QA	1630	1/1	0.81	0.24	-	55,55,55,55	0
57	MG	QV	104	1/1	0.85	0.33	-	52,52,52,52	0
57	MG	XA	1727	1/1	0.96	0.18	-	31,31,31,31	0
57	MG	RA	3340	1/1	0.70	0.47	-	56,56,56,56	0
57	MG	RA	3404	1/1	0.98	0.19	-	51,51,51,51	0
57	MG	RA	3379	1/1	0.97	0.17	-	44,44,44,44	0
57	MG	RA	3009	1/1	0.96	0.60	-	16,16,16,16	0
57	MG	YA	3281	1/1	0.92	0.07	-	28,28,28,28	0
57	MG	YA	3269	1/1	0.90	0.18	-	35,35,35,35	0
57	MG	RA	3258	1/1	0.98	0.26	-	32,32,32,32	0
57	MG	RA	3177	1/1	0.79	0.49	-	45,45,45,45	0
57	MG	RA	3257	1/1	0.94	0.55	-	48,48,48,48	0
57	MG	QA	1621	1/1	0.81	0.19	-	49,49,49,49	0
57	MG	YA	3271	1/1	0.97	0.30	-	25,25,25,25	0
57	MG	QA	1716	1/1	0.79	0.97	-	35,35,35,35	0
57	MG	RA	3160	1/1	0.89	0.36	-	58,58,58,58	0
57	MG	XA	1744	1/1	0.90	0.28	-	36,36,36,36	0
57	MG	R0	102	1/1	0.69	0.46	-	47,47,47,47	0
57	MG	YA	3439	1/1	0.78	0.33	-	53,53,53,53	0
57	MG	YA	3195	1/1	0.78	0.29	-	30,30,30,30	0
57	MG	YA	3402	1/1	0.95	0.48	-	14,14,14,14	0
57	MG	XA	1633	1/1	0.84	0.25	-	49,49,49,49	0
57	MG	YA	3291	1/1	0.88	0.88	-	34,34,34,34	0
57	MG	QA	1720	1/1	0.94	0.19	-	35,35,35,35	0
57	MG	YA	3349	1/1	0.68	0.42	-	63,63,63,63	0
57	MG	XA	1631	1/1	0.74	0.29	-	74,74,74,74	0
57	MG	RA	3387	1/1	0.91	0.41	-	24,24,24,24	0
57	MG	QA	1608	1/1	0.86	0.29	-	25,25,25,25	0
57	MG	YB	204	1/1	0.92	0.14	-	54,54,54,54	0
57	MG	YA	3367	1/1	0.72	0.30	-	57,57,57,57	0
57	MG	RA	3057	1/1	0.98	0.28	-	5,5,5,5	0
57	MG	YA	3228	1/1	0.76	1.27	-	51,51,51,51	0
57	MG	RA	3403	1/1	0.72	0.33	-	59,59,59,59	0
57	MG	YA	3263	1/1	0.90	0.47	-	50,50,50,50	0
57	MG	RA	3416	1/1	0.70	0.29	-	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	QA	1649	1/1	0.96	0.29	-	22,22,22,22	0
57	MG	YA	3179	1/1	0.70	0.46	-	64,64,64,64	0
57	MG	YA	3184	1/1	0.68	0.42	-	49,49,49,49	0
57	MG	YA	3446	1/1	0.55	0.34	-	49,49,49,49	0
57	MG	QA	1634	1/1	0.93	0.32	-	65,65,65,65	0
57	MG	YA	3194	1/1	0.91	0.17	-	56,56,56,56	0
57	MG	YP	202	1/1	0.88	0.39	-	38,38,38,38	0
57	MG	YA	3200	1/1	0.88	0.39	-	32,32,32,32	0
57	MG	YA	3001	1/1	0.89	0.79	-	28,28,28,28	0
57	MG	RA	3035	1/1	0.91	0.29	-	59,59,59,59	0
57	MG	XA	1693	1/1	0.86	0.15	-	25,25,25,25	0
57	MG	RA	3307	1/1	0.90	0.43	-	43,43,43,43	0
57	MG	YA	3295	1/1	0.85	0.38	-	46,46,46,46	0
57	MG	XA	1626	1/1	0.89	0.42	-	28,28,28,28	0
57	MG	YA	3296	1/1	0.97	0.49	-	34,34,34,34	0
57	MG	XA	1719	1/1	0.86	0.61	-	71,71,71,71	0
57	MG	RA	3381	1/1	0.93	0.70	-	11,11,11,11	0
57	MG	RA	3402	1/1	0.85	0.17	-	32,32,32,32	0
57	MG	QA	1729	1/1	0.86	0.16	-	54,54,54,54	0
57	MG	RA	3370	1/1	0.66	0.71	-	101,101,101,101	0
57	MG	YA	3187	1/1	0.86	0.48	-	35,35,35,35	0
57	MG	YA	3141	1/1	0.74	0.27	-	31,31,31,31	0
57	MG	YA	3303	1/1	0.70	0.44	-	47,47,47,47	0
57	MG	YA	3364	1/1	0.96	0.51	-	52,52,52,52	0
57	MG	YA	3229	1/1	0.97	0.29	-	54,54,54,54	0
57	MG	QA	1602	1/1	0.93	0.61	-	20,20,20,20	0
57	MG	YA	3235	1/1	0.87	0.46	-	19,19,19,19	0
57	MG	YA	3286	1/1	0.07	0.46	-	47,47,47,47	0
57	MG	YA	3197	1/1	0.93	0.27	-	23,23,23,23	0
57	MG	YA	3457	1/1	0.82	0.18	-	63,63,63,63	0
57	MG	QA	1732	1/1	0.93	0.42	-	60,60,60,60	0
57	MG	YA	3037	1/1	0.95	0.18	-	11,11,11,11	0
57	MG	RA	3020	1/1	0.99	0.36	-	9,9,9,9	0
57	MG	YA	3442	1/1	0.93	0.21	-	49,49,49,49	0
57	MG	RA	3328	1/1	0.88	0.45	-	37,37,37,37	0
57	MG	YA	3104	1/1	0.95	0.14	-	50,50,50,50	0
57	MG	RB	203	1/1	0.79	0.35	-	31,31,31,31	0
57	MG	QA	1710	1/1	0.68	0.51	-	59,59,59,59	0
57	MG	RA	3408	1/1	0.83	0.12	-	62,62,62,62	0
57	MG	RA	3023	1/1	0.94	0.54	-	3,3,3,3	0
57	MG	YA	3280	1/1	0.85	0.35	-	70,70,70,70	0
57	MG	RA	3353	1/1	0.79	0.39	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3264	1/1	0.74	0.52	-	60,60,60,60	0
57	MG	QA	1669	1/1	0.93	0.10	-	48,48,48,48	0
57	MG	YA	3247	1/1	0.94	0.46	-	30,30,30,30	0
57	MG	XA	1680	1/1	0.95	0.23	-	25,25,25,25	0
57	MG	RA	3424	1/1	0.91	0.21	-	45,45,45,45	0
57	MG	RA	3151	1/1	0.79	0.34	-	35,35,35,35	0
57	MG	QA	1733	1/1	0.76	0.35	-	57,57,57,57	0
57	MG	RA	3192	1/1	0.94	0.26	-	22,22,22,22	0
57	MG	R0	103	1/1	0.99	0.29	-	22,22,22,22	0
57	MG	QA	1622	1/1	0.96	0.19	-	20,20,20,20	0
57	MG	RA	3014	1/1	0.95	0.23	-	1,1,1,1	0
57	MG	QA	1647	1/1	0.52	0.23	-	72,72,72,72	0
57	MG	YA	3073	1/1	0.88	0.57	-	24,24,24,24	0
57	MG	QA	1677	1/1	0.79	0.19	-	86,86,86,86	0
57	MG	YA	3116	1/1	0.96	0.55	-	17,17,17,17	0
57	MG	YA	3151	1/1	0.88	0.54	-	15,15,15,15	0
57	MG	YA	3082	1/1	0.94	0.29	-	20,20,20,20	0
57	MG	RA	3202	1/1	0.94	0.10	-	40,40,40,40	0
57	MG	YA	3060	1/1	0.88	0.34	-	11,11,11,11	0
57	MG	YA	3133	1/1	0.95	0.60	-	28,28,28,28	0
57	MG	RA	3242	1/1	0.83	0.41	-	28,28,28,28	0
57	MG	YA	3318	1/1	0.71	0.81	-	48,48,48,48	0
57	MG	QA	1665	1/1	0.90	0.50	-	52,52,52,52	0
57	MG	YA	3034	1/1	0.96	0.24	-	24,24,24,24	0
57	MG	XA	1726	1/1	0.79	0.39	-	56,56,56,56	0
57	MG	YA	3279	1/1	0.82	0.17	-	71,71,71,71	0
57	MG	QA	1728	1/1	0.82	0.17	-	36,36,36,36	0
57	MG	YA	3370	1/1	0.89	0.48	-	39,39,39,39	0
57	MG	YB	203	1/1	0.89	0.35	-	16,16,16,16	0
57	MG	YA	3448	1/1	0.96	0.20	-	20,20,20,20	0
57	MG	YA	3342	1/1	0.74	0.79	-	43,43,43,43	0
57	MG	YA	3438	1/1	0.74	0.19	-	54,54,54,54	0
57	MG	YA	3413	1/1	0.92	0.19	-	36,36,36,36	0
57	MG	RA	3309	1/1	0.82	0.22	-	49,49,49,49	0
57	MG	RA	3263	1/1	0.83	0.29	-	50,50,50,50	0
57	MG	YA	3166	1/1	0.96	0.48	-	10,10,10,10	0
57	MG	RA	3187	1/1	0.72	0.40	-	42,42,42,42	0
57	MG	XA	1748	1/1	0.88	1.16	-	55,55,55,55	0
57	MG	RA	3427	1/1	0.84	0.28	-	56,56,56,56	0
57	MG	QA	1650	1/1	0.91	0.38	-	31,31,31,31	0
57	MG	QA	1717	1/1	0.88	0.43	-	55,55,55,55	0
57	MG	XA	1738	1/1	0.90	0.45	-	35,35,35,35	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3325	1/1	0.66	0.93	-	53,53,53,53	0
57	MG	QA	1731	1/1	0.54	0.35	-	54,54,54,54	0
57	MG	XA	1735	1/1	0.80	0.43	-	18,18,18,18	0
57	MG	QA	1721	1/1	0.88	1.37	-	46,46,46,46	0
57	MG	YA	3066	1/1	0.97	0.33	-	29,29,29,29	0
57	MG	RA	3269	1/1	0.74	0.49	-	50,50,50,50	0
57	MG	XA	1690	1/1	0.95	0.39	-	29,29,29,29	0
57	MG	YA	3144	1/1	0.98	0.46	-	41,41,41,41	0
57	MG	RA	3421	1/1	0.76	0.42	-	43,43,43,43	0
57	MG	YA	3256	1/1	0.95	0.17	-	15,15,15,15	0
57	MG	RA	3019	1/1	0.94	0.30	-	16,16,16,16	0
57	MG	XA	1733	1/1	0.99	0.38	-	8,8,8,8	0
57	MG	YA	3458	1/1	0.91	0.14	-	49,49,49,49	0
57	MG	YA	3272	1/1	0.97	0.37	-	49,49,49,49	0
57	MG	YA	3372	1/1	0.68	0.49	-	43,43,43,43	0
57	MG	QA	1661	1/1	0.88	0.26	-	57,57,57,57	0
57	MG	QA	1664	1/1	0.97	0.23	-	23,23,23,23	0
57	MG	QD	302	1/1	0.37	1.30	-	78,78,78,78	0
57	MG	YA	3365	1/1	0.83	0.65	-	24,24,24,24	0
57	MG	YA	3007	1/1	0.91	0.50	-	13,13,13,13	0
57	MG	XA	1658	1/1	0.93	0.21	-	25,25,25,25	0
57	MG	RA	3324	1/1	0.73	0.27	-	62,62,62,62	0
57	MG	RA	3333	1/1	0.72	0.46	-	50,50,50,50	0
57	MG	XA	1754	1/1	0.85	0.16	-	84,84,84,84	0
57	MG	XA	1617	1/1	0.97	0.56	-	36,36,36,36	0
57	MG	XA	1689	1/1	0.63	1.16	-	52,52,52,52	0
57	MG	YA	3207	1/1	0.98	0.61	-	13,13,13,13	0
57	MG	YA	3218	1/1	0.92	0.35	-	23,23,23,23	0
57	MG	YA	3366	1/1	0.88	0.47	-	29,29,29,29	0
57	MG	YA	3310	1/1	0.82	0.74	-	50,50,50,50	0
57	MG	RA	3200	1/1	0.91	0.36	-	20,20,20,20	0
57	MG	QA	1714	1/1	0.97	0.32	-	66,66,66,66	0
57	MG	XA	1651	1/1	0.86	0.41	-	29,29,29,29	0
57	MG	YA	3114	1/1	0.91	0.42	-	36,36,36,36	0
57	MG	Y5	101	1/1	0.96	0.13	-	7,7,7,7	0
57	MG	XA	1663	1/1	0.85	0.42	-	30,30,30,30	0
57	MG	RA	3117	1/1	0.96	0.56	-	28,28,28,28	0
57	MG	XA	1686	1/1	0.78	0.47	-	47,47,47,47	0
57	MG	YY	201	1/1	0.82	0.30	-	33,33,33,33	0
57	MG	RA	3218	1/1	0.79	0.18	-	39,39,39,39	0
57	MG	YA	3440	1/1	0.78	0.29	-	75,75,75,75	0
57	MG	RA	3284	1/1	0.78	0.67	-	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3183	1/1	0.95	0.50	-	67,67,67,67	0
57	MG	RA	3401	1/1	0.88	0.63	-	60,60,60,60	0
57	MG	RA	3293	1/1	0.91	0.59	-	21,21,21,21	0
57	MG	QA	1736	1/1	0.92	0.56	-	49,49,49,49	0
57	MG	RA	3418	1/1	0.92	0.24	-	39,39,39,39	0
57	MG	QA	1657	1/1	0.94	0.36	-	21,21,21,21	0
57	MG	YA	3351	1/1	0.70	0.45	-	48,48,48,48	0
57	MG	YA	3384	1/1	0.81	1.00	-	53,53,53,53	0
57	MG	YA	3196	1/1	0.98	0.40	-	22,22,22,22	0
57	MG	YA	3319	1/1	0.96	0.29	-	41,41,41,41	0
57	MG	Y0	102	1/1	0.94	0.10	-	24,24,24,24	0
57	MG	XA	1723	1/1	0.81	0.36	-	35,35,35,35	0
57	MG	RA	3152	1/1	0.88	0.84	-	33,33,33,33	0
57	MG	RA	3399	1/1	0.89	0.22	-	46,46,46,46	0
57	MG	YA	3212	1/1	0.95	0.66	-	25,25,25,25	0
57	MG	YA	3408	1/1	0.98	0.07	-	46,46,46,46	0
57	MG	RA	3215	1/1	0.88	0.32	-	29,29,29,29	0
57	MG	YA	3376	1/1	0.67	0.37	-	82,82,82,82	0
57	MG	YA	3137	1/1	0.98	0.26	-	5,5,5,5	0
57	MG	YA	3400	1/1	0.79	0.42	-	80,80,80,80	0
57	MG	RA	3228	1/1	0.87	0.25	-	47,47,47,47	0
57	MG	YA	3224	1/1	0.88	0.25	-	15,15,15,15	0
57	MG	YA	3049	1/1	0.98	0.43	-	4,4,4,4	0
57	MG	RA	3349	1/1	0.95	0.47	-	49,49,49,49	0
57	MG	YA	3332	1/1	0.86	0.66	-	36,36,36,36	0
57	MG	RA	3302	1/1	0.78	0.55	-	36,36,36,36	0
57	MG	RA	3004	1/1	0.99	0.55	-	3,3,3,3	0
57	MG	RA	3188	1/1	0.96	0.46	-	38,38,38,38	0
57	MG	QA	1642	1/1	0.98	0.19	-	51,51,51,51	0
57	MG	YA	3394	1/1	0.68	0.26	-	61,61,61,61	0
57	MG	RA	3374	1/1	0.91	0.35	-	18,18,18,18	0
57	MG	YA	3121	1/1	0.98	0.36	-	11,11,11,11	0
57	MG	XA	1691	1/1	0.95	0.18	-	27,27,27,27	0
57	MG	Y7	101	1/1	0.83	0.40	-	43,43,43,43	0
57	MG	QV	105	1/1	0.82	0.22	-	34,34,34,34	0
57	MG	RA	3225	1/1	0.96	0.18	-	23,23,23,23	0
57	MG	YA	3308	1/1	0.95	0.30	-	26,26,26,26	0
57	MG	RA	3182	1/1	0.69	0.41	-	56,56,56,56	0
57	MG	RA	3091	1/1	0.81	0.22	-	29,29,29,29	0
57	MG	YA	3356	1/1	0.71	0.20	-	55,55,55,55	0
57	MG	XA	1725	1/1	0.78	0.45	-	64,64,64,64	0
57	MG	RA	3425	1/1	0.78	0.49	-	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3412	1/1	0.83	0.42	-	57,57,57,57	0
57	MG	RA	3372	1/1	0.72	0.43	-	44,44,44,44	0
57	MG	YA	3430	1/1	0.83	0.16	-	43,43,43,43	0
57	MG	RA	3334	1/1	0.69	0.67	-	40,40,40,40	0
57	MG	QA	1603	1/1	0.92	0.19	-	53,53,53,53	0
57	MG	YA	3216	1/1	0.89	0.27	-	24,24,24,24	0
57	MG	XA	1629	1/1	0.85	0.15	-	53,53,53,53	0
57	MG	YA	3344	1/1	0.89	0.23	-	71,71,71,71	0
57	MG	RA	3344	1/1	0.91	0.23	-	39,39,39,39	0
57	MG	YA	3115	1/1	0.98	0.16	-	3,3,3,3	0
57	MG	YA	3392	1/1	0.60	0.31	-	52,52,52,52	0
57	MG	Y5	103	1/1	0.62	0.62	-	50,50,50,50	0
57	MG	QL	201	1/1	0.78	0.23	-	49,49,49,49	0
57	MG	YA	3002	1/1	0.98	0.19	-	5,5,5,5	0
57	MG	RA	3303	1/1	0.94	0.16	-	44,44,44,44	0
57	MG	YA	3214	1/1	0.93	0.23	-	34,34,34,34	0
57	MG	YA	3305	1/1	0.94	0.47	-	38,38,38,38	0
57	MG	QA	1694	1/1	0.93	0.17	-	31,31,31,31	0
57	MG	RA	3351	1/1	0.94	0.22	-	70,70,70,70	0
57	MG	XA	1649	1/1	0.95	0.22	-	13,13,13,13	0
57	MG	QA	1658	1/1	0.46	0.58	-	34,34,34,34	0
57	MG	YA	3250	1/1	0.82	0.54	-	67,67,67,67	0
57	MG	YQ	202	1/1	0.63	0.60	-	39,39,39,39	0
57	MG	YA	3357	1/1	0.75	0.50	-	34,34,34,34	0
57	MG	XA	1673	1/1	0.98	0.20	-	45,45,45,45	0
57	MG	YA	3257	1/1	0.91	0.32	-	51,51,51,51	0
57	MG	RA	3341	1/1	0.84	0.28	-	46,46,46,46	0
57	MG	QA	1620	1/1	0.86	0.57	-	30,30,30,30	0
57	MG	YA	3204	1/1	0.90	0.29	-	34,34,34,34	0
57	MG	YA	3431	1/1	0.72	0.36	-	65,65,65,65	0
57	MG	RA	3061	1/1	0.89	0.42	-	28,28,28,28	0
57	MG	RA	3322	1/1	0.92	0.27	-	30,30,30,30	0
57	MG	RA	3243	1/1	0.95	0.11	-	37,37,37,37	0
57	MG	RA	3039	1/1	0.92	0.49	-	7,7,7,7	0
57	MG	YA	3245	1/1	0.93	0.38	-	33,33,33,33	0
57	MG	YA	3453	1/1	0.91	0.21	-	33,33,33,33	0
57	MG	RA	3154	1/1	0.83	0.41	-	48,48,48,48	0
57	MG	QA	1702	1/1	0.91	0.14	-	99,99,99,99	0
57	MG	QA	1627	1/1	0.87	0.41	-	52,52,52,52	0
57	MG	YA	3473	1/1	0.98	0.40	-	8,8,8,8	0
57	MG	RA	3022	1/1	0.84	0.34	-	52,52,52,52	0
57	MG	RA	3397	1/1	0.85	0.39	-	34,34,34,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3074	1/1	0.97	0.43	-	13,13,13,13	0
57	MG	XA	1683	1/1	0.86	0.50	-	45,45,45,45	0
57	MG	XA	1661	1/1	0.88	0.44	-	28,28,28,28	0
57	MG	RA	3162	1/1	0.93	0.16	-	23,23,23,23	0
57	MG	YA	3347	1/1	0.80	0.39	-	44,44,44,44	0
57	MG	YA	3111	1/1	0.94	0.25	-	21,21,21,21	0
57	MG	YA	3261	1/1	0.79	0.39	-	54,54,54,54	0
57	MG	YA	3045	1/1	0.95	0.41	-	8,8,8,8	0
57	MG	YA	3444	1/1	0.94	0.16	-	50,50,50,50	0
57	MG	YA	3076	1/1	0.93	0.42	-	24,24,24,24	0
57	MG	RA	3275	1/1	0.66	0.63	-	79,79,79,79	0
57	MG	RA	3233	1/1	0.85	0.36	-	37,37,37,37	0
57	MG	RA	3043	1/1	0.95	0.47	-	7,7,7,7	0
57	MG	RA	3304	1/1	0.96	0.28	-	36,36,36,36	0
57	MG	YA	3181	1/1	0.53	0.30	-	58,58,58,58	0
57	MG	YA	3354	1/1	0.77	0.42	-	67,67,67,67	0
57	MG	YA	3159	1/1	0.94	0.39	-	26,26,26,26	0
57	MG	QA	1623	1/1	0.92	0.61	-	37,37,37,37	0
57	MG	YA	3298	1/1	0.94	0.67	-	41,41,41,41	0
57	MG	RA	3050	1/1	0.87	0.51	-	23,23,23,23	0
57	MG	YA	3307	1/1	0.85	0.23	-	43,43,43,43	0
57	MG	YA	3177	1/1	0.90	0.32	-	26,26,26,26	0
57	MG	YA	3244	1/1	0.89	0.74	-	34,34,34,34	0
57	MG	RA	3273	1/1	0.96	0.09	-	53,53,53,53	0
57	MG	RY	201	1/1	0.91	0.20	-	24,24,24,24	0
57	MG	QA	1609	1/1	0.85	0.32	-	57,57,57,57	0
57	MG	YA	3445	1/1	0.95	0.25	-	25,25,25,25	0
57	MG	RA	3096	1/1	0.94	0.73	-	29,29,29,29	0
57	MG	YA	3379	1/1	0.91	0.20	-	44,44,44,44	0
57	MG	RA	3319	1/1	0.94	0.15	-	95,95,95,95	0
57	MG	YA	3143	1/1	0.98	0.39	-	28,28,28,28	0
57	MG	RA	3016	1/1	0.97	0.08	-	7,7,7,7	0
57	MG	RA	3002	1/1	0.95	0.32	-	24,24,24,24	0
57	MG	YA	3385	1/1	0.94	0.27	-	40,40,40,40	0
57	MG	YA	3180	1/1	0.89	0.33	-	38,38,38,38	0
57	MG	YA	3172	1/1	0.69	0.36	-	43,43,43,43	0
57	MG	RA	3226	1/1	0.92	0.31	-	49,49,49,49	0
57	MG	QA	1675	1/1	0.90	0.18	-	36,36,36,36	0
57	MG	RA	3316	1/1	0.78	0.57	-	52,52,52,52	0
57	MG	RA	3028	1/1	0.91	0.34	-	34,34,34,34	0
57	MG	RA	3426	1/1	0.91	0.25	-	24,24,24,24	0
57	MG	YA	3412	1/1	0.81	0.34	-	49,49,49,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3315	1/1	0.96	0.43	-	25,25,25,25	0
57	MG	QA	1690	1/1	0.81	0.49	-	27,27,27,27	0
57	MG	XA	1634	1/1	0.93	0.30	-	17,17,17,17	0
57	MG	XA	1747	1/1	0.96	0.27	-	55,55,55,55	0
57	MG	RE	302	1/1	0.83	0.31	-	53,53,53,53	0
57	MG	YA	3283	1/1	0.84	0.59	-	66,66,66,66	0
57	MG	YA	3462	1/1	0.97	0.54	-	39,39,39,39	0
57	MG	YA	3252	1/1	0.88	0.46	-	47,47,47,47	0
57	MG	RA	3090	1/1	0.80	0.33	-	52,52,52,52	0
57	MG	YE	301	1/1	0.96	0.29	-	4,4,4,4	0
57	MG	XA	1700	1/1	0.67	0.59	-	36,36,36,36	0
57	MG	QA	1742	1/1	0.71	0.57	-	57,57,57,57	0
57	MG	YA	3215	1/1	0.87	0.26	-	15,15,15,15	0
57	MG	RA	3390	1/1	0.74	0.20	-	53,53,53,53	0
57	MG	YA	3123	1/1	0.98	0.32	-	5,5,5,5	0
57	MG	QA	1698	1/1	0.82	0.34	-	69,69,69,69	0
57	MG	RA	3383	1/1	0.95	0.34	-	26,26,26,26	0
57	MG	RQ	201	1/1	0.89	0.42	-	37,37,37,37	0
57	MG	RA	3268	1/1	0.86	0.44	-	35,35,35,35	0
57	MG	QA	1695	1/1	0.67	0.34	-	48,48,48,48	0
57	MG	RA	3105	1/1	0.91	0.15	-	38,38,38,38	0
57	MG	YA	3339	1/1	0.93	0.37	-	31,31,31,31	0
57	MG	RA	3210	1/1	0.77	0.37	-	29,29,29,29	0
57	MG	YA	3210	1/1	0.77	0.16	-	29,29,29,29	0
57	MG	RR	201	1/1	0.83	0.43	-	21,21,21,21	0
57	MG	YA	3345	1/1	0.94	0.26	-	29,29,29,29	0
57	MG	QA	1667	1/1	0.96	0.16	-	39,39,39,39	0
57	MG	QA	1646	1/1	0.89	0.53	-	70,70,70,70	0
57	MG	RA	3169	1/1	0.93	0.85	-	39,39,39,39	0
57	MG	RA	3104	1/1	0.93	0.17	-	34,34,34,34	0
57	MG	RA	3414	1/1	0.84	0.44	-	45,45,45,45	0
57	MG	RA	3364	1/1	0.90	0.20	-	67,67,67,67	0
57	MG	YA	3262	1/1	0.93	0.38	-	14,14,14,14	0
57	MG	YA	3359	1/1	0.91	0.39	-	52,52,52,52	0
57	MG	YA	3410	1/1	0.48	0.33	-	43,43,43,43	0
57	MG	YA	3100	1/1	0.93	0.39	-	23,23,23,23	0
57	MG	YA	3465	1/1	0.83	0.43	-	47,47,47,47	0
57	MG	QA	1676	1/1	0.96	0.32	-	40,40,40,40	0
57	MG	Y5	102	1/1	0.89	0.41	-	16,16,16,16	0
57	MG	QA	1638	1/1	0.87	0.22	-	67,67,67,67	0
57	MG	RA	3219	1/1	0.74	0.31	-	31,31,31,31	0
57	MG	RA	3201	1/1	0.92	0.46	-	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	XA	1729	1/1	0.72	1.08	-	48,48,48,48	0
57	MG	RA	3099	1/1	0.93	0.43	-	32,32,32,32	0
57	MG	RA	3359	1/1	0.92	0.35	-	42,42,42,42	0
57	MG	XA	1705	1/1	0.87	0.62	-	30,30,30,30	0
57	MG	QA	1607	1/1	0.95	0.50	-	26,26,26,26	0
57	MG	YV	201	1/1	0.93	0.33	-	11,11,11,11	0
57	MG	YA	3447	1/1	0.78	0.24	-	38,38,38,38	0
57	MG	QA	1653	1/1	0.97	0.34	-	25,25,25,25	0
57	MG	XV	102	1/1	0.94	0.28	-	0,0,0,0	0
57	MG	YA	3098	1/1	0.91	0.45	-	69,69,69,69	0
57	MG	YA	3035	1/1	0.91	0.26	-	26,26,26,26	0
57	MG	YA	3353	1/1	0.56	0.48	-	34,34,34,34	0
57	MG	RA	3164	1/1	0.96	0.25	-	34,34,34,34	0
57	MG	YA	3088	1/1	0.83	0.56	-	21,21,21,21	0
57	MG	RA	3224	1/1	0.93	0.48	-	37,37,37,37	0
57	MG	XA	1612	1/1	0.82	0.32	-	49,49,49,49	0
57	MG	YB	206	1/1	0.67	0.23	-	50,50,50,50	0
57	MG	QE	201	1/1	0.71	0.25	-	62,62,62,62	0
57	MG	QA	1615	1/1	0.93	0.20	-	59,59,59,59	0
57	MG	RA	3235	1/1	0.98	0.10	-	20,20,20,20	0
57	MG	RA	3321	1/1	0.90	0.39	-	37,37,37,37	0
57	MG	YA	3436	1/1	0.83	0.26	-	22,22,22,22	0
57	MG	RA	3037	1/1	0.93	0.19	-	1,1,1,1	0
57	MG	QA	1633	1/1	0.89	0.32	-	39,39,39,39	0
57	MG	QA	1709	1/1	0.83	0.59	-	45,45,45,45	0
57	MG	XA	1756	1/1	0.74	0.54	-	59,59,59,59	0
57	MG	RA	3137	1/1	0.95	0.32	-	22,22,22,22	0
57	MG	YA	3163	1/1	0.94	0.23	-	21,21,21,21	0
57	MG	RA	3250	1/1	0.96	0.31	-	31,31,31,31	0
57	MG	YA	3463	1/1	0.95	0.22	-	48,48,48,48	0
57	MG	RA	3373	1/1	0.96	0.14	-	52,52,52,52	0
57	MG	R0	101	1/1	0.92	0.29	-	14,14,14,14	0
57	MG	YA	3273	1/1	0.93	0.30	-	48,48,48,48	0
57	MG	RA	3305	1/1	0.92	0.17	-	24,24,24,24	0
57	MG	YA	3158	1/1	0.87	0.25	-	43,43,43,43	0
57	MG	RA	3298	1/1	0.57	0.75	-	79,79,79,79	0
57	MG	RB	205	1/1	0.80	0.39	-	58,58,58,58	0
57	MG	RA	3246	1/1	0.92	0.23	-	22,22,22,22	0
57	MG	YA	3118	1/1	0.96	0.28	-	23,23,23,23	0
57	MG	RA	3048	1/1	0.63	0.62	-	27,27,27,27	0
57	MG	XA	1674	1/1	0.98	0.09	-	18,18,18,18	0
57	MG	YA	3288	1/1	0.96	0.25	-	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	QA	1724	1/1	0.68	0.27	-	60,60,60,60	0
57	MG	RA	3285	1/1	0.83	0.47	-	35,35,35,35	0
57	MG	RA	3181	1/1	0.86	0.51	-	62,62,62,62	0
57	MG	RA	3358	1/1	0.87	1.03	-	57,57,57,57	0
57	MG	YA	3315	1/1	0.76	0.22	-	55,55,55,55	0
57	MG	XA	1701	1/1	0.95	0.37	-	30,30,30,30	0
57	MG	RA	3112	1/1	0.98	0.16	-	36,36,36,36	0
57	MG	RA	3300	1/1	0.44	0.72	-	44,44,44,44	0
57	MG	RA	3365	1/1	0.62	0.27	-	58,58,58,58	0
57	MG	RA	3136	1/1	0.94	0.36	-	61,61,61,61	0
57	MG	RA	3407	1/1	0.85	0.39	-	56,56,56,56	0
57	MG	RA	3089	1/1	0.77	0.50	-	33,33,33,33	0
57	MG	XA	1752	1/1	0.64	0.37	-	62,62,62,62	0
57	MG	RA	3211	1/1	0.89	0.10	-	26,26,26,26	0
57	MG	YA	3122	1/1	0.92	0.35	-	44,44,44,44	0
57	MG	RA	3123	1/1	0.93	0.40	-	33,33,33,33	0
57	MG	YA	3174	1/1	0.96	0.32	-	24,24,24,24	0
57	MG	XL	201	1/1	0.75	0.17	-	43,43,43,43	0
57	MG	YA	3125	1/1	0.99	0.28	-	13,13,13,13	0
57	MG	XA	1648	1/1	0.89	0.20	-	39,39,39,39	0
57	MG	YA	3322	1/1	0.77	0.67	-	42,42,42,42	0
57	MG	RA	3400	1/1	0.44	0.51	-	50,50,50,50	0
57	MG	XA	1641	1/1	0.96	0.11	-	38,38,38,38	0
57	MG	QA	1631	1/1	0.91	0.51	-	41,41,41,41	0
57	MG	XA	1720	1/1	0.71	0.83	-	62,62,62,62	0
57	MG	RA	3024	1/1	0.96	0.38	-	42,42,42,42	0
57	MG	QA	1703	1/1	0.63	0.30	-	57,57,57,57	0
57	MG	XA	1713	1/1	0.94	0.20	-	31,31,31,31	0
57	MG	RA	3274	1/1	0.96	0.28	-	41,41,41,41	0
57	MG	XA	1687	1/1	0.96	0.98	-	53,53,53,53	0
57	MG	YA	3267	1/1	0.83	0.85	-	49,49,49,49	0
57	MG	YA	3330	1/1	0.94	0.45	-	24,24,24,24	0
57	MG	RA	3313	1/1	0.84	0.36	-	50,50,50,50	0
57	MG	YA	3067	1/1	0.88	0.22	-	6,6,6,6	0
57	MG	RB	201	1/1	0.86	0.37	-	30,30,30,30	0
57	MG	YA	3165	1/1	0.96	0.27	-	37,37,37,37	0
57	MG	XA	1619	1/1	0.96	0.34	-	13,13,13,13	0
57	MG	RA	3405	1/1	0.96	0.49	-	52,52,52,52	0
57	MG	RA	3088	1/1	0.96	0.45	-	15,15,15,15	0
57	MG	QA	1611	1/1	0.96	0.33	-	33,33,33,33	0
57	MG	YA	3056	1/1	0.97	0.22	-	4,4,4,4	0
57	MG	XA	1758	1/1	0.81	0.67	-	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	YA	3095	1/1	0.91	0.77	-	16,16,16,16	0
57	MG	YA	3084	1/1	0.92	0.39	-	29,29,29,29	0
57	MG	YA	3292	1/1	0.85	0.50	-	33,33,33,33	0
57	MG	RA	3034	1/1	0.96	0.24	-	41,41,41,41	0
57	MG	YA	3368	1/1	0.64	0.51	-	36,36,36,36	0
57	MG	YA	3290	1/1	0.91	0.31	-	22,22,22,22	0
57	MG	QA	1617	1/1	0.92	0.38	-	37,37,37,37	0
57	MG	YA	3327	1/1	0.88	0.40	-	30,30,30,30	0
57	MG	YA	3085	1/1	0.98	0.17	-	7,7,7,7	0
57	MG	YA	3255	1/1	0.84	0.41	-	41,41,41,41	0
57	MG	RA	3270	1/1	0.79	0.56	-	35,35,35,35	0
57	MG	RA	3100	1/1	0.78	0.18	-	14,14,14,14	0
57	MG	YA	3321	1/1	0.94	0.22	-	36,36,36,36	0
57	MG	RA	3266	1/1	0.77	0.74	-	48,48,48,48	0
57	MG	YA	3415	1/1	0.96	0.51	-	24,24,24,24	0
57	MG	YA	3260	1/1	0.74	0.40	-	48,48,48,48	0
57	MG	YA	3173	1/1	0.94	0.22	-	43,43,43,43	0
57	MG	QA	1700	1/1	0.93	0.83	-	35,35,35,35	0
57	MG	RA	3207	1/1	0.95	0.49	-	20,20,20,20	0
57	MG	RA	3141	1/1	0.95	0.18	-	41,41,41,41	0
57	MG	XA	1714	1/1	0.61	0.83	-	54,54,54,54	0
57	MG	XA	1676	1/1	0.68	0.47	-	44,44,44,44	0
57	MG	YA	3320	1/1	0.97	0.21	-	56,56,56,56	0
57	MG	XV	104	1/1	0.93	0.15	-	16,16,16,16	0
57	MG	YA	3024	1/1	0.98	0.44	-	12,12,12,12	0
57	MG	YA	3009	1/1	0.97	0.46	-	10,10,10,10	0
57	MG	YA	3432	1/1	0.85	0.44	-	31,31,31,31	0
57	MG	RA	3222	1/1	0.86	0.46	-	30,30,30,30	0
57	MG	YA	3028	1/1	0.97	0.20	-	14,14,14,14	0
57	MG	YR	201	1/1	0.89	0.39	-	12,12,12,12	0
57	MG	RA	3113	1/1	0.91	0.25	-	33,33,33,33	0
57	MG	YA	3380	1/1	0.95	0.57	-	38,38,38,38	0
57	MG	YA	3301	1/1	0.58	0.85	-	65,65,65,65	0
57	MG	QA	1616	1/1	0.98	0.20	-	52,52,52,52	0
57	MG	XA	1698	1/1	0.91	0.47	-	112,112,112,112	0
57	MG	YA	3468	1/1	0.51	0.36	-	44,44,44,44	0
57	MG	YA	3023	1/1	0.96	0.40	-	2,2,2,2	0
57	MG	YA	3185	1/1	0.91	0.58	-	9,9,9,9	0
57	MG	YA	3381	1/1	0.82	0.27	-	35,35,35,35	0
57	MG	YA	3460	1/1	0.85	0.37	-	55,55,55,55	0
57	MG	RA	3231	1/1	0.88	0.61	-	30,30,30,30	0
57	MG	RA	3212	1/1	0.78	0.31	-	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
57	MG	RA	3196	1/1	0.89	0.65	-	39,39,39,39	0
57	MG	RA	3115	1/1	0.97	0.37	-	13,13,13,13	0
57	MG	YA	3276	1/1	0.85	0.38	-	53,53,53,53	0
57	MG	RA	3352	1/1	0.93	0.83	-	39,39,39,39	0
57	MG	YA	3390	1/1	0.71	0.26	-	54,54,54,54	0
57	MG	YA	3135	1/1	0.80	0.76	-	39,39,39,39	0
57	MG	YA	3284	1/1	0.83	0.35	-	57,57,57,57	0
57	MG	RA	3053	1/1	0.94	0.55	-	26,26,26,26	0
57	MG	RA	3111	1/1	0.92	0.20	-	38,38,38,38	0
57	MG	RA	3262	1/1	0.74	0.46	-	62,62,62,62	0
57	MG	RA	3267	1/1	0.96	0.34	-	51,51,51,51	0
57	MG	YA	3389	1/1	0.98	0.14	-	55,55,55,55	0
57	MG	QA	1738	1/1	0.88	0.11	-	42,42,42,42	0
57	MG	YA	3192	1/1	0.96	0.07	-	32,32,32,32	0
57	MG	RA	3237	1/1	0.82	0.39	-	54,54,54,54	0
57	MG	RA	3350	1/1	0.92	0.22	-	53,53,53,53	0
57	MG	YA	3387	1/1	0.87	0.21	-	49,49,49,49	0
57	MG	YA	3048	1/1	0.92	0.21	-	32,32,32,32	0
57	MG	XA	1709	1/1	0.67	1.07	-	63,63,63,63	0
57	MG	RA	3249	1/1	0.83	0.67	-	41,41,41,41	0
57	MG	QA	1713	1/1	0.94	0.36	-	32,32,32,32	0
57	MG	XA	1757	1/1	0.76	0.39	-	66,66,66,66	0
57	MG	QA	1628	1/1	0.83	0.16	-	61,61,61,61	0
57	MG	YA	3361	1/1	0.95	0.33	-	37,37,37,37	0
57	MG	YA	3268	1/1	0.72	0.38	-	51,51,51,51	0
57	MG	QA	1744	1/1	0.71	0.72	-	44,44,44,44	0
57	MG	YA	3383	1/1	0.83	0.23	-	47,47,47,47	0
57	MG	YB	202	1/1	0.94	0.56	-	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.