



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:59 PM GMT

PDB ID : 4V5E
Title : Insights into translational termination from the structure of RF2 bound to the ribosome
Authors : Weixlbaumer, A.; Jin, H.; Neubauer, C.; Voorhees, R.M.; Petry, S.; Kelley, A.C.; Ramakrishnan, V.
Deposited on : 2009-04-30
Resolution : 3.45 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

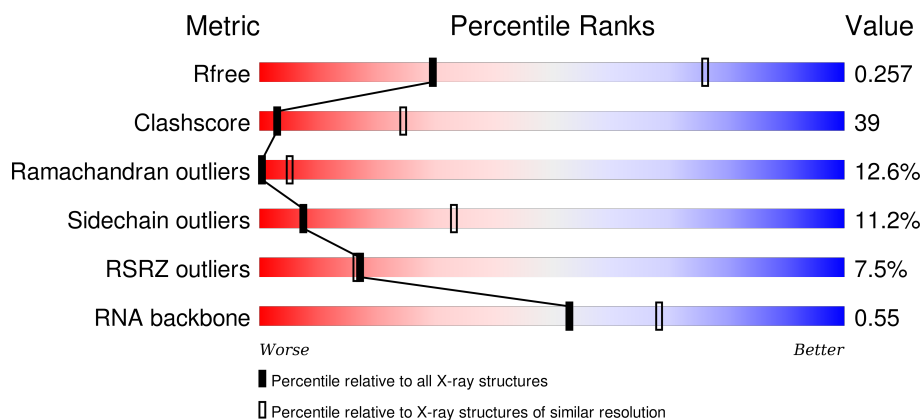
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.45 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.



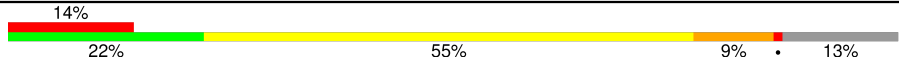
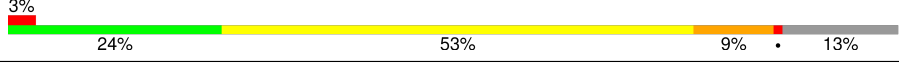
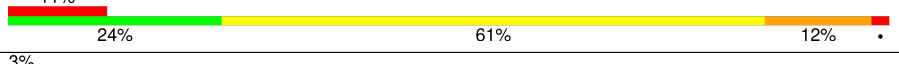
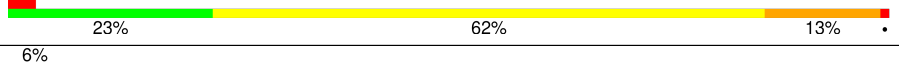
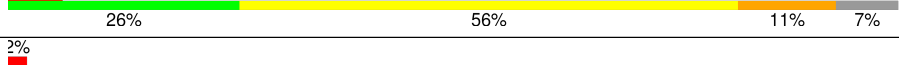
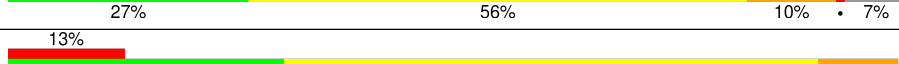
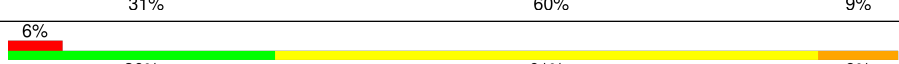
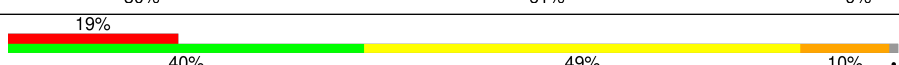
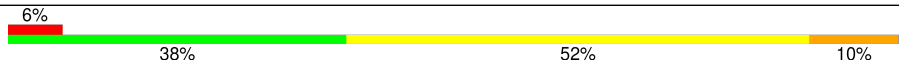

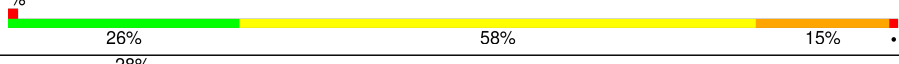
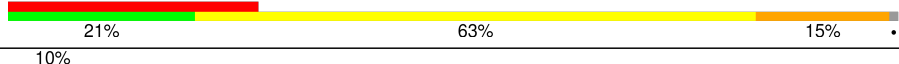
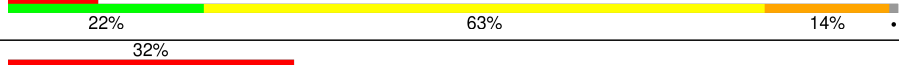
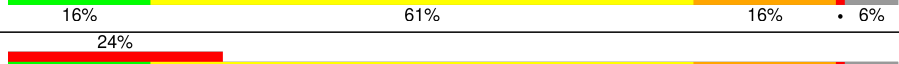
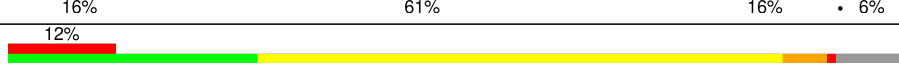
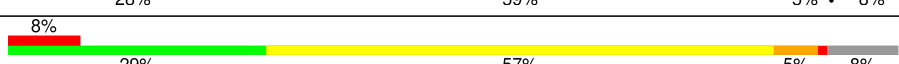
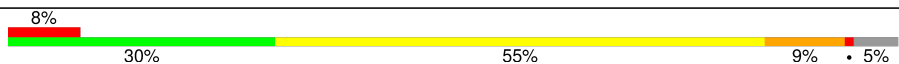
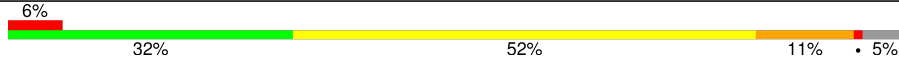
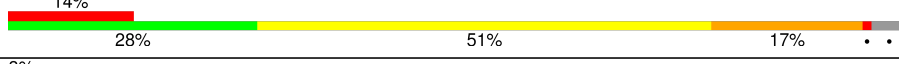
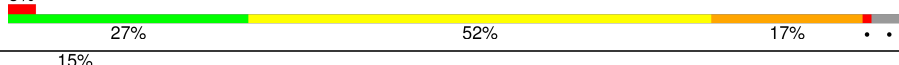





Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1000 (3.56-3.36)
Clashscore	102246	1090 (3.56-3.36)
Ramachandran outliers	100387	1057 (3.56-3.36)
Sidechain outliers	100360	1058 (3.56-3.36)
RSRZ outliers	91569	1005 (3.56-3.36)
RNA backbone	2183	1045 (4.10-2.80)

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	AA	1522	<div> <div>2%</div> <div> <div>26%</div> <div>60%</div> <div>12%</div> </div> <div>•</div> </div>
1	CA	1522	<div> <div>3%</div> <div> <div>26%</div> <div>60%</div> <div>12%</div> </div> <div>••</div> </div>
2	AB	256	<div> <div>15%</div> <div> <div>21%</div> <div>58%</div> <div>12%</div> <div>8%</div> </div> <div>•</div> </div>
2	CB	256	<div> <div>6%</div> <div> <div>21%</div> <div>57%</div> <div>12%</div> <div>8%</div> </div> <div>•</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	AC	239	
3	CC	239	
4	AD	209	
4	CD	209	
5	AE	162	
5	CE	162	
6	AF	101	
6	CF	101	
7	AG	156	
7	CG	156	
8	AH	138	
8	CH	138	
9	AI	128	
9	CI	128	
10	AJ	105	
10	CJ	105	
11	AK	129	
11	CK	129	
12	AL	132	
12	CL	132	
13	AM	126	
13	CM	126	
14	AN	61	
14	CN	61	
15	AO	89	

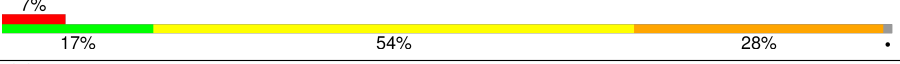
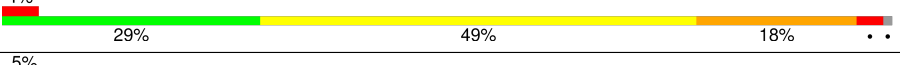
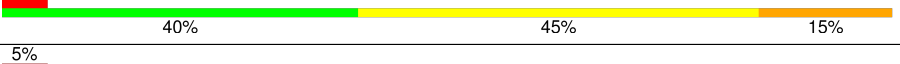
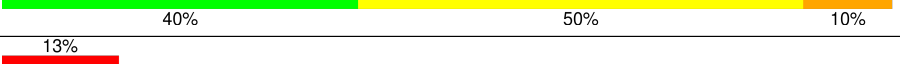

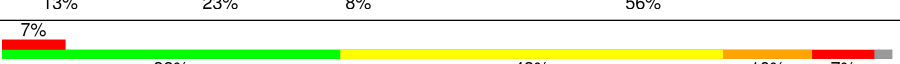
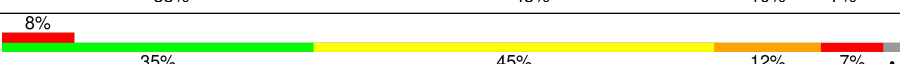



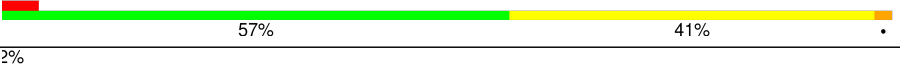
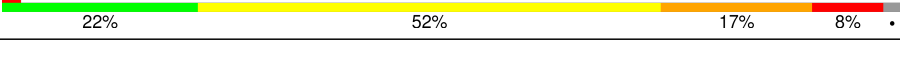
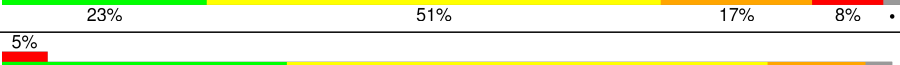
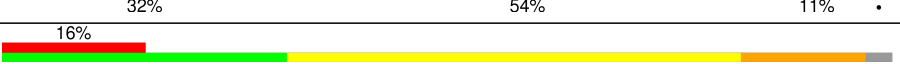
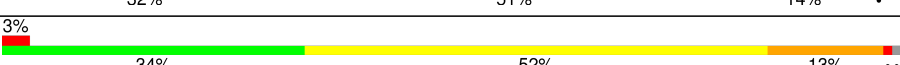
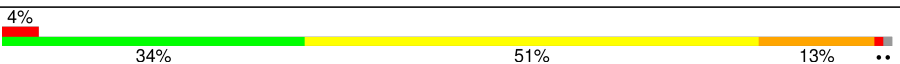

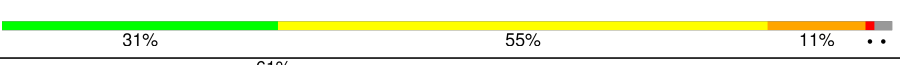
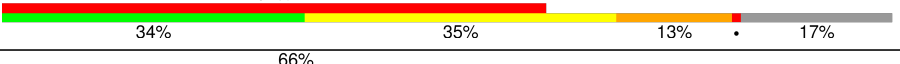
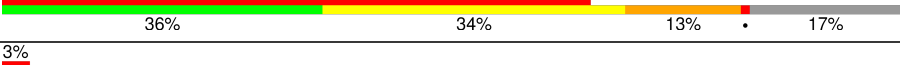

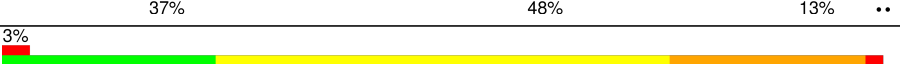
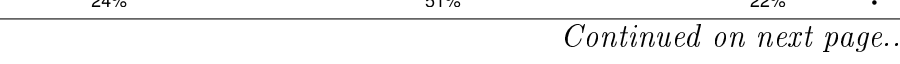


Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
15	CO	89	
16	AP	88	
16	CP	88	
17	AQ	105	
17	CQ	105	
18	AR	88	
18	CR	88	
19	AS	93	
19	CS	93	
20	AT	106	
20	CT	106	
21	AU	27	
21	CU	27	
22	AV	76	
22	AW	76	
22	CV	76	
22	CW	76	
23	AX	8	
23	CX	8	
24	AY	351	
24	CY	351	
25	B0	85	
25	D0	85	
26	B1	98	
26	D1	98	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
27	B2	72	
27	D2	72	
28	B3	60	
28	D3	60	
29	B4	71	
29	D4	71	
30	B5	60	
30	D5	60	
31	B6	54	
31	D6	54	
32	B7	49	
32	D7	49	
33	B8	65	
33	D8	65	
34	B9	37	
34	D9	37	
35	BA	2901	
35	DA	2901	
36	BB	122	
36	DB	122	
37	BC	229	
37	DC	229	
38	BD	276	
38	DD	276	
39	BE	206	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
39	DE	206	
40	BF	210	
40	DF	210	
41	BG	182	
41	DG	182	
42	BH	180	
42	DH	180	
43	BI	148	
44	BJ	130	
44	DJ	130	
45	BK	147	
45	DK	147	
46	BN	140	
46	DN	140	
47	BO	122	
47	DO	122	
48	BP	150	
48	DP	150	
49	BQ	141	
49	DQ	141	
50	BR	118	
50	DR	118	
51	BS	112	
51	DS	112	
52	BT	146	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
52	DT	146	
53	BU	118	
53	DU	118	
54	BV	101	
54	DV	101	
55	BW	113	
55	DW	113	
56	BX	96	
56	DX	96	
57	BY	110	
57	DY	110	
58	BZ	206	
58	DZ	206	
59	DI	148	

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
60	MG	AA	1611	-	-	-	X
60	MG	AA	1623	-	-	-	X
60	MG	AA	1625	-	-	-	X
60	MG	AA	1627	-	-	-	X
60	MG	AA	1632	-	-	-	X
60	MG	AA	1634	-	-	-	X
60	MG	AA	1650	-	-	-	X
60	MG	AA	1655	-	-	-	X
60	MG	AA	1656	-	-	-	X
60	MG	AA	1657	-	-	-	X
60	MG	AA	1669	-	-	-	X
60	MG	AA	1671	-	-	-	X
60	MG	AA	1672	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
60	MG	AA	1674	-	-	-	X
60	MG	AA	1683	-	-	-	X
60	MG	AA	1685	-	-	-	X
60	MG	AA	1714	-	-	-	X
60	MG	AA	1721	-	-	-	X
60	MG	AA	1735	-	-	-	X
60	MG	AA	1741	-	-	-	X
60	MG	AA	1745	-	-	-	X
60	MG	AA	1749	-	-	-	X
60	MG	AV	101	-	-	-	X
60	MG	AY	401	-	-	-	X
60	MG	B1	101	-	-	-	X
60	MG	B7	101	-	-	-	X
60	MG	BA	3004	-	-	-	X
60	MG	BA	3005	-	-	-	X
60	MG	BA	3009	-	-	-	X
60	MG	BA	3011	-	-	-	X
60	MG	BA	3012	-	-	-	X
60	MG	BA	3013	-	-	-	X
60	MG	BA	3015	-	-	-	X
60	MG	BA	3019	-	-	-	X
60	MG	BA	3020	-	-	-	X
60	MG	BA	3021	-	-	-	X
60	MG	BA	3023	-	-	-	X
60	MG	BA	3024	-	-	-	X
60	MG	BA	3026	-	-	-	X
60	MG	BA	3033	-	-	-	X
60	MG	BA	3035	-	-	-	X
60	MG	BA	3037	-	-	-	X
60	MG	BA	3042	-	-	-	X
60	MG	BA	3043	-	-	-	X
60	MG	BA	3044	-	-	-	X
60	MG	BA	3045	-	-	-	X
60	MG	BA	3047	-	-	-	X
60	MG	BA	3049	-	-	-	X
60	MG	BA	3050	-	-	-	X
60	MG	BA	3051	-	-	-	X
60	MG	BA	3056	-	-	-	X
60	MG	BA	3058	-	-	-	X
60	MG	BA	3061	-	-	-	X
60	MG	BA	3062	-	-	-	X
60	MG	BA	3064	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
60	MG	BA	3066	-	-	-	X
60	MG	BA	3067	-	-	-	X
60	MG	BA	3068	-	-	-	X
60	MG	BA	3069	-	-	-	X
60	MG	BA	3070	-	-	-	X
60	MG	BA	3071	-	-	-	X
60	MG	BA	3074	-	-	-	X
60	MG	BA	3076	-	-	-	X
60	MG	BA	3079	-	-	-	X
60	MG	BA	3082	-	-	-	X
60	MG	BA	3083	-	-	-	X
60	MG	BA	3088	-	-	-	X
60	MG	BA	3090	-	-	-	X
60	MG	BA	3098	-	-	-	X
60	MG	BA	3099	-	-	-	X
60	MG	BA	3101	-	-	-	X
60	MG	BA	3102	-	-	-	X
60	MG	BA	3103	-	-	-	X
60	MG	BA	3105	-	-	-	X
60	MG	BA	3106	-	-	-	X
60	MG	BA	3107	-	-	-	X
60	MG	BA	3108	-	-	-	X
60	MG	BA	3113	-	-	-	X
60	MG	BA	3114	-	-	-	X
60	MG	BA	3116	-	-	-	X
60	MG	BA	3123	-	-	-	X
60	MG	BA	3128	-	-	-	X
60	MG	BA	3138	-	-	-	X
60	MG	BA	3142	-	-	-	X
60	MG	BA	3145	-	-	-	X
60	MG	BA	3147	-	-	-	X
60	MG	BA	3155	-	-	-	X
60	MG	BA	3158	-	-	-	X
60	MG	BA	3159	-	-	-	X
60	MG	BA	3160	-	-	-	X
60	MG	BA	3163	-	-	-	X
60	MG	BA	3164	-	-	-	X
60	MG	BA	3165	-	-	-	X
60	MG	BA	3175	-	-	-	X
60	MG	BA	3182	-	-	-	X
60	MG	BA	3184	-	-	-	X
60	MG	BA	3185	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
60	MG	BA	3188	-	-	-	X
60	MG	BA	3196	-	-	-	X
60	MG	BA	3201	-	-	-	X
60	MG	BA	3202	-	-	-	X
60	MG	BA	3206	-	-	-	X
60	MG	BA	3213	-	-	-	X
60	MG	BA	3214	-	-	-	X
60	MG	BA	3219	-	-	-	X
60	MG	BA	3224	-	-	-	X
60	MG	BA	3225	-	-	-	X
60	MG	BA	3228	-	-	-	X
60	MG	BA	3233	-	-	-	X
60	MG	BA	3243	-	-	-	X
60	MG	BA	3252	-	-	-	X
60	MG	BA	3257	-	-	-	X
60	MG	BA	3264	-	-	-	X
60	MG	BA	3269	-	-	-	X
60	MG	BA	3271	-	-	-	X
60	MG	BA	3279	-	-	-	X
60	MG	BA	3280	-	-	-	X
60	MG	BA	3287	-	-	-	X
60	MG	BA	3296	-	-	-	X
60	MG	BA	3299	-	-	-	X
60	MG	BA	3300	-	-	-	X
60	MG	BA	3303	-	-	-	X
60	MG	BA	3305	-	-	-	X
60	MG	BA	3307	-	-	-	X
60	MG	BA	3318	-	-	-	X
60	MG	BA	3342	-	-	-	X
60	MG	BA	3346	-	-	-	X
60	MG	BA	3347	-	-	-	X
60	MG	BA	3348	-	-	-	X
60	MG	BA	3351	-	-	-	X
60	MG	BD	301	-	-	-	X
60	MG	CA	1603	-	-	-	X
60	MG	CA	1607	-	-	-	X
60	MG	CA	1610	-	-	-	X
60	MG	CA	1612	-	-	-	X
60	MG	CA	1616	-	-	-	X
60	MG	CA	1622	-	-	-	X
60	MG	CA	1624	-	-	-	X
60	MG	CA	1631	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
60	MG	CA	1633	-	-	-	X
60	MG	CA	1635	-	-	-	X
60	MG	CA	1645	-	-	-	X
60	MG	CA	1649	-	-	-	X
60	MG	CA	1658	-	-	-	X
60	MG	CA	1669	-	-	-	X
60	MG	CA	1674	-	-	-	X
60	MG	CA	1686	-	-	-	X
60	MG	CA	1695	-	-	-	X
60	MG	CA	1719	-	-	-	X
60	MG	CA	1722	-	-	-	X
60	MG	CA	1736	-	-	-	X
60	MG	CA	1746	-	-	-	X
60	MG	CA	1750	-	-	-	X
60	MG	CV	101	-	-	-	X
60	MG	CY	401	-	-	-	X
60	MG	D1	101	-	-	-	X
60	MG	DA	3002	-	-	-	X
60	MG	DA	3005	-	-	-	X
60	MG	DA	3006	-	-	-	X
60	MG	DA	3010	-	-	-	X
60	MG	DA	3012	-	-	-	X
60	MG	DA	3013	-	-	-	X
60	MG	DA	3014	-	-	-	X
60	MG	DA	3016	-	-	-	X
60	MG	DA	3020	-	-	-	X
60	MG	DA	3021	-	-	-	X
60	MG	DA	3022	-	-	-	X
60	MG	DA	3024	-	-	-	X
60	MG	DA	3025	-	-	-	X
60	MG	DA	3027	-	-	-	X
60	MG	DA	3033	-	-	-	X
60	MG	DA	3034	-	-	-	X
60	MG	DA	3036	-	-	-	X
60	MG	DA	3038	-	-	-	X
60	MG	DA	3043	-	-	-	X
60	MG	DA	3044	-	-	-	X
60	MG	DA	3046	-	-	-	X
60	MG	DA	3048	-	-	-	X
60	MG	DA	3052	-	-	-	X
60	MG	DA	3053	-	-	-	X
60	MG	DA	3055	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
60	MG	DA	3057	-	-	-	X
60	MG	DA	3059	-	-	-	X
60	MG	DA	3061	-	-	-	X
60	MG	DA	3062	-	-	-	X
60	MG	DA	3063	-	-	-	X
60	MG	DA	3065	-	-	-	X
60	MG	DA	3067	-	-	-	X
60	MG	DA	3068	-	-	-	X
60	MG	DA	3069	-	-	-	X
60	MG	DA	3070	-	-	-	X
60	MG	DA	3071	-	-	-	X
60	MG	DA	3072	-	-	-	X
60	MG	DA	3074	-	-	-	X
60	MG	DA	3075	-	-	-	X
60	MG	DA	3077	-	-	-	X
60	MG	DA	3079	-	-	-	X
60	MG	DA	3080	-	-	-	X
60	MG	DA	3081	-	-	-	X
60	MG	DA	3083	-	-	-	X
60	MG	DA	3084	-	-	-	X
60	MG	DA	3089	-	-	-	X
60	MG	DA	3091	-	-	-	X
60	MG	DA	3096	-	-	-	X
60	MG	DA	3097	-	-	-	X
60	MG	DA	3099	-	-	-	X
60	MG	DA	3100	-	-	-	X
60	MG	DA	3103	-	-	-	X
60	MG	DA	3104	-	-	-	X
60	MG	DA	3106	-	-	-	X
60	MG	DA	3107	-	-	-	X
60	MG	DA	3108	-	-	-	X
60	MG	DA	3109	-	-	-	X
60	MG	DA	3114	-	-	-	X
60	MG	DA	3116	-	-	-	X
60	MG	DA	3127	-	-	-	X
60	MG	DA	3129	-	-	-	X
60	MG	DA	3131	-	-	-	X
60	MG	DA	3139	-	-	-	X
60	MG	DA	3143	-	-	-	X
60	MG	DA	3146	-	-	-	X
60	MG	DA	3148	-	-	-	X
60	MG	DA	3151	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
60	MG	DA	3152	-	-	-	X
60	MG	DA	3156	-	-	-	X
60	MG	DA	3157	-	-	-	X
60	MG	DA	3159	-	-	-	X
60	MG	DA	3160	-	-	-	X
60	MG	DA	3161	-	-	-	X
60	MG	DA	3162	-	-	-	X
60	MG	DA	3163	-	-	-	X
60	MG	DA	3165	-	-	-	X
60	MG	DA	3166	-	-	-	X
60	MG	DA	3167	-	-	-	X
60	MG	DA	3170	-	-	-	X
60	MG	DA	3184	-	-	-	X
60	MG	DA	3186	-	-	-	X
60	MG	DA	3196	-	-	-	X
60	MG	DA	3197	-	-	-	X
60	MG	DA	3203	-	-	-	X
60	MG	DA	3206	-	-	-	X
60	MG	DA	3207	-	-	-	X
60	MG	DA	3214	-	-	-	X
60	MG	DA	3215	-	-	-	X
60	MG	DA	3220	-	-	-	X
60	MG	DA	3225	-	-	-	X
60	MG	DA	3226	-	-	-	X
60	MG	DA	3229	-	-	-	X
60	MG	DA	3234	-	-	-	X
60	MG	DA	3238	-	-	-	X
60	MG	DA	3245	-	-	-	X
60	MG	DA	3253	-	-	-	X
60	MG	DA	3258	-	-	-	X
60	MG	DA	3259	-	-	-	X
60	MG	DA	3265	-	-	-	X
60	MG	DA	3267	-	-	-	X
60	MG	DA	3269	-	-	-	X
60	MG	DA	3271	-	-	-	X
60	MG	DA	3287	-	-	-	X
60	MG	DA	3295	-	-	-	X
60	MG	DA	3298	-	-	-	X
60	MG	DA	3299	-	-	-	X
60	MG	DA	3304	-	-	-	X
60	MG	DA	3305	-	-	-	X
60	MG	DA	3317	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
60	MG	DA	3327	-	-	-	X
60	MG	DA	3344	-	-	-	X
60	MG	DA	3345	-	-	-	X
60	MG	DD	301	-	-	-	X
60	MG	DD	302	-	-	-	X
60	MG	DF	301	-	-	-	X
60	MG	DF	303	-	-	-	X
60	MG	DR	201	-	-	-	X
60	MG	DU	201	-	-	-	X

2 Entry composition

There are 61 unique types of molecules in this entry. The entry contains 304505 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1504	Total	C	N	O	P	0	0	0
			32329	14390	5992	10444	1503			
1	CA	1504	Total	C	N	O	P	0	0	0
			32329	14390	5992	10444	1503			

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	235	Total	C	N	O	S	0	0	1
			1901	1213	342	341	5			
2	CB	235	Total	C	N	O	S	0	0	1
			1901	1213	342	341	5			

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	207	Total	C	N	O	S	0	0	1
			1613	1016	315	281	1			
3	CC	207	Total	C	N	O	S	0	0	1
			1613	1016	315	281	1			

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			
4	CD	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	AE	151	Total	C	N	O	S	0	0	1
			1147	724	218	201	4			
5	CE	151	Total	C	N	O	S	0	0	1
			1147	724	218	201	4			

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			
6	CF	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	AG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			
7	CG	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	AH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			
8	CH	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	AI	127	Total	C	N	O		0	0	0
			1011	639	198	174				
9	CI	127	Total	C	N	O		0	0	0
			1011	639	198	174				

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AJ	99	Total	C	N	O	S	0	0	1
			795	499	157	138	1			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	CJ	99	Total	C	N	O	S	0	0	1
			795	499	157	138	1			

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

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

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	126	Total	C	N	O	S	0	0	1
			976	614	197	164	1			
12	CL	126	Total	C	N	O	S	0	0	1
			976	614	197	164	1			

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AM	121	Total	C	N	O	S	0	0	1
			956	591	198	165	2			
13	CM	121	Total	C	N	O	S	0	0	1
			956	591	198	165	2			

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14 TYPE Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			
14	CN	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	AO	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			
15	CO	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	AP	84	Total	C	N	O	S	0	0	1
			701	443	140	117	1			
16	CP	84	Total	C	N	O	S	0	0	1
			701	443	140	117	1			

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	100	Total	C	N	O	S	0	0	1
			824	528	152	142	2			
17	CQ	100	Total	C	N	O	S	0	0	1
			824	528	152	142	2			

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

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

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	79	Total	C	N	O	S	0	0	1
			630	403	115	110	2			
19	CS	79	Total	C	N	O	S	0	0	1
			630	403	115	110	2			

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			
20	CT	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	AU	25	Total	C	N	O	0	0	1
			209	128	51	30			
21	CU	25	Total	C	N	O	0	0	1
			209	128	51	30			

- Molecule 22 is a RNA chain called E-SITE TRNA PHE OR P-SITE TRNA PHE (UNMODIFIED BASES).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AV	76	Total	C	N	O	P	0	0	0
			1619	723	290	531	75			
22	AW	76	Total	C	N	O	P	0	0	0
			1619	723	290	531	75			
22	CV	76	Total	C	N	O	P	0	0	0
			1619	723	290	531	75			
22	CW	76	Total	C	N	O	P	0	0	0
			1619	723	290	531	75			

- Molecule 23 is a RNA chain called MRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AX	8	Total	C	N	O	P	0	0	0
			166	76	29	54	7			
23	CX	8	Total	C	N	O	P	0	0	0
			166	76	29	54	7			

- Molecule 24 is a protein called PEPTIDE CHAIN RELEASE FACTOR 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	AY	351	Total	C	N	O	S	0	0	0
			2799	1751	503	537	8			
24	CY	351	Total	C	N	O	S	0	0	0
			2799	1751	503	537	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AY	303	GLU	ARG	CONFLICT	UNP Q5SM01
CY	303	GLU	ARG	CONFLICT	UNP Q5SM01

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	B0	76	Total	C	N	O	S	0	0	0
			607	376	128	102	1			
25	D0	76	Total	C	N	O	S	0	0	0
			607	376	128	102	1			

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	B1	94	Total	C	N	O	S	0	0	1
			732	460	146	125	1			
26	D1	94	Total	C	N	O	S	0	0	1
			732	460	146	125	1			

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	B2	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			
27	D2	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	B3	60	Total	C	N	O	S	0	0	1
			468	298	91	78	1			
28	D3	60	Total	C	N	O	S	0	0	1
			468	298	91	78	1			

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	B4	31	Total	C	N	O	S	0	0	1
			226	142	37	43	4			
29	D4	31	Total	C	N	O	S	0	0	1
			226	142	37	43	4			

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	B5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	D5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	B6	45	Total	C	N	O	S	0	0	1
			381	235	78	64	4			
31	D6	45	Total	C	N	O	S	0	0	1
			381	235	78	64	4			

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	B7	49	Total	C	N	O	S	0	0	1
			419	257	105	55	2			
32	D7	49	Total	C	N	O	S	0	0	1
			419	257	105	55	2			

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	B8	64	Total	C	N	O	S	0	0	1
			508	326	102	78	2			
33	D8	64	Total	C	N	O	S	0	0	1
			508	326	102	78	2			

- Molecule 34 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	B9	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			
34	D9	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			

- Molecule 35 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BA	2886	Total	C	N	O	P	0	0	0
			62154	27663	11625	19981	2885			
35	DA	2886	Total	C	N	O	P	0	0	0
			62154	27663	11625	19981	2885			

- Molecule 36 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BB	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			
36	DB	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			

- Molecule 37 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
37	BC	191	Total	C	N	O	0	0	1
			1142	691	221	230			
37	DC	191	Total	C	N	O	0	0	1
			1142	691	221	230			

- Molecule 38 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BD	272	Total	C	N	O	S	0	0	1
			2105	1329	417	356	3			
38	DD	272	Total	C	N	O	S	0	0	1
			2105	1329	417	356	3			

- Molecule 39 is a protein called 50S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BE	205	Total	C	N	O	S	0	0	1
			1564	988	300	270	6			
39	DE	205	Total	C	N	O	S	0	0	1
			1564	988	300	270	6			

- Molecule 40 is a protein called 50S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BF	208	Total	C	N	O	S	0	0	1
			1624	1035	304	282	3			
40	DF	208	Total	C	N	O	S	0	0	1
			1624	1035	304	282	3			

- Molecule 41 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BG	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			
41	DG	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			

- Molecule 42 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BH	160	Total	C	N	O	S	0	0	1
			1223	773	229	220	1			
42	DH	160	Total	C	N	O	S	0	0	1
			1223	773	229	220	1			

- Molecule 43 is a protein called 50S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BI	146	Total	C	N	O	S	0	0	1
			1132	723	201	207	1			

- Molecule 44 is a protein called 50S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
44	BJ	130	Total	C	N	O	0	0	0
			651	390	130	131			
44	DJ	130	Total	C	N	O	0	0	0
			651	390	130	131			

- Molecule 45 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BK	141	Total	C	N	O	S	0	0	1
			1038	661	184	187	6			
45	DK	141	Total	C	N	O	S	0	0	1
			1038	661	184	187	6			

- Molecule 46 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	BN	139	Total	C	N	O	S	0	0	1
			1105	712	207	182	4			
46	DN	139	Total	C	N	O	S	0	0	1
			1105	712	207	182	4			

- Molecule 47 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	BO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
47	DO	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 48 is a protein called 50S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	BP	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			
48	DP	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			

- Molecule 49 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	BQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
49	DQ	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
50	BR	117	Total	C	N	O	0	0	0
			960	599	202	159			
50	DR	117	Total	C	N	O	0	0	0
			960	599	202	159			

- Molecule 51 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
51	BS	99	Total	C	N	O	0	0	1
			771	486	155	130			
51	DS	99	Total	C	N	O	0	0	1
			771	486	155	130			

- Molecule 52 is a protein called 50S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	BT	138	Total	C	N	O	S	0	0	1
			1142	710	235	196	1			
52	DT	138	Total	C	N	O	S	0	0	1
			1142	710	235	196	1			

- Molecule 53 is a protein called 50S RIBOSOMAL PROTEIN L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	BU	117	Total	C	N	O	S	0	0	0
			958	604	202	151	1			
53	DU	117	Total	C	N	O	S	0	0	0
			958	604	202	151	1			

- Molecule 54 is a protein called 50S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	BV	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			
54	DV	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 55 is a protein called 50S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	BW	113	Total	C	N	O	S	0	0	0
			896	563	176	155	2			
55	DW	113	Total	C	N	O	S	0	0	0
			896	563	176	155	2			

- Molecule 56 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
56	BX	93	Total	C	N	O	0	0	1
			726	471	132	123			
56	DX	93	Total	C	N	O	0	0	1
			726	471	132	123			

- Molecule 57 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	BY	101	Total	C	N	O	S	0	0	1
			776	500	149	123	4			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	DY	101	Total	C	N	O	S	0	0	1
			776	500	149	123	4			

- Molecule 58 is a protein called 50S RIBOSOMAL PROTEIN L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	BZ	177	Total	C	N	O	S	0	0	1
			1404	897	253	252	2			
58	DZ	177	Total	C	N	O	S	0	0	1
			1404	897	253	252	2			

- Molecule 59 is a protein called 50S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	DI	146	Total	C	N	O	S	0	0	1
			1133	724	201	207	1			

- Molecule 60 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	BA	354	Total	Mg	0	0
			354	354		
60	CA	157	Total	Mg	0	0
			157	157		
60	DQ	1	Total	Mg	0	0
			1	1		
60	DF	3	Total	Mg	0	0
			3	3		
60	CV	7	Total	Mg	0	0
			7	7		
60	AW	5	Total	Mg	0	0
			5	5		
60	DU	1	Total	Mg	0	0
			1	1		
60	B1	1	Total	Mg	0	0
			1	1		
60	DY	1	Total	Mg	0	0
			1	1		
60	BP	1	Total	Mg	0	0
			1	1		
60	DC	1	Total	Mg	0	0
			1	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	CY	1	Total 1	Mg 1	0	0
60	B5	2	Total 2	Mg 2	0	0
60	BB	4	Total 4	Mg 4	0	0
60	AE	1	Total 1	Mg 1	0	0
60	DB	4	Total 4	Mg 4	0	0
60	D3	1	Total 1	Mg 1	0	0
60	BF	1	Total 1	Mg 1	0	0
60	AV	7	Total 7	Mg 7	0	0
60	DR	1	Total 1	Mg 1	0	0
60	AA	157	Total 157	Mg 157	0	0
60	BQ	1	Total 1	Mg 1	0	0
60	D7	1	Total 1	Mg 1	0	0
60	BC	1	Total 1	Mg 1	0	0
60	AM	1	Total 1	Mg 1	0	0
60	BU	1	Total 1	Mg 1	0	0
60	CN	1	Total 1	Mg 1	0	0
60	DD	2	Total 2	Mg 2	0	0
60	DH	1	Total 1	Mg 1	0	0
60	B3	1	Total 1	Mg 1	0	0
60	DX	1	Total 1	Mg 1	0	0
60	DA	353	Total 353	Mg 353	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
60	B7	2	Total 2	Mg 2	0	0
60	AL	1	Total 1	Mg 1	0	0
60	D1	1	Total 1	Mg 1	0	0
60	BS	1	Total 1	Mg 1	0	0
60	CW	5	Total 5	Mg 5	0	0
60	D5	2	Total 2	Mg 2	0	0
60	BD	2	Total 2	Mg 2	0	0
60	AY	1	Total 1	Mg 1	0	0
60	CL	1	Total 1	Mg 1	0	0
60	BH	1	Total 1	Mg 1	0	0

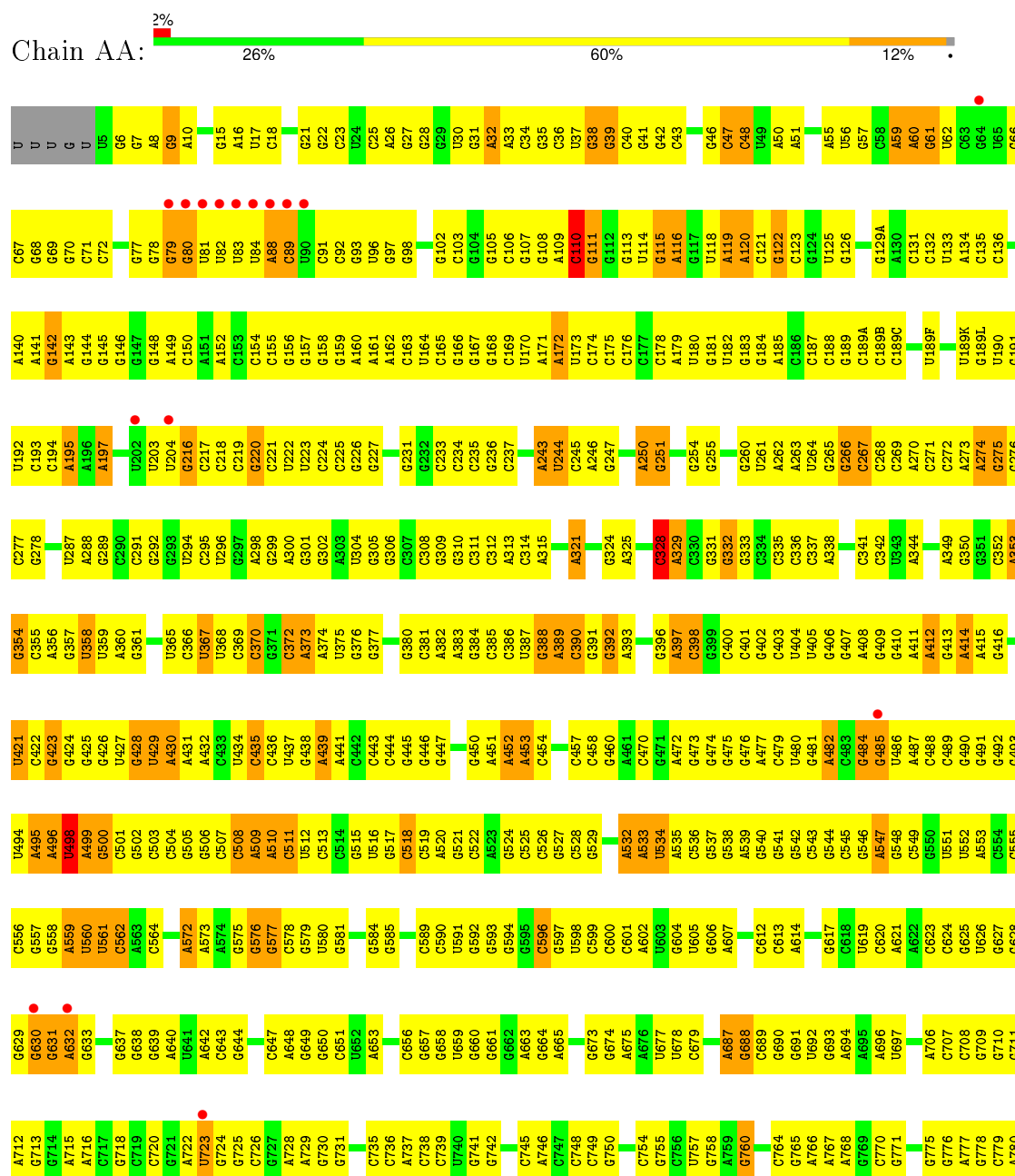
- Molecule 61 is ZINC ION (three-letter code: ZN) (formula: Zn).

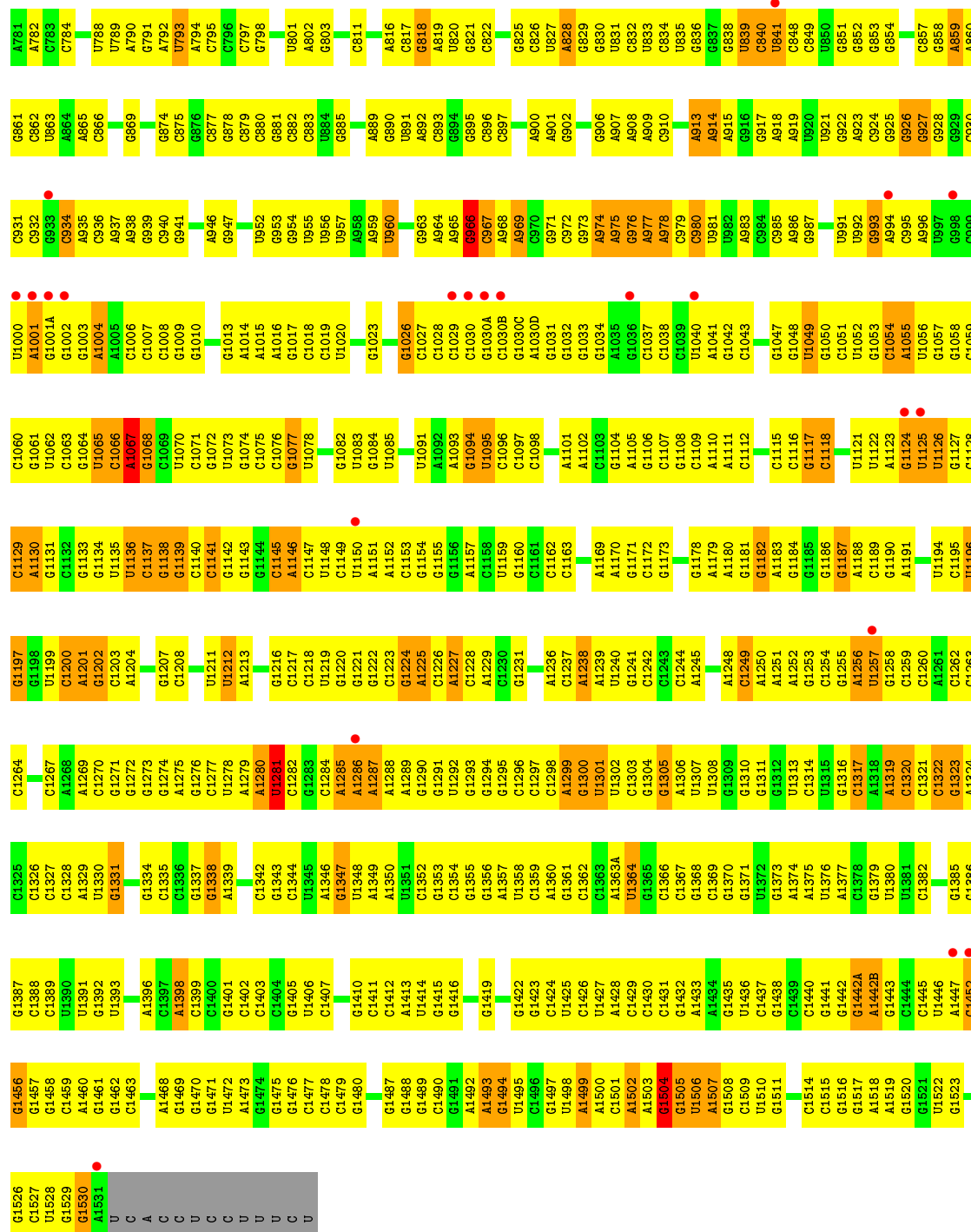
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	CN	1	Total 1	Zn 1	0	0
61	AN	1	Total 1	Zn 1	0	0
61	B9	1	Total 1	Zn 1	0	0
61	D9	1	Total 1	Zn 1	0	0
61	CD	1	Total 1	Zn 1	0	0
61	AD	1	Total 1	Zn 1	0	0

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

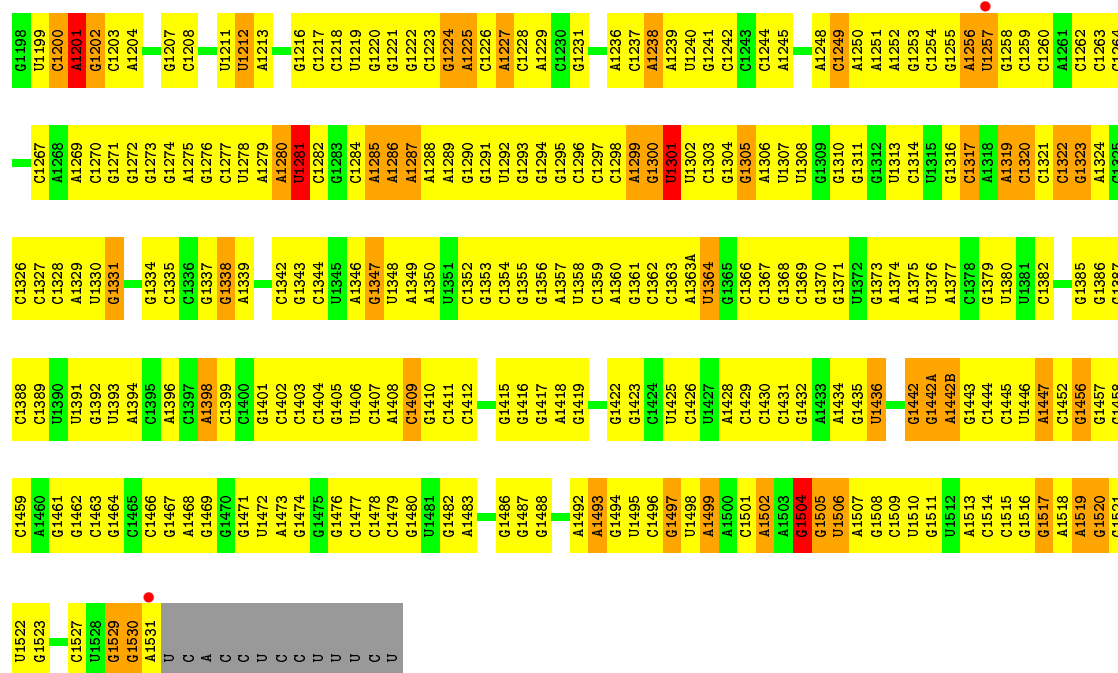




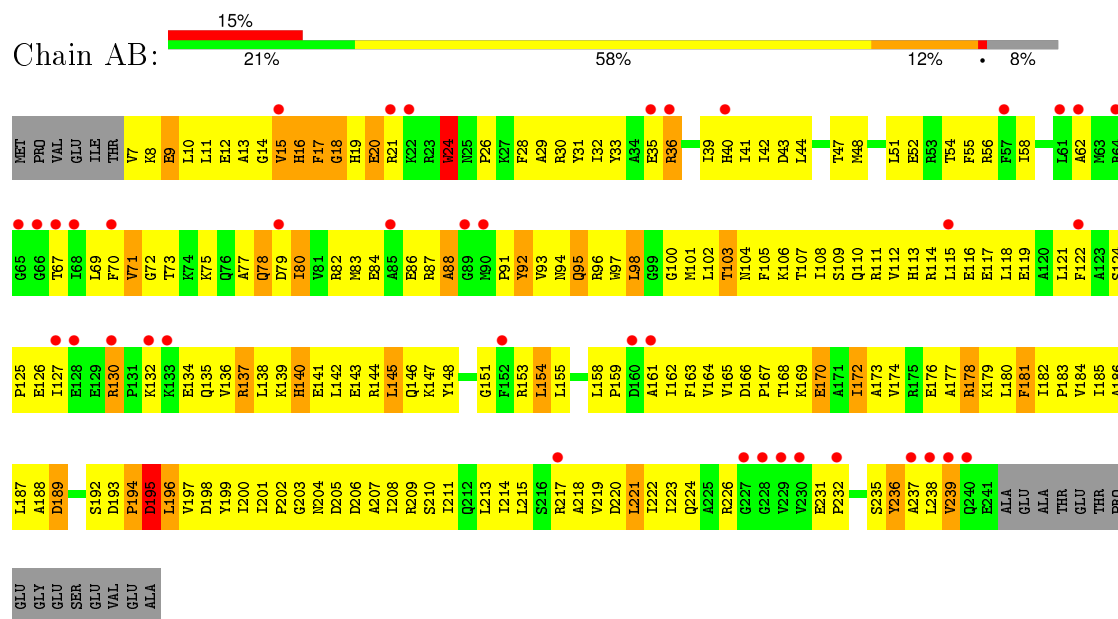
Molecule 1: 16S rRNA



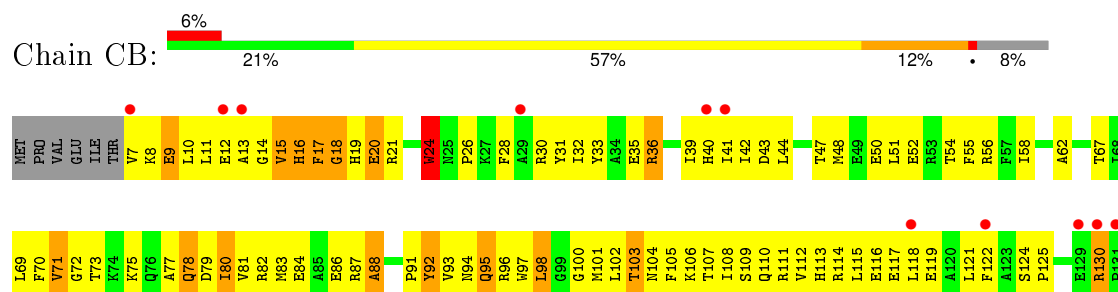
G1131	U1062	G1003	A935	A864	A782	G711	G629	C556	A495	A353	C194	A141	G69
G1132	C1063	A1004	C936	A865		A712	G630	G557	A496	G354	A195	G142	G70
G1133	G1064	A1005	A937	C966	U788	G713	G631	G558	A498	C355	A196	G143	C71
G1134	U1065	A1006	A938		U789	G714	A632	A559	A499	A356	A197	G144	C72
U1135	C1066	C1007	G939	G869	U790	A715	G633	U560	G500	G357		G145	
U1136	A1067	C1008	C940	G874	G791	A716		U561	G501	U358	U203	G146	
G1137	G1068	G1009	G941	C875	A792	G717	U636	C562	G502	A359	U204	G147	G73
G1138	U1069		A946	G876	U793	G718	G637	A563	G503	A360	G216		G79
G1139	C1070		G947	C877	A794	G719	G638	C564	G504	C217	G217	G148	G80
C1140	G1071		C948	G878	U795	C720	G639	U564	G505	C218	C218	G149	U81
C1141	G1072			C879	C796	G721	A640		G506	C219	C219	A151	U82
G1142	G1073		U952	C880	U797	A722	U641	A572	G507	A364	G220	C152	U83
G1143	U1074		G953	G881	G798	U723	A642	A573	C508	U365	C221	C153	U84
G1144	C1075		G954	G882		G724	C643	G575	A509	U366	U222	C154	A88
C1145	G1076		G955	C883	A802	G725	G644	U576	A510	U368	U223	C155	C89
C1146	G1077		U956	U884	G803	G726		G577	C511	C369	C224	G156	U90
C1147	U1078		U957	G885	G804	G727	C647	C578	U512	G370	C225	G157	C91
U1148					C811	A728	A648	G579	C513	G371	C226	G158	C92
U1149	G1082	G1023	A958			A729	G649	U580	C514	C372		G159	G93
U1150	U1083	G1024	A959	G888	A815	G730	G650	G581	G515	A373	U229	A160	U96
A1151	U1084	U1025	U960	A889	A816		C651		U516	A374		A161	G97
A1152	U1085	G1026	U961	G890	C817	C735	U652	G584	U517	U375	C233	A162	
C1153		C1027	C962	U891	G818	C736	A653	G585	C518	G376	C234	C163	
G1154	U1091	C1028	G963	A892	A819	A737			C519	G377	C235	U164	
G1155	A1092	C1029	A964	C893	U820	C738	C656	C589	A520	G378	G236	C165	
G1156	A1093	C1030	A965	G894	G821	C739	G657	C590	G521	G379	C237	C166	
U1157	G1094	G1030A	G966	G895	C822	U740	G658	U591	C522	G380		G167	A101
C1158	U1095	C1030B	C967	G896		G741	U659	G592	A523	C381	G104	G168	G102
U1159	U1096	A1030C	A968		G825	G742	G660	G593	G524	A382	A243	G105	C103
G1160	C1097	A1030D	A969	A900	C826	G743	G661	G594	C525	A383	U244	C106	
C1161	C1098	G1031	C970	A901	U827	C745	G662	G595	C526	G384	C245	U107	G107
C1162		G1032	G971	G902	A828	A746	A663	C596	G527	C385	A246	C108	G108
C1163		G1033	C972	G906	G829	C747	A664	C597	C528	U387	A172	A172	A109
G1164	U1102	G1034	G973	A907	U830	C748	A665	U598	G529	A388	U173	U173	C110
A1169	G1104	A1035	A974	A908	G831	C749	G673	C600	G530	C390	C176	C174	G111
A1170	A1105	G1036	A975	A909	U832	G750	G674	C801	U531	G391	G177	C175	
A1171	G1106	C1037	G976	C910	U833		A675	A802	A532	G392	C254	C178	G115
C1172	C1107	C1038	A977		C834	C754	G676	U603	A533	A397	G255		A116
G1173	U1107	U1039	A978		U835	G755	A677	G604	U534			U118	G117
	G1108	A1041	C979	A913	G836	C756	U677	U605	A535	A398	G260	U119	A118
	C1109	G1042	U981	A914	G837	U757	U678	G606	C536	A120	U261	G180	A120
G1178	A1110	C1043	U982		U838	G758	C679	A607	C537	A121	A262	G181	C121
A1179	A1111		U983	G917	U839	A759		A608	G538	G122	A263	G182	C122
A1180	C1112		A984	A918	C840	G760	A687		A539	G123	U264	G183	C123
G1181		A1046	C985	A919	U841	G761	G688	C612	G540	G124	G265	A185	G124
C1182	C1115	G1047	C986	U920	C848	C762	C689	G613	G541	G125	G266	C186	U125
A1183	C1116	G1048	A986	U921	C849	G763	G690	A614	G542	G126	C267	G187	U126
G1184	G1117	U1049	G987	G922	U850	C764	G691		C543	G127	C268		G127
G1185	C1118	G1050		A923	U851	G765	U692		G544	G128	C269		G128
G1186		C1051	U991	C924	G852	A766	G693	G617	C545	U129	A270	G189A	U129
G1187	U1121	U1052	U992	G925	G853	A767	A694	C618	A546	G129A	C271	C189B	G129A
A1188	U1122	G1053	G993	G926	G854	A768	A695	U619	U547	A130	C272	C189C	A130
C1189	A1123	C1054	A994	G927	A696		U697	C620	G548	C131	A273		C131
G1190	G1124	A1055	C995	G928		G775			C549	A274			C132
A1191	U1125	G1056	A996	G929	C857	G776			C550	G275			U189F
	U1126	G1057		C930	U858	A777	A706	C624	G551	U189K			U189K
G1127	G1058		C931	C931	A859	G778	C707	G625	U552	G189L			U189L
C1128	C1059		G932	G932	A860	G779	C708	G626	A415	U190			U190
U1194	U1195		U1000		A861	A780	G709	G627	G492	G191			U191
U1196	C1060		A1001		C862	A781		G628	G493	U192			U192
G1197	G1197		G1002		U863		G710		C555	C193			A140

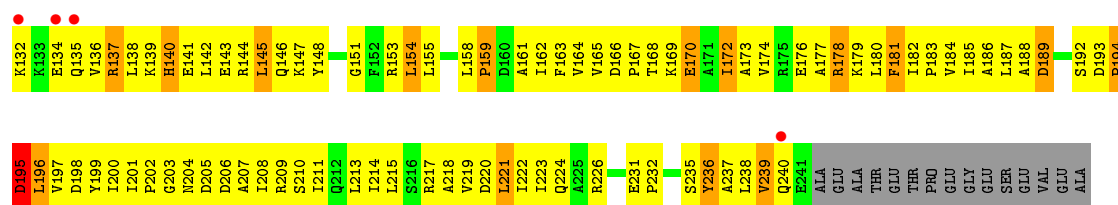


• Molecule 2: 30S RIBOSOMAL PROTEIN S2

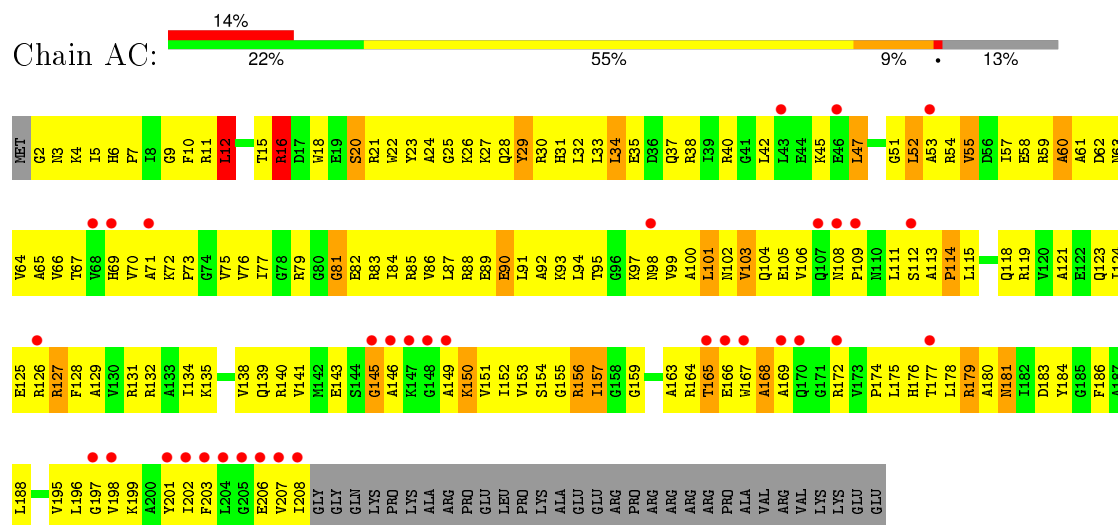


• Molecule 2: 30S RIBOSOMAL PROTEIN S2

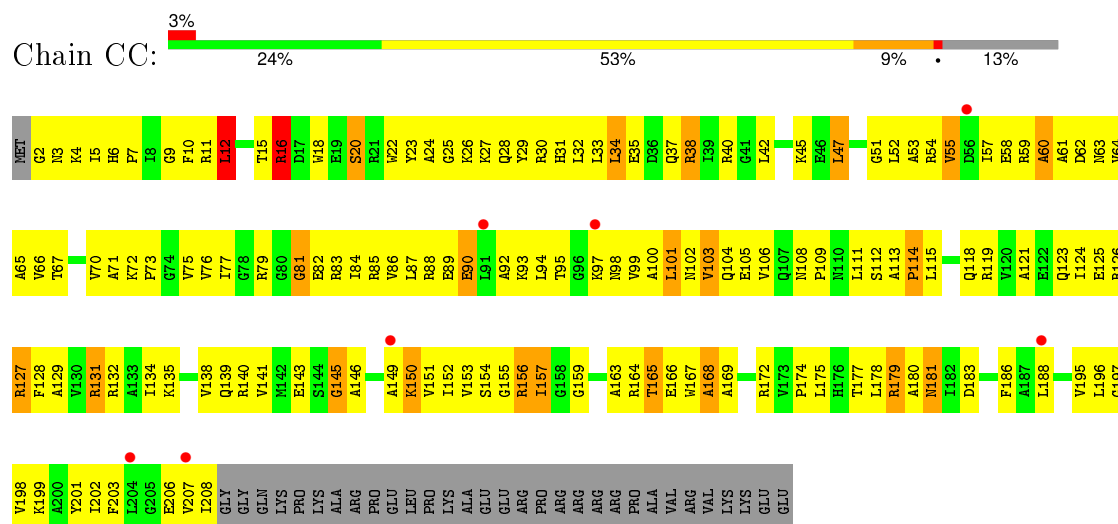




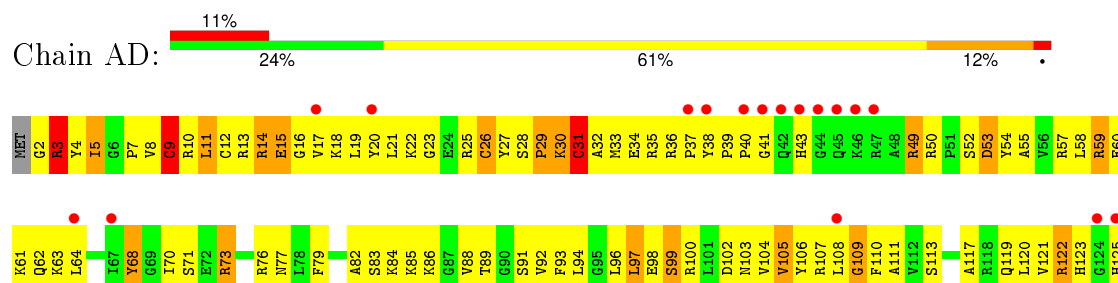
• Molecule 3: 30S RIBOSOMAL PROTEIN S3

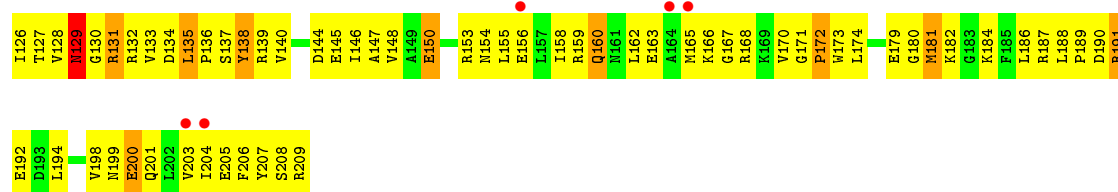


• Molecule 3: 30S RIBOSOMAL PROTEIN S3

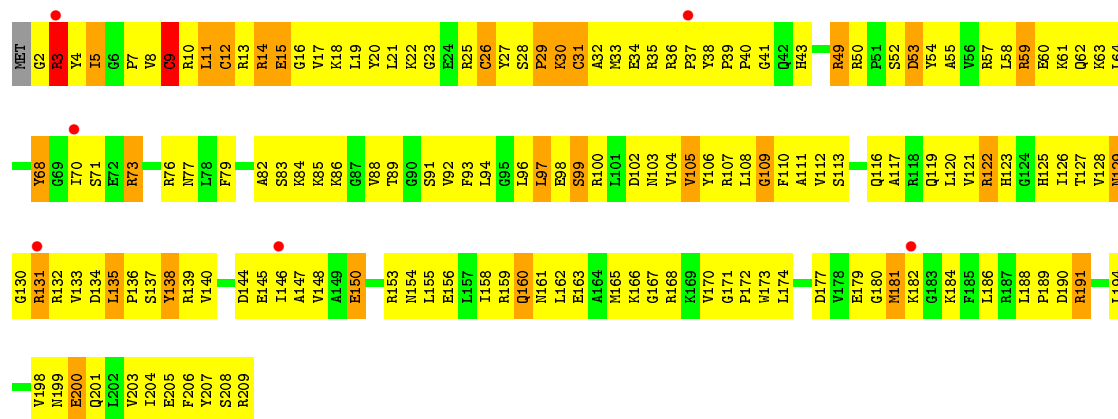


• Molecule 4: 30S RIBOSOMAL PROTEIN S4

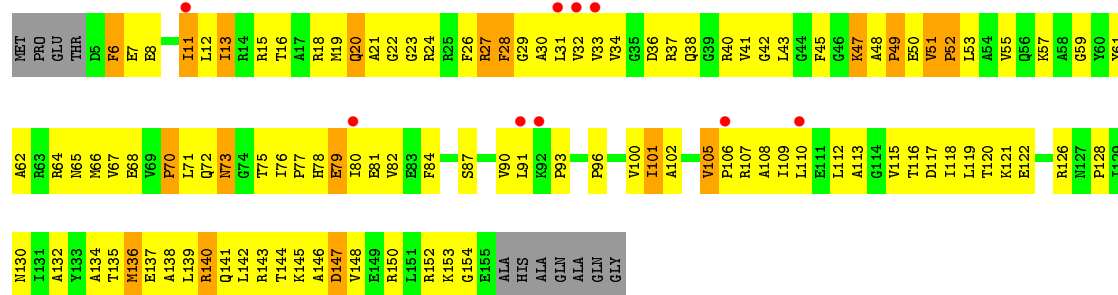




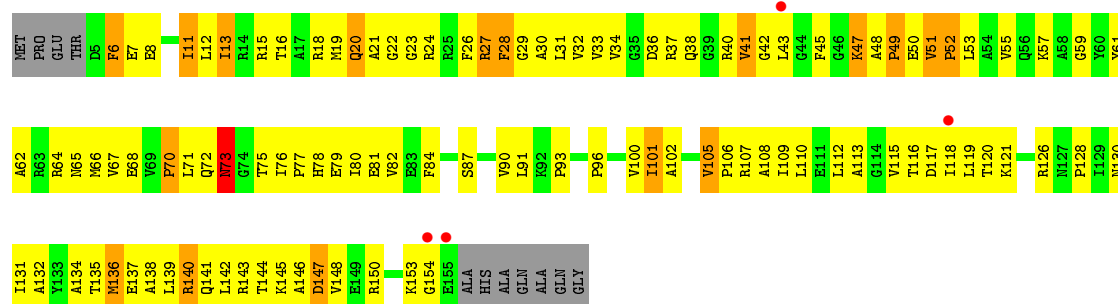
• Molecule 4: 30S RIBOSOMAL PROTEIN S4



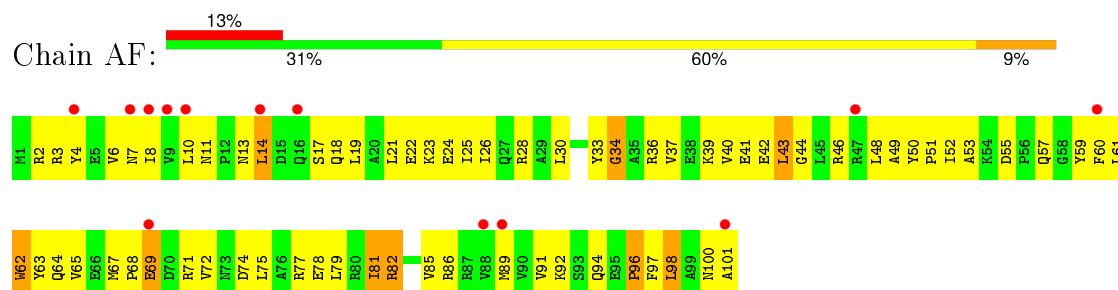
• Molecule 5: 30S RIBOSOMAL PROTEIN S5



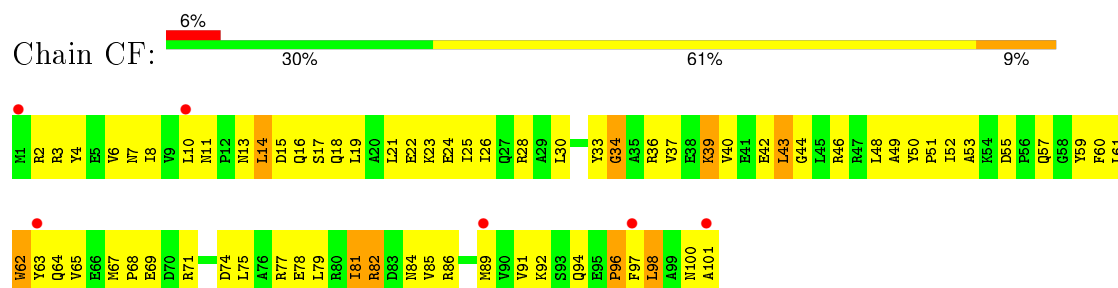
• Molecule 5: 30S RIBOSOMAL PROTEIN S5



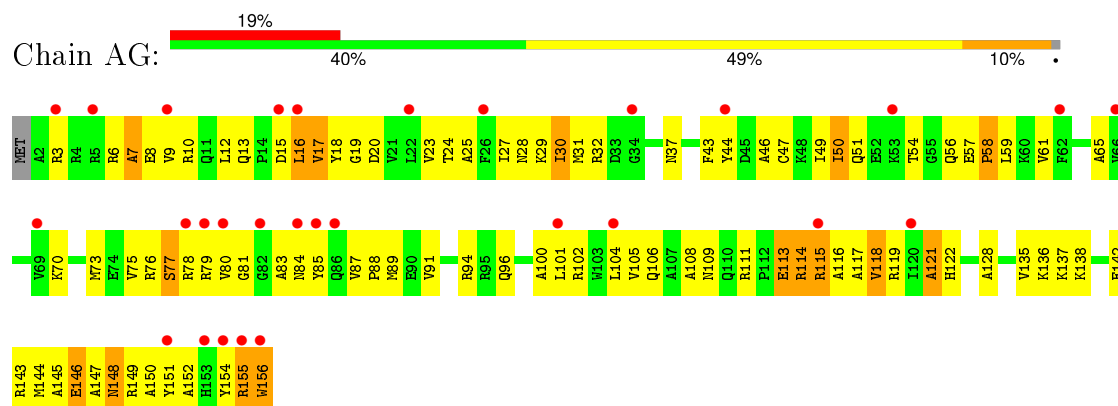
- Molecule 6: 30S RIBOSOMAL PROTEIN S6



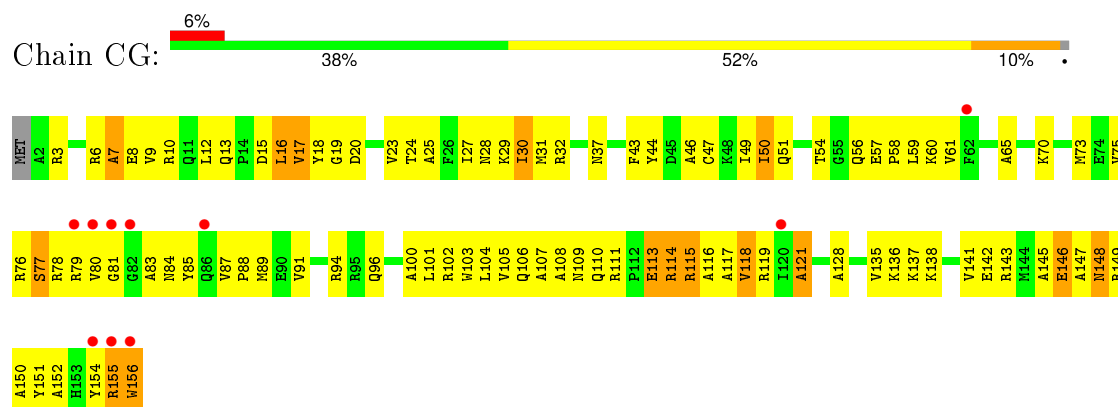
- Molecule 6: 30S RIBOSOMAL PROTEIN S6



- Molecule 7: 30S RIBOSOMAL PROTEIN S7

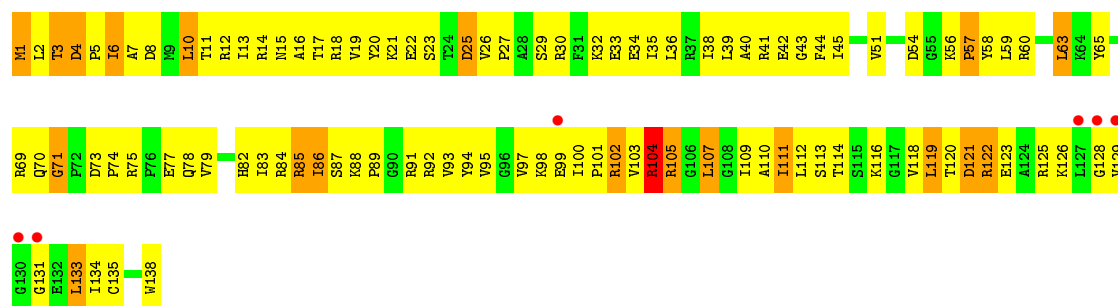


- Molecule 7: 30S RIBOSOMAL PROTEIN S7

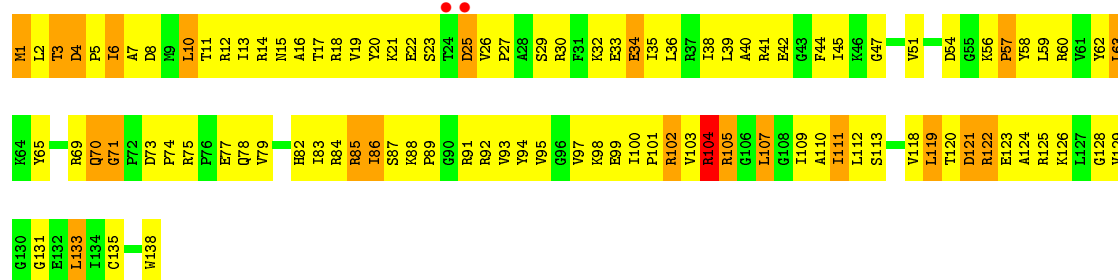


- Molecule 8: 30S RIBOSOMAL PROTEIN S8

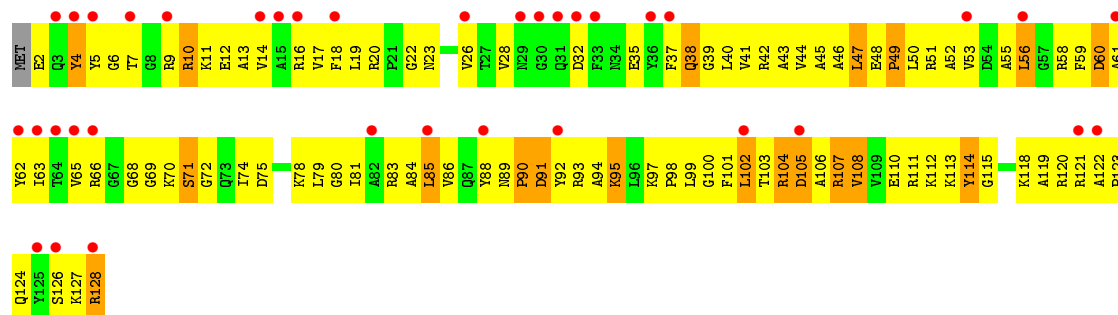




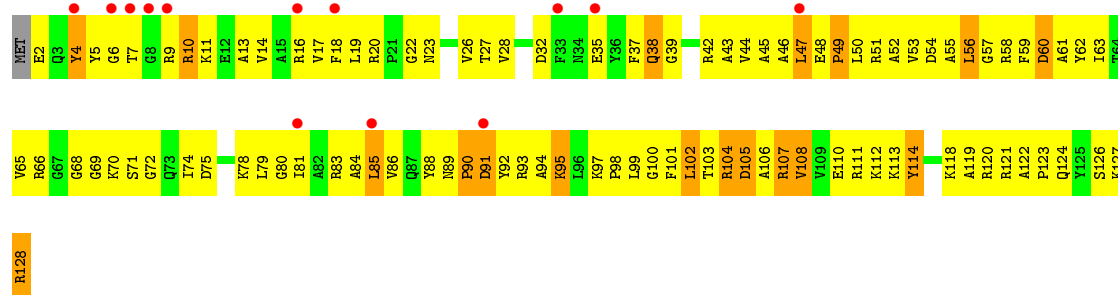
• Molecule 8: 30S RIBOSOMAL PROTEIN S8



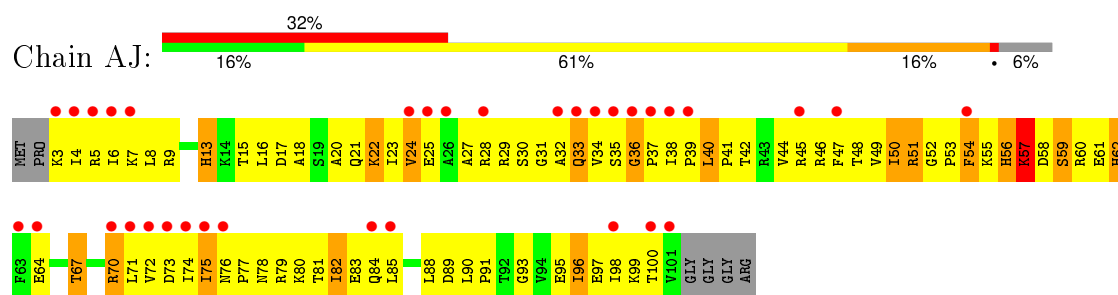
• Molecule 9: 30S RIBOSOMAL PROTEIN S9



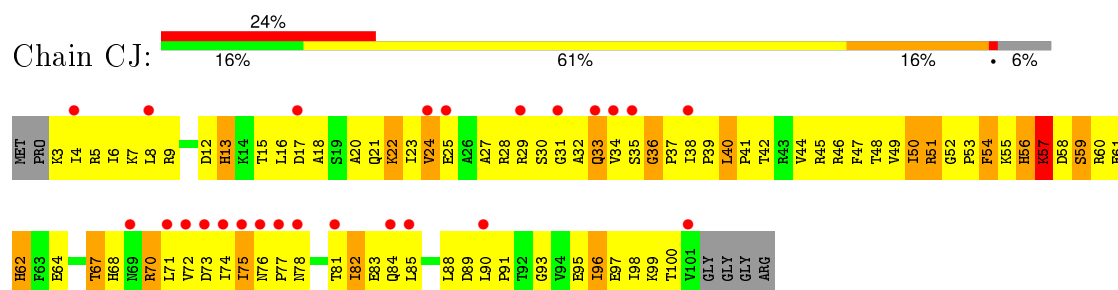
• Molecule 9: 30S RIBOSOMAL PROTEIN S9



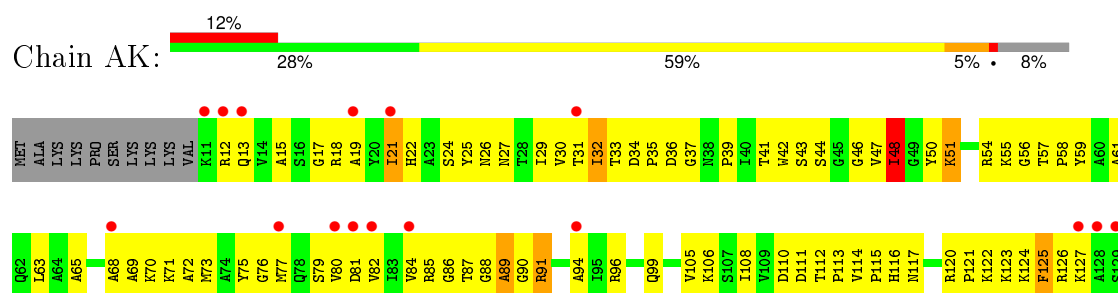
• Molecule 10: 30S RIBOSOMAL PROTEIN S10



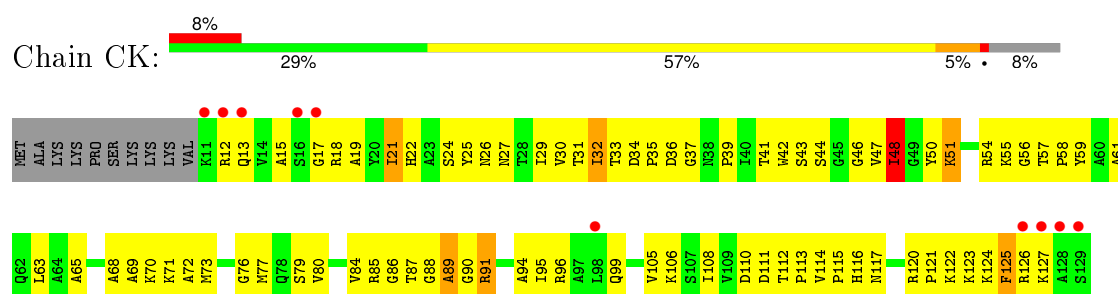
• Molecule 10: 30S RIBOSOMAL PROTEIN S10



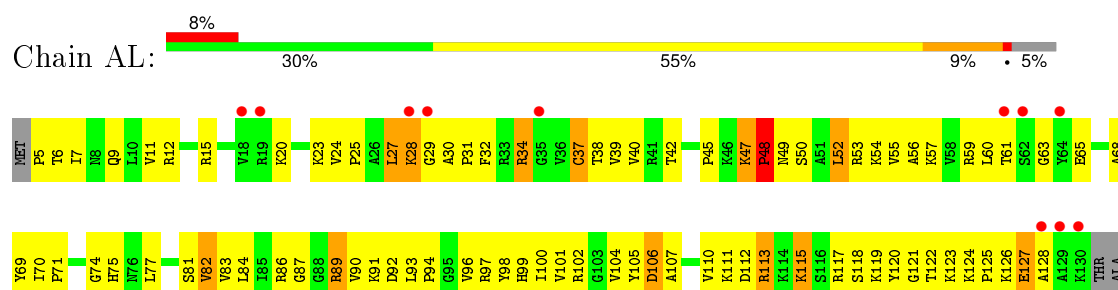
• Molecule 11: 30S RIBOSOMAL PROTEIN S11



• Molecule 11: 30S RIBOSOMAL PROTEIN S11



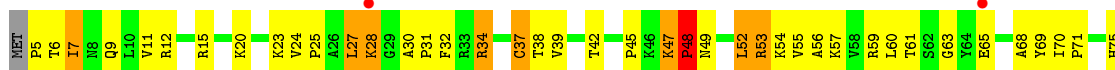
• Molecule 12: 30S RIBOSOMAL PROTEIN S12



ALA
LYS
LYS

• Molecule 12: 30S RIBOSOMAL PROTEIN S12

Chain CL: 

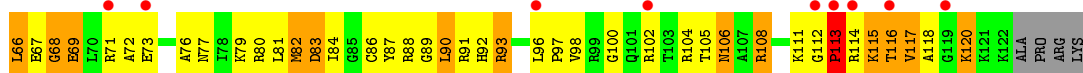




• Molecule 13: 30S RIBOSOMAL PROTEIN S13


Chain AM: 

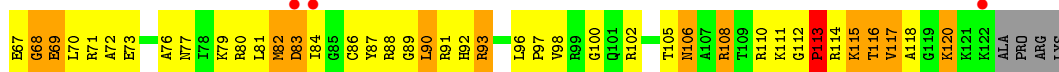




• Molecule 13: 30S RIBOSOMAL PROTEIN S13

Chain CM: 





• Molecule 14: 30S RIBOSOMAL PROTEIN S14 TYPE Z

Chain AN: 



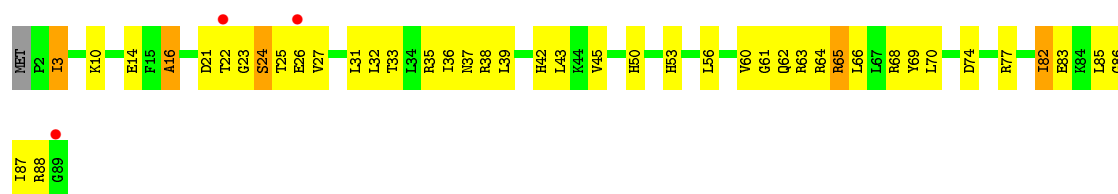
• Molecule 14: 30S RIBOSOMAL PROTEIN S14 TYPE Z

Chain CN: 

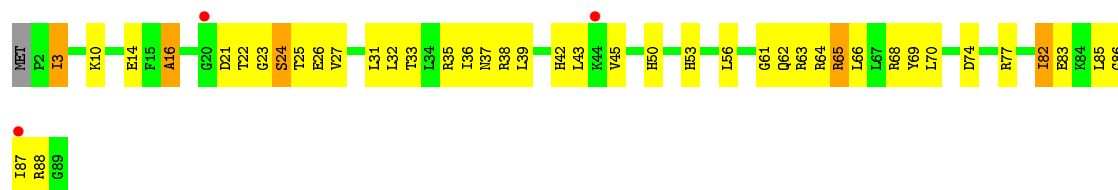


• Molecule 15: 30S RIBOSOMAL PROTEIN S15

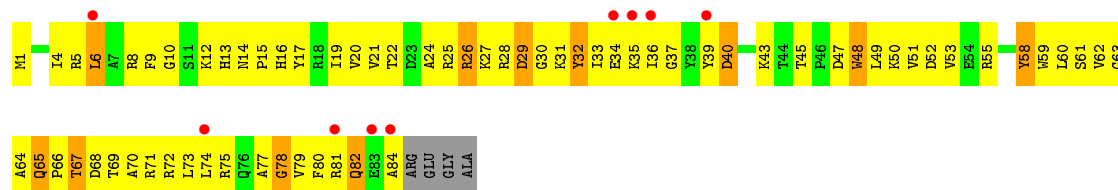
Chain AO: 



- Molecule 15: 30S RIBOSOMAL PROTEIN S15



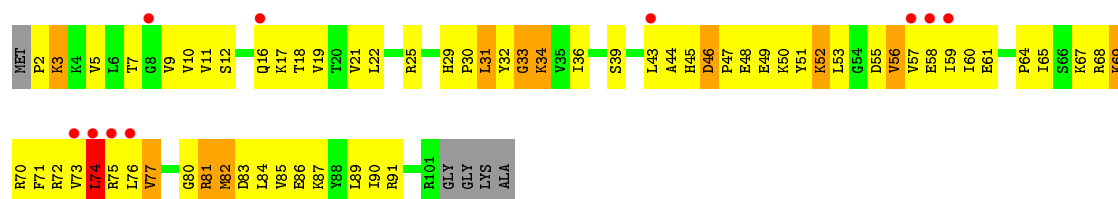
- Molecule 16: 30S RIBOSOMAL PROTEIN S16



- Molecule 16: 30S RIBOSOMAL PROTEIN S16

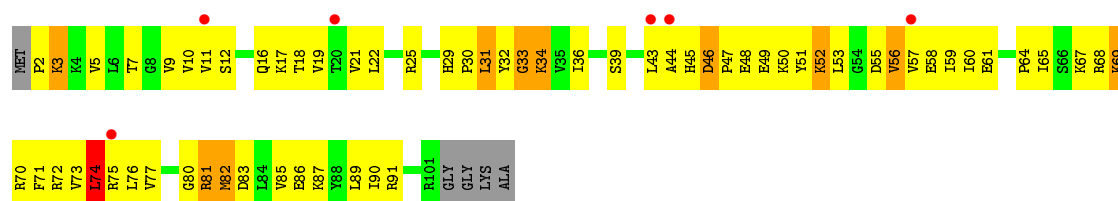


- Molecule 17: 30S RIBOSOMAL PROTEIN S17

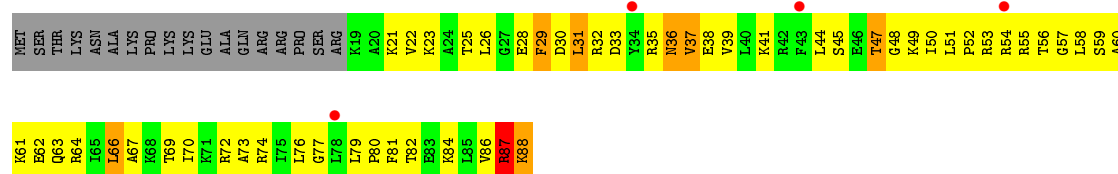
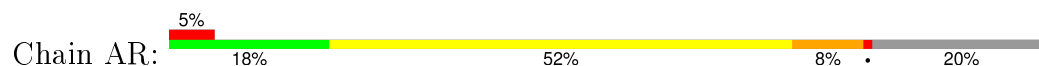


- Molecule 17: 30S RIBOSOMAL PROTEIN S17

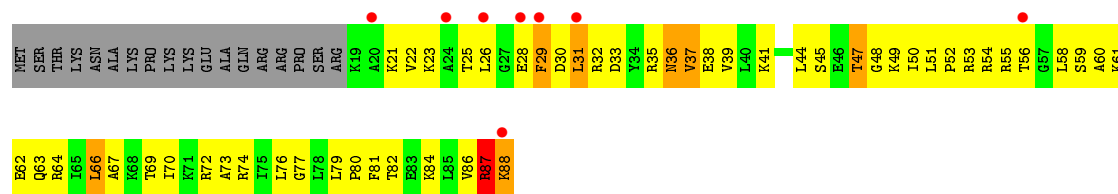
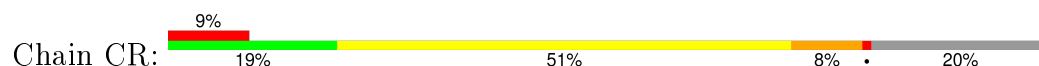




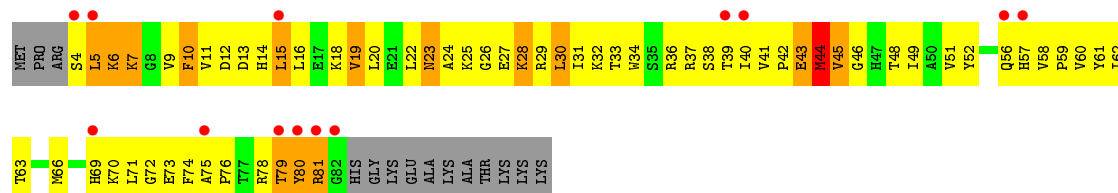
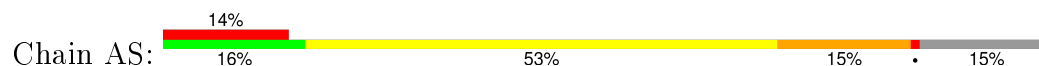
• Molecule 18: 30S RIBOSOMAL PROTEIN S18



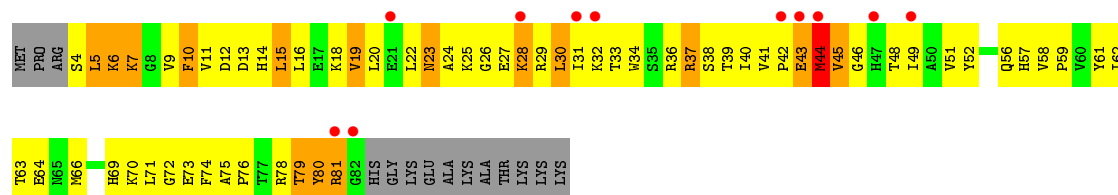
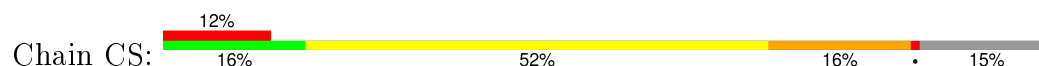
• Molecule 18: 30S RIBOSOMAL PROTEIN S18



• Molecule 19: 30S RIBOSOMAL PROTEIN S19

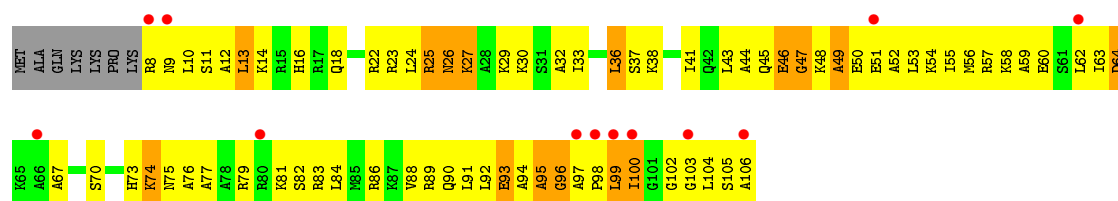


• Molecule 19: 30S RIBOSOMAL PROTEIN S19

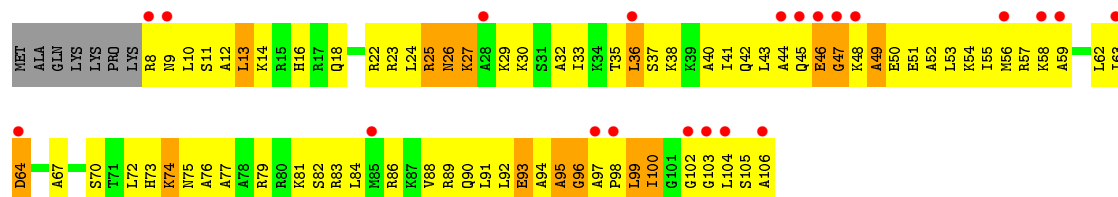


• Molecule 20: 30S RIBOSOMAL PROTEIN S20

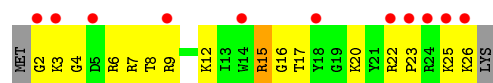




• Molecule 20: 30S RIBOSOMAL PROTEIN S20



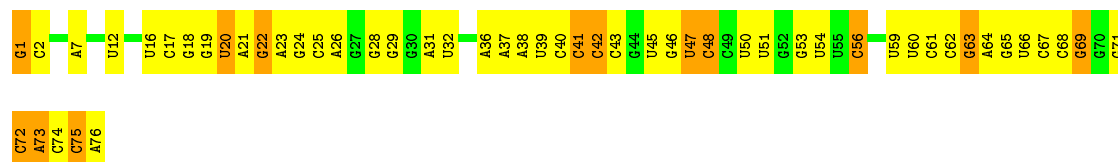
• Molecule 21: 30S RIBOSOMAL PROTEIN THX



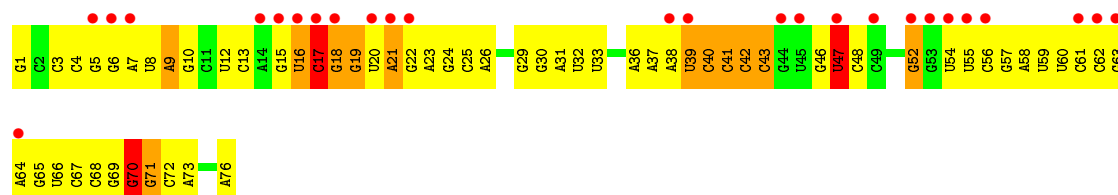
• Molecule 21: 30S RIBOSOMAL PROTEIN THX



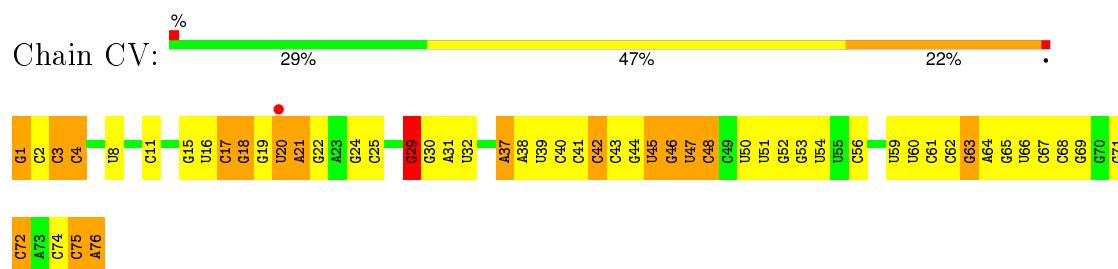
• Molecule 22: E-SITE TRNA PHE OR P-SITE TRNA PHE (UNMODIFIED BASES)



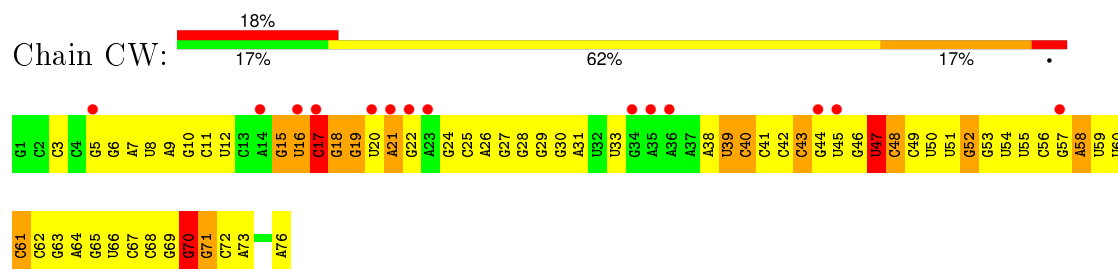
• Molecule 22: E-SITE TRNA PHE OR P-SITE TRNA PHE (UNMODIFIED BASES)



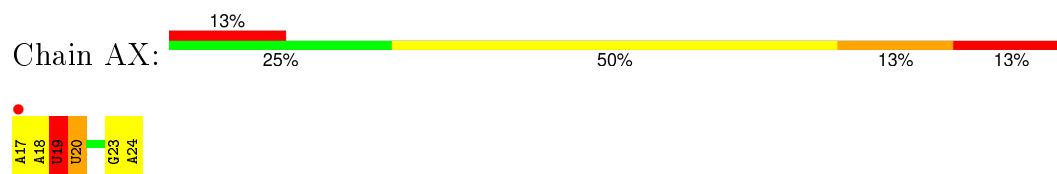
- Molecule 22: E-SITE TRNA PHE OR P-SITE TRNA PHE (UNMODIFIED BASES)



- Molecule 22: E-SITE TRNA PHE OR P-SITE TRNA PHE (UNMODIFIED BASES)



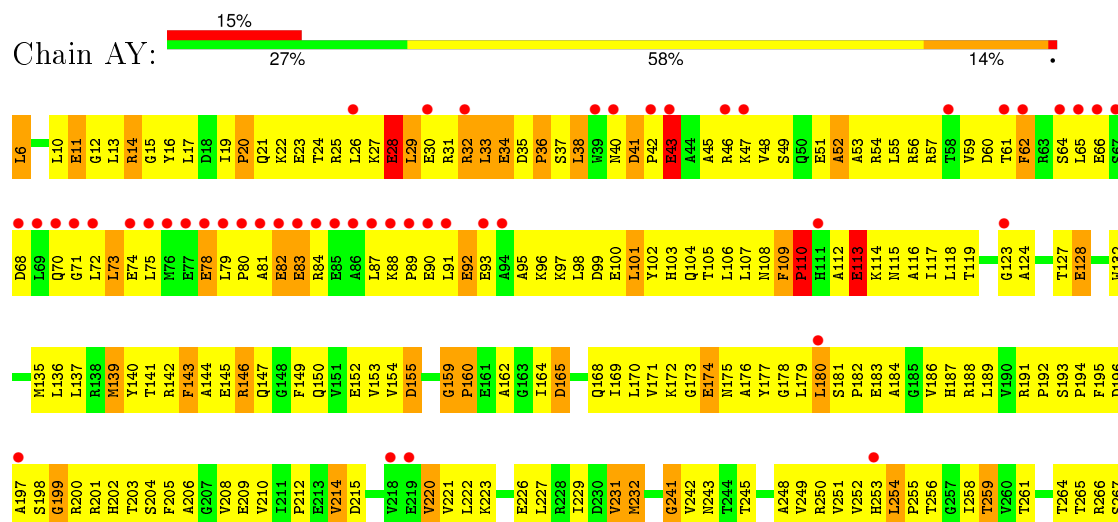
- Molecule 23: MRNA

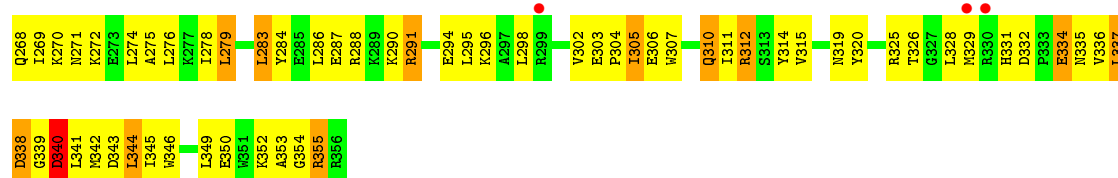


- Molecule 23: MRNA

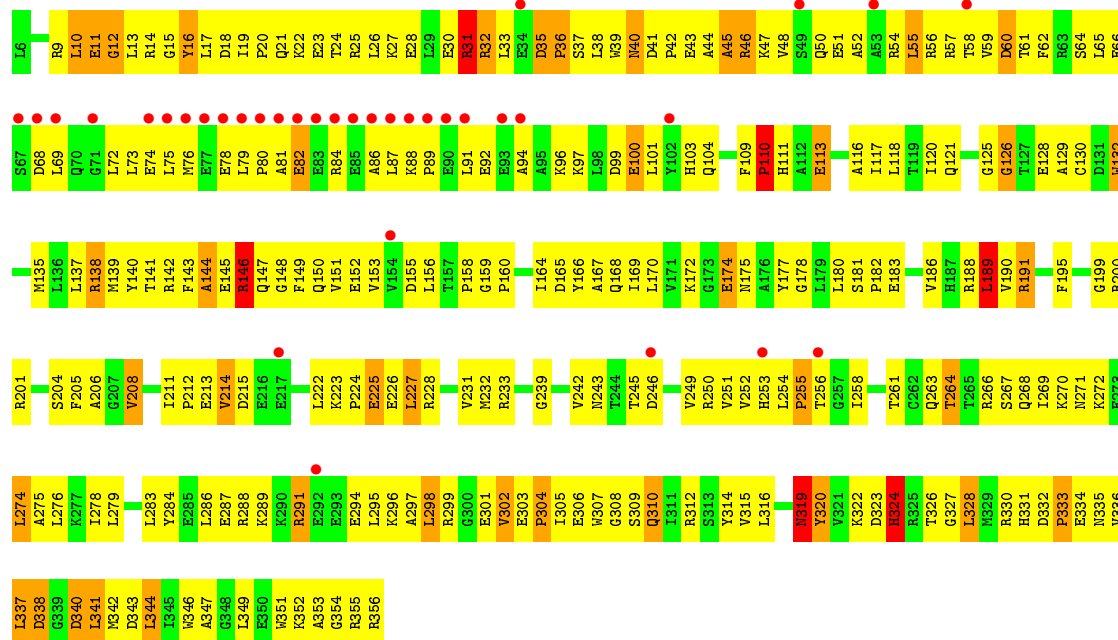


- Molecule 24: PEPTIDE CHAIN RELEASE FACTOR 2

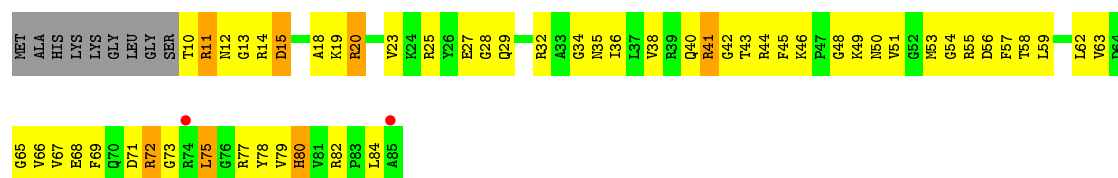




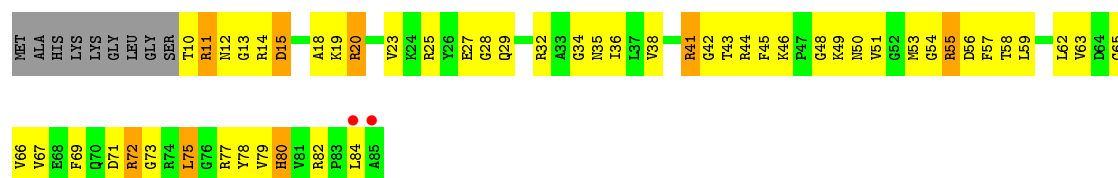
• Molecule 24: PEPTIDE CHAIN RELEASE FACTOR 2



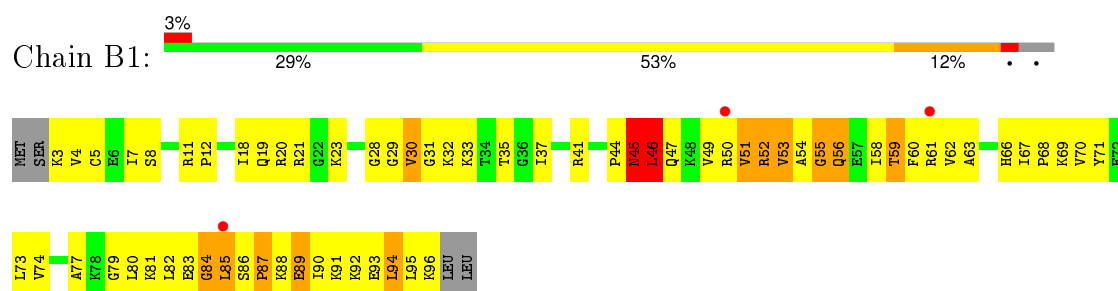
• Molecule 25: 50S RIBOSOMAL PROTEIN L27



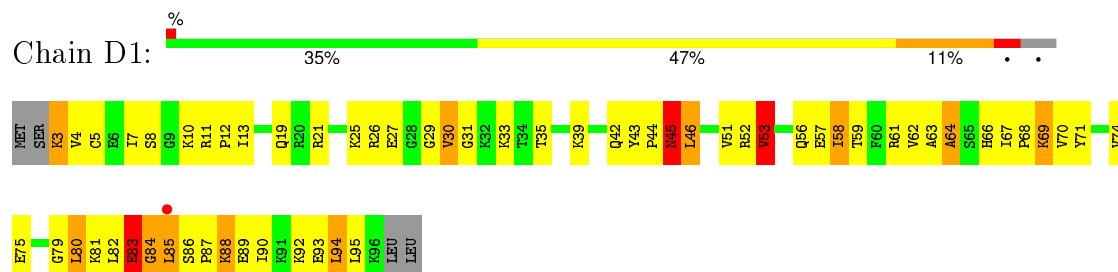
• Molecule 25: 50S RIBOSOMAL PROTEIN L27



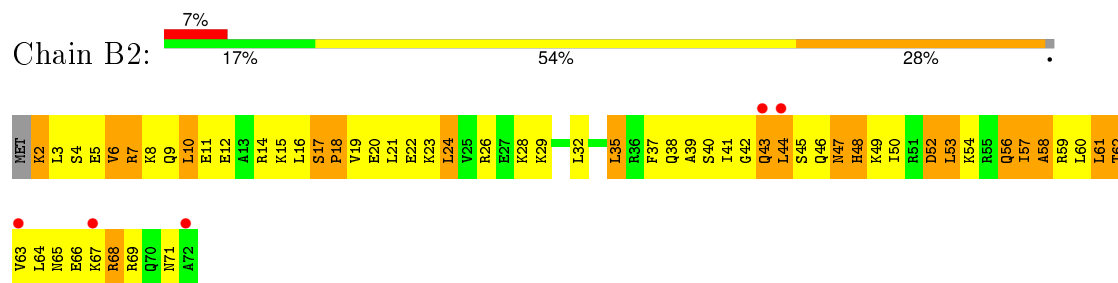
• Molecule 26: 50S RIBOSOMAL PROTEIN L28



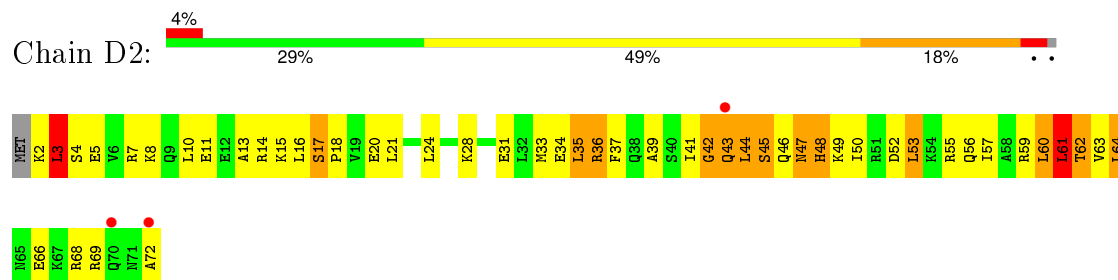
• Molecule 26: 50S RIBOSOMAL PROTEIN L28



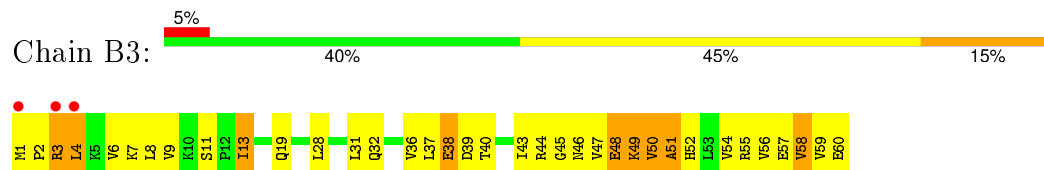
• Molecule 27: 50S RIBOSOMAL PROTEIN L29



• Molecule 27: 50S RIBOSOMAL PROTEIN L29

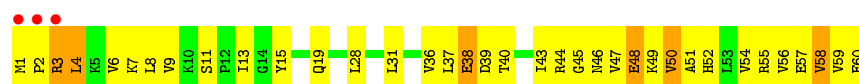


• Molecule 28: 50S RIBOSOMAL PROTEIN L30

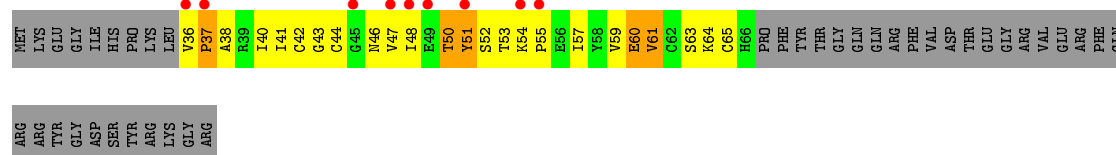
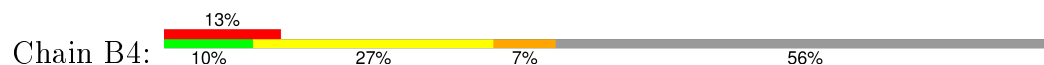


• Molecule 28: 50S RIBOSOMAL PROTEIN L30

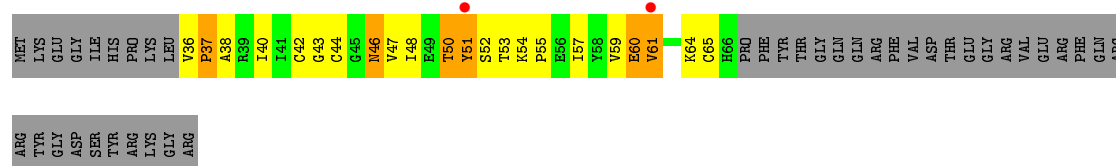
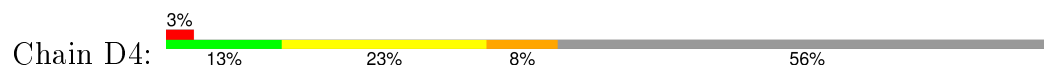




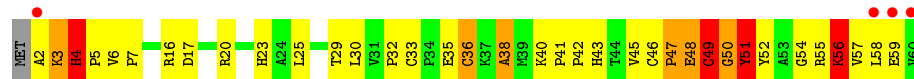
● Molecule 29: 50S RIBOSOMAL PROTEIN L31



● Molecule 29: 50S RIBOSOMAL PROTEIN L31



● Molecule 30: 50S RIBOSOMAL PROTEIN L32



● Molecule 30: 50S RIBOSOMAL PROTEIN L32



● Molecule 31: 50S RIBOSOMAL PROTEIN L33



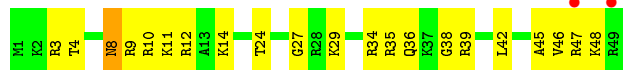
● Molecule 31: 50S RIBOSOMAL PROTEIN L33



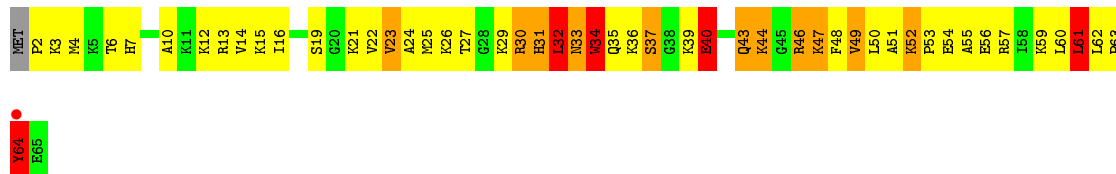
- Molecule 32: 50S RIBOSOMAL PROTEIN L34



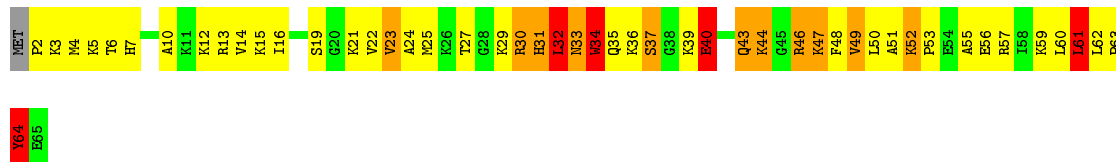
- Molecule 32: 50S RIBOSOMAL PROTEIN L34



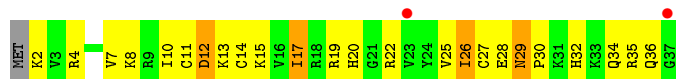
- Molecule 33: 50S RIBOSOMAL PROTEIN L35



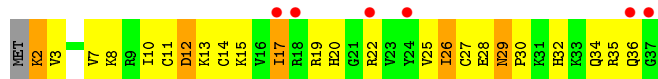
- Molecule 33: 50S RIBOSOMAL PROTEIN L35



- Molecule 34: 50S RIBOSOMAL PROTEIN L36



- Molecule 34: 50S RIBOSOMAL PROTEIN L36

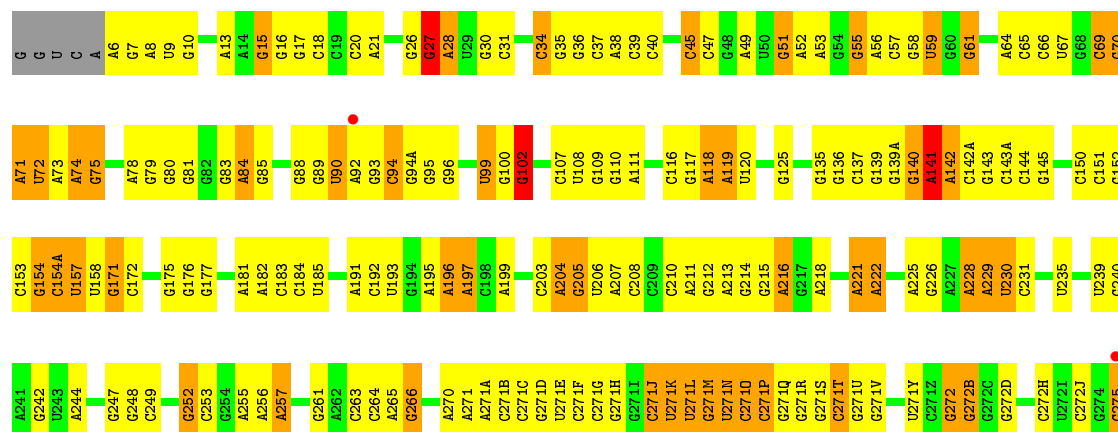


- Molecule 35: 23S RIBOSOMAL RNA



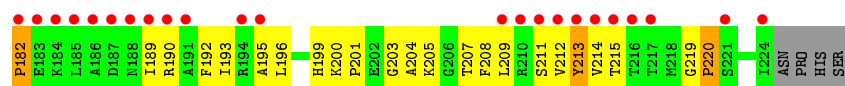
A1057	G989	C915	G848	A784	G707	G654A	C591	C509	A432	G351	C272J	U239	C153	U72	G
G1058	A990	G916	A849	G785	C708	C654B	G592	G512	C433	G352	G274	G240	G154	A73	G
	C991	A917	C850	G786	U709	G654C	G593		G436	G353	G275	A241	C154A	A74	C
U1061	C992	A918	U851	U787	G710	G654D			G437	G354	C279	G242	U157	U	
G1062	G993	G919	G852	A788	G711	C654E	G598	C617		G355		A243	U158	A78	A
G1063	C994		G853	G789	G712	G654F	G599	C618	A443		A283	G247	C172	G17	G
G1064	C995	U922	G854	C790	G713	C654G	G600	U519	C444	A389	U284	G248	G175	G80	A3
U1065	A996	C923	G855	G791	U714	G654H	C601	G520	C445	G360	C285	C249	G176	U9	U
U1066	G997	C924	C856	G792	G715	G654I	G602		C446	G361	C286		G177	G10	G
A1067	C998	C925	C857	A793	A716	G654J	A603	C523	C447	U362	C287		G178	G10	G
G1068	U999	G926	U858	G794	G717	G654K	G604	U524	A447	U363	C288		G179	G10	G
A1069	U999	G927	G859	C795	A718	G654L	C605	U525	U448	G363	A289		A84	A13	A
A1070	A1000	G927		C796	A719	G654M	U606		A449	A363A	G290		A182	A14	A
G1071	A1001	G928		C797	C720	G654N	U607	A528	G450	G363B	C291		C183	G15	G
C1072	G1002		G862		C721	G654O	A608	A529			C296	A255	C184	G16	G
			A863	A800	C722	G654P	A609	G530	A454	U363E	C297	A256	U185	G17	G
C1075	C1005	A933	G864	G801	A723	C654Q	G610	C531	C455		C298	G258	U186	G18	G
C1076	C1006		C865	A802	G724	G654R	G611	A532	C456	G370	G299	G259	U187	G19	G
A1077	A941		A866	G803	G725	G654S	G612	G533	A457	A371	G301	G260	C192	C20	C
U1078	G942		C867	U803		G654T	G613	U534	G458	G372	C302	G261	U193	A21	A
U1079	U943		U868	A804	G729	G654U	U614	U535	G459	U373	U303	A262	G194	G26	G
C1080	G944		G869	C806	C730	A654V	U614A	A536	A460	A374	G304	C263	A195	G27	G
U1081	A945		A870	U807	C731	A654W	G614B		C461		G305	C264	A196	G28	G
U1082	G946		U871	G808	G732	G656	A614C	C545		U380	U306	A265	A197	C97	G
				G809	G733	G657	G615	A547	U464		G307	G266	C198	U29	G
A1085	U1019	C951	G875	U810		G658		A548	G465	U383	G307		A199	G30	G
A1086	A1020	G952	U877	U811	U740	C659	G620	A549	G466	U384	A270		U200	G31	G
C1087	A1021	A953	A878	C812	G741	G660	A621	G549	A466	U385	A271		C201	C34	C
A1088	G1022	G954	G879	U813	G742	C661	G622	G551	G469	G386	A271A		U202	G35	G
G1089	U1023	C955	G880	C814	G743	G662	G623	U555	A470		C271B		C203	G36	G
U1090	G1024	G956	G881	C815	G744		G624	U556	A471	G389	C271C		G204	G37	G
G1091	G1025	A957	G882	C816		G665	G625	U557	A472	A390	C271D		G205	G109	G
U1092	U1026	U958	G883	C817	U747	G666	U626	U558	G473		U271E		U206	A38	A
G1093	A1027	A959	C884	G818			A627	G559	G474	U395	C271F		C207	A11	A
U1094	U1028	C961	C885	A819	A752	C671	G630	G560	G475	G396	C271G		C208	C40	C
A1095	A1029	G962	C886	A820	C753	C672	G631	U561	G476	G400	G271H		G212	G45	G
A1096	U1030	A887	C887	A821	C754	C673	A631	C564	A477		C271I		A213	G45	G
U1097		C888	C888		C755	G674	A632	C565	A478	C404	C271J		G214	A49	A
A1098	G1034	C964	C889	C825	C756	A675	A633	U566	A479	U405	U271K		G215	A49	A
U1099	U1035	C965	A890	U826		A676	C634	U567	A480	G406	U271L		A216	U50	U
C1100	G1036		G892	U827	G760		C635	A567	G481		G271M		G217	G51	G
U1101	U1037	C970	C893	U828	A761	G680	G636	U568	A482	C409	U271N		A218	A52	A
C1102	C1038	C971	C894	A829	G764	G681	A637	G573	A483	G410	C271O		G219	A53	A
A1103	U1040		U895	G830	G765	C682	G638	C574		G411	G271P		A221	G54	G
C1104		C975	A896	G831	C766	C683	U639	A575	A492	A412	G271Q		A222	G55	G
U1105		C976	C897	U832		G686	C640	U576	G493	C413	G271R		G225	A56	A
G1106	G1043	C977	A901	U833	G769	C691	C641	G577	G494		G271S		A226	C57	C
U1108	A1045	G978	C902	C834	G770	C692	G642		G495	A330	C271T		G226	G58	G
A1046	G1046	G979	C903	C835	G771	C693	A643	C580		C419	G271U		A227	U59	U
U1047	U1047	G980	C904	G836	U773	C694	A644	C581	A497	G420	G271V		A228	G60	G
C1109	C1049	A981	C905	C837	A774	C695	A645	C582	G498	U421			A229	G61	G
A1111	G1112	G982	C906	C838	G775	C696	A646	G583	U499	A422	U271Y		A230	A64	A
		C983	C907	C839	G776	A699	G647	C584	A502	G423	C271Z		U230	G65	G
G1116	G1051	A983	A909	C840	G777	G700	G648	C585	A503	G425	G272		C231	G66	G
C1117	C1052	A984	A910		U779		G649	A586	U504	C426	G272B		G234	U67	U
C1118	C1053	G985	A911	C844	G780	U703	G651	C587	A505	U427	G272C		U235	G68	G
	A1054	G986	C912	G845	A781	G704	C652	U588	A506	A428	G272H		C236	G69	G
G1125	G1055	G987	U913	C846	A782	A705	C653	C589	A507	G349	C272I		C237	G70	G
A1126	G1056	A988	C914	U847	A783	A706	A654	A590	G508	U431	U272J		C238	A71	A

G2191	G2192	G2193	G2194	G2195	G2196	G2197	G2198	G2199	G2200	G2201	G2202	G2203	G2204	G2205	G2206	G2207	G2208	G2209	G2210	G2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	G2219	G2220	G2221	G2222	G2223	G2224	G2225	G2226	G2227	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	G2239	G2240	G2241	G2242	G2243	G2244	G2245	G2246	G2247	G2248	G2249	G2250	G2251	G2252	G2253	G2254	G2255	G2256	G2257	G2258	G2259	G2260	G2261	G2262	G2263	G2264	G2265	G2266	G2267	G2268	G2269	G2270	G2271	G2272																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
G2131	U2132	G2133	G2134	G2135	G2136	G2137	G2138	G2139	G2140	G2141	G2142	G2143	G2144	G2145	G2146	G2147	G2148	G2149	G2150	G2151	G2152	G2153	G2154	G2155	G2156	G2157	G2158	G2159	G2160	G2161	G2162	G2163	G2164	G2165	G2166	G2167	G2168	G2169	G2170	G2171	G2172	G2173	G2174	G2175	G2176	G2177	G2178	G2179	G2180	G2181	G2182	G2183	G2184	G2185	G2186	G2187	G2188	G2189	G2190																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
U191	U192	U193	U194	U195	U196	U197	U198	U199	U200	U201	U202	U203	U204	U205	U206	U207	U208	U209	U210	U211	U212	U213	U214	U215	U216	U217	U218	U219	U220	U221	U222	U223	U224	U225	U226	U227	U228	U229	U230	U231	U232	U233	U234	U235	U236	U237	U238	U239	U240	U241	U242	U243	U244	U245	U246	U247	U248	U249	U250	U251	U252	U253	U254	U255	U256	U257	U258	U259	U260	U261	U262	U263	U264	U265	U266	U267	U268	U269	U270	U271	U272																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
A1127	A1128	A1129	A1130	A1131	A1132	A1133	A1134	A1135	A1136	A1137	A1138	A1139	A1140	A1141	A1142	A1143	A1144	A1145	A1146	A1147	A1148	A1149	A1150	A1151	A1152	A1153	A1154	A1155	A1156	A1157	A1158	A1159	A1160	A1161	A1162	A1163	A1164	A1165	A1166	A1167	A1168	A1169	A1170	A1171	A1172	A1173	A1174	A1175	A1176	A1177	A1178	A1179	A1180	A1181	A1182	A1183	A1184	A1185	A1186	A1187	A1188	A1189	A1190																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
G1364	G1365	G1366	G1367	G1368	G1369	G1370	G1371	G1372	G1373	G1374	G1375	G1376	G1377	G1378	G1379	G1380	G1381	G1382	G1383	G1384	G1385	G1386	G1387	G1388	G1389	G1390	G1391	G1392	G1393	G1394	G1395	G1396	G1397	G1398	G1399	G1400	G1401	G1402	G1403	G1404	G1405	G1406	G1407	G1408	G1409	G1410	G1411	G1412	G1413	G1414	G1415	G1416	G1417	G1418	G1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	G1427	G1428	G1429	G1430	G1431	G1432	G1433	G1434	G1435	G1436	G1437	G1438	G1439	G1440	G1441	G1442	G1443	G1444	G1445	G1446	G1447	G1448	G1449	G1450	G1451	G1452	G1453	G1454	G1455	G1456	G1457	G1458	G1459	G1460	G1461	G1462	G1463	G1464	G1465	G1466	G1467	G1468	G1469	G1470	G1471	G1472	G1473	G1474	G1475	G1476	G1477	G1478	G1479	G1480	G1481	G1482	G1483	G1484	G1485	G1486	G1487	G1488	G1489	G1490	G1491	G1492	G1493	G1494	G1495	G1496	G1497	G1498	G1499	G1500	G1501	G1502	G1503																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
C1504	C1505	C1506	C1507	C1508	C1509	A1509A	A1509B	C1510	C1511	C1512	C1513	C1514	C1515	C1516	C1517	C1518	C1519	C1520	C1521	C1522	C1523	C1524	C1525	C1526	C1527	A1528A	C1529	C1530	C1531	C1532	C1533	C1534	C1535	C1536	C1537	C1538	C1539	C1540	C1541	C1542	C1543	C1544	C1545	C1546	C1547	C1548	C1549	C1550	C1551	C1552	C1553	C1554	C1555	C1556	C1557	C1558	C1559	C1560	C1561	C1562	C1563	C1564	C1565	C1566	C1567	C1568	C1569	C1570	C1571	C1572	C1573	C1574	C1575	C1576	C1577	C1578	C1579	C1580	C1581	C1582	C1583	C1584	C1585	C1586	C1587	C1588	C1589	C1590	C1591	C1592	C1593	C1594	C1595	C1596	C1597	C1598	C1599	C1600	C1601	C1602	C1603	C1604	C1605	C1606	C1607	C1608	C1609	C1610	C1611	C1612	C1613	C1614	C1615	C1616	C1617	C1618	C1619	C1620	C1621	C1622	C1623	C1624	C1625	C1626	C1627	C1628	C1629	C1630	C1631	C1632	C1633	C1634	C1635	C1636	C1637	C1638	C1639	C1640	C1641	C1642	C1643	C1644	C1645	C1646	C1647	C1648	C1649	C1650	C1651	C1652	C1653	C1654	C1655	C1656	C1657	C1658	C1659	C1660	C1661	C1662	C1663	C1664	C1665	C1666	C1667	C1668	C1669	C1670	C1671	C1672	C1673	C1674	C1675	C1676	C1677	C1678	C1679	C1680	C1681	C1682	C1683	C1684	C1685	C1686	C1687	C1688	C1689	C1690	C1691	C1692	C1693	C1694	C1695	C1696	C1697	C1698	C1699	C1700	C1701	C1702	C1703	C1704	C1705	C1706	C1707	C1708	C1709	C1710	C1711	C1712	C1713	C1714	C1715	C1716	C1717	C1718	C1719	C1720	C1721	C1722	C1723	C1724	C1725	C1726	C1727	C1728	C1729	C1730	C1731	C1732	C1733	C1734	C1735	C1736	C1737	C1738	C1739	C1740	C1741	C1742	C1743	C1744	C1745	C1746	C1747	C1748	C1749	C1750	C1751	C1752	C1753	C1754	C1755	C1756	C1757	C1758	C1759	C1760	C1761	C1762	C1763	C1764	C1765	C1766	C1767	C1768	C1769	C1770	C1771	C1772	C1773	C1774	C1775	C1776	C1777	C1778	C1779	C1780	C1781	C1782	C1783	C1784	C1785	C1786	C1787	C1788	C1789	C1790	C1791	C1792	C1793	C1794	C1795	C1796	C1797	C1798	C1799	C1800	C1801	C1802	C1803	C1804	C1805	C1806	C1807	C1808	C1809	C1810	C1811	C1812	C1813	C1814	C1815	C1816	C1817	C1818	C1819	C1820	C1821	C1822	C1823	C1824	C1825	C1826	C1827	C1828	C1829	C1830	C1831	C1832	C1833	C1834	C1835	C1836	C1837	C1838	C1839	C1840	C1841	C1842	C1843	C1844	C1845	C1846	C1847	C1848	C1849	C1850	C1851	C1852	C1853	C1854	C1855	C1856	C1857	C1858	C1859	C1860	C1861	C1862	C1863	C1864	C1865	C1866	C1867	C1868	C1869	C1870	C1871	C1872	C1873	C1874	C1875	C1876	C1877	C1878	C1879	C1880	C1881	C1882	C1883	C1884	C1885	C1886	C1887	C1888	C1889	C1890	C1891	C1892	C1893	C1894	C1895	C1896	C1897	C1898	C1899	C1900	C1901	C1902	C1903	C1904	C1905	C1906	C1907	C1908	C1909	C1910	C1911	C1912	C1913	C1914	C1915	C1916	C1917	C1918	C1919	C1920	C1921	C1922	C1923	C1924	C1925	C1926	C1927	C1928	C1929	C1930	C1931	C1932	C1933	C1934	C1935	C1936	C1937	C1938	C1939	C1940	C1941	C1942	C1943	C1944	C1945	C1946	C1947	C1948	C1949	C1950	C1951	C1952	C1953	C1954	C1955	C1956	C1957	C1958	C1959	C1960	C1961	C1962	C1963	C1964	C1965	C1966	C1967	C1968	C1969	C1970	C1971	C1972	C1973	C1974	C1975	C1976	C1977	C1978	C1979	C1980	C1981	C1982	C1983	C1984	C1985	C1986	C1987	C1988	C1989	C1990	C1991	C1992	C1993	C1994	C1995	C1996	C1997	C1998	C1999	C2000	C2001	C2002	C2003	C2004	C2005	C2006	C2007	C2008	C2009	C2010	C2011	C2012	C2013	C2014	C2015	C2016	C2017	C2018	C2019	C2020	C2021	C2022	C2023	C2024	C2025	C2026	C2027	C2028	C2029	C2030	C2031	C2032	C2033	C2034	C2035	C2036	C2037	C2038	C2039	C2040	C2041	C2042	C2043	C2044	C2045	C2046	C2047	C2048	C2049	C2050	C2051	C2052	C2053	C2054	C2055	C2056	C2057	C2058	C2059	C2060	C2061	C2062	C2063	C2064	C2065	C2066	C2067	C2068	C2069	C2070	C2071	C2072	C2073	C2074	C2075	C2076	C2077	C2078	C2079	C2080	C2081	C2082	C2083	C2084	C2085	C2086	C2087	C2088	C2089	C2090	C2091	C2092	C2093	C2094	C2095	C2096	C2097	C2098	C2099	C2100	C2101	C2102	C2103	C2104	C2105	C2106	C2107	C2108	C2109	C2110	C2111	C2112	C2113	C2114	C2115	C2116	C2117	C2118	C2119	C2120	C2121	C2122	C2123	C2124	C2125	C2126	C2127	C2128	C2129	C2130	C2131	C2132	C2133	C2134	C2135	C2136	C2137	C2138	C2139	C2140	C2141	C2142	C2143	C2144	C2145	C2146	C2147	C2148	C2149	C2150	C2151	C2152	C2153	C2154	C2155	C2156	C2157	C2158	C2159	C2160	C2161	C2162	C2163	C2164	C2165	C2166	C2167	C2168	C2169	C2170	C2171	C2172	C2173	C2174	C2175	C2176	C2177	C2178	C2179	C2180	C2181	C2182	C2183	C2184	C2185	C2186	C2187	C2188	C2189	C2190

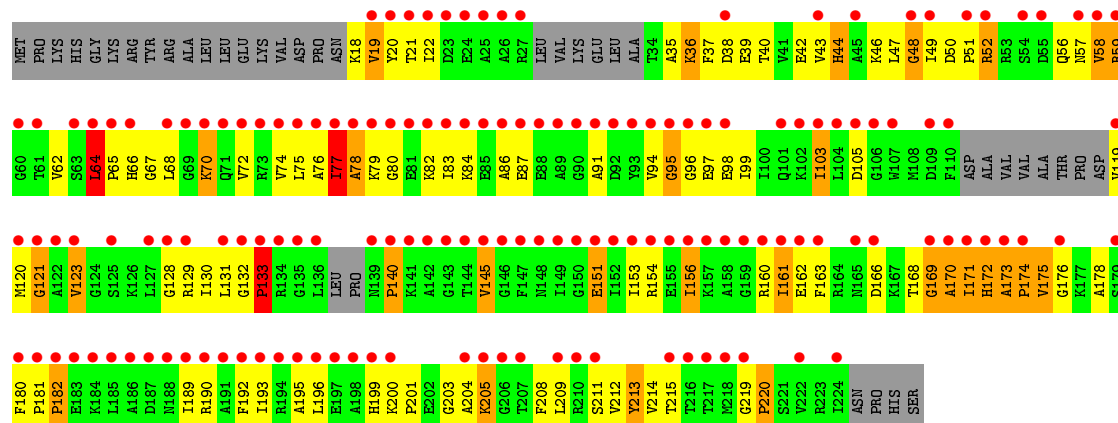


G1364	G1365	G1368	G1369	U1372	G1373	C1374	C1375	G1376	G1377	G1378	G1379	G1380	G1381	G1382	G1383	G1384	G1385	G1386	G1387	G1388	G1389	U1396	U1397	C1398	C1399	G1400	G1401	C1402	C1403	U1404	U1405	C1406	C1407	C1408	C1409	G1410	C1411	G1412	G1413	G1416	G1417	G1418	G1419	U1420	G1423	G1424	G1425	A1426	A1427	G1428	G1429	C1430	U1431	C1432	U1433																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
A1189	G1190	G1191	G1192	G1193	G1194	G1195	C1201	G1202	G1203	G1204	U1205	C1208	G1209	G1210	U1211	G1212	G1215	A1220	C1221	G1223	C1224	G1225	A1226	G1227	U1234	U1235	G1236	U1237	U1238	G1239	U1240	A1241	A1242	U1243	U1244	U1245	U1246	U1247	U1248	U1249	G1250	C1251	G1252	A1253	G1256	C1257	G1258	U1259	C1260	A1269	C1270	G1271	A1272	A1273	G1274	G1275	G1276	G1277	G1278	G1279	G1280	G1281	U1282	C1283	G1284	G1285	G1286	G1287	G1288	A1289	C1290	C1291	G1292	G1293	G1294	G1295	G1296	G1297	G1298	G1299	G1300	G1301	G1302	G1303	G1304	G1305	G1306	G1307	G1308	G1309	G1310	G1311	G1312	G1313	G1314	G1315	G1316	G1317	G1318	G1319	G1320	G1321	G1322	G1323	G1324	G1325	G1326	G1327	U1328	G1329	A330	A331	C332	C333	C334	C335	C336	C337	C338	C339	C340	C341	C342	C343	C344	C345	C346	C347	C348	C349	C350	C351	C352	C353	C354	C355	C356	C357	C358	C359	C360	C361	C362	C363	C364	C365	C366	C367	C368	C369	C370	C371	C372	C373	C374	C375	C376	C377	C378	C379	C380	C381	C382	C383	C384	C385	C386	C387	C388	C389	C390	C391	C392	C393	C394	C395	C396	C397	C398	C399	C400	C401	C402	C403	C404	C405	C406	C407	C408	C409	C410	C411	C412	C413	C414	C415	C416	C417	C418	C419	C420	C421	C422	C423	C424	C425	C426	C427	C428	C429	C430	C431	C432	C433	C434	C435	C436	C437	C438	C439	C440	C441	C442	C443	C444	C445	C446	C447	C448	C449	C450	C451	C452	C453	C454	C455	C456	C457	C458	C459	C460	C461	C462	C463	C464	C465	C466	C467	C468	C469	C470	C471	C472	C473	C474	C475	C476	C477	C478	C479	C480	C481	C482	C483	C484	C485	C486	C487	C488	C489	C490	C491	C492	C493	C494	C495	C496	C497	C498	C499	A500	A501	A502	A503	A504	A505	A506	A507	A508	A509	A510	A511	A512	A513	A514	A515	A516	A517	A518	A519	A520	A521	A522	A523	A524	A525	A526	A527	A528	A529	A530	A531	A532	A533	A534	A535	A536	A537	A538	A539	A540	A541	A542	A543	A544	A545	A546	A547	A548	A549	A550	A551	A552	A553	A554	A555	A556	A557	A558	A559	A560	A561	A562	A563	A564	A565	A566	A567	A568	A569	A570	A571	A572	A573	A574	A575	A576	A577	A578	A579	A580	A581	A582	A583	A584	A585	A586	A587	A588	A589	A590	C591	G592	G593	G594	G595	G596	G597	G598	G599	G600	G601	G602	G603	G604	G605	G606	G607	G608	G609	G610	G611	G612	G613	G614	G615	G616	G617	G618	G619	G620	G621	G622	G623	G624	G625	G626	G627	G628	G629	G630	G631	G632	G633	G634	G635	G636	G637	G638	G639	G640	G641	G642	G643	G644	G645	G646	G647	G648	G649	G650	G651	G652	G653	G654	G655	G656	G657	G658	G659	G660	G661	G662	G663	G664	G665	G666	G667	G668	G669	G670	G671	G672	G673	G674	G675	G676	G677	G678	G679	G680	G681	G682	G683	G684	G685	G686	G687	G688	G689	G690	G691	G692	G693	G694	G695	G696	G697	G698	G699	G700	G701	G702	G703	G704	G705	G706	G707	G708	G709	G710	G711	G712	G713	G714	G715	G716	G717	G718	G719	G720	G721	G722	G723	G724	G725	G726	G727	G728	G729	G730	G731	G732	G733	G734	G735	G736	G737	G738	G739	G740	G741	G742	G743	G744	G745	G746	G747	G748	G749	G750	G751	G752	G753	G754	G755	G756	G757	G758	G759	G760	G761	G762	G763	G764	G765	G766	G767	G768	G769	G770	G771	G772	G773	G774	G775	G776	G777	G778	G779	G780	G781	G782	G783	G784	G785	G786	G787	G788	G789	G790	G791	G792	G793	G794	G795	G796	G797	G798	G799	G800	G801	G802	G803	G804	G805	G806	G807	G808	G809	G810	G811	G812	G813	G814	G815	G816	G817	G818	G819	G820	G821	G822	G823	G824	G825	G826	G827	G828	G829	G830	G831	G832	G833	G834	G835	G836	G837	G838	G839	G840	G841	G842	G843	G844	G845	G846	G847	G848	G849	G850	G851	G852	G853	G854	G855	G856	G857	G858	G859	G860	G861	G862	G863	G864	G865	G866	G867	G868	G869	G870	G871	G872	G873	G874	G875	G876	G877	G878	G879	G880	G881	G882	G883	G884	G885	G886	G887	G888	G889	G890	G891	G892	G893	G894	G895	G896	G897	G898	G899	G900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	G1000	G1001	G1002	G1003	G1004	G1005	G1006	G1007	G1008	G1009	G1010	G1011	G1012	G1013	G1014	G1015	G1016	G1017	G1018	G1019	G1020	G1021	G1022	G1023	G1024	G1025	G1026	G1027	G1028	G1029	G1030	G1031	G1032	G1033	G1034	G1035	G1036	G1037	G1038	G1039	G1040	G1041	G1042	G1043	G1044	G1045	G1046	G1047	G1048	G1049	G1050	G1051	G1052	G1053	G1054	G1055	G1056	G1057	G1058	G1059	G1060	G1061	G1062	G1063	G1064	G1065	G1066	G1067	G1068	G1069	G1070	G1071	G1072	G1073	G1074	G1075	G1076	G1077	G1078	G1079	G1080	G1081	G1082	G1083	G1084	G1085	G1086	G1087	G1088	G1089	G1090	G1091	G1092	G1093	G1094	G1095	G1096	G1097	G1098	G1099	G1100	G1101	G1102	G1103	G1104	G1105	G1106	G1107	G1108	G1109	G1110	G1111	G1112	G1113	G1114	G1115	G1116	G1117	G1118	G1119	G1120	G1121	G1122	G1123	G1124	G1125	G1126	G1127	G1128	G1129	G1130	G1131	G1132	G1133	G1134	G1135	G1136	G1137	G1138	G1139	G1140	G1141	G1142	G1143	G1144	G1145	G1146	G1147	G1148	G1149	G1150	G1151	G1152	G1153	G1154	G1155	G1156	G1157	G1158	G1159	G1160	G1161	G1162	G1163	G1164	G1165	G1166	G1167	G1168	G1169	G1170	G1171	G1172	G1173	G1174	G1175	G1176	G1177	G1178	G1179	G1180	G1181	G1182	G1183	G1184	G1185	G1186	G1187	G1188	G1189	G1190	G1191	G1192	G1193	G1194	G1195	G1196	G1197	G1198	G1199	G1200	G1201	G1202	G1203	G1204	G1205	G1206	G1207	G1208	G1209	G1210	G1211	G1212	G1213	G1214	G1215	G1216	G1217	G1218	G1219	G1220	G1221	G1222	G1223	G1224	G1225	G1226	G1227	G1228	G1229	G1230	G1231	G1232	G1233	G1234	G1235	G1236	G1237	G1238	G1239	G1240	G1241	G1242	G1243	G1244	G1245	G1246	G1247	G1248	G1249	G1250	G1251	G1252	G1253	G1254	G1255	G1256	G1257	G1258	G1259	G1260	G1261	G1262	G1263	G1264	G1265	G1266	G1267	G1268	G1269	G1270	G1271	G1272	G1273	G1274	G1275	G1276	G1277	G1278	G1279	G1280	G1281	G1282	G1283	G1284	G1285	G1286	G1287	G1288	G1289	G1290	G1291	G1292	G1293	G1294	G1295	G1296	G1297	G1298	G1299	G1300	G1301	G1302	G1303	G1304	G1305	G1306	G1307	G1308	G1309	G1310	G1311	G1312	G1313	G1314	G1315	G1316	G1317	G1318	G1319	G1320	G1321	G1322	G1323	G1324	G1325	G1326	G1327	G1328	G1329	G1330	G1331	G1332	G1333	G1334	G1335	G1336	G1337	G1338	G1339	G1340	G1341	G1342	G1343	G1344	G1345	G1346	G1347	G1348	G1349	G1350	G1351	G1352	G1353	G1354	G1355	G1356	G1357	G1358	G1359	G1360	G1361	G1362	G1363	G1364	G1365	G1366	G1367	G1368	G1369	G1370	G1371	G1372	G1373	G1374	G1375	G1376	G1377	G1378	G1379	G1380	G1381	G1382	G1383	G1384	G1385	G1386	G1387	G1388	G1389	G1390	G1391	G1392	G1393	G1394	G1395	G1396	G1397	G1398	G1399	G1400	G1401	G1402	G1403	G1404	G1405	G1406	G1407	G1408	G1409	G1410	G1411	G1412	G1413	G1414	G1415	G1416	G1417	G1418	G1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	G1427	G1428	G1429	G1430	G1431	G1432	G1433	G1434	G1435	G1436	G1437	G1438	G1439	G1440	G1441	G1442	G1443	G1444	G1445	G1446	G1447	G1448	G1449	G1450	G1451	G1452	G1453	G1454	G1455	G1456	G1457	G1458	G1459	G1460	G1461	G1462	G1463	G1464	G1465	G1466	G1467	G1468	G1469	G1470	G1471	G1472	G1473	G1474	G1475	G1476	G1477	G1478	G1479	G1480	G1481	G1482	G1483	G1484	G1485	G1486	G1487	G1488	G1489	G1490	G1491	G1492	G1493	G1494	G1495	G1496	G1497	G1498	G1499	G1500	G1501	G1502	G1503	G1504	G1505	G1506	G1507	G1508	G1509	G1510	G1511	G1512	G1513	G1514	G1515	G1516	G1517	G1518	G1519	G1520	G1521	G1522	G1523	G1524	G1525	G1526	G1527	G1528	G1529	G1530	G1531	G1532	G1533	G1534	G1535	G1536	G1537	G1538	G1539	G1540	G1541	G1542	G1543	G1544	G1545	G1546	G1547	G1548	G1549	G1550	G1551	G1552	G1553	G1554	G1555	G1556	G1557	G1558	G1559	G1560	G1561	G1562	G1563	G1564	G1565	G1566	G1567	G1568	G1569	G1570	G1571	G1572	G1573	G1574	G1575	G1576	G1577	G1578	G1579	G1580	G1581	G1582	G1583	G1584	G1585	G1586	G1587	G1588	G1589	G1590	G1591	G1592	G1593	G1594	G1595

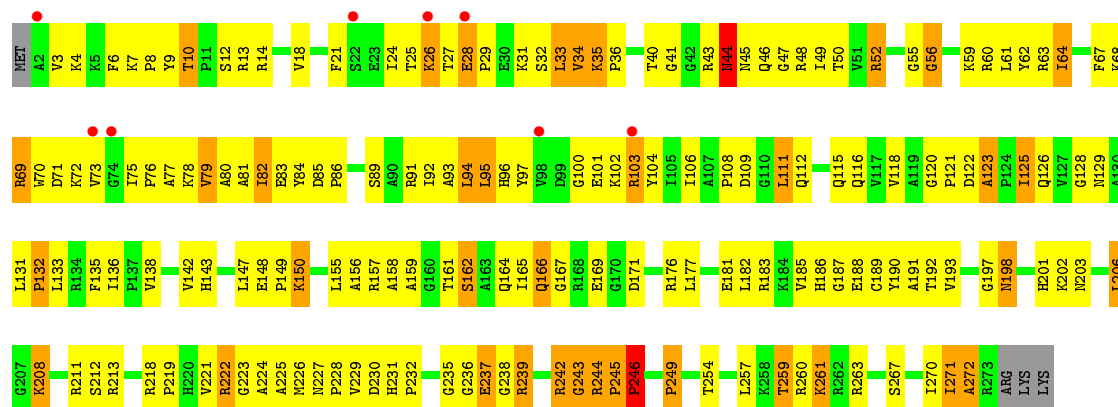
C2498	C2416	U2348	G2283	U2197	C2137	G2069	G1907	G1824	C1751	G1683	A1570	C1501	A1434
C2417	G2349	G2349	C2284	A2198	C2138	G2070	C1908	A1825	C1751	A1694	A1571	C1502	G1435
U2418	C2350	C2350	C2285	A2199	C2139	U2074	C1909	G1826	G1752	A1695	A1572	C1503	G1436
C2502	G2351	G2351	A2286	C2200	C2140	U2075	C1910	C1827	G1753	C1656	G1573	C1504	C1437
U2504	C2352	C2352	A2287	C2201	G2141	U2076	C1911	A1828	C1754	C1657	C1574	C1505	U1438
G2505	G2353	G2353	A2288	C2202	C2142	U2077	C1912	A1829	A1755	C1658	C1575	C1506	A1439
U2506	C2354	C2354	G2289	U2203	C2143	G2080	A1913	C1832	G1756	U1659	U1576	A1507	G1440
C2507	C2355	C2355	G2290	G2206	C2144	G2081	C1914	U1833	U1757	A1665	C1577	A1508	G1441
G2508	U2357	U2357	C2292	G2207	C2145	A2082	U1918	U1834	G1758	G1667	U1578	C1509	G1442
C2510	C2358	C2358	C2293	A2208	G2146	G2083	A1919	G1835	A1762	G1667	A1579	A1509A	
G2511	G2359	G2359	G2294	U2218	C2147	U2087	U1919	U1836	A1763	A1668	A1580	A1509B	A1445
C2512	G2360	G2360	C2295	G2219	C2148	G2086	U1923	C1838	G1764		C1584	G1510	G1446
U2513	A2361	A2361	U2296	G2220	U2150	G2087	C1924	G1839	C1765	G1674	A1586	G1511	G1447
C2514	C2362	C2362	G2297	G2221	G2151	G2088	C1925	G1840	U1766	A1587	A1587	U1512	
C2515	C2363	C2363	A2298	G2222	G2152	G2089	U1926	U1841	C1767	C1676	C1588	C1513	G1448
U2516	C2364	C2364	G2299	G2223	G2153	U2090	U1927	A1842		A1677	C1589	G1514	A1449
C2517	G2365	G2365	G2300	G2224	G2154	U2091	A1928	C1843	G1770	G1678	U1590	G1515	G1450
A2518	A2366	A2366	C2301	A2225	G2155	G2093	C1929	C1844	C1771		G1591	G1516	
U2519	G2367	G2367	G2302	C2226	C2156	G2094	G1930	G1845	A1772	G1681		G1517	A1482
C2520	C2368	C2368	G2303	U2233	G2157	C2095	U1931	G1846	A1773			U1518	A1483
	A2369	A2369	A2304	U2234	G2158	U2096	A1932	A1847	U1777	C1685	G1595	U1519	
G2523	C2370	C2370	A2305	C2235	G2159	C2097	G1933	U1851	U1778	C1686	A1596	G1520	G1489
	G2371	G2371	C2306	G2236	C2160	U2098	U1936	C1852	U1779	G1687	C1598	G1524	G1461
C2527	A2372	A2372	G2307	C2237	G2161	U2099	A1937	A1853	A1780	U1688	C1599	G1525	C1462
U2528	G2373	G2373	G2308	G2238	G2162	G2100	C1938	A1854	C1781	A1689	C1600	G1526	C2465
G2529	C2374	C2374	A2309	G2239	C2163	U2101	U1939	A1855	C1782	U1693	G1601	C1527	C1464
A2530	G2375	G2375	A2310	C2240	C2164	G2102	C2026	C1856	C1783	C1694	U1602	A1528	G1465
	C2447	C2447	U2312	A2241	G2165	G2103	U1940	G1857	A1784	G1695	A1603	G1529	G1466
C2533	C2448	C2448	C2313	G2242	U2167	G2104	C1941	C1858	A1785	C1696	C1607	C1530	C1467
A2534	U2449	U2449	G2314	U2243	C2168	G2107	U1946	A1859	A1786	G1697	A1608	C1531	C1468
G2535	G2382	G2382	G2315	U2244	A2169	C2108	C1947	G1860	A1789	A1698	A1609	C1532	A1469
C2536	C2383	C2383	C2316	U2245	G2170	U2109	G1948	G1862	C1790	A1700	A1610	C1533	A1472
U2537	G2384	G2384	C2317	G2246	A2171	G2112	G1949	G1863	A1791	A1701	G1613	A1544	G1473
C2538	C2385	C2385	G2318	A2247	U2172	U2113	A1952	U1864	G1792		A1614	A1545	C1474
			G2319	C2248	A2173	A2114	U1953	G1865	C1793	C1708	C1615	C1546	
C2540	G2389	G2389	G2320	U2249	C2174	A2115	U1954	C1866	U1794	G1709	A1616	C1547	A1477
A2541	U2390	U2390	G2321	G2250	C2175	G2116	U1955	A1877	C1795	C1710	C1617	C1548	G1478
U2542	G2391	G2391	C2322	C2259	A2176	G2117	U1956	C1878	U1796	C1711	A1618	C1549	G1479
G2543	A2392	A2392	A2327	C2260	C2177	U2118	C1958	A1879	C1797	C1712	G1624	C1550	G1480
U2544	C2393	C2393	G2328	C2261	C2178	A2119	U1959	C1880	U1798	G1713	G1625	C1551	U1481
	C2394	C2394	A2329	U2262	G2180	G2120	U1963	C1881	G1799	G1714	G1482	G1552	G1481
C2552	G2395	G2395	G2330	C2263	C2181	G2121	U1964	C1882	C1800	G1717	A1553	G1484	G1482
U2553	U2400	U2400	U2332	C2264	G2182	U2122	C1967	G1883	U1805	G1718	A1554		G1485
G2554	C2401	C2401	C2333	A2267	C2183	G2123	G1968	G1884	U1809	G1719	A1637	C1557	A1486
	C2402	C2402	G2334	C2268	C2184	G2124	A1969	A1885	U1638	U1720	C1638	C1558	G1487
C2555	G2403	G2403	A2335	A2269	G2185	G2125	A1970	C1886	C1640	U1721	U1639	G1559	U1488
U2556	C2404	C2404	A2336	C2271	G2186	G2126	A1971	C1887	A1722	A1640	U1640	G1560	U1489
C2557	G2405	G2405	A2337	U2272	C2187	G2127	A1972	C1888	G1811	U1739	A1641	G1561	A1490
	U2406	U2406	G2337	C2273	C2188	C2128	A1973	G1889	A1812	G1642	G1642	A1562	G1492
U2562	C2407	C2407	G2340	A2274	U2189	U2129	C1974	A1890	G1813	G1740	C1644	G1563	C1493
A2563	U2408	U2408	G2341	C2275	G2190	G2130	C1975	A1891	G1814	C1744	C1645	C1564	A1494
C2564	G2409	G2409	G2342	C2276	G2191	G2131	C1976	A1892	G1815		G1647	C1565	A1495
U2565	C2410	C2410	U2343	G2277	G2192	U2132	G1979	A1893	G1817	G1746	C1648	A1566	A1496
G2566	A2411	A2411	G2344	C2278	C2193	G2133	A1980	A1901	U1818	G1747	A1567	G1568	C1497
C2567	G2412	G2412	G2345	A2279	C2194	A2134	C1982	C1902	U1820	G1747A	G1651	G1569	
U2568	U2413	U2413	C2346	C2280	A2135	G2136	C1983	G1906		G1748	A1652		
G2569	C2414	C2414	G2347	G2282	C2196		U2068						



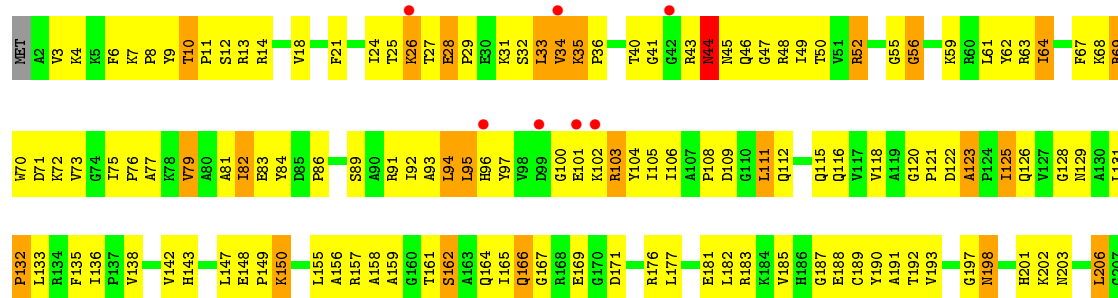
• Molecule 37: 50S RIBOSOMAL PROTEIN L1

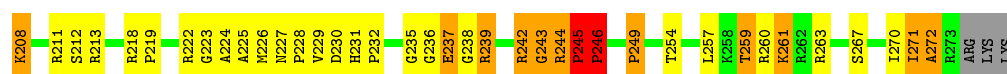


• Molecule 38: 50S RIBOSOMAL PROTEIN L2

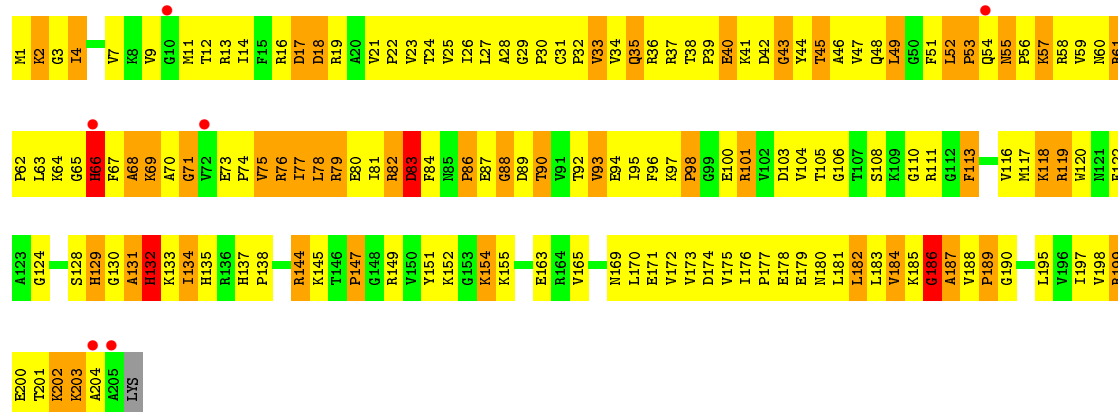


• Molecule 38: 50S RIBOSOMAL PROTEIN L2

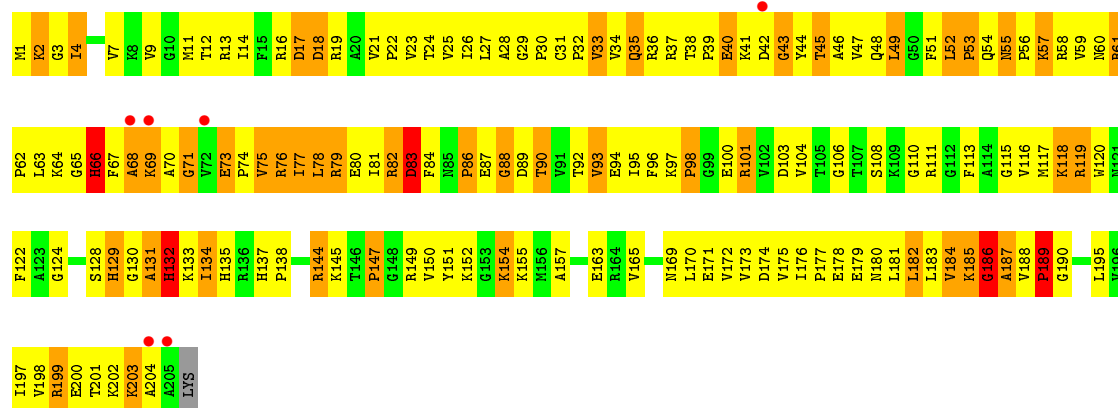




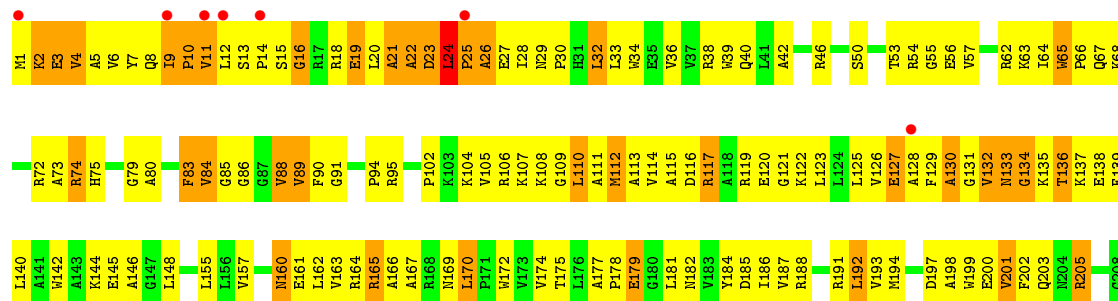
• Molecule 39: 50S RIBOSOMAL PROTEIN L3

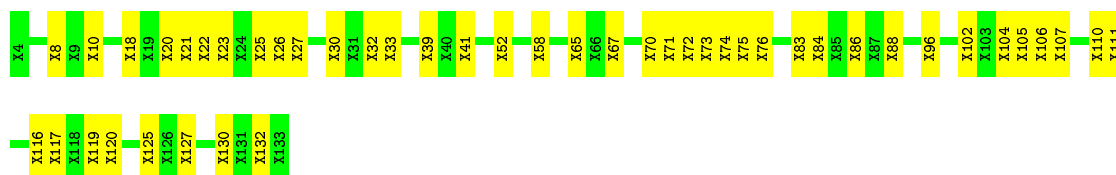


• Molecule 39: 50S RIBOSOMAL PROTEIN L3

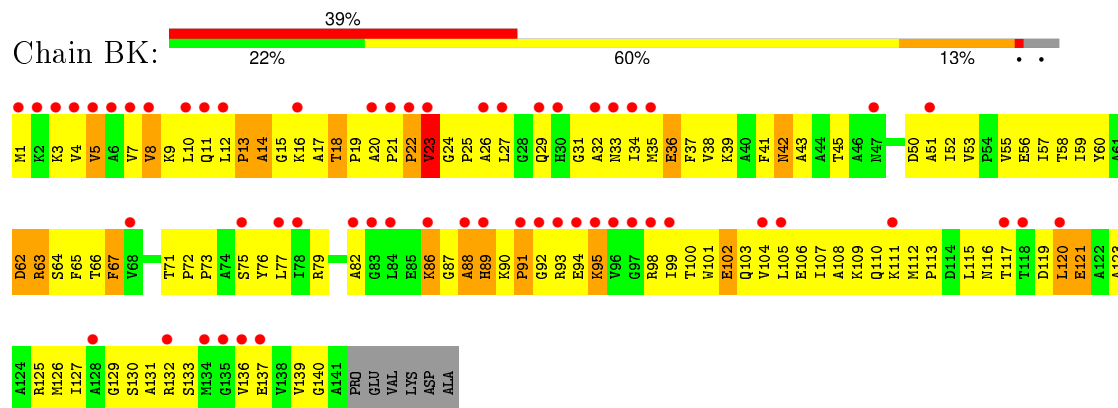


• Molecule 40: 50S RIBOSOMAL PROTEIN L4

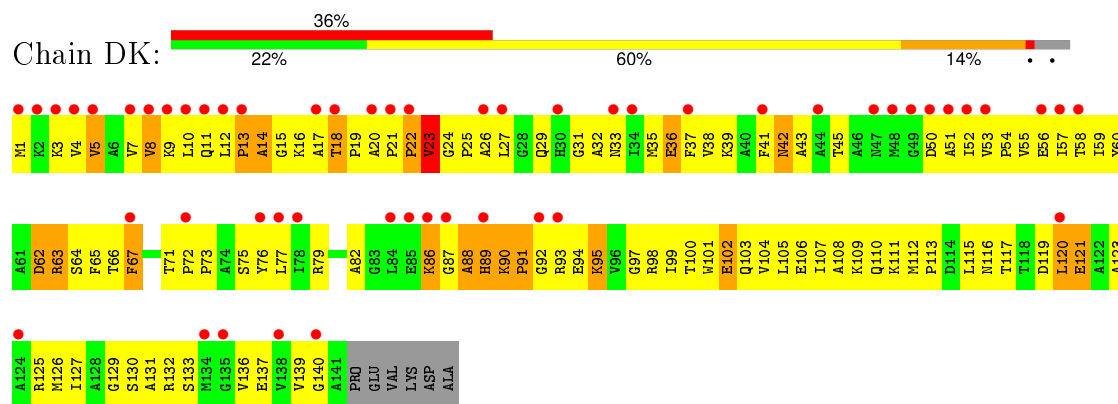




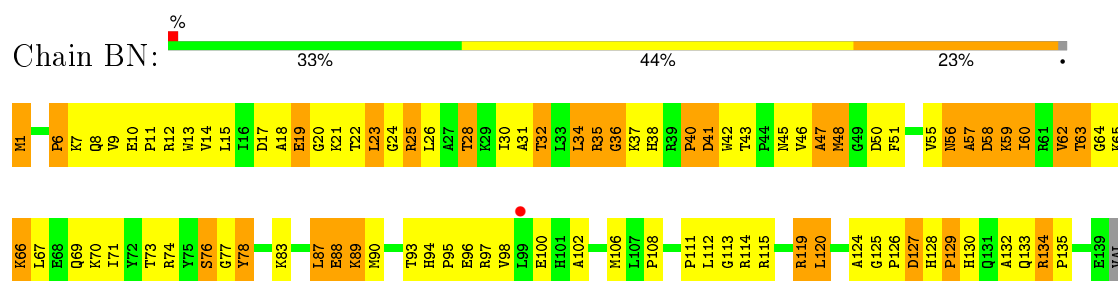
• Molecule 45: 50S RIBOSOMAL PROTEIN L11



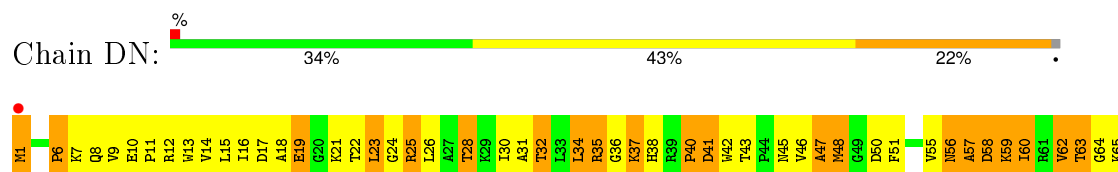
• Molecule 45: 50S RIBOSOMAL PROTEIN L11



• Molecule 46: 50S RIBOSOMAL PROTEIN L13



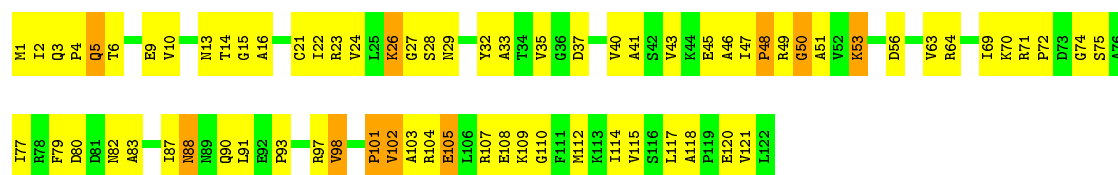
• Molecule 46: 50S RIBOSOMAL PROTEIN L13





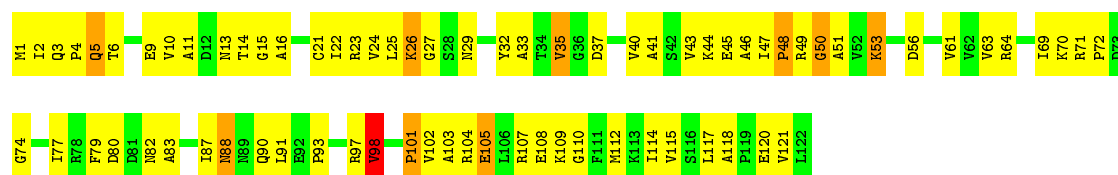
• Molecule 47: 50S RIBOSOMAL PROTEIN L14

Chain BO:



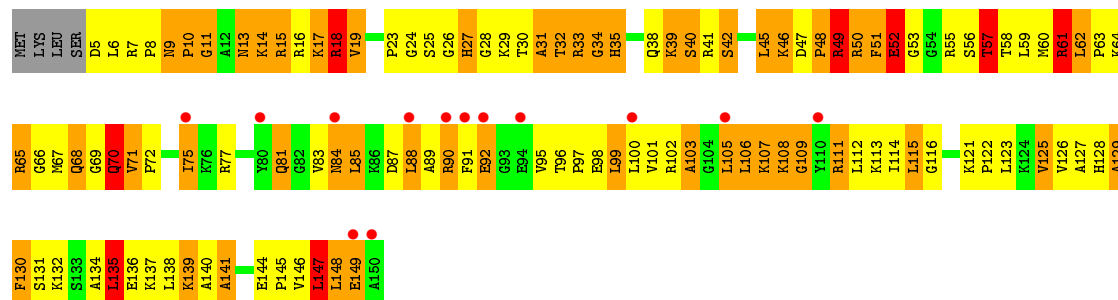
• Molecule 47: 50S RIBOSOMAL PROTEIN L14

Chain DO:



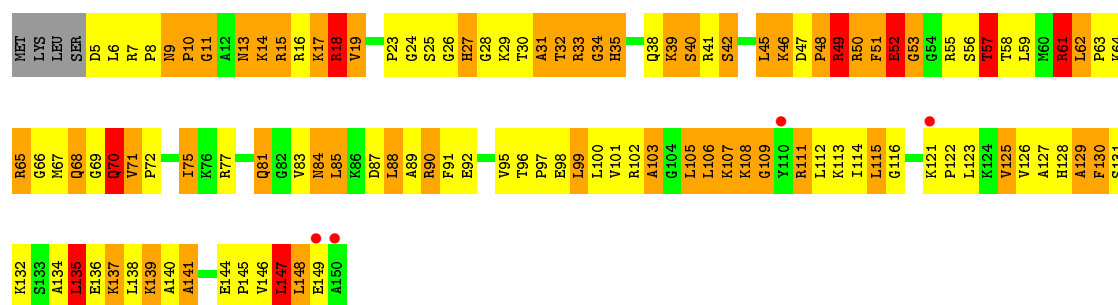
• Molecule 48: 50S RIBOSOMAL PROTEIN L15

Chain BP:

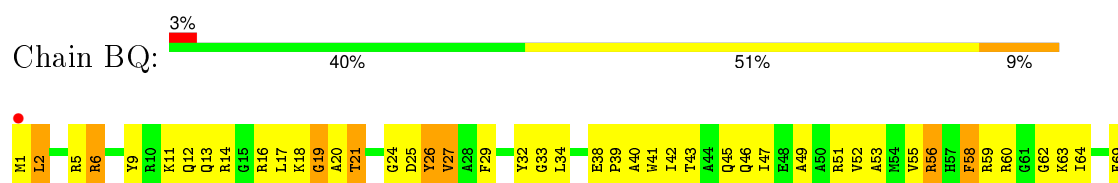


• Molecule 48: 50S RIBOSOMAL PROTEIN L15

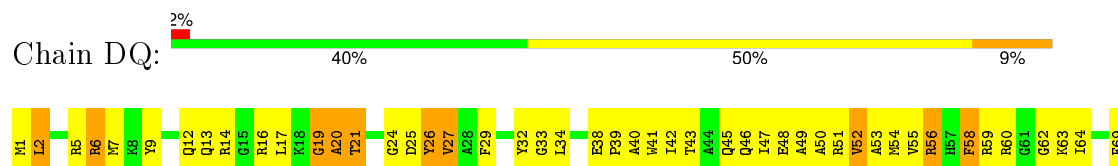
Chain DP:



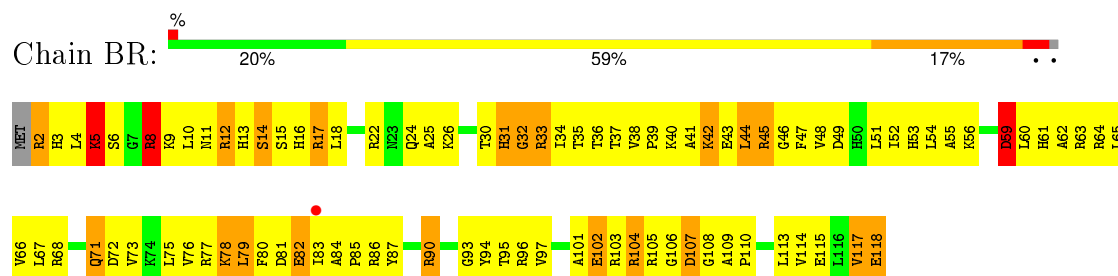
• Molecule 49: 50S RIBOSOMAL PROTEIN L16



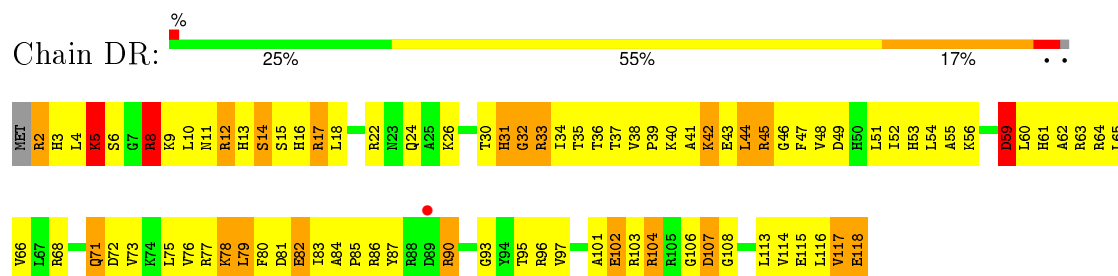
• Molecule 49: 50S RIBOSOMAL PROTEIN L16



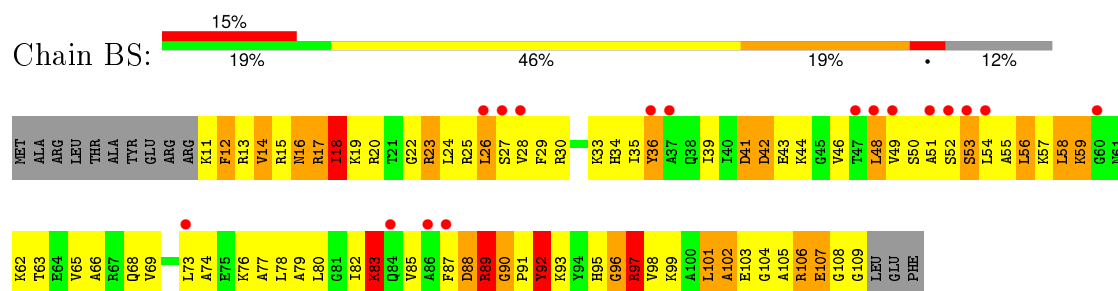
• Molecule 50: 50S RIBOSOMAL PROTEIN L17



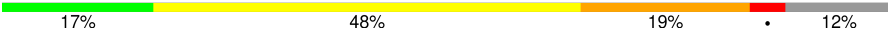
• Molecule 50: 50S RIBOSOMAL PROTEIN L17

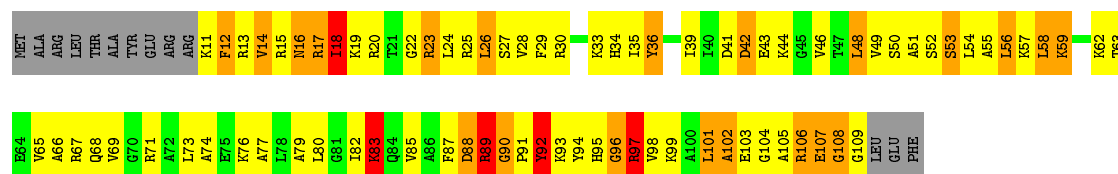


• Molecule 51: 50S RIBOSOMAL PROTEIN L18




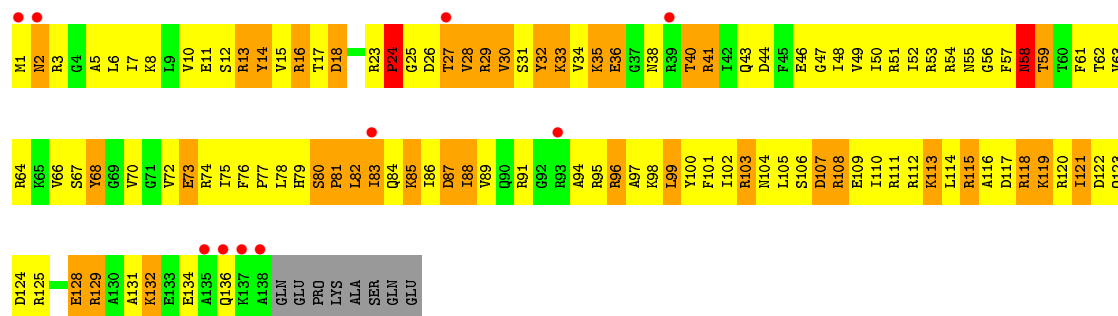
• Molecule 51: 50S RIBOSOMAL PROTEIN L18

Chain DS: 




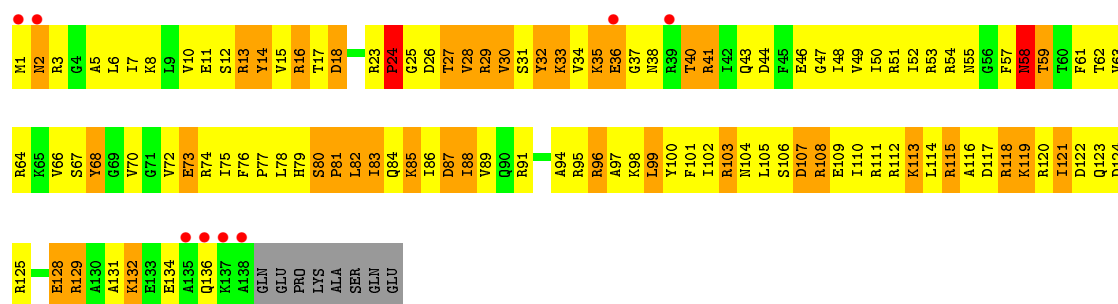
• Molecule 52: 50S RIBOSOMAL PROTEIN L19

Chain BT: 



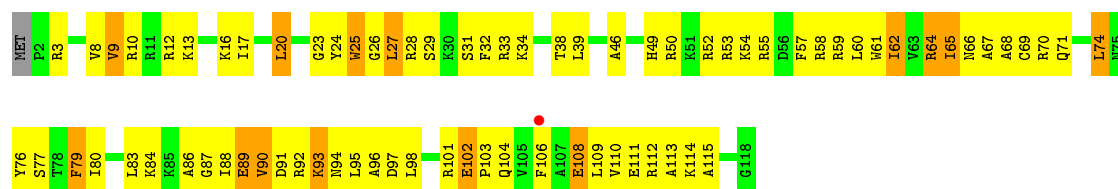
• Molecule 52: 50S RIBOSOMAL PROTEIN L19

Chain DT: 



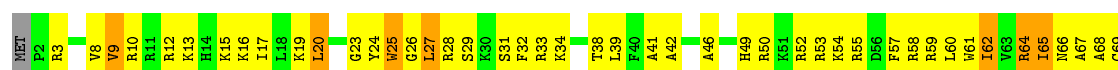
• Molecule 53: 50S RIBOSOMAL PROTEIN L20

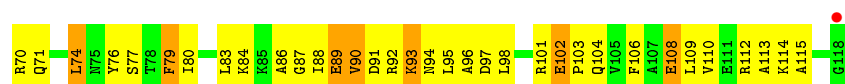
Chain BU: 



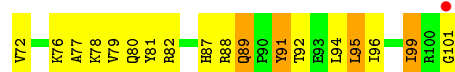
• Molecule 53: 50S RIBOSOMAL PROTEIN L20

Chain DU: 

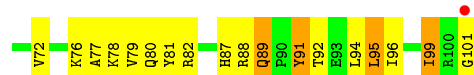
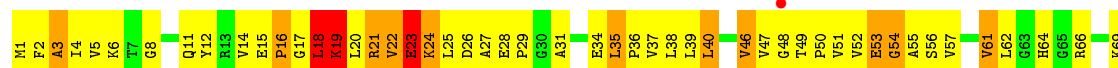




• Molecule 54: 50S RIBOSOMAL PROTEIN L21



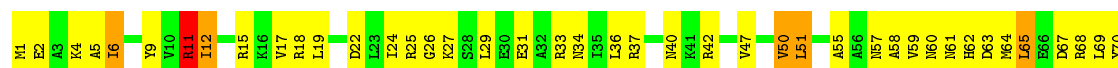
• Molecule 54: 50S RIBOSOMAL PROTEIN L21



• Molecule 55: 50S RIBOSOMAL PROTEIN L22

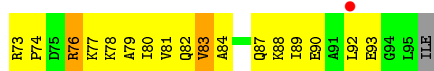


• Molecule 55: 50S RIBOSOMAL PROTEIN L22



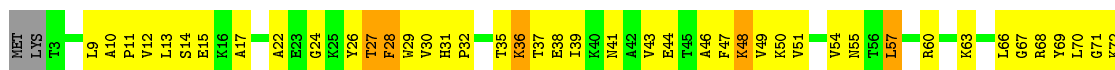
• Molecule 56: 50S RIBOSOMAL PROTEIN L23





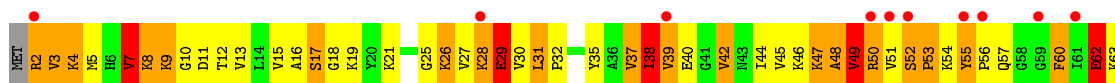
• Molecule 56: 50S RIBOSOMAL PROTEIN L23

Chain DX: 34% 55% 7%



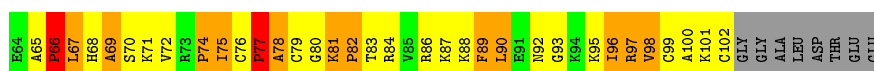
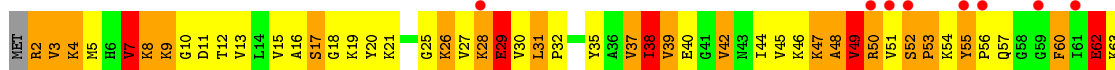
• Molecule 57: 50S RIBOSOMAL PROTEIN L24

Chain BY: 14% 17% 40% 29% 5% 8%



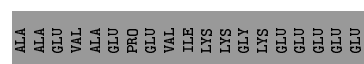
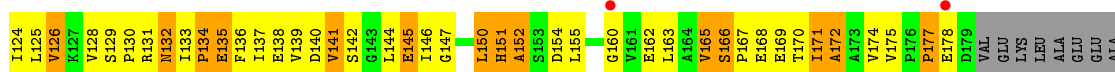
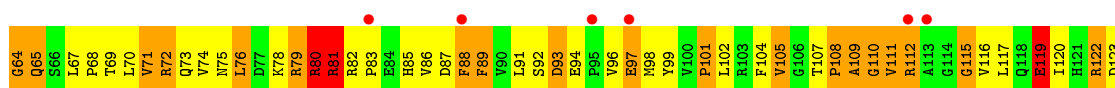
• Molecule 57: 50S RIBOSOMAL PROTEIN L24

Chain DY: 7% 16% 41% 28% 6% 8%

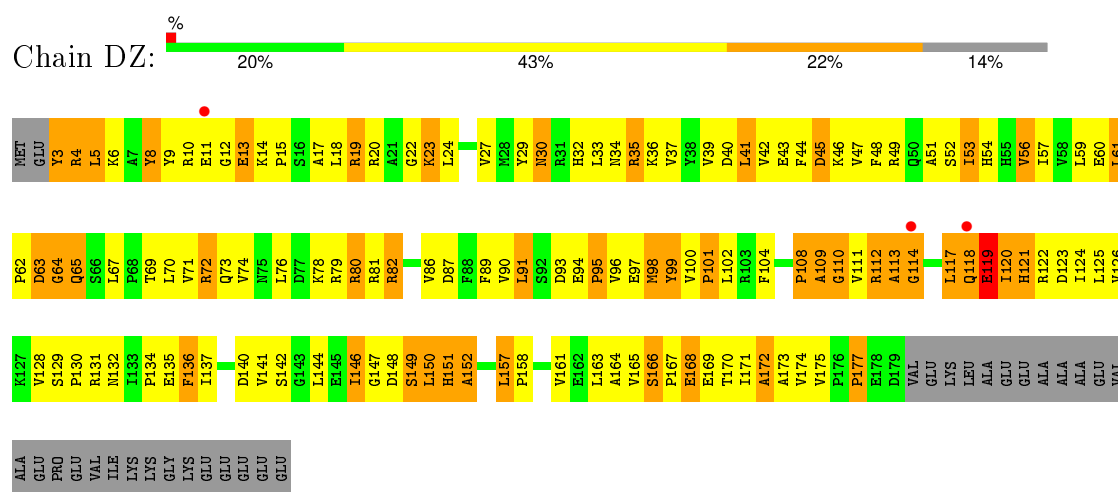


• Molecule 58: 50S RIBOSOMAL PROTEIN L25

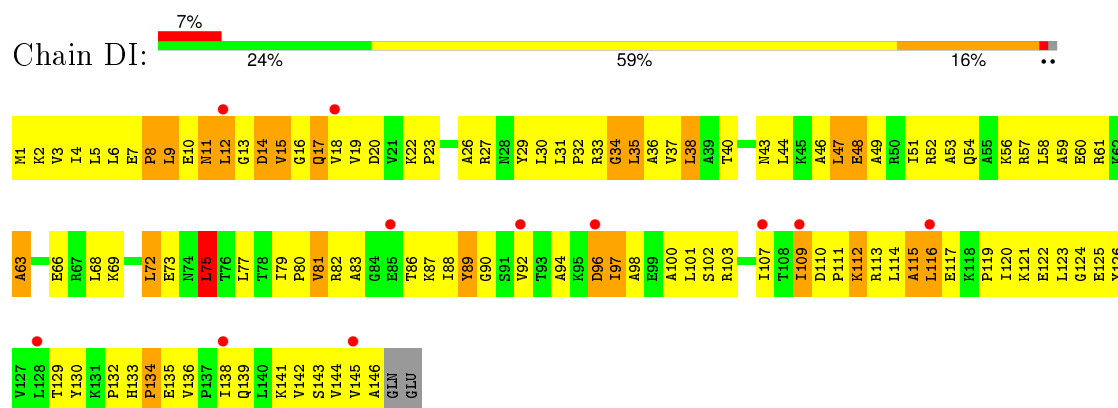
Chain BZ: 6% 19% 44% 21% 14%



• Molecule 58: 50S RIBOSOMAL PROTEIN L25



● Molecule 59: 50S RIBOSOMAL PROTEIN L9



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	211.34Å 450.91Å 614.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.57 – 3.45 49.57 – 3.45	Depositor EDS
% Data completeness (in resolution range)	99.6 (49.57-3.45) 99.6 (49.57-3.45)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 3.48Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.210 , 0.257 0.210 , 0.257	Depositor DCC
R_{free} test set	33079 reflections (4.55%)	DCC
Wilson B-factor (Å ²)	76.9	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 88.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	0 of 759980 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	304505	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.41% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AA	0.39	0/36190	0.69	9/56486 (0.0%)
1	CA	0.41	0/36190	0.69	11/56486 (0.0%)
2	AB	0.32	0/1936	0.61	0/2611
2	CB	0.32	0/1936	0.61	0/2611
3	AC	0.32	0/1637	0.57	0/2207
3	CC	0.35	0/1637	0.57	0/2207
4	AD	0.34	0/1733	0.58	0/2318
4	CD	0.36	0/1733	0.59	0/2318
5	AE	0.36	0/1163	0.61	0/1566
5	CE	0.37	0/1163	0.62	0/1566
6	AF	0.29	0/856	0.58	0/1154
6	CF	0.29	0/856	0.58	0/1154
7	AG	0.30	0/1276	0.54	0/1709
7	CG	0.33	0/1276	0.56	0/1709
8	AH	0.32	0/1136	0.62	0/1527
8	CH	0.33	0/1136	0.63	0/1527
9	AI	0.31	0/1029	0.60	0/1378
9	CI	0.33	0/1029	0.61	0/1378
10	AJ	0.33	0/808	0.60	0/1087
10	CJ	0.34	0/808	0.61	0/1087
11	AK	0.32	0/900	0.60	0/1213
11	CK	0.33	0/900	0.60	0/1213
12	AL	0.40	0/992	0.74	0/1329
12	CL	0.40	0/992	0.75	0/1329
13	AM	0.32	0/966	0.65	0/1294
13	CM	0.34	0/966	0.66	0/1294
14	AN	0.35	0/501	0.58	0/664
14	CN	0.38	0/501	0.60	0/664
15	AO	0.31	0/745	0.54	0/992
15	CO	0.32	0/745	0.55	0/992
16	AP	0.37	0/717	0.63	0/965
16	CP	0.37	0/717	0.63	0/965

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AQ	0.37	0/837	0.60	0/1119
17	CQ	0.37	0/837	0.60	0/1119
18	AR	0.32	0/579	0.61	0/768
18	CR	0.32	0/579	0.62	0/768
19	AS	0.37	0/643	0.60	0/867
19	CS	0.39	0/643	0.60	0/867
20	AT	0.29	0/765	0.55	0/1007
20	CT	0.29	0/765	0.56	0/1007
21	AU	0.44	0/213	0.53	0/279
21	CU	0.43	0/213	0.54	0/279
22	AV	0.52	0/1809	0.77	1/2819 (0.0%)
22	AW	0.42	0/1809	0.78	5/2819 (0.2%)
22	CV	0.53	0/1809	0.78	2/2819 (0.1%)
22	CW	0.39	0/1809	0.76	4/2819 (0.1%)
23	AX	0.53	0/185	0.79	1/286 (0.3%)
23	CX	0.56	0/185	0.71	0/286
24	AY	0.34	0/2847	0.66	0/3846
24	CY	0.36	0/2847	0.70	1/3846 (0.0%)
25	B0	0.42	0/615	0.72	0/819
25	D0	0.44	0/615	0.73	0/819
26	B1	0.44	0/739	0.79	1/983 (0.1%)
26	D1	0.49	0/739	0.77	0/983
27	B2	0.39	0/600	0.73	0/793
27	D2	0.44	0/600	0.75	1/793 (0.1%)
28	B3	0.44	0/473	0.74	0/636
28	D3	0.45	0/473	0.73	0/636
29	B4	0.38	0/229	0.53	0/311
29	D4	0.41	0/229	0.53	0/311
30	B5	0.46	0/473	0.83	0/639
30	D5	0.45	0/473	0.85	0/639
31	B6	0.62	1/388 (0.3%)	0.97	0/520
31	D6	0.71	1/388 (0.3%)	1.00	0/520
32	B7	0.48	0/427	0.70	0/563
32	D7	0.48	0/427	0.69	0/563
33	B8	0.63	0/516	0.88	0/681
33	D8	0.67	0/516	0.91	0/681
34	B9	0.42	0/302	0.77	1/397 (0.3%)
34	D9	0.45	0/302	0.77	1/397 (0.3%)
35	BA	0.53	1/69614 (0.0%)	0.74	40/108679 (0.0%)
35	DA	0.56	3/69614 (0.0%)	0.75	40/108679 (0.0%)
36	BB	0.50	2/2853 (0.1%)	0.87	4/4451 (0.1%)
36	DB	0.52	1/2853 (0.0%)	0.84	3/4451 (0.1%)
37	BC	0.36	0/1145	0.65	7/1556 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
37	DC	0.35	0/1145	0.66	7/1556 (0.4%)
38	BD	0.45	0/2155	0.68	1/2907 (0.0%)
38	DD	0.47	0/2155	0.68	1/2907 (0.0%)
39	BE	0.43	0/1597	0.76	1/2155 (0.0%)
39	DE	0.44	0/1597	0.76	1/2155 (0.0%)
40	BF	0.48	0/1659	0.77	0/2246
40	DF	0.49	0/1659	0.77	0/2246
41	BG	0.37	0/1499	0.69	0/2016
41	DG	0.41	0/1499	0.76	1/2016 (0.0%)
42	BH	0.36	0/1246	0.69	1/1684 (0.1%)
42	DH	0.37	0/1246	0.69	1/1684 (0.1%)
43	BI	0.31	0/1147	0.60	0/1553
45	BK	0.31	0/1057	0.57	0/1432
45	DK	0.31	0/1057	0.57	0/1432
46	BN	0.38	0/1132	0.69	0/1527
46	DN	0.41	0/1132	0.70	0/1527
47	BO	0.42	0/943	0.71	0/1269
47	DO	0.40	0/943	0.71	0/1269
48	BP	0.41	0/1131	0.78	1/1504 (0.1%)
48	DP	0.44	0/1131	0.78	1/1504 (0.1%)
49	BQ	0.44	0/1143	0.71	0/1527
49	DQ	0.46	0/1143	0.72	0/1527
50	BR	0.36	0/974	0.71	1/1302 (0.1%)
50	DR	0.37	0/974	0.72	1/1302 (0.1%)
51	BS	0.45	0/779	0.85	1/1038 (0.1%)
51	DS	0.56	0/779	0.89	1/1038 (0.1%)
52	BT	0.40	0/1156	0.74	0/1544
52	DT	0.41	0/1156	0.75	0/1544
53	BU	0.47	0/975	0.77	1/1297 (0.1%)
53	DU	0.47	0/975	0.80	1/1297 (0.1%)
54	BV	0.42	0/790	0.73	0/1057
54	DV	0.46	0/790	0.76	0/1057
55	BW	0.39	0/907	0.67	0/1216
55	DW	0.41	0/907	0.69	0/1216
56	BX	0.43	0/740	0.71	0/995
56	DX	0.44	0/740	0.72	0/995
57	BY	0.50	0/789	0.80	0/1053
57	DY	0.49	0/789	0.81	0/1053
58	BZ	0.41	0/1436	0.72	0/1951
58	DZ	0.41	0/1436	0.77	0/1951
59	DI	0.36	0/1148	0.73	0/1554
All	All	0.47	9/327803 (0.0%)	0.72	154/489223 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	9
1	CA	0	10
22	AW	3	0
22	CV	0	2
22	CW	3	0
23	AX	0	1
30	B5	0	1
30	D5	0	2
35	BA	2	40
35	DA	3	46
All	All	11	111

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	DB	86	G	P-OP1	-7.68	1.35	1.49
35	BA	568	U	C4-O4	7.25	1.29	1.23
36	BB	86	G	P-OP1	-7.23	1.36	1.49
36	BB	96	U	C2-O2	-6.42	1.16	1.22
31	D6	42	TRP	CB-CG	6.09	1.61	1.50

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	BB	85	G	OP1-P-O3'	-22.67	55.33	105.20
36	DB	85	G	OP1-P-O3'	-19.05	63.30	105.20
36	BB	85	G	OP2-P-O3'	13.54	134.99	105.20
36	DB	85	G	OP2-P-O3'	12.71	133.15	105.20
36	DB	86	G	O5'-P-OP1	11.85	124.92	110.70

5 of 11 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
22	AW	17	C	C1'
22	AW	47	U	C1'
22	AW	70	G	C3'
35	BA	1784	A	C3'
35	BA	1799	G	C3'

5 of 111 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	110	C	Sidechain
1	AA	324	G	Sidechain
1	AA	38	G	Sidechain
1	AA	388	G	Sidechain
1	AA	498	U	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32329	0	16318	1300	0
1	CA	32329	0	16318	1291	0
2	AB	1901	0	1951	253	0
2	CB	1901	0	1951	256	0
3	AC	1613	0	1677	193	0
3	CC	1613	0	1677	190	0
4	AD	1703	0	1763	215	0
4	CD	1703	0	1763	213	0
5	AE	1147	0	1207	140	0
5	CE	1147	0	1207	134	0
6	AF	843	0	857	93	0
6	CF	843	0	857	98	0
7	AG	1257	0	1296	112	0
7	CG	1257	0	1296	112	0
8	AH	1116	0	1177	160	0
8	CH	1116	0	1177	152	0
9	AI	1011	0	1043	164	0
9	CI	1011	0	1043	172	0
10	AJ	795	0	840	170	0
10	CJ	795	0	840	165	0
11	AK	885	0	904	101	0
11	CK	885	0	904	104	0
12	AL	976	0	1062	99	0
12	CL	976	0	1062	93	0
13	AM	956	0	1021	104	0
13	CM	956	0	1021	106	0
14	AN	492	0	529	59	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	CN	492	0	529	57	0
15	AO	734	0	771	52	0
15	CO	734	0	771	48	0
16	AP	701	0	720	100	0
16	CP	701	0	720	106	0
17	AQ	824	0	891	69	0
17	CQ	824	0	891	70	0
18	AR	574	0	644	78	0
18	CR	574	0	644	78	0
19	AS	630	0	652	97	0
19	CS	630	0	652	97	0
20	AT	763	0	861	112	0
20	CT	763	0	861	110	0
21	AU	209	0	221	18	0
21	CU	209	0	221	18	0
22	AV	1619	0	822	76	0
22	AW	1619	0	822	98	0
22	CV	1619	0	822	83	0
22	CW	1619	0	822	92	0
23	AX	166	0	87	17	0
23	CX	166	0	87	7	0
24	AY	2799	0	2809	362	0
24	CY	2799	0	2809	344	0
25	B0	607	0	628	82	0
25	D0	607	0	628	82	0
26	B1	732	0	808	113	0
26	D1	732	0	808	108	0
27	B2	598	0	653	85	0
27	D2	598	0	653	78	0
28	B3	468	0	523	59	3
28	D3	468	0	523	60	0
29	B4	226	0	229	33	0
29	D4	226	0	229	36	0
30	B5	459	0	480	64	0
30	D5	459	0	480	72	0
31	B6	381	0	391	117	0
31	D6	381	0	391	123	0
32	B7	419	0	467	25	0
32	D7	419	0	467	29	0
33	B8	508	0	576	122	0
33	D8	508	0	576	130	0
34	B9	299	0	324	33	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	D9	299	0	324	31	0
35	BA	62154	0	31337	2154	0
35	DA	62154	0	31337	2170	9
36	BB	2551	0	1295	103	6
36	DB	2551	0	1295	103	0
37	BC	1142	0	865	110	0
37	DC	1142	0	865	103	0
38	BD	2105	0	2182	255	0
38	DD	2105	0	2182	246	0
39	BE	1564	0	1629	245	0
39	DE	1564	0	1629	252	0
40	BF	1624	0	1677	227	0
40	DF	1624	0	1677	226	0
41	BG	1474	0	1535	288	0
41	DG	1474	0	1535	249	0
42	BH	1223	0	1282	214	0
42	DH	1223	0	1282	212	0
43	BI	1132	0	1218	120	0
44	BJ	651	0	146	35	0
44	DJ	651	0	146	36	0
45	BK	1038	0	1089	157	0
45	DK	1038	0	1089	184	0
46	BN	1105	0	1180	129	0
46	DN	1105	0	1180	122	0
47	BO	933	0	996	92	0
47	DO	933	0	996	94	0
48	BP	1114	0	1187	261	0
48	DP	1114	0	1187	259	0
49	BQ	1122	0	1179	121	0
49	DQ	1122	0	1179	123	0
50	BR	960	0	1021	134	0
50	DR	960	0	1020	134	0
51	BS	771	0	832	147	0
51	DS	771	0	832	149	0
52	BT	1142	0	1202	231	0
52	DT	1142	0	1202	231	0
53	BU	958	0	1015	134	0
53	DU	958	0	1015	139	0
54	BV	779	0	852	144	0
54	DV	779	0	852	149	0
55	BW	896	0	953	76	0
55	DW	896	0	953	77	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	BX	726	0	778	67	0
56	DX	726	0	778	65	0
57	BY	776	0	870	181	0
57	DY	776	0	870	182	0
58	BZ	1404	0	1432	232	0
58	DZ	1404	0	1432	245	0
59	DI	1133	0	1220	185	0
60	AA	157	0	0	0	0
60	AE	1	0	0	0	0
60	AL	1	0	0	0	0
60	AM	1	0	0	0	0
60	AV	7	0	0	0	0
60	AW	5	0	0	0	0
60	AY	1	0	0	0	0
60	B1	1	0	0	0	0
60	B3	1	0	0	0	0
60	B5	2	0	0	0	0
60	B7	2	0	0	0	0
60	BA	354	0	0	0	0
60	BB	4	0	0	0	0
60	BC	1	0	0	0	0
60	BD	2	0	0	0	0
60	BF	1	0	0	0	0
60	BH	1	0	0	0	0
60	BP	1	0	0	0	0
60	BQ	1	0	0	0	0
60	BS	1	0	0	0	0
60	BU	1	0	0	0	0
60	CA	157	0	0	0	0
60	CL	1	0	0	0	0
60	CN	1	0	0	0	0
60	CV	7	0	0	0	0
60	CW	5	0	0	0	0
60	CY	1	0	0	0	0
60	D1	1	0	0	0	0
60	D3	1	0	0	0	0
60	D5	2	0	0	0	0
60	D7	1	0	0	0	0
60	DA	353	0	0	0	0
60	DB	4	0	0	0	0
60	DC	1	0	0	0	0
60	DD	2	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	DF	3	0	0	0	0
60	DH	1	0	0	0	0
60	DQ	1	0	0	0	0
60	DR	1	0	0	0	0
60	DU	1	0	0	0	0
60	DX	1	0	0	0	0
60	DY	1	0	0	0	0
61	AD	1	0	0	0	0
61	AN	1	0	0	0	0
61	B9	1	0	0	0	0
61	CD	1	0	0	0	0
61	CN	1	0	0	0	0
61	D9	1	0	0	0	0
All	All	304505	0	207553	19772	9

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 39.

The worst 5 of 19772 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)
26:D1:81:LYS:CE	35:DA:271(H):G:H5'	1.21	1.60
26:B1:81:LYS:HE2	35:BA:271(H):G:C5'	1.23	1.59
26:D1:81:LYS:HE2	35:DA:271(H):G:C5'	1.31	1.54
26:B1:81:LYS:CE	35:BA:271(H):G:H5'	1.10	1.53
51:DS:97:ARG:NH2	51:DS:98:VAL:HA	1.57	1.18

The worst 5 of 9 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:B3:48:GLU:O	35:DA:654(L):G:OP2[3_455]	1.99	0.21
36:BB:97:G:N7	35:DA:654(J):A:OP1[3_455]	2.05	0.15
36:BB:97:G:OP2	35:DA:654(I):C:O2'[3_455]	2.06	0.14
36:BB:96:U:C3'	35:DA:654(I):C:O2'[3_455]	2.09	0.11
36:BB:96:U:O2	35:DA:654(K):C:OP1[3_455]	2.10	0.10

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	233/256 (91%)	155 (66%)	58 (25%)	20 (9%)	1	11
2	CB	233/256 (91%)	156 (67%)	56 (24%)	21 (9%)	1	10
3	AC	205/239 (86%)	125 (61%)	57 (28%)	23 (11%)	0	7
3	CC	205/239 (86%)	128 (62%)	55 (27%)	22 (11%)	0	8
4	AD	206/209 (99%)	134 (65%)	49 (24%)	23 (11%)	0	7
4	CD	206/209 (99%)	135 (66%)	49 (24%)	22 (11%)	0	8
5	AE	149/162 (92%)	98 (66%)	36 (24%)	15 (10%)	1	9
5	CE	149/162 (92%)	100 (67%)	34 (23%)	15 (10%)	1	9
6	AF	99/101 (98%)	75 (76%)	17 (17%)	7 (7%)	1	16
6	CF	99/101 (98%)	75 (76%)	17 (17%)	7 (7%)	1	16
7	AG	153/156 (98%)	108 (71%)	34 (22%)	11 (7%)	1	15
7	CG	153/156 (98%)	108 (71%)	34 (22%)	11 (7%)	1	15
8	AH	136/138 (99%)	92 (68%)	32 (24%)	12 (9%)	1	11
8	CH	136/138 (99%)	92 (68%)	32 (24%)	12 (9%)	1	11
9	AI	125/128 (98%)	83 (66%)	30 (24%)	12 (10%)	1	10
9	CI	125/128 (98%)	82 (66%)	31 (25%)	12 (10%)	1	10
10	AJ	97/105 (92%)	64 (66%)	21 (22%)	12 (12%)	0	5
10	CJ	97/105 (92%)	64 (66%)	21 (22%)	12 (12%)	0	5
11	AK	117/129 (91%)	89 (76%)	24 (20%)	4 (3%)	5	37
11	CK	117/129 (91%)	89 (76%)	24 (20%)	4 (3%)	5	37
12	AL	124/132 (94%)	89 (72%)	26 (21%)	9 (7%)	1	15
12	CL	124/132 (94%)	90 (73%)	25 (20%)	9 (7%)	1	15
13	AM	119/126 (94%)	82 (69%)	23 (19%)	14 (12%)	0	6
13	CM	119/126 (94%)	84 (71%)	21 (18%)	14 (12%)	0	6
14	AN	58/61 (95%)	39 (67%)	12 (21%)	7 (12%)	0	6

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	CN	58/61 (95%)	38 (66%)	12 (21%)	8 (14%)	0	4
15	AO	86/89 (97%)	59 (69%)	23 (27%)	4 (5%)	3	28
15	CO	86/89 (97%)	57 (66%)	25 (29%)	4 (5%)	3	28
16	AP	82/88 (93%)	51 (62%)	22 (27%)	9 (11%)	0	7
16	CP	82/88 (93%)	53 (65%)	20 (24%)	9 (11%)	0	7
17	AQ	98/105 (93%)	68 (69%)	17 (17%)	13 (13%)	0	4
17	CQ	98/105 (93%)	69 (70%)	17 (17%)	12 (12%)	0	6
18	AR	68/88 (77%)	45 (66%)	16 (24%)	7 (10%)	1	8
18	CR	68/88 (77%)	45 (66%)	16 (24%)	7 (10%)	1	8
19	AS	77/93 (83%)	36 (47%)	30 (39%)	11 (14%)	0	3
19	CS	77/93 (83%)	36 (47%)	30 (39%)	11 (14%)	0	3
20	AT	97/106 (92%)	68 (70%)	18 (19%)	11 (11%)	0	7
20	CT	97/106 (92%)	68 (70%)	18 (19%)	11 (11%)	0	7
21	AU	23/27 (85%)	18 (78%)	3 (13%)	2 (9%)	1	11
21	CU	23/27 (85%)	18 (78%)	3 (13%)	2 (9%)	1	11
24	AY	349/351 (99%)	246 (70%)	70 (20%)	33 (10%)	1	10
24	CY	349/351 (99%)	256 (73%)	61 (18%)	32 (9%)	1	10
25	B0	74/85 (87%)	58 (78%)	10 (14%)	6 (8%)	1	12
25	D0	74/85 (87%)	58 (78%)	10 (14%)	6 (8%)	1	12
26	B1	92/98 (94%)	65 (71%)	15 (16%)	12 (13%)	0	4
26	D1	92/98 (94%)	72 (78%)	12 (13%)	8 (9%)	1	11
27	B2	69/72 (96%)	40 (58%)	17 (25%)	12 (17%)	0	2
27	D2	69/72 (96%)	39 (56%)	20 (29%)	10 (14%)	0	3
28	B3	58/60 (97%)	43 (74%)	9 (16%)	6 (10%)	1	8
28	D3	58/60 (97%)	43 (74%)	9 (16%)	6 (10%)	1	8
29	B4	29/71 (41%)	14 (48%)	11 (38%)	4 (14%)	0	4
29	D4	29/71 (41%)	14 (48%)	11 (38%)	4 (14%)	0	4
30	B5	57/60 (95%)	40 (70%)	7 (12%)	10 (18%)	0	2
30	D5	57/60 (95%)	40 (70%)	7 (12%)	10 (18%)	0	2
31	B6	43/54 (80%)	17 (40%)	12 (28%)	14 (33%)	0	0
31	D6	43/54 (80%)	17 (40%)	13 (30%)	13 (30%)	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	B7	47/49 (96%)	44 (94%)	3 (6%)	0	100	100
32	D7	47/49 (96%)	44 (94%)	3 (6%)	0	100	100
33	B8	62/65 (95%)	38 (61%)	15 (24%)	9 (14%)	0	3
33	D8	62/65 (95%)	38 (61%)	15 (24%)	9 (14%)	0	3
34	B9	34/37 (92%)	23 (68%)	11 (32%)	0	100	100
34	D9	34/37 (92%)	24 (71%)	10 (29%)	0	100	100
37	BC	183/229 (80%)	64 (35%)	71 (39%)	48 (26%)	0	1
37	DC	183/229 (80%)	65 (36%)	72 (39%)	46 (25%)	0	1
38	BD	270/276 (98%)	199 (74%)	39 (14%)	32 (12%)	0	6
38	DD	270/276 (98%)	198 (73%)	40 (15%)	32 (12%)	0	6
39	BE	203/206 (98%)	124 (61%)	45 (22%)	34 (17%)	0	2
39	DE	203/206 (98%)	123 (61%)	44 (22%)	36 (18%)	0	2
40	BF	206/210 (98%)	149 (72%)	33 (16%)	24 (12%)	0	6
40	DF	206/210 (98%)	149 (72%)	33 (16%)	24 (12%)	0	6
41	BG	179/182 (98%)	92 (51%)	54 (30%)	33 (18%)	0	2
41	DG	179/182 (98%)	107 (60%)	46 (26%)	26 (14%)	0	3
42	BH	158/180 (88%)	90 (57%)	38 (24%)	30 (19%)	0	2
42	DH	158/180 (88%)	91 (58%)	36 (23%)	31 (20%)	0	2
43	BI	144/148 (97%)	100 (69%)	28 (19%)	16 (11%)	0	7
45	BK	139/147 (95%)	88 (63%)	33 (24%)	18 (13%)	0	5
45	DK	139/147 (95%)	87 (63%)	34 (24%)	18 (13%)	0	5
46	BN	137/140 (98%)	97 (71%)	20 (15%)	20 (15%)	0	3
46	DN	137/140 (98%)	99 (72%)	18 (13%)	20 (15%)	0	3
47	BO	120/122 (98%)	97 (81%)	17 (14%)	6 (5%)	3	25
47	DO	120/122 (98%)	98 (82%)	14 (12%)	8 (7%)	1	18
48	BP	144/150 (96%)	68 (47%)	36 (25%)	40 (28%)	0	0
48	DP	144/150 (96%)	68 (47%)	36 (25%)	40 (28%)	0	0
49	BQ	139/141 (99%)	111 (80%)	19 (14%)	9 (6%)	1	18
49	DQ	139/141 (99%)	114 (82%)	16 (12%)	9 (6%)	1	18
50	BR	115/118 (98%)	72 (63%)	29 (25%)	14 (12%)	0	6
50	DR	115/118 (98%)	70 (61%)	31 (27%)	14 (12%)	0	6

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	BS	97/112 (87%)	55 (57%)	22 (23%)	20 (21%)	0	1
51	DS	97/112 (87%)	54 (56%)	22 (23%)	21 (22%)	0	1
52	BT	136/146 (93%)	84 (62%)	23 (17%)	29 (21%)	0	1
52	DT	136/146 (93%)	85 (62%)	22 (16%)	29 (21%)	0	1
53	BU	115/118 (98%)	78 (68%)	27 (24%)	10 (9%)	1	11
53	DU	115/118 (98%)	77 (67%)	28 (24%)	10 (9%)	1	11
54	BV	99/101 (98%)	72 (73%)	13 (13%)	14 (14%)	0	4
54	DV	99/101 (98%)	72 (73%)	14 (14%)	13 (13%)	0	4
55	BW	111/113 (98%)	83 (75%)	22 (20%)	6 (5%)	2	23
55	DW	111/113 (98%)	83 (75%)	22 (20%)	6 (5%)	2	23
56	BX	91/96 (95%)	75 (82%)	14 (15%)	2 (2%)	8	47
56	DX	91/96 (95%)	74 (81%)	16 (18%)	1 (1%)	17	62
57	BY	99/110 (90%)	46 (46%)	20 (20%)	33 (33%)	0	0
57	DY	99/110 (90%)	47 (48%)	20 (20%)	32 (32%)	0	0
58	BZ	175/206 (85%)	102 (58%)	41 (23%)	32 (18%)	0	2
58	DZ	175/206 (85%)	110 (63%)	36 (21%)	29 (17%)	0	2
59	DI	144/148 (97%)	81 (56%)	42 (29%)	21 (15%)	0	3
All	All	12652/13582 (93%)	8336 (66%)	2725 (22%)	1591 (13%)	0	5

5 of 1591 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	15	VAL
2	AB	20	GLU
2	AB	88	ALA
2	AB	95	GLN
2	AB	195	ASP

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	AB	202/220 (92%)	184 (91%)	18 (9%)	12	46
2	CB	202/220 (92%)	184 (91%)	18 (9%)	12	46
3	AC	160/188 (85%)	149 (93%)	11 (7%)	19	59
3	CC	160/188 (85%)	150 (94%)	10 (6%)	22	62
4	AD	180/181 (99%)	159 (88%)	21 (12%)	7	30
4	CD	180/181 (99%)	159 (88%)	21 (12%)	7	30
5	AE	115/123 (94%)	103 (90%)	12 (10%)	9	38
5	CE	115/123 (94%)	101 (88%)	14 (12%)	6	28
6	AF	90/90 (100%)	86 (96%)	4 (4%)	35	73
6	CF	90/90 (100%)	86 (96%)	4 (4%)	35	73
7	AG	126/127 (99%)	117 (93%)	9 (7%)	18	58
7	CG	126/127 (99%)	118 (94%)	8 (6%)	22	62
8	AH	119/119 (100%)	105 (88%)	14 (12%)	6	30
8	CH	119/119 (100%)	105 (88%)	14 (12%)	6	30
9	AI	98/99 (99%)	88 (90%)	10 (10%)	9	39
9	CI	98/99 (99%)	88 (90%)	10 (10%)	9	39
10	AJ	88/92 (96%)	78 (89%)	10 (11%)	7	32
10	CJ	88/92 (96%)	78 (89%)	10 (11%)	7	32
11	AK	90/99 (91%)	84 (93%)	6 (7%)	20	60
11	CK	90/99 (91%)	84 (93%)	6 (7%)	20	60
12	AL	104/109 (95%)	98 (94%)	6 (6%)	25	65
12	CL	104/109 (95%)	96 (92%)	8 (8%)	16	53
13	AM	96/101 (95%)	83 (86%)	13 (14%)	5	25
13	CM	96/101 (95%)	83 (86%)	13 (14%)	5	25
14	AN	49/50 (98%)	46 (94%)	3 (6%)	23	63
14	CN	49/50 (98%)	46 (94%)	3 (6%)	23	63
15	AO	79/80 (99%)	76 (96%)	3 (4%)	40	76
15	CO	79/80 (99%)	76 (96%)	3 (4%)	40	76
16	AP	72/74 (97%)	64 (89%)	8 (11%)	8	34
16	CP	72/74 (97%)	64 (89%)	8 (11%)	8	34
17	AQ	94/97 (97%)	92 (98%)	2 (2%)	61	86
17	CQ	94/97 (97%)	92 (98%)	2 (2%)	61	86

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	AR	61/77 (79%)	57 (93%)	4 (7%)	21	61
18	CR	61/77 (79%)	57 (93%)	4 (7%)	21	61
19	AS	69/80 (86%)	61 (88%)	8 (12%)	7	31
19	CS	69/80 (86%)	61 (88%)	8 (12%)	7	31
20	AT	76/82 (93%)	70 (92%)	6 (8%)	15	52
20	CT	76/82 (93%)	70 (92%)	6 (8%)	15	52
21	AU	19/22 (86%)	18 (95%)	1 (5%)	28	67
21	CU	19/22 (86%)	19 (100%)	0	100	100
24	AY	298/298 (100%)	264 (89%)	34 (11%)	7	32
24	CY	298/298 (100%)	264 (89%)	34 (11%)	7	32
25	B0	61/67 (91%)	58 (95%)	3 (5%)	31	70
25	D0	61/67 (91%)	58 (95%)	3 (5%)	31	70
26	B1	78/83 (94%)	70 (90%)	8 (10%)	9	39
26	D1	78/83 (94%)	66 (85%)	12 (15%)	3	19
27	B2	66/67 (98%)	55 (83%)	11 (17%)	3	15
27	D2	66/67 (98%)	59 (89%)	7 (11%)	8	37
28	B3	51/52 (98%)	47 (92%)	4 (8%)	16	52
28	D3	51/52 (98%)	48 (94%)	3 (6%)	24	64
29	B4	27/63 (43%)	25 (93%)	2 (7%)	17	55
29	D4	27/63 (43%)	24 (89%)	3 (11%)	8	34
30	B5	51/52 (98%)	45 (88%)	6 (12%)	6	30
30	D5	51/52 (98%)	44 (86%)	7 (14%)	4	24
31	B6	43/52 (83%)	32 (74%)	11 (26%)	0	4
31	D6	43/52 (83%)	32 (74%)	11 (26%)	0	4
32	B7	41/42 (98%)	39 (95%)	2 (5%)	31	70
32	D7	41/42 (98%)	39 (95%)	2 (5%)	31	70
33	B8	53/55 (96%)	41 (77%)	12 (23%)	1	5
33	D8	53/55 (96%)	41 (77%)	12 (23%)	1	5
34	B9	33/34 (97%)	28 (85%)	5 (15%)	3	19
34	D9	33/34 (97%)	28 (85%)	5 (15%)	3	19
37	BC	61/181 (34%)	55 (90%)	6 (10%)	10	41

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	DC	61/181 (34%)	55 (90%)	6 (10%)	10	41
38	BD	213/218 (98%)	192 (90%)	21 (10%)	10	40
38	DD	213/218 (98%)	191 (90%)	22 (10%)	9	39
39	BE	165/166 (99%)	137 (83%)	28 (17%)	2	14
39	DE	165/166 (99%)	136 (82%)	29 (18%)	2	12
40	BF	165/166 (99%)	144 (87%)	21 (13%)	5	27
40	DF	165/166 (99%)	146 (88%)	19 (12%)	7	31
41	BG	155/156 (99%)	131 (84%)	24 (16%)	3	18
41	DG	155/156 (99%)	129 (83%)	26 (17%)	2	14
42	BH	132/148 (89%)	122 (92%)	10 (8%)	16	54
42	DH	132/148 (89%)	122 (92%)	10 (8%)	16	54
43	BI	122/124 (98%)	116 (95%)	6 (5%)	31	70
45	BK	106/111 (96%)	97 (92%)	9 (8%)	13	49
45	DK	106/111 (96%)	97 (92%)	9 (8%)	13	49
46	BN	117/119 (98%)	101 (86%)	16 (14%)	4	24
46	DN	117/119 (98%)	101 (86%)	16 (14%)	4	24
47	BO	100/100 (100%)	94 (94%)	6 (6%)	24	63
47	DO	100/100 (100%)	95 (95%)	5 (5%)	30	69
48	BP	112/116 (97%)	84 (75%)	28 (25%)	1	4
48	DP	112/116 (97%)	84 (75%)	28 (25%)	1	4
49	BQ	111/111 (100%)	97 (87%)	14 (13%)	5	27
49	DQ	111/111 (100%)	96 (86%)	15 (14%)	5	25
50	BR	100/101 (99%)	88 (88%)	12 (12%)	6	29
50	DR	100/101 (99%)	88 (88%)	12 (12%)	6	29
51	BS	77/88 (88%)	61 (79%)	16 (21%)	1	6
51	DS	77/88 (88%)	61 (79%)	16 (21%)	1	6
52	BT	120/127 (94%)	102 (85%)	18 (15%)	3	20
52	DT	120/127 (94%)	102 (85%)	18 (15%)	3	20
53	BU	92/94 (98%)	85 (92%)	7 (8%)	16	54
53	DU	92/94 (98%)	85 (92%)	7 (8%)	16	54
54	BV	82/82 (100%)	73 (89%)	9 (11%)	8	35

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	DV	82/82 (100%)	72 (88%)	10 (12%)	6	28
55	BW	91/92 (99%)	79 (87%)	12 (13%)	5	26
55	DW	91/92 (99%)	80 (88%)	11 (12%)	6	29
56	BX	74/78 (95%)	65 (88%)	9 (12%)	6	28
56	DX	74/78 (95%)	65 (88%)	9 (12%)	6	28
57	BY	84/91 (92%)	67 (80%)	17 (20%)	1	7
57	DY	84/91 (92%)	67 (80%)	17 (20%)	1	7
58	BZ	155/179 (87%)	128 (83%)	27 (17%)	2	13
58	DZ	155/179 (87%)	129 (83%)	26 (17%)	2	14
59	DI	122/124 (98%)	118 (97%)	4 (3%)	45	79
All	All	10446/11246 (93%)	9279 (89%)	1167 (11%)	7	33

5 of 1167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
55	BW	86	LEU
7	CG	114	ARG
52	DT	87	ASP
57	BY	15	VAL
2	CB	137	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 327 such sidechains are listed below:

Mol	Chain	Res	Type
51	BS	68	GLN
4	CD	74	GLN
49	DQ	123	HIS
53	BU	71	GLN
58	BZ	75	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1503/1522 (98%)	222 (14%)	34 (2%)
1	CA	1503/1522 (98%)	217 (14%)	34 (2%)
22	AV	75/76 (98%)	17 (22%)	1 (1%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	AW	75/76 (98%)	15 (20%)	3 (4%)
22	CV	75/76 (98%)	18 (24%)	0
22	CW	75/76 (98%)	16 (21%)	4 (5%)
23	AX	7/8 (87%)	1 (14%)	1 (14%)
23	CX	7/8 (87%)	1 (14%)	0
35	BA	2885/2901 (99%)	515 (17%)	58 (2%)
35	DA	2885/2901 (99%)	516 (17%)	57 (1%)
36	BB	118/122 (96%)	15 (12%)	3 (2%)
36	DB	118/122 (96%)	14 (11%)	3 (2%)
All	All	9326/9410 (99%)	1567 (16%)	198 (2%)

5 of 1567 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	9	G
1	AA	31	G
1	AA	32	A
1	AA	39	G
1	AA	47	C

5 of 198 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BA	2439	A
1	CA	372	C
35	DA	2225	A
35	BA	2542	A
1	CA	30	U

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 1098 ligands modelled in this entry, 1098 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	AA	1504/1522 (98%)	0.12	38 (2%) 61 54	43, 106, 183, 201	0
1	CA	1504/1522 (98%)	0.03	45 (2%) 54 47	35, 87, 183, 201	0
2	AB	235/256 (91%)	0.70	39 (16%) 2 2	76, 137, 191, 201	0
2	CB	235/256 (91%)	0.28	15 (6%) 23 21	51, 117, 180, 201	0
3	AC	207/239 (86%)	0.86	34 (16%) 2 3	71, 130, 177, 201	0
3	CC	207/239 (86%)	0.11	7 (3%) 49 42	48, 96, 159, 200	0
4	AD	208/209 (99%)	0.55	22 (10%) 8 8	53, 116, 168, 199	0
4	CD	208/209 (99%)	0.16	6 (2%) 55 48	41, 95, 158, 183	0
5	AE	151/162 (93%)	0.40	9 (5%) 25 22	48, 102, 156, 179	0
5	CE	151/162 (93%)	-0.09	4 (2%) 59 52	29, 86, 145, 193	0
6	AF	101/101 (100%)	0.85	13 (12%) 5 5	75, 120, 170, 189	0
6	CF	101/101 (100%)	0.34	6 (5%) 26 23	60, 116, 162, 184	0
7	AG	155/156 (99%)	0.96	29 (18%) 2 2	64, 137, 182, 201	0
7	CG	155/156 (99%)	0.25	10 (6%) 22 20	42, 89, 143, 193	0
8	AH	138/138 (100%)	0.41	6 (4%) 39 33	50, 101, 152, 201	0
8	CH	138/138 (100%)	0.03	2 (1%) 78 71	50, 97, 148, 188	0
9	AI	127/128 (99%)	1.38	36 (28%) 1 1	66, 148, 192, 201	0
9	CI	127/128 (99%)	0.66	13 (10%) 9 9	43, 97, 148, 183	0
10	AJ	99/105 (94%)	1.79	34 (34%) 0 0	64, 154, 198, 201	0
10	CJ	99/105 (94%)	1.07	25 (25%) 1 1	44, 122, 197, 201	0
11	AK	119/129 (92%)	0.83	16 (13%) 4 5	52, 100, 155, 172	0
11	CK	119/129 (92%)	0.36	10 (8%) 14 14	49, 89, 165, 183	0
12	AL	126/132 (95%)	0.44	11 (8%) 13 13	42, 81, 146, 193	0
12	CL	126/132 (95%)	0.40	8 (6%) 23 21	37, 75, 148, 201	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	AM	121/126 (96%)	0.86	18 (14%) 3 3	69, 133, 191, 201	0
13	CM	121/126 (96%)	0.26	4 (3%) 50 43	26, 96, 156, 189	0
14	AN	60/61 (98%)	0.84	9 (15%) 3 3	76, 124, 173, 187	0
14	CN	60/61 (98%)	-0.05	1 (1%) 73 66	40, 82, 118, 155	0
15	AO	88/89 (98%)	0.49	3 (3%) 49 42	43, 100, 153, 177	0
15	CO	88/89 (98%)	0.41	3 (3%) 49 42	55, 92, 138, 155	0
16	AP	84/88 (95%)	0.75	9 (10%) 8 8	59, 104, 142, 201	0
16	CP	84/88 (95%)	1.22	18 (21%) 1 1	56, 106, 157, 201	0
17	AQ	100/105 (95%)	0.48	10 (10%) 9 10	54, 96, 137, 165	0
17	CQ	100/105 (95%)	0.36	6 (6%) 25 22	53, 99, 152, 162	0
18	AR	70/88 (79%)	0.50	4 (5%) 27 24	62, 116, 160, 183	0
18	CR	70/88 (79%)	0.60	8 (11%) 7 7	51, 101, 157, 183	0
19	AS	79/93 (84%)	1.12	13 (16%) 2 3	91, 140, 191, 201	0
19	CS	79/93 (84%)	0.85	11 (13%) 4 4	51, 103, 193, 201	0
20	AT	99/106 (93%)	0.80	12 (12%) 6 7	55, 112, 165, 201	0
20	CT	99/106 (93%)	1.07	21 (21%) 1 1	68, 115, 177, 201	0
21	AU	25/27 (92%)	2.00	11 (44%) 0 0	78, 131, 167, 178	0
21	CU	25/27 (92%)	0.55	0 100 100	58, 85, 117, 123	0
22	AV	76/76 (100%)	-0.07	0 100 100	42, 85, 152, 176	0
22	AW	76/76 (100%)	1.54	26 (34%) 0 0	48, 184, 201, 201	0
22	CV	76/76 (100%)	-0.30	1 (1%) 79 72	35, 65, 135, 185	0
22	CW	76/76 (100%)	1.10	14 (18%) 2 2	30, 166, 198, 201	0
23	AX	8/8 (100%)	0.39	1 (12%) 5 6	67, 76, 160, 166	0
23	CX	8/8 (100%)	0.17	1 (12%) 5 6	46, 62, 153, 170	0
24	AY	351/351 (100%)	0.73	51 (14%) 3 4	31, 109, 190, 201	0
24	CY	351/351 (100%)	0.52	35 (9%) 9 10	25, 95, 188, 201	0
25	B0	76/85 (89%)	0.07	2 (2%) 59 52	25, 64, 105, 177	0
25	D0	76/85 (89%)	0.16	2 (2%) 59 52	10, 43, 103, 179	0
26	B1	94/98 (95%)	0.15	3 (3%) 51 45	23, 61, 123, 173	0
26	D1	94/98 (95%)	-0.11	1 (1%) 82 76	18, 52, 109, 155	0
27	B2	71/72 (98%)	0.29	5 (7%) 19 18	36, 85, 156, 201	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
27	D2	71/72 (98%)	0.06	3 (4%)	40	34	27, 76, 144, 186	0
28	B3	60/60 (100%)	0.33	3 (5%)	32	27	19, 56, 131, 197	0
28	D3	60/60 (100%)	0.18	3 (5%)	32	27	20, 51, 112, 201	0
29	B4	31/71 (43%)	1.33	9 (29%)	1	1	99, 184, 201, 201	0
29	D4	31/71 (43%)	0.22	2 (6%)	22	20	51, 140, 184, 200	0
30	B5	59/60 (98%)	-0.01	4 (6%)	20	19	22, 74, 170, 190	0
30	D5	59/60 (98%)	0.33	5 (8%)	13	13	7, 55, 183, 201	0
31	B6	45/54 (83%)	0.88	5 (11%)	7	8	39, 85, 140, 198	0
31	D6	45/54 (83%)	0.40	1 (2%)	65	59	24, 65, 117, 183	0
32	B7	49/49 (100%)	0.19	3 (6%)	25	22	7, 48, 129, 165	0
32	D7	49/49 (100%)	0.12	2 (4%)	41	35	7, 37, 113, 189	0
33	B8	64/65 (98%)	0.03	1 (1%)	74	68	17, 51, 125, 160	0
33	D8	64/65 (98%)	-0.19	0	100	100	8, 40, 120, 162	0
34	B9	36/37 (97%)	0.61	2 (5%)	28	25	45, 69, 127, 147	0
34	D9	36/37 (97%)	0.81	6 (16%)	2	2	40, 74, 133, 162	0
35	BA	2886/2901 (99%)	-0.07	87 (3%)	54	47	16, 58, 179, 201	0
35	DA	2886/2901 (99%)	-0.03	103 (3%)	46	40	14, 51, 181, 201	0
36	BB	119/122 (97%)	-0.10	0	100	100	46, 105, 160, 186	0
36	DB	119/122 (97%)	-0.19	0	100	100	34, 65, 99, 129	0
37	BC	191/229 (83%)	4.71	140 (73%)	0	0	91, 174, 201, 201	0
37	DC	191/229 (83%)	4.47	152 (79%)	0	0	104, 177, 201, 201	0
38	BD	272/276 (98%)	0.13	8 (2%)	55	48	27, 71, 122, 165	0
38	DD	272/276 (98%)	0.01	7 (2%)	59	52	25, 66, 108, 168	0
39	BE	205/206 (99%)	0.09	6 (2%)	55	48	22, 69, 152, 201	0
39	DE	205/206 (99%)	0.18	6 (2%)	55	48	16, 67, 144, 197	0
40	BF	208/210 (99%)	-0.18	7 (3%)	49	42	9, 52, 134, 194	0
40	DF	208/210 (99%)	-0.15	7 (3%)	49	42	9, 48, 140, 179	0
41	BG	181/182 (99%)	0.61	19 (10%)	8	9	64, 118, 173, 200	0
41	DG	181/182 (99%)	0.02	5 (2%)	56	50	30, 76, 137, 201	0
42	BH	160/180 (88%)	0.98	33 (20%)	1	1	50, 123, 181, 201	0
42	DH	160/180 (88%)	1.29	45 (28%)	1	1	63, 137, 186, 201	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
43	BI	146/148 (98%)	0.64	13 (8%) 12 12	41, 138, 187, 200	0
44	BJ	0/130	-	-	-	-
44	DJ	0/130	-	-	-	-
45	BK	141/147 (95%)	1.99	57 (40%) 0 0	85, 158, 195, 201	0
45	DK	141/147 (95%)	1.89	53 (37%) 0 0	99, 158, 197, 201	0
46	BN	139/140 (99%)	-0.07	1 (0%) 89 84	30, 70, 129, 164	0
46	DN	139/140 (99%)	-0.09	1 (0%) 89 84	24, 62, 122, 186	0
47	BO	122/122 (100%)	-0.24	0 100 100	28, 64, 101, 158	0
47	DO	122/122 (100%)	-0.11	0 100 100	25, 68, 101, 120	0
48	BP	146/150 (97%)	0.81	13 (8%) 12 12	27, 89, 163, 200	0
48	DP	146/150 (97%)	0.27	4 (2%) 58 51	25, 72, 147, 201	0
49	BQ	141/141 (100%)	0.02	4 (2%) 56 50	23, 65, 127, 198	0
49	DQ	141/141 (100%)	-0.22	3 (2%) 67 61	14, 53, 105, 196	0
50	BR	117/118 (99%)	-0.06	1 (0%) 85 79	33, 72, 126, 156	0
50	DR	117/118 (99%)	0.02	1 (0%) 85 79	26, 68, 122, 150	0
51	BS	99/112 (88%)	0.93	17 (17%) 2 2	60, 104, 165, 188	0
51	DS	99/112 (88%)	-0.12	0 100 100	25, 61, 120, 171	0
52	BT	138/146 (94%)	0.27	10 (7%) 18 17	44, 87, 164, 201	0
52	DT	138/146 (94%)	0.28	8 (5%) 26 23	39, 87, 172, 199	0
53	BU	117/118 (99%)	-0.27	1 (0%) 85 79	18, 55, 112, 140	0
53	DU	117/118 (99%)	-0.34	1 (0%) 85 79	12, 45, 111, 190	0
54	BV	101/101 (100%)	0.23	7 (6%) 20 18	34, 79, 137, 185	0
54	DV	101/101 (100%)	0.05	2 (1%) 68 62	25, 66, 141, 201	0
55	BW	113/113 (100%)	-0.12	2 (1%) 71 64	25, 57, 114, 201	0
55	DW	113/113 (100%)	-0.24	1 (0%) 85 79	16, 47, 115, 170	0
56	BX	93/96 (96%)	0.22	1 (1%) 82 76	31, 74, 129, 155	0
56	DX	93/96 (96%)	-0.10	0 100 100	33, 67, 114, 160	0
57	BY	101/110 (91%)	0.89	15 (14%) 3 3	27, 84, 157, 201	0
57	DY	101/110 (91%)	0.59	8 (7%) 15 15	25, 81, 162, 201	0
58	BZ	177/206 (85%)	0.38	13 (7%) 18 17	36, 98, 156, 201	0
58	DZ	177/206 (85%)	-0.01	3 (1%) 73 66	30, 83, 130, 192	0
59	DI	146/148 (98%)	0.53	11 (7%) 17 16	28, 109, 155, 183	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	22210/23252 (95%)	0.31	1666 (7%) 17 16	7, 84, 181, 201	0

The worst 5 of 1666 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
37	BC	215	THR	23.7
37	BC	214	VAL	22.6
37	BC	165	ASN	20.4
37	BC	90	GLY	17.4
19	AS	82	GLY	15.7

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
60	MG	BA	3102	1/1	0.92	0.73	78.73	47,47,47,47	0
60	MG	DA	3024	1/1	0.94	0.96	74.08	49,49,49,49	0
60	MG	DA	3038	1/1	0.97	0.56	72.69	47,47,47,47	0
60	MG	DA	3025	1/1	0.92	0.77	71.59	56,56,56,56	0
60	MG	BA	3066	1/1	0.96	0.95	69.00	50,50,50,50	0
60	MG	BA	3043	1/1	0.96	0.77	61.07	47,47,47,47	0
60	MG	BA	3165	1/1	0.95	0.69	60.65	47,47,47,47	0
60	MG	DA	3100	1/1	0.80	0.72	59.97	55,55,55,55	0
60	MG	DA	3065	1/1	0.95	0.55	57.59	53,53,53,53	0
60	MG	BA	3123	1/1	0.87	0.65	53.91	53,53,53,53	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	DA	3163	1/1	0.96	0.69	53.08	50,50,50,50	0
60	MG	BA	3049	1/1	0.97	0.61	50.55	47,47,47,47	0
60	MG	DA	3006	1/1	0.93	0.76	48.45	47,47,47,47	0
60	MG	DA	3265	1/1	0.96	0.60	46.62	53,53,53,53	0
60	MG	BA	3045	1/1	0.87	0.80	46.43	47,47,47,47	0
60	MG	BA	3042	1/1	0.93	1.01	43.94	47,47,47,47	0
60	MG	DA	3220	1/1	0.91	0.84	43.76	49,49,49,49	0
60	MG	DA	3053	1/1	0.97	0.60	43.14	47,47,47,47	0
60	MG	CA	1631	1/1	0.78	0.83	43.04	53,53,53,53	0
60	MG	BA	3158	1/1	0.96	0.85	42.30	49,49,49,49	0
60	MG	BA	3103	1/1	0.93	0.58	41.49	50,50,50,50	0
60	MG	DA	3203	1/1	0.96	0.45	41.48	47,47,47,47	0
60	MG	CA	1736	1/1	0.87	0.64	40.55	55,55,55,55	0
60	MG	DA	3143	1/1	0.63	0.45	40.31	47,47,47,47	1
60	MG	DA	3046	1/1	0.87	0.76	39.33	47,47,47,47	0
60	MG	BA	3099	1/1	0.88	0.78	38.26	55,55,55,55	0
60	MG	DA	3079	1/1	0.93	0.49	37.71	56,56,56,56	0
60	MG	DA	3269	1/1	0.88	0.61	37.41	52,52,52,52	0
60	MG	DA	3258	1/1	0.89	0.82	36.85	51,51,51,51	1
60	MG	BA	3106	1/1	0.95	0.72	35.83	51,51,51,51	0
60	MG	BA	3348	1/1	0.95	0.57	35.73	55,55,55,55	0
60	MG	BA	3101	1/1	0.95	0.69	35.41	47,47,47,47	0
60	MG	BA	3264	1/1	0.97	0.57	34.86	53,53,53,53	0
60	MG	BA	3303	1/1	0.83	0.75	34.00	55,55,55,55	0
60	MG	BA	3071	1/1	0.95	0.40	33.99	47,47,47,47	0
60	MG	DA	3327	1/1	0.68	0.46	33.96	55,55,55,55	0
60	MG	BA	3269	1/1	0.80	0.53	33.90	52,52,52,52	0
60	MG	BA	3033	1/1	0.95	0.54	33.88	47,47,47,47	0
60	MG	DA	3166	1/1	0.86	0.65	33.83	47,47,47,47	0
60	MG	BA	3024	1/1	0.91	0.63	33.79	56,56,56,56	0
60	MG	BA	3108	1/1	0.96	0.71	33.67	52,52,52,52	0
60	MG	AA	1655	1/1	0.81	0.41	33.55	52,52,52,52	0
60	MG	BA	3305	1/1	0.96	0.72	32.73	55,55,55,55	0
60	MG	DA	3245	1/1	0.95	0.56	32.50	53,53,53,53	0
60	MG	DA	3057	1/1	0.95	0.68	32.11	47,47,47,47	0
60	MG	DA	3151	1/1	0.95	0.52	31.74	51,51,51,51	0
60	MG	BA	3116	1/1	0.96	0.42	31.45	47,47,47,47	0
60	MG	BA	3287	1/1	0.65	0.40	30.87	51,51,51,51	0
60	MG	DA	3005	1/1	0.95	0.48	29.85	53,53,53,53	0
60	MG	CA	1622	1/1	0.94	0.85	29.72	57,57,57,57	0
60	MG	BA	3044	1/1	0.92	0.84	29.35	56,56,56,56	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	DA	3034	1/1	0.95	0.59	29.06	47,47,47,47	0
60	MG	DA	3081	1/1	0.93	0.57	28.45	52,52,52,52	0
60	MG	BA	3113	1/1	0.93	0.51	27.83	47,47,47,47	0
60	MG	BA	3082	1/1	0.82	0.67	27.75	51,51,51,51	0
60	MG	DA	3225	1/1	0.74	0.73	27.49	51,51,51,51	0
60	MG	BA	3013	1/1	0.98	0.43	27.23	47,47,47,47	0
60	MG	CA	1645	1/1	0.89	0.66	26.75	50,50,50,50	0
60	MG	BA	3005	1/1	0.95	0.76	26.53	47,47,47,47	0
60	MG	DA	3055	1/1	0.90	0.58	26.28	47,47,47,47	0
60	MG	BA	3160	1/1	0.97	0.33	26.12	47,47,47,47	0
60	MG	BA	3064	1/1	0.93	0.51	25.98	53,53,53,53	0
60	MG	DA	3067	1/1	0.95	0.63	25.94	50,50,50,50	0
60	MG	BA	3056	1/1	0.98	0.63	25.91	47,47,47,47	0
60	MG	DA	3152	1/1	0.95	0.45	25.75	47,47,47,47	0
60	MG	DA	3061	1/1	0.95	0.48	25.70	47,47,47,47	0
60	MG	BA	3228	1/1	0.92	0.77	25.49	52,52,52,52	0
60	MG	DA	3010	1/1	0.95	0.64	25.40	47,47,47,47	0
60	MG	DA	3295	1/1	0.95	0.75	25.38	55,55,55,55	0
60	MG	DA	3161	1/1	0.95	0.31	25.34	47,47,47,47	0
60	MG	DA	3062	1/1	0.96	0.44	25.27	48,48,48,48	0
60	MG	BA	3185	1/1	0.92	0.60	25.11	50,50,50,50	0
60	MG	BA	3219	1/1	0.92	0.86	25.06	49,49,49,49	0
60	MG	BA	3147	1/1	0.95	0.42	24.41	51,51,51,51	0
60	MG	DA	3159	1/1	0.95	0.83	23.20	49,49,49,49	0
60	MG	BA	3058	1/1	0.93	0.69	22.68	55,55,55,55	0
60	MG	BA	3020	1/1	0.97	0.58	22.68	47,47,47,47	0
60	MG	DA	3146	1/1	0.93	0.47	22.36	47,47,47,47	0
60	MG	BA	3068	1/1	0.98	0.48	22.36	47,47,47,47	0
60	MG	BA	3035	1/1	0.98	0.40	22.18	55,55,55,55	0
60	MG	DA	3103	1/1	0.81	0.47	22.14	47,47,47,47	0
60	MG	BA	3088	1/1	0.99	0.59	22.06	48,48,48,48	0
60	MG	BA	3023	1/1	0.96	0.78	21.98	49,49,49,49	0
60	MG	DA	3089	1/1	0.97	0.64	21.92	48,48,48,48	0
60	MG	DA	3059	1/1	0.86	0.78	21.54	55,55,55,55	0
60	MG	DA	3139	1/1	0.94	0.66	21.47	50,50,50,50	0
60	MG	BA	3062	1/1	0.94	0.52	20.99	47,47,47,47	0
60	MG	AA	1714	1/1	0.91	0.52	20.93	59,59,59,59	0
60	MG	DA	3107	1/1	0.97	0.59	20.85	51,51,51,51	0
60	MG	BA	3061	1/1	0.97	0.45	20.68	48,48,48,48	0
60	MG	DA	3043	1/1	0.93	1.02	20.19	47,47,47,47	0
60	MG	DA	3002	1/1	0.88	0.94	20.13	54,54,54,54	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	BA	3105	1/1	0.74	0.47	20.06	47,47,47,47	0
60	MG	BA	3224	1/1	0.86	0.43	20.00	51,51,51,51	0
60	MG	DA	3080	1/1	0.96	0.53	19.93	49,49,49,49	0
60	MG	BA	3090	1/1	0.98	0.46	19.92	48,48,48,48	0
60	MG	DA	3215	1/1	0.88	0.46	19.73	48,48,48,48	0
60	MG	BA	3280	1/1	0.89	0.42	19.66	57,57,57,57	0
60	MG	DA	3304	1/1	0.96	0.70	19.51	55,55,55,55	0
60	MG	AV	101	1/1	0.96	0.42	19.30	49,49,49,49	0
60	MG	DA	3287	1/1	0.75	0.47	19.07	51,51,51,51	0
60	MG	DA	3104	1/1	0.96	0.41	18.87	50,50,50,50	0
60	MG	DA	3012	1/1	0.86	0.35	18.71	47,47,47,47	0
60	MG	BA	3300	1/1	0.96	0.32	18.64	55,55,55,55	0
60	MG	BA	3296	1/1	0.83	0.67	18.50	55,55,55,55	0
60	MG	AA	1656	1/1	0.86	0.62	18.49	47,47,47,47	0
60	MG	BA	3213	1/1	0.93	0.44	18.25	58,58,58,58	0
60	MG	BA	3107	1/1	0.95	0.36	18.16	51,51,51,51	0
60	MG	DA	3165	1/1	0.91	0.28	18.04	47,47,47,47	0
60	MG	BA	3201	1/1	0.56	0.44	17.83	52,52,52,52	0
60	MG	DA	3021	1/1	0.97	0.53	17.69	47,47,47,47	0
60	MG	AY	401	1/1	0.89	0.56	17.68	55,55,55,55	0
60	MG	BA	3021	1/1	0.98	0.38	17.40	47,47,47,47	0
60	MG	BA	3351	1/1	0.85	0.48	17.39	55,55,55,55	0
60	MG	DA	3099	1/1	0.96	0.36	17.35	54,54,54,54	0
60	MG	DA	3020	1/1	0.98	0.56	17.26	47,47,47,47	0
60	MG	BA	3214	1/1	0.81	0.32	17.14	48,48,48,48	0
60	MG	DA	3096	1/1	0.97	0.53	17.11	60,60,60,60	0
60	MG	DA	3063	1/1	0.94	0.55	17.09	47,47,47,47	0
60	MG	DA	3036	1/1	0.96	0.40	17.03	55,55,55,55	0
60	MG	BA	3083	1/1	0.98	0.52	16.66	47,47,47,47	0
60	MG	BA	3069	1/1	0.97	0.36	16.01	48,48,48,48	0
60	MG	BA	3037	1/1	0.98	0.41	15.78	47,47,47,47	0
60	MG	CA	1624	1/1	0.90	0.37	15.75	51,51,51,51	0
60	MG	AA	1650	1/1	0.83	0.46	15.42	47,47,47,47	0
60	MG	DA	3186	1/1	0.96	0.55	15.16	50,50,50,50	0
60	MG	AA	1741	1/1	0.92	0.48	15.06	55,55,55,55	0
60	MG	BA	3009	1/1	0.96	0.66	15.01	47,47,47,47	0
60	MG	DA	3044	1/1	0.98	0.51	14.97	47,47,47,47	0
60	MG	BA	3243	1/1	0.95	0.50	14.97	53,53,53,53	0
60	MG	BA	3138	1/1	0.92	0.33	14.89	50,50,50,50	0
60	MG	BA	3257	1/1	0.94	0.34	14.85	51,51,51,51	0
60	MG	AA	1632	1/1	0.91	0.49	14.78	53,53,53,53	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	DA	3052	1/1	0.97	0.54	14.75	51,51,51,51	0
60	MG	DF	303	1/1	0.86	0.67	14.63	59,59,59,59	0
60	MG	AA	1735	1/1	0.83	0.55	14.62	55,55,55,55	0
60	MG	BA	3019	1/1	0.95	0.54	14.57	47,47,47,47	0
60	MG	DA	3114	1/1	0.96	0.38	14.53	47,47,47,47	0
60	MG	DA	3013	1/1	0.95	0.53	14.49	49,49,49,49	0
60	MG	DA	3074	1/1	0.97	0.42	14.30	52,52,52,52	0
60	MG	DA	3197	1/1	0.94	0.59	14.17	47,47,47,47	0
60	MG	CA	1719	1/1	0.72	0.35	14.09	55,55,55,55	1
60	MG	CA	1633	1/1	0.90	0.94	13.97	52,52,52,52	0
60	MG	AA	1745	1/1	0.94	0.64	13.93	55,55,55,55	0
60	MG	BA	3004	1/1	0.90	0.30	13.89	53,53,53,53	0
60	MG	DA	3106	1/1	0.79	0.40	13.86	47,47,47,47	0
60	MG	DA	3033	1/1	0.81	0.30	13.81	53,53,53,53	0
60	MG	CA	1695	1/1	0.86	0.37	13.49	56,56,56,56	0
60	MG	DD	301	1/1	0.92	0.58	13.30	47,47,47,47	0
60	MG	DA	3068	1/1	0.90	0.44	13.29	50,50,50,50	0
60	MG	DA	3077	1/1	0.94	0.35	12.98	48,48,48,48	0
60	MG	DA	3207	1/1	0.99	0.49	12.95	47,47,47,47	0
60	MG	CV	101	1/1	0.97	0.58	12.91	49,49,49,49	0
60	MG	BA	3142	1/1	0.71	0.39	12.67	47,47,47,47	0
60	MG	DA	3184	1/1	0.97	0.50	12.50	49,49,49,49	0
60	MG	CA	1669	1/1	0.96	0.32	12.32	47,47,47,47	0
60	MG	DA	3109	1/1	0.95	0.39	12.26	52,52,52,52	0
60	MG	BA	3070	1/1	0.98	0.40	12.08	50,50,50,50	0
60	MG	DA	3271	1/1	0.96	0.47	12.05	51,51,51,51	0
60	MG	DA	3226	1/1	0.92	0.38	12.05	51,51,51,51	0
60	MG	AA	1674	1/1	0.94	0.28	11.91	50,50,50,50	0
60	MG	DA	3097	1/1	0.84	0.53	11.84	56,56,56,56	0
60	MG	DA	3075	1/1	0.95	0.53	11.84	47,47,47,47	0
60	MG	DA	3069	1/1	0.98	0.34	11.83	47,47,47,47	0
60	MG	BA	3307	1/1	0.84	0.33	11.73	55,55,55,55	0
60	MG	DA	3196	1/1	0.95	0.35	11.71	52,52,52,52	0
60	MG	DA	3127	1/1	0.80	0.33	11.70	52,52,52,52	0
60	MG	DA	3162	1/1	0.77	0.35	11.67	47,47,47,47	0
60	MG	CA	1610	1/1	0.90	0.51	11.56	48,48,48,48	0
60	MG	BA	3026	1/1	0.94	0.39	11.43	47,47,47,47	0
60	MG	DA	3070	1/1	0.96	0.35	11.26	48,48,48,48	0
60	MG	BA	3299	1/1	0.97	0.42	11.21	55,55,55,55	0
60	MG	BA	3012	1/1	0.94	0.57	10.96	49,49,49,49	0
60	MG	DA	3206	1/1	0.87	0.34	10.87	50,50,50,50	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	BA	3011	1/1	0.97	0.32	10.69	47,47,47,47	0
60	MG	DA	3345	1/1	0.97	0.36	10.62	55,55,55,55	0
60	MG	BA	3079	1/1	0.94	0.44	10.58	49,49,49,49	0
60	MG	BA	3271	1/1	0.95	0.59	10.28	51,51,51,51	0
60	MG	CA	1686	1/1	0.94	0.35	10.22	57,57,57,57	0
60	MG	B7	101	1/1	0.90	0.51	10.02	49,49,49,49	0
60	MG	DA	3160	1/1	0.92	0.30	9.99	55,55,55,55	0
60	MG	CA	1635	1/1	0.89	0.43	9.97	49,49,49,49	0
60	MG	BA	3050	1/1	0.98	0.31	9.76	47,47,47,47	0
60	MG	DA	3157	1/1	0.92	0.34	9.68	48,48,48,48	0
60	MG	CA	1616	1/1	0.96	0.41	9.68	54,54,54,54	0
60	MG	DA	3148	1/1	0.98	0.37	9.65	51,51,51,51	0
60	MG	AA	1634	1/1	0.90	0.68	9.39	52,52,52,52	0
60	MG	DA	3116	1/1	0.94	0.37	9.38	50,50,50,50	0
60	MG	BA	3051	1/1	0.97	0.32	9.29	51,51,51,51	0
60	MG	DA	3072	1/1	0.98	0.25	9.28	47,47,47,47	0
60	MG	DA	3084	1/1	0.98	0.38	9.14	47,47,47,47	0
60	MG	DA	3253	1/1	0.88	0.33	9.13	49,49,49,49	0
60	MG	DA	3214	1/1	0.96	0.36	9.02	58,58,58,58	0
60	MG	CA	1603	1/1	0.97	0.33	9.02	61,61,61,61	0
60	MG	DA	3344	1/1	0.90	0.54	8.99	55,55,55,55	0
60	MG	AA	1749	1/1	0.98	0.38	8.91	55,55,55,55	0
60	MG	BA	3098	1/1	0.99	0.28	8.88	54,54,54,54	0
60	MG	AA	1685	1/1	0.94	0.28	8.80	57,57,57,57	0
60	MG	BD	301	1/1	0.94	0.46	8.61	47,47,47,47	0
60	MG	BA	3202	1/1	0.97	0.32	8.55	47,47,47,47	0
60	MG	DA	3016	1/1	0.97	0.51	8.43	47,47,47,47	0
60	MG	BA	3114	1/1	0.97	0.29	8.33	48,48,48,48	0
60	MG	DA	3317	1/1	0.82	0.32	8.25	55,55,55,55	0
60	MG	BA	3233	1/1	0.94	0.60	8.16	47,47,47,47	0
60	MG	DA	3027	1/1	0.93	0.46	8.09	47,47,47,47	0
60	MG	AA	1625	1/1	0.95	0.29	8.08	51,51,51,51	0
60	MG	BA	3347	1/1	0.97	0.29	7.94	55,55,55,55	0
60	MG	AA	1623	1/1	0.93	0.57	7.73	57,57,57,57	0
60	MG	BA	3342	1/1	0.95	0.28	7.72	55,55,55,55	0
60	MG	DA	3267	1/1	0.93	0.33	7.59	54,54,54,54	0
60	MG	BA	3252	1/1	0.96	0.34	7.54	49,49,49,49	0
60	MG	BA	3015	1/1	0.99	0.48	7.42	47,47,47,47	0
60	MG	CA	1722	1/1	0.74	0.44	7.20	55,55,55,55	0
60	MG	BA	3196	1/1	0.96	0.50	7.02	47,47,47,47	0
60	MG	CA	1649	1/1	0.94	0.45	6.91	47,47,47,47	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	BA	3067	1/1	0.89	0.34	6.87	50,50,50,50	0
60	MG	BA	3318	1/1	0.83	0.28	6.67	55,55,55,55	0
60	MG	BA	3164	1/1	0.98	0.24	6.64	47,47,47,47	0
60	MG	CY	401	1/1	0.95	0.57	6.58	55,55,55,55	0
60	MG	BA	3076	1/1	0.95	0.24	6.45	48,48,48,48	0
60	MG	DA	3234	1/1	0.97	0.52	6.43	47,47,47,47	0
60	MG	DA	3048	1/1	0.98	0.27	6.29	47,47,47,47	0
60	MG	BA	3206	1/1	0.95	0.30	6.29	47,47,47,47	0
60	MG	DA	3022	1/1	0.98	0.20	6.25	47,47,47,47	0
60	MG	BA	3188	1/1	0.91	0.36	6.17	57,57,57,57	0
60	MG	BA	3159	1/1	0.91	0.30	6.16	55,55,55,55	0
60	MG	BA	3074	1/1	0.95	0.40	6.15	47,47,47,47	0
60	MG	DA	3170	1/1	0.91	0.47	6.00	49,49,49,49	1
60	MG	BA	3128	1/1	0.94	0.21	5.94	50,50,50,50	0
60	MG	DA	3071	1/1	0.98	0.31	5.93	50,50,50,50	0
60	MG	DA	3014	1/1	0.99	0.32	5.92	47,47,47,47	0
60	MG	BA	3225	1/1	0.85	0.34	5.78	51,51,51,51	0
60	MG	DA	3298	1/1	0.94	0.30	5.66	55,55,55,55	0
60	MG	BA	3145	1/1	0.97	0.29	5.50	47,47,47,47	0
60	MG	AA	1721	1/1	0.95	0.48	5.24	55,55,55,55	1
60	MG	BA	3182	1/1	0.96	0.36	5.19	49,49,49,49	0
60	MG	CA	1607	1/1	0.91	0.34	5.07	47,47,47,47	0
60	MG	B1	101	1/1	0.92	0.53	5.01	55,55,55,55	0
60	MG	DA	3238	1/1	0.77	0.24	4.92	47,47,47,47	0
60	MG	DA	3108	1/1	0.98	0.20	4.90	51,51,51,51	0
60	MG	AA	1627	1/1	0.89	0.33	4.86	53,53,53,53	0
60	MG	DA	3305	1/1	0.93	0.25	4.81	55,55,55,55	0
60	MG	DA	3156	1/1	0.97	0.33	4.79	51,51,51,51	0
60	MG	BA	3346	1/1	0.87	0.45	4.58	55,55,55,55	0
60	MG	DA	3091	1/1	0.94	0.39	4.54	48,48,48,48	0
60	MG	AA	1683	1/1	0.69	0.48	4.46	47,47,47,47	0
60	MG	CA	1750	1/1	0.95	0.23	4.44	55,55,55,55	0
60	MG	D1	101	1/1	0.98	0.41	4.38	55,55,55,55	0
60	MG	BA	3155	1/1	0.97	0.30	4.12	51,51,51,51	0
60	MG	BA	3184	1/1	0.97	0.43	4.10	47,47,47,47	0
60	MG	DA	3167	1/1	0.80	0.25	3.97	47,47,47,47	0
60	MG	BA	3163	1/1	0.96	0.37	3.52	53,53,53,53	0
60	MG	DA	3259	1/1	0.85	0.33	3.44	58,58,58,58	0
60	MG	DA	3299	1/1	0.88	0.34	3.42	55,55,55,55	0
60	MG	CA	1746	1/1	0.98	0.22	3.41	55,55,55,55	0
60	MG	DA	3083	1/1	0.74	0.27	3.38	51,51,51,51	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	AA	1671	1/1	0.94	0.31	3.36	47,47,47,47	0
60	MG	DU	201	1/1	0.97	0.53	3.33	48,48,48,48	0
60	MG	BA	3175	1/1	0.81	0.30	3.24	49,49,49,49	1
60	MG	DA	3131	1/1	0.97	0.19	2.91	48,48,48,48	0
60	MG	CA	1674	1/1	0.82	0.22	2.66	50,50,50,50	0
60	MG	BA	3279	1/1	0.95	0.17	2.64	55,55,55,55	0
60	MG	DA	3229	1/1	0.80	0.34	2.55	52,52,52,52	0
60	MG	AA	1669	1/1	0.96	0.27	2.54	47,47,47,47	0
60	MG	DA	3129	1/1	0.94	0.21	2.46	50,50,50,50	0
60	MG	AA	1672	1/1	0.94	0.27	2.45	53,53,53,53	0
60	MG	DR	201	1/1	0.99	0.34	2.41	47,47,47,47	0
60	MG	CA	1658	1/1	0.93	0.27	2.31	49,49,49,49	0
60	MG	DF	301	1/1	0.86	0.27	2.27	47,47,47,47	0
60	MG	BA	3047	1/1	0.92	0.30	2.21	47,47,47,47	0
60	MG	DD	302	1/1	0.94	0.46	2.12	47,47,47,47	0
60	MG	AA	1657	1/1	0.53	0.27	2.06	54,54,54,54	0
60	MG	CA	1612	1/1	0.83	0.28	2.02	56,56,56,56	0
60	MG	AA	1679	1/1	0.83	0.20	1.98	53,53,53,53	0
60	MG	BA	3237	1/1	0.71	0.28	1.96	67,67,67,67	0
60	MG	AA	1694	1/1	0.64	0.21	1.92	56,56,56,56	0
60	MG	BA	3032	1/1	0.80	0.18	1.91	53,53,53,53	0
60	MG	AA	1608	1/1	0.95	0.24	1.80	47,47,47,47	0
60	MG	CA	1620	1/1	0.94	0.23	1.74	56,56,56,56	0
60	MG	AA	1611	1/1	0.89	0.52	1.71	48,48,48,48	0
60	MG	BA	3267	1/1	0.96	0.22	1.55	54,54,54,54	0
60	MG	AA	1654	1/1	0.97	0.16	1.42	53,53,53,53	0
60	MG	CA	1671	1/1	0.95	0.19	1.38	47,47,47,47	0
60	MG	BF	301	1/1	0.93	0.28	1.33	47,47,47,47	0
60	MG	AA	1754	1/1	0.84	0.24	1.08	55,55,55,55	0
60	MG	AA	1658	1/1	0.90	0.28	0.92	49,49,49,49	0
60	MG	BA	3205	1/1	0.92	0.17	0.83	50,50,50,50	0
60	MG	DA	3320	1/1	0.97	0.21	0.82	55,55,55,55	0
60	MG	BA	3321	1/1	0.95	0.21	0.73	55,55,55,55	0
60	MG	BA	3248	1/1	0.88	0.26	0.57	56,56,56,56	1
60	MG	DA	3312	1/1	0.93	0.19	0.53	55,55,55,55	0
60	MG	AA	1610	1/1	0.88	0.28	0.52	55,55,55,55	0
60	MG	AL	201	1/1	0.78	0.25	0.48	51,51,51,51	1
60	MG	AA	1722	1/1	0.97	0.28	0.38	55,55,55,55	0
61	ZN	CD	301	1/1	0.99	0.27	0.26	52,52,52,52	0
60	MG	CA	1754	1/1	0.87	0.24	0.25	55,55,55,55	0
60	MG	AA	1621	1/1	0.88	0.22	0.18	56,56,56,56	0
60	MG	BA	3313	1/1	0.95	0.19	0.17	55,55,55,55	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	CA	1675	1/1	0.79	0.19	0.16	48,48,48,48	1
60	MG	BA	3130	1/1	0.97	0.16	-0.01	48,48,48,48	0
60	MG	CA	1626	1/1	0.95	0.17	-0.12	53,53,53,53	0
60	MG	AA	1675	1/1	0.65	0.17	-0.27	48,48,48,48	0
61	ZN	AD	301	1/1	0.98	0.20	-0.59	52,52,52,52	0
60	MG	BA	3263	1/1	0.95	0.14	-0.61	56,56,56,56	0
60	MG	AA	1617	1/1	0.85	0.16	-0.74	54,54,54,54	0
60	MG	AA	1635	1/1	0.80	0.16	-1.13	47,47,47,47	0
60	MG	BA	3152	1/1	0.85	0.12	-1.14	50,50,50,50	0
60	MG	AA	1636	1/1	0.95	0.18	-1.16	49,49,49,49	0
60	MG	BA	3166	1/1	0.94	0.10	-1.35	47,47,47,47	0
60	MG	CA	1682	1/1	0.98	0.12	-1.41	53,53,53,53	0
60	MG	AA	1682	1/1	0.91	0.13	-1.42	53,53,53,53	0
61	ZN	CN	102	1/1	1.00	0.12	-1.43	60,60,60,60	0
60	MG	CA	1678	1/1	0.93	0.14	-1.46	49,49,49,49	0
61	ZN	D9	101	1/1	1.00	0.11	-1.52	55,55,55,55	1
61	ZN	AN	101	1/1	0.99	0.10	-1.55	60,60,60,60	1
60	MG	BA	3306	1/1	0.92	0.18	-1.56	55,55,55,55	0
60	MG	AA	1678	1/1	0.98	0.09	-1.57	49,49,49,49	0
60	MG	AA	1751	1/1	0.99	0.07	-1.65	55,55,55,55	0
60	MG	AA	1734	1/1	0.91	0.14	-1.95	55,55,55,55	0
60	MG	CA	1696	1/1	0.98	0.11	-2.08	62,62,62,62	0
61	ZN	B9	101	1/1	0.99	0.06	-2.44	55,55,55,55	0
60	MG	AA	1633	1/1	0.92	0.12	-2.60	55,55,55,55	0
60	MG	BA	3236	1/1	0.81	0.13	-2.69	47,47,47,47	0
60	MG	AW	103	1/1	0.91	0.08	-2.71	54,54,54,54	0
60	MG	DA	3306	1/1	0.91	0.10	-3.45	55,55,55,55	0
60	MG	CA	1653	1/1	0.98	0.07	-3.91	53,53,53,53	0
60	MG	AA	1748	1/1	0.65	0.39	-	55,55,55,55	0
60	MG	DA	3073	1/1	0.94	0.59	-	53,53,53,53	0
60	MG	AA	1710	1/1	0.87	0.13	-	55,55,55,55	0
60	MG	DA	3273	1/1	0.96	0.23	-	58,58,58,58	0
60	MG	DA	3050	1/1	0.94	0.52	-	47,47,47,47	0
60	MG	CN	101	1/1	0.92	0.37	-	55,55,55,55	0
60	MG	BA	3007	1/1	0.95	0.48	-	52,52,52,52	0
60	MG	BA	3177	1/1	0.91	0.86	-	47,47,47,47	0
60	MG	BA	3086	1/1	0.96	0.53	-	48,48,48,48	0
60	MG	BC	301	1/1	0.57	0.51	-	52,52,52,52	1
60	MG	AA	1612	1/1	0.93	0.13	-	52,52,52,52	0
60	MG	BA	3339	1/1	0.84	0.29	-	55,55,55,55	0
60	MG	DA	3255	1/1	0.94	0.48	-	60,60,60,60	0
60	MG	CA	1707	1/1	0.84	0.60	-	51,51,51,51	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	CA	1680	1/1	0.97	0.27	-	49,49,49,49	0
60	MG	BA	3040	1/1	0.97	0.61	-	47,47,47,47	0
60	MG	BA	3014	1/1	0.97	0.57	-	53,53,53,53	0
60	MG	BA	3277	1/1	0.91	0.75	-	57,57,57,57	0
60	MG	BA	3081	1/1	0.98	0.35	-	47,47,47,47	0
60	MG	DA	3135	1/1	0.95	0.50	-	54,54,54,54	0
60	MG	DB	204	1/1	0.92	0.24	-	55,55,55,55	0
60	MG	BA	3246	1/1	0.90	0.36	-	55,55,55,55	0
60	MG	AA	1725	1/1	0.90	1.07	-	54,54,54,54	0
60	MG	DA	3286	1/1	0.96	0.25	-	60,60,60,60	0
60	MG	DA	3054	1/1	0.91	0.36	-	51,51,51,51	0
60	MG	BA	3120	1/1	0.92	0.62	-	50,50,50,50	0
60	MG	DA	3085	1/1	0.89	0.40	-	47,47,47,47	0
60	MG	DA	3201	1/1	0.96	0.45	-	60,60,60,60	0
60	MG	BA	3034	1/1	0.94	0.37	-	50,50,50,50	0
60	MG	DA	3308	1/1	0.93	0.14	-	55,55,55,55	0
60	MG	DA	3123	1/1	0.91	0.25	-	64,64,64,64	1
60	MG	AA	1605	1/1	0.97	0.12	-	50,50,50,50	0
60	MG	AA	1673	1/1	0.81	0.11	-	52,52,52,52	0
60	MG	AA	1747	1/1	0.70	0.35	-	55,55,55,55	1
60	MG	BA	3046	1/1	0.98	0.42	-	47,47,47,47	0
60	MG	CA	1625	1/1	0.76	0.65	-	53,53,53,53	0
60	MG	BA	3266	1/1	0.88	0.57	-	59,59,59,59	0
60	MG	BA	3085	1/1	0.97	0.17	-	47,47,47,47	0
60	MG	CW	102	1/1	0.96	0.26	-	60,60,60,60	0
60	MG	DA	3316	1/1	0.85	0.60	-	55,55,55,55	0
60	MG	DA	3256	1/1	0.93	0.64	-	55,55,55,55	0
60	MG	DA	3348	1/1	0.95	0.34	-	55,55,55,55	0
60	MG	DA	3136	1/1	0.92	0.89	-	58,58,58,58	0
60	MG	CA	1670	1/1	0.53	0.77	-	69,69,69,69	0
60	MG	BA	3149	1/1	0.97	0.53	-	54,54,54,54	0
60	MG	BA	3354	1/1	0.91	0.31	-	55,55,55,55	0
60	MG	BA	3322	1/1	0.92	0.37	-	55,55,55,55	0
60	MG	BA	3282	1/1	0.86	0.43	-	57,57,57,57	0
60	MG	CA	1712	1/1	0.93	0.52	-	47,47,47,47	0
60	MG	AA	1742	1/1	0.83	0.34	-	55,55,55,55	0
60	MG	DY	201	1/1	0.92	0.26	-	55,55,55,55	0
60	MG	BA	3250	1/1	0.90	0.41	-	52,52,52,52	0
60	MG	CA	1605	1/1	0.90	0.57	-	59,59,59,59	0
60	MG	BA	3249	1/1	0.81	0.46	-	56,56,56,56	0
60	MG	BA	3183	1/1	0.81	0.62	-	56,56,56,56	0
60	MG	BA	3294	1/1	0.77	0.13	-	52,52,52,52	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	BA	3212	1/1	0.59	0.47	-	55,55,55,55	0
60	MG	AA	1718	1/1	0.69	0.23	-	55,55,55,55	0
60	MG	BA	3262	1/1	0.98	0.17	-	63,63,63,63	1
60	MG	AA	1666	1/1	0.82	0.65	-	57,57,57,57	0
60	MG	CA	1637	1/1	0.85	0.25	-	52,52,52,52	0
60	MG	DA	3274	1/1	0.83	0.49	-	63,63,63,63	0
60	MG	DA	3039	1/1	0.96	0.38	-	51,51,51,51	0
60	MG	AA	1604	1/1	0.95	0.39	-	61,61,61,61	0
60	MG	DA	3205	1/1	0.82	0.54	-	57,57,57,57	0
60	MG	BA	3109	1/1	0.95	0.29	-	48,48,48,48	0
60	MG	DA	3035	1/1	0.94	0.38	-	50,50,50,50	0
60	MG	DA	3281	1/1	0.80	0.37	-	57,57,57,57	0
60	MG	BA	3316	1/1	0.94	0.54	-	55,55,55,55	0
60	MG	BA	3135	1/1	0.67	0.71	-	58,58,58,58	0
60	MG	DA	3015	1/1	0.99	0.55	-	53,53,53,53	0
60	MG	AA	1644	1/1	0.87	0.37	-	49,49,49,49	0
60	MG	CA	1752	1/1	0.96	0.19	-	55,55,55,55	1
60	MG	DA	3173	1/1	0.93	0.25	-	58,58,58,58	0
60	MG	CA	1756	1/1	0.91	0.40	-	55,55,55,55	1
60	MG	DB	202	1/1	0.96	0.75	-	55,55,55,55	0
60	MG	DA	3102	1/1	0.97	0.73	-	47,47,47,47	0
60	MG	BA	3192	1/1	0.89	0.28	-	65,65,65,65	0
60	MG	AA	1620	1/1	0.92	0.30	-	55,55,55,55	0
60	MG	AV	103	1/1	0.92	0.25	-	54,54,54,54	1
60	MG	BA	3226	1/1	0.90	0.45	-	56,56,56,56	0
60	MG	BA	3054	1/1	0.87	0.76	-	47,47,47,47	0
60	MG	BA	3096	1/1	0.91	0.46	-	56,56,56,56	0
60	MG	AW	104	1/1	0.94	0.13	-	56,56,56,56	0
60	MG	DA	3247	1/1	0.83	0.32	-	55,55,55,55	1
60	MG	AA	1652	1/1	0.91	0.38	-	47,47,47,47	0
60	MG	AA	1613	1/1	0.59	0.27	-	56,56,56,56	0
60	MG	AA	1691	1/1	0.92	0.50	-	59,59,59,59	0
60	MG	DA	3149	1/1	0.86	0.24	-	47,47,47,47	0
60	MG	BA	3010	1/1	0.91	0.57	-	52,52,52,52	0
60	MG	BA	3112	1/1	0.90	0.32	-	48,48,48,48	0
60	MG	AA	1628	1/1	0.95	0.37	-	70,70,70,70	0
60	MG	CA	1748	1/1	0.91	0.44	-	55,55,55,55	1
60	MG	CA	1703	1/1	0.97	0.31	-	47,47,47,47	0
60	MG	DA	3278	1/1	0.96	0.63	-	51,51,51,51	0
60	MG	CA	1727	1/1	0.91	0.21	-	56,56,56,56	0
60	MG	AA	1702	1/1	0.98	0.32	-	47,47,47,47	0
60	MG	DA	3341	1/1	0.95	0.48	-	55,55,55,55	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	BA	3075	1/1	0.94	0.35	-	47,47,47,47	0
60	MG	BA	3025	1/1	0.94	0.45	-	55,55,55,55	0
60	MG	DA	3124	1/1	0.94	0.44	-	53,53,53,53	0
60	MG	AA	1739	1/1	0.88	0.23	-	55,55,55,55	1
60	MG	BA	3119	1/1	0.92	0.75	-	49,49,49,49	0
60	MG	DA	3105	1/1	0.80	0.84	-	48,48,48,48	0
60	MG	DA	3130	1/1	0.95	0.25	-	56,56,56,56	0
60	MG	BA	3291	1/1	0.94	0.40	-	54,54,54,54	0
60	MG	B5	102	1/1	0.91	0.59	-	53,53,53,53	0
60	MG	CA	1630	1/1	0.95	0.29	-	47,47,47,47	0
60	MG	AA	1707	1/1	0.91	0.46	-	49,49,49,49	0
60	MG	DA	3347	1/1	0.90	0.27	-	55,55,55,55	0
60	MG	CA	1734	1/1	0.83	0.24	-	55,55,55,55	1
60	MG	DA	3008	1/1	0.90	0.36	-	52,52,52,52	0
60	MG	AA	1638	1/1	0.82	0.25	-	52,52,52,52	0
60	MG	CV	105	1/1	0.85	0.25	-	50,50,50,50	0
60	MG	CA	1606	1/1	0.84	0.32	-	58,58,58,58	0
60	MG	BA	3170	1/1	0.95	0.40	-	50,50,50,50	0
60	MG	CA	1666	1/1	0.88	0.50	-	57,57,57,57	0
60	MG	AA	1649	1/1	0.87	0.15	-	53,53,53,53	0
60	MG	DA	3319	1/1	0.64	0.49	-	55,55,55,55	0
60	MG	BA	3028	1/1	0.99	0.46	-	52,52,52,52	0
60	MG	CA	1676	1/1	0.65	0.53	-	58,58,58,58	0
60	MG	DA	3288	1/1	0.90	0.22	-	66,66,66,66	0
60	MG	CA	1717	1/1	0.80	0.42	-	52,52,52,52	0
60	MG	DA	3262	1/1	0.84	0.32	-	52,52,52,52	0
60	MG	DA	3250	1/1	0.92	0.42	-	56,56,56,56	0
60	MG	DA	3087	1/1	0.81	0.58	-	48,48,48,48	0
60	MG	DA	3007	1/1	0.95	0.72	-	53,53,53,53	0
60	MG	BA	3340	1/1	0.93	0.62	-	55,55,55,55	0
60	MG	BA	3146	1/1	0.94	0.65	-	47,47,47,47	0
60	MG	BA	3136	1/1	0.96	0.75	-	50,50,50,50	0
60	MG	DA	3260	1/1	0.70	0.51	-	59,59,59,59	0
60	MG	DA	3326	1/1	0.90	0.53	-	55,55,55,55	0
60	MG	DA	3264	1/1	0.93	0.15	-	56,56,56,56	0
60	MG	CA	1619	1/1	0.96	0.21	-	55,55,55,55	0
60	MG	BA	3230	1/1	0.88	0.76	-	54,54,54,54	0
60	MG	DA	3180	1/1	0.76	0.22	-	52,52,52,52	0
60	MG	CA	1656	1/1	0.91	0.82	-	47,47,47,47	0
60	MG	CA	1693	1/1	0.83	0.74	-	59,59,59,59	0
60	MG	CA	1623	1/1	0.97	0.38	-	48,48,48,48	0
60	MG	CA	1735	1/1	0.96	0.17	-	55,55,55,55	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	DA	3095	1/1	0.98	0.76	-	47,47,47,47	0
60	MG	BA	3029	1/1	0.91	0.37	-	55,55,55,55	0
60	MG	DA	3224	1/1	0.79	0.37	-	52,52,52,52	0
60	MG	AV	104	1/1	0.93	0.07	-	54,54,54,54	0
60	MG	DA	3240	1/1	0.24	0.88	-	55,55,55,55	1
60	MG	DX	101	1/1	0.90	0.23	-	55,55,55,55	0
60	MG	AA	1642	1/1	0.47	0.32	-	55,55,55,55	0
60	MG	BA	3002	1/1	0.89	0.30	-	67,67,67,67	0
60	MG	AA	1696	1/1	0.81	0.34	-	62,62,62,62	0
60	MG	BA	3187	1/1	0.84	0.38	-	48,48,48,48	0
60	MG	DA	3223	1/1	0.88	0.32	-	49,49,49,49	0
60	MG	DB	203	1/1	0.91	0.74	-	55,55,55,55	0
60	MG	DA	3078	1/1	0.98	0.87	-	51,51,51,51	0
60	MG	BA	3232	1/1	0.94	0.53	-	53,53,53,53	0
60	MG	CA	1714	1/1	0.96	0.44	-	64,64,64,64	0
60	MG	DA	3280	1/1	0.78	0.66	-	57,57,57,57	0
60	MG	BA	3060	1/1	0.97	0.56	-	47,47,47,47	0
60	MG	BA	3173	1/1	0.86	0.34	-	56,56,56,56	0
60	MG	CA	1723	1/1	0.94	0.10	-	55,55,55,55	0
60	MG	BA	3216	1/1	0.92	0.28	-	49,49,49,49	0
60	MG	AA	1728	1/1	0.93	0.23	-	55,55,55,55	0
60	MG	BA	3195	1/1	0.88	0.42	-	52,52,52,52	0
60	MG	BA	3179	1/1	0.76	0.37	-	59,59,59,59	0
60	MG	BA	3323	1/1	0.95	0.86	-	55,55,55,55	0
60	MG	DA	3145	1/1	0.91	0.40	-	49,49,49,49	0
60	MG	AA	1640	1/1	0.94	0.42	-	48,48,48,48	0
60	MG	AA	1602	1/1	0.92	0.39	-	52,52,52,52	0
60	MG	CA	1685	1/1	0.88	0.30	-	47,47,47,47	0
60	MG	AA	1756	1/1	0.95	0.21	-	55,55,55,55	1
60	MG	AA	1647	1/1	0.80	0.36	-	62,62,62,62	0
60	MG	CA	1628	1/1	0.96	0.33	-	56,56,56,56	0
60	MG	AV	106	1/1	0.86	0.05	-	57,57,57,57	0
60	MG	CA	1615	1/1	0.66	0.69	-	64,64,64,64	0
60	MG	DA	3064	1/1	0.95	0.40	-	56,56,56,56	0
60	MG	DA	3003	1/1	0.76	0.41	-	67,67,67,67	0
60	MG	AA	1726	1/1	0.92	0.31	-	56,56,56,56	0
60	MG	BA	3337	1/1	0.83	0.16	-	55,55,55,55	0
60	MG	CA	1690	1/1	0.90	0.17	-	59,59,59,59	0
60	MG	DA	3049	1/1	0.93	0.43	-	47,47,47,47	0
60	MG	BB	201	1/1	0.89	0.63	-	67,67,67,67	0
60	MG	CA	1663	1/1	0.77	0.24	-	51,51,51,51	0
60	MG	BA	3302	1/1	0.96	0.64	-	55,55,55,55	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	AA	1738	1/1	0.96	0.08	-	55,55,55,55	0
60	MG	DA	3303	1/1	0.92	0.73	-	55,55,55,55	0
60	MG	DA	3279	1/1	0.91	0.28	-	55,55,55,55	0
60	MG	DA	3199	1/1	0.94	0.49	-	53,53,53,53	0
60	MG	BA	3038	1/1	0.98	0.49	-	51,51,51,51	0
60	MG	DA	3040	1/1	0.89	0.34	-	68,68,68,68	0
60	MG	BA	3087	1/1	0.97	0.32	-	49,49,49,49	0
60	MG	AV	105	1/1	0.88	0.21	-	50,50,50,50	1
60	MG	BA	3207	1/1	0.88	0.53	-	60,60,60,60	0
60	MG	DA	3185	1/1	0.86	0.53	-	56,56,56,56	0
60	MG	DA	3134	1/1	0.35	0.66	-	64,64,64,64	0
60	MG	BA	3260	1/1	0.95	0.18	-	57,57,57,57	0
60	MG	DA	3094	1/1	0.96	0.45	-	51,51,51,51	0
60	MG	AA	1661	1/1	0.97	0.42	-	52,52,52,52	0
60	MG	AA	1717	1/1	0.88	0.24	-	66,66,66,66	0
60	MG	DA	3342	1/1	0.96	0.31	-	55,55,55,55	0
60	MG	CA	1711	1/1	0.90	0.14	-	55,55,55,55	0
60	MG	AA	1690	1/1	0.95	0.66	-	52,52,52,52	0
60	MG	DA	3182	1/1	0.88	0.29	-	56,56,56,56	0
60	MG	DA	3121	1/1	0.97	0.42	-	50,50,50,50	0
60	MG	BA	3157	1/1	0.99	0.13	-	53,53,53,53	0
60	MG	DA	3200	1/1	0.88	0.96	-	58,58,58,58	0
60	MG	AA	1615	1/1	0.93	0.83	-	53,53,53,53	0
60	MG	AA	1711	1/1	0.91	0.28	-	47,47,47,47	0
60	MG	BA	3273	1/1	0.88	0.47	-	58,58,58,58	0
60	MG	BA	3349	1/1	0.90	0.53	-	55,55,55,55	0
60	MG	DA	3141	1/1	0.94	0.40	-	56,56,56,56	0
60	MG	AA	1697	1/1	0.81	0.35	-	52,52,52,52	0
60	MG	DA	3335	1/1	0.90	0.44	-	55,55,55,55	0
60	MG	CA	1749	1/1	0.87	0.37	-	55,55,55,55	0
60	MG	CA	1609	1/1	0.94	0.33	-	55,55,55,55	0
60	MG	DA	3249	1/1	0.88	0.20	-	56,56,56,56	0
60	MG	BA	3080	1/1	0.84	0.68	-	52,52,52,52	0
60	MG	DA	3332	1/1	0.93	0.52	-	55,55,55,55	0
60	MG	DA	3218	1/1	0.97	0.52	-	51,51,51,51	0
60	MG	BA	3222	1/1	0.78	0.32	-	49,49,49,49	0
60	MG	CA	1617	1/1	0.90	0.27	-	51,51,51,51	0
60	MG	CA	1643	1/1	0.59	0.58	-	49,49,49,49	0
60	MG	DA	3125	1/1	0.94	0.22	-	49,49,49,49	0
60	MG	D3	101	1/1	0.94	0.48	-	58,58,58,58	0
60	MG	DA	3041	1/1	0.97	0.33	-	47,47,47,47	0
60	MG	DA	3241	1/1	0.97	0.10	-	55,55,55,55	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	CA	1660	1/1	0.83	0.20	-	58,58,58,58	0
60	MG	BU	201	1/1	0.84	0.41	-	48,48,48,48	0
60	MG	BA	3141	1/1	0.83	0.58	-	49,49,49,49	0
60	MG	BA	3144	1/1	0.93	0.43	-	49,49,49,49	0
60	MG	BA	3008	1/1	0.97	0.41	-	55,55,55,55	0
60	MG	AA	1743	1/1	0.84	0.61	-	55,55,55,55	0
60	MG	B5	101	1/1	0.98	0.37	-	49,49,49,49	0
60	MG	BA	3330	1/1	0.92	0.24	-	55,55,55,55	0
60	MG	CA	1614	1/1	0.90	0.82	-	53,53,53,53	0
60	MG	CA	1668	1/1	0.91	0.84	-	58,58,58,58	0
60	MG	BA	3240	1/1	0.96	0.45	-	58,58,58,58	1
60	MG	CA	1738	1/1	0.90	0.90	-	55,55,55,55	0
60	MG	BA	3227	1/1	0.66	0.66	-	55,55,55,55	0
60	MG	AA	1626	1/1	0.97	0.29	-	53,53,53,53	0
60	MG	DA	3235	1/1	0.88	0.28	-	49,49,49,49	0
60	MG	BA	3072	1/1	0.87	0.72	-	53,53,53,53	0
60	MG	DA	3231	1/1	0.70	0.51	-	54,54,54,54	1
60	MG	DA	3282	1/1	0.79	0.35	-	57,57,57,57	0
60	MG	BA	3115	1/1	0.96	0.59	-	50,50,50,50	0
60	MG	CA	1721	1/1	0.89	0.28	-	58,58,58,58	0
60	MG	BA	3301	1/1	0.68	0.50	-	55,55,55,55	0
60	MG	BA	3312	1/1	0.93	0.72	-	55,55,55,55	0
60	MG	AA	1737	1/1	0.82	0.69	-	55,55,55,55	0
60	MG	DA	3026	1/1	0.96	0.45	-	55,55,55,55	0
60	MG	BA	3084	1/1	0.94	0.35	-	47,47,47,47	0
60	MG	DA	3088	1/1	0.95	0.39	-	49,49,49,49	0
60	MG	CA	1641	1/1	0.77	0.37	-	55,55,55,55	0
60	MG	AA	1659	1/1	0.56	0.31	-	57,57,57,57	0
60	MG	BA	3239	1/1	0.79	0.28	-	55,55,55,55	0
60	MG	DA	3115	1/1	0.93	0.24	-	48,48,48,48	0
60	MG	CA	1644	1/1	0.81	0.14	-	57,57,57,57	0
60	MG	DA	3296	1/1	0.93	0.64	-	55,55,55,55	0
60	MG	DA	3090	1/1	0.92	0.64	-	48,48,48,48	0
60	MG	BP	201	1/1	0.97	0.22	-	49,49,49,49	0
60	MG	AA	1606	1/1	0.93	0.31	-	59,59,59,59	0
60	MG	BA	3238	1/1	0.93	0.09	-	55,55,55,55	1
60	MG	CA	1745	1/1	0.88	0.23	-	55,55,55,55	0
60	MG	DA	3004	1/1	0.95	0.40	-	61,61,61,61	0
60	MG	AA	1637	1/1	0.69	0.50	-	53,53,53,53	0
60	MG	BA	3235	1/1	0.94	0.22	-	60,60,60,60	0
60	MG	BD	302	1/1	0.92	0.62	-	47,47,47,47	0
60	MG	AA	1700	1/1	0.91	0.23	-	51,51,51,51	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	AA	1667	1/1	0.83	0.27	-	47,47,47,47	0
60	MG	CA	1647	1/1	0.81	0.20	-	62,62,62,62	0
60	MG	AA	1732	1/1	0.65	0.55	-	55,55,55,55	0
60	MG	DA	3315	1/1	0.90	0.26	-	55,55,55,55	0
60	MG	AA	1720	1/1	0.74	0.52	-	58,58,58,58	1
60	MG	BA	3186	1/1	0.97	0.87	-	51,51,51,51	0
60	MG	CA	1667	1/1	0.89	0.41	-	47,47,47,47	0
60	MG	DA	3176	1/1	0.76	0.42	-	58,58,58,58	0
60	MG	AA	1607	1/1	0.97	0.46	-	58,58,58,58	0
60	MG	BA	3343	1/1	0.92	0.55	-	55,55,55,55	0
60	MG	CA	1700	1/1	0.87	0.25	-	54,54,54,54	0
60	MG	BA	3027	1/1	0.95	0.31	-	50,50,50,50	0
60	MG	DA	3323	1/1	0.87	0.52	-	55,55,55,55	0
60	MG	BA	3234	1/1	0.80	0.80	-	52,52,52,52	0
60	MG	CL	201	1/1	0.93	0.59	-	51,51,51,51	1
60	MG	BA	3272	1/1	0.89	0.26	-	59,59,59,59	1
60	MG	CA	1683	1/1	0.87	0.26	-	47,47,47,47	0
60	MG	BA	3319	1/1	0.74	0.33	-	55,55,55,55	0
60	MG	BB	204	1/1	0.92	0.23	-	55,55,55,55	0
60	MG	BA	3331	1/1	0.95	0.21	-	55,55,55,55	0
60	MG	AA	1701	1/1	0.89	0.32	-	51,51,51,51	0
60	MG	CA	1636	1/1	0.95	0.59	-	53,53,53,53	0
60	MG	DA	3174	1/1	0.94	0.33	-	52,52,52,52	0
60	MG	AA	1676	1/1	0.86	0.41	-	58,58,58,58	0
60	MG	CA	1684	1/1	0.89	0.12	-	49,49,49,49	0
60	MG	DA	3227	1/1	0.76	0.33	-	56,56,56,56	0
60	MG	DA	3082	1/1	0.97	0.71	-	47,47,47,47	0
60	MG	CA	1673	1/1	0.88	0.50	-	52,52,52,52	1
60	MG	AA	1646	1/1	0.89	0.76	-	50,50,50,50	0
60	MG	DA	3284	1/1	0.96	0.88	-	57,57,57,57	0
60	MG	DA	3221	1/1	0.92	0.55	-	54,54,54,54	0
60	MG	AA	1630	1/1	0.92	0.67	-	51,51,51,51	0
60	MG	AA	1660	1/1	0.90	0.12	-	58,58,58,58	0
60	MG	BA	3286	1/1	0.88	0.23	-	60,60,60,60	0
60	MG	AA	1687	1/1	0.81	0.21	-	48,48,48,48	0
60	MG	DA	3228	1/1	0.87	0.36	-	55,55,55,55	0
60	MG	DA	3011	1/1	0.82	0.53	-	52,52,52,52	0
60	MG	AA	1619	1/1	0.97	0.60	-	49,49,49,49	0
60	MG	DA	3244	1/1	0.96	0.45	-	47,47,47,47	0
60	MG	DA	3213	1/1	0.84	0.32	-	55,55,55,55	0
60	MG	CA	1639	1/1	0.92	0.31	-	48,48,48,48	0
60	MG	DA	3246	1/1	0.97	0.22	-	60,60,60,60	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	DA	3351	1/1	0.77	0.67	-	55,55,55,55	0
60	MG	BA	3297	1/1	0.96	0.52	-	55,55,55,55	0
60	MG	CA	1718	1/1	0.78	0.41	-	66,66,66,66	0
60	MG	CA	1755	1/1	0.92	0.49	-	55,55,55,55	0
60	MG	DA	3337	1/1	0.74	0.26	-	55,55,55,55	0
60	MG	AA	1622	1/1	0.86	0.22	-	48,48,48,48	0
60	MG	BA	3204	1/1	0.93	0.39	-	57,57,57,57	0
60	MG	DA	3066	1/1	0.92	0.53	-	52,52,52,52	0
60	MG	AA	1740	1/1	0.93	0.38	-	55,55,55,55	0
60	MG	BA	3244	1/1	0.90	0.23	-	60,60,60,60	0
60	MG	BA	3140	1/1	0.89	0.49	-	56,56,56,56	0
60	MG	AA	1719	1/1	0.95	0.14	-	56,56,56,56	0
60	MG	CA	1709	1/1	0.69	0.36	-	65,65,65,65	0
60	MG	CA	1692	1/1	0.94	0.45	-	59,59,59,59	0
60	MG	AA	1629	1/1	0.95	0.23	-	56,56,56,56	0
60	MG	BA	3336	1/1	0.69	0.62	-	55,55,55,55	0
60	MG	DA	3188	1/1	0.84	0.40	-	48,48,48,48	0
60	MG	BA	3169	1/1	0.95	0.55	-	51,51,51,51	0
60	MG	CW	105	1/1	0.79	0.57	-	53,53,53,53	0
60	MG	BA	3329	1/1	0.89	0.36	-	55,55,55,55	1
60	MG	CA	1688	1/1	0.81	0.16	-	48,48,48,48	0
60	MG	BA	3100	1/1	0.90	0.83	-	51,51,51,51	0
60	MG	DA	3172	1/1	0.97	0.52	-	50,50,50,50	0
60	MG	DA	3031	1/1	0.92	0.72	-	47,47,47,47	0
60	MG	CA	1724	1/1	0.96	0.15	-	57,57,57,57	1
60	MG	AA	1645	1/1	0.89	0.16	-	57,57,57,57	0
60	MG	CA	1731	1/1	0.83	0.35	-	55,55,55,55	0
60	MG	AE	201	1/1	0.89	0.77	-	57,57,57,57	0
60	MG	CA	1638	1/1	0.93	0.58	-	53,53,53,53	0
60	MG	BA	3092	1/1	0.91	0.61	-	50,50,50,50	0
60	MG	BA	3171	1/1	0.93	0.15	-	58,58,58,58	0
60	MG	AA	1716	1/1	0.56	1.12	-	52,52,52,52	0
60	MG	BA	3003	1/1	0.94	0.31	-	61,61,61,61	0
60	MG	BA	3311	1/1	0.91	0.39	-	55,55,55,55	0
60	MG	BA	3251	1/1	0.85	0.51	-	61,61,61,61	0
60	MG	DA	3338	1/1	0.91	0.73	-	55,55,55,55	0
60	MG	AA	1662	1/1	0.91	0.14	-	52,52,52,52	0
60	MG	AA	1729	1/1	0.84	0.24	-	55,55,55,55	0
60	MG	DA	3154	1/1	0.96	0.25	-	53,53,53,53	0
60	MG	DA	3171	1/1	0.97	0.70	-	51,51,51,51	0
60	MG	AA	1755	1/1	0.86	0.64	-	55,55,55,55	0
60	MG	BA	3122	1/1	0.83	0.41	-	64,64,64,64	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	BA	3217	1/1	0.89	0.70	-	51,51,51,51	0
60	MG	DA	3328	1/1	0.65	0.36	-	55,55,55,55	1
60	MG	DA	3346	1/1	0.93	0.82	-	55,55,55,55	0
60	MG	CA	1648	1/1	0.81	0.30	-	53,53,53,53	1
60	MG	CA	1657	1/1	0.96	0.31	-	54,54,54,54	0
60	MG	CA	1753	1/1	0.81	0.96	-	55,55,55,55	1
60	MG	AA	1648	1/1	0.70	0.13	-	62,62,62,62	0
60	MG	CA	1618	1/1	0.93	0.32	-	49,49,49,49	0
60	MG	DA	3314	1/1	0.88	0.26	-	55,55,55,55	1
60	MG	DA	3300	1/1	0.92	0.45	-	55,55,55,55	0
60	MG	DA	3032	1/1	0.94	0.33	-	50,50,50,50	0
60	MG	BA	3332	1/1	0.92	0.10	-	55,55,55,55	0
60	MG	BA	3274	1/1	0.85	0.68	-	63,63,63,63	0
60	MG	BA	3258	1/1	0.83	0.33	-	58,58,58,58	0
60	MG	DA	3331	1/1	0.89	0.08	-	55,55,55,55	1
60	MG	BA	3247	1/1	0.87	0.20	-	59,59,59,59	0
60	MG	AA	1698	1/1	0.76	0.34	-	53,53,53,53	1
60	MG	AA	1750	1/1	0.91	0.24	-	55,55,55,55	0
60	MG	CV	102	1/1	0.94	0.34	-	54,54,54,54	0
60	MG	AA	1651	1/1	0.87	0.74	-	54,54,54,54	0
60	MG	DA	3047	1/1	0.89	0.35	-	47,47,47,47	0
60	MG	BA	3268	1/1	0.94	0.71	-	59,59,59,59	0
60	MG	BA	3036	1/1	0.92	0.24	-	53,53,53,53	0
60	MG	CA	1646	1/1	0.90	0.41	-	62,62,62,62	0
60	MG	DA	3037	1/1	0.88	0.37	-	53,53,53,53	0
60	MG	CW	101	1/1	0.69	0.53	-	56,56,56,56	1
60	MG	DA	3142	1/1	0.72	0.54	-	49,49,49,49	0
60	MG	DA	3028	1/1	0.97	0.39	-	50,50,50,50	0
60	MG	BA	3200	1/1	0.83	0.26	-	60,60,60,60	0
60	MG	DA	3009	1/1	0.95	0.55	-	55,55,55,55	0
60	MG	CA	1732	1/1	0.93	0.20	-	55,55,55,55	0
60	MG	DA	3086	1/1	0.95	0.14	-	47,47,47,47	0
60	MG	AA	1746	1/1	0.82	0.28	-	55,55,55,55	1
60	MG	BA	3117	1/1	0.89	0.41	-	52,52,52,52	0
60	MG	DA	3023	1/1	0.98	0.80	-	47,47,47,47	0
60	MG	DA	3343	1/1	0.84	0.50	-	55,55,55,55	0
60	MG	BA	3265	1/1	0.85	0.46	-	47,47,47,47	0
60	MG	DA	3324	1/1	0.93	0.51	-	55,55,55,55	0
60	MG	BA	3110	1/1	0.98	0.43	-	49,49,49,49	0
60	MG	DA	3133	1/1	0.83	0.33	-	57,57,57,57	0
60	MG	DA	3257	1/1	0.91	0.66	-	55,55,55,55	0
60	MG	D5	102	1/1	0.95	0.35	-	53,53,53,53	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	BA	3290	1/1	0.91	0.37	-	57,57,57,57	0
60	MG	AA	1668	1/1	0.74	0.62	-	58,58,58,58	0
60	MG	AA	1603	1/1	0.91	0.23	-	57,57,57,57	0
60	MG	BA	3304	1/1	0.92	0.64	-	55,55,55,55	0
60	MG	BA	3194	1/1	0.89	0.27	-	53,53,53,53	0
60	MG	BA	3006	1/1	0.96	0.83	-	53,53,53,53	0
60	MG	BA	3181	1/1	0.71	0.25	-	53,53,53,53	0
60	MG	BA	3057	1/1	0.89	0.47	-	47,47,47,47	0
60	MG	AA	1677	1/1	0.84	0.31	-	55,55,55,55	1
60	MG	BA	3156	1/1	0.95	0.50	-	48,48,48,48	0
60	MG	DA	3112	1/1	0.92	0.32	-	52,52,52,52	0
60	MG	DA	3193	1/1	0.58	0.41	-	65,65,65,65	0
60	MG	AA	1664	1/1	0.92	0.32	-	60,60,60,60	0
60	MG	AV	102	1/1	0.95	0.28	-	54,54,54,54	0
60	MG	CA	1742	1/1	0.94	0.70	-	55,55,55,55	0
60	MG	DA	3195	1/1	0.97	0.23	-	53,53,53,53	0
60	MG	BA	3309	1/1	0.77	0.23	-	55,55,55,55	0
60	MG	BA	3245	1/1	0.91	0.38	-	53,53,53,53	0
60	MG	DA	3128	1/1	0.93	0.30	-	56,56,56,56	0
60	MG	BA	3308	1/1	0.98	0.50	-	55,55,55,55	0
60	MG	BA	3022	1/1	0.98	1.00	-	47,47,47,47	0
60	MG	DA	3322	1/1	0.95	0.76	-	55,55,55,55	0
60	MG	BA	3353	1/1	0.94	0.51	-	55,55,55,55	0
60	MG	DA	3019	1/1	0.95	0.59	-	54,54,54,54	0
60	MG	BA	3256	1/1	0.96	0.67	-	55,55,55,55	0
60	MG	CA	1744	1/1	0.82	0.44	-	55,55,55,55	0
60	MG	CW	103	1/1	0.87	0.44	-	54,54,54,54	1
60	MG	BA	3338	1/1	0.68	0.32	-	55,55,55,55	0
60	MG	DA	3294	1/1	0.67	0.52	-	49,49,49,49	1
60	MG	BA	3104	1/1	0.91	0.71	-	48,48,48,48	0
60	MG	BA	3189	1/1	0.81	0.37	-	59,59,59,59	0
60	MG	DA	3113	1/1	0.93	0.31	-	48,48,48,48	0
60	MG	CA	1659	1/1	0.83	0.21	-	57,57,57,57	0
60	MG	BA	3211	1/1	0.93	0.26	-	59,59,59,59	1
60	MG	DA	3340	1/1	0.98	0.35	-	55,55,55,55	0
60	MG	CA	1705	1/1	0.78	0.45	-	49,49,49,49	1
60	MG	CA	1681	1/1	0.72	0.62	-	66,66,66,66	0
60	MG	BA	3324	1/1	0.82	0.38	-	55,55,55,55	0
60	MG	BA	3208	1/1	0.91	0.41	-	51,51,51,51	0
60	MG	AA	1753	1/1	0.90	0.48	-	55,55,55,55	1
60	MG	CA	1699	1/1	0.95	0.17	-	53,53,53,53	1
60	MG	DA	3029	1/1	0.98	0.29	-	52,52,52,52	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	CA	1687	1/1	0.64	0.47	-	58,58,58,58	0
60	MG	DA	3219	1/1	0.77	0.38	-	66,66,66,66	0
60	MG	DA	3045	1/1	0.91	0.42	-	56,56,56,56	0
60	MG	DA	3266	1/1	0.93	0.51	-	47,47,47,47	0
60	MG	BA	3126	1/1	0.82	0.30	-	52,52,52,52	0
60	MG	CA	1654	1/1	0.90	0.73	-	57,57,57,57	0
60	MG	BA	3335	1/1	0.88	0.53	-	55,55,55,55	0
60	MG	CA	1601	1/1	0.93	0.27	-	56,56,56,56	0
60	MG	CV	103	1/1	0.60	0.27	-	54,54,54,54	0
60	MG	CA	1702	1/1	0.91	0.35	-	51,51,51,51	0
60	MG	BA	3333	1/1	0.92	0.72	-	55,55,55,55	0
60	MG	BA	3253	1/1	0.82	0.49	-	54,54,54,54	0
60	MG	BA	3241	1/1	0.79	0.28	-	61,61,61,61	1
60	MG	BA	3190	1/1	0.93	0.47	-	54,54,54,54	0
60	MG	BA	3078	1/1	0.92	0.64	-	56,56,56,56	0
60	MG	BA	3133	1/1	0.80	0.42	-	64,64,64,64	0
60	MG	BA	3176	1/1	0.95	0.57	-	48,48,48,48	0
60	MG	DA	3058	1/1	0.98	0.65	-	47,47,47,47	0
60	MG	CW	104	1/1	0.85	0.37	-	56,56,56,56	0
60	MG	CA	1640	1/1	0.98	0.76	-	47,47,47,47	0
60	MG	DA	3169	1/1	0.93	0.41	-	47,47,47,47	0
60	MG	CA	1713	1/1	0.90	0.39	-	54,54,54,54	0
60	MG	DA	3254	1/1	0.91	0.25	-	54,54,54,54	0
60	MG	BA	3283	1/1	0.90	0.33	-	65,65,65,65	0
60	MG	BA	3131	1/1	0.85	0.40	-	59,59,59,59	0
60	MG	CA	1661	1/1	0.87	0.58	-	52,52,52,52	0
60	MG	DA	3313	1/1	0.94	0.75	-	55,55,55,55	0
60	MG	BA	3121	1/1	0.97	0.25	-	50,50,50,50	0
60	MG	CA	1664	1/1	0.88	0.45	-	60,60,60,60	0
60	MG	CA	1613	1/1	0.68	0.22	-	52,52,52,52	0
60	MG	BA	3059	1/1	0.99	0.31	-	48,48,48,48	0
60	MG	CA	1621	1/1	0.83	0.20	-	48,48,48,48	0
60	MG	DA	3119	1/1	0.98	0.52	-	49,49,49,49	0
60	MG	AA	1618	1/1	0.92	0.20	-	51,51,51,51	1
60	MG	DH	201	1/1	0.94	0.13	-	50,50,50,50	0
60	MG	CV	106	1/1	0.77	0.18	-	57,57,57,57	1
60	MG	AA	1609	1/1	0.98	0.24	-	52,52,52,52	0
60	MG	CA	1611	1/1	0.95	0.25	-	52,52,52,52	0
60	MG	BA	3167	1/1	0.89	0.28	-	53,53,53,53	0
60	MG	BA	3197	1/1	0.97	0.43	-	58,58,58,58	0
60	MG	BA	3111	1/1	0.92	0.29	-	52,52,52,52	0
60	MG	CA	1634	1/1	0.92	0.17	-	47,47,47,47	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	BA	3295	1/1	0.95	0.16	-	49,49,49,49	0
60	MG	DA	3179	1/1	0.94	0.91	-	47,47,47,47	0
60	MG	BA	3041	1/1	0.98	0.63	-	47,47,47,47	0
60	MG	BA	3127	1/1	0.92	0.24	-	56,56,56,56	0
60	MG	DA	3283	1/1	0.77	0.49	-	65,65,65,65	0
60	MG	BA	3223	1/1	0.95	0.37	-	52,52,52,52	0
60	MG	DA	3252	1/1	0.93	0.47	-	61,61,61,61	1
60	MG	BA	3161	1/1	0.71	0.30	-	47,47,47,47	0
60	MG	AA	1731	1/1	0.88	0.24	-	55,55,55,55	0
60	MG	DA	3291	1/1	0.97	0.68	-	54,54,54,54	0
60	MG	AA	1706	1/1	0.91	0.24	-	51,51,51,51	0
60	MG	DA	3056	1/1	0.96	0.43	-	47,47,47,47	0
60	MG	CV	104	1/1	0.93	0.08	-	54,54,54,54	0
60	MG	BA	3001	1/1	0.89	0.30	-	54,54,54,54	0
60	MG	DA	3334	1/1	0.76	0.27	-	55,55,55,55	0
60	MG	BA	3255	1/1	0.98	0.28	-	55,55,55,55	0
60	MG	DA	3222	1/1	0.82	0.70	-	53,53,53,53	0
60	MG	DA	3233	1/1	0.94	0.65	-	53,53,53,53	0
60	MG	BA	3139	1/1	0.82	0.45	-	50,50,50,50	0
60	MG	CA	1715	1/1	0.89	0.64	-	59,59,59,59	0
60	MG	AA	1733	1/1	0.80	0.26	-	55,55,55,55	0
60	MG	DA	3261	1/1	0.94	0.23	-	57,57,57,57	0
60	MG	DA	3175	1/1	0.97	0.45	-	56,56,56,56	0
60	MG	BA	3097	1/1	0.91	0.34	-	47,47,47,47	0
60	MG	AA	1703	1/1	0.93	0.26	-	62,62,62,62	0
60	MG	DA	3093	1/1	0.88	0.73	-	50,50,50,50	0
60	MG	AA	1624	1/1	0.95	0.35	-	48,48,48,48	0
60	MG	BA	3118	1/1	0.94	0.53	-	49,49,49,49	0
60	MG	AA	1693	1/1	0.80	0.49	-	61,61,61,61	0
60	MG	BA	3030	1/1	0.85	0.62	-	47,47,47,47	0
60	MG	CA	1627	1/1	0.87	0.21	-	70,70,70,70	0
60	MG	AA	1704	1/1	0.83	0.26	-	49,49,49,49	1
60	MG	DA	3117	1/1	0.94	0.28	-	47,47,47,47	0
60	MG	DA	3098	1/1	0.91	0.27	-	47,47,47,47	0
60	MG	AA	1757	1/1	0.94	0.35	-	55,55,55,55	0
60	MG	BA	3344	1/1	0.88	0.89	-	55,55,55,55	0
60	MG	BA	3259	1/1	0.85	0.27	-	59,59,59,59	0
60	MG	CA	1739	1/1	0.89	0.15	-	55,55,55,55	0
60	MG	BA	3017	1/1	0.97	0.47	-	52,52,52,52	0
60	MG	BA	3275	1/1	0.89	0.39	-	59,59,59,59	0
60	MG	BA	3095	1/1	0.91	0.60	-	60,60,60,60	0
60	MG	BA	3293	1/1	0.98	0.47	-	55,55,55,55	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	AA	1601	1/1	0.91	0.20	-	56,56,56,56	0
60	MG	DA	3001	1/1	0.85	0.33	-	57,57,57,57	0
60	MG	DA	3318	1/1	0.83	0.23	-	55,55,55,55	0
60	MG	DA	3292	1/1	0.95	0.55	-	55,55,55,55	0
60	MG	AA	1631	1/1	0.97	0.23	-	47,47,47,47	0
60	MG	AA	1709	1/1	0.87	0.52	-	50,50,50,50	0
60	MG	CA	1691	1/1	0.87	0.69	-	52,52,52,52	0
60	MG	DA	3339	1/1	0.96	0.39	-	55,55,55,55	0
60	MG	BA	3039	1/1	0.87	0.25	-	68,68,68,68	0
60	MG	BA	3341	1/1	0.76	0.59	-	55,55,55,55	0
60	MG	DA	3289	1/1	0.98	0.45	-	54,54,54,54	0
60	MG	CA	1729	1/1	0.71	0.31	-	55,55,55,55	1
60	MG	BA	3288	1/1	0.95	0.22	-	66,66,66,66	0
60	MG	BA	3325	1/1	0.88	0.35	-	55,55,55,55	0
60	MG	BA	3289	1/1	0.94	0.44	-	54,54,54,54	0
60	MG	BA	3298	1/1	0.95	0.44	-	55,55,55,55	0
60	MG	DC	301	1/1	0.44	0.63	-	52,52,52,52	1
60	MG	BA	3137	1/1	0.84	0.57	-	52,52,52,52	0
60	MG	CA	1672	1/1	0.95	0.43	-	53,53,53,53	0
60	MG	DA	3126	1/1	0.96	0.79	-	47,47,47,47	0
60	MG	BA	3254	1/1	0.86	0.63	-	60,60,60,60	0
60	MG	AM	201	1/1	0.71	0.59	-	47,47,47,47	0
60	MG	CA	1662	1/1	0.92	0.29	-	52,52,52,52	0
60	MG	BA	3053	1/1	0.95	0.21	-	51,51,51,51	0
60	MG	BA	3180	1/1	0.86	0.40	-	56,56,56,56	0
60	MG	BA	3125	1/1	0.97	0.69	-	47,47,47,47	0
60	MG	BS	201	1/1	0.76	0.50	-	55,55,55,55	0
60	MG	AA	1724	1/1	0.95	0.51	-	59,59,59,59	0
60	MG	DA	3110	1/1	0.95	0.30	-	48,48,48,48	0
60	MG	DA	3297	1/1	0.94	0.45	-	55,55,55,55	0
60	MG	CA	1651	1/1	0.68	0.42	-	47,47,47,47	0
60	MG	AA	1653	1/1	0.77	0.89	-	60,60,60,60	0
60	MG	BA	3065	1/1	0.94	0.24	-	52,52,52,52	0
60	MG	BA	3073	1/1	0.95	0.42	-	52,52,52,52	0
60	MG	CA	1710	1/1	0.84	0.31	-	50,50,50,50	0
60	MG	CA	1629	1/1	0.81	0.45	-	51,51,51,51	0
60	MG	DA	3309	1/1	0.81	0.70	-	55,55,55,55	1
60	MG	AA	1616	1/1	0.57	0.55	-	64,64,64,64	0
60	MG	BA	3199	1/1	0.67	0.69	-	58,58,58,58	0
60	MG	BA	3284	1/1	0.86	0.68	-	57,57,57,57	0
60	MG	CA	1679	1/1	0.78	0.39	-	53,53,53,53	1
60	MG	DA	3290	1/1	0.89	0.44	-	57,57,57,57	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	DA	3190	1/1	0.79	0.27	-	59,59,59,59	0
60	MG	BA	3231	1/1	0.90	0.37	-	51,51,51,51	0
60	MG	AA	1639	1/1	0.90	0.22	-	53,53,53,53	0
60	MG	BA	3328	1/1	0.73	0.60	-	55,55,55,55	0
60	MG	BA	3153	1/1	0.85	0.43	-	53,53,53,53	0
60	MG	BA	3052	1/1	0.96	0.51	-	47,47,47,47	0
60	MG	AA	1663	1/1	0.95	0.28	-	51,51,51,51	0
60	MG	DA	3232	1/1	0.91	0.18	-	51,51,51,51	0
60	MG	AA	1614	1/1	0.97	0.09	-	52,52,52,52	0
60	MG	BA	3094	1/1	0.90	0.60	-	47,47,47,47	0
60	MG	AA	1730	1/1	0.74	0.44	-	55,55,55,55	0
60	MG	AW	105	1/1	0.86	0.14	-	53,53,53,53	0
60	MG	AA	1692	1/1	0.74	0.71	-	59,59,59,59	0
60	MG	DA	3243	1/1	0.97	0.14	-	61,61,61,61	1
60	MG	BA	3281	1/1	0.93	0.41	-	57,57,57,57	0
60	MG	BA	3016	1/1	0.94	0.88	-	47,47,47,47	0
60	MG	BH	201	1/1	0.95	0.13	-	50,50,50,50	0
60	MG	DA	3329	1/1	0.91	0.29	-	55,55,55,55	0
60	MG	CA	1665	1/1	0.86	0.46	-	50,50,50,50	0
60	MG	DA	3321	1/1	0.89	0.22	-	55,55,55,55	0
60	MG	AA	1641	1/1	0.91	0.40	-	47,47,47,47	0
60	MG	BA	3317	1/1	0.96	0.71	-	55,55,55,55	0
60	MG	DF	302	1/1	0.87	0.24	-	53,53,53,53	0
60	MG	DA	3217	1/1	0.93	0.16	-	49,49,49,49	0
60	MG	CA	1743	1/1	0.93	0.26	-	55,55,55,55	0
60	MG	DA	3268	1/1	0.94	0.87	-	59,59,59,59	0
60	MG	D7	101	1/1	0.88	0.41	-	54,54,54,54	0
60	MG	DA	3333	1/1	0.77	0.40	-	55,55,55,55	0
60	MG	DA	3189	1/1	0.96	0.16	-	57,57,57,57	0
60	MG	CA	1655	1/1	0.69	0.70	-	52,52,52,52	0
60	MG	BA	3031	1/1	0.97	0.28	-	50,50,50,50	0
60	MG	CA	1730	1/1	0.73	0.35	-	55,55,55,55	0
60	MG	BA	3242	1/1	0.94	0.38	-	47,47,47,47	0
60	MG	CA	1652	1/1	0.82	0.93	-	60,60,60,60	0
60	MG	AA	1752	1/1	0.92	0.19	-	55,55,55,55	0
60	MG	AA	1708	1/1	0.84	0.31	-	65,65,65,65	0
60	MG	BA	3350	1/1	0.90	0.33	-	55,55,55,55	0
60	MG	AA	1715	1/1	0.90	0.23	-	55,55,55,55	0
60	MG	AA	1713	1/1	0.87	0.16	-	64,64,64,64	0
60	MG	DA	3270	1/1	0.95	0.63	-	67,67,67,67	0
60	MG	DA	3251	1/1	0.91	0.19	-	52,52,52,52	0
60	MG	AA	1727	1/1	0.85	0.61	-	55,55,55,55	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	BA	3193	1/1	0.95	0.30	-	53,53,53,53	0
60	MG	DA	3211	1/1	0.95	0.50	-	57,57,57,57	0
60	MG	CA	1747	1/1	0.86	0.34	-	55,55,55,55	1
60	MG	AA	1686	1/1	0.81	0.44	-	58,58,58,58	1
60	MG	BA	3154	1/1	0.94	0.36	-	48,48,48,48	0
60	MG	CA	1694	1/1	0.88	0.47	-	61,61,61,61	0
60	MG	CA	1733	1/1	0.75	0.54	-	55,55,55,55	0
60	MG	DA	3277	1/1	0.98	0.77	-	57,57,57,57	0
60	MG	BA	3327	1/1	0.89	0.50	-	55,55,55,55	0
60	MG	BB	203	1/1	0.92	0.65	-	55,55,55,55	0
60	MG	DA	3330	1/1	0.79	0.21	-	55,55,55,55	0
60	MG	DA	3060	1/1	0.97	0.49	-	48,48,48,48	0
60	MG	BA	3292	1/1	0.84	0.67	-	55,55,55,55	0
60	MG	CA	1708	1/1	0.84	0.25	-	49,49,49,49	0
60	MG	DB	201	1/1	0.76	0.86	-	67,67,67,67	0
60	MG	AA	1684	1/1	0.87	0.17	-	49,49,49,49	0
60	MG	BA	3174	1/1	0.90	0.36	-	58,58,58,58	0
60	MG	BA	3089	1/1	0.97	0.56	-	48,48,48,48	0
60	MG	B3	101	1/1	0.96	0.59	-	58,58,58,58	0
60	MG	AA	1680	1/1	0.96	0.40	-	49,49,49,49	0
60	MG	DA	3236	1/1	0.97	0.88	-	52,52,52,52	0
60	MG	DA	3137	1/1	0.97	0.63	-	50,50,50,50	0
60	MG	DA	3276	1/1	0.92	0.77	-	58,58,58,58	0
60	MG	BA	3093	1/1	0.97	0.41	-	51,51,51,51	0
60	MG	BA	3150	1/1	0.90	0.48	-	51,51,51,51	0
60	MG	DA	3204	1/1	0.96	0.31	-	52,52,52,52	0
60	MG	DA	3302	1/1	0.83	0.52	-	55,55,55,55	0
60	MG	CA	1720	1/1	0.78	0.15	-	56,56,56,56	0
60	MG	CA	1602	1/1	0.92	0.25	-	52,52,52,52	0
60	MG	DA	3030	1/1	0.86	0.48	-	55,55,55,55	0
60	MG	DA	3242	1/1	0.88	0.21	-	58,58,58,58	1
60	MG	DA	3177	1/1	0.46	0.55	-	49,49,49,49	0
60	MG	BA	3143	1/1	0.84	0.30	-	57,57,57,57	0
60	MG	CA	1716	1/1	0.80	0.28	-	55,55,55,55	0
60	MG	DA	3164	1/1	0.95	0.69	-	53,53,53,53	0
60	MG	DA	3293	1/1	0.88	0.23	-	52,52,52,52	0
60	MG	DA	3092	1/1	0.86	0.45	-	51,51,51,51	1
60	MG	DA	3285	1/1	0.83	0.25	-	55,55,55,55	0
60	MG	BA	3191	1/1	0.94	0.18	-	61,61,61,61	0
60	MG	BA	3210	1/1	0.95	0.39	-	57,57,57,57	0
60	MG	DA	3132	1/1	0.89	0.29	-	59,59,59,59	0
60	MG	AA	1736	1/1	0.88	0.26	-	55,55,55,55	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	BA	3198	1/1	0.96	0.67	-	53,53,53,53	0
60	MG	DA	3212	1/1	0.95	0.21	-	59,59,59,59	0
60	MG	DA	3158	1/1	0.87	0.48	-	53,53,53,53	0
60	MG	DA	3140	1/1	0.90	0.39	-	50,50,50,50	1
60	MG	DA	3101	1/1	0.95	0.50	-	51,51,51,51	0
60	MG	DA	3275	1/1	0.90	0.68	-	59,59,59,59	0
60	MG	DA	3349	1/1	0.79	0.52	-	55,55,55,55	0
60	MG	CA	1608	1/1	0.98	0.41	-	52,52,52,52	0
60	MG	CA	1704	1/1	0.97	0.64	-	62,62,62,62	0
60	MG	CA	1740	1/1	0.79	0.33	-	55,55,55,55	0
60	MG	BA	3326	1/1	0.91	0.79	-	55,55,55,55	0
60	MG	BA	3048	1/1	0.96	0.59	-	47,47,47,47	0
60	MG	DA	3216	1/1	0.88	0.55	-	60,60,60,60	0
60	MG	DA	3191	1/1	0.85	0.29	-	54,54,54,54	0
60	MG	BA	3215	1/1	0.92	0.74	-	60,60,60,60	0
60	MG	CA	1728	1/1	0.97	0.41	-	55,55,55,55	0
60	MG	AA	1705	1/1	0.79	0.20	-	51,51,51,51	0
60	MG	BA	3220	1/1	0.88	0.63	-	54,54,54,54	0
60	MG	DA	3310	1/1	0.94	0.21	-	55,55,55,55	0
60	MG	AA	1665	1/1	0.94	0.77	-	50,50,50,50	0
60	MG	DA	3311	1/1	0.96	0.65	-	55,55,55,55	0
60	MG	DA	3230	1/1	0.90	0.10	-	49,49,49,49	0
60	MG	DA	3352	1/1	0.79	0.55	-	55,55,55,55	0
60	MG	DA	3183	1/1	0.69	0.24	-	53,53,53,53	0
60	MG	BA	3162	1/1	0.91	0.84	-	50,50,50,50	0
60	MG	DA	3336	1/1	0.84	0.26	-	55,55,55,55	1
60	MG	AA	1695	1/1	0.84	0.34	-	62,62,62,62	0
60	MG	DA	3353	1/1	0.86	0.66	-	55,55,55,55	0
60	MG	AA	1712	1/1	0.85	0.41	-	54,54,54,54	0
60	MG	BA	3132	1/1	0.89	0.31	-	57,57,57,57	0
60	MG	DA	3051	1/1	0.97	0.18	-	47,47,47,47	0
60	MG	BA	3334	1/1	0.92	0.30	-	55,55,55,55	0
60	MG	DA	3350	1/1	0.94	0.44	-	55,55,55,55	0
60	MG	CA	1698	1/1	0.91	0.32	-	52,52,52,52	0
60	MG	BA	3278	1/1	0.97	0.30	-	51,51,51,51	0
60	MG	BA	3218	1/1	0.94	0.58	-	66,66,66,66	0
60	MG	CA	1741	1/1	0.92	0.53	-	55,55,55,55	0
60	MG	AA	1699	1/1	0.72	0.46	-	54,54,54,54	1
60	MG	CA	1725	1/1	0.93	0.32	-	59,59,59,59	0
60	MG	CA	1726	1/1	0.87	0.82	-	54,54,54,54	0
60	MG	DA	3150	1/1	0.99	0.61	-	54,54,54,54	0
60	MG	DA	3122	1/1	0.73	0.44	-	50,50,50,50	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	AA	1744	1/1	0.88	0.28	-	55,55,55,55	0
60	MG	DA	3210	1/1	0.87	0.53	-	66,66,66,66	0
60	MG	BA	3148	1/1	0.91	0.17	-	47,47,47,47	0
60	MG	DA	3118	1/1	0.86	0.42	-	52,52,52,52	0
60	MG	BA	3270	1/1	0.95	0.72	-	67,67,67,67	0
60	MG	DA	3237	1/1	0.90	0.76	-	60,60,60,60	0
60	MG	BA	3315	1/1	0.85	0.40	-	55,55,55,55	1
60	MG	DA	3018	1/1	0.92	0.45	-	52,52,52,52	0
60	MG	CA	1751	1/1	0.85	0.28	-	55,55,55,55	0
60	MG	DA	3076	1/1	0.94	0.36	-	47,47,47,47	0
60	MG	BA	3077	1/1	0.92	0.51	-	51,51,51,51	0
60	MG	DA	3325	1/1	0.89	0.90	-	55,55,55,55	0
60	MG	AA	1681	1/1	0.88	0.31	-	66,66,66,66	0
60	MG	BA	3352	1/1	0.95	0.35	-	55,55,55,55	0
60	MG	D5	101	1/1	0.95	0.16	-	49,49,49,49	0
60	MG	BA	3091	1/1	0.78	0.39	-	51,51,51,51	0
60	MG	DA	3194	1/1	0.91	0.50	-	53,53,53,53	0
60	MG	CA	1677	1/1	0.67	0.25	-	55,55,55,55	1
60	MG	DA	3138	1/1	0.85	0.48	-	52,52,52,52	0
60	MG	DA	3111	1/1	0.92	0.26	-	49,49,49,49	0
60	MG	AV	107	1/1	0.55	0.61	-	54,54,54,54	1
60	MG	AW	101	1/1	0.80	0.68	-	56,56,56,56	1
60	MG	BA	3310	1/1	0.91	0.22	-	55,55,55,55	0
60	MG	BA	3221	1/1	0.94	0.67	-	53,53,53,53	0
60	MG	BA	3285	1/1	0.88	0.25	-	55,55,55,55	0
60	MG	DA	3198	1/1	0.99	0.51	-	58,58,58,58	0
60	MG	CA	1701	1/1	0.96	0.42	-	51,51,51,51	0
60	MG	DQ	201	1/1	0.92	0.74	-	55,55,55,55	0
60	MG	CA	1697	1/1	0.93	0.16	-	62,62,62,62	0
60	MG	BA	3178	1/1	0.87	0.29	-	52,52,52,52	0
60	MG	BA	3124	1/1	0.90	0.29	-	49,49,49,49	0
60	MG	BA	3229	1/1	0.90	0.16	-	49,49,49,49	0
60	MG	DA	3272	1/1	0.82	0.37	-	59,59,59,59	1
60	MG	AA	1643	1/1	0.87	0.17	-	56,56,56,56	0
60	MG	DA	3153	1/1	0.93	0.12	-	50,50,50,50	0
60	MG	BA	3134	1/1	0.89	0.27	-	54,54,54,54	0
60	MG	DA	3042	1/1	0.96	0.79	-	47,47,47,47	0
60	MG	BA	3276	1/1	0.88	0.49	-	58,58,58,58	0
60	MG	DA	3017	1/1	0.92	0.67	-	47,47,47,47	0
60	MG	BB	202	1/1	0.96	0.42	-	55,55,55,55	0
60	MG	BA	3314	1/1	0.86	0.34	-	55,55,55,55	0
60	MG	DA	3147	1/1	0.96	0.44	-	47,47,47,47	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	DA	3155	1/1	0.99	0.42	-	48,48,48,48	0
60	MG	BA	3063	1/1	0.99	0.26	-	56,56,56,56	0
60	MG	CA	1642	1/1	0.92	0.60	-	56,56,56,56	0
60	MG	CA	1706	1/1	0.92	0.19	-	51,51,51,51	0
60	MG	DA	3178	1/1	0.89	0.50	-	48,48,48,48	0
60	MG	DA	3301	1/1	0.87	0.62	-	55,55,55,55	0
60	MG	CA	1632	1/1	0.84	0.11	-	55,55,55,55	0
60	MG	CA	1737	1/1	0.89	0.40	-	55,55,55,55	1
60	MG	BA	3151	1/1	0.87	0.28	-	47,47,47,47	0
60	MG	BA	3209	1/1	0.86	0.48	-	66,66,66,66	0
60	MG	DA	3239	1/1	0.77	0.20	-	67,67,67,67	1
60	MG	DA	3168	1/1	0.96	0.19	-	53,53,53,53	0
60	MG	DA	3263	1/1	0.84	0.44	-	63,63,63,63	0
60	MG	AA	1688	1/1	0.80	0.45	-	63,63,63,63	1
60	MG	CA	1650	1/1	0.95	0.67	-	54,54,54,54	0
60	MG	DA	3144	1/1	0.65	0.30	-	57,57,57,57	0
60	MG	AA	1670	1/1	0.87	0.32	-	69,69,69,69	0
60	MG	BA	3018	1/1	0.97	0.54	-	54,54,54,54	0
60	MG	AA	1689	1/1	0.60	0.80	-	59,59,59,59	1
60	MG	BQ	201	1/1	0.97	0.78	-	55,55,55,55	0
60	MG	CV	107	1/1	0.83	0.30	-	54,54,54,54	0
60	MG	DA	3209	1/1	0.88	0.47	-	51,51,51,51	0
60	MG	DA	3307	1/1	0.94	0.26	-	55,55,55,55	0
60	MG	DA	3248	1/1	0.98	0.15	-	59,59,59,59	1
60	MG	CA	1689	1/1	0.96	0.24	-	63,63,63,63	1
60	MG	BA	3168	1/1	0.92	0.36	-	47,47,47,47	0
60	MG	DA	3192	1/1	0.96	0.19	-	61,61,61,61	1
60	MG	B7	102	1/1	0.90	0.35	-	54,54,54,54	0
60	MG	BA	3055	1/1	0.96	0.66	-	47,47,47,47	0
60	MG	CA	1757	1/1	0.92	0.20	-	55,55,55,55	0
60	MG	BA	3172	1/1	0.93	0.30	-	52,52,52,52	0
60	MG	BA	3129	1/1	0.82	0.34	-	56,56,56,56	0
60	MG	BA	3320	1/1	0.78	0.44	-	55,55,55,55	0
60	MG	DA	3202	1/1	0.63	0.59	-	52,52,52,52	1
60	MG	AA	1723	1/1	0.89	0.36	-	57,57,57,57	0
60	MG	BA	3203	1/1	0.97	0.39	-	52,52,52,52	0
60	MG	CA	1604	1/1	0.96	0.20	-	50,50,50,50	0
60	MG	AW	102	1/1	0.88	0.11	-	60,60,60,60	1
60	MG	DA	3187	1/1	0.98	0.55	-	51,51,51,51	0
60	MG	BA	3345	1/1	0.91	0.24	-	55,55,55,55	0
60	MG	BA	3261	1/1	0.95	0.55	-	52,52,52,52	0
60	MG	DA	3181	1/1	0.73	0.63	-	59,59,59,59	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
60	MG	DA	3208	1/1	0.96	0.24	-	60,60,60,60	0
60	MG	DA	3120	1/1	0.93	0.91	-	49,49,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.