



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 03:44 AM UTC

PDB ID : 8CQW / pdb_00008cqw
Title : Crystal structure of the Candida albicans 80S ribosome in complex with Hygromycin B
Authors : Kolosova, O.; Zgadzay, Y.; Yusupov, M.
Deposited on : 2023-03-07
Resolution : 3.05 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

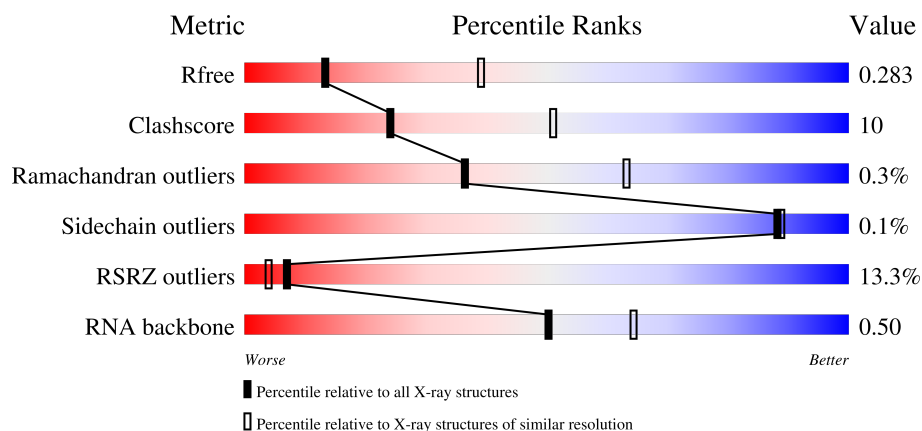
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)
RNA backbone	3983	1079 (3.30-2.82)

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

Mol	Chain	Length	Quality of chain
1	1	3359	2% 47% 41% 8% .
1	AS	3359	3% 48% 38% 9% .
2	3	121	64% 34% .
2	AT	121	% 69% 30% .

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Mol	Chain	Length	Quality of chain
3	4	158	
3	AU	158	
4	AW	254	
4	j	254	
5	AX	389	
5	k	389	
6	AY	363	
6	l	363	
7	AZ	298	
7	m	298	
8	BA	176	
8	n	176	
9	BB	241	
9	o	241	
10	BC	262	
10	p	262	
11	BD	191	
11	q	191	
12	BE	220	
12	r	220	
13	BF	174	
13	s	174	
14	BG	202	
14	t	202	
15	BH	131	

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Mol	Chain	Length	Quality of chain
15	u	131	
16	BI	204	
16	v	204	
17	BJ	200	
17	w	200	
18	BK	185	
18	x	185	
19	BL	186	
19	y	186	
20	BM	190	
20	z	190	
21	0	172	
21	BN	172	
22	2	160	
22	BO	160	
23	5	124	
23	BP	124	
24	6	137	
24	BQ	137	
25	7	155	
25	BR	155	
26	8	142	
26	BS	142	
27	9	127	
27	BT	127	

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Mol	Chain	Length	Quality of chain
28	AA	136	
28	BU	136	
29	AB	149	
29	BV	149	
30	AC	63	
30	BW	63	
31	AD	106	
31	BX	106	
32	AE	112	
32	BY	112	
33	AF	131	
33	BZ	131	
34	AG	107	
34	CA	107	
35	AH	122	
35	CB	122	
36	AI	120	
36	CC	120	
37	AJ	99	
37	CD	99	
38	AK	90	
38	CE	90	
39	AL	78	
39	CF	78	
40	AM	51	

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Mol	Chain	Length	Quality of chain
40	CG	51	
41	AN	52	
41	CH	52	
42	AO	25	
42	CI	25	
43	AP	106	
43	CJ	106	
44	AQ	92	
44	CK	92	
45	CL	267	
45	i	267	
46	B	1787	
46	CM	1787	
47	C	261	
47	CN	261	
48	CO	256	
48	D	256	
49	CP	249	
49	E	249	
50	CQ	251	
50	F	251	
51	CR	262	
51	G	262	
52	CS	225	
52	H	225	

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Mol	Chain	Length	Quality of chain
53	CT	236	
53	I	236	
54	CU	186	
54	J	186	
55	CV	206	
55	K	206	
56	CW	189	
56	L	189	
57	CX	118	
57	M	118	
58	CY	155	
58	N	155	
59	CZ	143	
59	O	143	
60	DA	151	
60	P	151	
61	DB	132	
61	Q	132	
62	DC	142	
62	R	142	
63	DD	142	
63	S	142	
64	DE	137	
64	T	137	
65	DF	145	

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Mol	Chain	Length	Quality of chain
65	U	145	
66	DG	145	
66	V	145	
67	DH	119	
67	W	119	
68	DI	87	
68	X	87	
69	DJ	130	
69	Y	130	
70	DK	145	
70	Z	145	
71	DL	135	
71	a	135	
72	DM	105	
72	b	105	
73	DN	119	
73	c	119	
74	DO	82	
74	d	82	
75	DP	67	
75	e	67	
76	DQ	56	
76	f	56	
77	DR	63	
77	g	63	

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Mol	Chain	Length	Quality of chain
78	DS	193	
78	h	193	
79	AR	317	
79	DT	317	
80	P0	312	
80	p0	312	
81	12	165	
82	L1	217	
82	l1	217	

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
83	MG	8	202	-	-	-	X

2 Entry composition [i](#)

There are 87 unique types of molecules in this entry. The entry contains 408804 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 25S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	3208	Total	C	N	O	P	0	0	0
			68581	30637	12330	22406	3208			
1	AS	3227	Total	C	N	O	P	0	0	0
			68985	30817	12402	22539	3227			

- Molecule 2 is a RNA chain called 5S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	3	121	Total	C	N	O	P	0	0	0
			2579	1153	463	842	121			
2	AT	121	Total	C	N	O	P	0	0	0
			2579	1153	463	842	121			

- Molecule 3 is a RNA chain called 5.8S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	4	157	Total	C	N	O	P	0	0	0
			3333	1491	583	1102	157			
3	AU	157	Total	C	N	O	P	0	0	0
			3333	1491	583	1102	157			

- Molecule 4 is a protein called 60S ribosomal protein L2-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	j	249	Total	C	N	O	S	0	0	0
			1888	1180	376	330	2			
4	AW	249	Total	C	N	O	S	0	0	0
			1888	1180	376	330	2			

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	k	386	Total	C	N	O	S	0	0	0
			3077	1950	582	538	7			
5	AX	386	Total	C	N	O	S	0	0	0
			3077	1950	582	538	7			

- Molecule 6 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	l	361	Total	C	N	O	S	0	0	0
			2751	1729	529	490	3			
6	AY	361	Total	C	N	O	S	0	0	0
			2751	1729	529	490	3			

- Molecule 7 is a protein called Uncharacterized protein CaJ7.0206.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	m	296	Total	C	N	O	S	0	0	0
			2426	1544	422	458	2			
7	AZ	292	Total	C	N	O	S	0	0	0
			2394	1526	416	450	2			

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	n	157	Total	C	N	O	S	0	0	0
			1242	796	226	219	1			
8	BA	153	Total	C	N	O		0	0	0
			1210	777	221	212				

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	o	233	Total	C	N	O	S	0	0	0
			1876	1203	344	328	1			
9	BB	234	Total	C	N	O	S	0	0	0
			1885	1208	345	331	1			

- Molecule 10 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	p	233	Total	C	N	O	S	0	0	0
			1805	1156	321	325	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	BC	229	Total	C	N	O	S	0	0	0
			1778	1140	316	319	3			

- Molecule 11 is a protein called 60S ribosomal protein L9-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	q	189	Total	C	N	O	S	0	0	0
			1510	953	275	278	4			
11	BD	190	Total	C	N	O	S	0	0	0
			1519	958	276	281	4			

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	r	208	Total	C	N	O	S	0	0	0
			1689	1069	322	291	7			
12	BE	208	Total	C	N	O	S	0	0	0
			1689	1069	322	291	7			

- Molecule 13 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	s	171	Total	C	N	O	S	0	0	0
			1371	857	260	250	4			
13	BF	171	Total	C	N	O	S	0	0	0
			1371	857	260	250	4			

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	t	200	Total	C	N	O	0	0	0
			1610	1009	318	283			
14	BG	200	Total	C	N	O	0	0	0
			1610	1009	318	283			

- Molecule 15 is a protein called 60S ribosomal protein L14-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	u	130	Total	C	N	O	S	0	0	0
			1029	660	193	175	1			
15	BH	130	Total	C	N	O	S	0	0	0
			1029	660	193	175	1			

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	v	203	Total	C	N	O	S	0	0	0
			1713	1075	356	280	2			
16	BI	203	Total	C	N	O	S	0	0	0
			1713	1075	356	280	2			

- Molecule 17 is a protein called Ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	w	199	Total	C	N	O	S	0	0	0
			1590	1025	294	269	2			
17	BJ	199	Total	C	N	O	S	0	0	0
			1590	1025	294	269	2			

- Molecule 18 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	x	173	Total	C	N	O	0	0	0
			1387	856	280	251			
18	BK	176	Total	C	N	O	0	0	0
			1406	868	284	254			

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
19	y	185	Total	C	N	O	0	0	0
			1458	916	297	245			
19	BL	185	Total	C	N	O	0	0	0
			1458	916	297	245			

- Molecule 20 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	z	179	Total	C	N	O	S	0	0	0
			1457	901	310	243	3			
20	BM	179	Total	C	N	O	S	0	0	0
			1457	901	310	243	3			

- Molecule 21 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	0	170	Total	C	N	O	S	0	0	0
			1423	921	258	241	3			
21	BN	170	Total	C	N	O	S	0	0	0
			1423	921	258	241	3			

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	2	159	Total	C	N	O	S	0	0	0
			1262	798	241	221	2			
22	BO	159	Total	C	N	O	S	0	0	0
			1262	798	241	221	2			

- Molecule 23 is a protein called 60S ribosomal protein L22-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	5	102	Total	C	N	O		0	0	0
			826	536	137	153				
23	BP	102	Total	C	N	O		0	0	0
			826	536	137	153				

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	6	131	Total	C	N	O	S	0	0	0
			977	615	183	171	8			
24	BQ	131	Total	C	N	O	S	0	0	0
			977	615	183	171	8			

- Molecule 25 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	7	118	Total	C	N	O	S	0	0	0
			945	591	192	161	1			
25	BR	98	Total	C	N	O	S	0	0	0
			801	501	162	137	1			

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	8	120	Total	C	N	O	S	0	0	0
			965	616	173	175	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BS	119	Total	C	N	O	S	0	0	0
			960	613	172	174	1			

- Molecule 27 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	9	126	Total	C	N	O		0	0	0
			989	618	190	181				
27	BT	126	Total	C	N	O		0	0	0
			989	618	190	181				

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	AA	135	Total	C	N	O	S	0	0	0
			1087	705	197	183	2			
28	BU	135	Total	C	N	O	S	0	0	0
			1087	705	197	183	2			

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	AB	148	Total	C	N	O	S	0	0	0
			1170	741	231	197	1			
29	BV	148	Total	C	N	O	S	0	0	0
			1170	741	231	197	1			

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	AC	62	Total	C	N	O		0	0	0
			493	307	105	81				
30	BW	61	Total	C	N	O		0	0	0
			488	304	104	80				

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	AD	96	Total	C	N	O	S	0	0	0
			729	469	121	137	2			
31	BX	96	Total	C	N	O	S	0	0	0
			729	469	121	137	2			

- Molecule 32 is a protein called 60S ribosomal protein L31-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	AE	110	Total	C	N	O	S	0	0	0
			894	565	168	159	2			
32	BY	110	Total	C	N	O	S	0	0	0
			894	565	168	159	2			

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	AF	124	Total	C	N	O	S	0	0	0
			1000	638	194	167	1			
33	BZ	124	Total	C	N	O	S	0	0	0
			1004	641	195	167	1			

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	AG	106	Total	C	N	O	S	0	0	0
			847	543	161	142	1			
34	CA	106	Total	C	N	O	S	0	0	0
			847	543	161	142	1			

- Molecule 35 is a protein called 60S ribosomal protein L34-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	AH	112	Total	C	N	O	S	0	0	0
			887	547	182	154	4			
35	CB	112	Total	C	N	O	S	0	0	0
			887	547	182	154	4			

- Molecule 36 is a protein called Ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	AI	120	Total	C	N	O	S	0	0	0
			992	629	195	167	1			
36	CC	118	Total	C	N	O		0	0	0
			979	621	193	165				

- Molecule 37 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	AJ	97	Total	C	N	O	S	0	0	0
			758	471	156	130	1			
37	CD	97	Total	C	N	O	S	0	0	0
			758	471	156	130	1			

- Molecule 38 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	AK	86	Total	C	N	O	S	0	0	0
			677	413	148	110	6			
38	CE	86	Total	C	N	O	S	0	0	0
			677	413	148	110	6			

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
39	AL	77	Total	C	N	O	0	0	0
			617	393	115	109			
39	CF	77	Total	C	N	O	0	0	0
			617	393	115	109			

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
40	AM	50	Total	C	N	O	0	0	0
			438	275	97	66			
40	CG	50	Total	C	N	O	0	0	0
			438	275	97	66			

- Molecule 41 is a protein called 60S ribosomal protein L40-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	AN	52	Total	C	N	O	S	0	0	0
			419	260	86	67	6			
41	CH	51	Total	C	N	O	S	0	0	0
			411	255	85	66	5			

- Molecule 42 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	AO	25	Total	C	N	O	S	0	0	0
			236	144	63	28	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	CI	24	Total	C	N	O	S	0	0	0
			227	138	61	27	1			

- Molecule 43 is a protein called 60S ribosomal protein L42-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	AP	103	Total	C	N	O	S	0	0	0
			828	521	165	137	5			
43	CJ	103	Total	C	N	O	S	0	0	0
			828	521	165	137	5			

- Molecule 44 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	AQ	91	Total	C	N	O	S	0	0	0
			698	430	140	124	4			
44	CK	91	Total	C	N	O	S	0	0	0
			698	430	140	124	4			

- Molecule 45 is a protein called 60S ribosomal protein CAALFM_C304810CA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	i	120	Total	C	N	O		0	0	0
			922	558	165	199				
45	CL	121	Total	C	N	O		0	0	0
			931	563	166	202				

- Molecule 46 is a RNA chain called 18S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	B	1741	Total	C	N	O	P	0	0	0
			37113	16590	6583	12199	1741			
46	CM	1765	Total	C	N	O	P	0	0	0
			37621	16818	6670	12368	1765			

- Molecule 47 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	C	208	Total	C	N	O	S	0	0	0
			1627	1041	284	297	5			
47	CN	208	Total	C	N	O	S	0	0	0
			1627	1041	284	297	5			

- Molecule 48 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	D	214	Total	C	N	O	S	0	0	0
			1724	1094	313	313	4			
48	CO	214	Total	C	N	O	S	0	0	0
			1724	1094	313	313	4			

- Molecule 49 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	E	217	Total	C	N	O	S	0	0	0
			1629	1039	289	296	5			
49	CP	217	Total	C	N	O	S	0	0	0
			1629	1039	289	296	5			

- Molecule 50 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	F	223	Total	C	N	O	S	0	0	0
			1707	1087	311	305	4			
50	CQ	223	Total	C	N	O	S	0	0	0
			1707	1087	311	305	4			

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	G	259	Total	C	N	O	S	0	0	0
			2051	1304	385	357	5			
51	CR	260	Total	C	N	O	S	0	0	0
			2055	1306	386	358	5			

- Molecule 52 is a protein called Ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	H	206	Total	C	N	O	S	0	0	0
			1614	1008	301	301	4			
52	CS	206	Total	C	N	O	S	0	0	0
			1614	1008	301	301	4			

- Molecule 53 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	I	226	Total	C	N	O	S	0	0	0
			1820	1133	351	330	6			
53	CT	236	Total	C	N	O	S	0	0	0
			1904	1184	369	345	6			

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	J	184	Total	C	N	O	S	0	0	0
			1485	950	268	267				
54	CU	183	Total	C	N	O	S	0	0	0
			1475	944	265	266				

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	K	203	Total	C	N	O	S	0	0	0
			1579	973	322	283	1			
55	CV	203	Total	C	N	O	S	0	0	0
			1579	973	322	283	1			

- Molecule 56 is a protein called Ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	L	178	Total	C	N	O	S	0	0	0
			1453	918	286	248	1			
56	CW	178	Total	C	N	O	S	0	0	0
			1453	918	286	248	1			

- Molecule 57 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	M	98	Total	C	N	O	S	0	0	0
			817	531	135	150	1			
57	CX	94	Total	C	N	O	S	0	0	0
			791	515	131	144	1			

- Molecule 58 is a protein called 40S ribosomal protein S11A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	N	144	Total	C	N	O	S	0	0	0
			1150	734	215	198	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	CY	141	Total	C	N	O	S	0	0	0
			1129	722	212	192	3			

- Molecule 59 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	O	116	Total	C	N	O	S	0	0	0
			885	550	158	172	5			
59	CZ	119	Total	C	N	O	S	0	0	0
			913	566	163	179	5			

- Molecule 60 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
60	P	150	Total	C	N	O	S	0	0	0
			1187	757	219	210	1			
60	DA	150	Total	C	N	O	S	0	0	0
			1187	757	219	210	1			

- Molecule 61 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
61	Q	127	Total	C	N	O	S	0	0	0
			942	579	186	174	3			
61	DB	127	Total	C	N	O	S	0	0	0
			942	579	186	174	3			

- Molecule 62 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
62	R	129	Total	C	N	O	S	0	0	0
			1018	649	185	177	7			
62	DC	130	Total	C	N	O	S	0	0	0
			1029	655	189	178	7			

- Molecule 63 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
63	S	140	Total	C	N	O	S	0	0	0
			1091	700	198	192	1			
63	DD	140	Total	C	N	O	S	0	0	0
			1091	700	198	192	1			

- Molecule 64 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
64	T	124	Total	C	N	O	S	0	0	0
			997	628	183	185	1			
64	DE	124	Total	C	N	O	S	0	0	0
			997	628	183	185	1			

- Molecule 65 is a protein called 40S ribosomal protein S18-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
65	U	144	Total	C	N	O	S	0	0	0
			1187	744	233	207	3			
65	DF	141	Total	C	N	O	S	0	0	0
			1161	727	227	204	3			

- Molecule 66 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
66	V	141	Total	C	N	O	S	0	0	0
			1100	689	210	200	1			
66	DG	141	Total	C	N	O	S	0	0	0
			1100	689	210	200	1			

- Molecule 67 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
67	W	102	Total	C	N	O	S	0	0	0
			808	509	150	147	2			
67	DH	97	Total	C	N	O	S	0	0	0
			763	481	140	140	2			

- Molecule 68 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
68	X	87	Total	C	N	O	S	0	0	0
			676	415	126	133	2			
68	DI	87	Total	C	N	O	S	0	0	0
			676	415	126	133	2			

- Molecule 69 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
69	Y	129	Total	C	N	O	S	0	0	0
			1032	655	191	183	3			
69	DJ	129	Total	C	N	O	S	0	0	0
			1032	655	191	183	3			

- Molecule 70 is a protein called Ribosomal protein S23 (S12).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
70	Z	143	Total	C	N	O	S	0	0	0
			1110	701	219	188	2			
70	DK	143	Total	C	N	O	S	0	0	0
			1110	701	219	188	2			

- Molecule 71 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
71	a	134	Total	C	N	O		0	0	0
			1086	677	218	191				
71	DL	132	Total	C	N	O		0	0	0
			1072	670	216	186				

- Molecule 72 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
72	b	72	Total	C	N	O		0	0	0
			578	369	103	106				
72	DM	71	Total	C	N	O		0	0	0
			570	365	102	103				

- Molecule 73 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
73	c	98	Total	C	N	O	S	0	0	0
			779	482	163	128	6			
73	DN	97	Total	C	N	O	S	0	0	0
			770	477	161	126	6			

- Molecule 74 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
74	d	81	Total	C	N	O	S	0	0	0
			614	383	110	114	7			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
74	DO	81	Total	C	N	O	S	0	0	0
			614	383	110	114	7			

- Molecule 75 is a protein called 40S ribosomal protein S28-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
75	e	62	Total	C	N	O	S	0	0	0
			487	299	98	88	2			
75	DP	61	Total	C	N	O	S	0	0	0
			476	293	94	87	2			

- Molecule 76 is a protein called 40S ribosomal protein S29A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
76	f	55	Total	C	N	O	S	0	0	0
			454	281	94	75	4			
76	DQ	54	Total	C	N	O	S	0	0	0
			449	278	93	74	4			

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
77	g	60	Total	C	N	O	S	0	0	0
			474	297	96	79	2			
77	DR	58	Total	C	N	O	S	0	0	0
			461	289	93	77	2			

- Molecule 78 is a protein called Ubiquitin-40S ribosomal protein S31 fusion protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
78	h	70	Total	C	N	O	S	0	0	0
			574	362	113	93	6			
78	DS	70	Total	C	N	O	S	0	0	0
			574	362	113	93	6			

- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
79	AR	311	Total	C	N	O	S	0	0	0
			2398	1519	412	462	5			
79	DT	306	Total	C	N	O	S	0	0	0
			2357	1494	402	456	5			

- Molecule 80 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
80	P0	107	Total	C	N	O	S	0	0	0
			845	542	150	150	3			
80	p0	79	Total	C	N	O	S	0	0	0
			635	404	114	115	2			

- Molecule 81 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
81	12	63	Total	C	N	O	S	0	0	0
			480	297	85	96	2			

- Molecule 82 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
82	L1	217	Total	C	N	O	S	0	0	0
			1711	1096	294	312	9			
82	11	217	Total	C	N	O	S	0	0	0
			1711	1096	294	312	9			

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
83	1	530	Total	Mg	0	0
			530	530		
83	3	14	Total	Mg	0	0
			14	14		
83	4	12	Total	Mg	0	0
			12	12		
83	j	3	Total	Mg	0	0
			3	3		
83	k	4	Total	Mg	0	0
			4	4		
83	o	3	Total	Mg	0	0
			3	3		
83	r	2	Total	Mg	0	0
			2	2		
83	s	1	Total	Mg	0	0
			1	1		
83	u	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
83	v	3	Total 3	Mg 3	0	0
83	w	3	Total 3	Mg 3	0	0
83	x	3	Total 3	Mg 3	0	0
83	y	1	Total 1	Mg 1	0	0
83	0	5	Total 5	Mg 5	0	0
83	2	3	Total 3	Mg 3	0	0
83	5	1	Total 1	Mg 1	0	0
83	6	3	Total 3	Mg 3	0	0
83	8	2	Total 2	Mg 2	0	0
83	9	2	Total 2	Mg 2	0	0
83	AB	2	Total 2	Mg 2	0	0
83	AC	1	Total 1	Mg 1	0	0
83	AD	1	Total 1	Mg 1	0	0
83	AE	2	Total 2	Mg 2	0	0
83	AF	1	Total 1	Mg 1	0	0
83	AG	2	Total 2	Mg 2	0	0
83	AH	2	Total 2	Mg 2	0	0
83	AJ	1	Total 1	Mg 1	0	0
83	AK	1	Total 1	Mg 1	0	0
83	AM	1	Total 1	Mg 1	0	0
83	AP	2	Total 2	Mg 2	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
83	B	152	Total 152	Mg 152	0	0
83	D	1	Total 1	Mg 1	0	0
83	G	2	Total 2	Mg 2	0	0
83	I	2	Total 2	Mg 2	0	0
83	J	1	Total 1	Mg 1	0	0
83	K	1	Total 1	Mg 1	0	0
83	L	1	Total 1	Mg 1	0	0
83	Q	1	Total 1	Mg 1	0	0
83	R	1	Total 1	Mg 1	0	0
83	V	1	Total 1	Mg 1	0	0
83	Y	3	Total 3	Mg 3	0	0
83	Z	2	Total 2	Mg 2	0	0
83	a	1	Total 1	Mg 1	0	0
83	f	1	Total 1	Mg 1	0	0
83	AR	1	Total 1	Mg 1	0	0
83	AS	278	Total 278	Mg 278	0	0
83	AT	9	Total 9	Mg 9	0	0
83	AU	2	Total 2	Mg 2	0	0
83	AW	4	Total 4	Mg 4	0	0
83	BB	2	Total 2	Mg 2	0	0
83	BE	2	Total 2	Mg 2	0	0

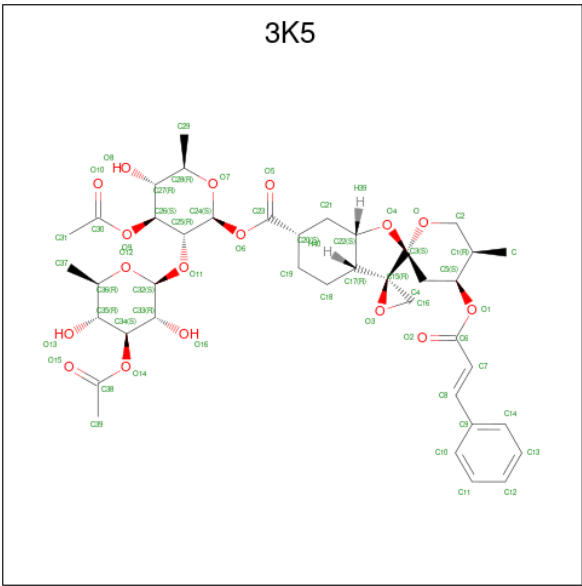
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
83	BF	1	Total 1	Mg 1	0	0
83	BH	1	Total 1	Mg 1	0	0
83	BJ	3	Total 3	Mg 3	0	0
83	BK	1	Total 1	Mg 1	0	0
83	BN	1	Total 1	Mg 1	0	0
83	BQ	1	Total 1	Mg 1	0	0
83	BV	1	Total 1	Mg 1	0	0
83	BZ	2	Total 2	Mg 2	0	0
83	CA	1	Total 1	Mg 1	0	0
83	CJ	1	Total 1	Mg 1	0	0
83	CK	1	Total 1	Mg 1	0	0
83	CL	3	Total 3	Mg 3	0	0
83	CM	102	Total 102	Mg 102	0	0
83	CO	1	Total 1	Mg 1	0	0
83	CP	1	Total 1	Mg 1	0	0
83	CQ	1	Total 1	Mg 1	0	0
83	DA	1	Total 1	Mg 1	0	0
83	DB	3	Total 3	Mg 3	0	0
83	DG	2	Total 2	Mg 2	0	0
83	DQ	1	Total 1	Mg 1	0	0

- Molecule 84 is 3-O-acetyl-2-O-(3-O-acetyl-6-deoxy-beta-D-glucopyranosyl)-6-deoxy-1-O-[[(2R,2'S,3a'R,4'S,5''R,6'S,7a'S)-5''-methyl-4''-{[(2E)-3-phenylprop-2-enoyl]oxy}decahydrodis piro[oxirane-2,3'-[1]benzofuran-2',2''-pyran]-6'-yl]carbonyl]-beta-D-glucopyranose (CCD ID:

3K5) (formula: C₄₀H₅₂O₁₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
84	1	1	Total	C	O	0	0
			57	40	17		
84	AS	1	Total	C	O	0	0
			57	40	17		

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

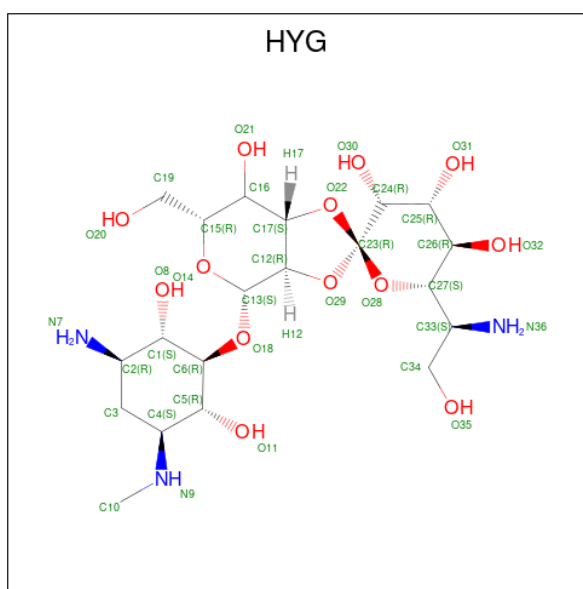
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
85	AH	1	Total	Zn	0	0
			1	1		
85	AK	1	Total	Zn	0	0
			1	1		
85	AN	1	Total	Zn	0	0
			1	1		
85	AP	1	Total	Zn	0	0
			1	1		
85	AQ	1	Total	Zn	0	0
			1	1		
85	c	1	Total	Zn	0	0
			1	1		
85	d	1	Total	Zn	0	0
			1	1		
85	f	1	Total	Zn	0	0
			1	1		
85	h	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
85	CB	1	Total	Zn	0	0
			1	1		
85	CE	1	Total	Zn	0	0
			1	1		
85	CH	1	Total	Zn	0	0
			1	1		
85	CJ	1	Total	Zn	0	0
			1	1		
85	CK	1	Total	Zn	0	0
			1	1		
85	DN	1	Total	Zn	0	0
			1	1		
85	DQ	1	Total	Zn	0	0
			1	1		
85	DS	1	Total	Zn	0	0
			1	1		

- Molecule 86 is HYGROMYCIN B (CCD ID: HYG) (formula: $C_{20}H_{37}N_3O_{13}$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
86	B	1	Total	C	N	O	0	0
			36	20	3	13		
86	CM	1	Total	C	N	O	0	0
			36	20	3	13		

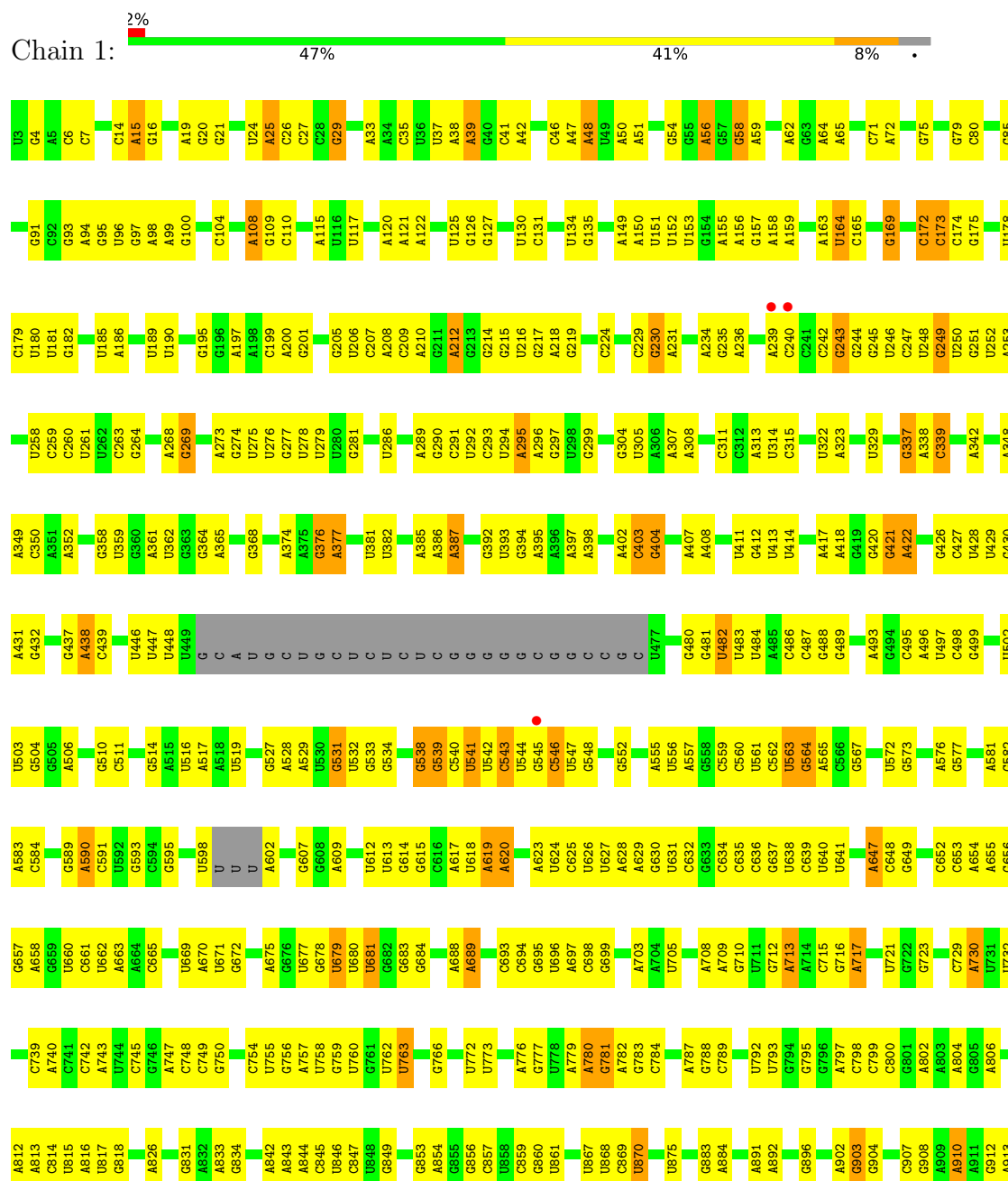
- Molecule 87 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
87	1	9	Total 9	O 9	0	0
87	4	3	Total 3	O 3	0	0
87	B	6	Total 6	O 6	0	0
87	AS	12	Total 12	O 12	0	0

3 Residue-property plots

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

• Molecule 1: 25S



G	G1944	A1838	U1761	C1859	A1589	C1416	A1522	G1246	U1178	A1089	U991
A	A1945	G1841	G1762	G1660	U1590	G1417	C1323	A1247	C1179	A1090	C996
G	U1946	C1842	C1763	U1661	U1591	U1324	U1324	U1248	U1019	U180	G997
C				G1662	C1592	U1421	U1325	U1249	C1181	G1092	A998
U				A1663	C1593	C1422	C1326	U1250	G1182	U1093	G920
G	G1949	C1845	U1768	G1664	U1594	U1423	U1327	C1251	C1183	A1094	A921
C	U			C1665	C1504	A1424	A1328	U1184	U1184		U1004
U	U			G1666	A1598		C1329	C1252		A1099	U1005
C	U			C1667	U1599		U1329	C1253		G1100	C923
G	U			U1678	A1600	G1427	U1330	U1254		C1188	C924
C	U			A1679	U1601	U1428	U1331	U1255		U1104	A925
U	U			U1778	U1602	U1429	C1332	U1256		U1106	U926
U	U				U1603	G1430	A1333	G1257	A1189	U1104	
G	U			U1684		A1431	U1339	G1258	G1190	U1106	
G	U			U1685		U1519	A1338	A1259	A1191	U1107	
A	U			C1685		A1520	U1341	C1194			C1011
G	U					C1523	G1432	U1261			U1012
C	U			U1690	G1606	U1433	U1340	G1260	A1193		U1013
C	U			U1691	G1607	U1434	U1341	U1261			C934
C	U			U1692		U1435	G1342	U1262			U835
U	U			U1693		G1436	C1343	U1263			
U	U			A1693			C1343	U1264			
U	U			C1694		A1442	U1344	U1265			
C	U			A1695		U1443	A1531	A1266			
U	U			G1696		U1444	U1346	A1267	A1200	U1117	
U	U					A1445	U1347	C1268	A1201		C944
U	U			U1790		G1446	U1348	A1269	G1202		C945
A	U			U1791			U1349	U1270	U1124	U1024	
G	U			C1705			G1350	U1271	A1125	U1028	
A	U			C1706		U1454		U1272	G1130	U1030	
G	U			U1713		C1455	C1354	C1273	G1132	U1031	
C	U			G1714		A1456		U1206	C1027	G949	
A	U			G1715		A1457		U1207	A1129	C1028	
G	U							U1217			U850
C	U			U1825				G1218			U851
C	U			U1826							U952
C	U			U1827							C953
C	U			U1828							C954
G	U			U1829							C955
U	U			U1830							U956
U	U			U1831							C957
U	U			U1832							G959
U	U			U1833							
U	U			U1834							U962
U	U			U1835							A963
U	U			U1836							G964
U	U			U1837							C965
U	U			U1838							A966
A	U			U1839							G967
C	U			U1840							
C	U			U1841							U972
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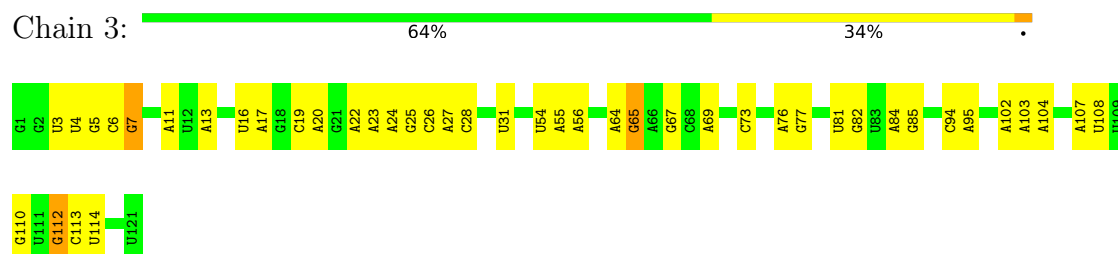




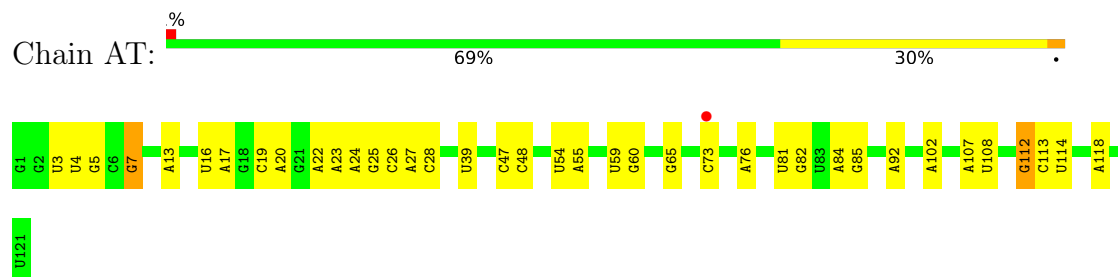




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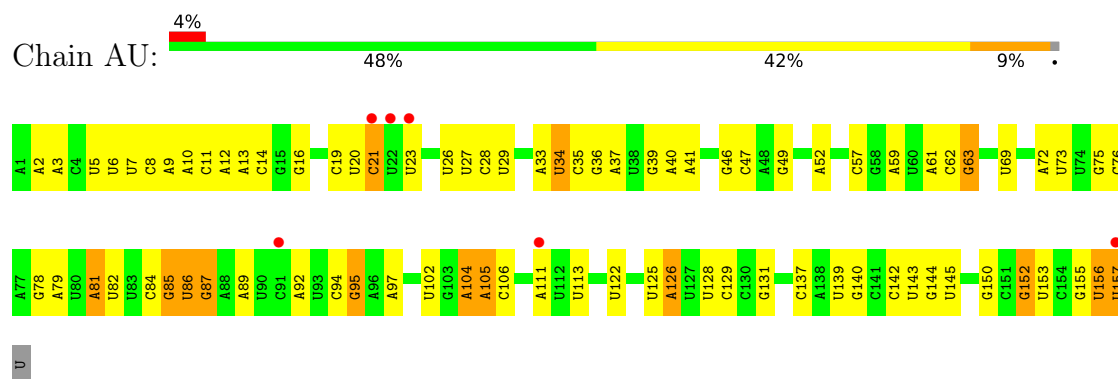
- Molecule 2: 5S



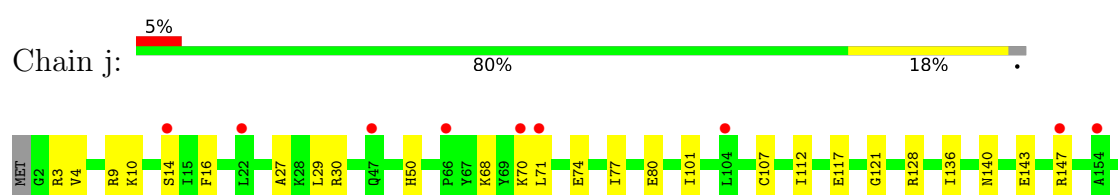
- Molecule 3: 5.8S



- Molecule 3: 5.8S

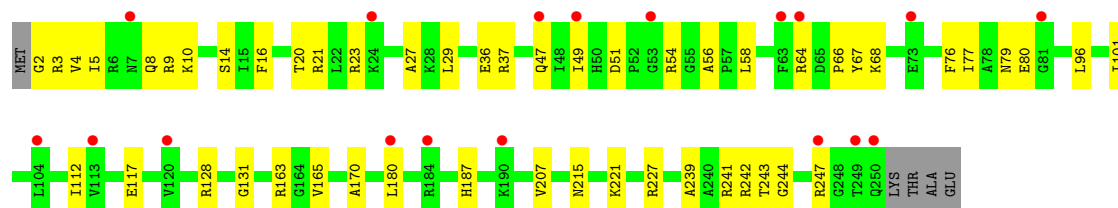
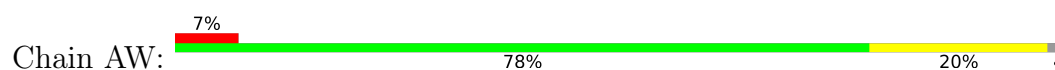


- Molecule 4: 60S ribosomal protein L2-B

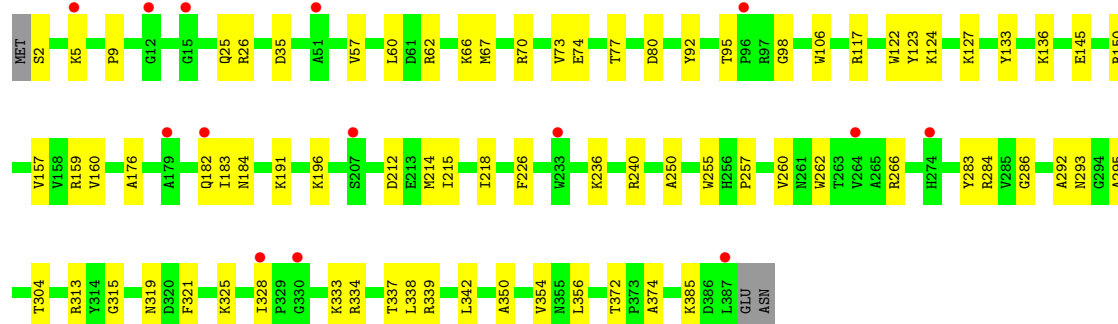
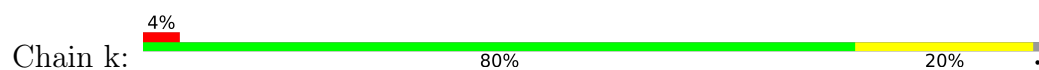




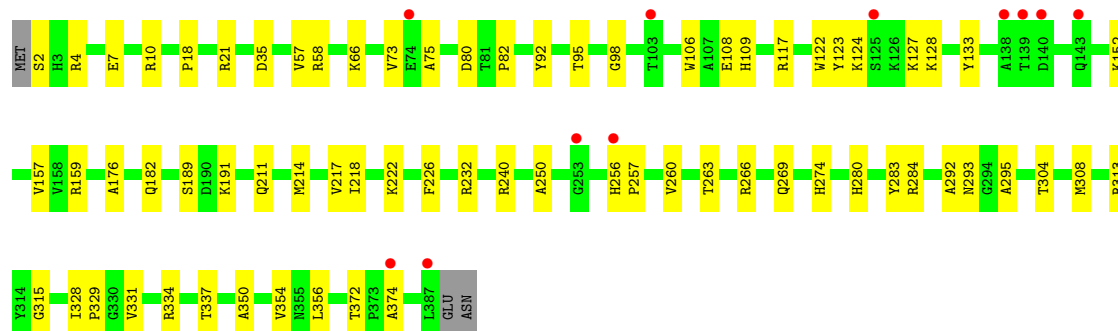
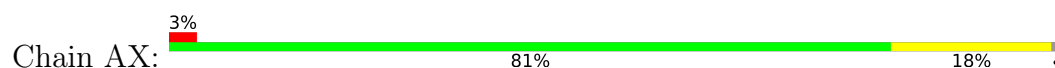
- Molecule 4: 60S ribosomal protein L2-B



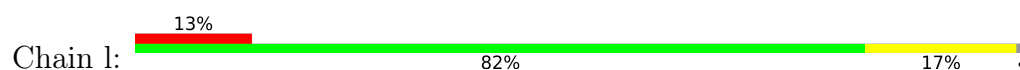
- Molecule 5: 60S ribosomal protein L3

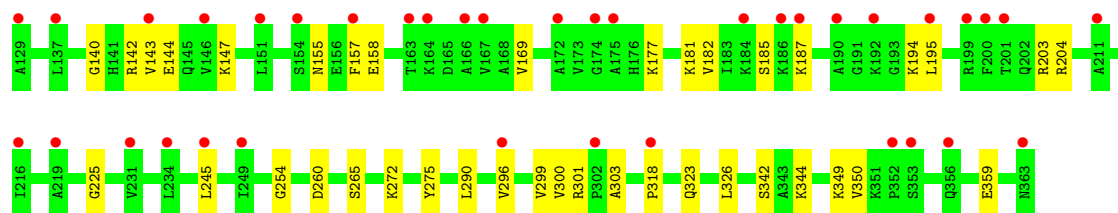


- Molecule 5: 60S ribosomal protein L3

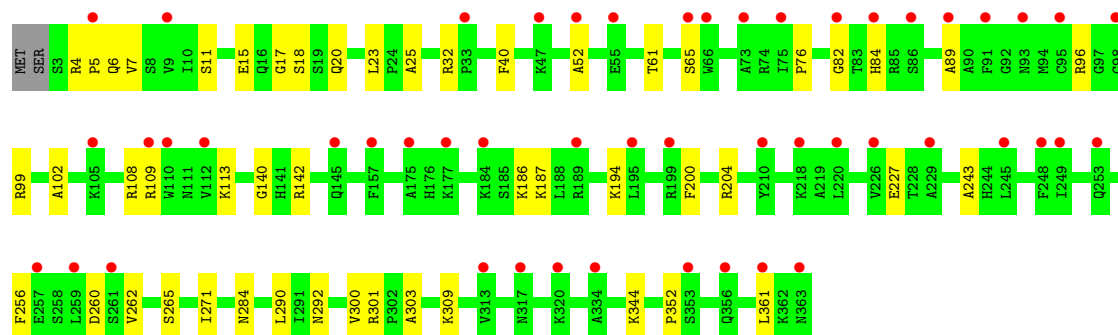
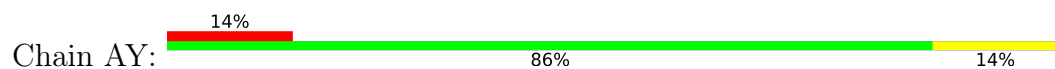


- Molecule 6: 60S ribosomal protein L4-B

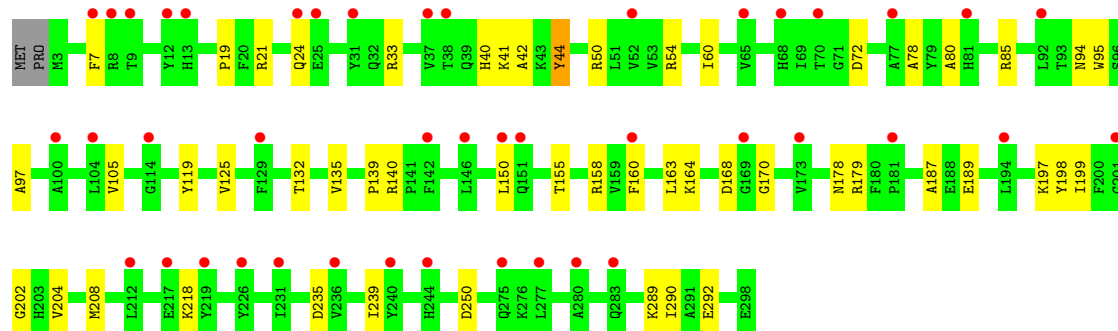
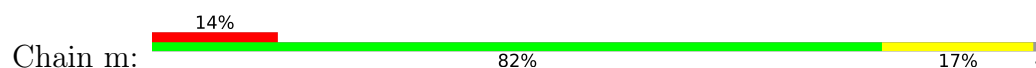




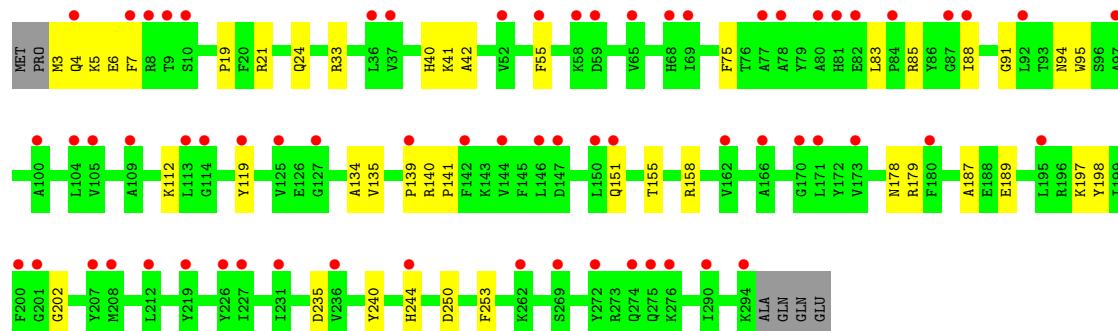
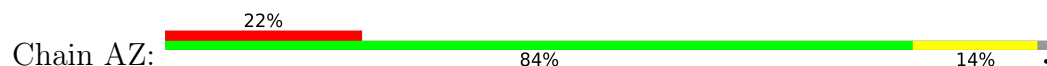
• Molecule 6: 60S ribosomal protein L4-B



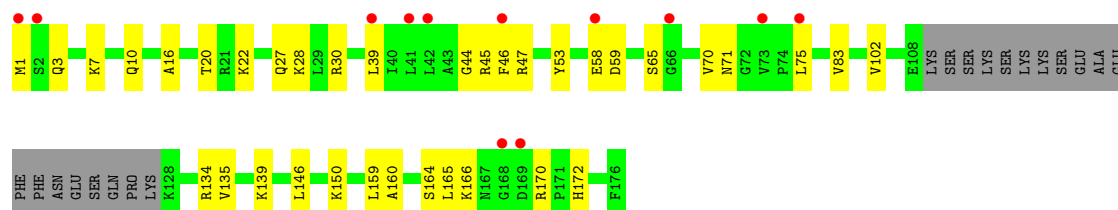
• Molecule 7: Uncharacterized protein CaJ7.0206



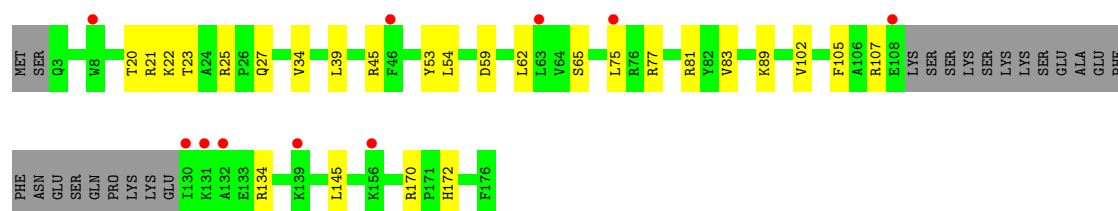
• Molecule 7: Uncharacterized protein CaJ7.0206



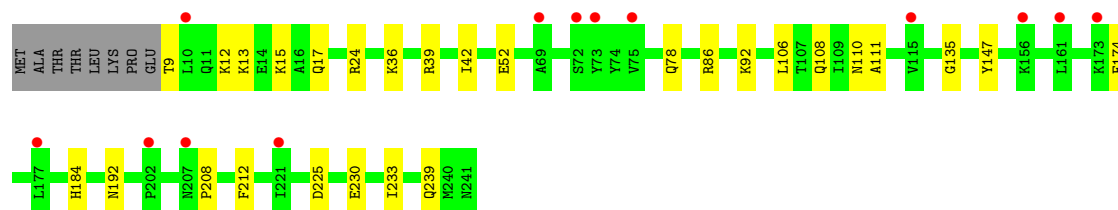
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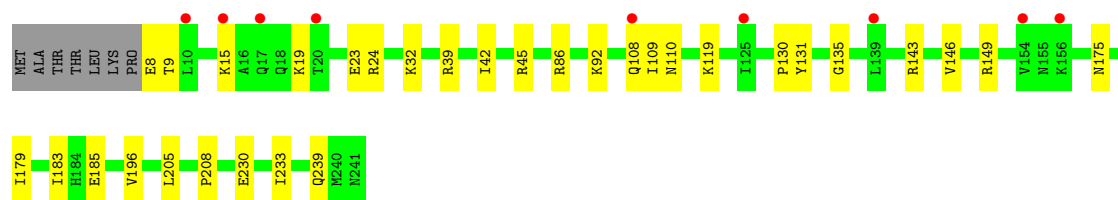
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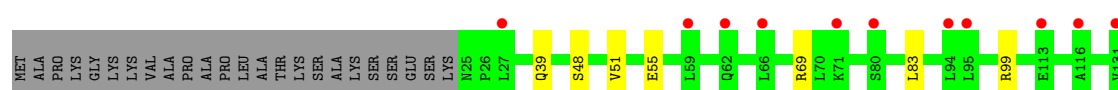
Chain o: 5% 85% 12%

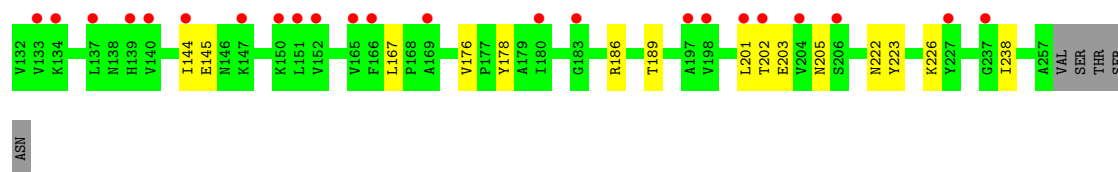


Chain BB:

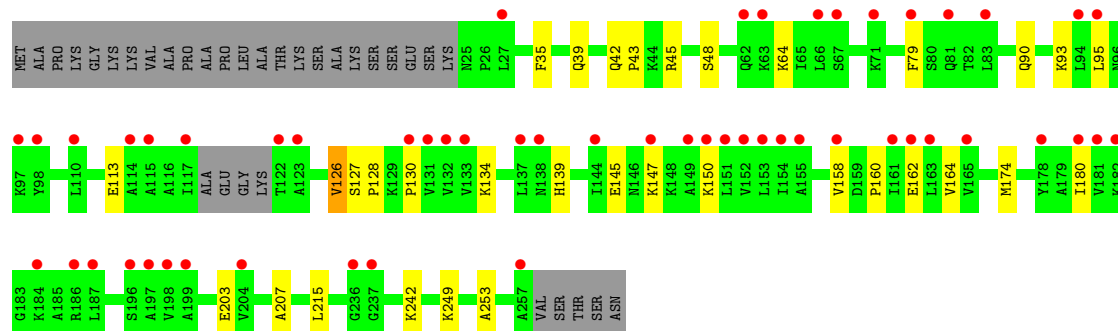
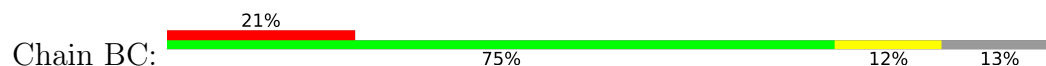


Chain p: 13% 81% 8% 11%

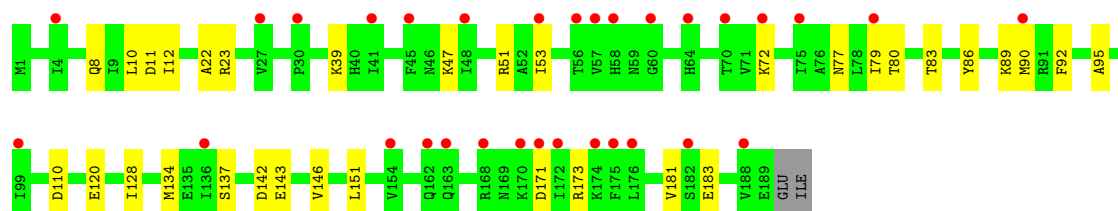
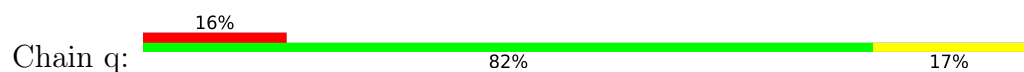




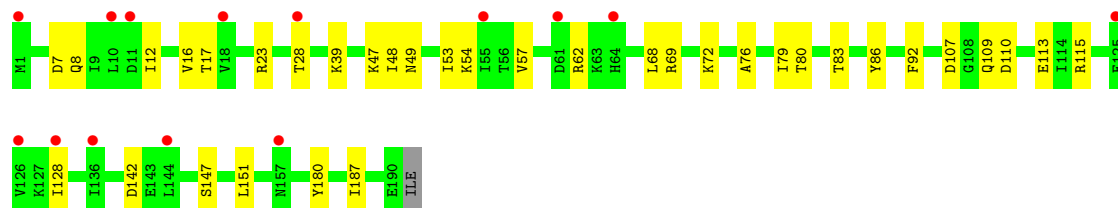
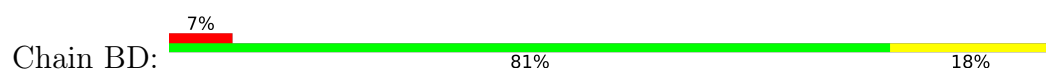
• Molecule 10: 60S ribosomal protein L8



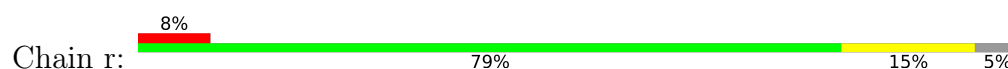
• Molecule 11: 60S ribosomal protein L9-B



• Molecule 11: 60S ribosomal protein L9-B

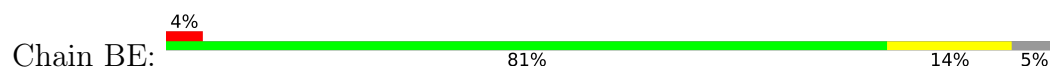


• Molecule 12: 60S ribosomal protein L10

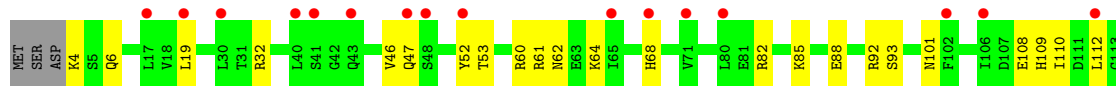
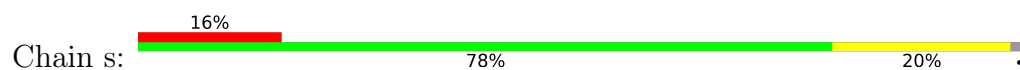




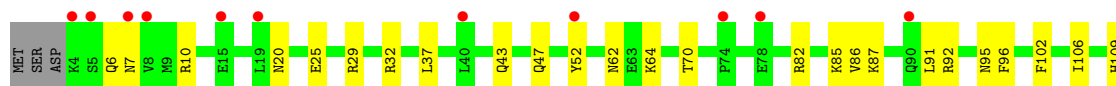
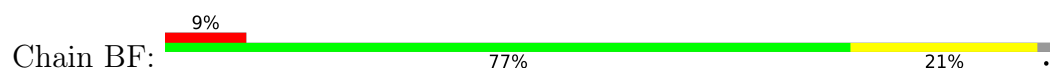
- Molecule 12: 60S ribosomal protein L10



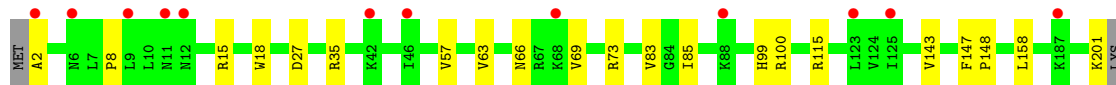
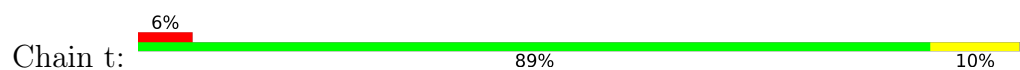
- Molecule 13: 60S ribosomal protein L11-B



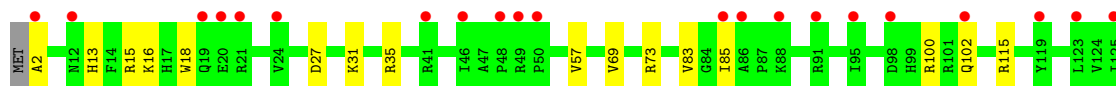
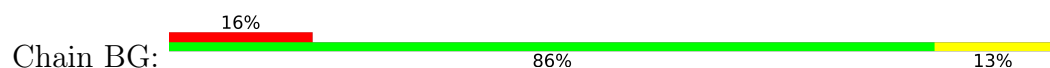
- Molecule 13: 60S ribosomal protein L11-B



- Molecule 14: 60S ribosomal protein L13

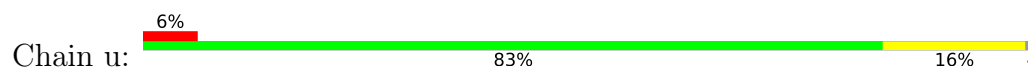


- Molecule 14: 60S ribosomal protein L13

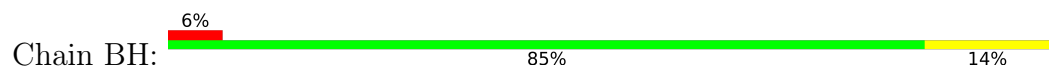




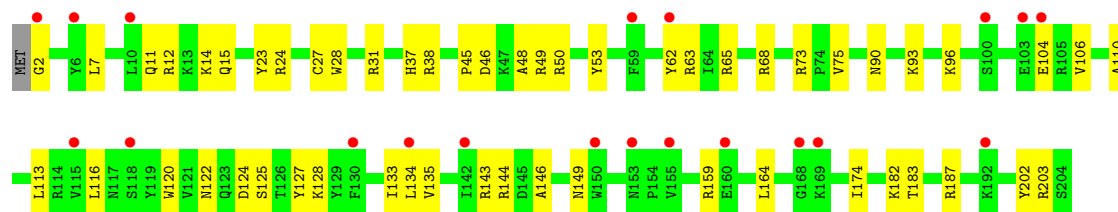
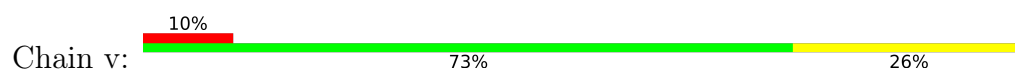
- Molecule 15: 60S ribosomal protein L14-B



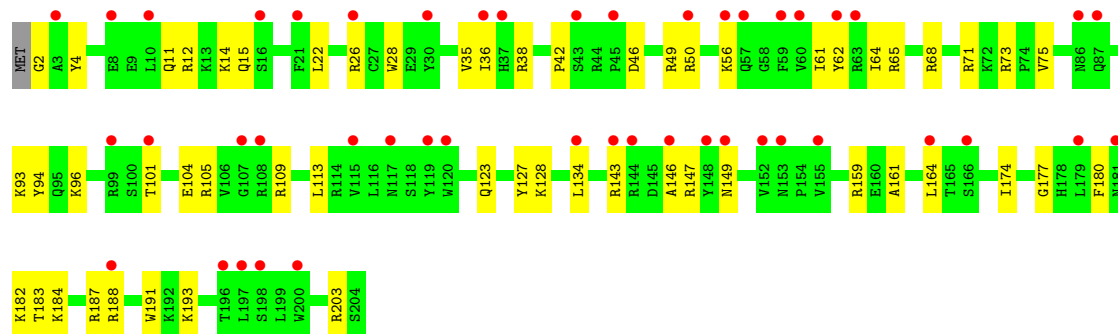
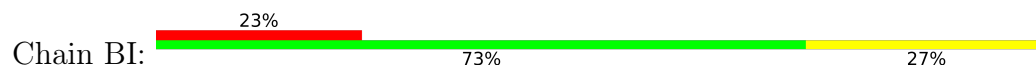
- Molecule 15: 60S ribosomal protein L14-B



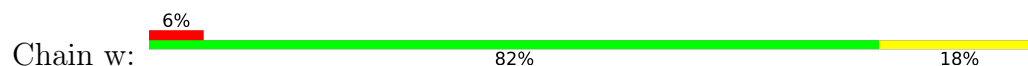
- Molecule 16: 60S ribosomal protein L15-A



- Molecule 16: 60S ribosomal protein L15-A

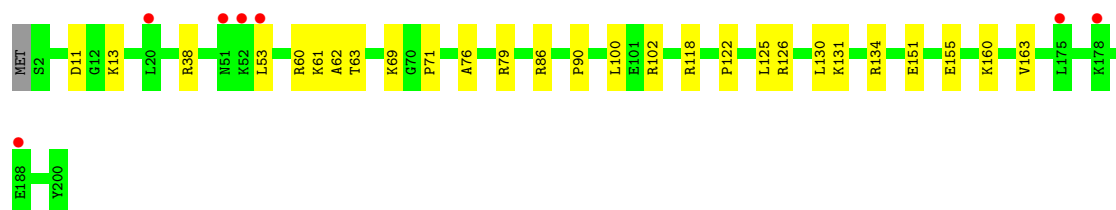
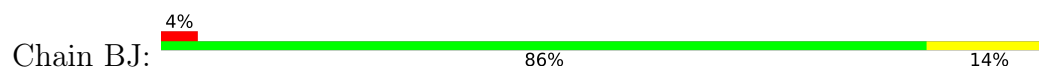


- Molecule 17: Ribosomal protein L13

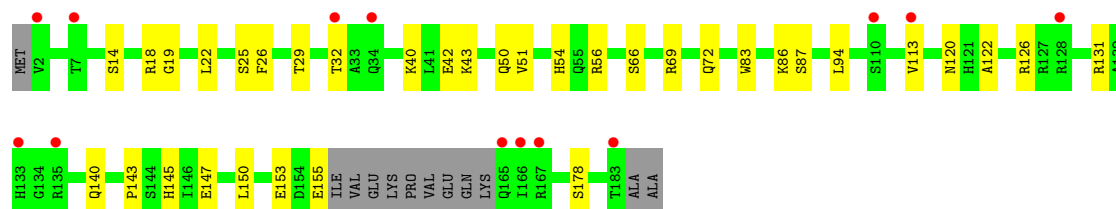
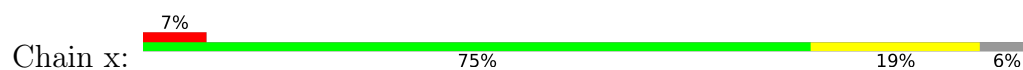




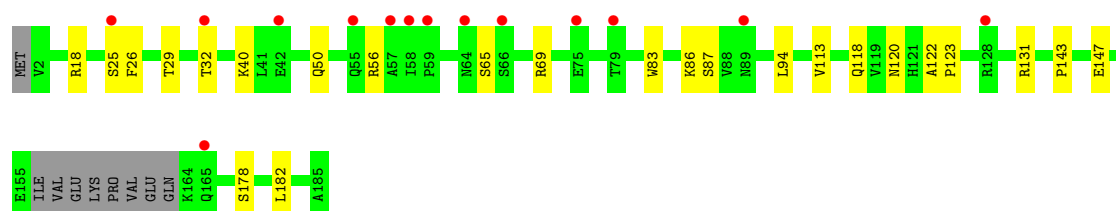
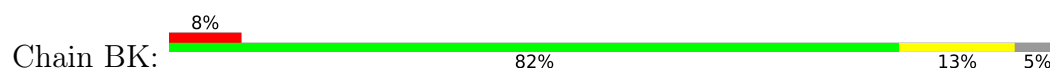
- Molecule 17: Ribosomal protein L13



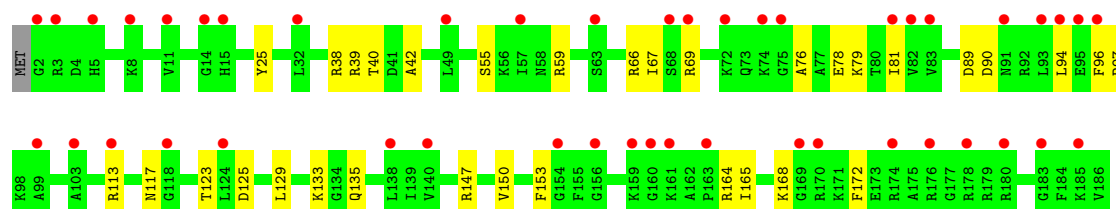
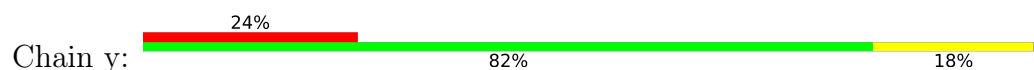
- Molecule 18: Ribosomal protein L22



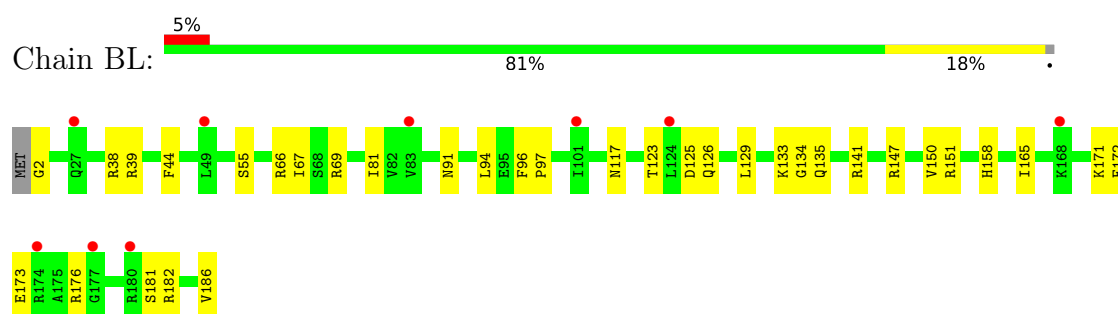
- Molecule 18: Ribosomal protein L22



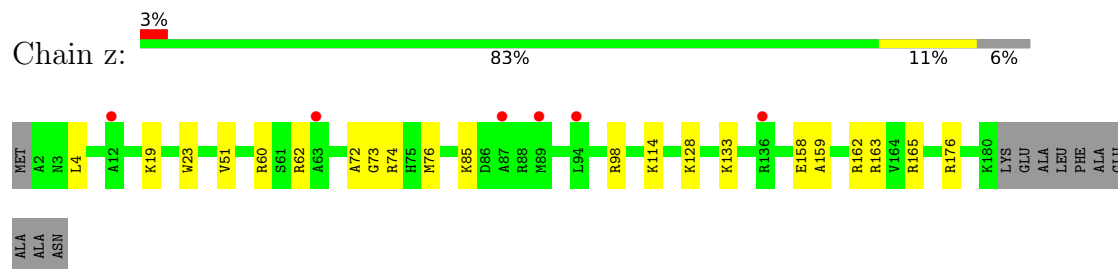
- Molecule 19: 60S ribosomal protein L18-A



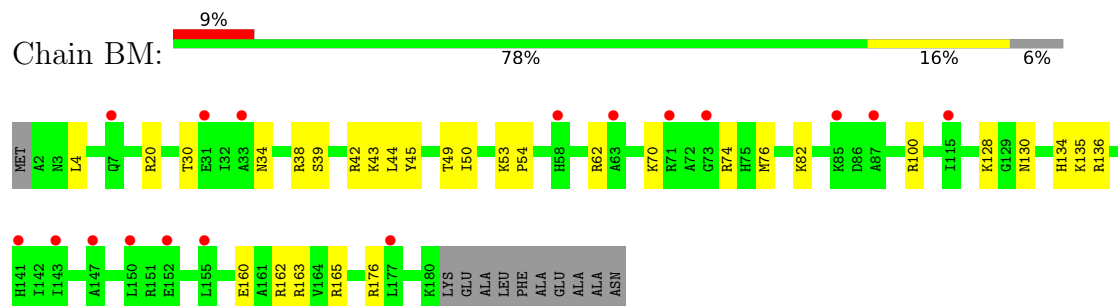
- Molecule 19: 60S ribosomal protein L18-A



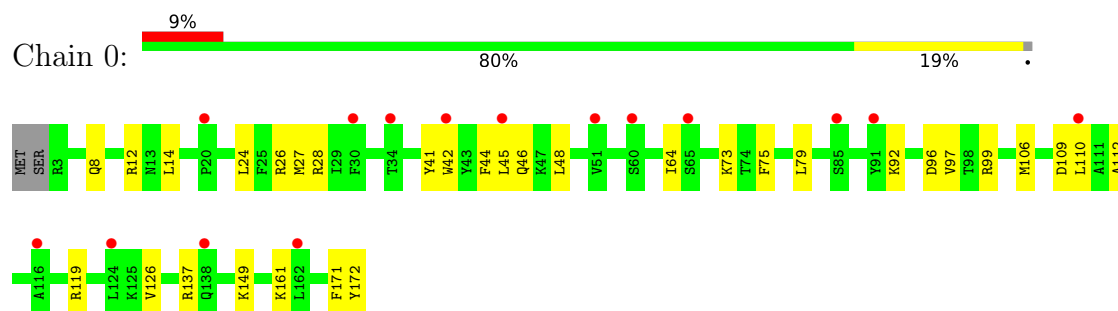
- Molecule 20: 60S ribosomal protein L19-A



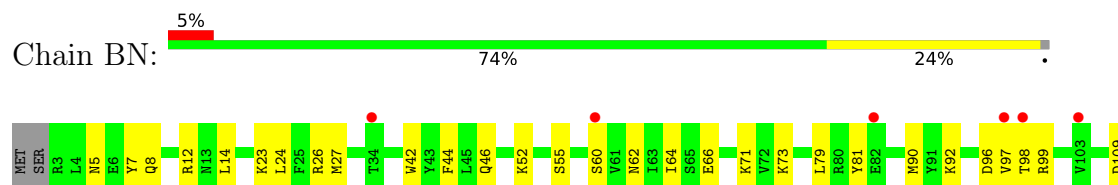
- Molecule 20: 60S ribosomal protein L19-A



- Molecule 21: 60S ribosomal protein L20

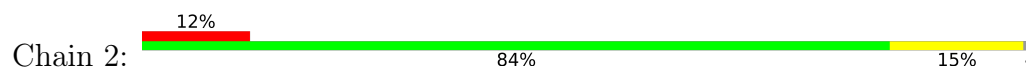


- Molecule 21: 60S ribosomal protein L20

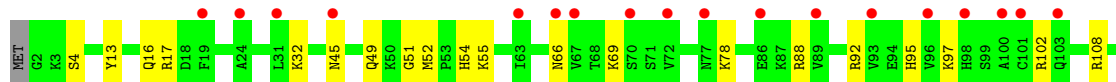
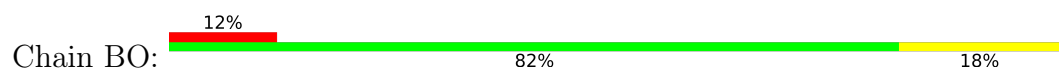




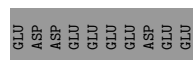
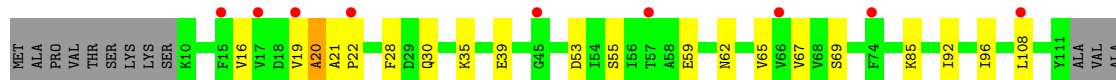
- Molecule 22: 60S ribosomal protein L21-A



- Molecule 22: 60S ribosomal protein L21-A



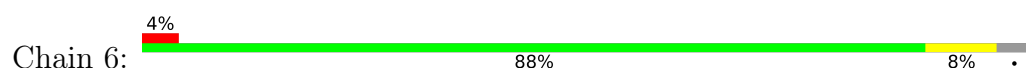
- Molecule 23: 60S ribosomal protein L22-B



- Molecule 23: 60S ribosomal protein L22-B

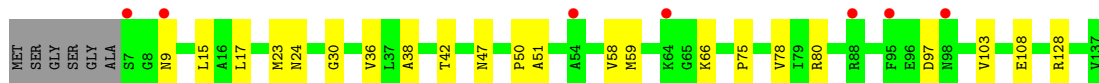
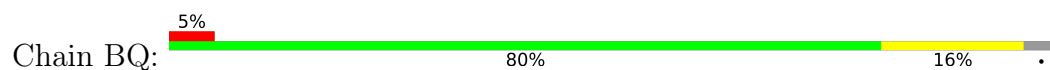


- Molecule 24: 60S ribosomal protein L23-A

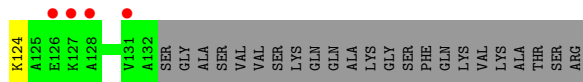
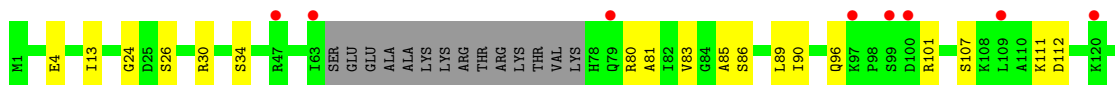




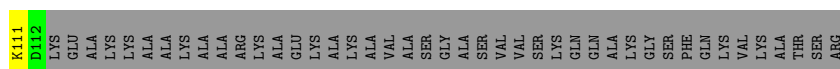
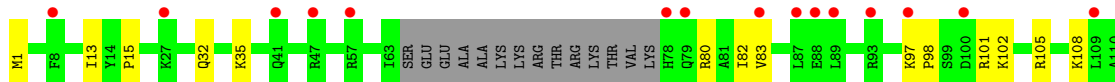
- Molecule 24: 60S ribosomal protein L23-A



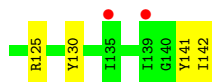
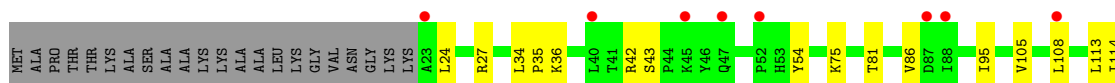
- Molecule 25: 60S ribosomal protein L24-A



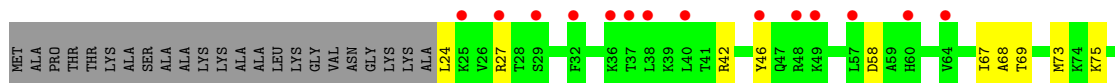
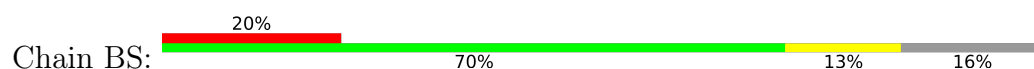
- Molecule 25: 60S ribosomal protein L24-A



- Molecule 26: 60S ribosomal protein L25

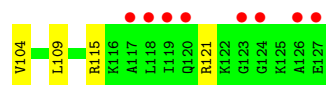
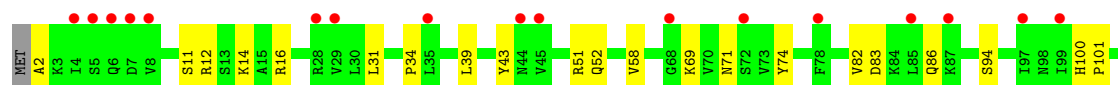
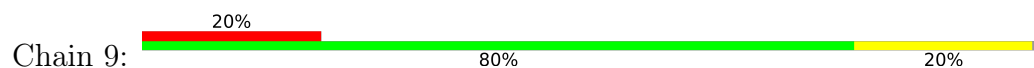


- Molecule 26: 60S ribosomal protein L25

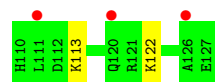
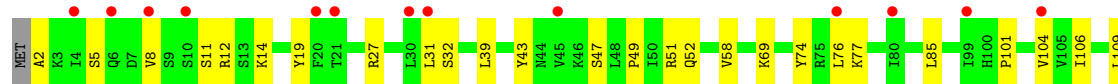
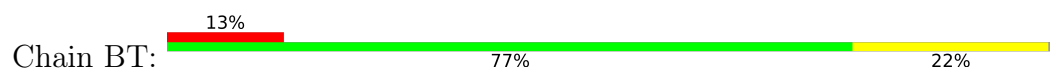




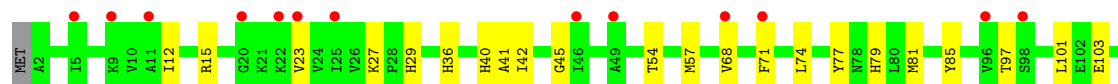
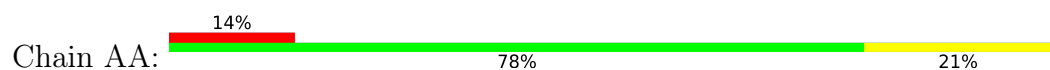
• Molecule 27: Ribosomal protein L24



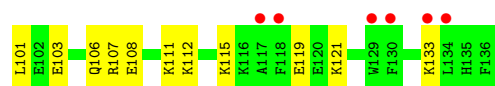
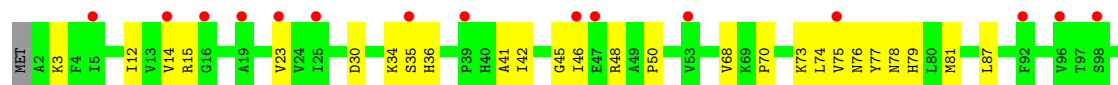
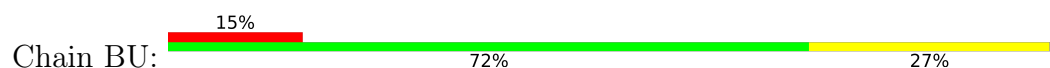
• Molecule 27: Ribosomal protein L24



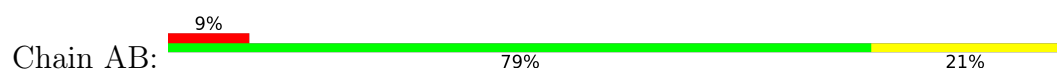
• Molecule 28: 60S ribosomal protein L27

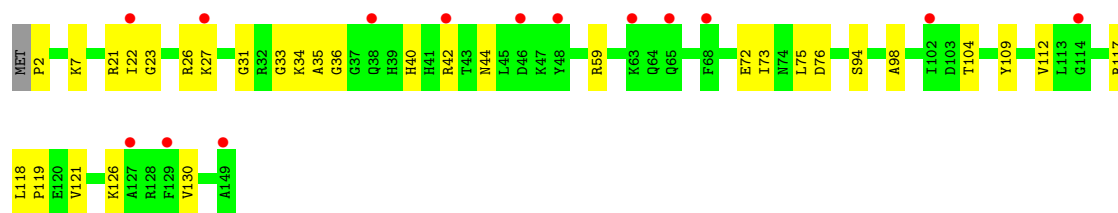


• Molecule 28: 60S ribosomal protein L27

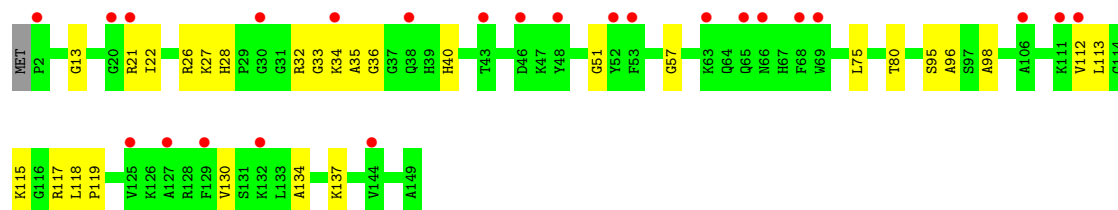
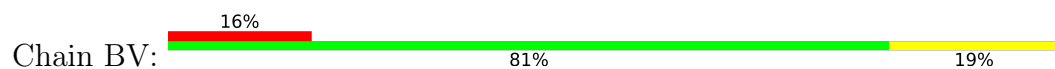


• Molecule 29: 60S ribosomal protein L28

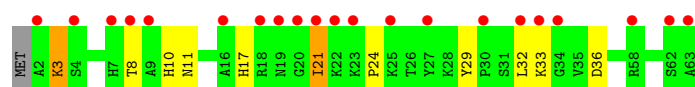
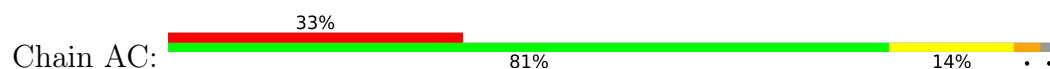




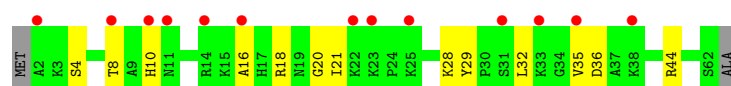
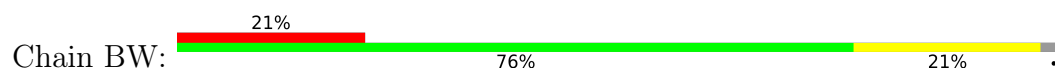
- Molecule 29: 60S ribosomal protein L28



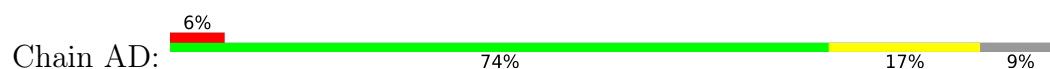
- Molecule 30: 60S ribosomal protein L29



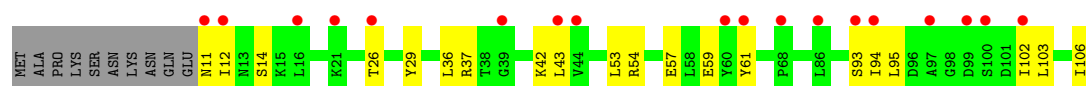
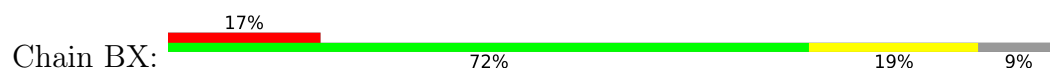
- Molecule 30: 60S ribosomal protein L29



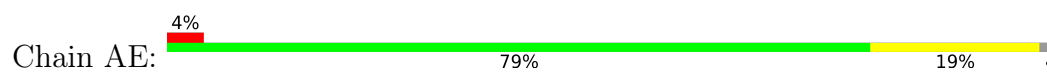
- Molecule 31: 60S ribosomal protein L30



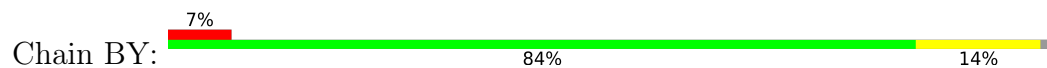
- Molecule 31: 60S ribosomal protein L30



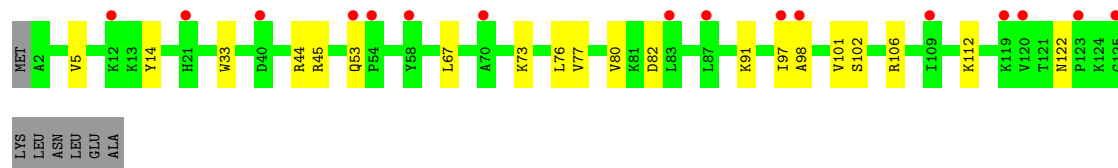
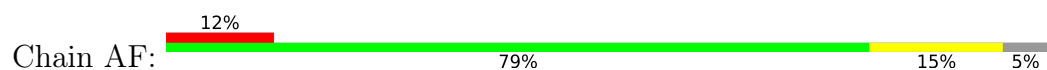
- Molecule 32: 60S ribosomal protein L31-B



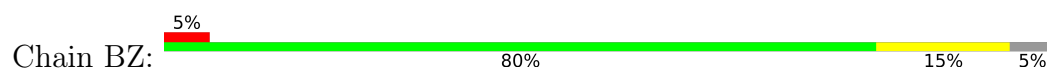
- Molecule 32: 60S ribosomal protein L31-B



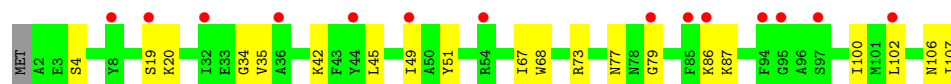
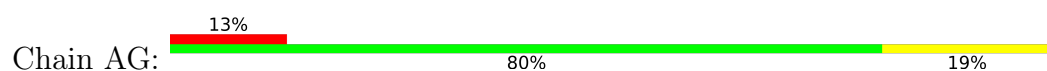
- Molecule 33: 60S ribosomal protein L32



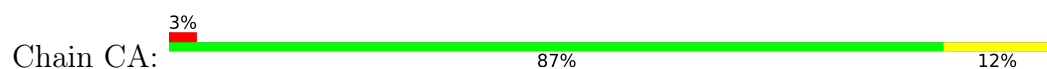
- Molecule 33: 60S ribosomal protein L32



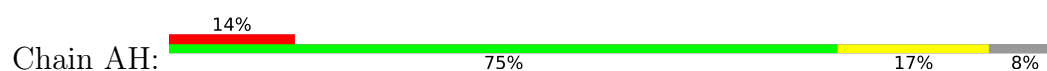
- Molecule 34: 60S ribosomal protein L33-A

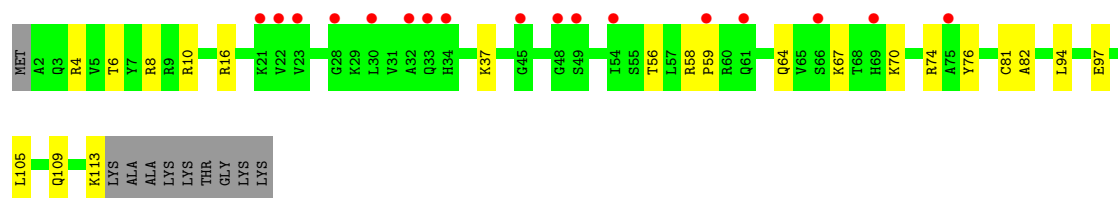


- Molecule 34: 60S ribosomal protein L33-A



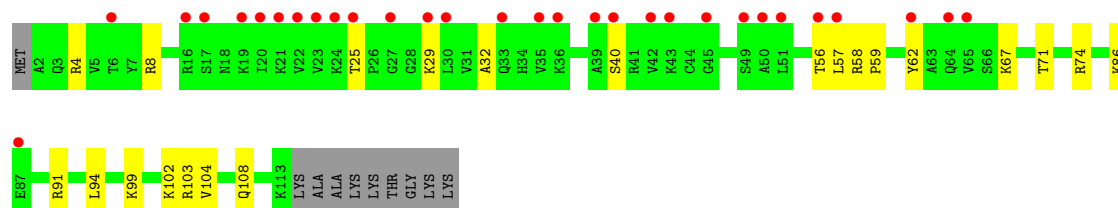
- Molecule 35: 60S ribosomal protein L34-B





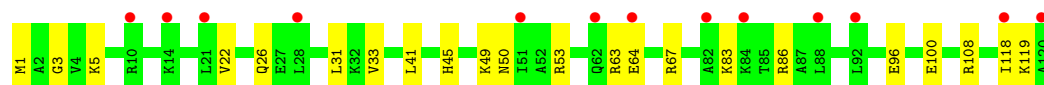
- Molecule 35: 60S ribosomal protein L34-B

Chain CB: 25% 74% 18% 8%



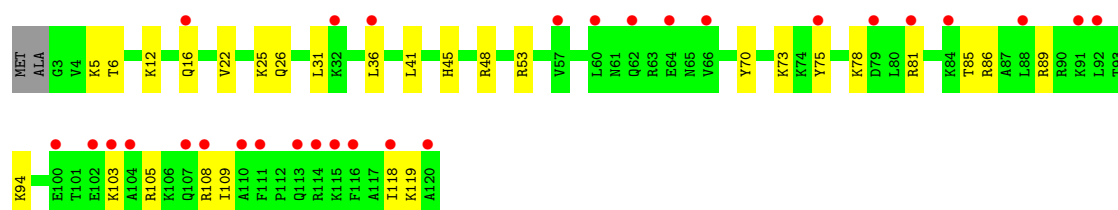
- Molecule 36: Ribosomal protein L29

Chain AI: 11% 82% 18%



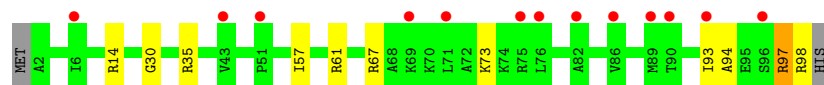
- Molecule 36: Ribosomal protein L29

Chain CC: 24% 75% 23%



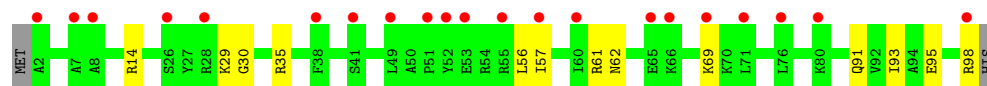
- Molecule 37: 60S ribosomal protein L36

Chain AJ: 13% 87% 10%



- Molecule 37: 60S ribosomal protein L36

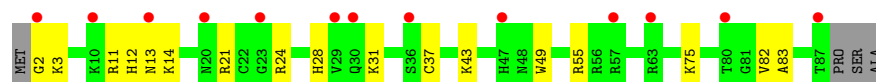
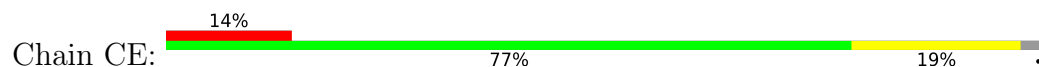
Chain CD: 21% 85% 13%



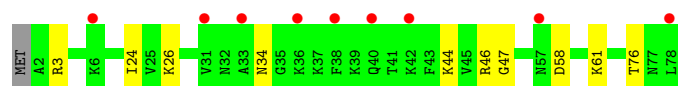
• Molecule 38: 60S ribosomal protein L37-B



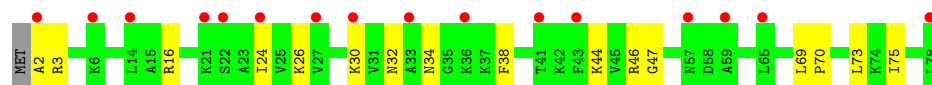
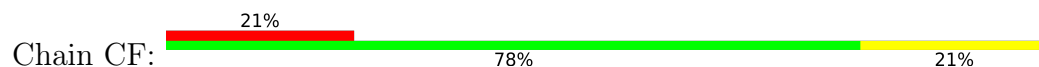
• Molecule 38: 60S ribosomal protein L37-B



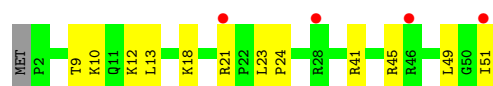
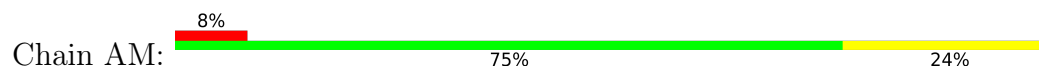
• Molecule 39: 60S ribosomal protein L38



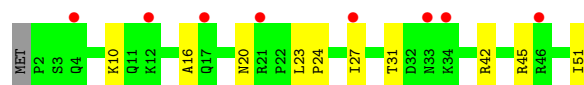
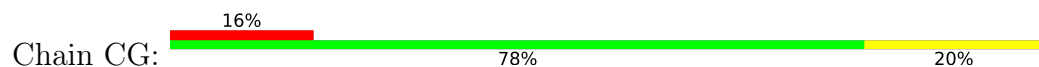
• Molecule 39: 60S ribosomal protein L38



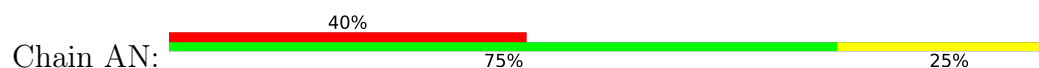
• Molecule 40: 60S ribosomal protein L39



• Molecule 40: 60S ribosomal protein L39

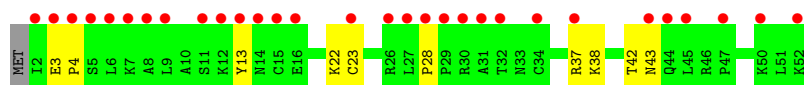
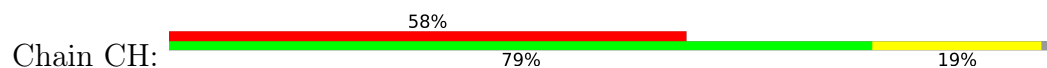


• Molecule 41: 60S ribosomal protein L40-B

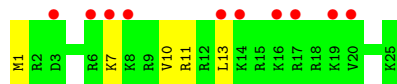
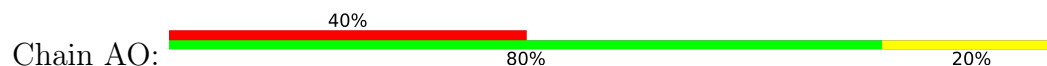




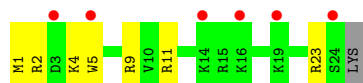
- Molecule 41: 60S ribosomal protein L40-B



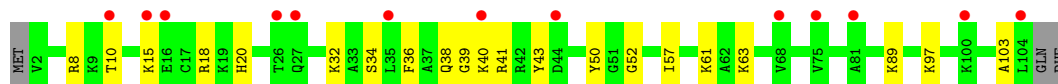
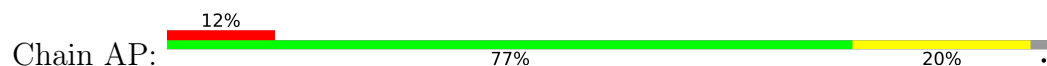
- Molecule 42: 60S ribosomal protein L41



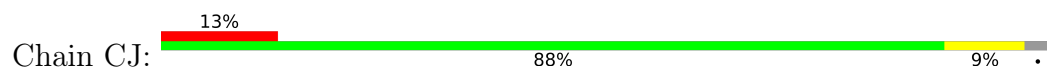
- Molecule 42: 60S ribosomal protein L41



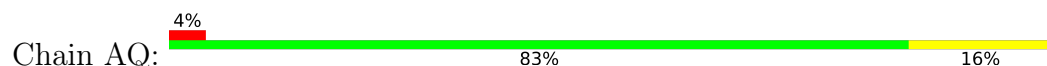
- Molecule 43: 60S ribosomal protein L42-B



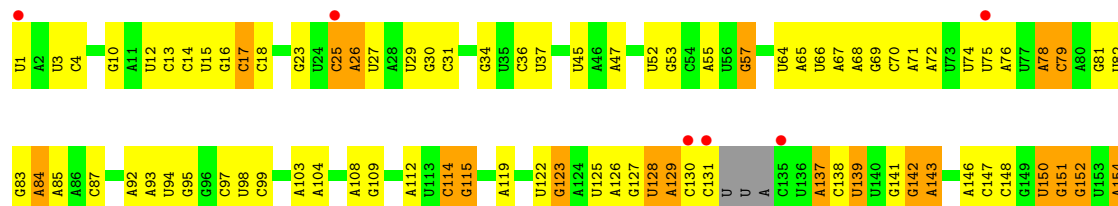
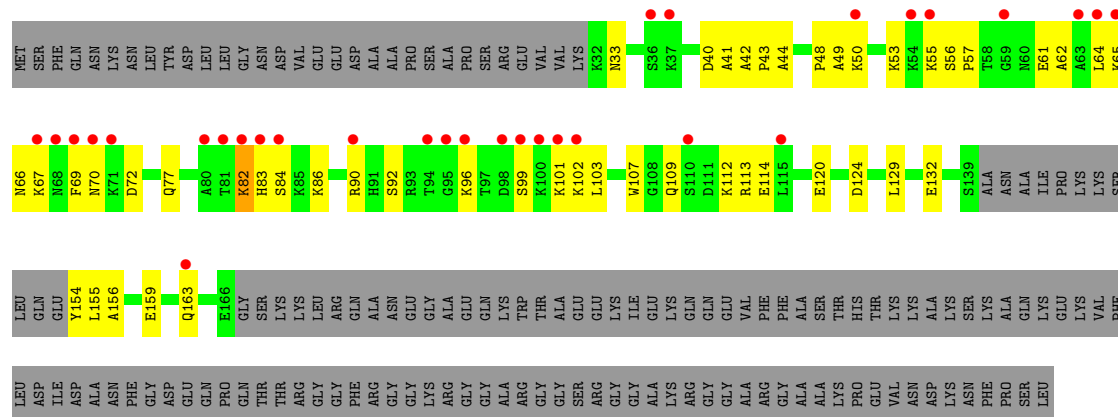
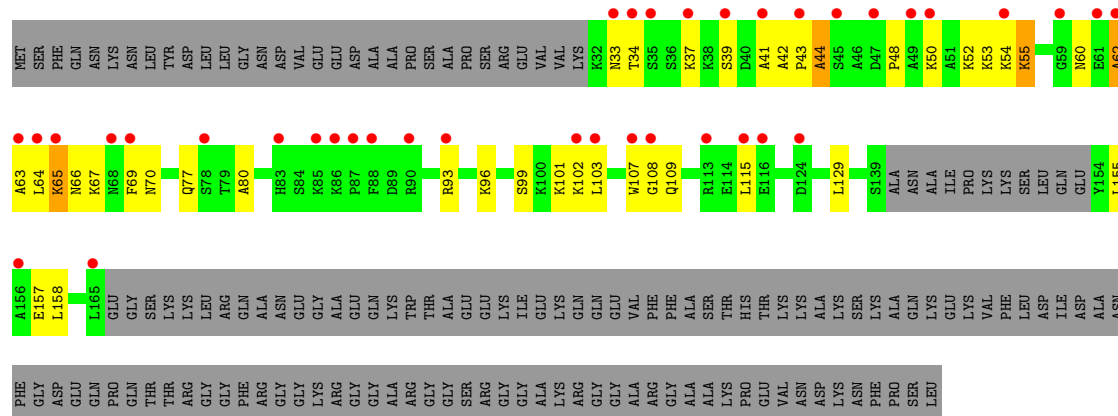
- Molecule 43: 60S ribosomal protein L42-B

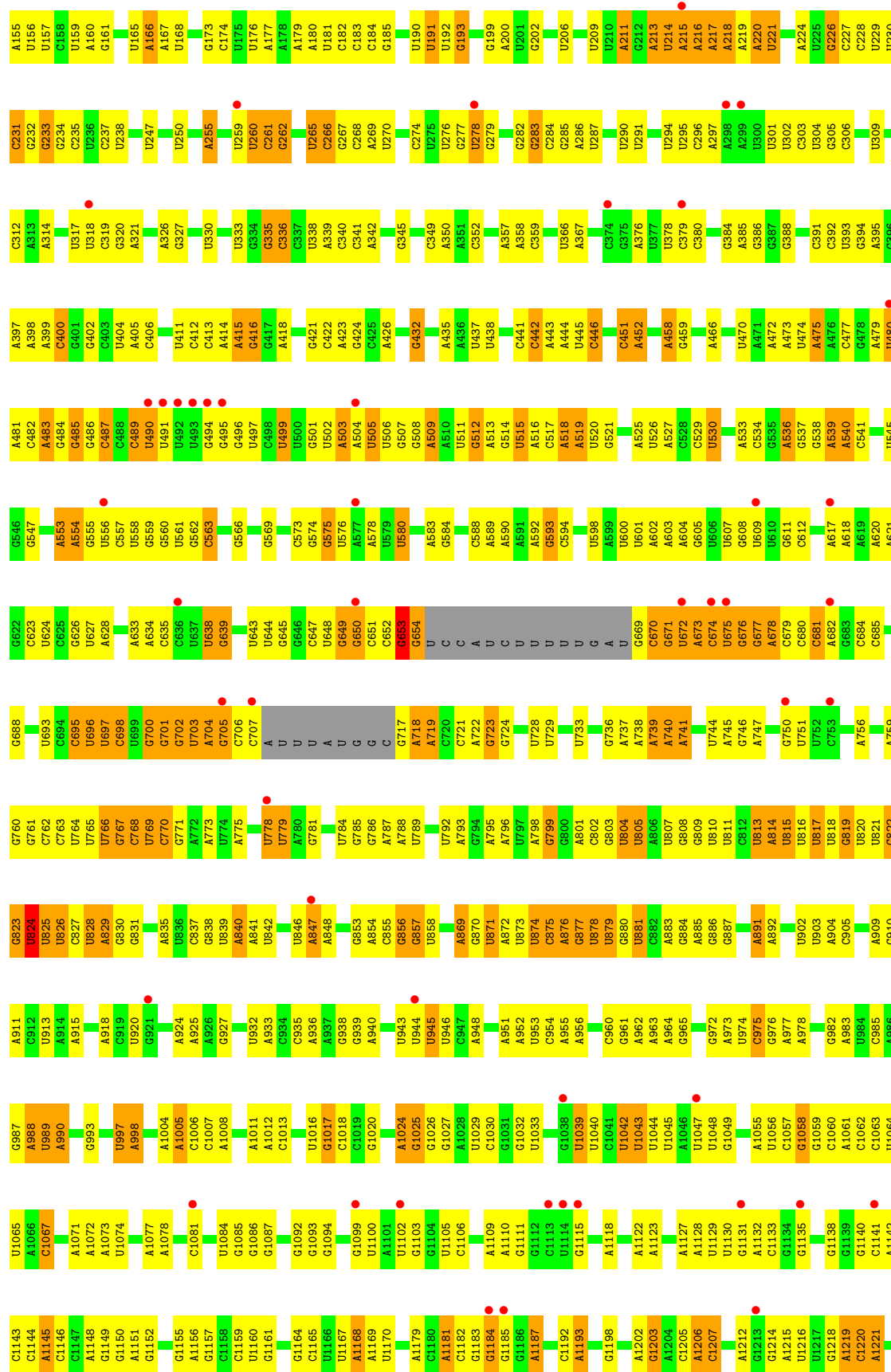


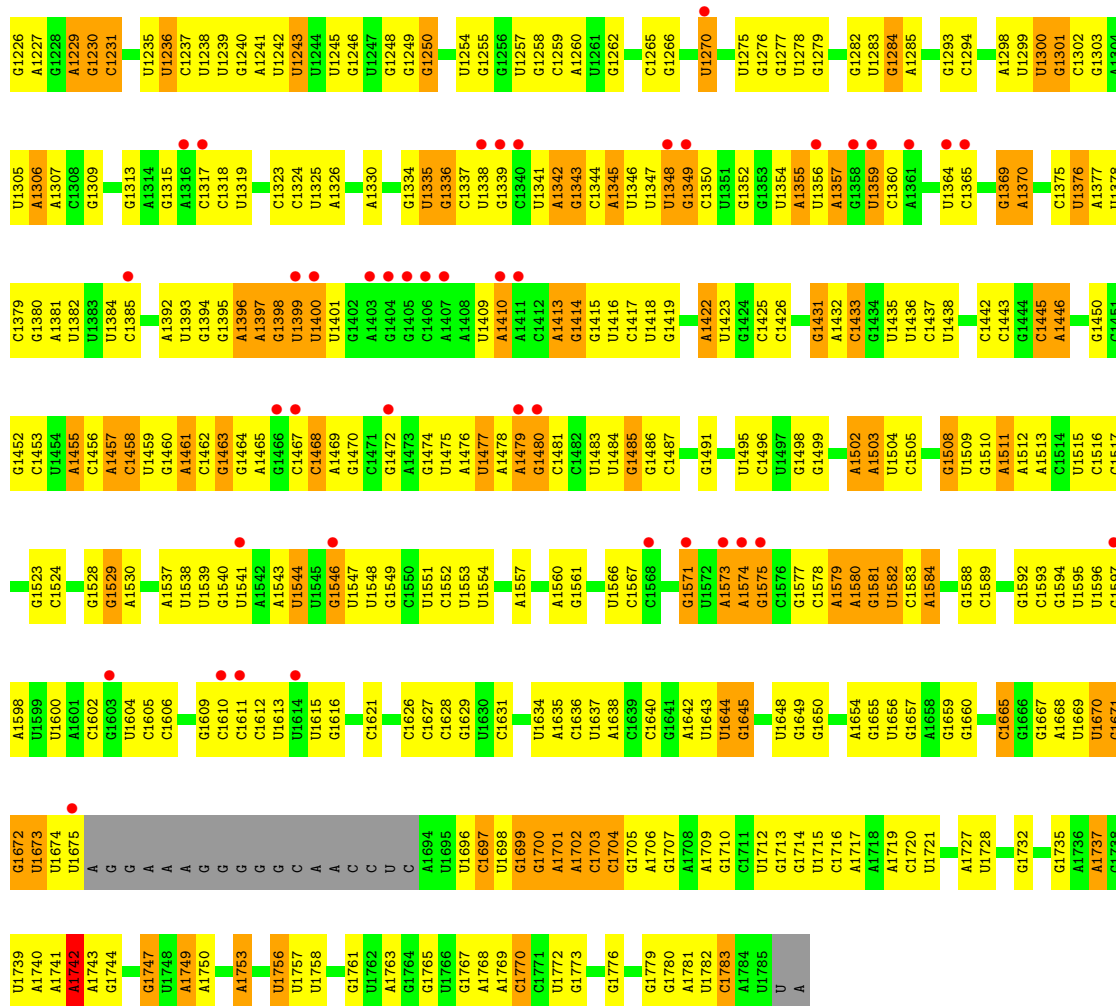
- Molecule 44: 60S ribosomal protein L43-A



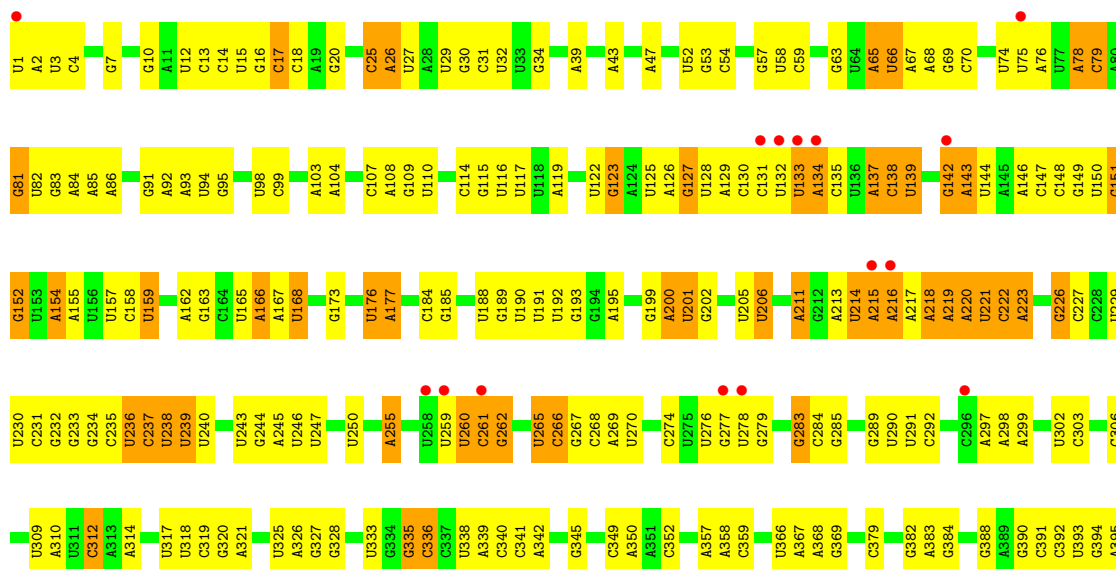
- Molecule 44: 60S ribosomal protein L43-A

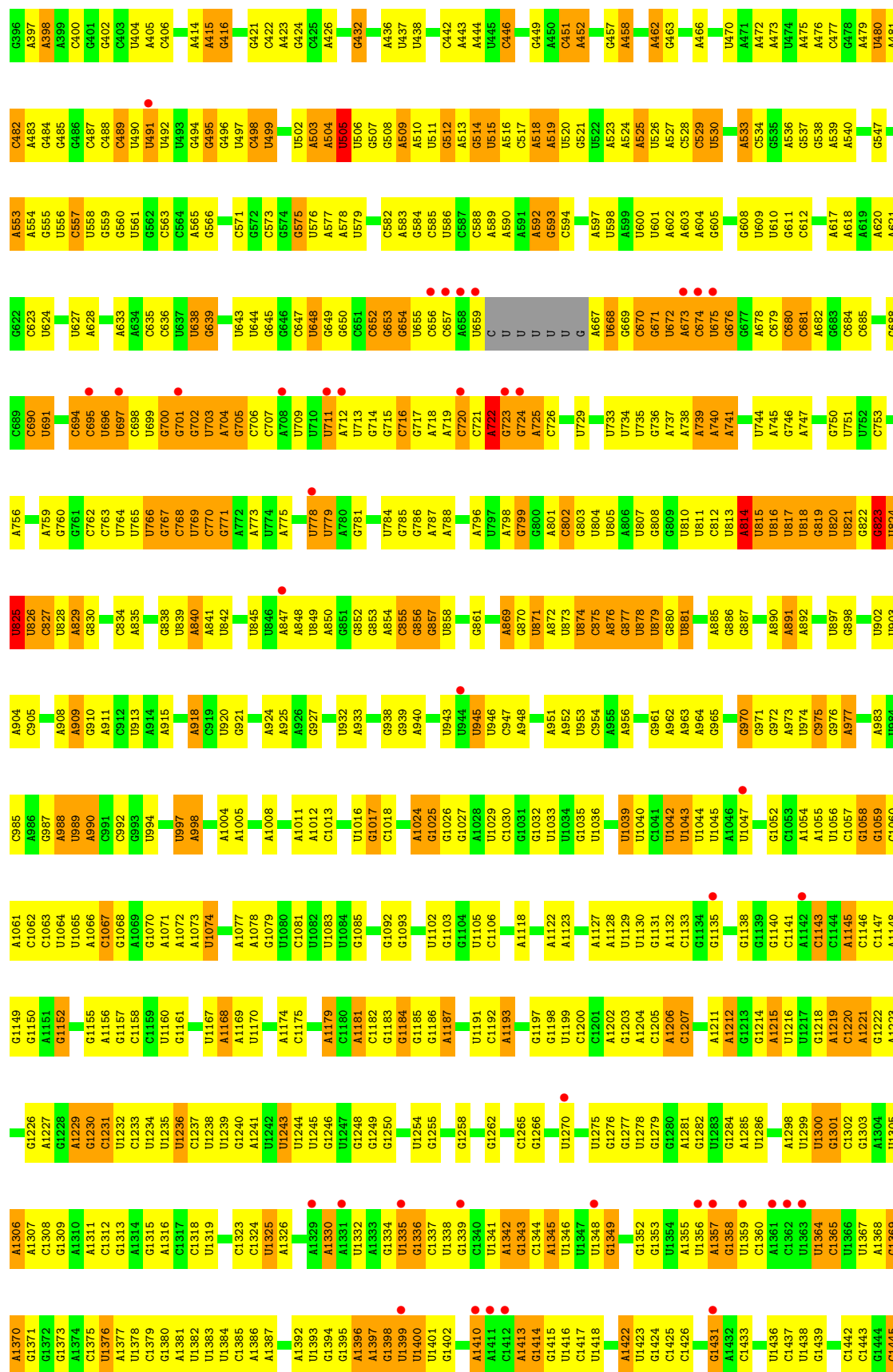


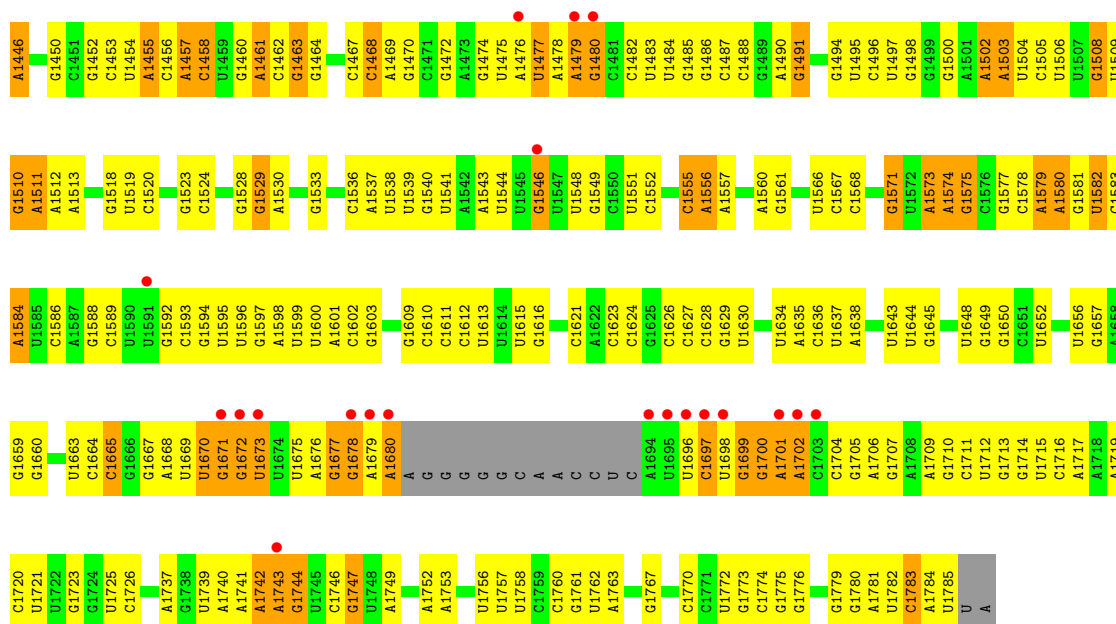




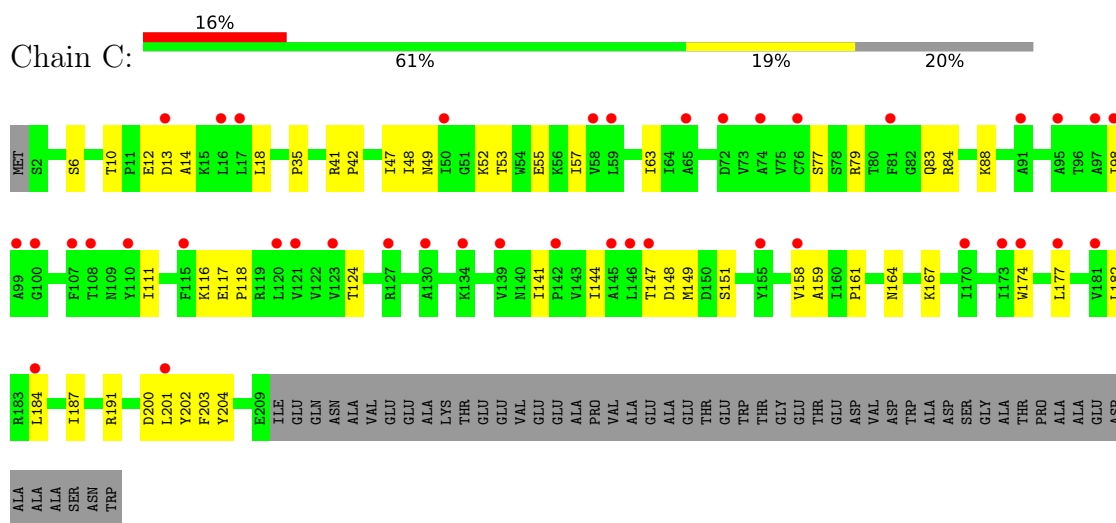
• Molecule 46: 18S



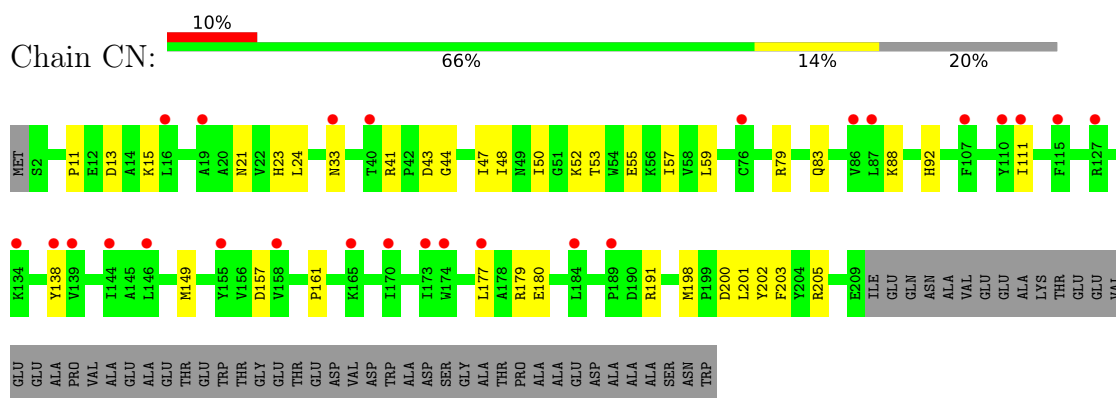


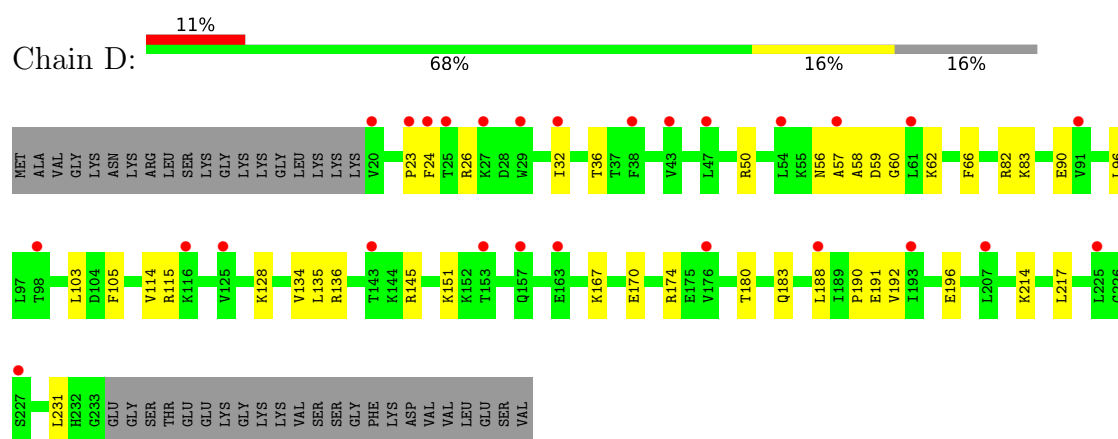


• Molecule 47: 40S ribosomal protein S0

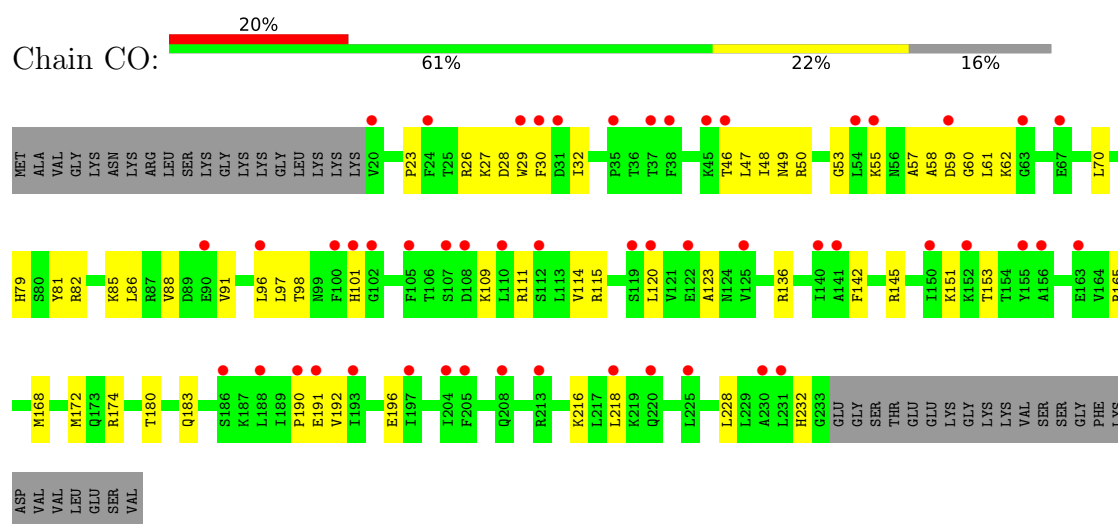


• Molecule 48: 40S ribosomal protein S1

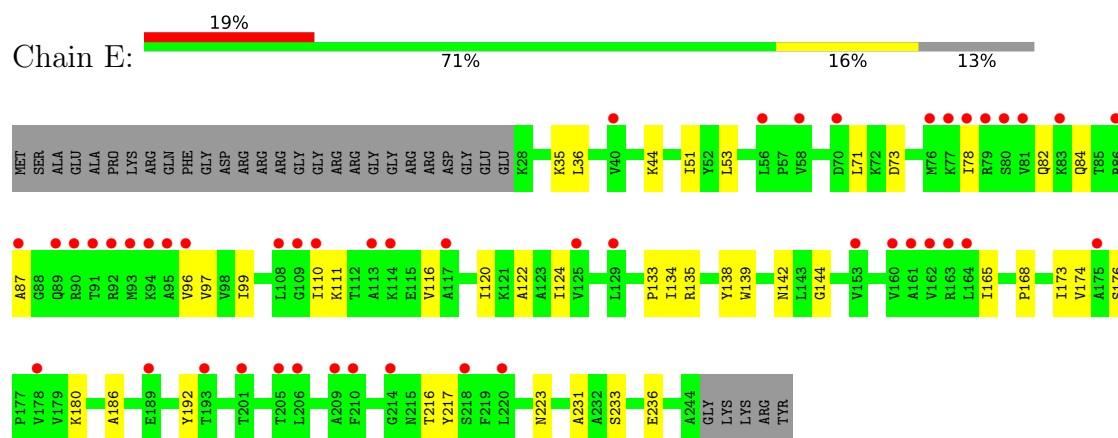




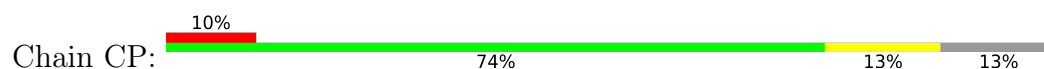
- Molecule 48: 40S ribosomal protein S1

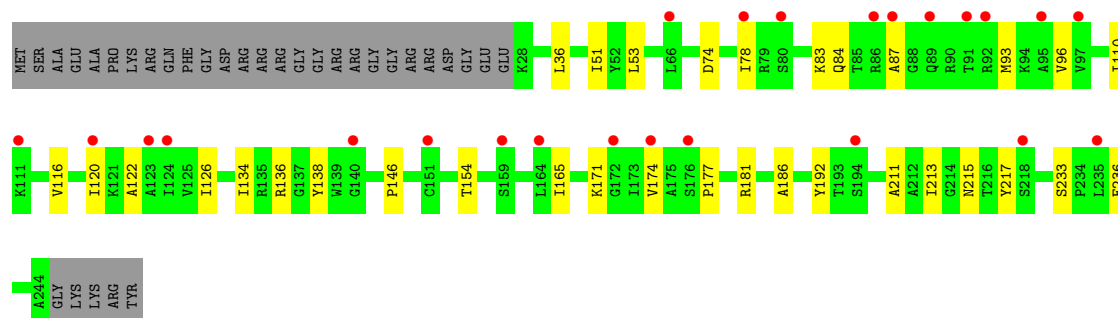


- Molecule 49: Ribosomal protein S5

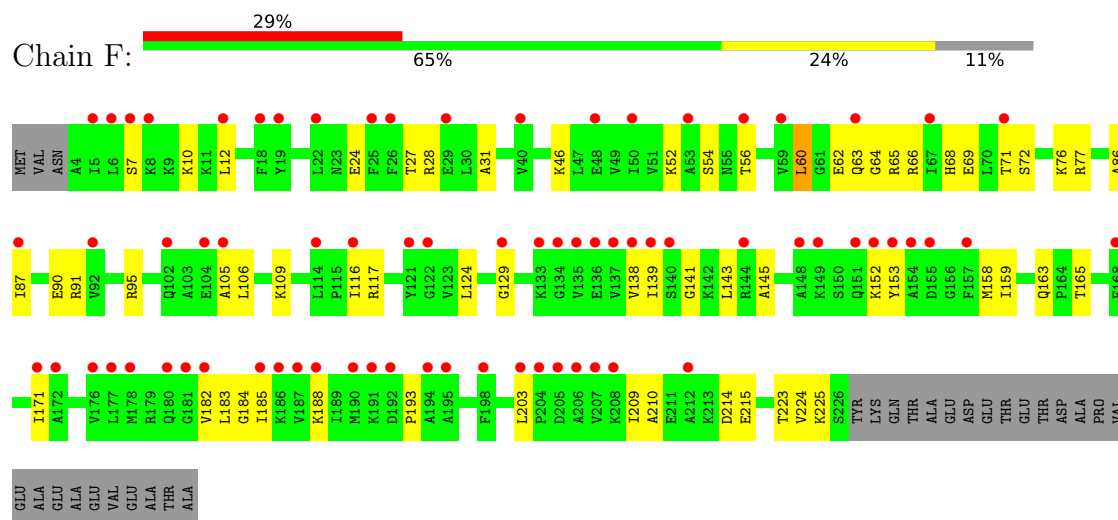


- Molecule 49: Ribosomal protein S5

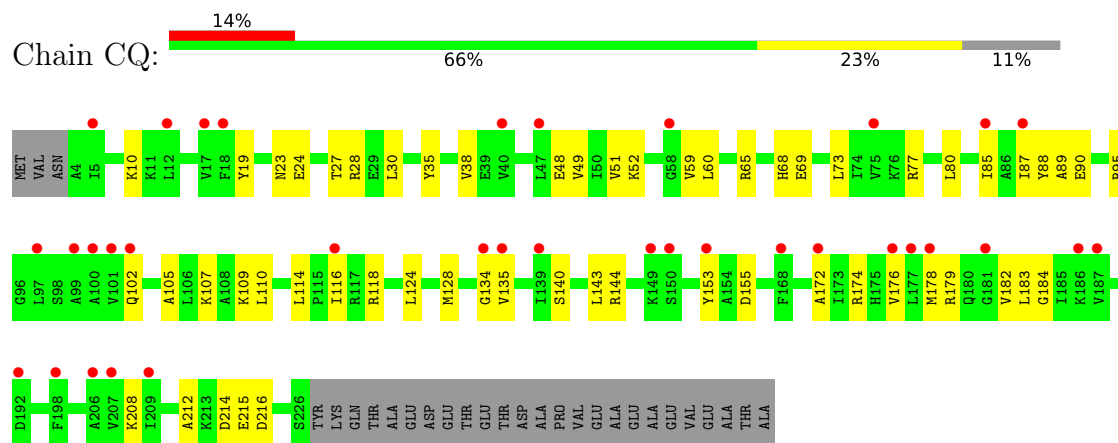




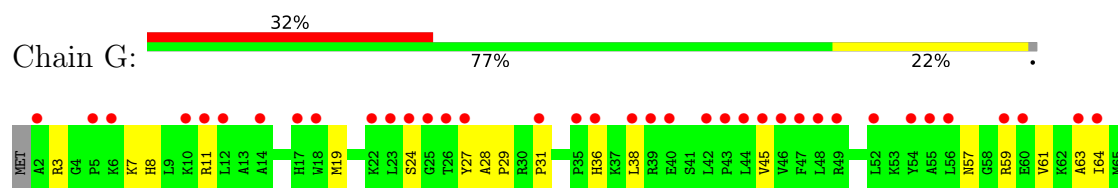
- Molecule 50: Ribosomal protein S3

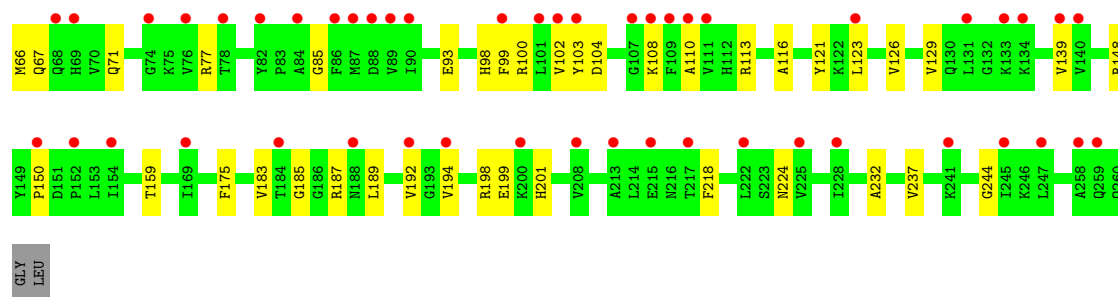


- Molecule 50: Ribosomal protein S3

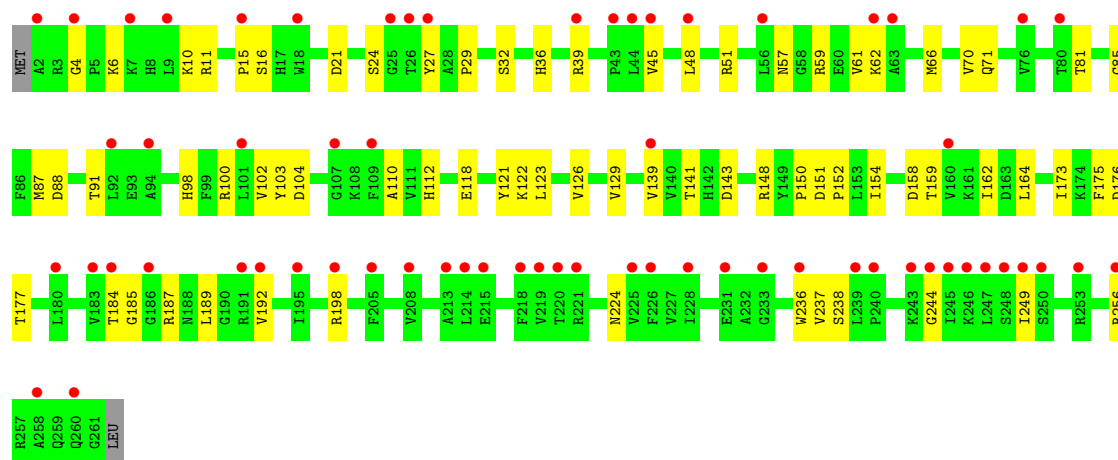
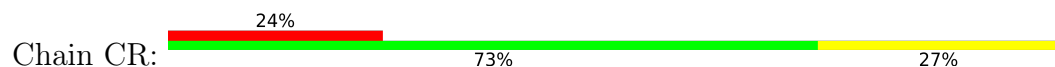


- Molecule 51: 40S ribosomal protein S4

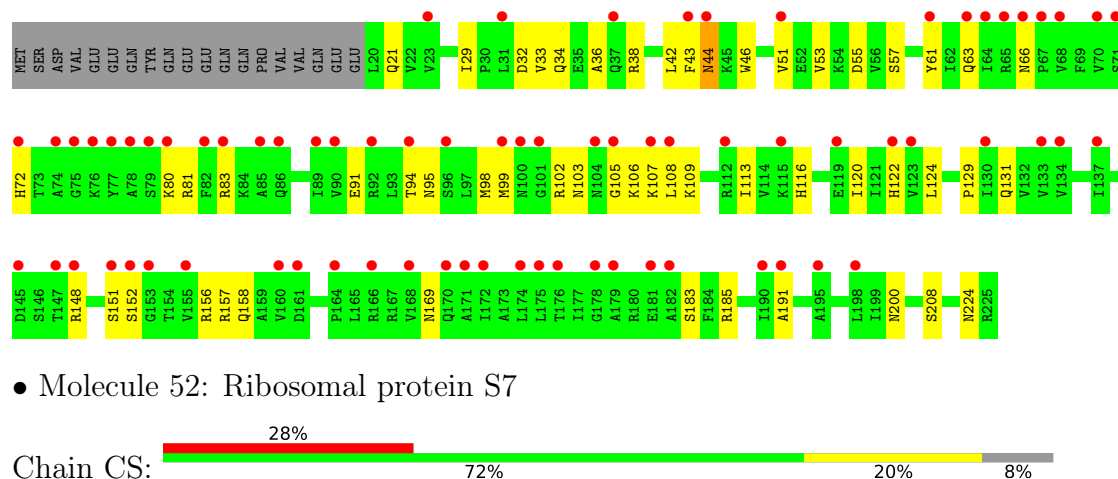




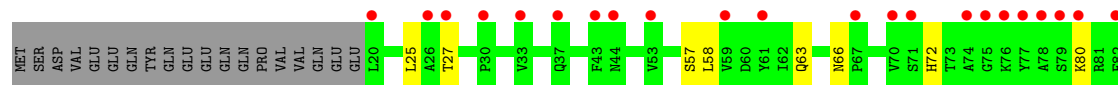
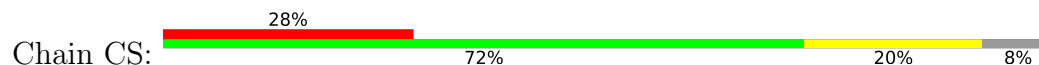
- Molecule 51: 40S ribosomal protein S4

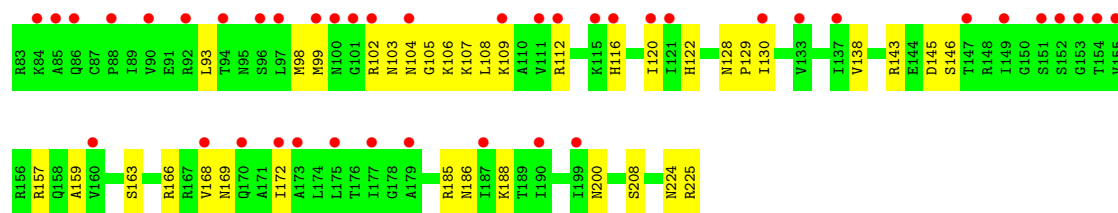


- Molecule 52: Ribosomal protein S7

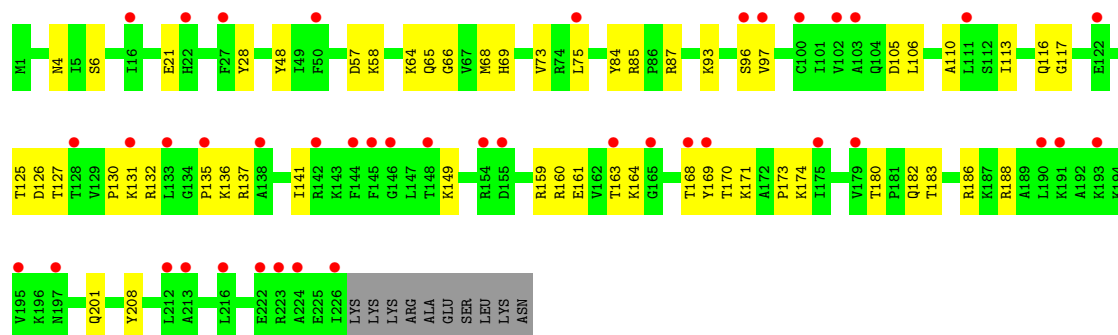
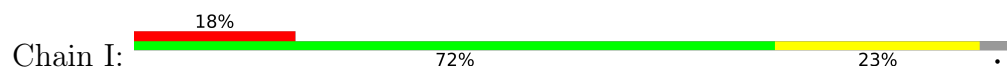


- Molecule 52: Ribosomal protein S7

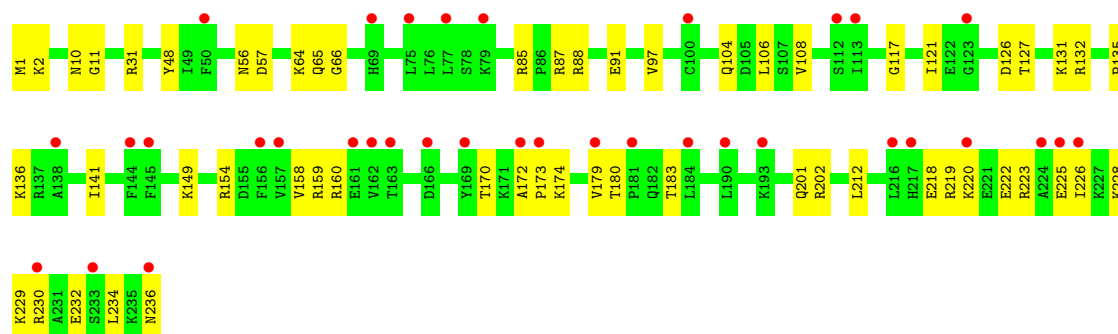
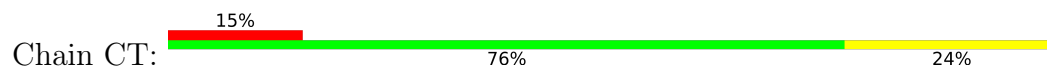




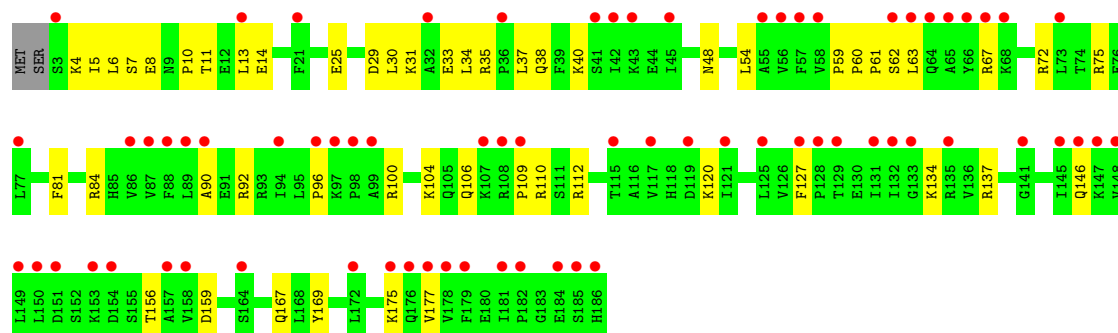
• Molecule 53: 40S ribosomal protein S6



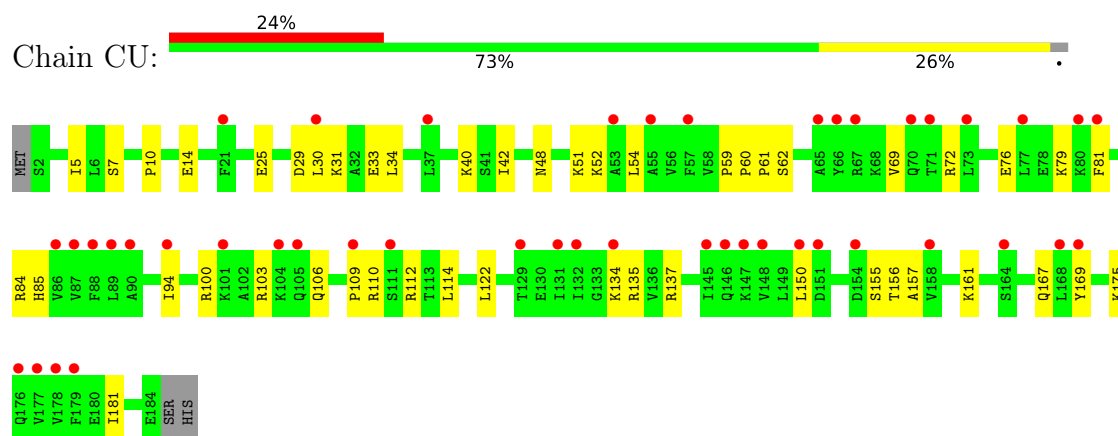
• Molecule 53: 40S ribosomal protein S6



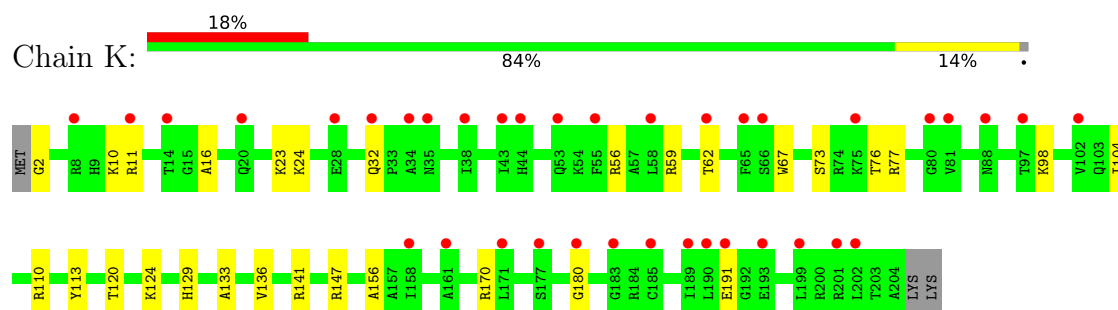
• Molecule 54: 40S ribosomal protein S7



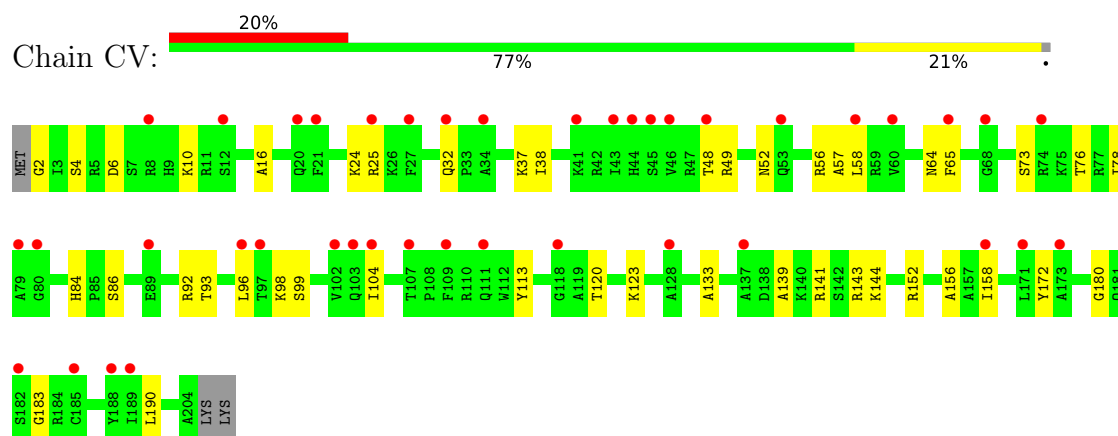
- Molecule 54: 40S ribosomal protein S7



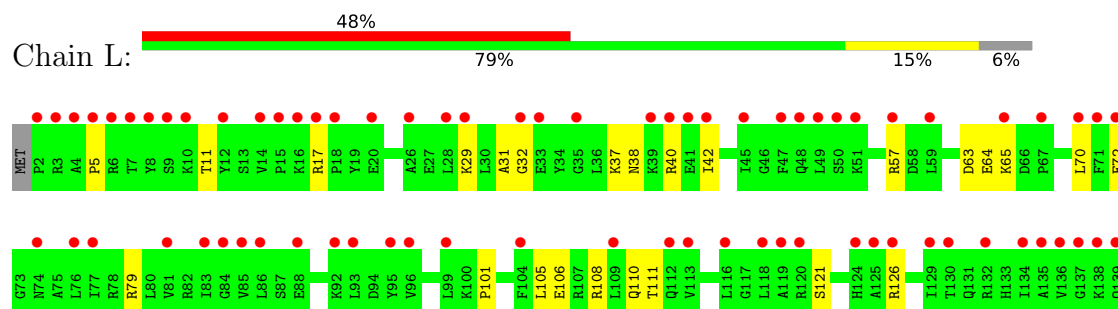
- Molecule 55: 40S ribosomal protein S8

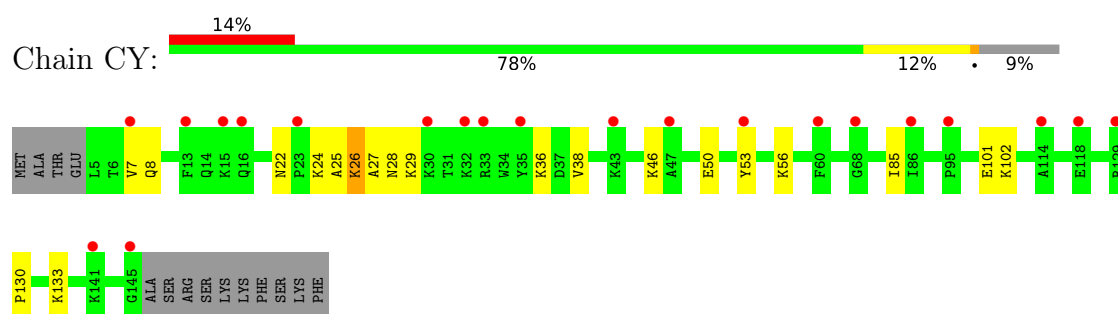


- Molecule 55: 40S ribosomal protein S8

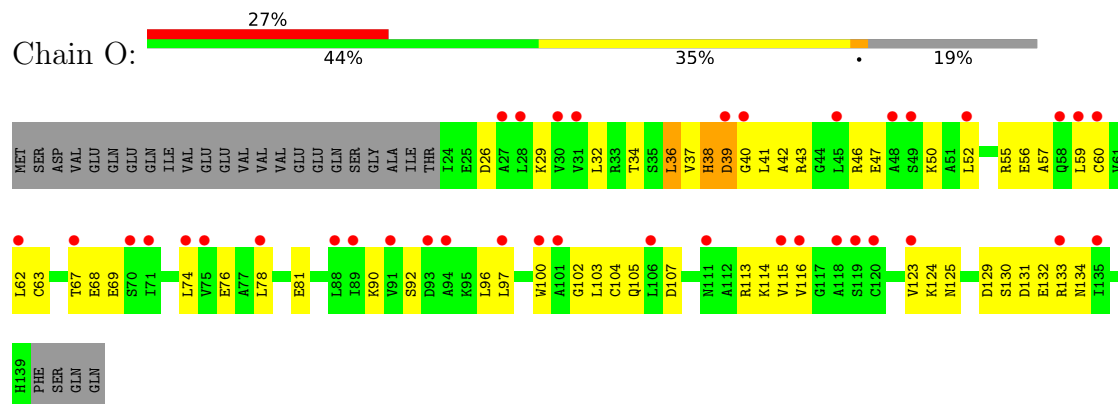


- Molecule 56: Ribosomal protein S4

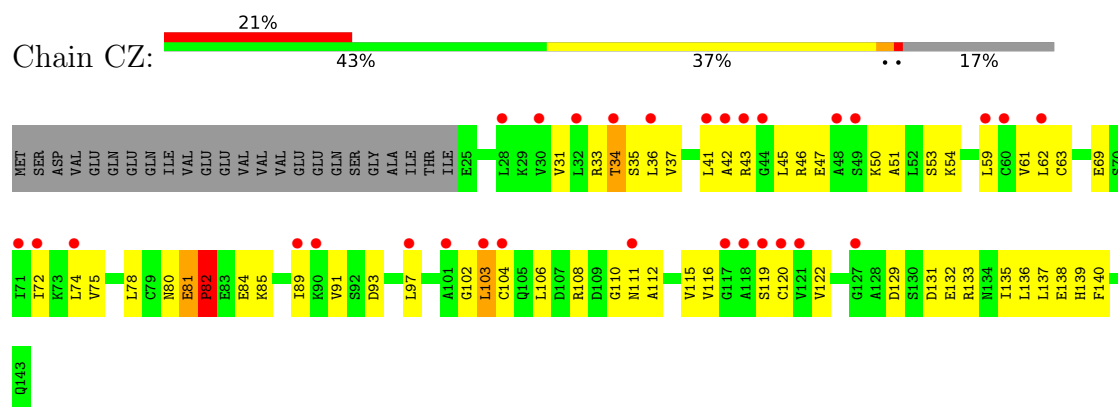




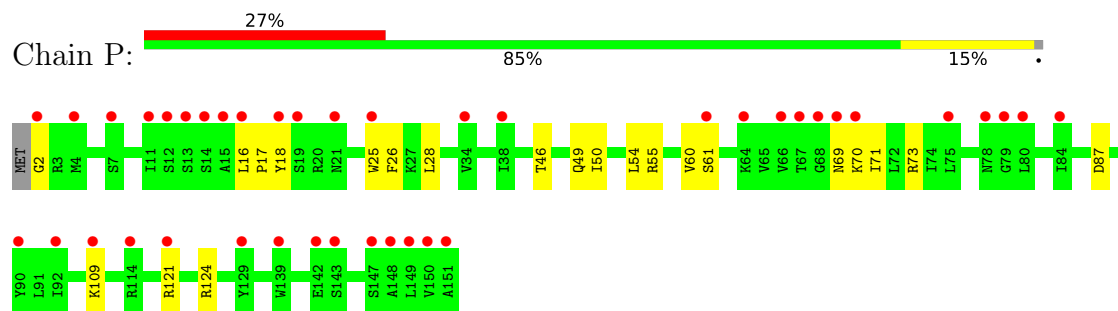
- Molecule 59: 40S ribosomal protein S12



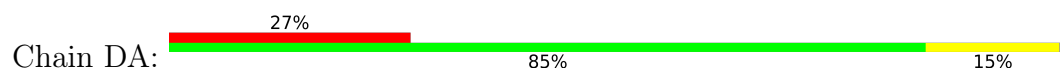
- Molecule 59: 40S ribosomal protein S12

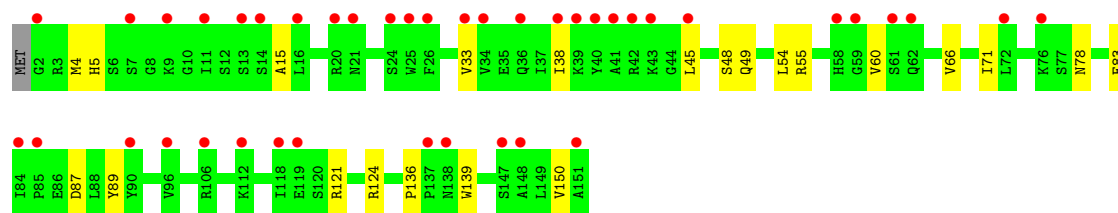


- Molecule 60: 40S ribosomal protein S13

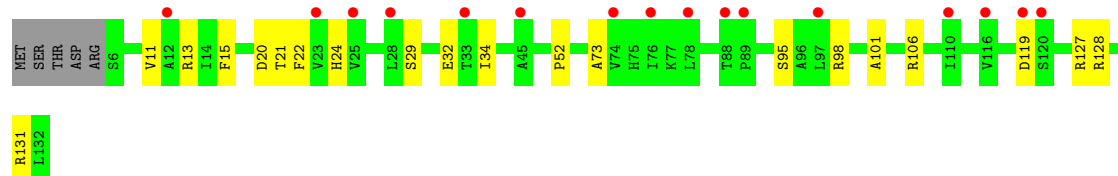
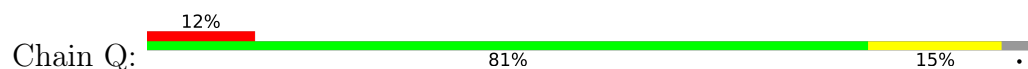


- Molecule 60: 40S ribosomal protein S13

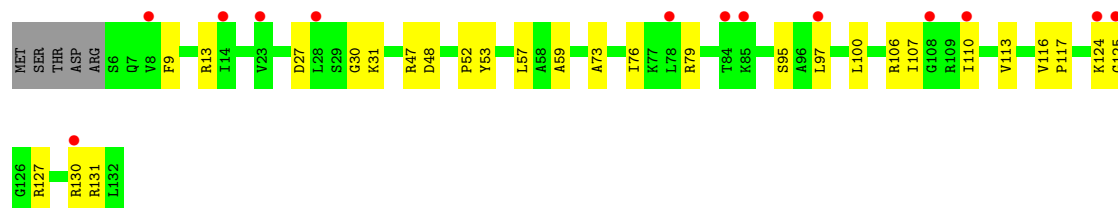
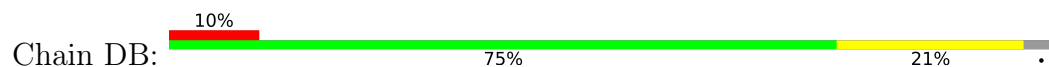




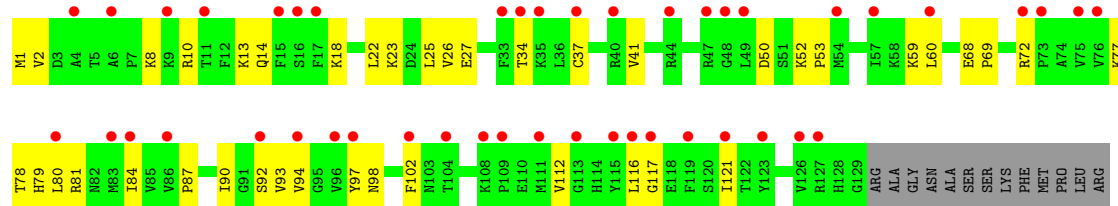
- Molecule 61: 40S ribosomal protein S14-A



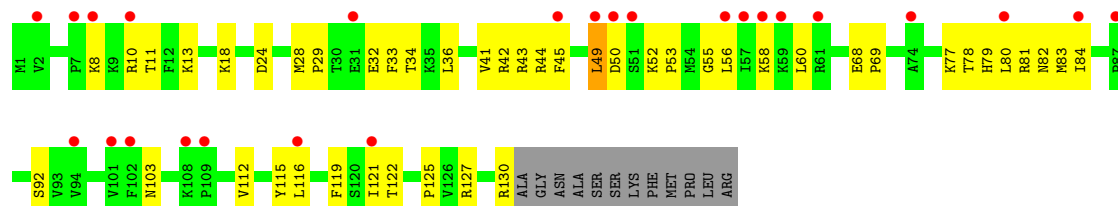
- Molecule 61: 40S ribosomal protein S14-A



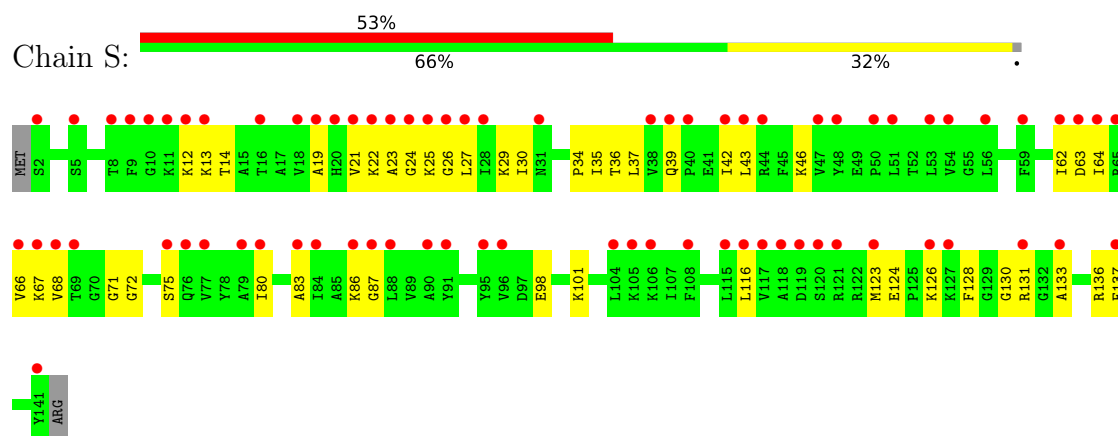
- Molecule 62: 40S ribosomal protein S15



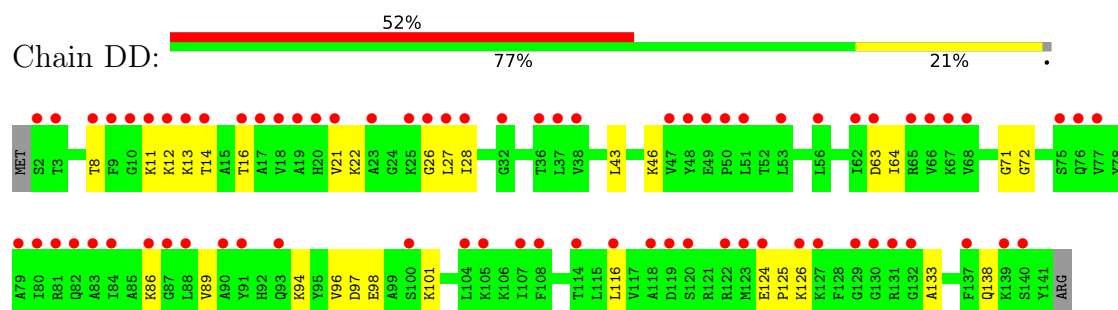
- Molecule 62: 40S ribosomal protein S15



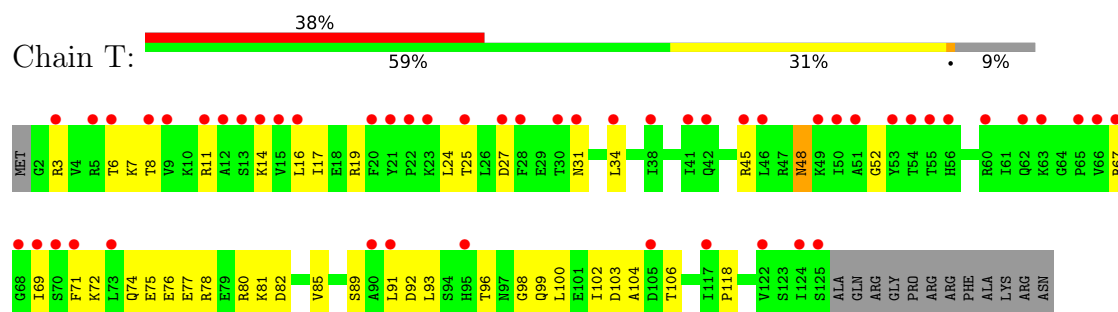
- Molecule 63: 40S ribosomal protein S16



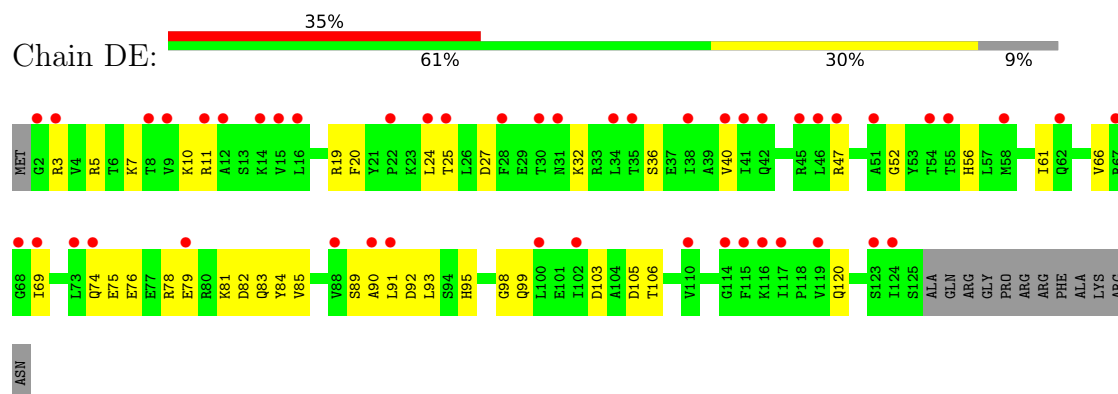
- Molecule 63: 40S ribosomal protein S16



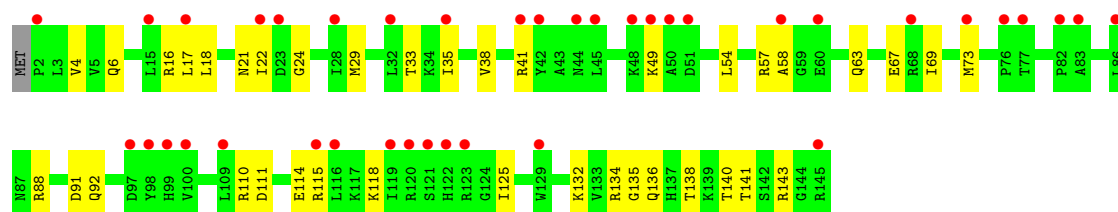
- Molecule 64: 40S ribosomal protein S17-B



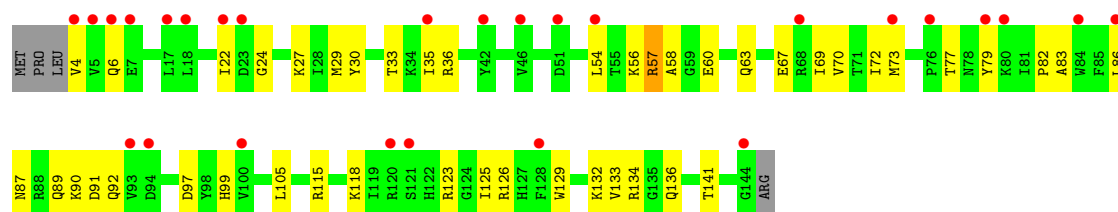
- Molecule 64: 40S ribosomal protein S17-B



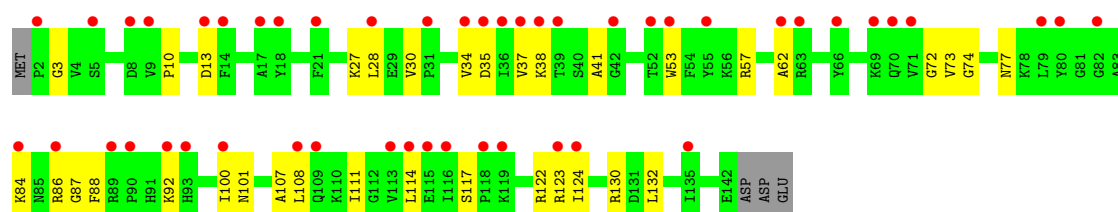
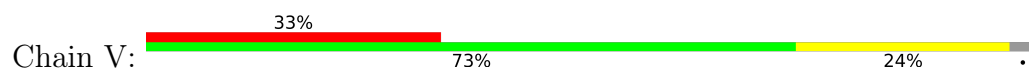
- Molecule 65: 40S ribosomal protein S18-B



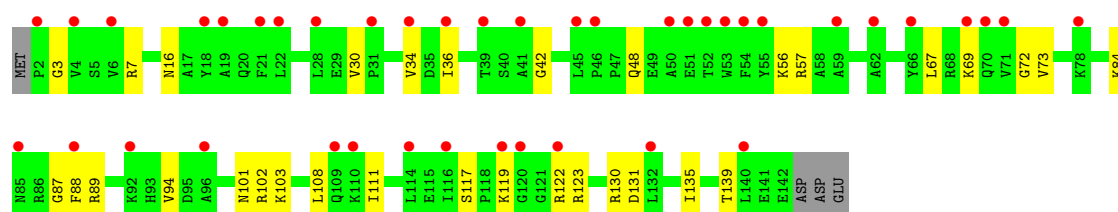
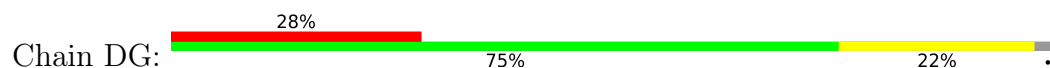
• Molecule 65: 40S ribosomal protein S18-B



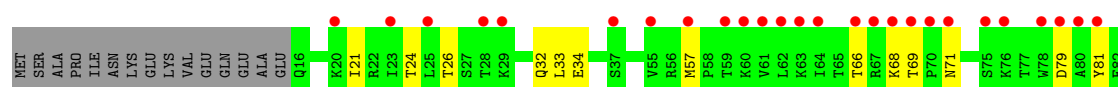
• Molecule 66: 40S ribosomal protein S19-A

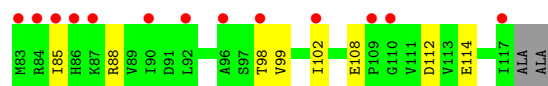


• Molecule 66: 40S ribosomal protein S19-A

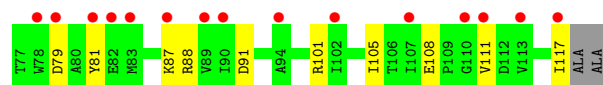
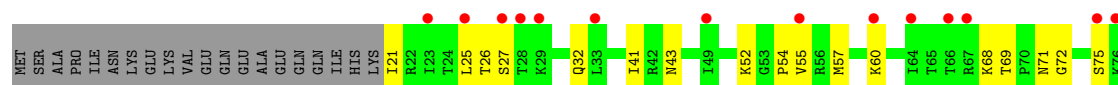


• Molecule 67: Ribosomal protein S10





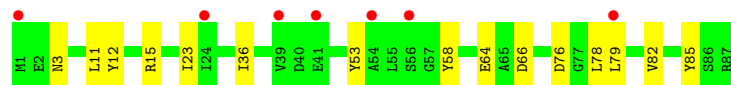
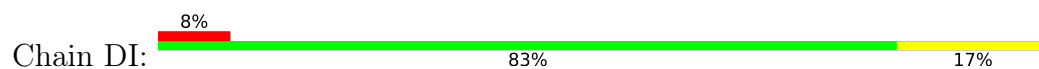
● Molecule 67: Ribosomal protein S10



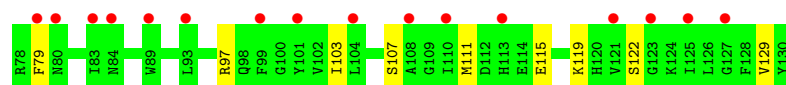
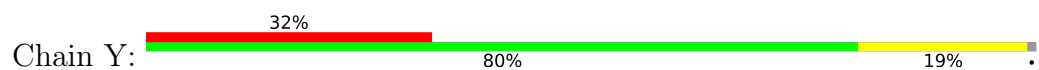
● Molecule 68: 40S ribosomal protein S21



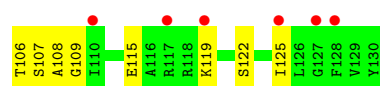
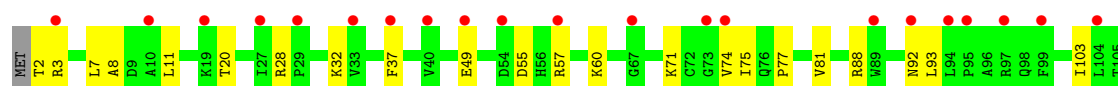
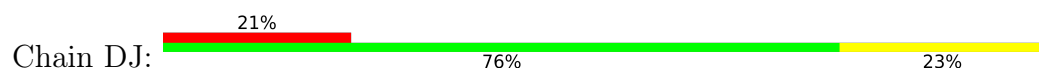
● Molecule 68: 40S ribosomal protein S21



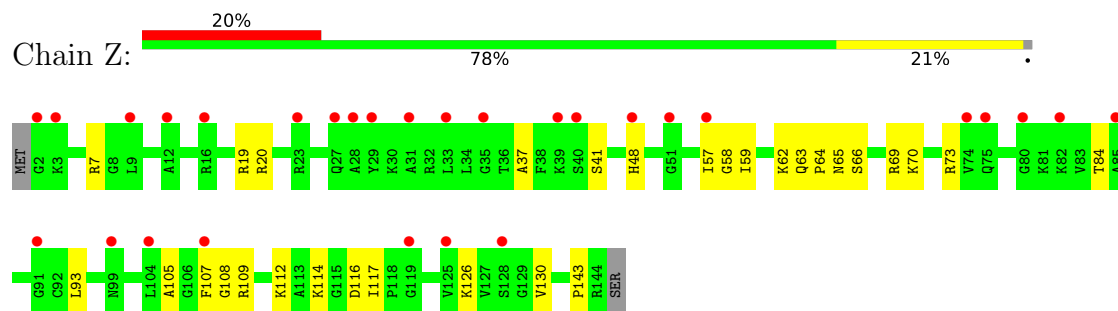
● Molecule 69: 40S ribosomal protein S22-A



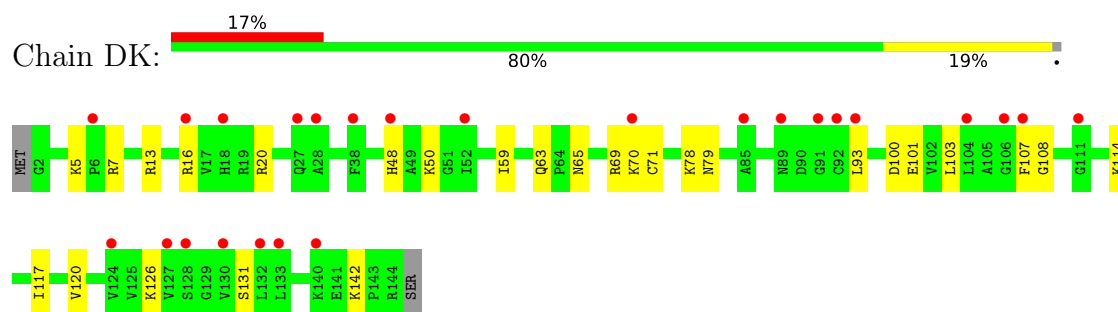
● Molecule 69: 40S ribosomal protein S22-A



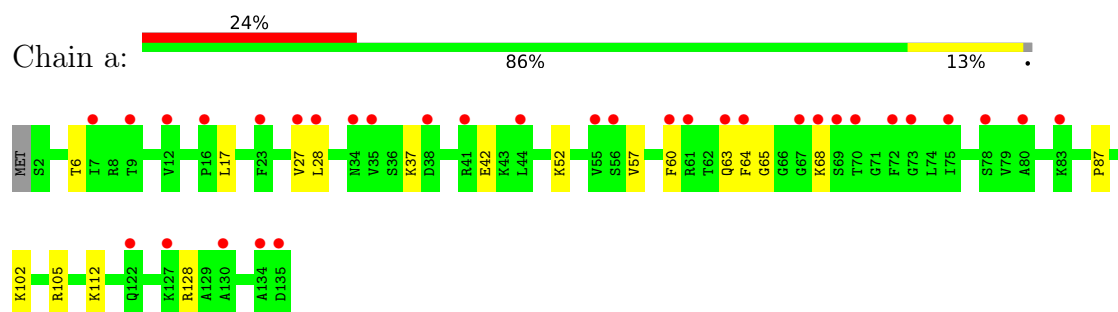
- Molecule 70: Ribosomal protein S23 (S12)



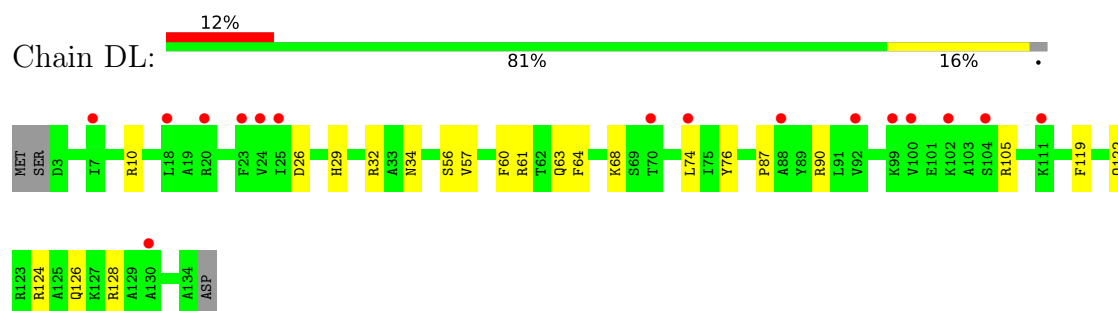
- Molecule 70: Ribosomal protein S23 (S12)



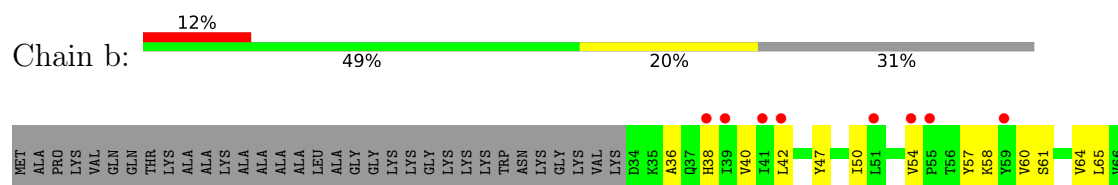
- Molecule 71: 40S ribosomal protein S24



- Molecule 71: 40S ribosomal protein S24

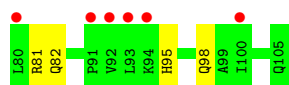
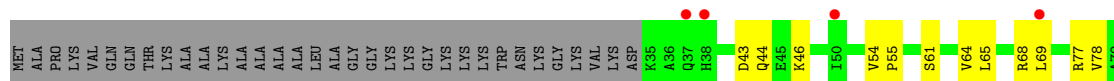


- Molecule 72: 40S ribosomal protein S25

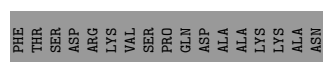




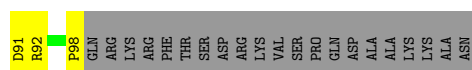
- Molecule 72: 40S ribosomal protein S25



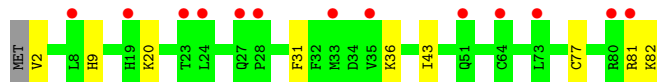
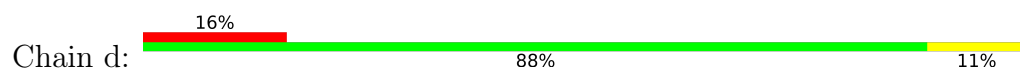
- Molecule 73: 40S ribosomal protein S26



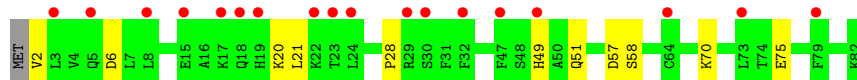
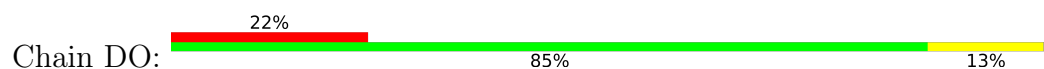
- Molecule 73: 40S ribosomal protein S26

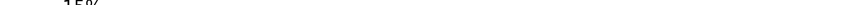


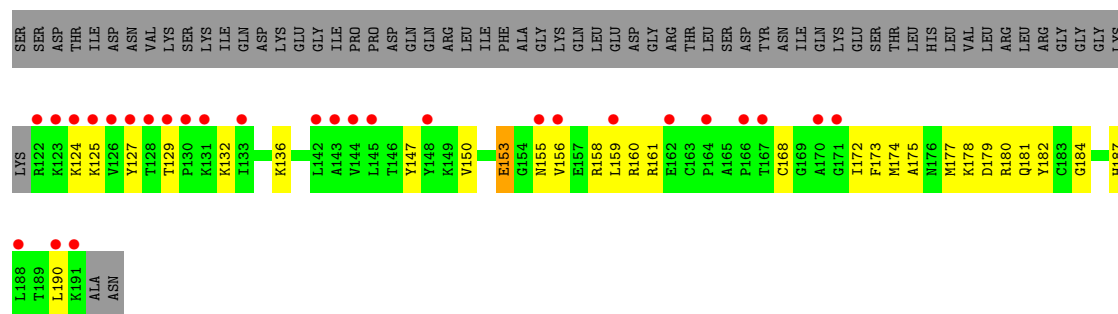
- Molecule 74: 40S ribosomal protein S27



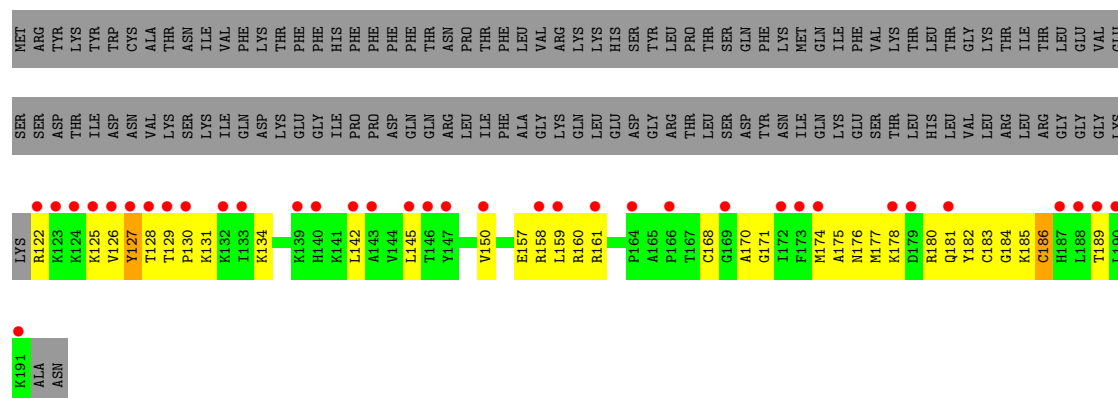
- Molecule 74: 40S ribosomal protein S27



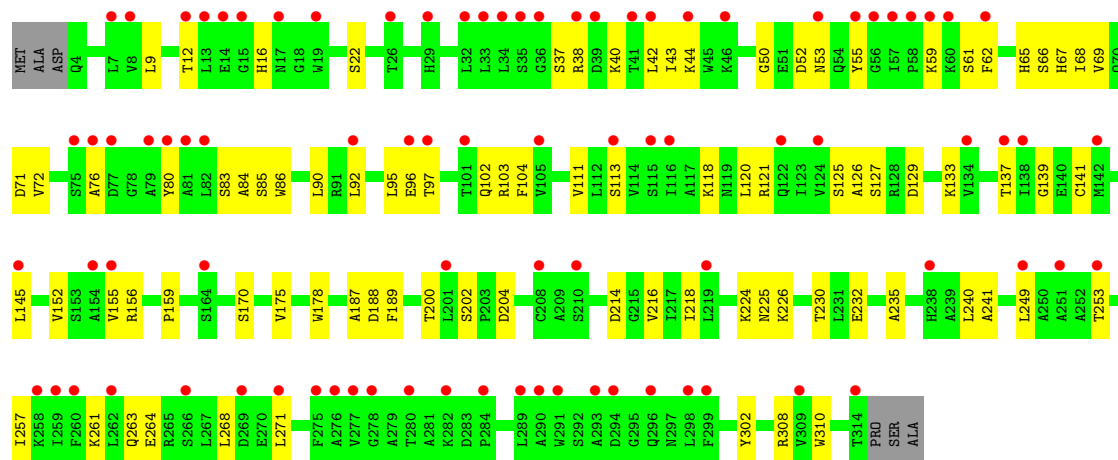
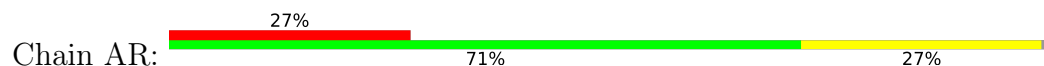
- Chain h: 



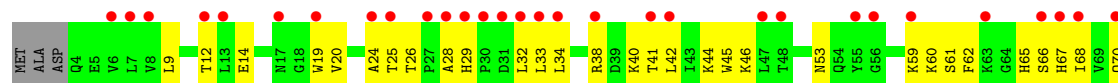
- Molecule 78: Ubiquitin-40S ribosomal protein S31 fusion protein

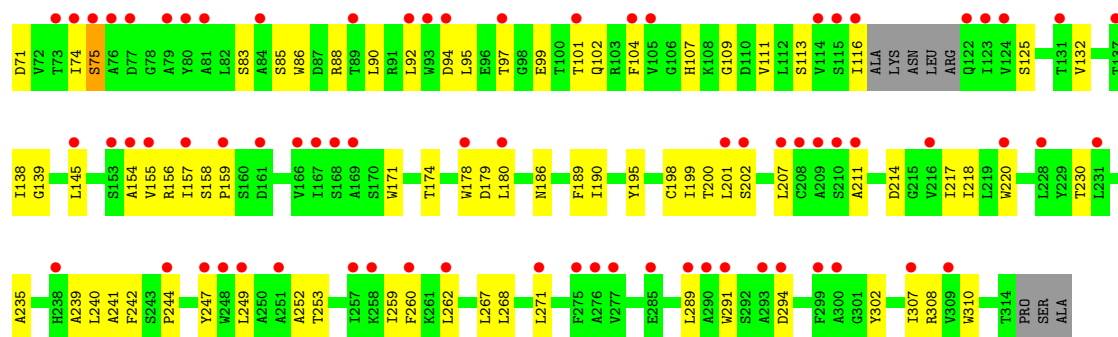


- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein

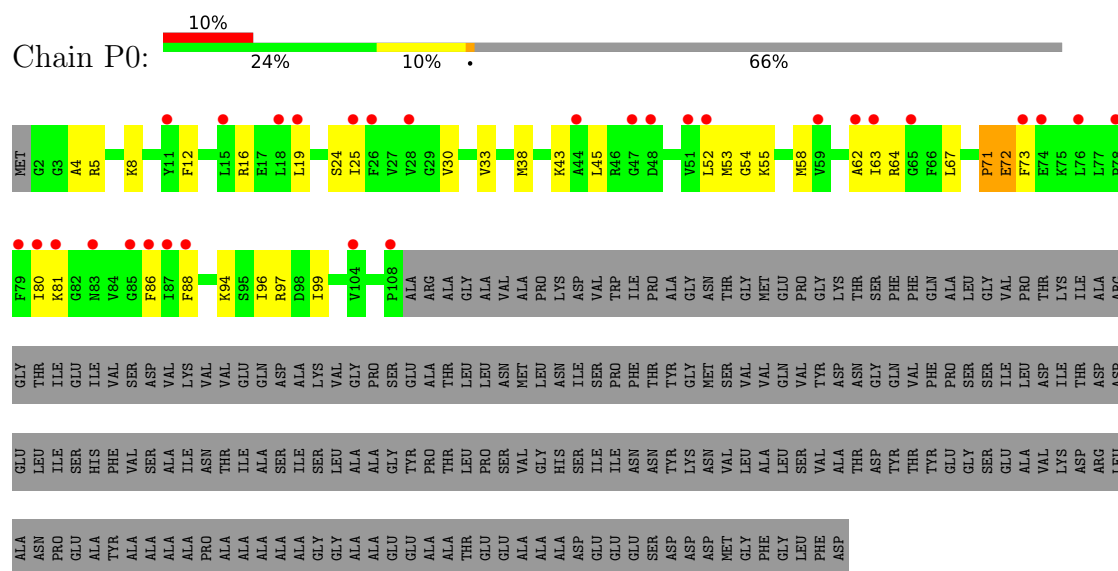


- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein

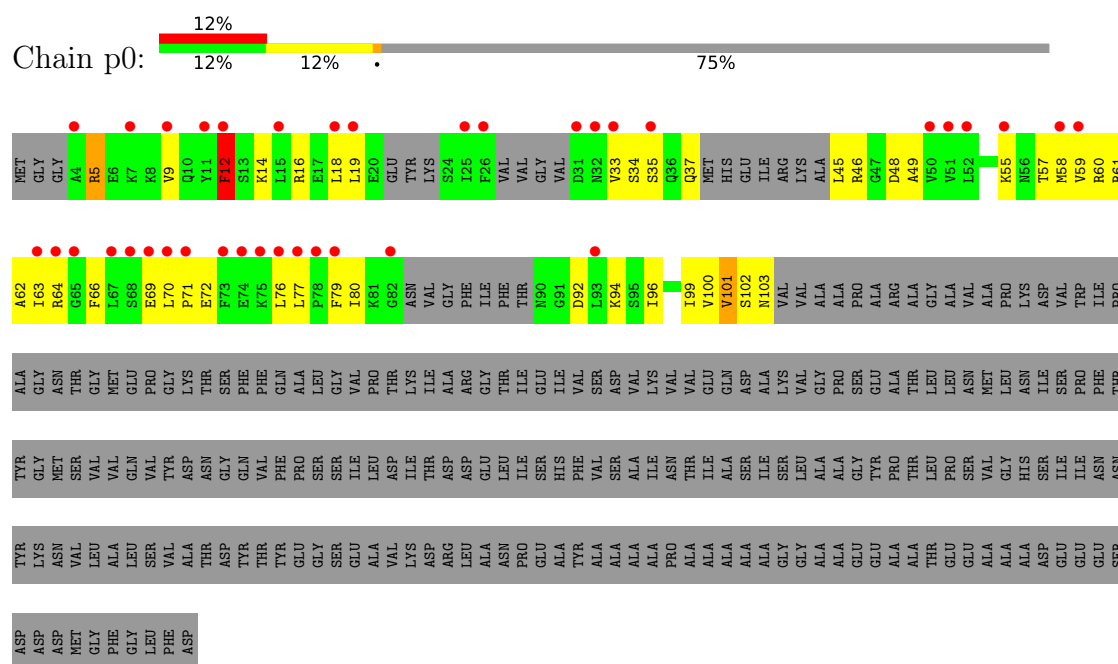




• Molecule 80: 60S acidic ribosomal protein P0



• Molecule 80: 60S acidic ribosomal protein P0



Chain 12:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	298.81Å 292.84Å 450.18Å 90.00° 100.11° 90.00°	Depositor
Resolution (Å)	163.72 – 3.05 163.72 – 3.05	Depositor EDS
% Data completeness (in resolution range)	99.1 (163.72-3.05) 89.6 (163.72-3.05)	Depositor EDS
R_{merge}	0.84	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.00 (at 3.07Å)	Xtriage
Refinement program	PHENIX (1.19rc4_4035: ???)	Depositor
R, R_{free}	0.283 , 0.307 (Not available) , 0.283	Depositor DCC
R_{free} test set	2000 reflections (0.14%)	wwPDB-VP
Wilson B-factor (Å ²)	50.5	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	408804	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.31% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3K5, HYG, 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	1	0.18	0/76756	0.44	8/119655 (0.0%)
1	AS	0.17	0/77209	0.42	3/120366 (0.0%)
2	3	0.15	0/2884	0.32	0/4492
2	AT	0.15	0/2884	0.32	0/4492
3	4	0.15	0/3724	0.38	1/5798 (0.0%)
3	AU	0.15	0/3724	0.38	1/5798 (0.0%)
4	AW	0.14	0/1922	0.36	0/2581
4	j	0.17	0/1922	0.41	0/2581
5	AX	0.15	0/3145	0.40	0/4231
5	k	0.16	0/3145	0.42	0/4231
6	AY	0.14	0/2799	0.38	0/3777
6	l	0.16	0/2799	0.42	0/3777
7	AZ	0.14	0/2447	0.36	0/3294
7	m	0.16	0/2479	0.43	0/3337
8	BA	0.14	0/1231	0.38	0/1662
8	n	0.15	0/1263	0.38	0/1703
9	BB	0.14	0/1918	0.35	0/2575
9	o	0.16	0/1909	0.38	0/2563
10	BC	0.27	0/1807	0.51	0/2434
10	p	0.17	0/1835	0.42	0/2472
11	BD	0.15	0/1537	0.39	0/2067
11	q	0.17	0/1528	0.42	0/2055
12	BE	0.17	0/1724	0.42	0/2314
12	r	0.22	0/1724	0.42	0/2314
13	BF	0.15	0/1390	0.40	0/1861
13	s	0.17	0/1390	0.44	0/1861
14	BG	0.17	0/1637	0.42	0/2195
14	t	0.16	0/1637	0.40	0/2195
15	BH	0.14	0/1044	0.38	0/1407
15	u	0.18	0/1044	0.40	0/1407
16	BI	0.14	0/1753	0.39	0/2347
16	v	0.17	0/1753	0.39	0/2347

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	BJ	0.17	0/1620	0.40	0/2167
17	w	0.16	0/1620	0.39	0/2167
18	BK	0.15	0/1429	0.38	0/1920
18	x	0.14	0/1410	0.38	0/1895
19	BL	0.14	0/1482	0.34	0/1985
19	y	0.14	0/1482	0.37	0/1985
20	BM	0.14	0/1475	0.40	0/1961
20	z	0.16	0/1475	0.37	0/1961
21	0	0.15	0/1457	0.39	0/1962
21	BN	0.15	0/1457	0.36	0/1962
22	2	0.18	0/1285	0.44	0/1723
22	BO	0.15	0/1285	0.38	0/1723
23	5	0.31	0/841	0.50	0/1133
23	BP	0.16	0/841	0.47	0/1133
24	6	0.14	0/993	0.38	0/1339
24	BQ	0.14	0/993	0.38	0/1339
25	7	0.14	0/958	0.30	0/1267
25	BR	0.13	0/814	0.28	0/1079
26	8	0.14	0/981	0.36	0/1326
26	BS	0.11	0/976	0.32	0/1319
27	9	0.13	0/999	0.34	0/1334
27	BT	0.12	0/999	0.36	0/1334
28	AA	0.13	0/1112	0.34	0/1488
28	BU	0.13	0/1112	0.36	0/1488
29	AB	0.14	0/1199	0.38	0/1607
29	BV	0.16	0/1199	0.36	0/1607
30	AC	0.19	0/503	0.56	0/668
30	BW	0.15	0/498	0.38	0/661
31	AD	0.13	0/738	0.32	0/994
31	BX	0.12	0/738	0.38	0/994
32	AE	0.14	0/907	0.40	0/1219
32	BY	0.15	0/907	0.43	0/1219
33	AF	0.15	0/1021	0.37	0/1368
33	BZ	0.14	0/1025	0.40	0/1372
34	AG	0.13	0/866	0.35	0/1165
34	CA	0.20	0/866	0.38	0/1165
35	AH	0.14	0/896	0.39	0/1195
35	CB	0.13	0/896	0.39	0/1195
36	AI	0.14	0/1003	0.37	0/1336
36	CC	0.13	0/990	0.37	0/1319
37	AJ	0.34	0/763	0.56	1/1012 (0.1%)
37	CD	0.12	0/763	0.37	0/1012
38	AK	0.15	0/690	0.39	0/916

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
38	CE	0.18	0/690	0.38	0/916
39	AL	0.12	0/623	0.35	0/831
39	CF	0.17	0/623	0.46	0/831
40	AM	0.14	0/447	0.32	0/594
40	CG	0.15	0/447	0.42	0/594
41	AN	0.27	0/425	0.57	0/563
41	CH	0.26	0/417	0.54	0/553
42	AO	0.23	0/237	0.42	0/304
42	CI	0.15	0/228	0.37	0/293
43	AP	0.16	0/840	0.39	0/1110
43	CJ	0.17	0/840	0.36	0/1110
44	AQ	0.16	0/705	0.39	0/940
44	CK	0.13	0/705	0.37	0/940
45	CL	0.33	0/942	0.78	0/1258
45	i	0.41	0/933	0.90	3/1246 (0.2%)
46	B	0.19	0/41511	0.46	11/64681 (0.0%)
46	CM	0.19	0/42081	0.46	12/65573 (0.0%)
47	C	0.12	0/1666	0.34	0/2273
47	CN	0.14	0/1666	0.39	0/2273
48	CO	0.17	0/1750	0.45	0/2354
48	D	0.13	0/1750	0.36	0/2354
49	CP	0.16	0/1657	0.38	0/2248
49	E	0.13	0/1657	0.34	0/2248
50	CQ	0.19	0/1731	0.53	0/2324
50	F	0.16	0/1731	0.48	1/2324 (0.0%)
51	CR	0.15	0/2096	0.37	0/2822
51	G	0.13	0/2092	0.36	0/2817
52	CS	0.18	0/1631	0.40	0/2199
52	H	0.34	0/1631	0.55	0/2199
53	CT	0.14	0/1929	0.42	0/2571
53	I	0.13	0/1845	0.37	0/2464
54	CU	0.34	0/1499	0.47	0/2016
54	J	0.15	0/1510	0.39	0/2031
55	CV	0.15	0/1606	0.38	0/2150
55	K	0.16	0/1606	0.38	0/2150
56	CW	0.13	0/1478	0.35	0/1978
56	L	0.13	0/1478	0.35	0/1978
57	CX	0.20	0/809	0.55	0/1092
57	M	0.19	0/836	0.63	0/1130
58	CY	0.16	0/1154	0.38	0/1553
58	N	0.15	0/1175	0.40	0/1582
59	CZ	0.25	0/921	0.88	5/1240 (0.4%)
59	O	0.35	0/892	0.93	3/1203 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
60	DA	0.14	0/1210	0.37	0/1631
60	P	0.13	0/1210	0.35	0/1631
61	DB	0.15	0/953	0.41	0/1279
61	Q	0.35	0/953	0.53	0/1279
62	DC	0.19	0/1049	0.55	1/1409 (0.1%)
62	R	0.20	0/1038	0.52	0/1395
63	DD	0.15	0/1109	0.41	0/1486
63	S	0.36	0/1109	0.67	2/1486 (0.1%)
64	DE	0.18	0/1009	0.55	0/1354
64	T	0.20	0/1009	0.52	0/1354
65	DF	0.24	0/1178	0.52	0/1579
65	U	0.16	0/1205	0.43	0/1615
66	DG	0.16	0/1120	0.43	0/1508
66	V	0.17	0/1120	0.49	0/1508
67	DH	0.16	0/772	0.45	0/1045
67	W	0.15	0/818	0.41	0/1106
68	DI	0.18	0/683	0.48	0/918
68	X	0.15	0/683	0.39	0/918
69	DJ	0.16	0/1049	0.40	0/1412
69	Y	0.14	0/1049	0.34	0/1412
70	DK	0.16	0/1128	0.43	0/1505
70	Z	0.16	0/1128	0.49	0/1505
71	DL	0.13	0/1086	0.35	0/1447
71	a	0.14	0/1100	0.34	0/1466
72	DM	0.16	0/577	0.47	0/778
72	b	0.15	0/585	0.37	0/789
73	DN	0.14	0/782	0.39	0/1048
73	c	0.16	0/791	0.40	0/1060
74	DO	0.15	0/624	0.44	0/843
74	d	0.13	0/624	0.38	0/843
75	DP	0.15	0/478	0.52	0/640
75	e	0.13	0/489	0.43	0/654
76	DQ	0.21	0/461	0.47	0/613
76	f	0.14	0/466	0.40	0/620
77	DR	0.29	0/469	0.74	0/626
77	g	0.22	0/482	0.49	0/642
78	DS	0.38	0/585	0.88	2/778 (0.3%)
78	h	0.40	0/585	0.75	0/778
79	AR	0.14	0/2451	0.38	0/3337
79	DT	0.19	0/2409	0.52	0/3280
80	P0	0.17	0/857	0.44	0/1148
80	p0	0.45	0/638	0.88	1/845 (0.1%)
81	12	0.20	0/486	0.53	0/653

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
82	L1	0.21	0/1737	0.43	0/2335
82	l1	0.35	0/1737	0.60	0/2335
All	All	0.18	0/437098	0.44	55/641006 (0.0%)

There are no bond length outliers.

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	CM	823	G	C4'-C3'-O3'	9.09	123.04	109.40
1	1	3163	U	OP1-P-O3'	-8.86	81.41	108.00
1	1	3163	U	OP2-P-O3'	-8.22	83.34	108.00
46	B	653	G	O5'-P-OP2	-7.93	84.20	108.00
1	1	1653	C	C3'-C2'-O2'	-7.60	103.20	114.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	68581	0	34467	1209	0
1	AS	68985	0	34671	1173	0
2	3	2579	0	1304	35	0
2	AT	2579	0	1304	27	0
3	4	3333	0	1684	70	0
3	AU	3333	0	1684	66	0
4	AW	1888	0	1962	44	0
4	j	1888	0	1962	44	0
5	AX	3077	0	3166	56	0
5	k	3077	0	3166	64	0
6	AY	2751	0	2879	38	0
6	l	2751	0	2879	54	0
7	AZ	2394	0	2361	35	0
7	m	2426	0	2389	37	0
8	BA	1210	0	1285	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	n	1242	0	1321	28	0
9	BB	1885	0	1977	20	0
9	o	1876	0	1971	20	0
10	BC	1778	0	1897	23	0
10	p	1805	0	1925	15	0
11	BD	1519	0	1588	28	0
11	q	1510	0	1582	23	0
12	BE	1689	0	1731	19	0
12	r	1689	0	1731	26	0
13	BF	1371	0	1410	26	0
13	s	1371	0	1410	25	0
14	BG	1610	0	1686	23	0
14	t	1610	0	1686	20	0
15	BH	1029	0	1116	24	0
15	u	1029	0	1116	22	0
16	BI	1713	0	1764	47	0
16	v	1713	0	1763	46	0
17	BJ	1590	0	1705	19	0
17	w	1590	0	1705	26	0
18	BK	1406	0	1431	19	0
18	x	1387	0	1408	25	0
19	BL	1458	0	1556	28	0
19	y	1458	0	1556	28	0
20	BM	1457	0	1564	31	0
20	z	1457	0	1564	27	0
21	0	1423	0	1480	30	0
21	BN	1423	0	1480	29	0
22	2	1262	0	1314	17	0
22	BO	1262	0	1314	22	0
23	5	826	0	843	13	0
23	BP	826	0	843	22	0
24	6	977	0	1026	9	0
24	BQ	977	0	1026	13	0
25	7	945	0	1010	15	0
25	BR	801	0	840	15	0
26	8	965	0	1019	19	0
26	BS	960	0	1014	13	0
27	9	989	0	1064	21	0
27	BT	989	0	1064	20	0
28	AA	1087	0	1154	19	0
28	BU	1087	0	1154	26	0
29	AB	1170	0	1203	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	BV	1170	0	1203	27	0
30	AC	493	0	520	10	0
30	BW	488	0	515	10	0
31	AD	729	0	775	13	0
31	BX	729	0	775	15	0
32	AE	894	0	941	18	0
32	BY	894	0	941	10	0
33	AF	1000	0	1069	13	0
33	BZ	1004	0	1077	13	0
34	AG	847	0	893	17	0
34	CA	847	0	893	10	0
35	AH	887	0	947	19	0
35	CB	887	0	947	20	0
36	AI	992	0	1093	19	0
36	CC	979	0	1076	22	0
37	AJ	758	0	838	10	0
37	CD	758	0	838	11	0
38	AK	677	0	697	16	0
38	CE	677	0	696	17	0
39	AL	617	0	675	7	0
39	CF	617	0	675	14	0
40	AM	438	0	475	10	0
40	CG	438	0	475	9	0
41	AN	419	0	460	11	0
41	CH	411	0	448	6	0
42	AO	236	0	285	5	0
42	CI	227	0	272	7	0
43	AP	828	0	893	22	0
43	CJ	828	0	893	11	0
44	AQ	698	0	734	13	0
44	CK	698	0	734	17	0
45	CL	931	0	908	50	0
45	i	922	0	902	39	0
46	B	37113	0	18673	824	0
46	CM	37621	0	18927	896	0
47	C	1627	0	1644	37	0
47	CN	1627	0	1644	30	0
48	CO	1724	0	1805	48	0
48	D	1724	0	1805	30	0
49	CP	1629	0	1728	30	0
49	E	1629	0	1728	32	0
50	CQ	1707	0	1807	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	F	1707	0	1807	45	0
51	CR	2055	0	2137	51	0
51	G	2051	0	2134	43	0
52	CS	1614	0	1688	39	0
52	H	1614	0	1688	47	0
53	CT	1904	0	1994	53	0
53	I	1820	0	1896	44	0
54	CU	1475	0	1567	37	0
54	J	1485	0	1574	37	0
55	CV	1579	0	1602	38	0
55	K	1579	0	1602	26	0
56	CW	1453	0	1532	32	0
56	L	1453	0	1532	25	0
57	CX	791	0	805	44	0
57	M	817	0	828	39	0
58	CY	1129	0	1183	15	0
58	N	1150	0	1201	17	0
59	CZ	913	0	934	49	0
59	O	885	0	915	47	0
60	DA	1187	0	1249	17	0
60	P	1187	0	1249	18	0
61	DB	942	0	981	26	0
61	Q	942	0	981	15	0
62	DC	1029	0	1078	36	0
62	R	1018	0	1065	38	0
63	DD	1091	0	1155	26	0
63	S	1091	0	1155	42	0
64	DE	997	0	1053	37	0
64	T	997	0	1053	36	0
65	DF	1161	0	1205	33	0
65	U	1187	0	1237	31	0
66	DG	1100	0	1114	26	0
66	V	1100	0	1114	29	0
67	DH	763	0	824	20	0
67	W	808	0	871	17	0
68	DI	676	0	677	17	0
68	X	676	0	677	22	0
69	DJ	1032	0	1066	27	0
69	Y	1032	0	1066	19	0
70	DK	1110	0	1182	24	0
70	Z	1110	0	1181	26	0
71	DL	1072	0	1123	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
71	a	1086	0	1132	16	0
72	DM	570	0	609	15	0
72	b	578	0	613	16	0
73	DN	770	0	825	24	0
73	c	779	0	832	15	0
74	DO	614	0	630	10	0
74	d	614	0	627	7	0
75	DP	476	0	510	22	0
75	e	487	0	523	15	0
76	DQ	449	0	427	12	0
76	f	454	0	432	10	0
77	DR	461	0	499	17	0
77	g	474	0	515	15	0
78	DS	574	0	606	34	0
78	h	574	0	606	30	0
79	AR	2398	0	2374	60	0
79	DT	2357	0	2325	81	0
80	P0	845	0	884	34	0
80	p0	635	0	663	37	0
81	12	480	0	477	31	0
82	L1	1711	0	1817	66	0
82	l1	1711	0	1817	117	0
83	0	5	0	0	0	0
83	1	530	0	0	0	0
83	2	3	0	0	0	0
83	3	14	0	0	0	0
83	4	12	0	0	0	0
83	5	1	0	0	0	0
83	6	3	0	0	0	0
83	8	2	0	0	0	0
83	9	2	0	0	0	0
83	AB	2	0	0	0	0
83	AC	1	0	0	0	0
83	AD	1	0	0	0	0
83	AE	2	0	0	0	0
83	AF	1	0	0	0	0
83	AG	2	0	0	0	0
83	AH	2	0	0	0	0
83	AJ	1	0	0	0	0
83	AK	1	0	0	0	0
83	AM	1	0	0	0	0
83	AP	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	AR	1	0	0	0	0
83	AS	278	0	0	0	0
83	AT	9	0	0	0	0
83	AU	2	0	0	0	0
83	AW	4	0	0	0	0
83	B	152	0	0	0	0
83	BB	2	0	0	0	0
83	BE	2	0	0	0	0
83	BF	1	0	0	0	0
83	BH	1	0	0	0	0
83	BJ	3	0	0	0	0
83	BK	1	0	0	0	0
83	BN	1	0	0	0	0
83	BQ	1	0	0	0	0
83	BV	1	0	0	0	0
83	BZ	2	0	0	0	0
83	CA	1	0	0	0	0
83	CJ	1	0	0	0	0
83	CK	1	0	0	0	0
83	CL	3	0	0	0	0
83	CM	102	0	0	0	0
83	CO	1	0	0	0	0
83	CP	1	0	0	0	0
83	CQ	1	0	0	0	0
83	D	1	0	0	0	0
83	DA	1	0	0	0	0
83	DB	3	0	0	0	0
83	DG	2	0	0	0	0
83	DQ	1	0	0	0	0
83	G	2	0	0	0	0
83	I	2	0	0	0	0
83	J	1	0	0	0	0
83	K	1	0	0	0	0
83	L	1	0	0	0	0
83	Q	1	0	0	0	0
83	R	1	0	0	0	0
83	V	1	0	0	0	0
83	Y	3	0	0	0	0
83	Z	2	0	0	0	0
83	a	1	0	0	0	0
83	f	1	0	0	0	0
83	j	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	k	4	0	0	0	0
83	o	3	0	0	0	0
83	r	2	0	0	0	0
83	s	1	0	0	0	0
83	u	2	0	0	0	0
83	v	3	0	0	0	0
83	w	3	0	0	0	0
83	x	3	0	0	0	0
83	y	1	0	0	0	0
84	1	57	0	52	7	0
84	AS	57	0	52	8	0
85	AH	1	0	0	0	0
85	AK	1	0	0	0	0
85	AN	1	0	0	0	0
85	AP	1	0	0	0	0
85	AQ	1	0	0	0	0
85	CB	1	0	0	0	0
85	CE	1	0	0	0	0
85	CH	1	0	0	0	0
85	CJ	1	0	0	0	0
85	CK	1	0	0	0	0
85	DN	1	0	0	0	0
85	DQ	1	0	0	0	0
85	DS	1	0	0	0	0
85	c	1	0	0	0	0
85	d	1	0	0	0	0
85	f	1	0	0	0	0
85	h	1	0	0	0	0
86	B	36	0	36	0	0
86	CM	36	0	36	2	0
87	1	9	0	0	1	0
87	4	3	0	0	1	0
87	AS	12	0	0	0	0
87	B	6	0	0	0	0
All	All	408804	0	304392	7016	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 7016 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)
46:B:671:G:H3'	46:B:672:U:H5'	1.35	1.08
1:1:1233:G:H1	1:1:1247:A:N6	1.49	1.07
48:D:180:THR:HG22	48:D:183:GLN:OE1	1.61	0.99
48:CO:57:ALA:O	48:CO:61:LEU:HD13	1.63	0.97
54:CU:25:GLU:HB2	54:CU:31:LYS:HG3	1.47	0.97

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AW	247/254 (97%)	239 (97%)	8 (3%)	0	100	100
4	j	247/254 (97%)	239 (97%)	8 (3%)	0	100	100
5	AX	384/389 (99%)	372 (97%)	12 (3%)	0	100	100
5	k	384/389 (99%)	372 (97%)	12 (3%)	0	100	100
6	AY	359/363 (99%)	349 (97%)	10 (3%)	0	100	100
6	l	359/363 (99%)	348 (97%)	11 (3%)	0	100	100
7	AZ	290/298 (97%)	278 (96%)	12 (4%)	0	100	100
7	m	294/298 (99%)	281 (96%)	12 (4%)	1 (0%)	36	63
8	BA	149/176 (85%)	147 (99%)	2 (1%)	0	100	100
8	n	153/176 (87%)	150 (98%)	3 (2%)	0	100	100
9	BB	232/241 (96%)	226 (97%)	5 (2%)	1 (0%)	30	57
9	o	223/241 (92%)	215 (96%)	7 (3%)	1 (0%)	30	57
10	BC	225/262 (86%)	210 (93%)	11 (5%)	4 (2%)	6	24
10	p	231/262 (88%)	223 (96%)	7 (3%)	1 (0%)	30	57
11	BD	188/191 (98%)	184 (98%)	4 (2%)	0	100	100
11	q	187/191 (98%)	182 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	BE	204/220 (93%)	199 (98%)	5 (2%)	0	100	100
12	r	204/220 (93%)	201 (98%)	3 (2%)	0	100	100
13	BF	169/174 (97%)	163 (96%)	6 (4%)	0	100	100
13	s	169/174 (97%)	161 (95%)	8 (5%)	0	100	100
14	BG	198/202 (98%)	193 (98%)	5 (2%)	0	100	100
14	t	198/202 (98%)	196 (99%)	2 (1%)	0	100	100
15	BH	128/131 (98%)	124 (97%)	4 (3%)	0	100	100
15	u	128/131 (98%)	125 (98%)	3 (2%)	0	100	100
16	BI	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
16	v	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
17	BJ	197/200 (98%)	195 (99%)	2 (1%)	0	100	100
17	w	197/200 (98%)	195 (99%)	2 (1%)	0	100	100
18	BK	172/185 (93%)	167 (97%)	5 (3%)	0	100	100
18	x	169/185 (91%)	166 (98%)	3 (2%)	0	100	100
19	BL	183/186 (98%)	179 (98%)	4 (2%)	0	100	100
19	y	183/186 (98%)	179 (98%)	4 (2%)	0	100	100
20	BM	177/190 (93%)	173 (98%)	4 (2%)	0	100	100
20	z	177/190 (93%)	174 (98%)	3 (2%)	0	100	100
21	0	168/172 (98%)	166 (99%)	2 (1%)	0	100	100
21	BN	168/172 (98%)	166 (99%)	2 (1%)	0	100	100
22	2	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
22	BO	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
23	5	100/124 (81%)	89 (89%)	10 (10%)	1 (1%)	12	37
23	BP	100/124 (81%)	87 (87%)	11 (11%)	2 (2%)	6	21
24	6	129/137 (94%)	126 (98%)	3 (2%)	0	100	100
24	BQ	129/137 (94%)	126 (98%)	3 (2%)	0	100	100
25	7	114/155 (74%)	103 (90%)	11 (10%)	0	100	100
25	BR	94/155 (61%)	90 (96%)	4 (4%)	0	100	100
26	8	118/142 (83%)	116 (98%)	2 (2%)	0	100	100
26	BS	117/142 (82%)	115 (98%)	2 (2%)	0	100	100
27	9	124/127 (98%)	123 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	BT	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
28	AA	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
28	BU	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
29	AB	146/149 (98%)	139 (95%)	7 (5%)	0	100	100
29	BV	146/149 (98%)	139 (95%)	7 (5%)	0	100	100
30	AC	60/63 (95%)	57 (95%)	1 (2%)	2 (3%)	3	13
30	BW	59/63 (94%)	58 (98%)	1 (2%)	0	100	100
31	AD	94/106 (89%)	93 (99%)	1 (1%)	0	100	100
31	BX	94/106 (89%)	92 (98%)	2 (2%)	0	100	100
32	AE	108/112 (96%)	106 (98%)	2 (2%)	0	100	100
32	BY	108/112 (96%)	103 (95%)	5 (5%)	0	100	100
33	AF	122/131 (93%)	122 (100%)	0	0	100	100
33	BZ	122/131 (93%)	122 (100%)	0	0	100	100
34	AG	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
34	CA	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
35	AH	110/122 (90%)	108 (98%)	2 (2%)	0	100	100
35	CB	110/122 (90%)	107 (97%)	3 (3%)	0	100	100
36	AI	118/120 (98%)	114 (97%)	4 (3%)	0	100	100
36	CC	116/120 (97%)	114 (98%)	2 (2%)	0	100	100
37	AJ	95/99 (96%)	93 (98%)	2 (2%)	0	100	100
37	CD	95/99 (96%)	94 (99%)	1 (1%)	0	100	100
38	AK	84/90 (93%)	81 (96%)	3 (4%)	0	100	100
38	CE	84/90 (93%)	81 (96%)	3 (4%)	0	100	100
39	AL	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
39	CF	75/78 (96%)	68 (91%)	7 (9%)	0	100	100
40	AM	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	5	21
40	CG	48/51 (94%)	48 (100%)	0	0	100	100
41	AN	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
41	CH	49/52 (94%)	46 (94%)	1 (2%)	2 (4%)	2	10
42	AO	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
42	CI	22/25 (88%)	22 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	AP	101/106 (95%)	100 (99%)	1 (1%)	0	100	100
43	CJ	101/106 (95%)	100 (99%)	1 (1%)	0	100	100
44	AQ	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
44	CK	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	CL	117/267 (44%)	91 (78%)	22 (19%)	4 (3%)	3	13
45	i	116/267 (43%)	91 (78%)	23 (20%)	2 (2%)	7	25
47	C	206/261 (79%)	201 (98%)	5 (2%)	0	100	100
47	CN	206/261 (79%)	198 (96%)	8 (4%)	0	100	100
48	CO	212/256 (83%)	204 (96%)	8 (4%)	0	100	100
48	D	212/256 (83%)	207 (98%)	5 (2%)	0	100	100
49	CP	215/249 (86%)	209 (97%)	6 (3%)	0	100	100
49	E	215/249 (86%)	210 (98%)	5 (2%)	0	100	100
50	CQ	221/251 (88%)	211 (96%)	10 (4%)	0	100	100
50	F	221/251 (88%)	213 (96%)	8 (4%)	0	100	100
51	CR	258/262 (98%)	254 (98%)	4 (2%)	0	100	100
51	G	257/262 (98%)	253 (98%)	4 (2%)	0	100	100
52	CS	204/225 (91%)	196 (96%)	8 (4%)	0	100	100
52	H	204/225 (91%)	185 (91%)	17 (8%)	2 (1%)	12	37
53	CT	234/236 (99%)	231 (99%)	3 (1%)	0	100	100
53	I	224/236 (95%)	221 (99%)	3 (1%)	0	100	100
54	CU	181/186 (97%)	171 (94%)	9 (5%)	1 (1%)	21	48
54	J	182/186 (98%)	172 (94%)	10 (6%)	0	100	100
55	CV	201/206 (98%)	199 (99%)	2 (1%)	0	100	100
55	K	201/206 (98%)	200 (100%)	1 (0%)	0	100	100
56	CW	176/189 (93%)	175 (99%)	1 (1%)	0	100	100
56	L	176/189 (93%)	175 (99%)	1 (1%)	0	100	100
57	CX	92/118 (78%)	86 (94%)	6 (6%)	0	100	100
57	M	96/118 (81%)	81 (84%)	13 (14%)	2 (2%)	5	21
58	CY	139/155 (90%)	133 (96%)	4 (3%)	2 (1%)	9	29
58	N	142/155 (92%)	137 (96%)	5 (4%)	0	100	100
59	CZ	117/143 (82%)	90 (77%)	22 (19%)	5 (4%)	2	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	O	114/143 (80%)	89 (78%)	23 (20%)	2 (2%)	6	24
60	DA	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
60	P	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
61	DB	125/132 (95%)	120 (96%)	5 (4%)	0	100	100
61	Q	125/132 (95%)	119 (95%)	5 (4%)	1 (1%)	16	42
62	DC	128/142 (90%)	111 (87%)	17 (13%)	0	100	100
62	R	127/142 (89%)	115 (91%)	11 (9%)	1 (1%)	16	42
63	DD	138/142 (97%)	134 (97%)	4 (3%)	0	100	100
63	S	138/142 (97%)	132 (96%)	6 (4%)	0	100	100
64	DE	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
64	T	122/137 (89%)	118 (97%)	4 (3%)	0	100	100
65	DF	139/145 (96%)	133 (96%)	5 (4%)	1 (1%)	18	45
65	U	142/145 (98%)	137 (96%)	5 (4%)	0	100	100
66	DG	139/145 (96%)	133 (96%)	5 (4%)	1 (1%)	18	45
66	V	139/145 (96%)	136 (98%)	3 (2%)	0	100	100
67	DH	95/119 (80%)	93 (98%)	2 (2%)	0	100	100
67	W	100/119 (84%)	97 (97%)	3 (3%)	0	100	100
68	DI	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
68	X	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
69	DJ	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
69	Y	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
70	DK	141/145 (97%)	139 (99%)	2 (1%)	0	100	100
70	Z	141/145 (97%)	138 (98%)	3 (2%)	0	100	100
71	DL	130/135 (96%)	130 (100%)	0	0	100	100
71	a	132/135 (98%)	130 (98%)	2 (2%)	0	100	100
72	DM	69/105 (66%)	65 (94%)	4 (6%)	0	100	100
72	b	70/105 (67%)	69 (99%)	1 (1%)	0	100	100
73	DN	95/119 (80%)	93 (98%)	2 (2%)	0	100	100
73	c	96/119 (81%)	93 (97%)	3 (3%)	0	100	100
74	DO	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
74	d	79/82 (96%)	75 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	DP	59/67 (88%)	53 (90%)	6 (10%)	0	100	100
75	e	60/67 (90%)	57 (95%)	3 (5%)	0	100	100
76	DQ	52/56 (93%)	50 (96%)	2 (4%)	0	100	100
76	f	53/56 (95%)	51 (96%)	2 (4%)	0	100	100
77	DR	56/63 (89%)	52 (93%)	3 (5%)	1 (2%)	6	24
77	g	58/63 (92%)	55 (95%)	3 (5%)	0	100	100
78	DS	68/193 (35%)	57 (84%)	10 (15%)	1 (2%)	8	28
78	h	68/193 (35%)	55 (81%)	13 (19%)	0	100	100
79	AR	309/317 (98%)	292 (94%)	17 (6%)	0	100	100
79	DT	302/317 (95%)	281 (93%)	19 (6%)	2 (1%)	18	45
80	P0	105/312 (34%)	81 (77%)	21 (20%)	3 (3%)	3	16
80	p0	69/312 (22%)	46 (67%)	20 (29%)	3 (4%)	2	10
81	12	61/165 (37%)	36 (59%)	25 (41%)	0	100	100
82	L1	215/217 (99%)	166 (77%)	46 (21%)	3 (1%)	9	29
82	l1	215/217 (99%)	131 (61%)	72 (34%)	12 (6%)	1	7
All	All	22741/25499 (89%)	21725 (96%)	951 (4%)	65 (0%)	36	63

5 of 65 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	AC	21	ILE
40	AM	49	LEU
45	i	55	LYS
59	O	130	SER
41	CH	3	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AW	190/194 (98%)	190 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	j	190/194 (98%)	190 (100%)	0	100	100
5	AX	325/328 (99%)	325 (100%)	0	100	100
5	k	325/328 (99%)	325 (100%)	0	100	100
6	AY	290/292 (99%)	290 (100%)	0	100	100
6	l	290/292 (99%)	290 (100%)	0	100	100
7	AZ	247/252 (98%)	247 (100%)	0	100	100
7	m	250/252 (99%)	250 (100%)	0	100	100
8	BA	132/154 (86%)	132 (100%)	0	100	100
8	n	136/154 (88%)	136 (100%)	0	100	100
9	BB	198/204 (97%)	198 (100%)	0	100	100
9	o	197/204 (97%)	197 (100%)	0	100	100
10	BC	191/216 (88%)	191 (100%)	0	100	100
10	p	193/216 (89%)	193 (100%)	0	100	100
11	BD	169/170 (99%)	169 (100%)	0	100	100
11	q	168/170 (99%)	168 (100%)	0	100	100
12	BE	178/186 (96%)	177 (99%)	1 (1%)	78	81
12	r	178/186 (96%)	178 (100%)	0	100	100
13	BF	146/149 (98%)	146 (100%)	0	100	100
13	s	146/149 (98%)	146 (100%)	0	100	100
14	BG	166/168 (99%)	166 (100%)	0	100	100
14	t	166/168 (99%)	166 (100%)	0	100	100
15	BH	108/109 (99%)	108 (100%)	0	100	100
15	u	108/109 (99%)	108 (100%)	0	100	100
16	BI	177/178 (99%)	177 (100%)	0	100	100
16	v	177/178 (99%)	177 (100%)	0	100	100
17	BJ	166/167 (99%)	166 (100%)	0	100	100
17	w	166/167 (99%)	166 (100%)	0	100	100
18	BK	145/154 (94%)	145 (100%)	0	100	100
18	x	144/154 (94%)	144 (100%)	0	100	100
19	BL	153/154 (99%)	153 (100%)	0	100	100
19	y	153/154 (99%)	153 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	BM	146/153 (95%)	145 (99%)	1 (1%)	76	80
20	z	146/153 (95%)	146 (100%)	0	100	100
21	0	155/157 (99%)	155 (100%)	0	100	100
21	BN	155/157 (99%)	155 (100%)	0	100	100
22	2	133/134 (99%)	133 (100%)	0	100	100
22	BO	133/134 (99%)	133 (100%)	0	100	100
23	5	93/112 (83%)	93 (100%)	0	100	100
23	BP	93/112 (83%)	93 (100%)	0	100	100
24	6	101/104 (97%)	101 (100%)	0	100	100
24	BQ	101/104 (97%)	101 (100%)	0	100	100
25	7	97/127 (76%)	97 (100%)	0	100	100
25	BR	86/127 (68%)	86 (100%)	0	100	100
26	8	107/121 (88%)	107 (100%)	0	100	100
26	BS	107/121 (88%)	107 (100%)	0	100	100
27	9	111/112 (99%)	111 (100%)	0	100	100
27	BT	111/112 (99%)	111 (100%)	0	100	100
28	AA	117/118 (99%)	117 (100%)	0	100	100
28	BU	117/118 (99%)	117 (100%)	0	100	100
29	AB	120/121 (99%)	120 (100%)	0	100	100
29	BV	120/121 (99%)	120 (100%)	0	100	100
30	AC	48/49 (98%)	48 (100%)	0	100	100
30	BW	48/49 (98%)	48 (100%)	0	100	100
31	AD	81/90 (90%)	81 (100%)	0	100	100
31	BX	81/90 (90%)	81 (100%)	0	100	100
32	AE	98/100 (98%)	98 (100%)	0	100	100
32	BY	98/100 (98%)	98 (100%)	0	100	100
33	AF	109/115 (95%)	109 (100%)	0	100	100
33	BZ	110/115 (96%)	110 (100%)	0	100	100
34	AG	91/92 (99%)	91 (100%)	0	100	100
34	CA	91/92 (99%)	91 (100%)	0	100	100
35	AH	95/102 (93%)	95 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	CB	95/102 (93%)	95 (100%)	0	100	100
36	AI	106/106 (100%)	106 (100%)	0	100	100
36	CC	105/106 (99%)	105 (100%)	0	100	100
37	AJ	77/79 (98%)	76 (99%)	1 (1%)	61	74
37	CD	77/79 (98%)	77 (100%)	0	100	100
38	AK	70/73 (96%)	70 (100%)	0	100	100
38	CE	70/73 (96%)	70 (100%)	0	100	100
39	AL	68/69 (99%)	68 (100%)	0	100	100
39	CF	68/69 (99%)	68 (100%)	0	100	100
40	AM	46/47 (98%)	46 (100%)	0	100	100
40	CG	46/47 (98%)	46 (100%)	0	100	100
41	AN	47/47 (100%)	47 (100%)	0	100	100
41	CH	46/47 (98%)	46 (100%)	0	100	100
42	AO	24/24 (100%)	24 (100%)	0	100	100
42	CI	23/24 (96%)	23 (100%)	0	100	100
43	AP	88/91 (97%)	88 (100%)	0	100	100
43	CJ	88/91 (97%)	88 (100%)	0	100	100
44	AQ	72/73 (99%)	72 (100%)	0	100	100
44	CK	72/73 (99%)	72 (100%)	0	100	100
45	CL	100/212 (47%)	99 (99%)	1 (1%)	68	77
45	i	99/212 (47%)	99 (100%)	0	100	100
47	C	176/215 (82%)	176 (100%)	0	100	100
47	CN	176/215 (82%)	176 (100%)	0	100	100
48	CO	194/229 (85%)	194 (100%)	0	100	100
48	D	194/229 (85%)	194 (100%)	0	100	100
49	CP	175/198 (88%)	175 (100%)	0	100	100
49	E	175/198 (88%)	175 (100%)	0	100	100
50	CQ	174/196 (89%)	174 (100%)	0	100	100
50	F	174/196 (89%)	174 (100%)	0	100	100
51	CR	218/220 (99%)	218 (100%)	0	100	100
51	G	218/220 (99%)	218 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	CS	178/197 (90%)	178 (100%)	0	100	100
52	H	178/197 (90%)	177 (99%)	1 (1%)	78	81
53	CT	204/204 (100%)	204 (100%)	0	100	100
53	I	195/204 (96%)	195 (100%)	0	100	100
54	CU	164/167 (98%)	164 (100%)	0	100	100
54	J	165/167 (99%)	165 (100%)	0	100	100
55	CV	157/160 (98%)	157 (100%)	0	100	100
55	K	157/160 (98%)	157 (100%)	0	100	100
56	CW	153/160 (96%)	153 (100%)	0	100	100
56	L	153/160 (96%)	153 (100%)	0	100	100
57	CX	88/104 (85%)	88 (100%)	0	100	100
57	M	90/104 (86%)	90 (100%)	0	100	100
58	CY	122/134 (91%)	122 (100%)	0	100	100
58	N	124/134 (92%)	124 (100%)	0	100	100
59	CZ	101/123 (82%)	101 (100%)	0	100	100
59	O	98/123 (80%)	96 (98%)	2 (2%)	48	69
60	DA	129/130 (99%)	129 (100%)	0	100	100
60	P	129/130 (99%)	129 (100%)	0	100	100
61	DB	97/102 (95%)	97 (100%)	0	100	100
61	Q	97/102 (95%)	97 (100%)	0	100	100
62	DC	112/121 (93%)	112 (100%)	0	100	100
62	R	111/121 (92%)	111 (100%)	0	100	100
63	DD	114/116 (98%)	114 (100%)	0	100	100
63	S	114/116 (98%)	114 (100%)	0	100	100
64	DE	112/122 (92%)	112 (100%)	0	100	100
64	T	112/122 (92%)	111 (99%)	1 (1%)	70	78
65	DF	125/129 (97%)	125 (100%)	0	100	100
65	U	128/129 (99%)	128 (100%)	0	100	100
66	DG	113/117 (97%)	113 (100%)	0	100	100
66	V	113/117 (97%)	113 (100%)	0	100	100
67	DH	87/105 (83%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	W	92/105 (88%)	92 (100%)	0	100	100
68	DI	71/71 (100%)	71 (100%)	0	100	100
68	X	71/71 (100%)	71 (100%)	0	100	100
69	DJ	112/113 (99%)	112 (100%)	0	100	100
69	Y	112/113 (99%)	112 (100%)	0	100	100
70	DK	116/118 (98%)	116 (100%)	0	100	100
70	Z	116/118 (98%)	116 (100%)	0	100	100
71	DL	109/112 (97%)	109 (100%)	0	100	100
71	a	111/112 (99%)	111 (100%)	0	100	100
72	DM	63/85 (74%)	63 (100%)	0	100	100
72	b	64/85 (75%)	64 (100%)	0	100	100
73	DN	83/102 (81%)	83 (100%)	0	100	100
73	c	84/102 (82%)	84 (100%)	0	100	100
74	DO	72/73 (99%)	72 (100%)	0	100	100
74	d	72/73 (99%)	72 (100%)	0	100	100
75	DP	53/58 (91%)	53 (100%)	0	100	100
75	e	54/58 (93%)	54 (100%)	0	100	100
76	DQ	47/48 (98%)	47 (100%)	0	100	100
76	f	47/48 (98%)	47 (100%)	0	100	100
77	DR	50/54 (93%)	50 (100%)	0	100	100
77	g	51/54 (94%)	51 (100%)	0	100	100
78	DS	62/175 (35%)	60 (97%)	2 (3%)	34	60
78	h	62/175 (35%)	59 (95%)	3 (5%)	23	50
79	AR	259/263 (98%)	259 (100%)	0	100	100
79	DT	255/263 (97%)	255 (100%)	0	100	100
80	P0	92/247 (37%)	92 (100%)	0	100	100
80	p0	71/247 (29%)	69 (97%)	2 (3%)	38	63
81	12	53/137 (39%)	53 (100%)	0	100	100
82	L1	196/196 (100%)	196 (100%)	0	100	100
82	l1	196/196 (100%)	194 (99%)	2 (1%)	68	77
All	All	19544/21471 (91%)	19527 (100%)	17 (0%)	88	89

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
82	l1	215	ARG
80	p0	12	PHE
78	h	160	ARG
12	BE	3	ARG
20	BM	130	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 170 such sidechains are listed below:

Mol	Chain	Res	Type
20	BM	134	HIS
53	CT	22	HIS
30	BW	6	ASN
45	CL	33	ASN
57	CX	17	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3203/3359 (95%)	594 (18%)	44 (1%)
1	AS	3223/3359 (95%)	625 (19%)	52 (1%)
2	3	120/121 (99%)	9 (7%)	0
2	AT	120/121 (99%)	9 (7%)	0
3	4	156/158 (98%)	23 (14%)	3 (1%)
3	AU	156/158 (98%)	23 (14%)	3 (1%)
46	B	1736/1787 (97%)	433 (24%)	42 (2%)
46	CM	1762/1787 (98%)	454 (25%)	55 (3%)
All	All	10476/10850 (96%)	2170 (20%)	199 (1%)

5 of 2170 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	15	A
1	1	24	U
1	1	25	A
1	1	29	G
1	1	39	A

5 of 199 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AS	2183	U
3	AU	156	U
1	AS	2447	G
1	AS	2789	A
46	CM	176	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1231 ligands modelled in this entry, 1227 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
84	3K5	AS	3401	-	63,63,63	0.31	0	84,95,95	0.98	4 (4%)
86	HYG	B	1953	83	36,39,39	0.66	1 (2%)	44,60,60	1.10	4 (9%)
86	HYG	CM	1902	83	36,39,39	0.71	1 (2%)	44,60,60	1.23	5 (11%)
84	3K5	1	3402	-	63,63,63	0.35	0	84,95,95	0.93	6 (7%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	3K5	AS	3401	-	-	3/29/121/121	0/7/7/7
86	HYG	B	1953	83	-	5/12/87/87	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	HYG	CM	1902	83	-	7/12/87/87	0/4/4/4
84	3K5	1	3402	-	-	6/29/121/121	0/7/7/7

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	CM	1902	HYG	C4-N9	3.19	1.50	1.47
86	B	1953	HYG	C4-N9	3.14	1.50	1.47

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	AS	3401	3K5	O14-C34-C33	4.65	118.45	107.76
84	AS	3401	3K5	C34-O14-C38	3.79	123.60	117.72
86	CM	1902	HYG	C16-C17-C12	-3.74	104.56	113.50
86	B	1953	HYG	C16-C17-C12	-3.41	105.34	113.50
86	CM	1902	HYG	O29-C12-C13	3.30	119.32	110.89

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	1	3402	3K5	O15-C38-O14-C34
84	AS	3401	3K5	O15-C38-O14-C34
86	B	1953	HYG	N36-C33-C34-O35
86	CM	1902	HYG	O28-C27-C33-C34
84	1	3402	3K5	C39-C38-O14-C34

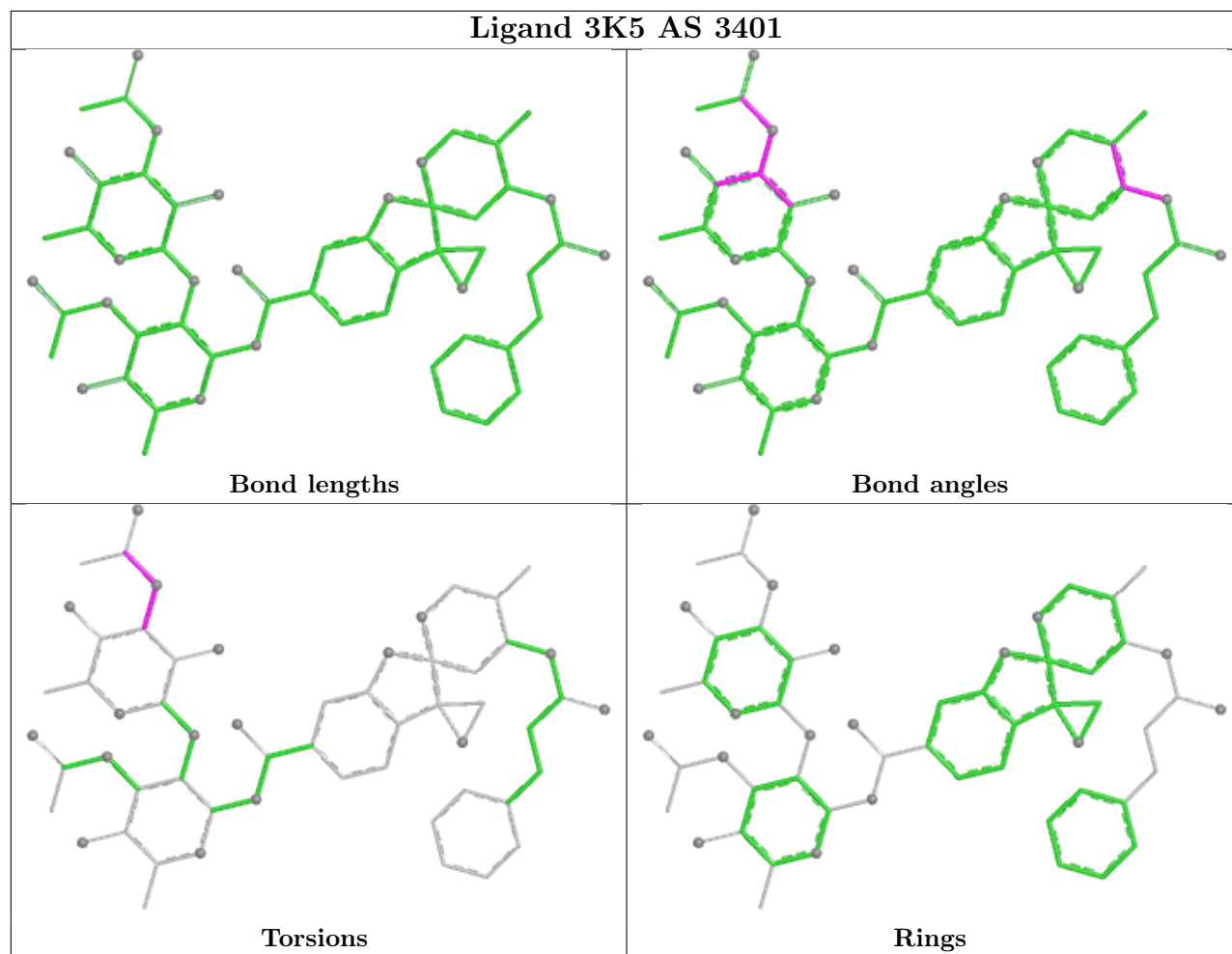
There are no ring outliers.

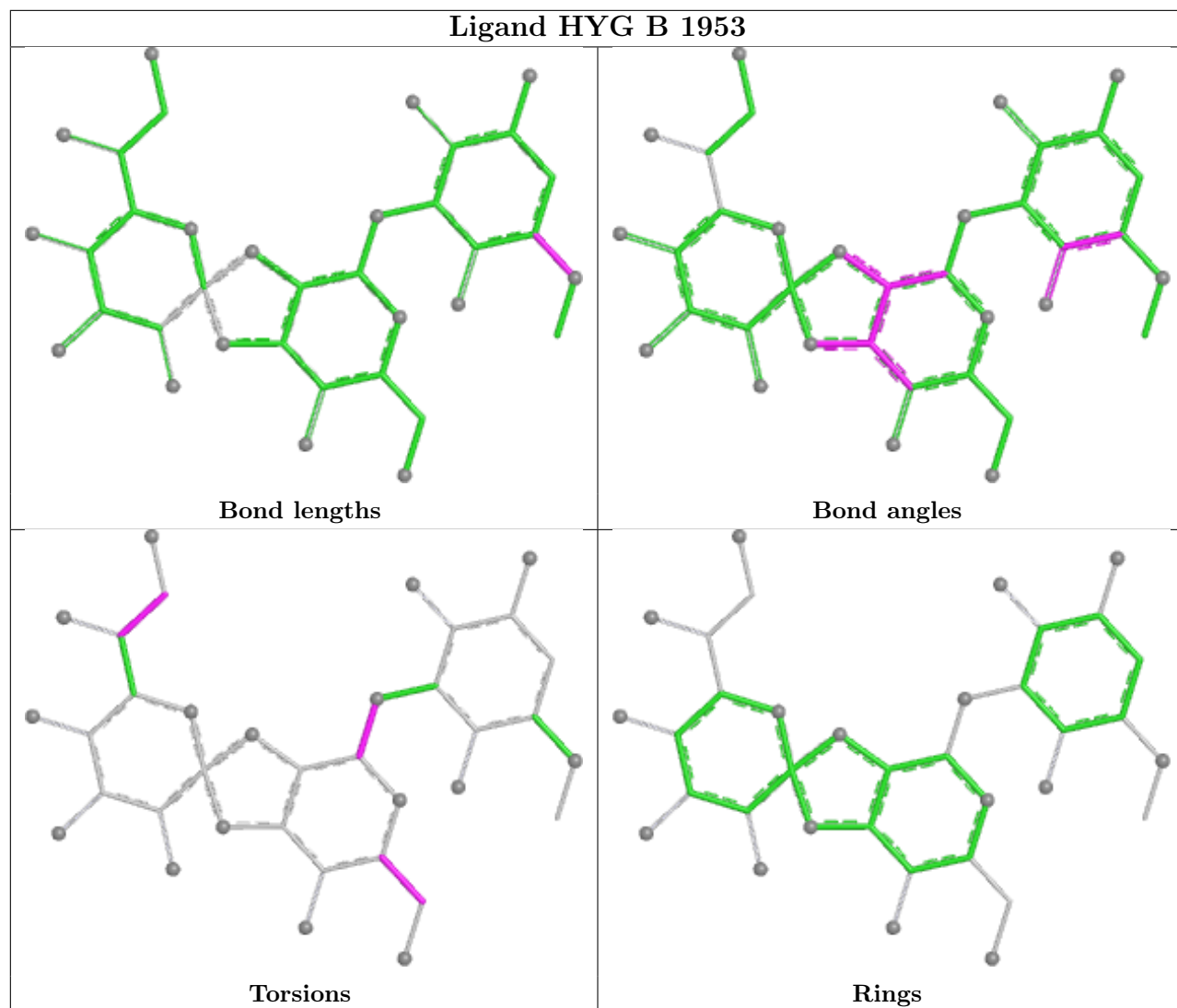
3 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
84	AS	3401	3K5	8	0
86	CM	1902	HYG	2	0
84	1	3402	3K5	7	0

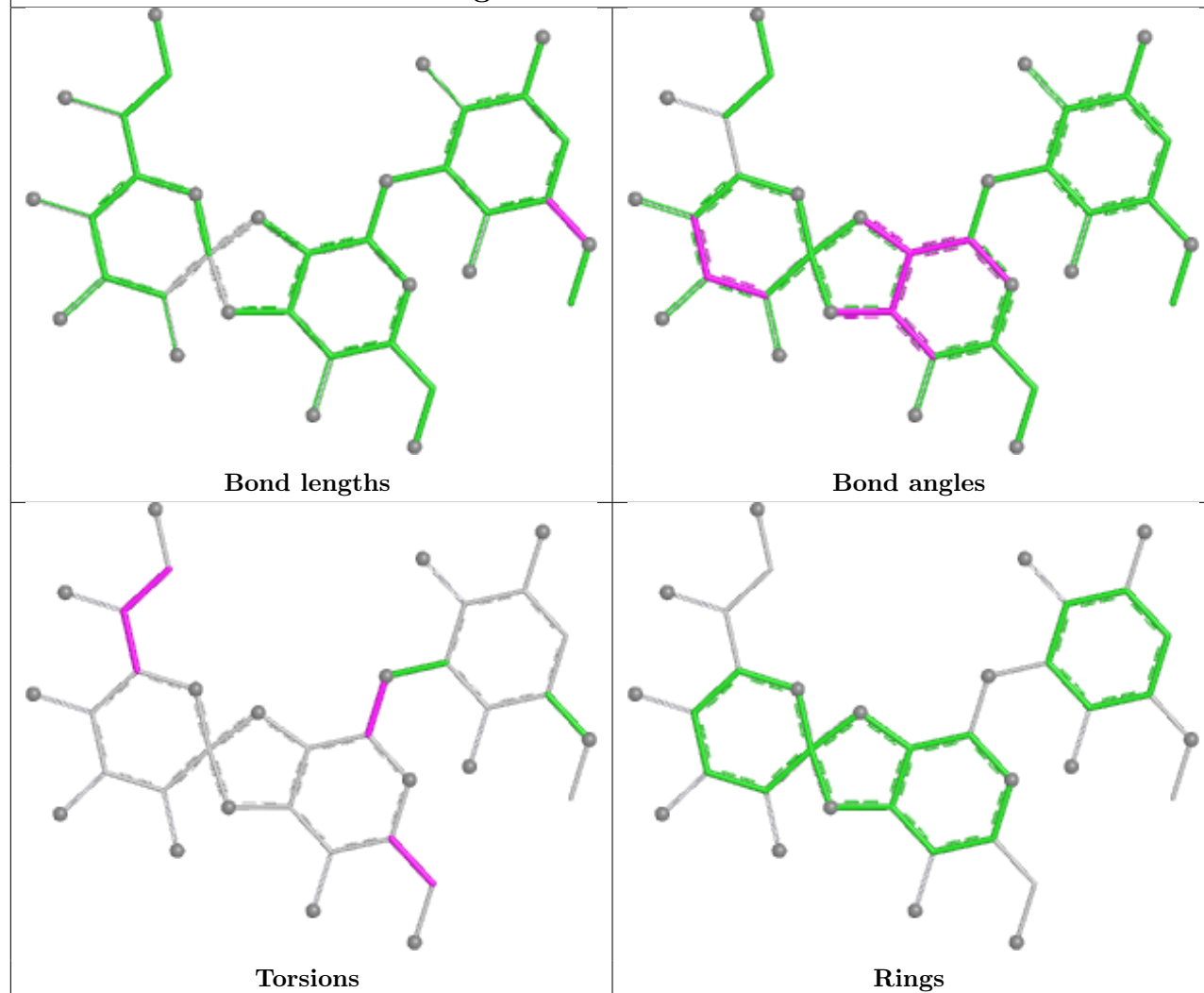
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

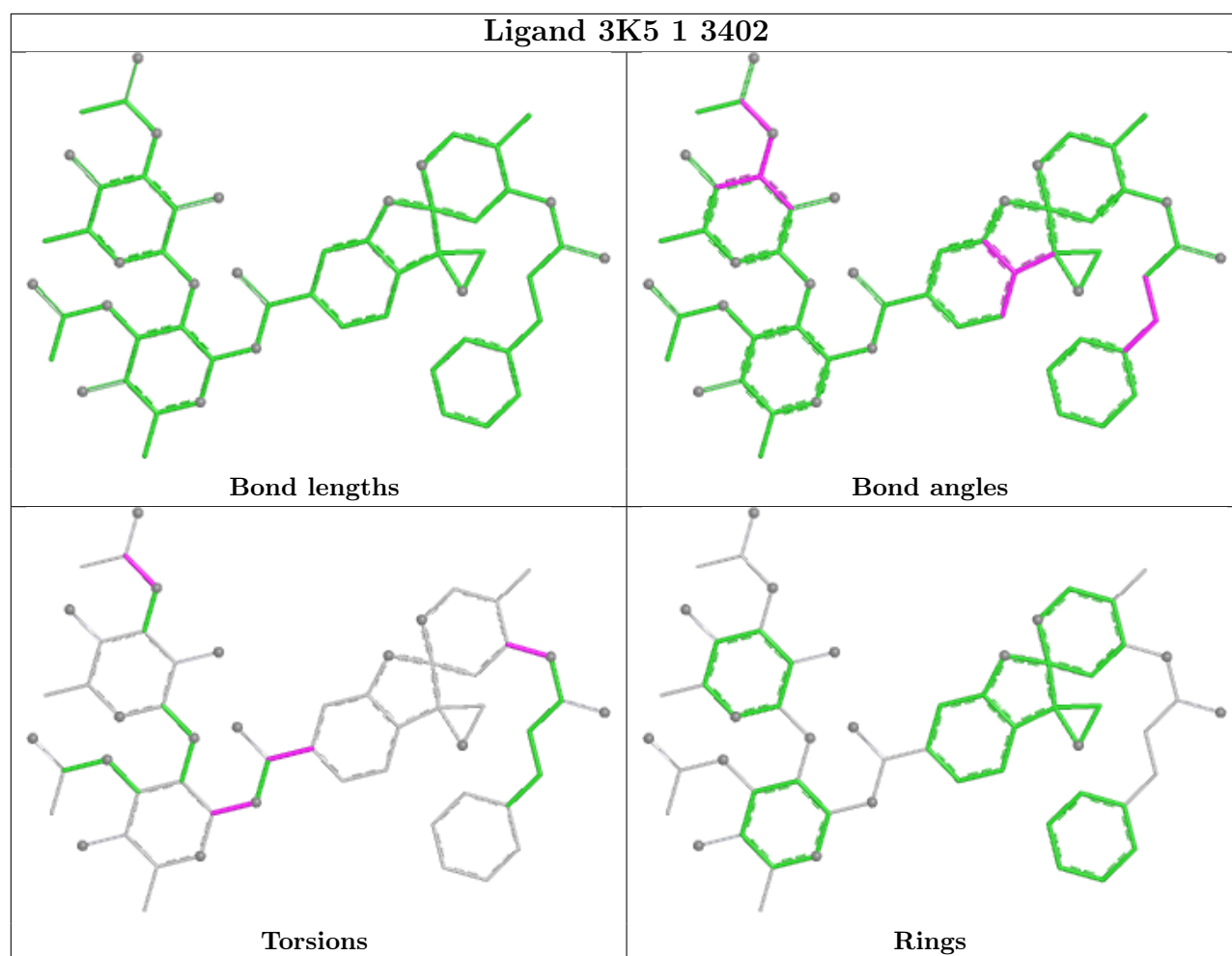
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





Ligand HYG CM 1902





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	1	3208/3359 (95%)	0.31	78 (2%) 59 37	32, 64, 173, 334	0
1	AS	3227/3359 (96%)	0.29	97 (3%) 52 30	34, 69, 204, 323	0
2	3	121/121 (100%)	0.29	0 100 100	50, 78, 100, 136	0
2	AT	121/121 (100%)	0.19	1 (0%) 82 63	39, 70, 93, 145	0
3	4	157/158 (99%)	0.12	1 (0%) 85 69	46, 67, 117, 169	0
3	AU	157/158 (99%)	0.44	6 (3%) 44 24	55, 89, 136, 219	0
4	AW	249/254 (98%)	0.81	18 (7%) 21 11	37, 72, 95, 108	0
4	j	249/254 (98%)	0.78	13 (5%) 33 16	28, 52, 74, 143	0
5	AX	386/389 (99%)	0.49	11 (2%) 55 32	34, 56, 85, 150	0
5	k	386/389 (99%)	0.63	14 (3%) 46 25	29, 58, 78, 116	0
6	AY	361/363 (99%)	1.12	50 (13%) 6 4	44, 73, 101, 132	0
6	l	361/363 (99%)	1.03	48 (13%) 7 4	35, 70, 105, 135	0
7	AZ	292/298 (97%)	1.45	66 (22%) 2 1	44, 93, 124, 140	0
7	m	296/298 (99%)	1.25	43 (14%) 6 3	50, 87, 119, 141	0
8	BA	153/176 (86%)	0.82	10 (6%) 25 12	48, 68, 103, 132	0
8	n	157/176 (89%)	0.85	12 (7%) 20 10	53, 75, 101, 138	0
9	BB	234/241 (97%)	0.54	9 (3%) 44 24	35, 55, 113, 167	0
9	o	233/241 (96%)	0.90	13 (5%) 30 15	38, 63, 123, 164	0
10	BC	229/262 (87%)	1.44	54 (23%) 2 1	76, 117, 159, 188	0
10	p	233/262 (88%)	1.08	34 (14%) 6 3	51, 76, 125, 148	0
11	BD	190/191 (99%)	0.99	14 (7%) 20 10	48, 74, 106, 155	0
11	q	189/191 (98%)	1.21	31 (16%) 4 2	52, 77, 97, 127	0
12	BE	208/220 (94%)	0.56	9 (4%) 40 21	33, 51, 99, 134	0
12	r	208/220 (94%)	0.89	18 (8%) 16 9	40, 65, 101, 119	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
13	BF	171/174 (98%)	1.02	16 (9%)	14 7	53, 81, 114, 127	0
13	s	171/174 (98%)	1.34	28 (16%)	4 2	58, 92, 116, 131	0
14	BG	200/202 (99%)	1.13	33 (16%)	4 2	48, 92, 133, 154	0
14	t	200/202 (99%)	0.80	12 (6%)	27 14	43, 75, 110, 143	0
15	BH	130/131 (99%)	0.70	8 (6%)	26 13	43, 65, 96, 128	0
15	u	130/131 (99%)	0.83	8 (6%)	26 13	52, 70, 89, 103	0
16	BI	203/204 (99%)	1.50	46 (22%)	2 1	54, 84, 106, 118	0
16	v	203/204 (99%)	1.11	20 (9%)	13 6	36, 57, 71, 85	0
17	BJ	199/200 (99%)	0.46	7 (3%)	47 26	34, 51, 86, 120	0
17	w	199/200 (99%)	0.75	12 (6%)	27 14	33, 55, 82, 103	0
18	BK	176/185 (95%)	1.00	14 (7%)	18 9	44, 63, 91, 123	0
18	x	173/185 (93%)	0.90	13 (7%)	20 10	33, 59, 92, 120	0
19	BL	185/186 (99%)	0.82	9 (4%)	35 17	45, 69, 85, 104	0
19	y	185/186 (99%)	1.36	45 (24%)	2 1	41, 66, 85, 100	0
20	BM	179/190 (94%)	0.92	17 (9%)	14 7	48, 77, 137, 169	0
20	z	179/190 (94%)	0.84	6 (3%)	48 27	45, 68, 126, 145	0
21	0	170/172 (98%)	0.92	15 (8%)	15 8	46, 64, 87, 137	0
21	BN	170/172 (98%)	0.61	8 (4%)	36 19	39, 58, 77, 105	0
22	2	159/160 (99%)	1.03	19 (11%)	9 5	44, 63, 111, 147	0
22	BO	159/160 (99%)	0.97	20 (12%)	8 4	37, 60, 113, 147	0
23	5	102/124 (82%)	1.00	9 (8%)	15 8	73, 109, 140, 160	0
23	BP	102/124 (82%)	1.15	14 (13%)	6 4	89, 125, 151, 162	0
24	6	131/137 (95%)	0.71	6 (4%)	37 19	37, 55, 76, 86	0
24	BQ	131/137 (95%)	0.74	7 (5%)	32 16	32, 53, 77, 116	0
25	7	118/155 (76%)	0.92	12 (10%)	12 6	38, 76, 126, 143	0
25	BR	98/155 (63%)	1.00	15 (15%)	5 3	39, 70, 128, 138	0
26	8	120/142 (84%)	0.89	10 (8%)	17 9	53, 71, 91, 98	0
26	BS	119/142 (83%)	1.29	28 (23%)	2 1	62, 93, 113, 128	0
27	9	126/127 (99%)	1.41	25 (19%)	3 1	55, 80, 98, 113	0
27	BT	126/127 (99%)	1.09	16 (12%)	8 4	59, 91, 123, 140	0
28	AA	135/136 (99%)	1.20	19 (14%)	6 3	56, 84, 111, 143	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
28	BU	135/136 (99%)	1.25	21 (15%)	5 2	78, 113, 137, 159	0
29	AB	148/149 (99%)	1.06	14 (9%)	14 7	34, 63, 95, 123	0
29	BV	148/149 (99%)	1.16	24 (16%)	4 2	44, 73, 96, 118	0
30	AC	62/63 (98%)	1.60	21 (33%)	1 0	39, 77, 122, 143	0
30	BW	61/63 (96%)	1.40	13 (21%)	2 1	38, 76, 112, 135	0
31	AD	96/106 (90%)	0.72	6 (6%)	26 13	53, 73, 95, 108	0
31	BX	96/106 (90%)	1.13	18 (18%)	3 2	78, 103, 128, 152	0
32	AE	110/112 (98%)	0.66	4 (3%)	46 25	46, 64, 109, 134	0
32	BY	110/112 (98%)	0.90	8 (7%)	21 10	42, 72, 120, 146	0
33	AF	124/131 (94%)	1.09	16 (12%)	7 4	33, 65, 83, 94	0
33	BZ	124/131 (94%)	0.80	7 (5%)	30 15	37, 63, 87, 107	0
34	AG	106/107 (99%)	1.05	14 (13%)	7 4	45, 61, 78, 99	0
34	CA	106/107 (99%)	0.56	3 (2%)	55 32	36, 51, 73, 91	0
35	AH	112/122 (91%)	1.28	17 (15%)	5 3	46, 70, 113, 139	0
35	CB	112/122 (91%)	1.44	30 (26%)	1 1	50, 95, 128, 158	0
36	AI	120/120 (100%)	1.13	13 (10%)	11 5	60, 83, 106, 128	0
36	CC	118/120 (98%)	1.45	29 (24%)	2 1	74, 100, 125, 135	0
37	AJ	97/99 (97%)	1.04	13 (13%)	7 4	50, 70, 102, 166	0
37	CD	97/99 (97%)	1.37	21 (21%)	2 1	77, 98, 125, 155	0
38	AK	86/90 (95%)	0.87	6 (6%)	22 11	28, 54, 95, 109	0
38	CE	86/90 (95%)	1.11	13 (15%)	5 3	48, 71, 100, 135	0
39	AL	77/78 (98%)	1.17	9 (11%)	9 5	72, 94, 125, 153	0
39	CF	77/78 (98%)	1.47	16 (20%)	2 1	83, 115, 157, 165	0
40	AM	50/51 (98%)	1.01	4 (8%)	18 9	42, 61, 84, 95	0
40	CG	50/51 (98%)	1.41	8 (16%)	5 2	55, 76, 97, 105	0
41	AN	52/52 (100%)	2.11	21 (40%)	0 0	65, 96, 120, 128	0
41	CH	51/52 (98%)	2.34	30 (58%)	0 0	60, 95, 115, 127	0
42	AO	25/25 (100%)	1.74	10 (40%)	1 0	55, 66, 82, 88	0
42	CI	24/25 (96%)	1.49	6 (25%)	2 1	43, 58, 68, 74	0
43	AP	103/106 (97%)	0.85	13 (12%)	8 4	36, 62, 100, 118	0
43	CJ	103/106 (97%)	0.98	14 (13%)	7 4	44, 72, 107, 121	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
44	AQ	91/92 (98%)	0.79	4 (4%)	39 20	39, 57, 97, 108	0
44	CK	91/92 (98%)	0.84	6 (6%)	24 12	48, 72, 104, 123	0
45	CL	121/267 (45%)	1.42	31 (25%)	1 1	59, 88, 120, 144	0
45	i	120/267 (44%)	1.76	38 (31%)	1 1	59, 103, 135, 152	0
46	B	1741/1787 (97%)	0.75	96 (5%)	30 16	48, 89, 173, 457	0
46	CM	1765/1787 (98%)	0.62	75 (4%)	40 21	41, 79, 180, 457	0
47	C	208/261 (79%)	1.25	41 (19%)	3 1	80, 109, 137, 148	0
47	CN	208/261 (79%)	1.17	26 (12%)	8 4	53, 97, 127, 165	0
48	CO	214/256 (83%)	1.42	51 (23%)	2 1	65, 113, 138, 164	0
48	D	214/256 (83%)	1.04	27 (12%)	8 4	58, 92, 111, 131	0
49	CP	217/249 (87%)	0.92	24 (11%)	10 5	42, 73, 102, 120	0
49	E	217/249 (87%)	1.43	47 (21%)	2 1	69, 97, 121, 146	0
50	CQ	223/251 (88%)	1.16	35 (15%)	5 2	49, 76, 133, 174	0
50	F	223/251 (88%)	1.72	73 (32%)	1 0	70, 107, 152, 178	0
51	CR	260/262 (99%)	1.54	63 (24%)	2 1	58, 88, 110, 151	0
51	G	259/262 (98%)	1.67	85 (32%)	1 0	63, 96, 116, 156	0
52	CS	206/225 (91%)	1.70	64 (31%)	1 1	65, 99, 137, 191	0
52	H	206/225 (91%)	1.84	74 (35%)	1 0	67, 103, 143, 168	0
53	CT	236/236 (100%)	1.24	35 (14%)	5 3	54, 94, 139, 159	0
53	I	226/236 (95%)	1.21	42 (18%)	3 2	59, 96, 142, 175	0
54	CU	183/186 (98%)	1.45	45 (24%)	2 1	67, 124, 165, 174	0
54	J	184/186 (98%)	1.88	71 (38%)	1 0	76, 126, 156, 173	0
55	CV	203/206 (98%)	1.29	41 (20%)	3 1	38, 70, 120, 148	0
55	K	203/206 (98%)	1.15	37 (18%)	3 2	43, 79, 123, 140	0
56	CW	178/189 (94%)	1.66	48 (26%)	1 1	59, 93, 121, 136	0
56	L	178/189 (94%)	2.06	91 (51%)	0 0	74, 108, 129, 143	0
57	CX	94/118 (79%)	1.02	9 (9%)	13 7	62, 85, 123, 142	0
57	M	98/118 (83%)	1.70	36 (36%)	1 0	84, 117, 142, 158	0
58	CY	141/155 (90%)	1.24	21 (14%)	5 3	39, 67, 95, 149	0
58	N	144/155 (92%)	1.18	21 (14%)	6 3	48, 77, 113, 139	0
59	CZ	119/143 (83%)	1.46	30 (25%)	1 1	124, 157, 177, 180	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
59	O	116/143 (81%)	1.69	38 (32%)	1	0	136, 175, 196, 203	0
60	DA	150/151 (99%)	1.52	41 (27%)	1	1	54, 89, 117, 134	0
60	P	150/151 (99%)	1.52	41 (27%)	1	1	46, 88, 116, 122	0
61	DB	127/132 (96%)	1.16	13 (10%)	12	6	57, 97, 123, 132	0
61	Q	127/132 (96%)	1.02	16 (12%)	8	4	44, 79, 96, 107	0
62	DC	130/142 (91%)	1.39	25 (19%)	3	1	50, 89, 130, 144	0
62	R	129/142 (90%)	1.77	45 (34%)	1	0	63, 100, 137, 151	0
63	DD	140/142 (98%)	2.15	74 (52%)	0	0	58, 98, 130, 143	0
63	S	140/142 (98%)	2.31	75 (53%)	0	0	67, 112, 148, 152	0
64	DE	124/137 (90%)	1.85	48 (38%)	1	0	67, 108, 158, 166	0
64	T	124/137 (90%)	2.04	52 (41%)	0	0	80, 121, 166, 176	0
65	DF	141/145 (97%)	1.36	27 (19%)	3	1	54, 92, 124, 156	0
65	U	144/145 (99%)	1.53	39 (27%)	1	1	62, 90, 114, 157	0
66	DG	141/145 (97%)	1.54	41 (29%)	1	1	60, 90, 119, 148	0
66	V	141/145 (97%)	1.88	48 (34%)	1	0	79, 107, 140, 162	0
67	DH	97/119 (81%)	1.64	29 (29%)	1	1	49, 94, 122, 150	0
67	W	102/119 (85%)	1.82	39 (38%)	1	0	71, 121, 149, 158	0
68	DI	87/87 (100%)	0.93	7 (8%)	18	9	61, 83, 114, 149	0
68	X	87/87 (100%)	1.14	12 (13%)	6	4	76, 102, 126, 133	0
69	DJ	129/130 (99%)	1.33	27 (20%)	2	1	50, 69, 87, 96	0
69	Y	129/130 (99%)	1.75	41 (31%)	1	0	59, 84, 105, 113	0
70	DK	143/145 (98%)	1.23	25 (17%)	4	2	43, 64, 88, 116	0
70	Z	143/145 (98%)	1.33	29 (20%)	3	1	56, 78, 97, 115	0
71	DL	132/135 (97%)	1.19	16 (12%)	8	5	71, 110, 133, 174	0
71	a	134/135 (99%)	1.48	33 (24%)	2	1	68, 112, 130, 144	0
72	DM	71/105 (67%)	1.19	10 (14%)	6	3	89, 120, 143, 148	0
72	b	72/105 (68%)	1.31	13 (18%)	3	2	85, 111, 134, 154	0
73	DN	97/119 (81%)	1.37	18 (18%)	3	2	52, 75, 129, 137	0
73	c	98/119 (82%)	1.46	24 (24%)	2	1	53, 83, 123, 135	0
74	DO	81/82 (98%)	1.46	18 (22%)	2	1	73, 99, 160, 173	0
74	d	81/82 (98%)	1.38	13 (16%)	5	2	73, 99, 156, 170	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
75	DP	61/67 (91%)	1.07	9 (14%) 5 3	78, 101, 129, 148	0
75	e	62/67 (92%)	1.45	13 (20%) 2 1	91, 111, 131, 138	0
76	DQ	54/56 (96%)	1.38	12 (22%) 2 1	51, 65, 93, 103	0
76	f	55/56 (98%)	1.82	17 (30%) 1 1	75, 92, 118, 141	0
77	DR	58/63 (92%)	1.52	15 (25%) 1 1	63, 101, 161, 173	0
77	g	60/63 (95%)	1.60	16 (26%) 1 1	75, 105, 154, 169	0
78	DS	70/193 (36%)	2.33	36 (51%) 0 0	95, 163, 181, 196	0
78	h	70/193 (36%)	1.88	28 (40%) 1 0	113, 160, 185, 191	0
79	AR	311/317 (98%)	1.61	86 (27%) 1 1	114, 155, 178, 192	0
79	DT	306/317 (96%)	1.72	103 (33%) 1 0	100, 145, 174, 196	0
80	P0	107/312 (34%)	1.52	30 (28%) 1 1	104, 127, 144, 157	0
80	p0	79/312 (25%)	2.19	37 (46%) 0 0	119, 138, 155, 161	0
81	12	63/165 (38%)	0.98	6 (9%) 14 7	98, 132, 151, 157	0
82	L1	217/217 (100%)	1.00	28 (12%) 7 4	91, 127, 164, 224	0
82	l1	217/217 (100%)	1.36	51 (23%) 2 1	109, 137, 164, 197	0
All	All	33588/36349 (92%)	0.97	4460 (13%) 7 4	28, 80, 154, 457	0

The worst 5 of 4460 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
67	W	81	TYR	9.5
51	G	110	ALA	9.5
50	F	206	ALA	9.0
1	AS	1263	U	8.2
66	V	18	TYR	7.9

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 oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
83	MG	1	3715	1/1	-0.02	0.38	76,76,76,76	0
83	MG	1	3921	1/1	0.15	0.20	67,67,67,67	0
83	MG	B	1928	1/1	0.16	0.32	108,108,108,108	0
83	MG	J	201	1/1	0.31	0.16	129,129,129,129	0
83	MG	1	3841	1/1	0.36	0.18	73,73,73,73	0
83	MG	CM	1819	1/1	0.41	0.24	74,74,74,74	0
83	MG	8	201	1/1	0.43	0.26	62,62,62,62	0
83	MG	8	202	1/1	0.46	0.61	79,79,79,79	0
83	MG	1	3868	1/1	0.50	0.18	54,54,54,54	0
83	MG	B	1898	1/1	0.52	0.31	60,60,60,60	0
83	MG	B	1851	1/1	0.52	0.19	53,53,53,53	0
83	MG	9	202	1/1	0.53	0.23	81,81,81,81	0
83	MG	1	3651	1/1	0.53	0.36	77,77,77,77	0
85	ZN	d	101	1/1	0.53	0.17	285,285,285,285	0
83	MG	AS	3676	1/1	0.54	0.17	72,72,72,72	0
83	MG	u	202	1/1	0.54	0.12	51,51,51,51	0
83	MG	1	3630	1/1	0.54	0.34	59,59,59,59	0
83	MG	1	3669	1/1	0.56	0.33	76,76,76,76	0
83	MG	AJ	101	1/1	0.57	0.22	82,82,82,82	0
83	MG	CM	1876	1/1	0.57	0.21	51,51,51,51	0
83	MG	1	3930	1/1	0.57	0.23	81,81,81,81	0
83	MG	1	3803	1/1	0.58	0.27	92,92,92,92	0
83	MG	1	3527	1/1	0.58	0.32	72,72,72,72	0
83	MG	CL	301	1/1	0.59	0.17	40,40,40,40	0
83	MG	AS	3601	1/1	0.59	0.15	124,124,124,124	0
83	MG	B	1924	1/1	0.60	0.30	69,69,69,69	0
83	MG	4	207	1/1	0.61	0.27	64,64,64,64	0
83	MG	f	102	1/1	0.61	0.14	81,81,81,81	0
83	MG	1	3776	1/1	0.61	0.38	57,57,57,57	0
83	MG	B	1941	1/1	0.61	0.13	58,58,58,58	0
83	MG	AS	3631	1/1	0.62	0.16	66,66,66,66	0
83	MG	1	3856	1/1	0.62	0.15	66,66,66,66	0
83	MG	4	203	1/1	0.62	0.16	57,57,57,57	0
83	MG	Y	201	1/1	0.63	0.12	58,58,58,58	0
83	MG	AG	201	1/1	0.63	0.25	86,86,86,86	0
83	MG	DG	201	1/1	0.63	0.30	52,52,52,52	0
83	MG	1	3688	1/1	0.63	0.35	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3716	1/1	0.64	0.14	77,77,77,77	0
83	MG	s	201	1/1	0.64	0.20	62,62,62,62	0
83	MG	1	3867	1/1	0.64	0.18	51,51,51,51	0
83	MG	1	3470	1/1	0.64	0.27	53,53,53,53	0
83	MG	1	3722	1/1	0.65	0.19	61,61,61,61	0
83	MG	CM	1859	1/1	0.65	0.18	60,60,60,60	0
83	MG	B	1890	1/1	0.65	0.16	53,53,53,53	0
83	MG	a	201	1/1	0.65	0.12	76,76,76,76	0
83	MG	B	1829	1/1	0.65	0.14	64,64,64,64	0
83	MG	1	3713	1/1	0.66	0.13	51,51,51,51	0
83	MG	G	302	1/1	0.66	0.32	63,63,63,63	0
83	MG	1	3890	1/1	0.66	0.19	46,46,46,46	0
83	MG	1	3796	1/1	0.66	0.15	84,84,84,84	0
83	MG	B	1875	1/1	0.66	0.31	75,75,75,75	0
83	MG	1	3476	1/1	0.67	0.15	58,58,58,58	0
83	MG	DB	203	1/1	0.67	0.14	52,52,52,52	0
83	MG	B	1939	1/1	0.68	0.14	78,78,78,78	0
83	MG	I	301	1/1	0.68	0.25	99,99,99,99	0
83	MG	CM	1880	1/1	0.68	0.18	66,66,66,66	0
83	MG	1	3699	1/1	0.68	0.21	54,54,54,54	0
83	MG	AS	3519	1/1	0.68	0.24	42,42,42,42	0
83	MG	AS	3597	1/1	0.68	0.10	28,28,28,28	0
83	MG	1	3681	1/1	0.69	0.21	52,52,52,52	0
83	MG	1	3914	1/1	0.69	0.18	57,57,57,57	0
83	MG	CM	1864	1/1	0.69	0.18	73,73,73,73	0
83	MG	B	1896	1/1	0.69	0.09	61,61,61,61	0
83	MG	1	3797	1/1	0.69	0.18	77,77,77,77	0
83	MG	B	1922	1/1	0.69	0.20	66,66,66,66	0
83	MG	1	3598	1/1	0.69	0.20	56,56,56,56	0
83	MG	1	3837	1/1	0.69	0.13	34,34,34,34	0
83	MG	1	3432	1/1	0.70	0.14	48,48,48,48	0
83	MG	1	3923	1/1	0.70	0.20	64,64,64,64	0
83	MG	1	3694	1/1	0.70	0.14	39,39,39,39	0
83	MG	1	3931	1/1	0.70	0.16	61,61,61,61	0
83	MG	1	3517	1/1	0.70	0.15	58,58,58,58	0
83	MG	B	1856	1/1	0.70	0.15	47,47,47,47	0
83	MG	BF	201	1/1	0.70	0.14	44,44,44,44	0
83	MG	B	1862	1/1	0.70	0.16	68,68,68,68	0
83	MG	1	3438	1/1	0.71	0.19	31,31,31,31	0
83	MG	1	3483	1/1	0.71	0.13	38,38,38,38	0
83	MG	o	303	1/1	0.71	0.17	57,57,57,57	0
83	MG	1	3842	1/1	0.71	0.11	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3493	1/1	0.72	0.19	51,51,51,51	0
83	MG	B	1810	1/1	0.72	0.23	45,45,45,45	0
83	MG	k	404	1/1	0.72	0.17	79,79,79,79	0
83	MG	CM	1882	1/1	0.72	0.22	66,66,66,66	0
83	MG	1	3584	1/1	0.72	0.14	41,41,41,41	0
83	MG	CM	1822	1/1	0.72	0.19	44,44,44,44	0
83	MG	1	3876	1/1	0.72	0.14	42,42,42,42	0
83	MG	1	3655	1/1	0.73	0.18	54,54,54,54	0
83	MG	j	302	1/1	0.73	0.12	53,53,53,53	0
83	MG	BZ	202	1/1	0.73	0.13	66,66,66,66	0
83	MG	1	3543	1/1	0.73	0.21	62,62,62,62	0
83	MG	CM	1816	1/1	0.73	0.20	27,27,27,27	0
83	MG	1	3854	1/1	0.74	0.27	61,61,61,61	0
83	MG	CM	1821	1/1	0.74	0.15	35,35,35,35	0
83	MG	AS	3602	1/1	0.74	0.15	59,59,59,59	0
83	MG	CM	1836	1/1	0.74	0.15	48,48,48,48	0
83	MG	AS	3622	1/1	0.74	0.09	47,47,47,47	0
83	MG	AS	3627	1/1	0.74	0.15	57,57,57,57	0
83	MG	1	3891	1/1	0.74	0.18	65,65,65,65	0
83	MG	1	3648	1/1	0.74	0.12	44,44,44,44	0
83	MG	1	3783	1/1	0.74	0.18	48,48,48,48	0
83	MG	1	3468	1/1	0.74	0.21	38,38,38,38	0
83	MG	1	3871	1/1	0.74	0.18	67,67,67,67	0
83	MG	1	3597	1/1	0.74	0.34	60,60,60,60	0
83	MG	1	3618	1/1	0.75	0.13	34,34,34,34	0
83	MG	1	3700	1/1	0.75	0.22	47,47,47,47	0
83	MG	1	3545	1/1	0.75	0.23	51,51,51,51	0
83	MG	1	3674	1/1	0.75	0.17	83,83,83,83	0
83	MG	1	3631	1/1	0.75	0.25	64,64,64,64	0
83	MG	AS	3646	1/1	0.75	0.12	35,35,35,35	0
83	MG	AS	3652	1/1	0.75	0.11	51,51,51,51	0
83	MG	1	3547	1/1	0.75	0.11	42,42,42,42	0
83	MG	1	3746	1/1	0.75	0.13	66,66,66,66	0
83	MG	1	3909	1/1	0.75	0.18	79,79,79,79	0
83	MG	1	3553	1/1	0.75	0.24	54,54,54,54	0
83	MG	r	302	1/1	0.75	0.18	50,50,50,50	0
83	MG	1	3913	1/1	0.76	0.18	55,55,55,55	0
83	MG	V	201	1/1	0.76	0.28	48,48,48,48	0
83	MG	1	3524	1/1	0.76	0.24	44,44,44,44	0
83	MG	B	1926	1/1	0.76	0.20	41,41,41,41	0
83	MG	3	202	1/1	0.76	0.11	59,59,59,59	0
83	MG	3	214	1/1	0.76	0.14	82,82,82,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3587	1/1	0.76	0.13	58,58,58,58	0
83	MG	AS	3562	1/1	0.76	0.13	50,50,50,50	0
83	MG	B	1944	1/1	0.76	0.10	76,76,76,76	0
83	MG	1	3583	1/1	0.76	0.21	52,52,52,52	0
83	MG	0	201	1/1	0.76	0.19	70,70,70,70	0
83	MG	1	3652	1/1	0.77	0.18	43,43,43,43	0
83	MG	AS	3580	1/1	0.77	0.12	42,42,42,42	0
83	MG	CM	1853	1/1	0.77	0.25	72,72,72,72	0
83	MG	B	1877	1/1	0.77	0.22	53,53,53,53	0
83	MG	CM	1860	1/1	0.77	0.21	41,41,41,41	0
83	MG	B	1827	1/1	0.77	0.13	37,37,37,37	0
83	MG	1	3671	1/1	0.77	0.20	52,52,52,52	0
83	MG	5	201	1/1	0.77	0.12	64,64,64,64	0
83	MG	1	3732	1/1	0.77	0.12	26,26,26,26	0
83	MG	CM	1818	1/1	0.77	0.18	38,38,38,38	0
83	MG	B	1806	1/1	0.77	0.13	67,67,67,67	0
83	MG	AS	3637	1/1	0.77	0.24	97,97,97,97	0
83	MG	1	3838	1/1	0.78	0.14	61,61,61,61	0
83	MG	6	203	1/1	0.78	0.16	42,42,42,42	0
83	MG	1	3564	1/1	0.78	0.14	57,57,57,57	0
83	MG	1	3502	1/1	0.78	0.13	41,41,41,41	0
83	MG	1	3591	1/1	0.78	0.14	58,58,58,58	0
83	MG	1	3622	1/1	0.78	0.23	42,42,42,42	0
83	MG	AS	3641	1/1	0.78	0.28	48,48,48,48	0
83	MG	AH	202	1/1	0.78	0.14	55,55,55,55	0
83	MG	1	3861	1/1	0.78	0.12	56,56,56,56	0
83	MG	1	3747	1/1	0.78	0.08	45,45,45,45	0
83	MG	AT	207	1/1	0.78	0.19	68,68,68,68	0
83	MG	1	3830	1/1	0.78	0.23	43,43,43,43	0
83	MG	DA	201	1/1	0.78	0.26	57,57,57,57	0
83	MG	1	3832	1/1	0.78	0.18	56,56,56,56	0
83	MG	1	3754	1/1	0.78	0.22	61,61,61,61	0
83	MG	0	204	1/1	0.78	0.18	45,45,45,45	0
83	MG	1	3677	1/1	0.79	0.19	55,55,55,55	0
83	MG	1	3554	1/1	0.79	0.09	40,40,40,40	0
83	MG	B	1943	1/1	0.79	0.07	68,68,68,68	0
83	MG	1	3555	1/1	0.79	0.10	46,46,46,46	0
83	MG	1	3781	1/1	0.79	0.12	82,82,82,82	0
83	MG	AS	3673	1/1	0.79	0.13	45,45,45,45	0
83	MG	AS	3581	1/1	0.79	0.11	46,46,46,46	0
83	MG	B	1850	1/1	0.79	0.10	24,24,24,24	0
83	MG	0	202	1/1	0.79	0.10	39,39,39,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	BN	201	1/1	0.79	0.11	59,59,59,59	0
83	MG	1	3858	1/1	0.79	0.15	48,48,48,48	0
83	MG	CM	1898	1/1	0.79	0.12	44,44,44,44	0
83	MG	CM	1899	1/1	0.79	0.17	31,31,31,31	0
83	MG	CO	301	1/1	0.79	0.25	34,34,34,34	0
83	MG	AS	3615	1/1	0.79	0.16	50,50,50,50	0
83	MG	CL	303	1/1	0.79	0.19	41,41,41,41	0
83	MG	3	210	1/1	0.79	0.19	59,59,59,59	0
83	MG	B	1866	1/1	0.79	0.20	78,78,78,78	0
83	MG	1	3563	1/1	0.80	0.21	50,50,50,50	0
83	MG	CM	1808	1/1	0.80	0.21	58,58,58,58	0
83	MG	1	3466	1/1	0.80	0.19	43,43,43,43	0
83	MG	B	1927	1/1	0.80	0.11	57,57,57,57	0
83	MG	9	201	1/1	0.80	0.76	70,70,70,70	0
83	MG	1	3873	1/1	0.80	0.09	40,40,40,40	0
83	MG	1	3848	1/1	0.80	0.18	78,78,78,78	0
83	MG	1	3595	1/1	0.80	0.14	42,42,42,42	0
83	MG	CM	1837	1/1	0.80	0.19	39,39,39,39	0
83	MG	1	3686	1/1	0.80	0.18	60,60,60,60	0
83	MG	1	3893	1/1	0.80	0.17	52,52,52,52	0
83	MG	B	1893	1/1	0.80	0.30	43,43,43,43	0
83	MG	1	3530	1/1	0.80	0.18	52,52,52,52	0
83	MG	1	3559	1/1	0.80	0.16	46,46,46,46	0
83	MG	B	1902	1/1	0.80	0.32	60,60,60,60	0
83	MG	B	1907	1/1	0.80	0.10	44,44,44,44	0
83	MG	AS	3675	1/1	0.80	0.12	55,55,55,55	0
83	MG	B	1909	1/1	0.80	0.16	35,35,35,35	0
83	MG	AS	3427	1/1	0.80	0.10	43,43,43,43	0
83	MG	AS	3491	1/1	0.80	0.17	64,64,64,64	0
83	MG	B	1911	1/1	0.80	0.23	60,60,60,60	0
83	MG	B	1916	1/1	0.80	0.17	69,69,69,69	0
83	MG	1	3727	1/1	0.80	0.09	38,38,38,38	0
83	MG	1	3902	1/1	0.81	0.23	51,51,51,51	0
83	MG	1	3607	1/1	0.81	0.12	51,51,51,51	0
83	MG	1	3866	1/1	0.81	0.08	62,62,62,62	0
83	MG	1	3645	1/1	0.81	0.22	47,47,47,47	0
83	MG	1	3625	1/1	0.81	0.38	95,95,95,95	0
83	MG	1	3518	1/1	0.81	0.25	57,57,57,57	0
83	MG	B	1934	1/1	0.81	0.14	102,102,102,102	0
83	MG	1	3928	1/1	0.81	0.21	59,59,59,59	0
83	MG	AS	3662	1/1	0.81	0.08	57,57,57,57	0
83	MG	AS	3666	1/1	0.81	0.11	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3560	1/1	0.81	0.10	52,52,52,52	0
83	MG	1	3800	1/1	0.81	0.17	62,62,62,62	0
83	MG	AS	3573	1/1	0.81	0.14	30,30,30,30	0
83	MG	1	3849	1/1	0.81	0.24	47,47,47,47	0
83	MG	BB	301	1/1	0.81	0.12	28,28,28,28	0
83	MG	BE	302	1/1	0.81	0.10	48,48,48,48	0
83	MG	1	3714	1/1	0.81	0.19	43,43,43,43	0
83	MG	BJ	303	1/1	0.81	0.11	30,30,30,30	0
83	MG	AS	3585	1/1	0.81	0.20	44,44,44,44	0
83	MG	3	206	1/1	0.81	0.12	47,47,47,47	0
83	MG	1	3672	1/1	0.81	0.11	57,57,57,57	0
83	MG	1	3692	1/1	0.81	0.13	176,176,176,176	0
83	MG	1	3442	1/1	0.82	0.30	52,52,52,52	0
83	MG	AE	202	1/1	0.82	0.07	63,63,63,63	0
83	MG	1	3720	1/1	0.82	0.18	23,23,23,23	0
83	MG	B	1938	1/1	0.82	0.26	70,70,70,70	0
83	MG	1	3639	1/1	0.82	0.16	54,54,54,54	0
83	MG	1	3726	1/1	0.82	0.19	43,43,43,43	0
83	MG	CL	302	1/1	0.82	0.37	59,59,59,59	0
83	MG	B	1942	1/1	0.82	0.16	67,67,67,67	0
83	MG	1	3798	1/1	0.82	0.13	41,41,41,41	0
83	MG	1	3419	1/1	0.82	0.15	47,47,47,47	0
83	MG	B	1949	1/1	0.82	0.17	47,47,47,47	0
83	MG	B	1899	1/1	0.82	0.18	73,73,73,73	0
83	MG	CM	1820	1/1	0.82	0.21	27,27,27,27	0
83	MG	B	1817	1/1	0.82	0.24	45,45,45,45	0
83	MG	AS	3629	1/1	0.82	0.14	38,38,38,38	0
83	MG	AS	3630	1/1	0.82	0.07	50,50,50,50	0
83	MG	1	3489	1/1	0.82	0.13	49,49,49,49	0
83	MG	1	3594	1/1	0.82	0.23	72,72,72,72	0
83	MG	B	1846	1/1	0.82	0.10	57,57,57,57	0
83	MG	B	1912	1/1	0.82	0.12	81,81,81,81	0
83	MG	1	3911	1/1	0.82	0.12	63,63,63,63	0
83	MG	CM	1874	1/1	0.82	0.15	66,66,66,66	0
83	MG	AS	3414	1/1	0.82	0.27	47,47,47,47	0
83	MG	B	1918	1/1	0.82	0.14	59,59,59,59	0
83	MG	AS	3490	1/1	0.82	0.12	35,35,35,35	0
83	MG	1	3568	1/1	0.82	0.23	44,44,44,44	0
83	MG	1	3683	1/1	0.82	0.12	104,104,104,104	0
83	MG	AT	202	1/1	0.82	0.25	55,55,55,55	0
83	MG	AT	203	1/1	0.82	0.20	57,57,57,57	0
83	MG	1	3495	1/1	0.82	0.22	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AW	304	1/1	0.82	0.25	84,84,84,84	0
83	MG	AS	3538	1/1	0.82	0.11	32,32,32,32	0
83	MG	AS	3616	1/1	0.83	0.15	45,45,45,45	0
83	MG	AS	3621	1/1	0.83	0.14	53,53,53,53	0
83	MG	1	3428	1/1	0.83	0.30	47,47,47,47	0
83	MG	AS	3624	1/1	0.83	0.10	41,41,41,41	0
83	MG	1	3523	1/1	0.83	0.18	42,42,42,42	0
83	MG	CM	1806	1/1	0.83	0.10	28,28,28,28	0
83	MG	AS	3628	1/1	0.83	0.15	33,33,33,33	0
83	MG	4	206	1/1	0.83	0.15	24,24,24,24	0
83	MG	1	3661	1/1	0.83	0.09	33,33,33,33	0
83	MG	AS	3455	1/1	0.83	0.10	29,29,29,29	0
83	MG	AS	3482	1/1	0.83	0.13	67,67,67,67	0
83	MG	AS	3638	1/1	0.83	0.18	59,59,59,59	0
83	MG	1	3444	1/1	0.83	0.25	45,45,45,45	0
83	MG	1	3766	1/1	0.83	0.15	44,44,44,44	0
83	MG	1	3455	1/1	0.83	0.28	32,32,32,32	0
83	MG	AS	3661	1/1	0.83	0.19	64,64,64,64	0
83	MG	AS	3516	1/1	0.83	0.25	40,40,40,40	0
83	MG	B	1886	1/1	0.83	0.15	95,95,95,95	0
83	MG	1	3877	1/1	0.83	0.10	52,52,52,52	0
83	MG	AH	203	1/1	0.83	0.14	29,29,29,29	0
83	MG	1	3929	1/1	0.83	0.10	77,77,77,77	0
83	MG	CM	1877	1/1	0.83	0.12	47,47,47,47	0
83	MG	B	1802	1/1	0.83	0.25	45,45,45,45	0
83	MG	1	3552	1/1	0.83	0.17	50,50,50,50	0
83	MG	AT	204	1/1	0.83	0.20	64,64,64,64	0
83	MG	1	3836	1/1	0.83	0.16	31,31,31,31	0
83	MG	1	3729	1/1	0.83	0.35	50,50,50,50	0
83	MG	1	3895	1/1	0.83	0.12	44,44,44,44	0
83	MG	0	205	1/1	0.83	0.34	55,55,55,55	0
83	MG	B	1833	1/1	0.83	0.26	32,32,32,32	0
83	MG	1	3862	1/1	0.83	0.15	80,80,80,80	0
83	MG	BH	201	1/1	0.84	0.08	43,43,43,43	0
83	MG	1	3853	1/1	0.84	0.13	33,33,33,33	0
83	MG	B	1836	1/1	0.84	0.19	51,51,51,51	0
83	MG	AS	3618	1/1	0.84	0.18	45,45,45,45	0
83	MG	Z	202	1/1	0.84	0.15	58,58,58,58	0
83	MG	1	3433	1/1	0.84	0.28	45,45,45,45	0
83	MG	1	3855	1/1	0.84	0.11	43,43,43,43	0
83	MG	1	3721	1/1	0.84	0.18	43,43,43,43	0
83	MG	1	3908	1/1	0.84	0.09	23,23,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	CM	1811	1/1	0.84	0.21	59,59,59,59	0
83	MG	1	3812	1/1	0.84	0.20	46,46,46,46	0
83	MG	AS	3473	1/1	0.84	0.11	16,16,16,16	0
83	MG	AB	202	1/1	0.84	0.21	76,76,76,76	0
83	MG	AS	3632	1/1	0.84	0.16	38,38,38,38	0
83	MG	1	3603	1/1	0.84	0.13	50,50,50,50	0
83	MG	1	3724	1/1	0.84	0.16	49,49,49,49	0
83	MG	1	3491	1/1	0.84	0.17	32,32,32,32	0
83	MG	AS	3642	1/1	0.84	0.16	46,46,46,46	0
83	MG	CM	1848	1/1	0.84	0.28	52,52,52,52	0
83	MG	AS	3512	1/1	0.84	0.17	20,20,20,20	0
83	MG	CM	1858	1/1	0.84	0.14	42,42,42,42	0
83	MG	1	3668	1/1	0.84	0.11	32,32,32,32	0
83	MG	AS	3518	1/1	0.84	0.19	43,43,43,43	0
83	MG	B	1940	1/1	0.84	0.15	76,76,76,76	0
83	MG	1	3793	1/1	0.84	0.11	18,18,18,18	0
83	MG	AS	3539	1/1	0.84	0.19	59,59,59,59	0
83	MG	AS	3540	1/1	0.84	0.19	37,37,37,37	0
83	MG	1	3839	1/1	0.84	0.08	55,55,55,55	0
83	MG	B	1897	1/1	0.84	0.12	42,42,42,42	0
83	MG	w	303	1/1	0.84	0.14	56,56,56,56	0
83	MG	B	1946	1/1	0.84	0.21	32,32,32,32	0
83	MG	1	3794	1/1	0.84	0.22	68,68,68,68	0
83	MG	B	1952	1/1	0.84	0.22	48,48,48,48	0
83	MG	1	3569	1/1	0.84	0.24	38,38,38,38	0
83	MG	1	3537	1/1	0.84	0.17	51,51,51,51	0
83	MG	1	3525	1/1	0.84	0.19	44,44,44,44	0
83	MG	1	3423	1/1	0.85	0.15	42,42,42,42	0
83	MG	1	3918	1/1	0.85	0.12	43,43,43,43	0
83	MG	k	401	1/1	0.85	0.11	58,58,58,58	0
83	MG	B	1919	1/1	0.85	0.26	50,50,50,50	0
83	MG	AS	3600	1/1	0.85	0.14	46,46,46,46	0
83	MG	1	3719	1/1	0.85	0.07	27,27,27,27	0
83	MG	AE	201	1/1	0.85	0.11	62,62,62,62	0
83	MG	AS	3426	1/1	0.85	0.17	30,30,30,30	0
83	MG	B	1864	1/1	0.85	0.18	42,42,42,42	0
83	MG	B	1865	1/1	0.85	0.13	25,25,25,25	0
83	MG	1	3881	1/1	0.85	0.18	25,25,25,25	0
83	MG	1	3924	1/1	0.85	0.14	69,69,69,69	0
83	MG	1	3675	1/1	0.85	0.20	52,52,52,52	0
83	MG	1	3575	1/1	0.85	0.16	28,28,28,28	0
83	MG	w	302	1/1	0.85	0.31	52,52,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3753	1/1	0.85	0.26	55,55,55,55	0
83	MG	1	3580	1/1	0.85	0.19	61,61,61,61	0
83	MG	B	1807	1/1	0.85	0.20	40,40,40,40	0
83	MG	CM	1883	1/1	0.85	0.12	45,45,45,45	0
83	MG	CM	1891	1/1	0.85	0.20	26,26,26,26	0
83	MG	1	3896	1/1	0.85	0.16	43,43,43,43	0
83	MG	1	3503	1/1	0.85	0.09	32,32,32,32	0
83	MG	1	3434	1/1	0.85	0.22	41,41,41,41	0
83	MG	1	3807	1/1	0.85	0.09	54,54,54,54	0
83	MG	1	3585	1/1	0.85	0.19	44,44,44,44	0
83	MG	B	1910	1/1	0.85	0.10	54,54,54,54	0
83	MG	DG	202	1/1	0.85	0.11	63,63,63,63	0
83	MG	1	3815	1/1	0.85	0.17	30,30,30,30	0
85	ZN	CB	201	1/1	0.85	0.14	202,202,202,202	0
83	MG	AS	3605	1/1	0.86	0.22	38,38,38,38	0
83	MG	1	3925	1/1	0.86	0.10	37,37,37,37	0
83	MG	B	1835	1/1	0.86	0.18	21,21,21,21	0
83	MG	1	3926	1/1	0.86	0.23	53,53,53,53	0
83	MG	B	1844	1/1	0.86	0.13	55,55,55,55	0
83	MG	AS	3449	1/1	0.86	0.14	40,40,40,40	0
83	MG	AS	3450	1/1	0.86	0.18	38,38,38,38	0
83	MG	AS	3626	1/1	0.86	0.19	40,40,40,40	0
83	MG	1	3401	1/1	0.86	0.29	30,30,30,30	0
83	MG	1	3885	1/1	0.86	0.09	53,53,53,53	0
83	MG	1	3804	1/1	0.86	0.12	30,30,30,30	0
83	MG	1	3579	1/1	0.86	0.09	36,36,36,36	0
83	MG	1	3892	1/1	0.86	0.10	53,53,53,53	0
83	MG	3	203	1/1	0.86	0.15	31,31,31,31	0
83	MG	AS	3500	1/1	0.86	0.10	32,32,32,32	0
83	MG	CM	1823	1/1	0.86	0.16	34,34,34,34	0
83	MG	CM	1827	1/1	0.86	0.21	34,34,34,34	0
83	MG	CM	1835	1/1	0.86	0.22	54,54,54,54	0
83	MG	1	3693	1/1	0.86	0.10	37,37,37,37	0
83	MG	1	3894	1/1	0.86	0.15	57,57,57,57	0
83	MG	CM	1845	1/1	0.86	0.13	29,29,29,29	0
83	MG	1	3778	1/1	0.86	0.19	57,57,57,57	0
83	MG	CM	1850	1/1	0.86	0.12	58,58,58,58	0
83	MG	AS	3643	1/1	0.86	0.16	39,39,39,39	0
83	MG	1	3593	1/1	0.86	0.17	35,35,35,35	0
83	MG	1	3457	1/1	0.86	0.10	20,20,20,20	0
83	MG	AS	3653	1/1	0.86	0.15	68,68,68,68	0
83	MG	B	1887	1/1	0.86	0.23	47,47,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	CM	1868	1/1	0.86	0.18	64,64,64,64	0
83	MG	CM	1872	1/1	0.86	0.19	45,45,45,45	0
83	MG	1	3906	1/1	0.86	0.13	27,27,27,27	0
83	MG	AS	3544	1/1	0.86	0.12	28,28,28,28	0
83	MG	AS	3671	1/1	0.86	0.13	32,32,32,32	0
83	MG	AS	3547	1/1	0.86	0.11	35,35,35,35	0
83	MG	4	209	1/1	0.86	0.07	54,54,54,54	0
83	MG	1	3835	1/1	0.86	0.08	25,25,25,25	0
83	MG	AS	3678	1/1	0.86	0.12	42,42,42,42	0
83	MG	1	3515	1/1	0.86	0.20	21,21,21,21	0
83	MG	1	3653	1/1	0.86	0.07	39,39,39,39	0
83	MG	1	3498	1/1	0.86	0.21	39,39,39,39	0
83	MG	1	3657	1/1	0.86	0.15	22,22,22,22	0
83	MG	DB	201	1/1	0.86	0.13	38,38,38,38	0
83	MG	1	3526	1/1	0.86	0.12	48,48,48,48	0
83	MG	AS	3599	1/1	0.86	0.28	50,50,50,50	0
83	MG	1	3875	1/1	0.86	0.11	42,42,42,42	0
83	MG	1	3799	1/1	0.86	0.10	33,33,33,33	0
83	MG	1	3664	1/1	0.86	0.20	32,32,32,32	0
86	HYG	B	1953	36/36	0.86	0.14	49,77,94,99	0
83	MG	1	3827	1/1	0.87	0.14	50,50,50,50	0
83	MG	B	1892	1/1	0.87	0.15	40,40,40,40	0
83	MG	B	1823	1/1	0.87	0.14	31,31,31,31	0
83	MG	B	1824	1/1	0.87	0.21	26,26,26,26	0
83	MG	B	1825	1/1	0.87	0.15	32,32,32,32	0
83	MG	AS	3644	1/1	0.87	0.13	59,59,59,59	0
83	MG	1	3500	1/1	0.87	0.16	37,37,37,37	0
83	MG	AS	3648	1/1	0.87	0.17	32,32,32,32	0
83	MG	1	3879	1/1	0.87	0.11	39,39,39,39	0
83	MG	B	1830	1/1	0.87	0.21	46,46,46,46	0
83	MG	B	1905	1/1	0.87	0.13	38,38,38,38	0
83	MG	Q	201	1/1	0.87	0.20	49,49,49,49	0
83	MG	1	3880	1/1	0.87	0.21	58,58,58,58	0
83	MG	B	1908	1/1	0.87	0.19	46,46,46,46	0
83	MG	1	3765	1/1	0.87	0.13	38,38,38,38	0
83	MG	AS	3596	1/1	0.87	0.08	37,37,37,37	0
83	MG	1	3920	1/1	0.87	0.20	49,49,49,49	0
83	MG	1	3884	1/1	0.87	0.10	65,65,65,65	0
83	MG	AS	3412	1/1	0.87	0.16	23,23,23,23	0
83	MG	B	1845	1/1	0.87	0.18	35,35,35,35	0
83	MG	1	3617	1/1	0.87	0.08	37,37,37,37	0
83	MG	AS	3603	1/1	0.87	0.16	38,38,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3643	1/1	0.87	0.12	27,27,27,27	0
83	MG	AS	3606	1/1	0.87	0.07	32,32,32,32	0
83	MG	1	3540	1/1	0.87	0.23	42,42,42,42	0
83	MG	1	3740	1/1	0.87	0.18	53,53,53,53	0
83	MG	B	1859	1/1	0.87	0.16	34,34,34,34	0
83	MG	AS	3467	1/1	0.87	0.12	57,57,57,57	0
83	MG	1	3647	1/1	0.87	0.14	45,45,45,45	0
83	MG	1	3789	1/1	0.87	0.15	21,21,21,21	0
83	MG	CK	102	1/1	0.87	0.14	32,32,32,32	0
83	MG	1	3680	1/1	0.87	0.08	30,30,30,30	0
83	MG	1	3845	1/1	0.87	0.15	37,37,37,37	0
83	MG	1	3872	1/1	0.87	0.12	48,48,48,48	0
83	MG	1	3725	1/1	0.87	0.17	40,40,40,40	0
83	MG	AS	3504	1/1	0.87	0.24	50,50,50,50	0
83	MG	1	3817	1/1	0.87	0.10	32,32,32,32	0
85	ZN	DQ	102	1/1	0.87	0.27	118,118,118,118	0
83	MG	B	1815	1/1	0.87	0.25	51,51,51,51	0
83	MG	B	1931	1/1	0.88	0.17	47,47,47,47	0
83	MG	AS	3474	1/1	0.88	0.21	41,41,41,41	0
83	MG	B	1814	1/1	0.88	0.13	53,53,53,53	0
83	MG	B	1882	1/1	0.88	0.20	49,49,49,49	0
83	MG	1	3734	1/1	0.88	0.15	14,14,14,14	0
83	MG	1	3844	1/1	0.88	0.12	48,48,48,48	0
83	MG	1	3464	1/1	0.88	0.23	48,48,48,48	0
83	MG	1	3682	1/1	0.88	0.19	85,85,85,85	0
83	MG	AS	3507	1/1	0.88	0.13	20,20,20,20	0
83	MG	1	3887	1/1	0.88	0.07	58,58,58,58	0
83	MG	AS	3515	1/1	0.88	0.14	31,31,31,31	0
83	MG	CM	1824	1/1	0.88	0.08	28,28,28,28	0
83	MG	1	3539	1/1	0.88	0.09	24,24,24,24	0
83	MG	CM	1833	1/1	0.88	0.24	42,42,42,42	0
83	MG	B	1828	1/1	0.88	0.17	39,39,39,39	0
83	MG	B	1947	1/1	0.88	0.15	63,63,63,63	0
83	MG	1	3611	1/1	0.88	0.26	24,24,24,24	0
83	MG	AS	3649	1/1	0.88	0.13	48,48,48,48	0
83	MG	1	3718	1/1	0.88	0.12	35,35,35,35	0
83	MG	B	1900	1/1	0.88	0.25	50,50,50,50	0
83	MG	AS	3657	1/1	0.88	0.18	17,17,17,17	0
83	MG	1	3763	1/1	0.88	0.17	28,28,28,28	0
83	MG	1	3548	1/1	0.88	0.13	43,43,43,43	0
83	MG	K	301	1/1	0.88	0.06	27,27,27,27	0
83	MG	AS	3667	1/1	0.88	0.11	92,92,92,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3691	1/1	0.88	0.20	22,22,22,22	0
83	MG	1	3824	1/1	0.88	0.12	47,47,47,47	0
83	MG	1	3529	1/1	0.88	0.08	38,38,38,38	0
83	MG	1	3829	1/1	0.88	0.12	25,25,25,25	0
83	MG	1	3413	1/1	0.88	0.21	31,31,31,31	0
83	MG	1	3663	1/1	0.88	0.14	54,54,54,54	0
83	MG	AR	401	1/1	0.88	0.18	48,48,48,48	0
83	MG	AS	3404	1/1	0.88	0.27	19,19,19,19	0
83	MG	CM	1884	1/1	0.88	0.17	54,54,54,54	0
83	MG	CM	1890	1/1	0.88	0.11	24,24,24,24	0
83	MG	AT	206	1/1	0.88	0.14	61,61,61,61	0
83	MG	1	3833	1/1	0.88	0.19	41,41,41,41	0
83	MG	AS	3413	1/1	0.88	0.17	24,24,24,24	0
83	MG	1	3697	1/1	0.88	0.09	50,50,50,50	0
83	MG	AS	3420	1/1	0.88	0.11	15,15,15,15	0
83	MG	1	3679	1/1	0.88	0.13	27,27,27,27	0
83	MG	1	3599	1/1	0.88	0.16	36,36,36,36	0
83	MG	AS	3428	1/1	0.88	0.23	37,37,37,37	0
83	MG	AS	3441	1/1	0.88	0.21	29,29,29,29	0
83	MG	1	3705	1/1	0.88	0.11	34,34,34,34	0
83	MG	1	3731	1/1	0.88	0.10	37,37,37,37	0
83	MG	B	1868	1/1	0.88	0.09	59,59,59,59	0
83	MG	1	3706	1/1	0.88	0.12	36,36,36,36	0
83	MG	r	301	1/1	0.89	0.19	34,34,34,34	0
83	MG	B	1805	1/1	0.89	0.17	57,57,57,57	0
83	MG	Y	202	1/1	0.89	0.18	71,71,71,71	0
83	MG	1	3717	1/1	0.89	0.17	42,42,42,42	0
83	MG	AS	3524	1/1	0.89	0.19	27,27,27,27	0
83	MG	AS	3537	1/1	0.89	0.20	41,41,41,41	0
83	MG	1	3889	1/1	0.89	0.11	69,69,69,69	0
83	MG	1	3600	1/1	0.89	0.13	35,35,35,35	0
83	MG	B	1923	1/1	0.89	0.15	57,57,57,57	0
83	MG	1	3558	1/1	0.89	0.13	47,47,47,47	0
83	MG	CM	1825	1/1	0.89	0.25	31,31,31,31	0
83	MG	1	3658	1/1	0.89	0.10	39,39,39,39	0
83	MG	AS	3550	1/1	0.89	0.20	19,19,19,19	0
83	MG	B	1879	1/1	0.89	0.20	46,46,46,46	0
83	MG	AS	3658	1/1	0.89	0.10	28,28,28,28	0
83	MG	1	3863	1/1	0.89	0.12	29,29,29,29	0
83	MG	AS	3565	1/1	0.89	0.23	31,31,31,31	0
83	MG	AS	3665	1/1	0.89	0.12	51,51,51,51	0
83	MG	CM	1849	1/1	0.89	0.14	50,50,50,50	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3417	1/1	0.89	0.21	23,23,23,23	0
83	MG	AS	3419	1/1	0.89	0.12	27,27,27,27	0
83	MG	1	3684	1/1	0.89	0.25	54,54,54,54	0
83	MG	1	3701	1/1	0.89	0.18	59,59,59,59	0
83	MG	AS	3674	1/1	0.89	0.18	44,44,44,44	0
83	MG	B	1935	1/1	0.89	0.17	56,56,56,56	0
83	MG	1	3723	1/1	0.89	0.06	16,16,16,16	0
83	MG	AS	3677	1/1	0.89	0.14	45,45,45,45	0
83	MG	2	203	1/1	0.89	0.08	37,37,37,37	0
83	MG	AS	3442	1/1	0.89	0.22	45,45,45,45	0
83	MG	AS	3447	1/1	0.89	0.35	48,48,48,48	0
83	MG	1	3759	1/1	0.89	0.08	49,49,49,49	0
83	MG	1	3621	1/1	0.89	0.10	54,54,54,54	0
83	MG	1	3662	1/1	0.89	0.15	42,42,42,42	0
83	MG	AT	209	1/1	0.89	0.15	52,52,52,52	0
83	MG	1	3690	1/1	0.89	0.08	25,25,25,25	0
83	MG	AS	3468	1/1	0.89	0.10	37,37,37,37	0
83	MG	1	3773	1/1	0.89	0.12	32,32,32,32	0
83	MG	1	3774	1/1	0.89	0.10	29,29,29,29	0
83	MG	AS	3481	1/1	0.89	0.13	25,25,25,25	0
83	MG	BJ	302	1/1	0.89	0.16	58,58,58,58	0
83	MG	1	3775	1/1	0.89	0.14	32,32,32,32	0
83	MG	B	1903	1/1	0.89	0.17	87,87,87,87	0
83	MG	4	212	1/1	0.89	0.08	60,60,60,60	0
83	MG	1	3463	1/1	0.89	0.16	18,18,18,18	0
83	MG	1	3818	1/1	0.89	0.11	38,38,38,38	0
83	MG	k	403	1/1	0.89	0.13	57,57,57,57	0
83	MG	1	3562	1/1	0.89	0.15	48,48,48,48	0
83	MG	1	3654	1/1	0.89	0.13	70,70,70,70	0
83	MG	B	1839	1/1	0.90	0.30	48,48,48,48	0
83	MG	B	1842	1/1	0.90	0.15	25,25,25,25	0
83	MG	1	3628	1/1	0.90	0.22	48,48,48,48	0
83	MG	1	3429	1/1	0.90	0.23	24,24,24,24	0
83	MG	1	3851	1/1	0.90	0.08	19,19,19,19	0
83	MG	CM	1801	1/1	0.90	0.21	41,41,41,41	0
83	MG	CM	1805	1/1	0.90	0.13	18,18,18,18	0
83	MG	B	1847	1/1	0.90	0.13	35,35,35,35	0
83	MG	1	3809	1/1	0.90	0.07	57,57,57,57	0
83	MG	1	3577	1/1	0.90	0.14	12,12,12,12	0
83	MG	B	1855	1/1	0.90	0.16	79,79,79,79	0
83	MG	1	3770	1/1	0.90	0.12	46,46,46,46	0
83	MG	B	1858	1/1	0.90	0.12	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3771	1/1	0.90	0.10	38,38,38,38	0
83	MG	3	212	1/1	0.90	0.15	59,59,59,59	0
83	MG	1	3608	1/1	0.90	0.32	67,67,67,67	0
83	MG	1	3860	1/1	0.90	0.11	46,46,46,46	0
83	MG	1	3497	1/1	0.90	0.17	11,11,11,11	0
83	MG	AG	202	1/1	0.90	0.12	52,52,52,52	0
83	MG	B	1869	1/1	0.90	0.17	41,41,41,41	0
83	MG	B	1870	1/1	0.90	0.10	42,42,42,42	0
83	MG	1	3901	1/1	0.90	0.09	29,29,29,29	0
83	MG	1	3484	1/1	0.90	0.12	34,34,34,34	0
83	MG	B	1950	1/1	0.90	0.08	40,40,40,40	0
83	MG	CM	1843	1/1	0.90	0.10	26,26,26,26	0
83	MG	1	3904	1/1	0.90	0.14	32,32,32,32	0
83	MG	G	301	1/1	0.90	0.11	72,72,72,72	0
83	MG	AM	101	1/1	0.90	0.16	54,54,54,54	0
83	MG	AS	3536	1/1	0.90	0.12	35,35,35,35	0
83	MG	1	3905	1/1	0.90	0.10	27,27,27,27	0
83	MG	CM	1857	1/1	0.90	0.11	48,48,48,48	0
83	MG	B	1803	1/1	0.90	0.17	28,28,28,28	0
83	MG	j	303	1/1	0.90	0.10	19,19,19,19	0
83	MG	1	3730	1/1	0.90	0.22	55,55,55,55	0
83	MG	k	402	1/1	0.90	0.12	54,54,54,54	0
83	MG	1	3427	1/1	0.90	0.23	16,16,16,16	0
83	MG	CM	1871	1/1	0.90	0.15	22,22,22,22	0
83	MG	1	3619	1/1	0.90	0.11	33,33,33,33	0
83	MG	AS	3552	1/1	0.90	0.16	27,27,27,27	0
83	MG	Y	203	1/1	0.90	0.23	41,41,41,41	0
83	MG	1	3620	1/1	0.90	0.13	21,21,21,21	0
83	MG	1	3735	1/1	0.90	0.24	33,33,33,33	0
83	MG	B	1821	1/1	0.90	0.20	31,31,31,31	0
83	MG	AT	201	1/1	0.90	0.11	21,21,21,21	0
83	MG	AS	3575	1/1	0.90	0.09	33,33,33,33	0
83	MG	1	3739	1/1	0.90	0.17	28,28,28,28	0
83	MG	1	3411	1/1	0.90	0.15	10,10,10,10	0
83	MG	CM	1897	1/1	0.90	0.18	41,41,41,41	0
83	MG	AS	3408	1/1	0.90	0.09	28,28,28,28	0
83	MG	AS	3588	1/1	0.90	0.09	21,21,21,21	0
83	MG	AT	208	1/1	0.90	0.13	27,27,27,27	0
83	MG	CP	301	1/1	0.90	0.24	32,32,32,32	0
83	MG	1	3673	1/1	0.90	0.14	47,47,47,47	0
83	MG	v	303	1/1	0.90	0.10	72,72,72,72	0
83	MG	1	3494	1/1	0.90	0.17	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3623	1/1	0.90	0.08	40,40,40,40	0
83	MG	1	3508	1/1	0.90	0.16	33,33,33,33	0
84	3K5	1	3402	57/57	0.90	0.17	26,53,74,90	0
84	3K5	AS	3401	57/57	0.90	0.15	41,66,88,90	0
85	ZN	AH	201	1/1	0.90	0.10	138,138,138,138	0
83	MG	1	3843	1/1	0.90	0.27	62,62,62,62	0
85	ZN	h	201	1/1	0.90	0.09	209,209,209,209	0
83	MG	AS	3421	1/1	0.90	0.33	19,19,19,19	0
83	MG	1	3698	1/1	0.90	0.18	58,58,58,58	0
83	MG	1	3762	1/1	0.90	0.13	31,31,31,31	0
86	HYG	CM	1902	36/36	0.90	0.12	34,53,79,89	0
83	MG	CM	1813	1/1	0.91	0.24	35,35,35,35	0
83	MG	1	3542	1/1	0.91	0.16	28,28,28,28	0
83	MG	1	3487	1/1	0.91	0.05	11,11,11,11	0
83	MG	1	3567	1/1	0.91	0.07	20,20,20,20	0
83	MG	1	3430	1/1	0.91	0.10	50,50,50,50	0
83	MG	B	1818	1/1	0.91	0.09	33,33,33,33	0
83	MG	0	203	1/1	0.91	0.11	75,75,75,75	0
83	MG	1	3490	1/1	0.91	0.15	44,44,44,44	0
83	MG	B	1933	1/1	0.91	0.10	57,57,57,57	0
83	MG	1	3473	1/1	0.91	0.18	13,13,13,13	0
83	MG	1	3626	1/1	0.91	0.16	46,46,46,46	0
83	MG	1	3507	1/1	0.91	0.17	9,9,9,9	0
83	MG	1	3736	1/1	0.91	0.17	39,39,39,39	0
83	MG	1	3780	1/1	0.91	0.18	32,32,32,32	0
83	MG	AS	3567	1/1	0.91	0.09	45,45,45,45	0
83	MG	CM	1839	1/1	0.91	0.17	36,36,36,36	0
83	MG	CM	1841	1/1	0.91	0.27	45,45,45,45	0
83	MG	AS	3434	1/1	0.91	0.18	18,18,18,18	0
83	MG	B	1891	1/1	0.91	0.10	41,41,41,41	0
83	MG	1	3446	1/1	0.91	0.10	71,71,71,71	0
83	MG	AS	3672	1/1	0.91	0.08	29,29,29,29	0
83	MG	1	3514	1/1	0.91	0.17	30,30,30,30	0
83	MG	CM	1851	1/1	0.91	0.12	28,28,28,28	0
83	MG	1	3787	1/1	0.91	0.22	23,23,23,23	0
83	MG	CM	1855	1/1	0.91	0.17	29,29,29,29	0
83	MG	1	3907	1/1	0.91	0.18	74,74,74,74	0
83	MG	AS	3591	1/1	0.91	0.16	52,52,52,52	0
83	MG	AS	3593	1/1	0.91	0.07	16,16,16,16	0
83	MG	AD	201	1/1	0.91	0.14	59,59,59,59	0
83	MG	AS	3465	1/1	0.91	0.14	19,19,19,19	0
83	MG	CM	1865	1/1	0.91	0.17	45,45,45,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3637	1/1	0.91	0.09	49,49,49,49	0
83	MG	1	3790	1/1	0.91	0.10	49,49,49,49	0
83	MG	AS	3469	1/1	0.91	0.25	25,25,25,25	0
83	MG	AS	3472	1/1	0.91	0.24	36,36,36,36	0
83	MG	B	1951	1/1	0.91	0.11	29,29,29,29	0
83	MG	1	3535	1/1	0.91	0.14	34,34,34,34	0
83	MG	AS	3476	1/1	0.91	0.24	34,34,34,34	0
83	MG	AU	202	1/1	0.91	0.18	31,31,31,31	0
83	MG	1	3425	1/1	0.91	0.12	36,36,36,36	0
83	MG	1	3840	1/1	0.91	0.06	14,14,14,14	0
83	MG	CM	1885	1/1	0.91	0.10	26,26,26,26	0
83	MG	BB	302	1/1	0.91	0.12	53,53,53,53	0
83	MG	BE	301	1/1	0.91	0.17	33,33,33,33	0
83	MG	1	3496	1/1	0.91	0.11	31,31,31,31	0
83	MG	1	3755	1/1	0.91	0.14	34,34,34,34	0
83	MG	1	3758	1/1	0.91	0.14	33,33,33,33	0
83	MG	AS	3623	1/1	0.91	0.21	32,32,32,32	0
83	MG	AS	3496	1/1	0.91	0.21	40,40,40,40	0
83	MG	1	3922	1/1	0.91	0.24	42,42,42,42	0
83	MG	AS	3502	1/1	0.91	0.18	34,34,34,34	0
83	MG	CJ	202	1/1	0.91	0.09	21,21,21,21	0
83	MG	1	3614	1/1	0.91	0.19	86,86,86,86	0
83	MG	1	3760	1/1	0.91	0.09	55,55,55,55	0
83	MG	B	1913	1/1	0.91	0.11	49,49,49,49	0
83	MG	B	1914	1/1	0.91	0.07	47,47,47,47	0
83	MG	B	1860	1/1	0.91	0.08	78,78,78,78	0
85	ZN	AP	201	1/1	0.91	0.09	181,181,181,181	0
83	MG	CM	1804	1/1	0.91	0.21	25,25,25,25	0
83	MG	AS	3634	1/1	0.91	0.07	52,52,52,52	0
83	MG	1	3586	1/1	0.91	0.12	47,47,47,47	0
83	MG	CM	1807	1/1	0.91	0.20	37,37,37,37	0
83	MG	1	3443	1/1	0.91	0.18	44,44,44,44	0
83	MG	AS	3640	1/1	0.91	0.15	46,46,46,46	0
83	MG	AS	3435	1/1	0.92	0.21	30,30,30,30	0
83	MG	1	3459	1/1	0.92	0.07	20,20,20,20	0
83	MG	B	1930	1/1	0.92	0.13	60,60,60,60	0
83	MG	1	3741	1/1	0.92	0.22	18,18,18,18	0
83	MG	1	3821	1/1	0.92	0.20	43,43,43,43	0
83	MG	4	205	1/1	0.92	0.07	33,33,33,33	0
83	MG	1	3900	1/1	0.92	0.15	29,29,29,29	0
83	MG	AS	3457	1/1	0.92	0.09	23,23,23,23	0
83	MG	AS	3460	1/1	0.92	0.14	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3612	1/1	0.92	0.11	25,25,25,25	0
83	MG	AS	3462	1/1	0.92	0.24	31,31,31,31	0
83	MG	B	1937	1/1	0.92	0.17	47,47,47,47	0
83	MG	1	3859	1/1	0.92	0.11	77,77,77,77	0
83	MG	CM	1814	1/1	0.92	0.11	19,19,19,19	0
83	MG	CM	1815	1/1	0.92	0.15	28,28,28,28	0
83	MG	1	3744	1/1	0.92	0.17	23,23,23,23	0
83	MG	AP	203	1/1	0.92	0.13	73,73,73,73	0
83	MG	4	210	1/1	0.92	0.07	34,34,34,34	0
83	MG	1	3825	1/1	0.92	0.09	39,39,39,39	0
83	MG	1	3576	1/1	0.92	0.16	31,31,31,31	0
83	MG	1	3644	1/1	0.92	0.08	20,20,20,20	0
83	MG	AS	3480	1/1	0.92	0.10	29,29,29,29	0
83	MG	B	1945	1/1	0.92	0.19	56,56,56,56	0
83	MG	B	1884	1/1	0.92	0.08	97,97,97,97	0
83	MG	CM	1826	1/1	0.92	0.10	34,34,34,34	0
83	MG	1	3864	1/1	0.92	0.14	41,41,41,41	0
83	MG	CM	1828	1/1	0.92	0.23	22,22,22,22	0
83	MG	CM	1832	1/1	0.92	0.18	14,14,14,14	0
83	MG	1	3510	1/1	0.92	0.11	23,23,23,23	0
83	MG	1	3788	1/1	0.92	0.17	23,23,23,23	0
83	MG	AS	3635	1/1	0.92	0.21	44,44,44,44	0
83	MG	AS	3495	1/1	0.92	0.21	33,33,33,33	0
83	MG	1	3513	1/1	0.92	0.17	23,23,23,23	0
83	MG	AS	3497	1/1	0.92	0.11	26,26,26,26	0
83	MG	1	3462	1/1	0.92	0.14	19,19,19,19	0
83	MG	D	301	1/1	0.92	0.14	38,38,38,38	0
83	MG	1	3792	1/1	0.92	0.14	32,32,32,32	0
83	MG	1	3915	1/1	0.92	0.06	17,17,17,17	0
83	MG	1	3649	1/1	0.92	0.17	38,38,38,38	0
83	MG	u	201	1/1	0.92	0.11	28,28,28,28	0
83	MG	1	3403	1/1	0.92	0.20	25,25,25,25	0
83	MG	B	1826	1/1	0.92	0.13	43,43,43,43	0
83	MG	B	1901	1/1	0.92	0.12	43,43,43,43	0
83	MG	AS	3523	1/1	0.92	0.19	29,29,29,29	0
83	MG	1	3451	1/1	0.92	0.10	26,26,26,26	0
83	MG	AS	3660	1/1	0.92	0.08	27,27,27,27	0
83	MG	AS	3525	1/1	0.92	0.23	32,32,32,32	0
83	MG	AS	3528	1/1	0.92	0.13	41,41,41,41	0
83	MG	AS	3529	1/1	0.92	0.09	55,55,55,55	0
83	MG	CM	1870	1/1	0.92	0.13	30,30,30,30	0
83	MG	AS	3533	1/1	0.92	0.18	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3534	1/1	0.92	0.17	38,38,38,38	0
83	MG	AS	3535	1/1	0.92	0.19	27,27,27,27	0
83	MG	1	3601	1/1	0.92	0.09	61,61,61,61	0
83	MG	B	1904	1/1	0.92	0.07	36,36,36,36	0
83	MG	1	3407	1/1	0.92	0.30	23,23,23,23	0
83	MG	CM	1881	1/1	0.92	0.09	11,11,11,11	0
83	MG	x	201	1/1	0.92	0.18	16,16,16,16	0
83	MG	1	3551	1/1	0.92	0.09	36,36,36,36	0
83	MG	1	3424	1/1	0.92	0.17	14,14,14,14	0
83	MG	AS	3546	1/1	0.92	0.14	15,15,15,15	0
83	MG	CM	1888	1/1	0.92	0.08	47,47,47,47	0
83	MG	AS	3403	1/1	0.92	0.19	5,5,5,5	0
83	MG	1	3883	1/1	0.92	0.07	28,28,28,28	0
83	MG	CM	1895	1/1	0.92	0.19	21,21,21,21	0
83	MG	AS	3405	1/1	0.92	0.23	16,16,16,16	0
83	MG	AS	3556	1/1	0.92	0.16	37,37,37,37	0
83	MG	1	3769	1/1	0.92	0.12	21,21,21,21	0
83	MG	1	3609	1/1	0.92	0.06	20,20,20,20	0
83	MG	1	3846	1/1	0.92	0.09	44,44,44,44	0
83	MG	1	3660	1/1	0.92	0.07	25,25,25,25	0
83	MG	AS	3568	1/1	0.92	0.17	39,39,39,39	0
83	MG	1	3538	1/1	0.92	0.14	48,48,48,48	0
83	MG	1	3810	1/1	0.92	0.12	20,20,20,20	0
83	MG	AS	3577	1/1	0.92	0.22	30,30,30,30	0
83	MG	DQ	101	1/1	0.92	0.09	42,42,42,42	0
83	MG	AS	3578	1/1	0.92	0.19	27,27,27,27	0
83	MG	3	204	1/1	0.92	0.19	32,32,32,32	0
83	MG	1	3612	1/1	0.92	0.09	27,27,27,27	0
83	MG	AS	3584	1/1	0.92	0.18	37,37,37,37	0
83	MG	BJ	301	1/1	0.92	0.14	22,22,22,22	0
83	MG	3	208	1/1	0.92	0.09	47,47,47,47	0
83	MG	3	209	1/1	0.92	0.18	48,48,48,48	0
83	MG	1	3687	1/1	0.92	0.12	39,39,39,39	0
83	MG	BZ	201	1/1	0.92	0.17	41,41,41,41	0
83	MG	3	211	1/1	0.92	0.15	34,34,34,34	0
83	MG	1	3516	1/1	0.93	0.15	30,30,30,30	0
83	MG	AS	3614	1/1	0.93	0.09	16,16,16,16	0
83	MG	B	1888	1/1	0.93	0.21	52,52,52,52	0
83	MG	B	1808	1/1	0.93	0.14	29,29,29,29	0
83	MG	1	3590	1/1	0.93	0.12	17,17,17,17	0
83	MG	CM	1810	1/1	0.93	0.12	46,46,46,46	0
83	MG	1	3431	1/1	0.93	0.18	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3565	1/1	0.93	0.15	44,44,44,44	0
83	MG	o	301	1/1	0.93	0.06	21,21,21,21	0
83	MG	AS	3503	1/1	0.93	0.15	21,21,21,21	0
83	MG	1	3436	1/1	0.93	0.14	23,23,23,23	0
83	MG	AS	3505	1/1	0.93	0.07	12,12,12,12	0
83	MG	R	201	1/1	0.93	0.11	83,83,83,83	0
83	MG	AS	3508	1/1	0.93	0.06	46,46,46,46	0
83	MG	B	1820	1/1	0.93	0.11	22,22,22,22	0
83	MG	AS	3514	1/1	0.93	0.16	22,22,22,22	0
83	MG	1	3478	1/1	0.93	0.12	20,20,20,20	0
83	MG	1	3820	1/1	0.93	0.06	29,29,29,29	0
83	MG	1	3916	1/1	0.93	0.08	45,45,45,45	0
83	MG	AS	3636	1/1	0.93	0.10	42,42,42,42	0
83	MG	Z	201	1/1	0.93	0.29	54,54,54,54	0
83	MG	AS	3520	1/1	0.93	0.14	20,20,20,20	0
83	MG	AS	3639	1/1	0.93	0.12	37,37,37,37	0
83	MG	AS	3522	1/1	0.93	0.11	30,30,30,30	0
83	MG	1	3445	1/1	0.93	0.16	25,25,25,25	0
83	MG	1	3919	1/1	0.93	0.32	51,51,51,51	0
83	MG	v	302	1/1	0.93	0.08	19,19,19,19	0
83	MG	AS	3526	1/1	0.93	0.07	27,27,27,27	0
83	MG	1	3624	1/1	0.93	0.19	24,24,24,24	0
83	MG	AS	3647	1/1	0.93	0.13	45,45,45,45	0
83	MG	1	3574	1/1	0.93	0.11	22,22,22,22	0
83	MG	CM	1847	1/1	0.93	0.15	27,27,27,27	0
83	MG	AS	3532	1/1	0.93	0.26	23,23,23,23	0
83	MG	AS	3651	1/1	0.93	0.07	17,17,17,17	0
83	MG	1	3418	1/1	0.93	0.13	33,33,33,33	0
83	MG	1	3439	1/1	0.93	0.17	20,20,20,20	0
83	MG	AS	3654	1/1	0.93	0.05	17,17,17,17	0
83	MG	AS	3655	1/1	0.93	0.18	55,55,55,55	0
83	MG	x	202	1/1	0.93	0.06	20,20,20,20	0
83	MG	1	3505	1/1	0.93	0.05	22,22,22,22	0
83	MG	1	3831	1/1	0.93	0.15	80,80,80,80	0
83	MG	1	3578	1/1	0.93	0.19	27,27,27,27	0
83	MG	CM	1861	1/1	0.93	0.07	24,24,24,24	0
83	MG	CM	1862	1/1	0.93	0.12	29,29,29,29	0
83	MG	1	3665	1/1	0.93	0.05	24,24,24,24	0
83	MG	1	3667	1/1	0.93	0.05	16,16,16,16	0
83	MG	CM	1866	1/1	0.93	0.07	25,25,25,25	0
83	MG	1	3733	1/1	0.93	0.20	11,11,11,11	0
83	MG	CM	1869	1/1	0.93	0.12	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3784	1/1	0.93	0.16	30,30,30,30	0
83	MG	B	1848	1/1	0.93	0.14	30,30,30,30	0
83	MG	1	3633	1/1	0.93	0.10	40,40,40,40	0
83	MG	1	3453	1/1	0.93	0.12	33,33,33,33	0
83	MG	1	3454	1/1	0.93	0.06	9,9,9,9	0
83	MG	1	3702	1/1	0.93	0.14	33,33,33,33	0
83	MG	B	1857	1/1	0.93	0.14	37,37,37,37	0
83	MG	B	1929	1/1	0.93	0.09	37,37,37,37	0
83	MG	AS	3566	1/1	0.93	0.13	26,26,26,26	0
83	MG	1	3703	1/1	0.93	0.21	48,48,48,48	0
83	MG	1	3704	1/1	0.93	0.12	30,30,30,30	0
83	MG	1	3469	1/1	0.93	0.15	28,28,28,28	0
83	MG	CM	1886	1/1	0.93	0.20	40,40,40,40	0
83	MG	CM	1887	1/1	0.93	0.18	16,16,16,16	0
83	MG	AS	3574	1/1	0.93	0.06	17,17,17,17	0
83	MG	1	3795	1/1	0.93	0.14	37,37,37,37	0
83	MG	1	3493	1/1	0.93	0.19	30,30,30,30	0
83	MG	AS	3459	1/1	0.93	0.13	50,50,50,50	0
83	MG	AS	3579	1/1	0.93	0.17	38,38,38,38	0
83	MG	1	3847	1/1	0.93	0.06	36,36,36,36	0
83	MG	1	3709	1/1	0.93	0.14	25,25,25,25	0
83	MG	B	1867	1/1	0.93	0.08	49,49,49,49	0
83	MG	4	204	1/1	0.93	0.14	25,25,25,25	0
83	MG	1	3749	1/1	0.93	0.13	20,20,20,20	0
83	MG	AS	3589	1/1	0.93	0.16	21,21,21,21	0
83	MG	AS	3590	1/1	0.93	0.15	33,33,33,33	0
83	MG	1	3898	1/1	0.93	0.05	16,16,16,16	0
83	MG	AS	3470	1/1	0.93	0.19	31,31,31,31	0
83	MG	B	1874	1/1	0.93	0.16	37,37,37,37	0
83	MG	1	3850	1/1	0.93	0.06	22,22,22,22	0
83	MG	1	3710	1/1	0.93	0.09	38,38,38,38	0
83	MG	B	1878	1/1	0.93	0.16	14,14,14,14	0
83	MG	1	3426	1/1	0.93	0.13	24,24,24,24	0
83	MG	1	3646	1/1	0.93	0.19	48,48,48,48	0
83	MG	1	3471	1/1	0.93	0.13	21,21,21,21	0
83	MG	AS	3604	1/1	0.93	0.22	46,46,46,46	0
85	ZN	CJ	201	1/1	0.93	0.10	211,211,211,211	0
83	MG	AS	3486	1/1	0.93	0.11	28,28,28,28	0
83	MG	1	3615	1/1	0.93	0.15	51,51,51,51	0
83	MG	AS	3607	1/1	0.93	0.10	37,37,37,37	0
83	MG	B	1811	1/1	0.94	0.16	27,27,27,27	0
83	MG	B	1813	1/1	0.94	0.12	19,19,19,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	B	1883	1/1	0.94	0.16	23,23,23,23	0
83	MG	1	3415	1/1	0.94	0.23	23,23,23,23	0
83	MG	1	3482	1/1	0.94	0.23	23,23,23,23	0
83	MG	AS	3659	1/1	0.94	0.09	18,18,18,18	0
83	MG	AS	3471	1/1	0.94	0.21	51,51,51,51	0
83	MG	1	3557	1/1	0.94	0.14	34,34,34,34	0
83	MG	1	3659	1/1	0.94	0.10	24,24,24,24	0
83	MG	1	3602	1/1	0.94	0.06	28,28,28,28	0
83	MG	1	3504	1/1	0.94	0.10	21,21,21,21	0
83	MG	1	3886	1/1	0.94	0.09	27,27,27,27	0
83	MG	AS	3669	1/1	0.94	0.19	56,56,56,56	0
83	MG	1	3604	1/1	0.94	0.14	25,25,25,25	0
83	MG	1	3801	1/1	0.94	0.08	29,29,29,29	0
83	MG	1	3606	1/1	0.94	0.13	58,58,58,58	0
83	MG	y	201	1/1	0.94	0.09	12,12,12,12	0
83	MG	1	3519	1/1	0.94	0.13	41,41,41,41	0
83	MG	1	3634	1/1	0.94	0.10	43,43,43,43	0
83	MG	3	205	1/1	0.94	0.15	27,27,27,27	0
83	MG	1	3696	1/1	0.94	0.10	19,19,19,19	0
83	MG	1	3666	1/1	0.94	0.10	27,27,27,27	0
83	MG	2	201	1/1	0.94	0.16	75,75,75,75	0
83	MG	AS	3501	1/1	0.94	0.10	40,40,40,40	0
83	MG	2	202	1/1	0.94	0.10	34,34,34,34	0
83	MG	1	3560	1/1	0.94	0.14	24,24,24,24	0
83	MG	B	1843	1/1	0.94	0.16	21,21,21,21	0
83	MG	1	3814	1/1	0.94	0.07	33,33,33,33	0
83	MG	1	3520	1/1	0.94	0.16	25,25,25,25	0
83	MG	AU	201	1/1	0.94	0.08	40,40,40,40	0
83	MG	1	3610	1/1	0.94	0.17	47,47,47,47	0
83	MG	AW	303	1/1	0.94	0.08	34,34,34,34	0
83	MG	3	213	1/1	0.94	0.13	49,49,49,49	0
83	MG	1	3458	1/1	0.94	0.19	8,8,8,8	0
83	MG	CM	1873	1/1	0.94	0.18	40,40,40,40	0
83	MG	1	3412	1/1	0.94	0.24	19,19,19,19	0
83	MG	CM	1875	1/1	0.94	0.08	18,18,18,18	0
83	MG	1	3777	1/1	0.94	0.17	21,21,21,21	0
83	MG	B	1852	1/1	0.94	0.11	26,26,26,26	0
83	MG	CM	1878	1/1	0.94	0.17	33,33,33,33	0
83	MG	AC	101	1/1	0.94	0.08	41,41,41,41	0
83	MG	1	3485	1/1	0.94	0.11	37,37,37,37	0
83	MG	1	3779	1/1	0.94	0.20	33,33,33,33	0
83	MG	1	3546	1/1	0.94	0.11	36,36,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3828	1/1	0.94	0.08	36,36,36,36	0
83	MG	AS	3425	1/1	0.94	0.17	17,17,17,17	0
83	MG	1	3592	1/1	0.94	0.21	43,43,43,43	0
83	MG	AS	3527	1/1	0.94	0.08	35,35,35,35	0
83	MG	4	211	1/1	0.94	0.08	11,11,11,11	0
83	MG	B	1863	1/1	0.94	0.17	58,58,58,58	0
83	MG	1	3910	1/1	0.94	0.08	64,64,64,64	0
83	MG	1	3486	1/1	0.94	0.16	18,18,18,18	0
83	MG	AS	3437	1/1	0.94	0.15	33,33,33,33	0
83	MG	1	3678	1/1	0.94	0.15	19,19,19,19	0
83	MG	CM	1802	1/1	0.94	0.24	15,15,15,15	0
83	MG	CM	1901	1/1	0.94	0.08	20,20,20,20	0
83	MG	CM	1903	1/1	0.94	0.08	38,38,38,38	0
83	MG	1	3467	1/1	0.94	0.17	37,37,37,37	0
83	MG	AS	3444	1/1	0.94	0.13	15,15,15,15	0
83	MG	1	3712	1/1	0.94	0.10	41,41,41,41	0
83	MG	1	3488	1/1	0.94	0.24	9,9,9,9	0
83	MG	DB	202	1/1	0.94	0.14	57,57,57,57	0
83	MG	1	3414	1/1	0.94	0.20	20,20,20,20	0
83	MG	AS	3541	1/1	0.94	0.09	49,49,49,49	0
83	MG	AS	3542	1/1	0.94	0.15	37,37,37,37	0
83	MG	CM	1812	1/1	0.94	0.13	41,41,41,41	0
83	MG	B	1873	1/1	0.94	0.14	48,48,48,48	0
83	MG	AS	3545	1/1	0.94	0.20	15,15,15,15	0
83	MG	1	3531	1/1	0.94	0.16	39,39,39,39	0
83	MG	o	302	1/1	0.94	0.12	16,16,16,16	0
83	MG	AS	3548	1/1	0.94	0.11	26,26,26,26	0
83	MG	AS	3549	1/1	0.94	0.31	33,33,33,33	0
83	MG	1	3751	1/1	0.94	0.17	43,43,43,43	0
83	MG	1	3878	1/1	0.94	0.15	34,34,34,34	0
83	MG	AS	3553	1/1	0.94	0.09	46,46,46,46	0
83	MG	AS	3554	1/1	0.94	0.15	18,18,18,18	0
83	MG	AS	3463	1/1	0.94	0.16	34,34,34,34	0
83	MG	B	1832	1/1	0.95	0.17	19,19,19,19	0
83	MG	1	3650	1/1	0.95	0.11	34,34,34,34	0
83	MG	1	3441	1/1	0.95	0.21	29,29,29,29	0
83	MG	AS	3650	1/1	0.95	0.08	7,7,7,7	0
83	MG	1	3571	1/1	0.95	0.14	15,15,15,15	0
83	MG	B	1838	1/1	0.95	0.14	20,20,20,20	0
83	MG	CM	1829	1/1	0.95	0.13	25,25,25,25	0
83	MG	CM	1830	1/1	0.95	0.17	25,25,25,25	0
83	MG	AS	3475	1/1	0.95	0.09	22,22,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3813	1/1	0.95	0.11	27,27,27,27	0
83	MG	CM	1834	1/1	0.95	0.22	28,28,28,28	0
83	MG	1	3511	1/1	0.95	0.18	14,14,14,14	0
83	MG	1	3549	1/1	0.95	0.17	32,32,32,32	0
83	MG	1	3897	1/1	0.95	0.15	52,52,52,52	0
83	MG	AS	3569	1/1	0.95	0.13	33,33,33,33	0
83	MG	AS	3571	1/1	0.95	0.16	14,14,14,14	0
83	MG	1	3816	1/1	0.95	0.15	28,28,28,28	0
83	MG	CM	1844	1/1	0.95	0.13	26,26,26,26	0
83	MG	AS	3487	1/1	0.95	0.14	20,20,20,20	0
83	MG	AS	3663	1/1	0.95	0.15	42,42,42,42	0
83	MG	1	3737	1/1	0.95	0.15	15,15,15,15	0
83	MG	AS	3576	1/1	0.95	0.14	24,24,24,24	0
83	MG	1	3857	1/1	0.95	0.08	40,40,40,40	0
83	MG	1	3738	1/1	0.95	0.11	21,21,21,21	0
83	MG	CM	1852	1/1	0.95	0.06	24,24,24,24	0
83	MG	AS	3494	1/1	0.95	0.15	31,31,31,31	0
83	MG	1	3903	1/1	0.95	0.12	56,56,56,56	0
83	MG	1	3512	1/1	0.95	0.17	49,49,49,49	0
83	MG	1	3437	1/1	0.95	0.18	19,19,19,19	0
83	MG	1	3823	1/1	0.95	0.11	34,34,34,34	0
83	MG	AS	3586	1/1	0.95	0.16	15,15,15,15	0
83	MG	AS	3587	1/1	0.95	0.09	14,14,14,14	0
83	MG	1	3474	1/1	0.95	0.25	21,21,21,21	0
83	MG	CM	1863	1/1	0.95	0.11	44,44,44,44	0
83	MG	j	301	1/1	0.95	0.06	15,15,15,15	0
83	MG	AS	3406	1/1	0.95	0.21	17,17,17,17	0
83	MG	1	3782	1/1	0.95	0.10	28,28,28,28	0
83	MG	1	3448	1/1	0.95	0.16	14,14,14,14	0
83	MG	AS	3594	1/1	0.95	0.10	34,34,34,34	0
83	MG	1	3532	1/1	0.95	0.16	15,15,15,15	0
83	MG	1	3450	1/1	0.95	0.17	32,32,32,32	0
83	MG	AS	3509	1/1	0.95	0.09	29,29,29,29	0
83	MG	AS	3511	1/1	0.95	0.23	50,50,50,50	0
83	MG	B	1801	1/1	0.95	0.07	69,69,69,69	0
83	MG	AW	301	1/1	0.95	0.11	30,30,30,30	0
83	MG	AS	3418	1/1	0.95	0.24	19,19,19,19	0
83	MG	1	3748	1/1	0.95	0.14	28,28,28,28	0
83	MG	1	3869	1/1	0.95	0.07	37,37,37,37	0
83	MG	1	3870	1/1	0.95	0.13	43,43,43,43	0
83	MG	1	3479	1/1	0.95	0.15	35,35,35,35	0
83	MG	1	3481	1/1	0.95	0.11	12,12,12,12	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3610	1/1	0.95	0.06	35,35,35,35	0
83	MG	AS	3611	1/1	0.95	0.12	29,29,29,29	0
83	MG	B	1932	1/1	0.95	0.07	18,18,18,18	0
83	MG	AS	3613	1/1	0.95	0.11	28,28,28,28	0
83	MG	1	3406	1/1	0.95	0.22	26,26,26,26	0
83	MG	AS	3430	1/1	0.95	0.27	31,31,31,31	0
83	MG	AS	3432	1/1	0.95	0.13	12,12,12,12	0
83	MG	1	3834	1/1	0.95	0.19	21,21,21,21	0
83	MG	1	3638	1/1	0.95	0.14	9,9,9,9	0
83	MG	AS	3436	1/1	0.95	0.16	10,10,10,10	0
83	MG	B	1936	1/1	0.95	0.08	25,25,25,25	0
83	MG	AS	3530	1/1	0.95	0.15	34,34,34,34	0
83	MG	AS	3625	1/1	0.95	0.17	42,42,42,42	0
83	MG	AS	3531	1/1	0.95	0.11	45,45,45,45	0
83	MG	1	3561	1/1	0.95	0.07	26,26,26,26	0
83	MG	1	3506	1/1	0.95	0.07	26,26,26,26	0
83	MG	1	3695	1/1	0.95	0.16	32,32,32,32	0
83	MG	1	3541	1/1	0.95	0.07	34,34,34,34	0
83	MG	w	301	1/1	0.95	0.08	22,22,22,22	0
83	MG	1	3521	1/1	0.95	0.13	26,26,26,26	0
83	MG	CM	1809	1/1	0.95	0.12	67,67,67,67	0
83	MG	1	3882	1/1	0.95	0.12	39,39,39,39	0
83	MG	B	1822	1/1	0.95	0.18	22,22,22,22	0
83	MG	1	3670	1/1	0.95	0.09	47,47,47,47	0
83	MG	1	3616	1/1	0.95	0.16	22,22,22,22	0
83	MG	AS	3461	1/1	0.95	0.17	23,23,23,23	0
83	MG	1	3522	1/1	0.95	0.06	24,24,24,24	0
83	MG	1	3768	1/1	0.95	0.07	27,27,27,27	0
83	MG	CM	1817	1/1	0.95	0.11	19,19,19,19	0
83	MG	AS	3464	1/1	0.95	0.16	21,21,21,21	0
83	MG	1	3460	1/1	0.95	0.15	15,15,15,15	0
83	MG	1	3888	1/1	0.95	0.16	28,28,28,28	0
83	MG	1	3410	1/1	0.95	0.18	7,7,7,7	0
83	MG	1	3808	1/1	0.95	0.11	28,28,28,28	0
83	MG	AS	3620	1/1	0.96	0.15	26,26,26,26	0
83	MG	B	1917	1/1	0.96	0.11	24,24,24,24	0
83	MG	AS	3424	1/1	0.96	0.18	15,15,15,15	0
83	MG	B	1853	1/1	0.96	0.19	27,27,27,27	0
83	MG	1	3536	1/1	0.96	0.15	15,15,15,15	0
83	MG	B	1921	1/1	0.96	0.08	24,24,24,24	0
83	MG	AK	102	1/1	0.96	0.05	12,12,12,12	0
83	MG	AS	3429	1/1	0.96	0.15	17,17,17,17	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3743	1/1	0.96	0.10	25,25,25,25	0
83	MG	AS	3431	1/1	0.96	0.18	8,8,8,8	0
83	MG	1	3589	1/1	0.96	0.12	16,16,16,16	0
83	MG	1	3745	1/1	0.96	0.14	30,30,30,30	0
83	MG	1	3573	1/1	0.96	0.10	23,23,23,23	0
83	MG	AS	3633	1/1	0.96	0.05	43,43,43,43	0
83	MG	B	1861	1/1	0.96	0.08	45,45,45,45	0
83	MG	1	3509	1/1	0.96	0.17	20,20,20,20	0
83	MG	AS	3439	1/1	0.96	0.13	32,32,32,32	0
83	MG	1	3447	1/1	0.96	0.12	10,10,10,10	0
83	MG	1	3416	1/1	0.96	0.14	25,25,25,25	0
83	MG	AS	3443	1/1	0.96	0.19	11,11,11,11	0
83	MG	1	3927	1/1	0.96	0.06	22,22,22,22	0
83	MG	AS	3446	1/1	0.96	0.21	22,22,22,22	0
83	MG	1	3461	1/1	0.96	0.13	13,13,13,13	0
83	MG	B	1809	1/1	0.96	0.06	79,79,79,79	0
83	MG	1	3752	1/1	0.96	0.11	39,39,39,39	0
83	MG	1	3819	1/1	0.96	0.19	13,13,13,13	0
83	MG	B	1812	1/1	0.96	0.10	17,17,17,17	0
83	MG	B	1871	1/1	0.96	0.11	63,63,63,63	0
83	MG	CM	1842	1/1	0.96	0.09	45,45,45,45	0
83	MG	B	1872	1/1	0.96	0.12	40,40,40,40	0
83	MG	1	3785	1/1	0.96	0.13	20,20,20,20	0
83	MG	1	3786	1/1	0.96	0.06	24,24,24,24	0
83	MG	CM	1846	1/1	0.96	0.08	18,18,18,18	0
83	MG	1	3822	1/1	0.96	0.05	23,23,23,23	0
83	MG	B	1876	1/1	0.96	0.11	54,54,54,54	0
83	MG	AS	3555	1/1	0.96	0.15	11,11,11,11	0
83	MG	1	3422	1/1	0.96	0.22	14,14,14,14	0
83	MG	AS	3558	1/1	0.96	0.05	25,25,25,25	0
83	MG	AS	3466	1/1	0.96	0.13	25,25,25,25	0
83	MG	AS	3561	1/1	0.96	0.18	18,18,18,18	0
83	MG	CM	1854	1/1	0.96	0.20	27,27,27,27	0
83	MG	1	3632	1/1	0.96	0.12	20,20,20,20	0
83	MG	AS	3563	1/1	0.96	0.13	17,17,17,17	0
83	MG	B	1819	1/1	0.96	0.19	16,16,16,16	0
83	MG	B	1881	1/1	0.96	0.12	51,51,51,51	0
83	MG	x	203	1/1	0.96	0.13	24,24,24,24	0
83	MG	1	3656	1/1	0.96	0.11	28,28,28,28	0
83	MG	3	207	1/1	0.96	0.09	51,51,51,51	0
83	MG	B	1885	1/1	0.96	0.07	45,45,45,45	0
83	MG	AS	3572	1/1	0.96	0.14	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	1	3757	1/1	0.96	0.23	19,19,19,19	0
83	MG	1	3899	1/1	0.96	0.16	31,31,31,31	0
83	MG	1	3613	1/1	0.96	0.16	24,24,24,24	0
83	MG	AS	3478	1/1	0.96	0.11	16,16,16,16	0
83	MG	1	3596	1/1	0.96	0.10	36,36,36,36	0
83	MG	I	302	1/1	0.96	0.06	31,31,31,31	0
83	MG	1	3456	1/1	0.96	0.07	6,6,6,6	0
83	MG	AS	3484	1/1	0.96	0.04	22,22,22,22	0
83	MG	1	3405	1/1	0.96	0.21	21,21,21,21	0
83	MG	AS	3582	1/1	0.96	0.15	16,16,16,16	0
83	MG	AS	3583	1/1	0.96	0.22	30,30,30,30	0
83	MG	AT	205	1/1	0.96	0.15	22,22,22,22	0
83	MG	1	3581	1/1	0.96	0.08	24,24,24,24	0
83	MG	AS	3489	1/1	0.96	0.08	29,29,29,29	0
83	MG	B	1894	1/1	0.96	0.11	27,27,27,27	0
83	MG	B	1895	1/1	0.96	0.10	37,37,37,37	0
83	MG	4	201	1/1	0.96	0.23	41,41,41,41	0
83	MG	1	3641	1/1	0.96	0.15	7,7,7,7	0
83	MG	1	3642	1/1	0.96	0.17	16,16,16,16	0
83	MG	AW	302	1/1	0.96	0.07	29,29,29,29	0
83	MG	B	1834	1/1	0.96	0.10	29,29,29,29	0
83	MG	AS	3592	1/1	0.96	0.10	20,20,20,20	0
83	MG	1	3711	1/1	0.96	0.05	22,22,22,22	0
83	MG	1	3544	1/1	0.96	0.26	19,19,19,19	0
83	MG	AS	3595	1/1	0.96	0.18	31,31,31,31	0
83	MG	CM	1896	1/1	0.96	0.05	4,4,4,4	0
83	MG	B	1837	1/1	0.96	0.13	26,26,26,26	0
83	MG	1	3556	1/1	0.96	0.06	35,35,35,35	0
83	MG	AS	3598	1/1	0.96	0.04	24,24,24,24	0
83	MG	AB	201	1/1	0.96	0.07	9,9,9,9	0
83	MG	1	3874	1/1	0.96	0.10	45,45,45,45	0
83	MG	B	1906	1/1	0.96	0.11	12,12,12,12	0
83	MG	BK	201	1/1	0.96	0.16	11,11,11,11	0
83	MG	1	3802	1/1	0.96	0.13	19,19,19,19	0
83	MG	1	3912	1/1	0.96	0.06	26,26,26,26	0
83	MG	AS	3410	1/1	0.96	0.18	26,26,26,26	0
83	MG	CA	201	1/1	0.96	0.08	33,33,33,33	0
83	MG	AS	3510	1/1	0.96	0.15	28,28,28,28	0
83	MG	1	3689	1/1	0.96	0.07	33,33,33,33	0
83	MG	1	3452	1/1	0.96	0.15	19,19,19,19	0
83	MG	AS	3609	1/1	0.96	0.06	8,8,8,8	0
83	MG	AS	3513	1/1	0.96	0.13	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AF	201	1/1	0.96	0.12	23,23,23,23	0
83	MG	AS	3415	1/1	0.96	0.22	22,22,22,22	0
85	ZN	AQ	101	1/1	0.96	0.05	65,65,65,65	0
83	MG	1	3805	1/1	0.96	0.07	27,27,27,27	0
83	MG	1	3806	1/1	0.96	0.06	32,32,32,32	0
83	MG	1	3917	1/1	0.96	0.07	79,79,79,79	0
83	MG	1	3570	1/1	0.96	0.17	28,28,28,28	0
83	MG	AS	3617	1/1	0.96	0.07	25,25,25,25	0
83	MG	AS	3521	1/1	0.96	0.21	28,28,28,28	0
83	MG	AS	3619	1/1	0.96	0.08	20,20,20,20	0
83	MG	1	3640	1/1	0.97	0.20	27,27,27,27	0
83	MG	1	3756	1/1	0.97	0.13	31,31,31,31	0
83	MG	AS	3485	1/1	0.97	0.15	15,15,15,15	0
83	MG	1	3421	1/1	0.97	0.21	3,3,3,3	0
83	MG	1	3629	1/1	0.97	0.09	25,25,25,25	0
83	MG	AS	3488	1/1	0.97	0.25	15,15,15,15	0
83	MG	AS	3438	1/1	0.97	0.18	17,17,17,17	0
83	MG	1	3742	1/1	0.97	0.10	32,32,32,32	0
83	MG	AS	3543	1/1	0.97	0.08	23,23,23,23	0
83	MG	AS	3440	1/1	0.97	0.16	17,17,17,17	0
83	MG	AS	3492	1/1	0.97	0.10	16,16,16,16	0
83	MG	1	3728	1/1	0.97	0.17	18,18,18,18	0
83	MG	AS	3402	1/1	0.97	0.05	46,46,46,46	0
83	MG	1	3761	1/1	0.97	0.06	18,18,18,18	0
83	MG	1	3533	1/1	0.97	0.13	25,25,25,25	0
83	MG	AS	3445	1/1	0.97	0.06	22,22,22,22	0
83	MG	AS	3499	1/1	0.97	0.07	6,6,6,6	0
83	MG	1	3480	1/1	0.97	0.16	16,16,16,16	0
83	MG	B	1915	1/1	0.97	0.09	31,31,31,31	0
83	MG	CM	1879	1/1	0.97	0.12	26,26,26,26	0
83	MG	AS	3448	1/1	0.97	0.10	33,33,33,33	0
83	MG	1	3404	1/1	0.97	0.13	30,30,30,30	0
83	MG	AS	3557	1/1	0.97	0.09	20,20,20,20	0
83	MG	AS	3409	1/1	0.97	0.11	9,9,9,9	0
83	MG	AS	3451	1/1	0.97	0.12	26,26,26,26	0
83	MG	AS	3506	1/1	0.97	0.09	18,18,18,18	0
83	MG	AS	3453	1/1	0.97	0.13	14,14,14,14	0
83	MG	AS	3454	1/1	0.97	0.08	20,20,20,20	0
83	MG	AS	3564	1/1	0.97	0.04	12,12,12,12	0
83	MG	CM	1889	1/1	0.97	0.12	33,33,33,33	0
83	MG	B	1889	1/1	0.97	0.15	37,37,37,37	0
83	MG	AS	3411	1/1	0.97	0.18	13,13,13,13	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	CM	1893	1/1	0.97	0.09	17,17,17,17	0
83	MG	B	1948	1/1	0.97	0.17	22,22,22,22	0
83	MG	6	201	1/1	0.97	0.12	23,23,23,23	0
83	MG	6	202	1/1	0.97	0.13	27,27,27,27	0
83	MG	AS	3570	1/1	0.97	0.13	16,16,16,16	0
83	MG	4	202	1/1	0.97	0.17	10,10,10,10	0
83	MG	CM	1900	1/1	0.97	0.11	35,35,35,35	0
83	MG	1	3492	1/1	0.97	0.09	31,31,31,31	0
83	MG	1	3477	1/1	0.97	0.09	14,14,14,14	0
83	MG	AS	3517	1/1	0.97	0.09	22,22,22,22	0
83	MG	1	3501	1/1	0.97	0.14	12,12,12,12	0
83	MG	CM	1838	1/1	0.97	0.11	32,32,32,32	0
83	MG	v	301	1/1	0.97	0.07	21,21,21,21	0
83	MG	1	3750	1/1	0.97	0.14	39,39,39,39	0
83	MG	AS	3422	1/1	0.97	0.06	20,20,20,20	0
83	MG	AS	3423	1/1	0.97	0.13	25,25,25,25	0
83	MG	1	3707	1/1	0.97	0.04	3,3,3,3	0
83	MG	4	208	1/1	0.97	0.11	8,8,8,8	0
83	MG	1	3791	1/1	0.97	0.11	46,46,46,46	0
83	MG	L	201	1/1	0.97	0.18	41,41,41,41	0
83	MG	B	1816	1/1	0.97	0.21	17,17,17,17	0
83	MG	1	3417	1/1	0.97	0.08	13,13,13,13	0
83	MG	1	3852	1/1	0.97	0.13	24,24,24,24	0
83	MG	AS	3477	1/1	0.97	0.12	14,14,14,14	0
85	ZN	f	101	1/1	0.97	0.07	71,71,71,71	0
83	MG	1	3627	1/1	0.97	0.14	11,11,11,11	0
83	MG	BQ	201	1/1	0.97	0.13	14,14,14,14	0
85	ZN	CH	101	1/1	0.97	0.10	75,75,75,75	0
83	MG	AS	3645	1/1	0.97	0.10	26,26,26,26	0
83	MG	AS	3479	1/1	0.97	0.12	30,30,30,30	0
85	ZN	DS	201	1/1	0.97	0.06	134,134,134,134	0
83	MG	1	3685	1/1	0.97	0.14	33,33,33,33	0
83	MG	AS	3433	1/1	0.97	0.20	17,17,17,17	0
83	MG	AS	3608	1/1	0.98	0.04	21,21,21,21	0
83	MG	1	3572	1/1	0.98	0.10	11,11,11,11	0
83	MG	CM	1803	1/1	0.98	0.13	13,13,13,13	0
83	MG	B	1854	1/1	0.98	0.05	58,58,58,58	0
83	MG	1	3449	1/1	0.98	0.15	11,11,11,11	0
83	MG	AS	3458	1/1	0.98	0.13	1,1,1,1	0
83	MG	1	3472	1/1	0.98	0.10	10,10,10,10	0
83	MG	1	3605	1/1	0.98	0.05	22,22,22,22	0
83	MG	B	1880	1/1	0.98	0.12	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	AS	3551	1/1	0.98	0.11	23,23,23,23	0
83	MG	CM	1894	1/1	0.98	0.25	16,16,16,16	0
83	MG	AS	3407	1/1	0.98	0.05	0,0,0,0	0
83	MG	1	3826	1/1	0.98	0.05	36,36,36,36	0
83	MG	1	3811	1/1	0.98	0.04	6,6,6,6	0
83	MG	1	3566	1/1	0.98	0.10	3,3,3,3	0
83	MG	1	3409	1/1	0.98	0.04	12,12,12,12	0
83	MG	CM	1856	1/1	0.98	0.12	24,24,24,24	0
83	MG	B	1840	1/1	0.98	0.14	38,38,38,38	0
83	MG	B	1841	1/1	0.98	0.18	36,36,36,36	0
83	MG	AS	3559	1/1	0.98	0.09	8,8,8,8	0
83	MG	AS	3498	1/1	0.98	0.10	26,26,26,26	0
83	MG	CQ	301	1/1	0.98	0.06	3,3,3,3	0
83	MG	1	3420	1/1	0.98	0.12	17,17,17,17	0
83	MG	B	1804	1/1	0.98	0.14	14,14,14,14	0
83	MG	AS	3416	1/1	0.98	0.05	47,47,47,47	0
83	MG	1	3588	1/1	0.98	0.10	26,26,26,26	0
83	MG	AS	3664	1/1	0.98	0.09	29,29,29,29	0
83	MG	1	3435	1/1	0.98	0.08	0,0,0,0	0
83	MG	CM	1867	1/1	0.98	0.10	34,34,34,34	0
83	MG	1	3865	1/1	0.98	0.03	25,25,25,25	0
83	MG	1	3465	1/1	0.98	0.09	10,10,10,10	0
83	MG	AS	3668	1/1	0.98	0.05	63,63,63,63	0
85	ZN	AK	101	1/1	0.98	0.07	55,55,55,55	0
85	ZN	AN	101	1/1	0.98	0.06	73,73,73,73	0
83	MG	1	3534	1/1	0.98	0.05	15,15,15,15	0
83	MG	BV	201	1/1	0.98	0.19	25,25,25,25	0
83	MG	CM	1831	1/1	0.98	0.08	44,44,44,44	0
83	MG	AS	3670	1/1	0.98	0.08	11,11,11,11	0
83	MG	B	1849	1/1	0.98	0.13	32,32,32,32	0
83	MG	1	3635	1/1	0.98	0.07	37,37,37,37	0
83	MG	1	3636	1/1	0.98	0.04	22,22,22,22	0
83	MG	B	1920	1/1	0.98	0.06	68,68,68,68	0
85	ZN	DN	201	1/1	0.98	0.03	59,59,59,59	0
83	MG	AS	3452	1/1	0.98	0.14	19,19,19,19	0
83	MG	1	3676	1/1	0.98	0.09	41,41,41,41	0
83	MG	AS	3483	1/1	0.98	0.11	13,13,13,13	0
83	MG	CM	1840	1/1	0.98	0.18	24,24,24,24	0
83	MG	1	3440	1/1	0.99	0.17	2,2,2,2	0
83	MG	1	3499	1/1	0.99	0.16	13,13,13,13	0
83	MG	1	3528	1/1	0.99	0.09	32,32,32,32	0
83	MG	1	3475	1/1	0.99	0.16	3,3,3,3	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
83	MG	B	1831	1/1	0.99	0.14	23,23,23,23	0
83	MG	3	201	1/1	0.99	0.10	0,0,0,0	0
83	MG	AS	3679	1/1	0.99	0.06	28,28,28,28	0
85	ZN	c	201	1/1	0.99	0.03	51,51,51,51	0
83	MG	1	3772	1/1	0.99	0.12	18,18,18,18	0
83	MG	B	1925	1/1	0.99	0.06	28,28,28,28	0
83	MG	1	3550	1/1	0.99	0.12	9,9,9,9	0
83	MG	1	3764	1/1	0.99	0.13	18,18,18,18	0
85	ZN	CE	101	1/1	0.99	0.03	66,66,66,66	0
83	MG	AS	3456	1/1	0.99	0.15	7,7,7,7	0
83	MG	AP	202	1/1	0.99	0.03	12,12,12,12	0
85	ZN	CK	101	1/1	0.99	0.03	84,84,84,84	0
83	MG	1	3408	1/1	0.99	0.03	47,47,47,47	0
83	MG	1	3582	1/1	0.99	0.18	31,31,31,31	0
83	MG	CM	1892	1/1	0.99	0.14	9,9,9,9	0
83	MG	1	3767	1/1	0.99	0.03	26,26,26,26	0
83	MG	AS	3656	1/1	0.99	0.04	45,45,45,45	0
83	MG	1	3708	1/1	1.00	0.07	11,11,11,11	0

6.5 Other polymers [i](#)

There are no such residues in this entry.