



wwPDB X-ray Structure Validation Summary Report i

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PDB ID : 4V7U
Title : Crystal structure of the E. coli ribosome bound to erythromycin.
Authors : Dunkle, J.A.; Xiong, L.; Mankin, A.S.; Cate, J.H.D.
Deposited on : 2010-08-15
Resolution : 3.10 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

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

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

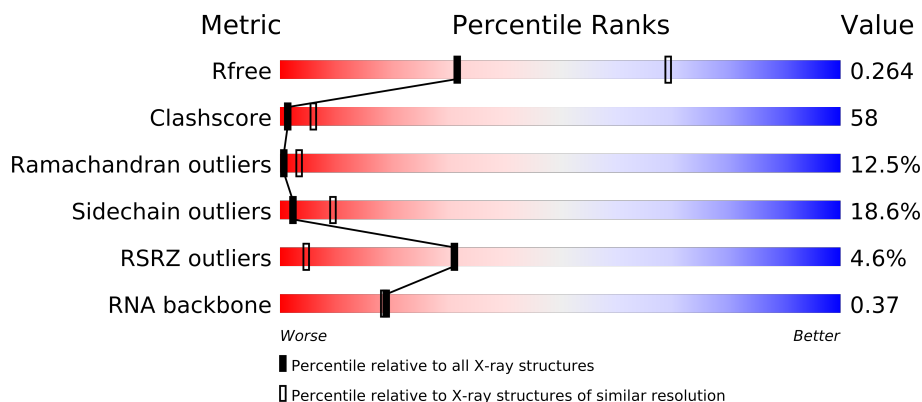
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.16 November 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable23397
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable23397

1 Overall quality at a glance

The reported resolution of this entry is 3.10 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}	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)
RNA backbone	1838	1047 (3.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	AA	1533	
2	AB	218	
2	CB	218	
3	AC	206	
3	CC	206	
4	AD	205	
4	CD	205	
5	AE	150	
5	CE	150	
6	AF	100	
6	CF	100	
7	AG	151	

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Mol	Chain	Length	Quality of chain
8	AH	129	
8	CH	129	
9	AI	127	
9	CI	127	
10	AJ	98	
10	CJ	98	
11	AK	117	
11	CK	117	
12	AL	123	
12	CL	123	
13	AM	114	
14	AN	100	
14	CN	100	
15	AO	88	
15	CO	88	
16	AP	82	
17	AQ	80	
17	CQ	80	
18	AR	55	
18	CR	55	
19	AS	79	
19	CS	79	
20	AT	85	
20	CT	85	
21	AU	51	
21	CU	51	
22	BA	2904	
22	DA	2904	
23	BB	118	
24	BC	271	
24	DC	271	
25	BD	209	
25	DD	209	
26	BE	201	
26	DE	201	
27	BF	177	
28	BG	176	
28	DG	176	
29	BH	149	
29	DH	149	
30	BI	141	
30	DI	141	

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Mol	Chain	Length	Quality of chain
31	BJ	142	
31	DJ	142	
32	BK	122	
32	DK	122	
33	BL	143	
33	DL	143	
34	BM	136	
34	DM	136	
35	BN	120	
35	DN	120	
36	BO	116	
36	DO	116	
37	BP	114	
37	DP	114	
38	BQ	117	
38	DQ	117	
39	BR	103	
39	DR	103	
40	BS	110	
40	DS	110	
41	BT	93	
41	DT	93	
42	BU	102	
42	DU	102	
43	BV	94	
43	DV	94	
44	BW	79	
44	DW	79	
45	BX	77	
45	DX	77	
46	BY	63	
46	DY	63	
47	BZ	58	
47	DZ	58	
48	B0	56	
48	D0	56	
49	B1	50	
49	D1	50	
50	B2	46	
50	D2	46	
51	B3	64	
51	D3	64	

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Mol	Chain	Length	Quality of chain
52	B4	38	
52	D4	38	
53	CA	1530	
54	CG	150	
55	CM	113	
56	CP	80	
57	DB	117	
58	DF	178	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
59	MG	AA	1604	-	X
59	MG	AA	1612	-	X
59	MG	AA	1617	-	X
59	MG	AA	1620	-	X
59	MG	AA	1624	-	X
59	MG	AA	1625	-	X
59	MG	AA	1639	-	X
59	MG	BA	3004	-	X
59	MG	BA	3011	-	X
59	MG	BA	3014	-	X
59	MG	BA	3018	-	X
59	MG	BA	3019	-	X
59	MG	BA	3020	-	X
59	MG	BA	3025	-	X
59	MG	BA	3027	-	X
59	MG	BA	3030	-	X
59	MG	BA	3034	-	X
59	MG	BA	3036	-	X
59	MG	BA	3039	-	X
59	MG	BA	3040	-	X
59	MG	BA	3041	-	X
59	MG	BA	3044	-	X
59	MG	BA	3047	-	X
59	MG	BA	3048	-	X
59	MG	BA	3055	-	X
59	MG	BA	3056	-	X
59	MG	BA	3057	-	X
59	MG	BA	3059	-	X
59	MG	BA	3060	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
59	MG	BA	3061	-	X
59	MG	BA	3063	-	X
59	MG	BA	3070	-	X
59	MG	BA	3075	-	X
59	MG	BA	3077	-	X
59	MG	BA	3082	-	X
59	MG	BA	3083	-	X
59	MG	BA	3084	-	X
59	MG	BA	3086	-	X
59	MG	BA	3087	-	X
59	MG	BA	3091	-	X
59	MG	BA	3097	-	X
59	MG	BA	3100	-	X
59	MG	BA	3103	-	X
59	MG	BA	3104	-	X
59	MG	BA	3107	-	X
59	MG	BA	3108	-	X
59	MG	BA	3110	-	X
59	MG	BA	3112	-	X
59	MG	BA	3118	-	X
59	MG	BA	3121	-	X
59	MG	BA	3123	-	X
59	MG	BA	3124	-	X
59	MG	BA	3125	-	X
59	MG	BA	3128	-	X
59	MG	BA	3130	-	X
59	MG	BA	3132	-	X
59	MG	BA	3133	-	X
59	MG	BA	3134	-	X
59	MG	BA	3135	-	X
59	MG	BB	201	-	X
59	MG	CA	1612	-	X
59	MG	CA	1614	-	X
59	MG	CA	1624	-	X
59	MG	CA	1625	-	X
59	MG	CA	1626	-	X
59	MG	CA	1627	-	X
59	MG	CA	1628	-	X
59	MG	CA	1640	-	X
59	MG	DA	3002	-	X
59	MG	DA	3005	-	X
59	MG	DA	3010	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
59	MG	DA	3013	-	X
59	MG	DA	3014	-	X
59	MG	DA	3015	-	X
59	MG	DA	3016	-	X
59	MG	DA	3020	-	X
59	MG	DA	3026	-	X
59	MG	DA	3028	-	X
59	MG	DA	3029	-	X
59	MG	DA	3033	-	X
59	MG	DA	3045	-	X
59	MG	DA	3047	-	X
59	MG	DA	3049	-	X
59	MG	DA	3051	-	X
59	MG	DA	3057	-	X
59	MG	DA	3058	-	X
59	MG	DA	3059	-	X
59	MG	DA	3060	-	X
59	MG	DA	3062	-	X
59	MG	DA	3063	-	X
59	MG	DA	3064	-	X
59	MG	DA	3074	-	X
59	MG	DA	3075	-	X
59	MG	DA	3077	-	X
59	MG	DA	3078	-	X
59	MG	DA	3079	-	X
59	MG	DA	3082	-	X
59	MG	DA	3091	-	X
59	MG	DA	3097	-	X
59	MG	DA	3099	-	X
59	MG	DA	3108	-	X
59	MG	DA	3109	-	X
59	MG	DA	3125	-	X
59	MG	DA	3127	-	X
59	MG	DA	3129	-	X
59	MG	DA	3130	-	X
59	MG	DA	3133	-	X
59	MG	DJ	201	-	X

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 284525 atoms, of which 0 are hydrogen and 0 are deuterium.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1533	Total	C	N	O	P	0	0	0
			32895	14671	6036	10655	1533			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	218	Total	C	N	O	S	0	0	0
			1705	1081	305	312	7			
2	CB	218	Total	C	N	O	S	0	0	0
			1705	1081	305	312	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	206	Total	C	N	O	S	0	0	0
			1625	1028	305	289	3			
3	CC	206	Total	C	N	O	S	0	0	0
			1625	1028	305	289	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			
4	CD	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	150	Total	C	N	O	S	0	0	0
			1106	687	211	202	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	CE	150	Total	C	N	O	S	0	0	0
			1106	687	211	202	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	100	Total	C	N	O	S	0	0	0
			818	515	148	149	6			
6	CF	100	Total	C	N	O	S	0	0	0
			818	515	148	149	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	151	Total	C	N	O	S	0	0	0
			1182	735	227	216	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			
8	CH	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			
9	CI	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0	0
			787	493	150	143	1			
10	CJ	98	Total	C	N	O	S	0	0	0
			787	493	150	143	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AK	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			
11	CK	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			
12	CL	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AM	114	Total	C	N	O	S	0	0	0
			884	546	178	157	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			
14	CN	95	Total	C	N	O	S	0	0	0
			769	480	159	127	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0	0
			714	439	144	130	1			
15	CO	88	Total	C	N	O	S	0	0	0
			714	439	144	130	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0	0
			649	406	128	114	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AQ	80	Total	C	N	O	S	0	0	0
			649	411	121	114	3			
17	CQ	80	Total	C	N	O	S	0	0	0
			649	411	121	114	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	AR	55	Total	C	N	O	S	0	0	0
			456	288	86	82				
18	CR	55	Total	C	N	O	S	0	0	0
			456	288	86	82				

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AS	79	Total	C	N	O	S	0	0	0
			638	408	120	108	2			
19	CS	79	Total	C	N	O	S	0	0	0
			638	408	120	108	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AT	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			
20	CT	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	AU	51	Total	C	N	O	S	0	0	0
			426	265	86	74	1			
21	CU	51	Total	C	N	O	S	0	0	0
			426	265	86	74	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	BA	2854	Total	C	N	O	P	0	0	0
			61274	27334	11279	19807	2854			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	DA	2841	Total	C	N	O	P	0	0	0
			60995	27210	11229	19715	2841			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	BB	118	Total	C	N	O	P	0	0	0
			2529	1126	464	821	118			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	BC	271	Total	C	N	O	S	0	0	0
			2083	1288	423	365	7			
24	DC	271	Total	C	N	O	S	0	0	0
			2083	1288	423	365	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	BD	209	Total	C	N	O	S	0	0	0
			1565	979	288	294	4			
25	DD	209	Total	C	N	O	S	0	0	0
			1565	979	288	294	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	BE	201	Total	C	N	O	S	0	0	0
			1552	974	283	290	5			
26	DE	201	Total	C	N	O	S	0	0	0
			1552	974	283	290	5			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	BF	177	Total	C	N	O	S	0	0	0
			1411	899	249	257	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	BG	176	Total	C	N	O	S	0	0	0
			1323	832	243	246	2			
28	DG	176	Total	C	N	O	S	0	0	0
			1323	832	243	246	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	BH	149	Total	C	N	O	S	0	0	0
			1111	699	197	214	1			
29	DH	149	Total	C	N	O	S	0	0	0
			1111	699	197	214	1			

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	BI	141	Total	C	N	O	S	0	0	0
			1032	651	179	196	6			
30	DI	141	Total	C	N	O	S	0	0	0
			1032	651	179	196	6			

- Molecule 31 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	BJ	142	Total	C	N	O	S	0	0	0
			1129	714	212	199	4			
31	DJ	142	Total	C	N	O	S	0	0	0
			1129	714	212	199	4			

- Molecule 32 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BK	122	Total	C	N	O	S	0	0	0
			939	587	180	166	6			
32	DK	122	Total	C	N	O	S	0	0	0
			939	587	180	166	6			

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	BL	143	Total	C	N	O	S	0	0	0
			1045	649	206	189	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	DL	143	Total	C	N	O	S	0	0	0
			1045	649	206	189	1			

- Molecule 34 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BM	136	Total	C	N	O	S	0	0	0
			1074	686	205	177	6			
34	DM	136	Total	C	N	O	S	0	0	0
			1074	686	205	177	6			

- Molecule 35 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BN	120	Total	C	N	O	S	0	0	0
			961	593	196	167	5			
35	DN	120	Total	C	N	O	S	0	0	0
			961	593	196	167	5			

- Molecule 36 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	BO	116	Total	C	N	O	S	0	0	0
			892	552	178	162				
36	DO	116	Total	C	N	O	S	0	0	0
			892	552	178	162				

- Molecule 37 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BP	114	Total	C	N	O	S	0	0	0
			917	574	179	163	1			
37	DP	114	Total	C	N	O	S	0	0	0
			917	574	179	163	1			

- Molecule 38 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BQ	117	Total	C	N	O	S	0	0	0
			947	604	192	151				
38	DQ	117	Total	C	N	O	S	0	0	0
			947	604	192	151				

- Molecule 39 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BR	103	Total	C	N	O	S	0	0	0
			816	516	153	145	2			
39	DR	103	Total	C	N	O	S	0	0	0
			816	516	153	145	2			

- Molecule 40 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BS	110	Total	C	N	O	S	0	0	0
			857	532	166	156	3			
40	DS	110	Total	C	N	O	S	0	0	0
			857	532	166	156	3			

- Molecule 41 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BT	93	Total	C	N	O	S	0	0	0
			739	466	139	132	2			
41	DT	93	Total	C	N	O	S	0	0	0
			739	466	139	132	2			

- Molecule 42 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
42	BU	102	Total	C	N	O	0	0	0
			780	492	146	142			
42	DU	102	Total	C	N	O	0	0	0
			780	492	146	142			

- Molecule 43 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BV	94	Total	C	N	O	S	0	0	0
			753	479	137	134	3			
43	DV	94	Total	C	N	O	S	0	0	0
			753	479	137	134	3			

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	BW	79	Total	C	N	O	S	0	0	0
			596	367	120	108	1			
44	DW	79	Total	C	N	O	S	0	0	0
			596	367	120	108	1			

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BX	77	Total	C	N	O	S	0	0	0
			625	388	129	106	2			
45	DX	77	Total	C	N	O	S	0	0	0
			625	388	129	106	2			

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	BY	63	Total	C	N	O	S	0	0	0
			509	313	99	95	2			
46	DY	63	Total	C	N	O	S	0	0	0
			509	313	99	95	2			

- Molecule 47 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	BZ	58	Total	C	N	O	S	0	0	0
			449	281	87	79	2			
47	DZ	58	Total	C	N	O	S	0	0	0
			449	281	87	79	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	B0	56	Total	C	N	O	S	0	0	0
			444	269	94	80	1			
48	D0	56	Total	C	N	O	S	0	0	0
			444	269	94	80	1			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	B1	50	Total	C	N	O	0	0	0
			410	263	75	72			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
49	D1	50	Total	C	N	O	0	0	0
			410	263	75	72			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	B2	46	Total	C	N	O	S	0	0	0
			377	228	90	57	2			
50	D2	46	Total	C	N	O	S	0	0	0
			377	228	90	57	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	B3	64	Total	C	N	O	S	0	0	0
			504	323	105	74	2			
51	D3	64	Total	C	N	O	S	0	0	0
			504	323	105	74	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	B4	38	Total	C	N	O	S	0	0	0
			302	185	65	48	4			
52	D4	38	Total	C	N	O	S	0	0	0
			302	185	65	48	4			

- Molecule 53 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	CA	1530	Total	C	N	O	P	0	0	0
			32831	14642	6024	10635	1530			

- Molecule 54 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	CG	150	Total	C	N	O	S	0	0	0
			1175	730	226	215	4			

- Molecule 55 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	CM	113	Total	C	N	O	S	0	0	0
			877	541	177	156	3			

- Molecule 56 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	CP	80	Total	C	N	O	S	0	0	0
			639	400	126	112	1			

- Molecule 57 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	DB	117	Total	C	N	O	P	0	0	0
			2507	1116	459	815	117			

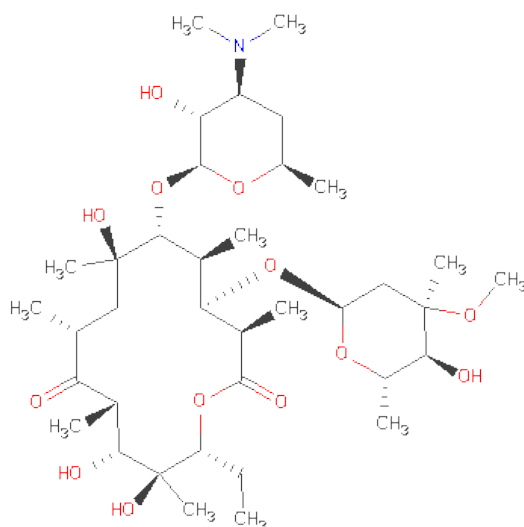
- Molecule 58 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	DF	178	Total	C	N	O	S	0	0	0
			1420	905	251	258	6			

- Molecule 59 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
59	BB	4	Total	Mg	0	0
			4	4		
59	BA	135	Total	Mg	0	0
			135	135		
59	CA	42	Total	Mg	0	0
			42	42		
59	DJ	1	Total	Mg	0	0
			1	1		
59	AA	41	Total	Mg	0	0
			41	41		
59	AN	2	Total	Mg	0	0
			2	2		
59	DA	133	Total	Mg	0	0
			133	133		
59	DC	2	Total	Mg	0	0
			2	2		
59	DB	1	Total	Mg	0	0
			1	1		

- Molecule 60 is ERYTHROMYCIN A (three-letter code: ERY) (formula: $C_{37}H_{67}NO_{13}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
60	BA	1	Total	C	N	O	0	0
			51	37	1	13		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
61	B4	1	Total	Zn	0	0
			1	1		
61	D4	1	Total	Zn	0	0
			1	1		

- Molecule 62 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	AA	197	Total	O	0	0
			197	197		
62	AE	1	Total	O	0	0
			1	1		
62	AL	1	Total	O	0	0
			1	1		
62	AN	7	Total	O	0	0
			7	7		
62	AT	1	Total	O	0	0
			1	1		
62	AU	1	Total	O	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
62	BA	605	Total O 605 605	0	0
62	BB	19	Total O 19 19	0	0
62	BC	7	Total O 7 7	0	0
62	BD	3	Total O 3 3	0	0
62	BE	1	Total O 1 1	0	0
62	BL	4	Total O 4 4	0	0
62	BN	2	Total O 2 2	0	0
62	BR	1	Total O 1 1	0	0
62	BT	2	Total O 2 2	0	0
62	BV	1	Total O 1 1	0	0
62	B3	3	Total O 3 3	0	0
62	B4	2	Total O 2 2	0	0
62	CA	195	Total O 195 195	0	0
62	CE	3	Total O 3 3	0	0
62	CL	1	Total O 1 1	0	0
62	CN	3	Total O 3 3	0	0
62	CT	4	Total O 4 4	0	0
62	CU	1	Total O 1 1	0	0
62	DA	600	Total O 600 600	0	0
62	DB	3	Total O 3 3	0	0
62	DC	13	Total O 13 13	0	0

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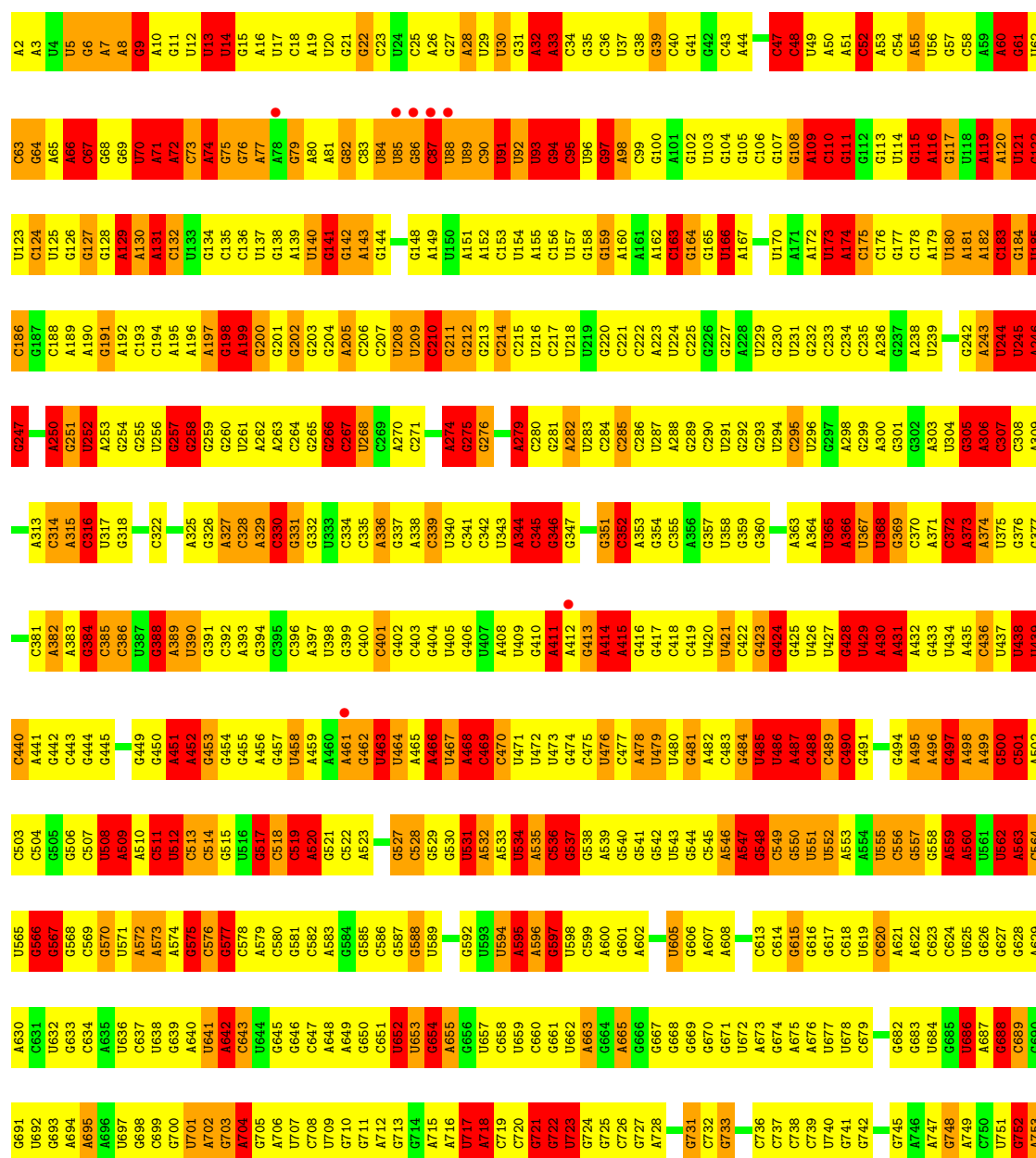
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
62	DD	2	Total 2	O 2	0	0
62	DE	4	Total 4	O 4	0	0
62	DJ	3	Total 3	O 3	0	0
62	DL	4	Total 4	O 4	0	0
62	DN	2	Total 2	O 2	0	0
62	DT	2	Total 2	O 2	0	0
62	DU	2	Total 2	O 2	0	0
62	DV	2	Total 2	O 2	0	0
62	D2	1	Total 1	O 1	0	0
62	D3	1	Total 1	O 1	0	0
62	D4	4	Total 4	O 4	0	0

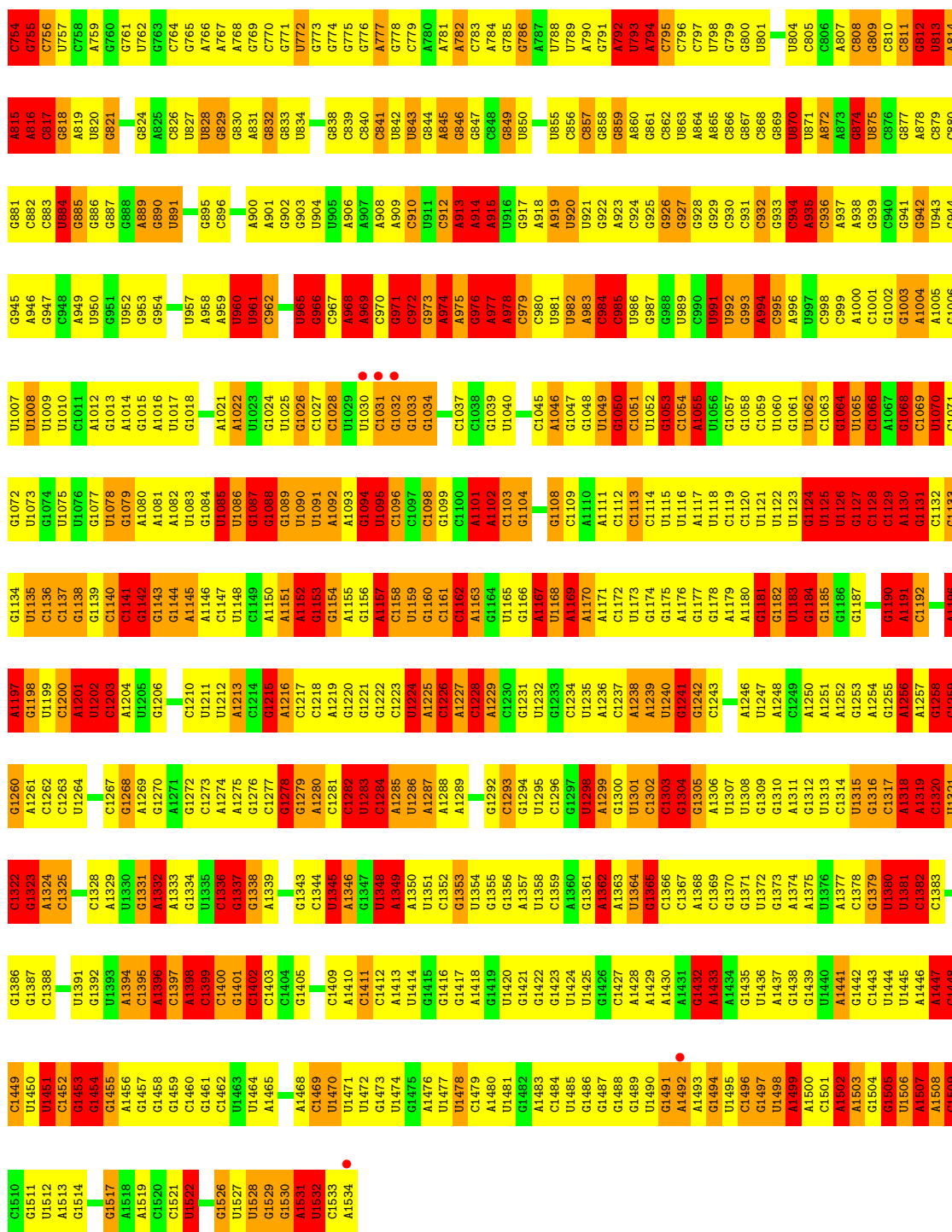
3 Residue-property plots

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

• Molecule 1: 16S rRNA

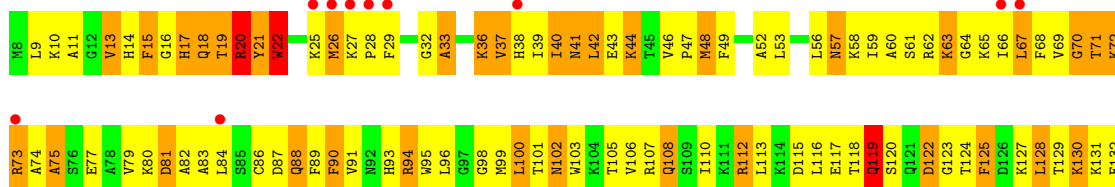
Chain AA: 

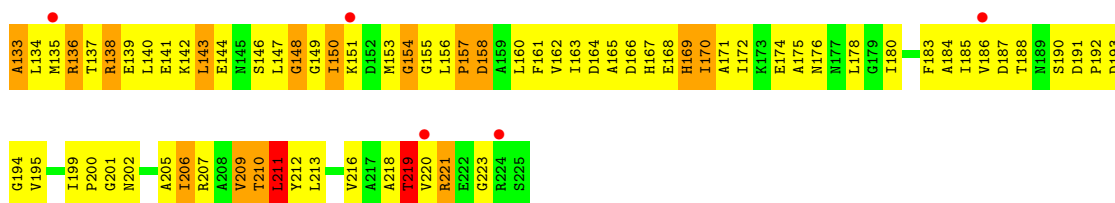




• Molecule 2: 30S ribosomal protein S2

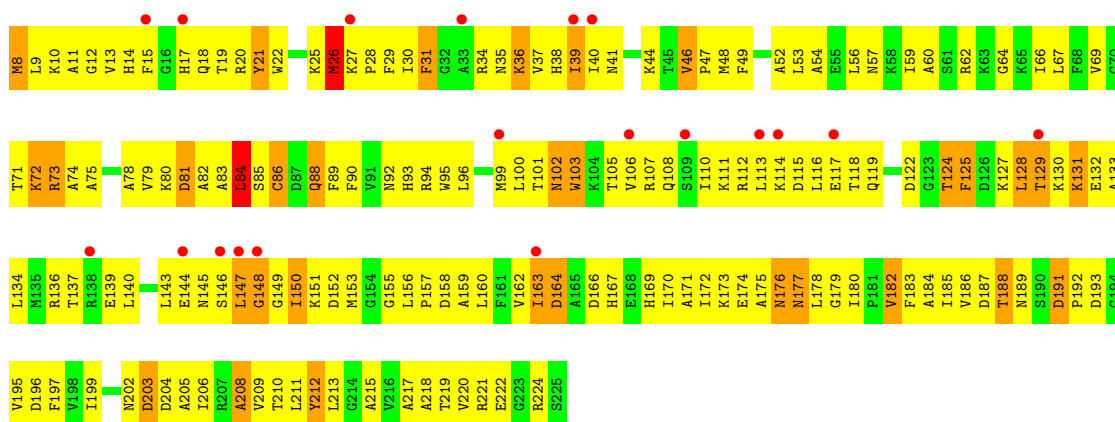
Chain AB:





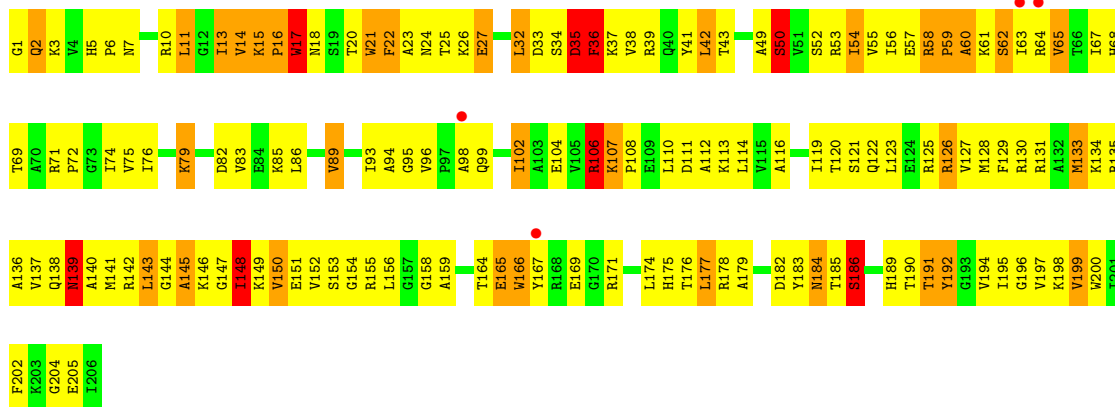
• Molecule 2: 30S ribosomal protein S2

Chain CB:



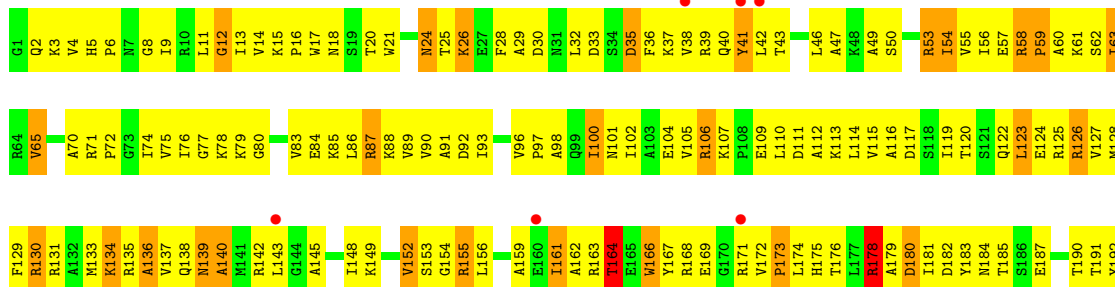
• Molecule 3: 30S ribosomal protein S3

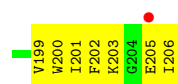
Chain AC:



• Molecule 3: 30S ribosomal protein S3

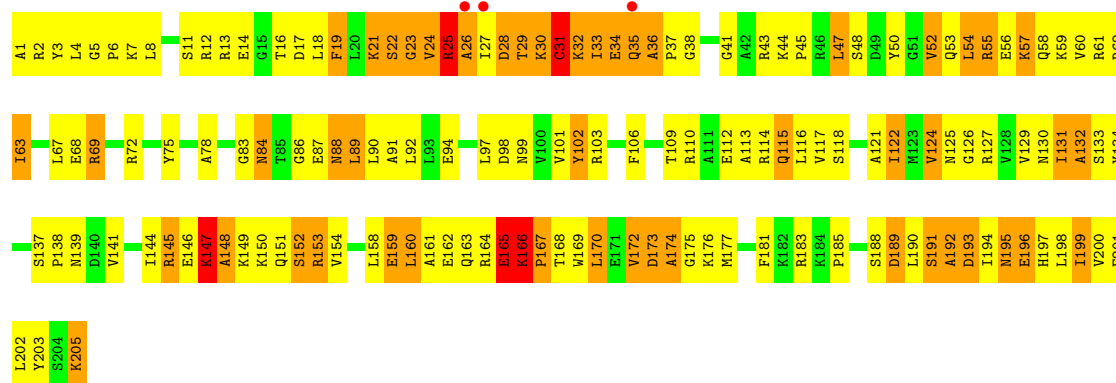
Chain CC:





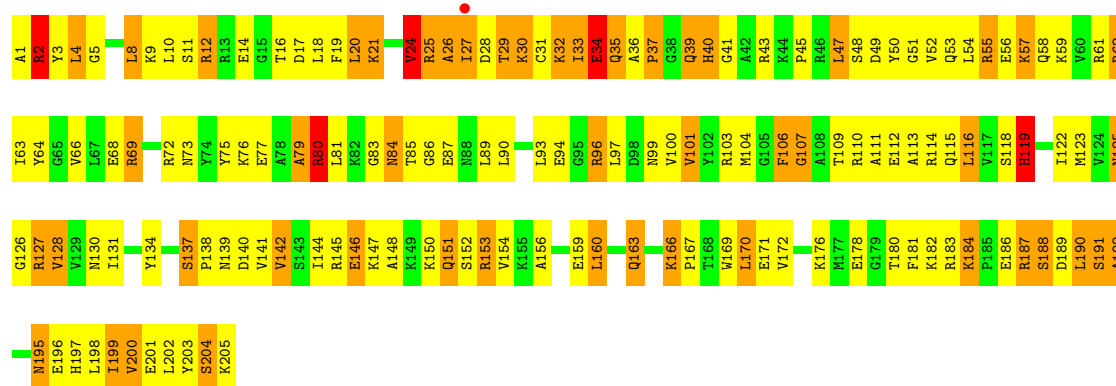
• Molecule 4: 30S ribosomal protein S4

Chain AD:



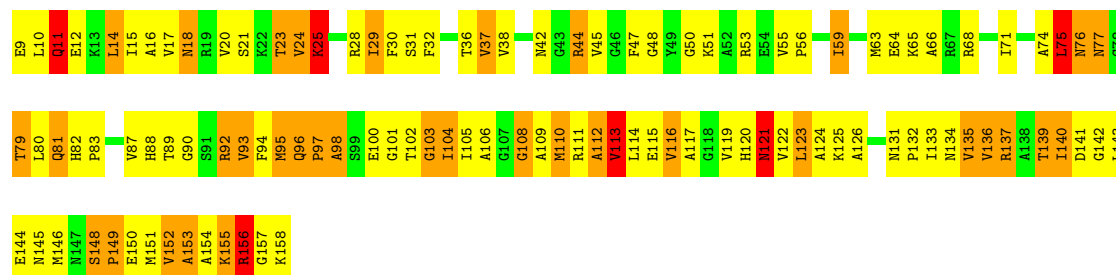
• Molecule 4: 30S ribosomal protein S4

Chain CD:



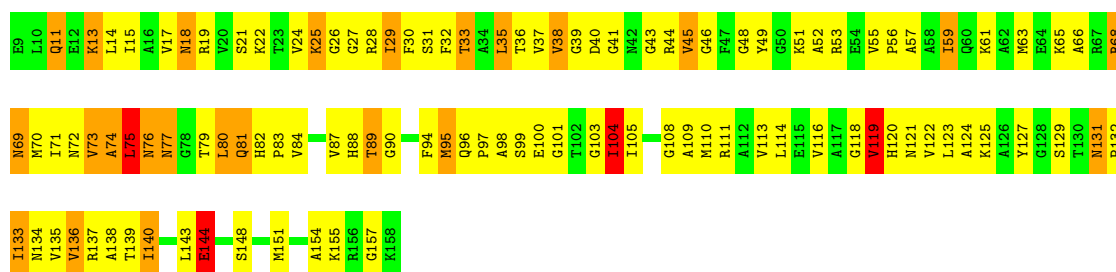
• Molecule 5: 30S ribosomal protein S5

Chain AE:



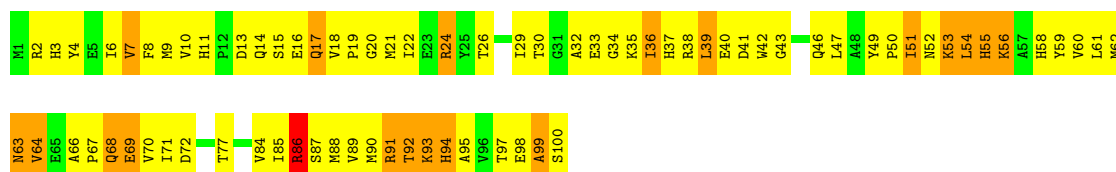
• Molecule 5: 30S ribosomal protein S5

Chain CE:



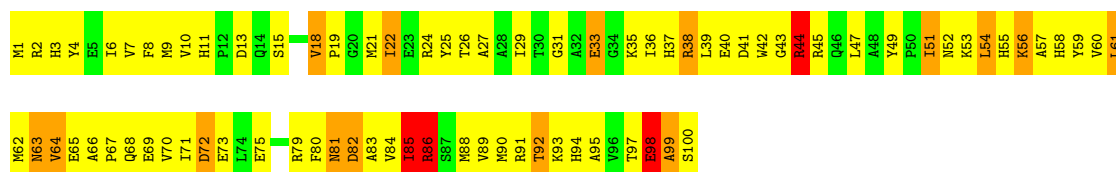
- Molecule 6: 30S ribosomal protein S6

Chain AF:



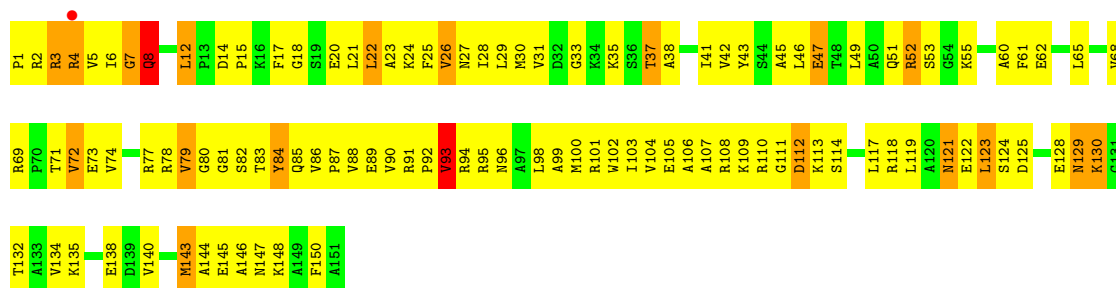
- Molecule 6: 30S ribosomal protein S6

Chain CF:



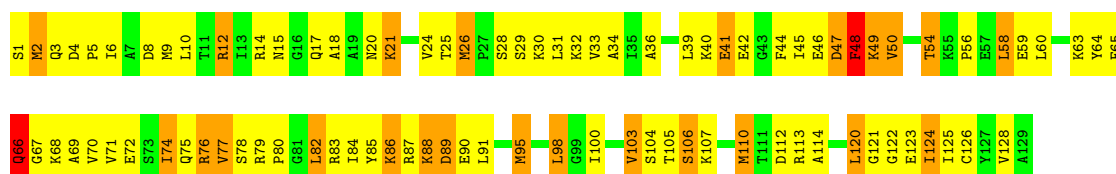
- Molecule 7: 30S ribosomal protein S7

Chain AG:



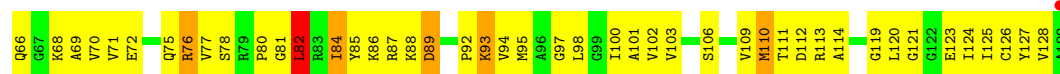
- Molecule 8: 30S ribosomal protein S8

Chain AH:



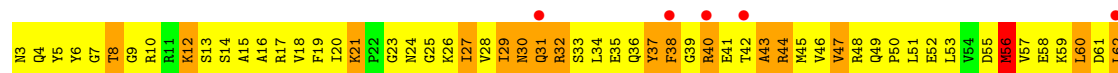
- Molecule 8: 30S ribosomal protein S8

Chain CH:



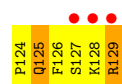
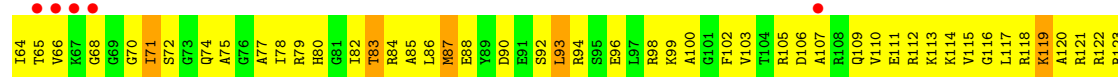
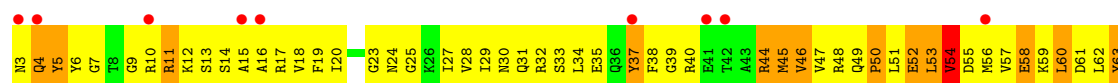
• Molecule 9: 30S ribosomal protein S9

Chain AI:



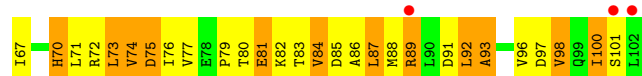
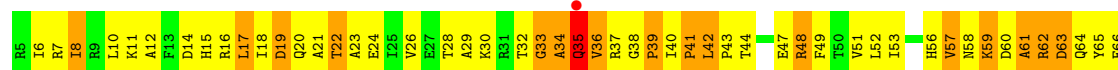
• Molecule 9: 30S ribosomal protein S9

Chain CI:



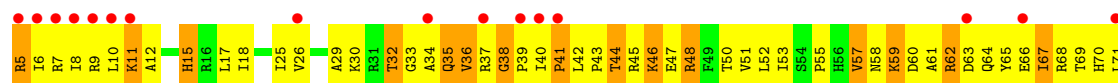
• Molecule 10: 30S ribosomal protein S10

Chain AJ:

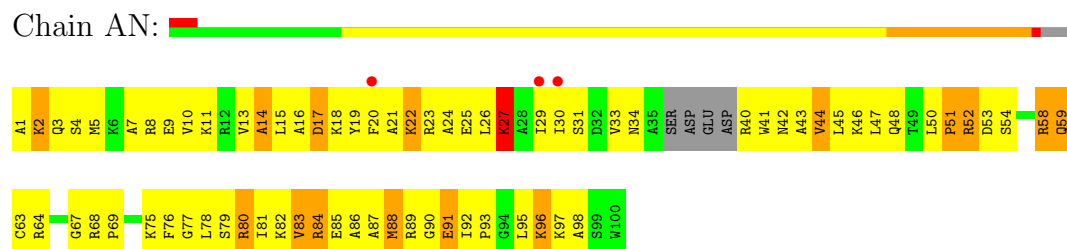


• Molecule 10: 30S ribosomal protein S10

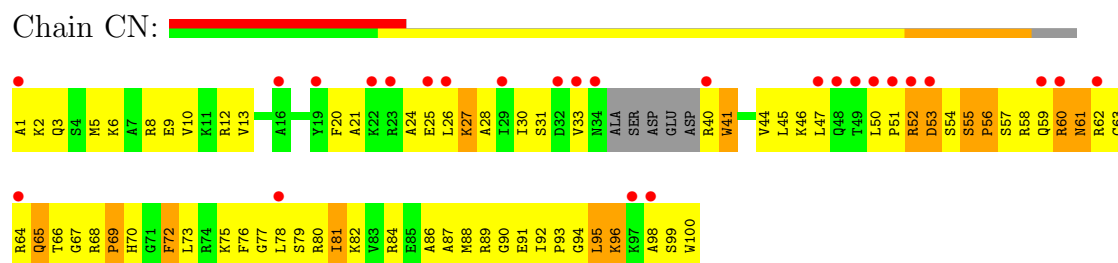
Chain CJ:



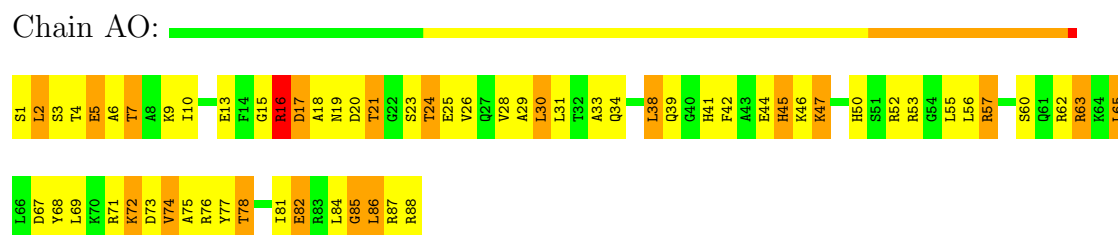
- Molecule 14: 30S ribosomal protein S14



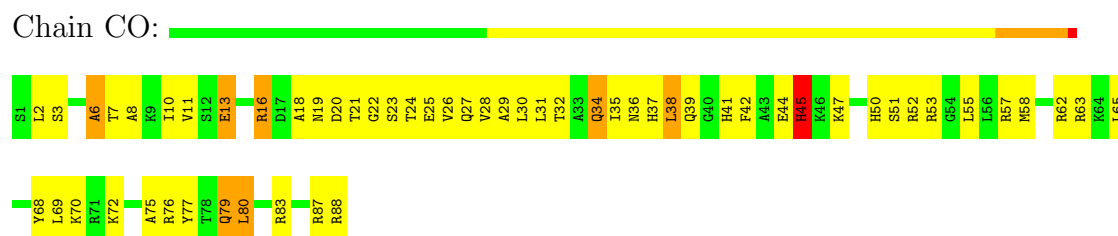
- Molecule 14: 30S ribosomal protein S14



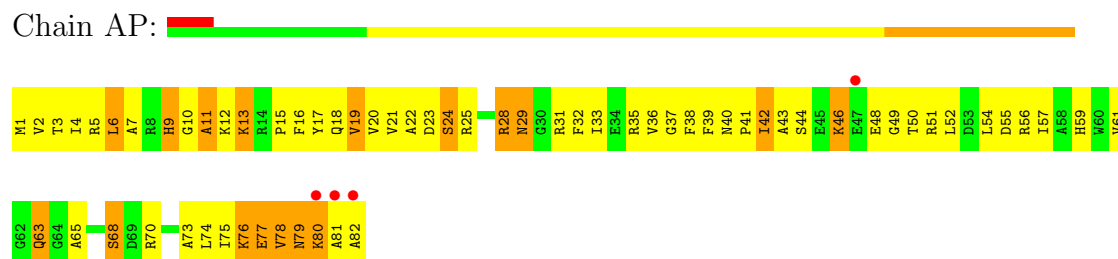
- Molecule 15: 30S ribosomal protein S15



- Molecule 15: 30S ribosomal protein S15

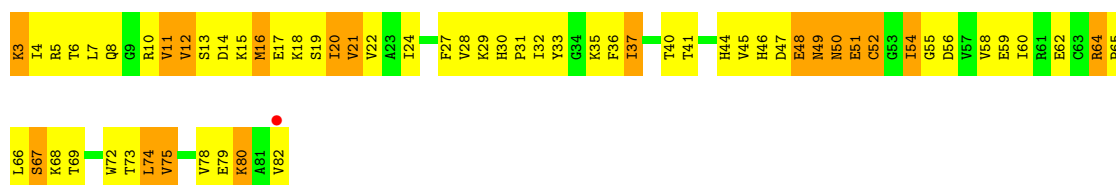


- Molecule 16: 30S ribosomal protein S16



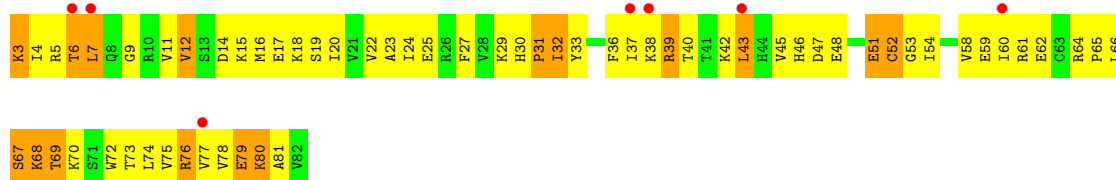
- Molecule 17: 30S ribosomal protein S17





- Molecule 17: 30S ribosomal protein S17

Chain CQ:



- Molecule 18: 30S ribosomal protein S18

Chain AR:



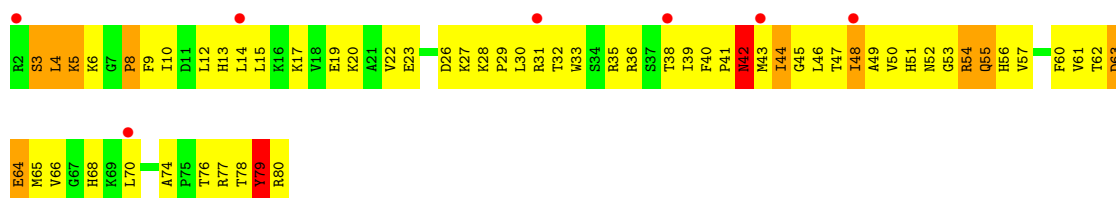
- Molecule 18: 30S ribosomal protein S18

Chain CR:



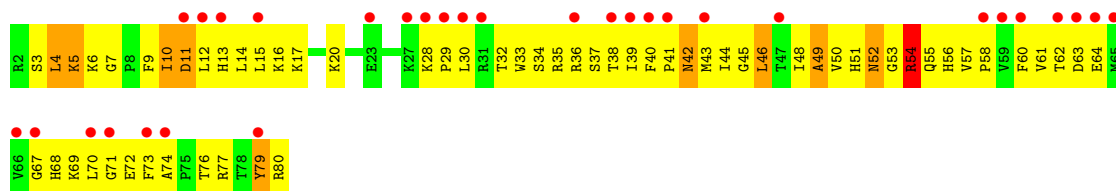
- Molecule 19: 30S ribosomal protein S19

Chain AS:



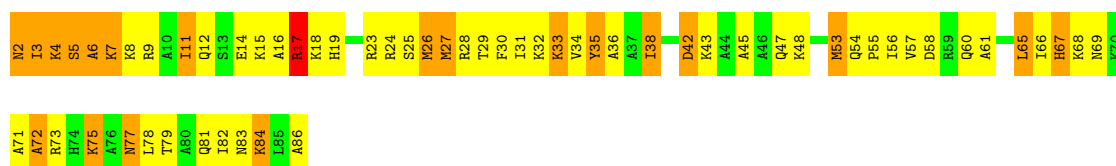
- Molecule 19: 30S ribosomal protein S19

Chain CS:



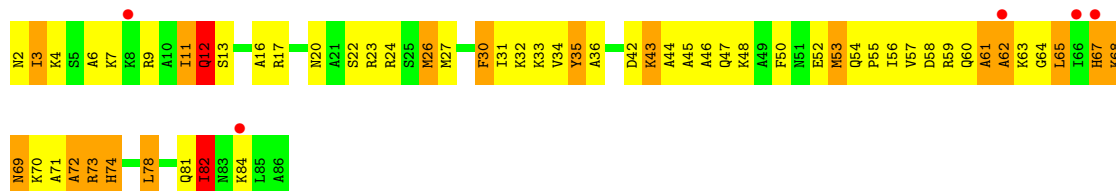
- Molecule 20: 30S ribosomal protein S20

Chain AT:



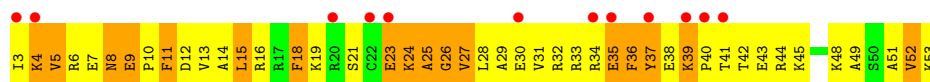
• Molecule 20: 30S ribosomal protein S20

Chain CT:



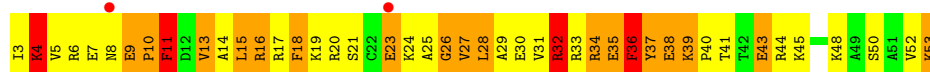
• Molecule 21: 30S ribosomal protein S21

Chain AU:



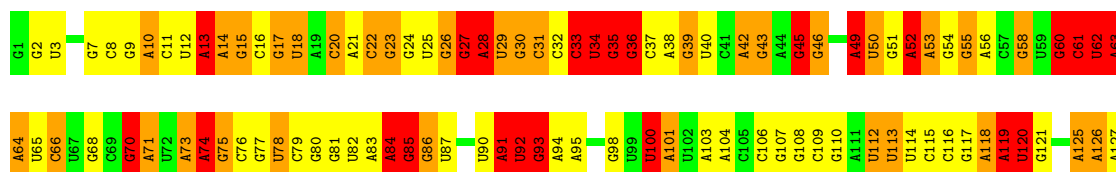
• Molecule 21: 30S ribosomal protein S21

Chain CU:



• Molecule 22: 23S rRNA

Chain BA:



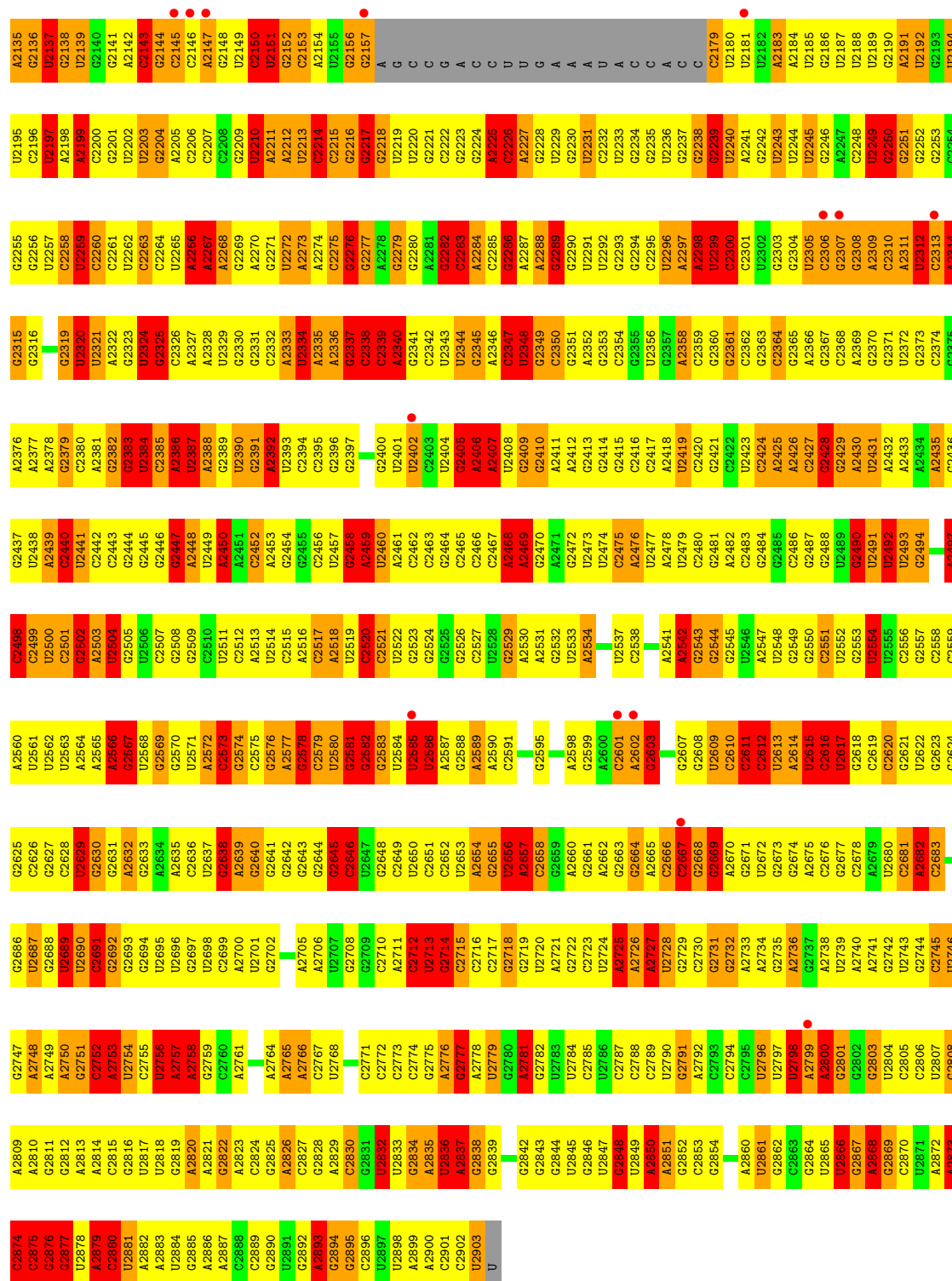
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U1203	A1204	A1205	G1206	C1207	A1208	G1209	G1210	G1211	G1212	G1213	G1214	G1215	G1216	G1217	G1218	G1219	G1220	C1221	C1222	C1223	G1224	A1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266																																																																																																																										
G1079	A1080	C1081	U1082	U1083	A1084	A1085	A1086	G1087	A1088	A1089	A1090	G1091	C1092	G1093	A1094	A1095	A1096	U1097	A1098	G1099	C1100	U1101	C1102	A1103	C1104	U1105	A1106	G1107	U1108	C1109	G1110	A1111	C1112	U1113	C1114	G1115	C1116	C1117	C1118	U1119	G1120	C1121	G1122	C1123	G1124	G1125	A1126	A1127	C1128	A1129	U1130	C1131	U1132	A1133	U1134	C1135	U1136	C1137	G1138																																																																																																																														
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U1203	A1204	A1205	G1206	C1207	A1208	G1209	G1210	G1211	G1212	G1213	G1214	G1215	G1216	G1217	G1218	G1219	G1220	C1221	C1222	C1223	G1224	A1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266																																																																																																																										
U1267	A1268	A1269	C1270	G1271	A1272	U1273	A1274	G1275	A1276	G1277	C1278	G1281	U1282	C1283	A1284	A1285	A1286	A1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	A1301	A1302	G1303	A1304	C1305	C1306	G1309	C1310	G1311	U1312	C1313	C1314	C1315	U1316	G1317	U1318	C1319	C1320	C1321	A1322	C1323	G1324	C1325	A1326	U1327	U1328	U1329																																																																																																																															
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A825	U826	U827	U828	C829	C830	C831	U832	C833	C834	C835	C836	C837	C838	C839	C840	C841	U842	C843	C844	C845	C846	U847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948																																																														
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C1013	A1014	U1015	G1016	C1017	U1018	U1019	A1020	C1021	G1022	U1023	C1024	G1025	C1026	A1027	A1028	A1029	A1030	C1031	C1032	C1033	C1034	A1035	A1036	A1037	A1038	A1039	A1040	G1041	C1042	C1043	C1044	C1045	A1046	C1047	C1048	C1049	C1050	C1051	C1052	C1053	A1054	C1055	C1056	A1057	C1058	C1059	C1060	C1061	C1062	C1063	C1064	C1065	C1066	C1067	C1068	C1069	A1070	C1071	C1072	A1073	C1074	C1075	C1076	A1077	U1078																																																																																																																								
C1079	A1080	C1081	U1082	U1083	A1084	A1085	A1086	G1087	A1088	A1089	A1090	G1091	C1092	G1093	A1094	A1095	A1096	U1097	A1098	G1099	C1100	U1101	C1102	A1103	C1104	U1105	A1106	G1107	U1108	C1109	G1110	A1111	C1112	U1113	C1114	G1115	C1116	C1117	C1118	U1119	G1120	C1121	G1122	C1123	G1124	G1125	A1126	A1127	C1128	A1129	U1130	C1131	U1132	A1133	U1134	C1135	U1136	C1137	G1138																																																																																																																														
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C2295	U1397	G1521	U1457	G1587	A1655	G1721	A1786	G1850	A1918	A1981		U	C2047	A2031	G2133	A2134	U2197	C2201	G2251	G2314	C2351
U2296	C1398	A1522	U1458	U1587	C1656	A1722	A1787	U1851	A1919	U1982	G2047	U	G2048	C2042	G2134	A2135	U2198	C2202	G2252	A2314	C2352
A2297	C1399	U1523	U1459	U1589	U1657	U1725	C1788	U1852	G1921	G1983	G2049	U	A2049	A2032	G2135	A2136	U2199	C2203	G2253	G2315	C2353
U2298	U1400	U1524	U1460	U1590	C1658	U1726	A1789	U1853	G1922	U1984	U2048	U	C2050	C2043	G2136	A2137	U2200	C2204	A2247	G2316	C2354
C2300	C1461	A1525	C1461	A1591	U1659	C1727	C1790	U1854	G1923	G1985	A2051	C	A2051	C2044	G2137	A2138	U2201	C2205	U2248	A2311	C2355
C2301	U1402	C1526	C1462	A1592	C1662	U1728	G1792	U1855	U1924	U1986	A2052	C	A2052	C2045	G2138	A2139	U2202	C2206	U2249	U2312	C2356
U2302	A1403	G1527	C1463	A1593	C1663	U1729	C1793	U1856	C1924	U1987	G2053	U	A2053	C2046	G2139	A2140	U2203	C2207	U2250	U2313	C2357
G2303	C1404		G1464	U1594	A1664	U1730	C1794	U1857	C1925	U1988	G2054	U	A2054	C2047	G2140	A2141	U2204	C2208	U2251	G2318	C2358
G2304	U1405	C1533	U1465	U1595	A1665	U1731	C1795	U1858	U1926	U1989	G2055	G	A2055	C2048	G2141	A2142	U2205	C2209	G2254	A2319	C2359
U2305	U1406	U1534	U1466	U1600	C1666	U1732	C1796	U1859	A1927	U1990	G2056	G	A2056	C2049	G2142	A2143	U2206	C2210	U2243	G2320	C2360
C2306	G1407	U1535	U1467	U1602	C1667	U1733	C1797	U1860	U1928	U1991	G2057	U	A2057	C2050	G2143	A2144	U2207	C2211	U2244	U2321	C2361
C2307	U1408	A1536	U1468	U1603	A1668	G1734	U1798	U1864	G1929	U1993		U		C2051	G2144	A2145	U2208	C2212	U2245	U2322	C2362
G2308	U1409	C1537	U1469	A1604	C1670	A1735	G1799	U1865	U1930	U1994	A2060	G	A2060	C2052	G2145	A2146	U2209	C2213	U2246	U2323	C2363
A2309	U1410	U1538	A1470	U1605	C1671	U1736	C1800	U1866	U1931	U1995	G2061	G	G2061	C2053	G2146	A2147	U2210	C2214	U2247	U2324	C2364
U2310	U1411	U1539	G1471	U1606	A1672	U1737	C1801	A1867	G1932	U1996	A2062	G	A2062	C2054	G2147	A2148	U2211	C2215	A2248	U2325	C2365
A2311	U1412	U1540	C1472	C1606	A1673	G1738	A1802	C1868	U1933	G1997	G2063	G	G2063	C2055	G2148	A2149	U2212	C2216	U2249	U2326	C2366
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C2313	C1414	C1541	U1474	A1608	G1675	G1740	C1807	C1870	U1935	U1999	C2065	C	C2065	C2057	G2150	A2151	U2214	C2218	U2251	U2328	C2368
A2314	U1415	U1542	U1475	A1609	A1676	G1741	U1808	A1871	A1936	U2000	C2066	U	C2066	C2058	G2151	A2152	U2215	C2219	U2252	U2329	C2369
G2315	G1416	U1543	U1476	U1610	A1677	U1742	C1809	A1872	U1937	C2001	G2067	U	G2067	C2059	G2152	A2153	U2216	C2220	U2253	U2330	C2370
C2318	U1417	A1544	U1477	C1611	A1678	G1743	A1809	C1873	U1938	G2002	G2068	U	G2068	C2060	G2153	A2154	U2217	C2221	U2254	U2331	C2371
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U2320	A1419	C1546	U1480	G1613	U1680	A1745	G1813	A1875	U1940	U2006	A2070		A2070	C2062	G2155	A2156	U2219	C2223	U2256	U2333	C2373
C2321	G1421	C1547	U1481	C1614	G1681	U1746	G1814	C1876	C1941	U2007	C2071		C2071	C2063	G2156	A2157	U2220	C2224	U2257	U2334	C2374
U2322	G1422	U1548	U1482	C1615	G1682	U1747	G1815	A1877	U1942	U2008	C2072		C2072	C2064	G2157	A2158	U2221	C2225	U2258	U2335	C2375
C2326	G1423		U1485	U1553	U1683	U1748	C1816	C1878	U1943	U2009				C2065	G2158	A2159	U2222	C2226	U2259	U2336	C2376
A2327	U1424	U1554	U1486	U1554	U1687	U1749	C1817	C1879	G1945	U2011	U2075		U2075	C2066	G2159	A2160	U2223	C2227	U2260	U2337	C2377
U2328	G1425	C1555	U1487	U1555	U1688	G1756	C1818	C1882	G1946	G2012	A2076		A2076	C2067	G2160	A2161	U2224	C2228	U2261	U2338	C2378
C2329	U1426	U1556	U1488	G1556	U1689	A1755	C1819	C1883	U1947	U2013	A2077		A2077	C2068	G2161	A2162	U2225	C2229	U2262	U2339	C2379
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C2326	C1428	C1558	U1490	C1558	A1690	A1757	U1821	C1885	U1949	U2015	U2079		U2079	C2070	G2163	A2164	U2227	C2231	U2264	U2341	C2381
A2327	G1429	U1559	C1491	U1559	A1691	A1758	U1822	U1886	U1950	U2016	A2080		A2080	C2071	G2164	A2165	U2228	C2232	U2265	U2342	C2382
U2332	U1430	C1560	G1492	U1560	U1692	A1759	C1823	U1887	U1951	U2017	U2076		U2076	C2072	G2165	A2166	U2229	C2233	U2266	U2343	C2383
C2330	A1431	C1561	C1493	C1561	U1693	U1758	G1824	C1888	U1952	U2018	A2082		A2082	C2073	G2166	A2167	U2230	C2234	U2267	U2344	C2384
G2331	G1432	U1562	A1494	U1562	C1694	A1759	U1825	U1890	U1953	U2019	G2083		G2083	C2074	G2167	A2168	U2231	C2235	U2268	U2345	C2385
C2332	A1433	U1563	A1495	U1563	G1695	C1760	U1826	A1890	U1954	U2020	U2084		U2084	C2075	G2168	A2169	U2232	C2236	U2269	U2346	C2386
A2333	U1434	C1564	A1496	C1564	G1696	C1761	U1827	C1894	U1955	U2021	U2085		U2085	C2076	G2169	A2170	U2233	C2237	U2270	U2347	C2387
U2334	A1435	C1565	U1497	C1565	U1697	A1762	U1828	U1897	U1956	U2022	U2086		U2086	C2077	G2170	A2171	U2234	C2238	U2271	U2348	C2388
A2335	C1436	U1566	C1498	A1566	A1698	C1763	A1829	G1897	U1957	U2023	G2087		G2087	C2078	G2171	A2172	U2235	C2239	U2272	U2349	C2389
C2336	C1437	C1567	C1499	U1567	U1699	C1764	U1830	U1897	U1958	U2024	A2094		A2094	C2079	G2172	A2173	U2236	C2240	U2273	U2350	C2390
G2337	U1438	G1568	U1500	G1568	A1700	U1765	C1832	U1898	U1959	G2025	C2095		C2095	C2080	G2173	A2174	U2237	C2241	U2274	U2351	C2391
C2338	A1439	A1569	G1501	A1569	A1701	G1766	U1833	A1900	C1961	U1960	U2092		U2092	C2081	G2174	A2175	U2238	C2242	U2275	U2352	C2392
C2339	U1440	A1570	U1502	A1570	G1702	C1768	U1834	A1901	C1962	U1961	U2093		U2093	C2082	G2175	A2176	U2239	C2243	U2276	U2353	C2393
A2340	G1441	A1571	A1503	A1571	C1703	U1769	U1835	U1902	U1963	U1962	U2094		U2094	C2083	G2176	A2177	U2240	C2244	U2277	U2354	C2394
U2341	U1442	A1572	A1504	A1572	C1706		C1836	C1905	U1964	C1963	A2095		A2095	C2084	G2177	A2178	U2241	C2245	U2278	U2355	C2395
C2342	U1443	G1573	A1505	G1573	G1707	A1773	C1837	G1906	U1965	C1964	C2096		C2096	C2085	G2178	A2179	U2242	C2246	U2279	U2356	C2396
U2343	G1444	C1574	U1506	C1574	C1708	C1774	U1838	G1907	C1966	U1965	U2097		U2097	C2086	G2179	A2180	U2243	C2247	U2280	U2357	C2397
C2344	G1445	C1575	U1507	C1575	U1708	U1775	U1839	G1908	U1967	U1966	U2098		U2098	C2087	G2180	A2181	U2244	C2248	U2281	U2358	C2398
G2345	U1446	U1576	A1508	U1576	C1709	U1776	U1840	C1909	U1968	U1967	U2099		U2099	C2088	G2181	A2182	U2245	C2249	U2282	U2359	C2399
A2346	C1447	C1577	A1509	C1577	A1711	U1776	U1841	C1906	U1969	U1968	U2100		U2100	C2089	G2182	A2183	U2246	C2250	U2283	U2360	C2400
U2348	U1448	U1578	G1510	U1578	U1712	U1777	U1842	U1909	U1970	U1969	C2103		C2103	C2090	G2183	A2184	U2247	C2251	U2284	U2361	C2401
C2349	G1449	A1579	C1511	A1579	A1713	U1778	U1843	G1910	U1971	U1970	C2104		C2104	C2091	G2184	A2185	U2248	C2252	U2285	U2362	C2402
U2350	U1450	A1580	C1512	A1580	U1714	U1779	U1844	U1911	G1972	U1971	A2205		A2205	C2092	G2185	A2186	U2249	C2253	U2286	U2363	C2403
C2351	G1451	G1581	U1513	G1581	G1715	A1780	C1845	U1912	G1973	U1972	U2105		U2105	C2093	G2186	A2187	U2250	C2254	U2287	U2364	C2404
U2352	C1452	C1582	U1514	C1582	U1716	U1781	U1846	A1913	C1974	U1973	G2107		G2107	C2094	G2187	A2188	U2251	C2255	U2288	U2365	C2405
A1453	A1453	A1583	A1515	A1583	A1717	U1782	G1846	C1914	G1975	U1974				C2095	G2188	A2189	U2252	C2256	U2289	U2366	C2406
G1454	U1454	U1584	C1516	U1584	A1718	A1783	U1847	U1915	G1976	U1975	A2206		A2206	C2096	G2189	A2190	U2253	C2257	U2290	U2367	C2407
C1455	U1455	U1585	C1517	U1585	G1719	A1784	U1848	U1916	U1977	U1976	C2207		C2207	C2097	G2190	A2191	U2254	C2258	U2291	U2368	C2408
U1520	U1520	A1586		A1586	U1720	A1785	U1849	U1917	U1978	U1977	C2208		C2208	C2098	G2191	A2192	U2255	C2259	U2292	U2369	C2409



G1099	G1036	G376	G315	U82	C791	G729	A666	U606	U545	A482	A422	A362	C302
C1100	U101	G977	G916	C853	A792	A730	U667	U607	U546	A483	A423	G363	G303
U1101	A1040	G978	A917	C854	A793	C731	A668	A608	A547	C484	A424	C364	U304
C1102	G1041	A979	A918	G855	A794	C732	G669	A609	G548	C485	G425	U365	C305
A1103	G1042	A980	A919	G856	C795	G733	A670	C610	A549	C486	G426	C366	U306
C1104	C1043	A981	A920	G857	C796	A734	C671	C611	C550	C487	U427	G367	G307
U1105	C1044	C982	C921	G858	C797	A735	C672	G612	C551	G488	A428	A368	G308
G1106	C1045	A983	C922	G859	C798	C736	C673	A613	U552	C489	A429	U369	A309
U1107	A1046	A984	G923	U860	C674	C737	A675	A614	G553	C490	A430	G370	A310
A1108	G1047	C985	G924	U861	A676	A738	A675	U615	U554	A491	U431	A371	A311
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G1110	C1049	C987	G926	A863	A678	C740	C677	G617	U558	G493	C433	U373	G313
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G1112	G1051	C989	A928	C865	A680	A742	C679	G619	G560	A497	C435	C375	G315
U1113	C1052	A990	U929	A866	C681	A743	C680	G620	C561	U498	C436	G376	C316
C1114	C1053	C991	G930	C867	U744	U744	G682	A621	G562	U499	U437	G377	G317
G1115	A1054	C992	U931	U868	C745	G745	G683	G622	U563	G500	G438	C378	C318
U1116	G1055	G993	U932	G869	C746	U746	U683	G623	A563	A439	A439	G379	G319
C1117	G1056	C994	A933	U870	U747	U747	G684	G624	C564	A501	C440	G380	A320
G1118	A1057	C995	U934	U871	U748	G748	A685	G625	C565	A502	U441	C381	U321
U1119	U1058	A996	C935	U872	C749	A749	U686	A626	U566	A503	G442	A322	G327
G1120	G1059	C997	A936	U873	A750	A750	C687	A627	U567	A504	A443	A323	U328
C1121	U1060	C998	C937	G874	A751	A751	U688	G628	U568	A505	A444	A324	A384
U1122	G1061	U999	G938	G875	A752	A752	A689	G629	U569	A506	C445	G325	G385
C1123	G1062	A1000	G939	C876	A753	A753	G690	G630	G570	A507	G446	G326	G386
G1124	G1063	A1001	G940	A877	U754	U754	C691	A631	U571	A508	A447	G327	U387
G1125	C1064	G1002	A941	A878	U755	U755	C692	A632	U572	C509	U448	A328	G388
U1126	U1065	G1003	G942	G	A756	A756	A693	A633	U573	C510	A449	G329	G389
C1127	U1066	U1004	A943	G	C757	G757	U694	C634	A574	U511	G450	A330	U390
G1128	A1067	C1005	C944	G	C758	C758	G695	C635	A575	U512	U451	A331	A391
U1129	G1068	C1006	A945	G	G759	G759	U696	G636	U576	A513	G452	A332	U392
G1130	A1069	C1007	C946	U	G760	G760	A699	A637	U577	A514	A453	C333	C393
C1131	U1070	A1008	A947	U	A761	A761	G700	A638	G578	A515	A454	C334	C394
U1132	G1071	C1009	C948	C	U762	U762	G701	U639	G579	C516	C455	C335	U395
A1133	C1072	A1010	G949	A	G763	G763	U702	C940	U580	C517	C456	C336	G396
G1135	A1073	G1011	G950	U	A764	A764	U703	U641	C581	G518	A457	C337	U397
C1136	G1074	U1012	C951	C	G765	G765	G704	U642	A582	U519	G458	C338	G398
U1137	C1075	C1013	G952	C	U766	U766	A705	A643	G583	U520	U459	U339	U399
G1138	A1077	U1015	G953	C	G770	G770	U706	A644	C584	C523	A460	A340	A400
U1139	U1078	G1016	G954	G	C771	C771	G707	C945	G585	G524	C461	A341	A401
C1200	C1079	C1017	U955	A	U772	U772	G708	U646	A586	U525	C462	A342	A402
U1201	G1080	U1018	C956	C	C773	C773	U709	G647	C587	A526	G463	C343	U403
G1202	U1081	U1019	C957	U	U774	U774	G711	G648	U588	G527	U464	A344	A404
U1203	U1082	A1020	U958	A	G775	G775	G712	C649	U589	A528	G465	A345	U405
A1204	U1083	A1021	A959	C	G776	G776	G713	C650	A590	A529	A466	A346	A406
G1206	A1084	G1022	C961	C898	U777	U777	G714	G651	U591	G530	G467	A347	G407
C1207	A1085	U1023	G962	A899	G778	G778	U715	U652	A592	C531	G468	A348	G408
G1208	A1086	G1024	U963	C840	U779	U779	A716	U653	U593	A532	G469	U349	G409
U1209	G1087	G1025	C964	C841	G780	G780	C717	A654	U594	G533	A470	G350	G410
G1210	A1088	G1026	C965	C902	U781	U781	U718	A655	C595	U534	A471	C351	G411
C1211	U1089	A1027	G966	C903	A782	A782	C719	G656	U596	G535	A472	A352	A412
G1212	A1090	A1028	G967	G904	G783	G783	U720	U657	G597	G536	G473	C353	C413
A1213	C1091	A1029	U970	U909	A784	A784	A721	U658	U598	G537	C474	A354	C414
G1214	C1092	G1030	G971	A910	G785	G785	U724	C660	A599	A538	C475	U355	A415
C1215	G1093	G1031	G972	A911	U847	U847	G725	G661	G601	G539	G476	G356	U416
G1216	U1094	A1032	A973	G912	C848	C848	G726	A661	A602	C540	A477	C357	C417
U1217	U1097	G1033	G974	U913	A849	A849	G727	G663	A603	G542	A478	U358	C418
G1218	U1098	U1035	A975	G914	U850	U850	G728	U665	G604	G543	A479	U359	U419
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U2076	U2016	G1954	A1890	G1828	G1768	C1708	U1648	G1588	C1526	G1465	A1403	A1341	G1281	G1221
A2077	U2017	U1955	A1899	A1829	U1769	U1709	G1649	U1589	G1527	U1466	U1404	G1343	U1282	U1222
C2078	G2018	U1956	C1893	G1830	G1770	G1710	A1650	A1590	A1528	U1467	U1405	G1344	G1283	G1223
U2079	A2019	C1957	C1894	G1831	C1771	A1711	G1651	A1591	G1529	U1468		G1345	A1285	U1224
A2080	A2020	C1958	C1895	G1832	A1772	U1712	A1652	A1592	G1530	U1469	G1408	G1346	U1284	G1225
U2081	C2021	G1959	G1896	C1833	A1773	A1713	G1653	A1593	C1531	A1470		A1347	A1286	A1226
A2082	U2022	A1960		U1834	C1774	U1714	A1654	U1594	A1532	G1471	U1411	C1348	A1287	G1227
C2023	C2023	G1961	A1899	G1835	C1775	G1715	A1655	U1595	C1533	G1472	U1412	C1349	A1288	G1228
G2024	G2024	C1962	A1900	G1836	C1776	U1716	G1656	A1596	G1534	G1473	A1413	G1350	C1289	C1229
C2025	C2025	U1963	A1901	C1837	G1777	A1717	U1657	A1597	A1535	U1474	A1414	G1351	C1290	A1230
U2086	U2026	G1964	G1902	G1838	U1778	G1718	C1658	A1598	G1536	U1475	U1415	G1352	G1291	U1231
G2027	G2027	G1965	G1903	C1839	U1779	G1719	G1659	U1599	G1537	U1476	U1416	A1353	G1292	G1232
A2088	U2028	A1966	G1904	G1840	A1780	U1720	G1660	G1600	G1538	A1477	C1417	A1354	C1293	G1233
C2089	G2029	C1967	G1905	U1841	U1781	U1721	G1661	G1601	U1539	G1478	U1418	G1355	U1294	U1234
A2090	A2030	G1968	G1906	U1842	U1782	A1722	A1662	U1602	G1540	G1479	A1419	G1356	C1295	U1235
C2091	A2031	A1969	G1907	A1843	A1783	G1723	G1663	A1603	C1541	G1480	A1421	C1357	G1296	G1236
G2092	G2032	U1970	G1910	C1844	A1784	G1724	A1664	C1604	C1542	U1481	G1422	G1358	C1297	A1237
C2093	A2033	U1971	G1911	G1845	A1785	U1725	A1665	G1605	G1543	G1482	G1423	A1359	C1298	G1238
A2094	U2034	G1972	U1912	G1846	A1786	C1726	G1666	A1544	A1545	G1483	G1424	G1360	C1299	G1239
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U2098	C2037	U1975	G1914	G1849	A1789	U1729	A1669	A1609						
U2099	U2038	U1976	U1915	G1850	C1790	C1730	C1670	A1610	A1549	A1427	A1427	G1364	G1303	C1243
G2100	G2040	A1978	U1917		G1792	C1732	U1671	C1611	C1550	A1428		A1365	A1304	C1244
A2101	U2041	U1979	A1884		G1793	C1733	A1672	C1612	A1551	A1429		A1366	C1305	G1245
G2102	A2042	U1985	U1885	G1861	C1794	G1734	G1673	G1613	A1552	G1430		A1367	C1306	U1246
C2103	G2043	U1986	A1886	G1862	A1794	G1735	G1674	A1614	A1553	G1431	G1374	A1367	A1307	A1247
C2104	C2044	U1987	C1920	G1863	C1795	C1736	C1675	C1615	C1554	G1432	G1375	A1368	A1308	G1248
U2105	C2045	U1988	G1921	G1864	U1796	U1736	A1676	G1616	G1555	A1494	A1433	G1377	G1309	U1249
G2106	G2046	G1989	U1916	G1865	G1797	U1737	A1677	C1566	C1557	A1495	A1434	U1372	G1310	G1250
U2107	U2047	C1995	G1925	G1866	U1798	G1738	A1678	C1567	A1496	U1497	G1435	U1373	G1311	C1251
A2108	G2048	U1986	U1926	G1867	G1799	A1739	A1679	C1568	C1558	U1498	G1436	G1374	U1312	G1252
U2109	G2049	A1987	G1927	G1868	C1800	G1740	U1680	G1620	U1559	C1498	U1437	C1375	A1253	A1254
G2110	C2050	U1988	A1928	U1864	A1802	U1742	G1682	G1622	C1561	G1500	U1438	G1376	A1254	
U	A2051	G1989	G1929	U1865	A1803	G1743	G1683	G1623	U1562	G1501	U1440	A1378		G1255
G	A2052	C1990	G1930	A1866	C1804	A1744	G1684	U1624	U1563	A1502	G1441	U1379	G1317	U1257
U	G2053	U1991	U1931	G1867	A1805	A1745	G1685	C1625	A1564	A1503	U1442	G1380	C1319	U1258
A	A2054	U1992	A1932	C1868	C1806	A1746	G1686	A1626	C1565	A1504	U1443	G1381	G1320	U1259
G	G2055	U1993	G1933	G1869	G1807	U1747	G1687	G1627	A1566	A1505	G1444	G1382	A1321	G1260
G	G2056	C1994	C1934	C1870	A1808	C1748	U1688	G1628	G1567	U1506	G1445	A1383	G1322	C1261
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U	A2058	C1996	A1936	A1872	A1810	G1750	A1690	A1630	A1569	A1508	C1447	A1385	G1324	U1263
A	A2059	C1997	A1937	G1873	G1811	U1751	C1691	G1631	A1570	A1509	G1448	C1386	U1325	A1264
G	A2060	A1998	A1938	C1874	U1812	C1752	U1692	A1632	A1571	G1510	G1449	A1387	U1326	A1265
G	G2061	C1999	U1939	G1875	U1813	G1753	U1693	G1633	A1572	G1511	G1450	A1387	A1327	G1266
U	A2062	C2000	U1940	A1876	G1814	A1754	G1694	A1634	G1573	C1512	C1451	G1388	A1328	U1267
G	C2063	C2001	C1941	A1877	A1815	A1755	G1695	A1635	C1574	U1513	G1452	G1389	U1329	A1268
G	C2064	G2002	U1942	G1878	C1816	G1756	G1696	U1636	C1575	G1514	A1453	U1391	C1330	A1269
G	C2065		U1943	C1879	G1817	A1757	G1697	A1637	U1576	A1515	C1454	A1392	G1331	C1270
A	C2066		U1944	U1880	U1818	U1758	U1698	A1638	C1577	G1516	G1455	A1393	G1332	G1271
G	G2067	U2007	A1945	C1881	A1819	A1759	G1699	C1639	U1578	G1517	G1456	U1394	G1333	A1272
G	U2068	C2008	U1946	U1882	U1820	C1760	A1640	C1618		G1518	U1457	A1395	G1334	U1273
C	G2069	A2009	G1947	U1883	A1821	C1761	A1701	A1641	G1581	U1519	U1458	U1396	C1335	A1274
U	A2070	G2010	G1948	G1884	C1822	A1762	G1702	C1582	G1520	G1459	G1459	A1336	C1336	A1275
U	A2071	U2011	G1949	A1885	G1823	G1763	G1703	G1643	G1521	G1460	U1460	C1397	G1337	A1276
U	G2072	G2012	U1950	U1886	G1824	C1764	C1704	C1644	A1522	C1461	G1338	C1399	G1338	G1277
C2073	C2073	A2013	U1951	U1886	U1825	U1765	G1705	C1645	U1523	U1400	G1339	U1400	G1339	G1278
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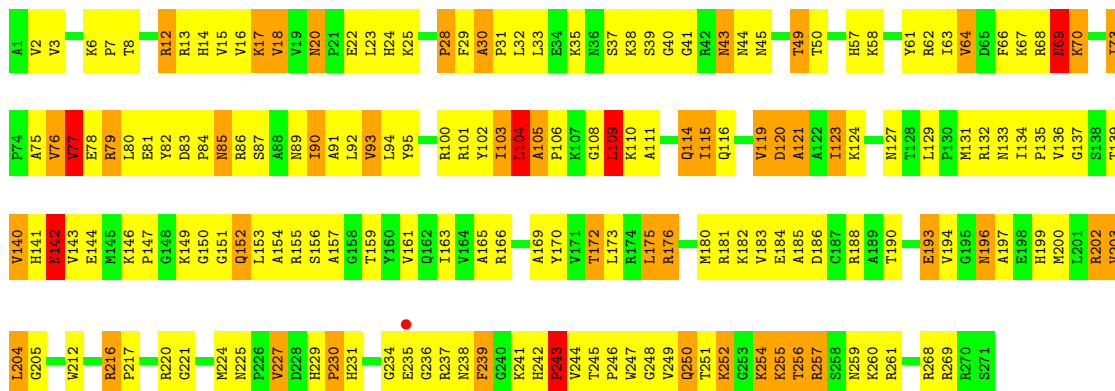


• Molecule 23: 5S rRNA

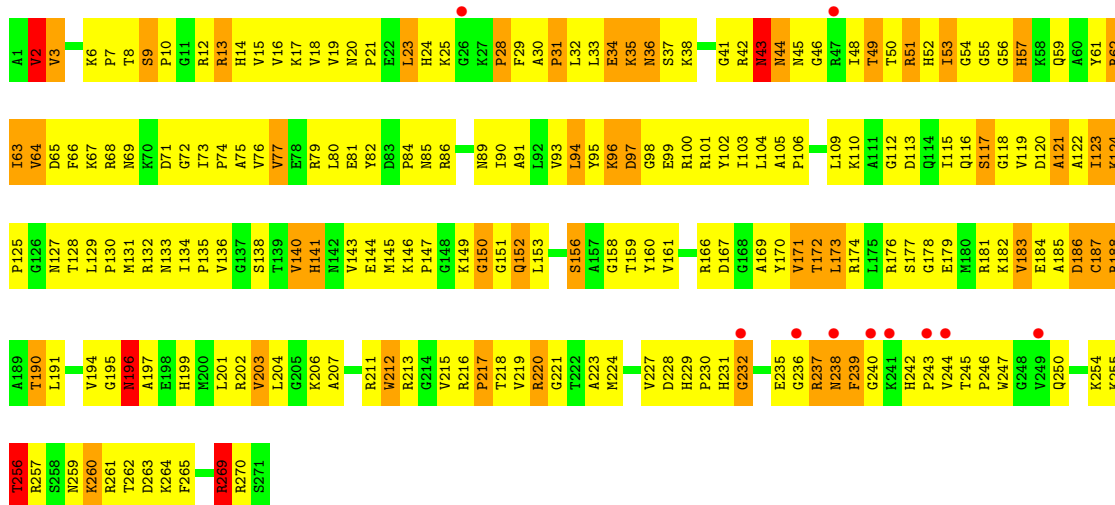
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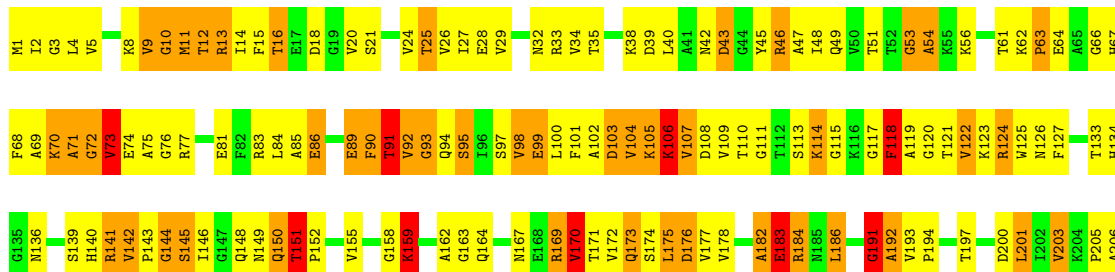
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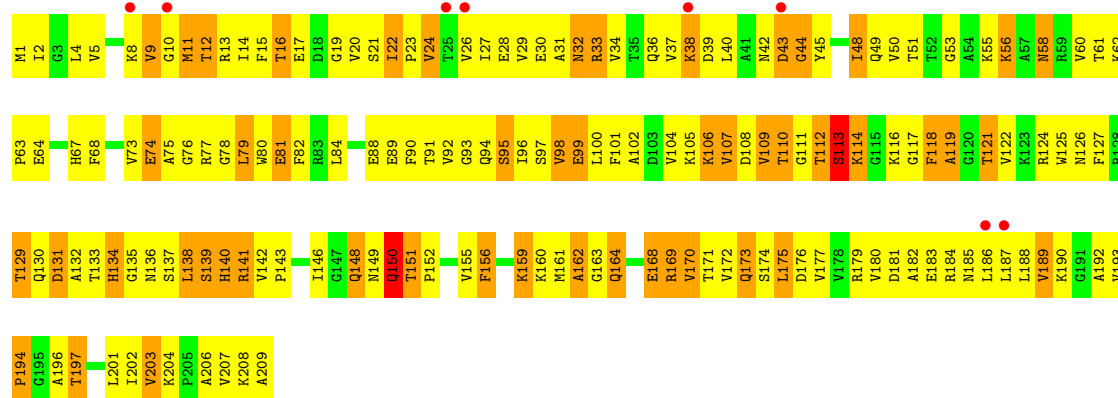
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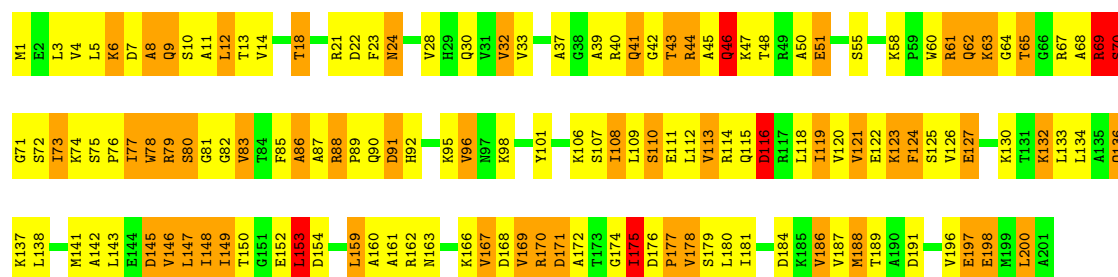
- Molecule 25: 50S ribosomal protein L3

Chain DD:



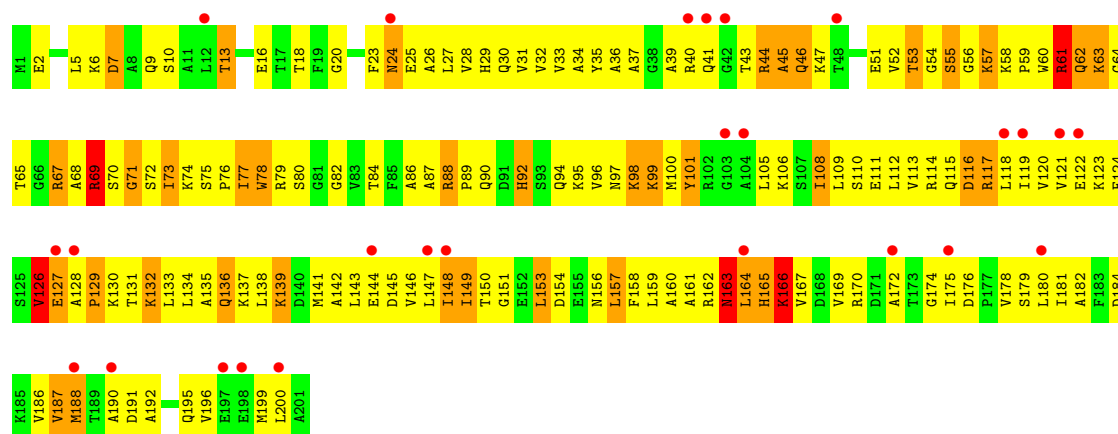
- Molecule 26: 50S ribosomal protein L4

Chain BE:



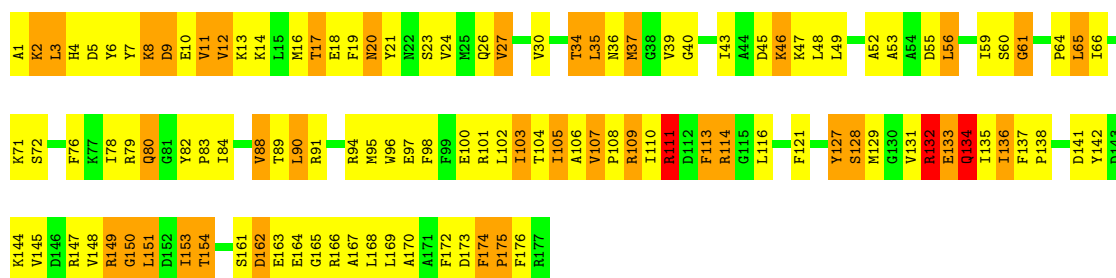
- Molecule 26: 50S ribosomal protein L4

Chain DE:



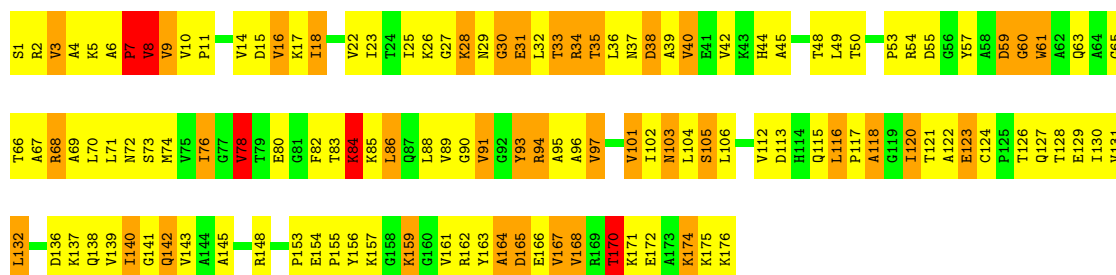
- Molecule 27: 50S ribosomal protein L5

Chain BF:



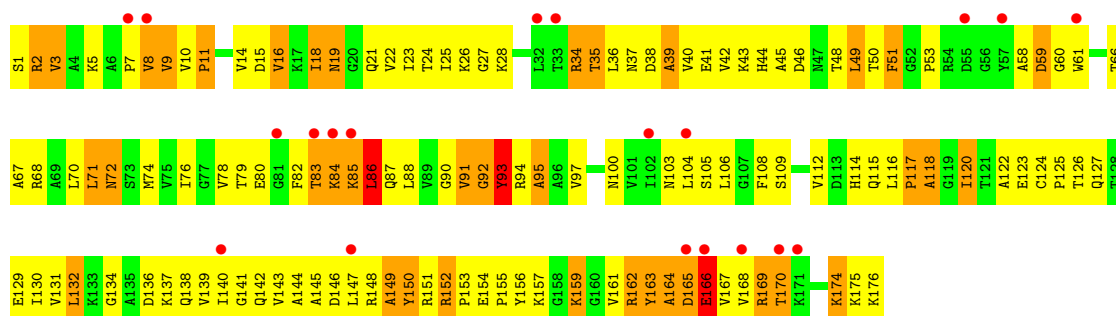
• Molecule 28: 50S ribosomal protein L6

Chain BG:



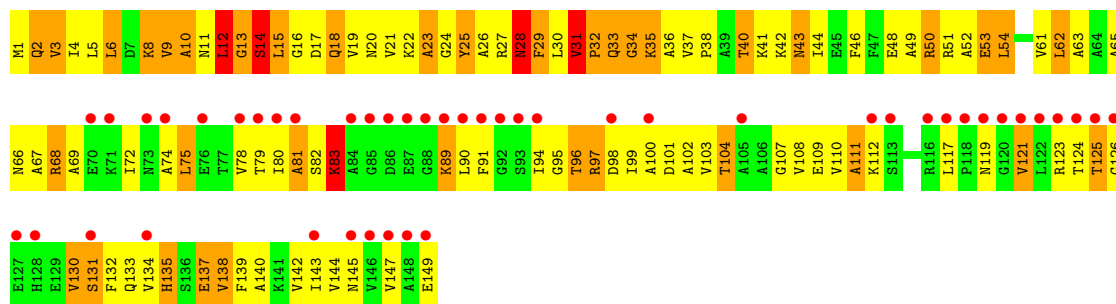
• Molecule 28: 50S ribosomal protein L6

Chain DG:



• Molecule 29: 50S ribosomal protein L9

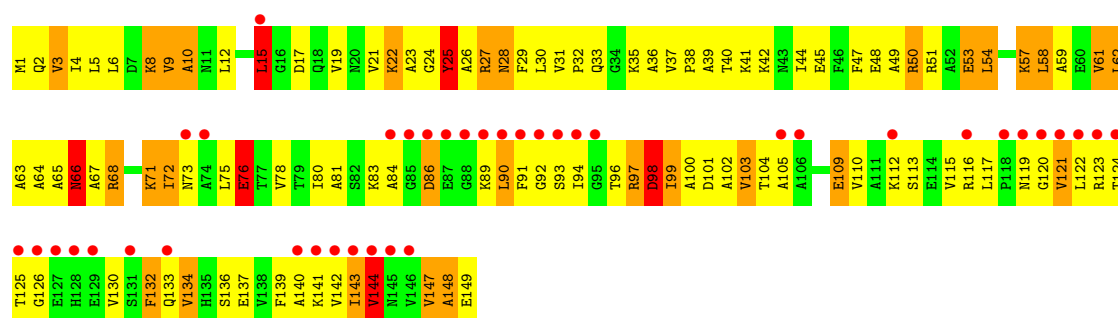
Chain BH:



• Molecule 29: 50S ribosomal protein L9

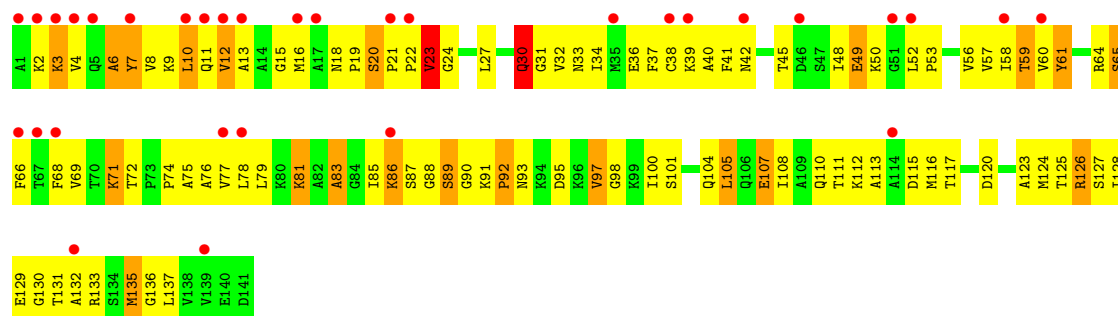
Chain DH:





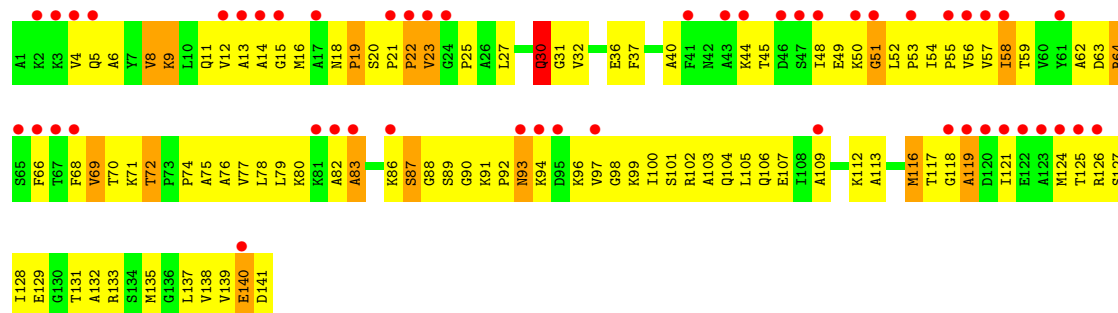
- Molecule 30: 50S ribosomal protein L11

Chain BI:



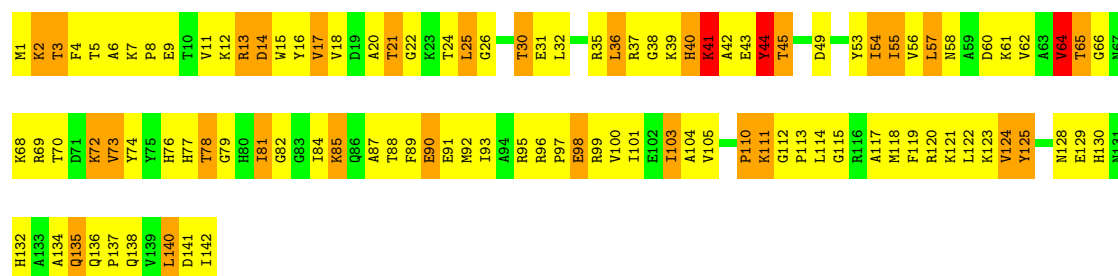
- Molecule 30: 50S ribosomal protein L11

Chain DI:



- Molecule 31: 50S ribosomal protein L13

Chain BJ:

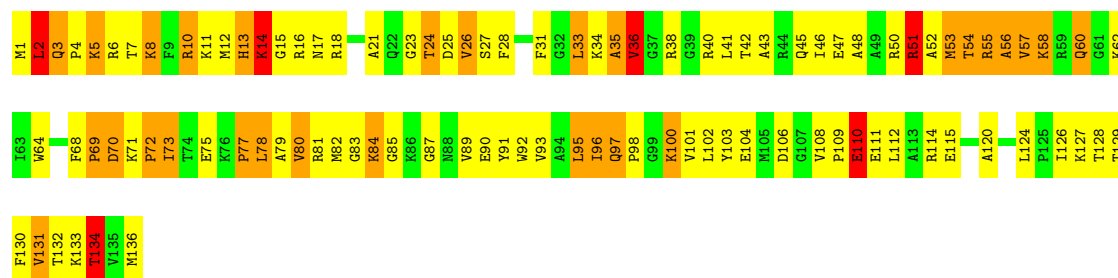


- Molecule 31: 50S ribosomal protein L13

Chain DJ:

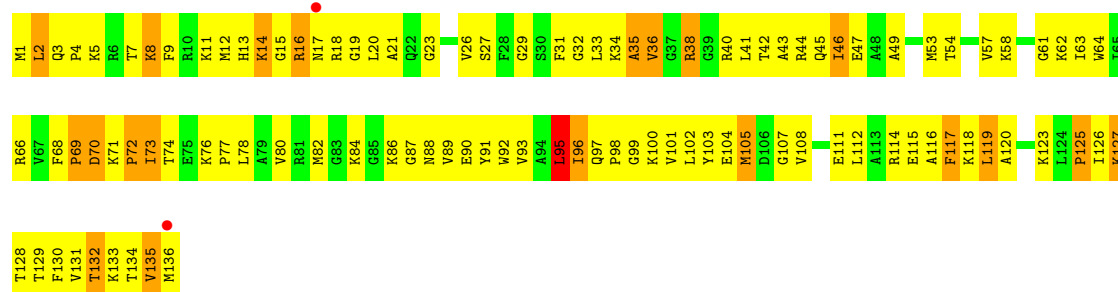
- Molecule 34: 50S ribosomal protein L16

Chain BM:



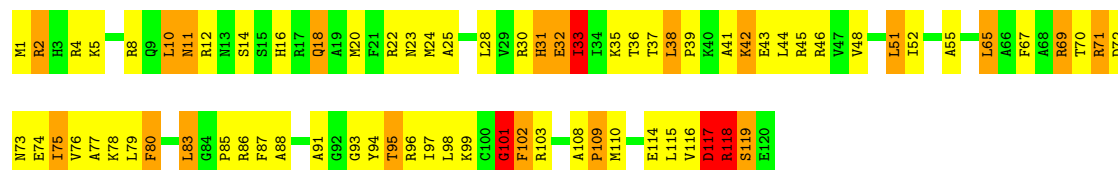
- Molecule 34: 50S ribosomal protein L16

Chain DM:



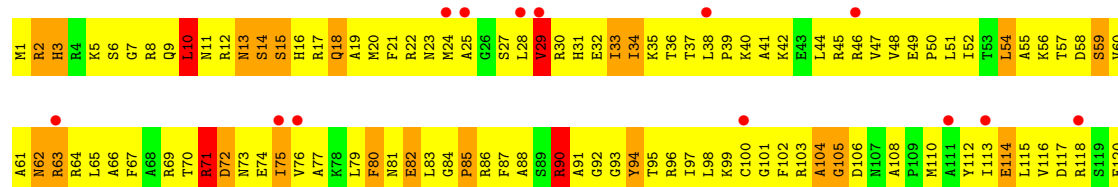
- Molecule 35: 50S ribosomal protein L17

Chain BN:



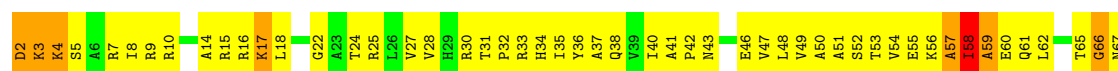
- Molecule 35: 50S ribosomal protein L17

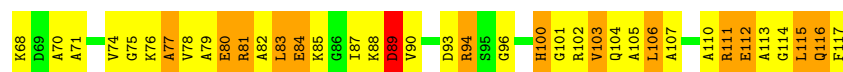
Chain DN:



- Molecule 36: 50S ribosomal protein L18

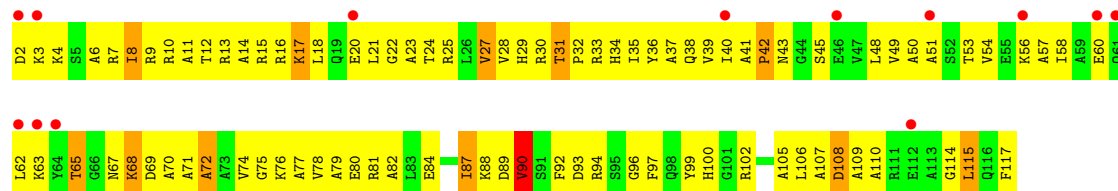
Chain BO:





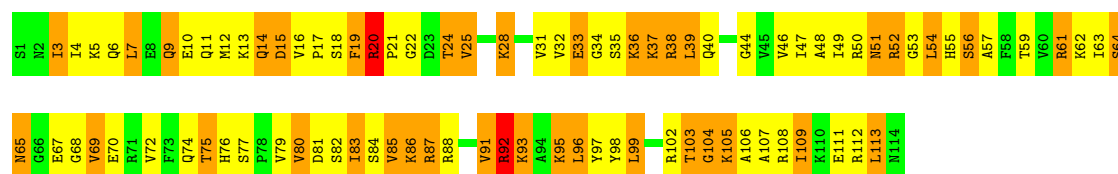
• Molecule 36: 50S ribosomal protein L18

Chain DO:



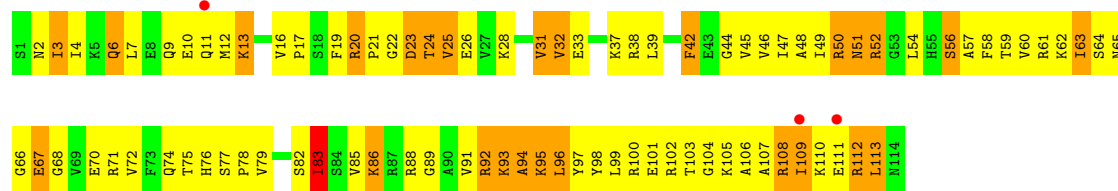
• Molecule 37: 50S ribosomal protein L19

Chain BP:



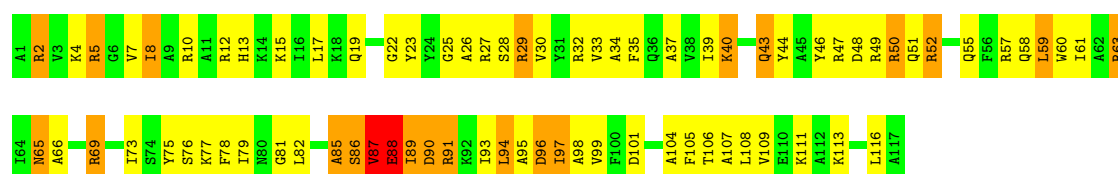
• Molecule 37: 50S ribosomal protein L19

Chain DP:



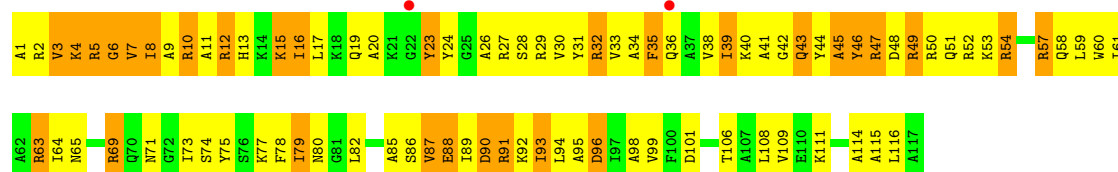
• Molecule 38: 50S ribosomal protein L20

Chain BQ:



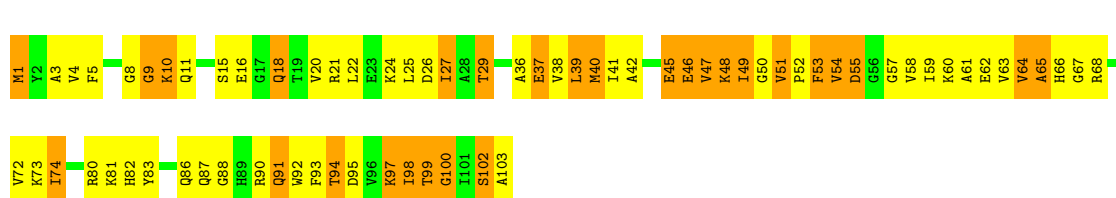
• Molecule 38: 50S ribosomal protein L20

Chain DQ:



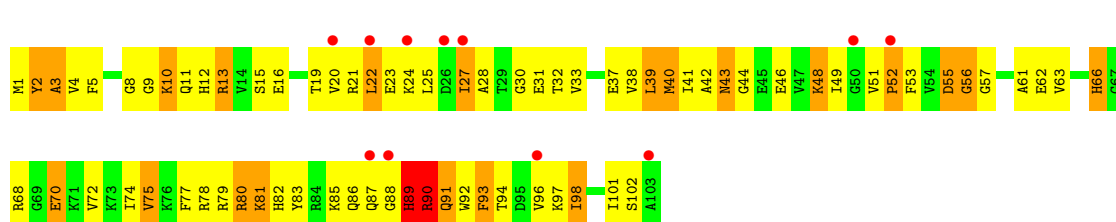
- Molecule 39: 50S ribosomal protein L21

Chain BR:



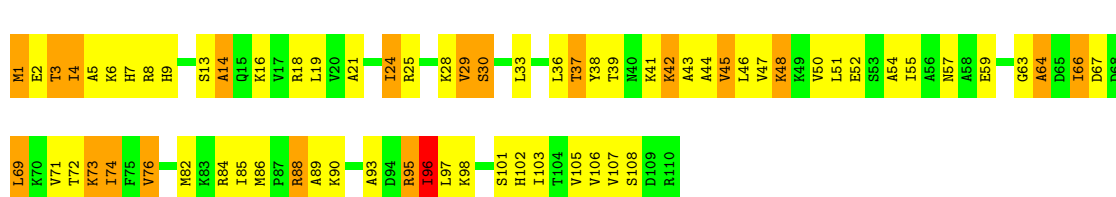
- Molecule 39: 50S ribosomal protein L21

Chain DR:



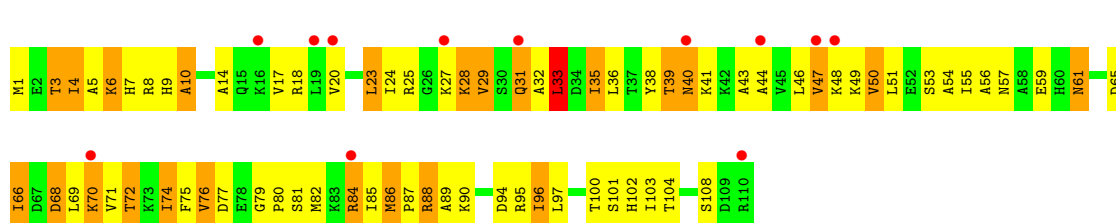
- Molecule 40: 50S ribosomal protein L22

Chain BS:



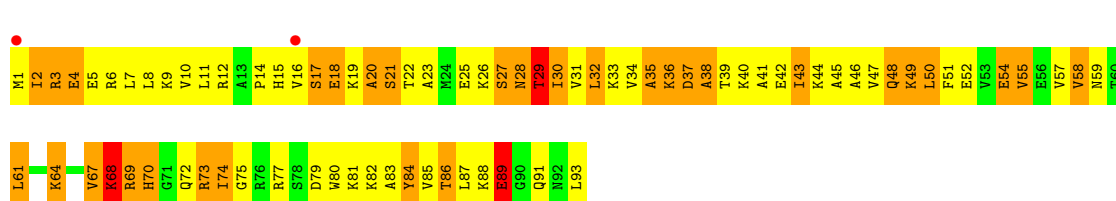
- Molecule 40: 50S ribosomal protein L22

Chain DS:



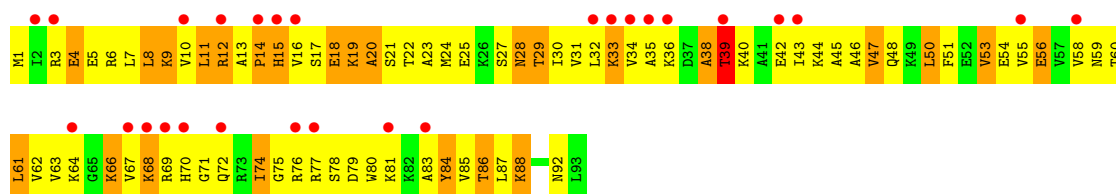
- Molecule 41: 50S ribosomal protein L23

Chain BT:



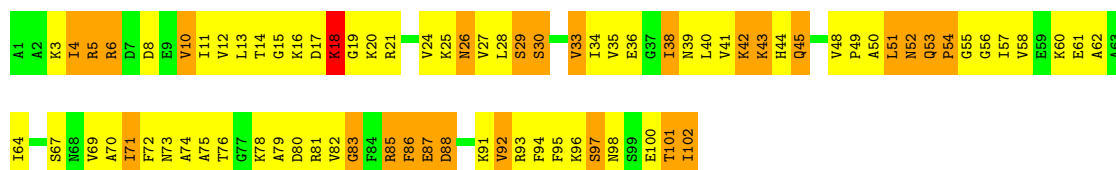
- Molecule 41: 50S ribosomal protein L23

Chain DT:



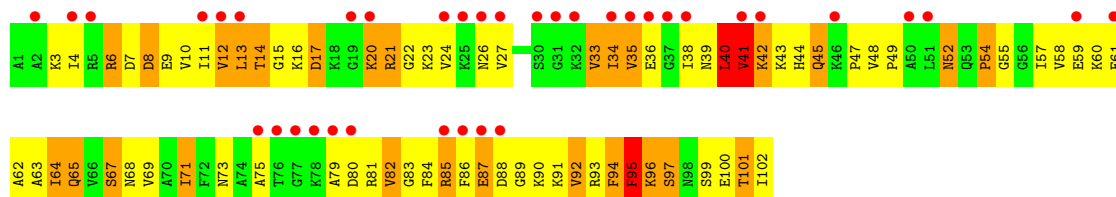
- Molecule 42: 50S ribosomal protein L24

Chain BU:



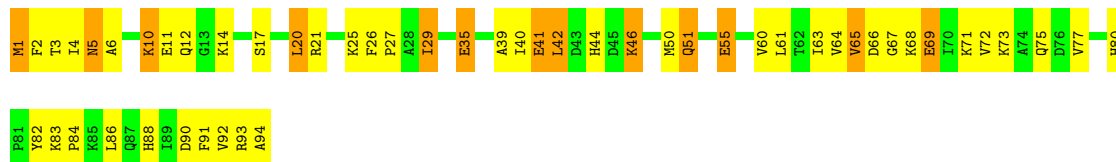
- Molecule 42: 50S ribosomal protein L24

Chain DU:



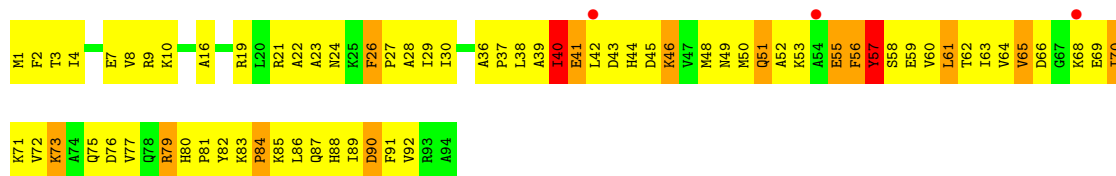
- Molecule 43: 50S ribosomal protein L25

Chain BV:



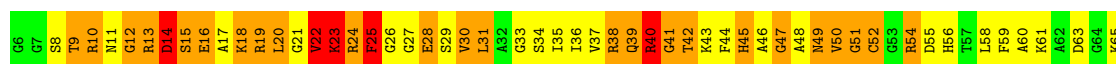
- Molecule 43: 50S ribosomal protein L25

Chain DV:



- Molecule 44: 50S ribosomal protein L27

Chain BW:





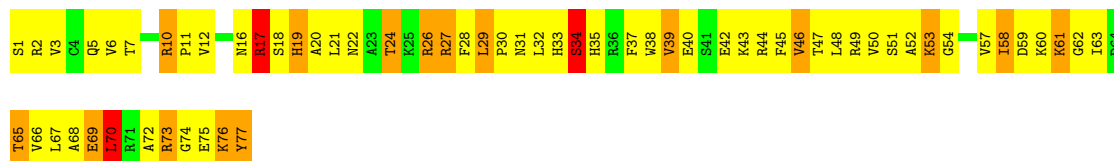
- Molecule 44: 50S ribosomal protein L27

Chain DW:



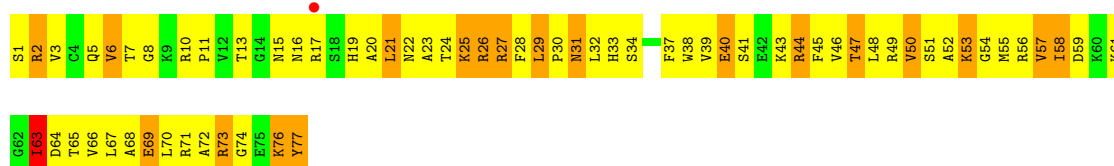
- Molecule 45: 50S ribosomal protein L28

Chain BX:



- Molecule 45: 50S ribosomal protein L28

Chain DX:



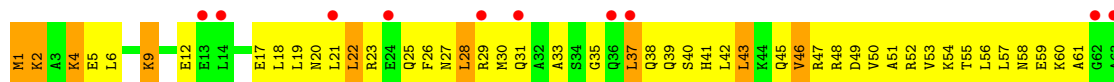
- Molecule 46: 50S ribosomal protein L29

Chain BY:



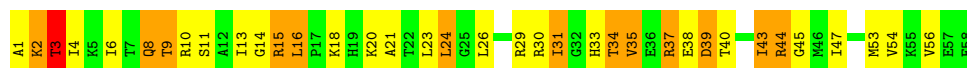
- Molecule 46: 50S ribosomal protein L29

Chain DY:



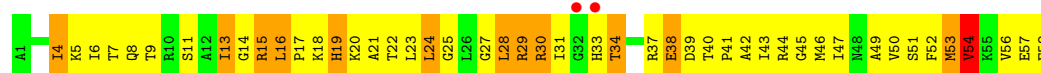
- Molecule 47: 50S ribosomal protein L30

Chain BZ:



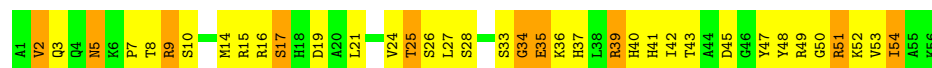
- Molecule 47: 50S ribosomal protein L30

Chain DZ: 



- Molecule 48: 50S ribosomal protein L32

Chain B0: 



- Molecule 48: 50S ribosomal protein L32

Chain D0: 



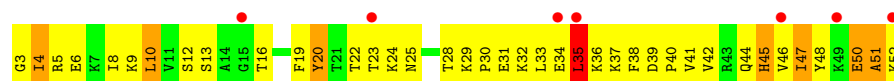
- Molecule 49: 50S ribosomal protein L33

Chain B1: 



- Molecule 49: 50S ribosomal protein L33

Chain D1: 



- Molecule 50: 50S ribosomal protein L34

Chain B2: 



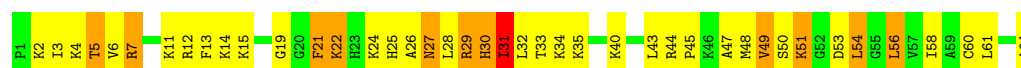
- Molecule 50: 50S ribosomal protein L34

Chain D2: 



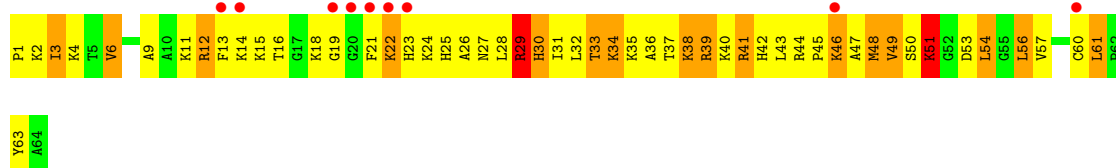
- Molecule 51: 50S ribosomal protein L35

Chain B3: 



- Molecule 51: 50S ribosomal protein L35

Chain D3: 



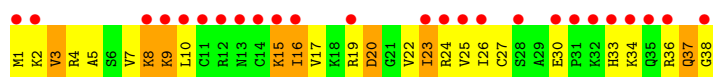
- Molecule 52: 50S ribosomal protein L36

Chain B4: 



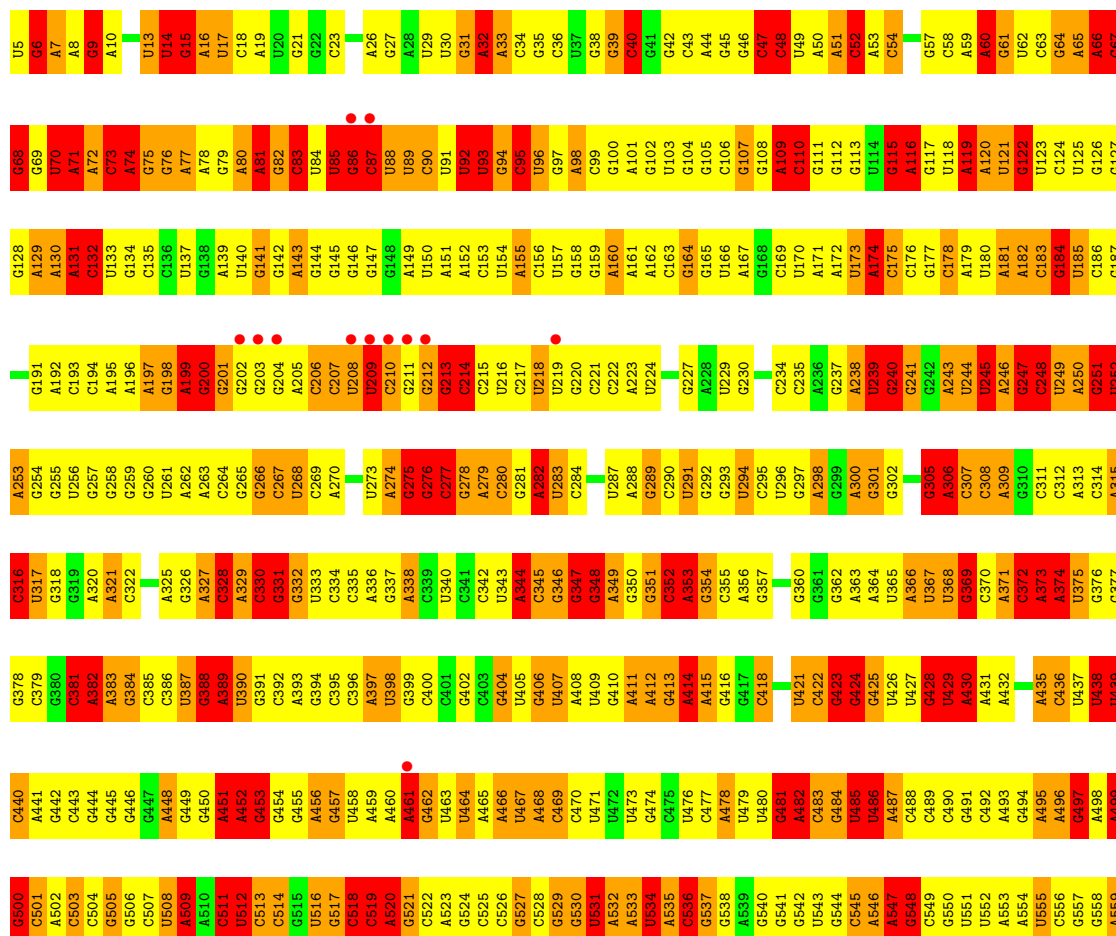
- Molecule 52: 50S ribosomal protein L36

Chain D4: 



- Molecule 53: 16S rRNA

Chain CA: 

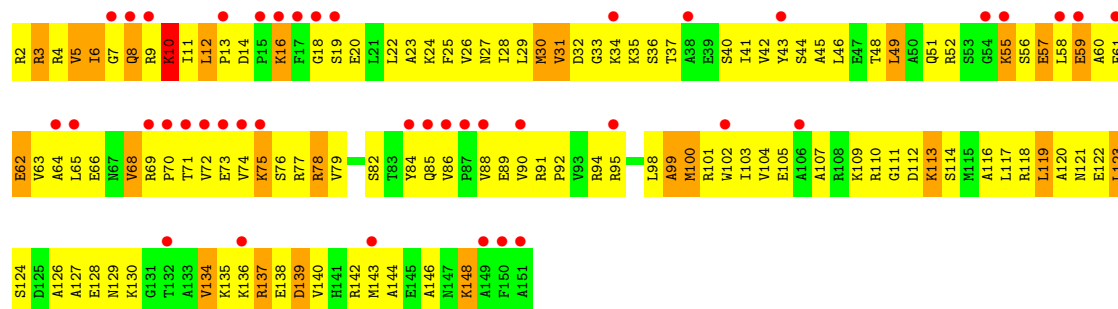


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A1437	A1374	U1313	A1252	A1191	A1130	C1069	A1005	U943	A878	U613	G752	G688	U651	U561
G1438	A1375	G1253	G1253	C1192	G1312	U1070	G1006	G944	C879	A814	A753	C689	U624	U562
G1439	U1376	U1315	A1254	G1193	U1332	C1071	U1007	G945	C880	A815	C754	C690	U625	A563
U1440	A1377	G1255	G1255	U1194	G1133	G1072	U1008	A946	G881	A816	G755	G691	C564	C564
A1441	C1378	C1317	A1256	C1195	G1134	U1073	U1009	G947	C882	C817	C756	U692	U565	U565
A1442	A1379	A1318	A1257	A1196	U1135	G1074	U1010	C948	C883	G818	U757	G693	G666	G666
C1443	U1380	A1319	G1258	A1197	C1136	U1075	C1011	A949	U884	A819	C758	A694	A629	G667
A1446	C1382	C1320	G1259	G1198	G1137	U1076	A1012	U950	U885	U820	G761	A695	A630	G668
A1447	C1383	U1321	C1260	U1199	G1138	G1077	G1013	G886	G886	G821	U762	A696	U632	G668
C1448	A1281	C1322	A1281	C1200	G1139	U1078	A1014	U952	G951	U822	G763	G697	G630	C570
C1449	C1262	G1323	C1262	A1201	C1140	G1079	G1015	G953	A889	C824	G764	G700	C634	U571
C1485	A1324	C1263	C1263	U1202	G1141	A1080	A1016	G954	G890	G825	C765	U701	A635	A572
U1450	G1386	C1325	U1284	C1203	G1142	A1081	U1017	U955	U891	A825	G766	G702	U636	A573
U1451	C1387	U1326	C1265	G1206	G1143	U1082	G1018	U956	A892	U826	G767	A703	C637	A574
C1452	C1388	C1327	G1266	G1207	G1144	U1083	A1019	A958	A906	C826	A766	A702	C637	G575
G1453	G1267	C1268	C1268	C1207	A1145	U1084	A1019	A959	A907	U827	A767	G703	C637	G575
G1454	C1268	G1268	G1268	C1208	A1146	U1085	A1021	U960	A908	U828	A768	A704	A640	C576
G1455	A1269	C1209	C1209	C1209	C1147	U1086	U1022	U961	C896	G829	G769	G705	U641	C576
C1456	G1270	U1211	U1211	U1211	U1148	G1087	U1023	C962	C897	G830	C770	A706	A642	C578
G1457	A1271	C1149	C1149	C1149	C1149	G1088	G1024	C963	C898	G832	G771	U707	A643	A579
C1458	G1272	A1150	A1150	G1089	A1151	U1090	G1025	A964	A900	U833	U772	C708	U644	C580
G1459	C1273	A1151	A1151	G1090	U1090	U1090	G1026	U965	A901	U834	G773	U709	G646	C582
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C1462	G1276	G1154	G1154	A1093	U1093	A1093	U1030	A968	A906	U836	A777	A712	A648	G584
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C1465	A1279	A1157	A1157	U1096	C1096	U1096	G1033	C970	A909	C941	C779	A715	G654	C587
A1466	G1280	C1158	C1158	C1097	G1097	U1097	G1034	C971	A909	U842	A780	A716	G654	C588
C1467	C1281	U1159	U1159	C1098	C1097	U1097	G1035	C972	C910	U843	A781	U717	A655	U589
A1468	C1282	U1160	U1160	G1099	G1098	U1098	A1036	A973	U911	G844	C782	A718	G656	U590
G1469	U1283	C1161	C1161	U1099	G1099	U1099	A1036	A974	C912	A845	C783	C719	U657	U591
U1470	C1284	A1162	A1162	A1101	C1101	A975	C1037	A975	A913	G846	A784	C720	C658	G592
U1471	A1285	A1163	A1163	A1102	G1102	G1102	G1038	A976	A914	C947	G785	G721	U659	U593
C1472	U1286	G1164	G1164	C1103	C1103	U1097	U1040	A978	U916	U849	A787	G722	C660	U594
U1473	A1287	U1165	U1165	C1104	G1104	U1098	G1041	C979	G917	U850	U788	U723	A595	A595
C1474	C1287	C1227	C1227	U1166	G1166	A1105	A1042	C980	A918	G851	U789	A728	A663	A596
A1475	A1288	G1167	G1167	A1105	G1166	A1105	A1042	C980	A918	G851	U789	A728	A663	A596
U1476	A1289	U1168	U1168	C1107	A1167	G1106	G1043	C981	A919	G852	A790	A729	A664	G597
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U1478	G1291	C1170	C1170	G1108	G1169	G1108	G1047	A983	U921	U854	A792	G731	G666	C599
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C1481	C1296	U1173	U1173	C1112	C1112	U1109	U1049	U986	A923	C556	C795	G734	G669	A602
A1482	G1297	G1174	G1174	C1113	C1113	U1109	U1050	G987	G926	G861	C796	G735	G670	U603
C1483	U1298	U1175	U1175	C1114	C1114	U1109	C1051	G988	G927	C862	C797	C736	U672	G604
C1484	A1299	G1176	G1176	U1115	U1115	U1109	U1052	U989	G928	C863	C797	C737	U673	U605
U1485	G1300	A1177	A1177	U1116	G1053	C990	G1053	C990	G929	U863	G799	C738	A674	G606
G1486	U1301	G1178	G1178	U1117	C1054	U991	C1054	C991	C930	A864	G800	C739	A675	A608
G1487	C1302	A1179	A1179	U1118	U1118	U1109	A1055	U992	C931	C865	U801	U740	A676	A609
G1488	C1303	U1241	U1241	C1119	C1119	U1109	U1056	U992	C932	C867	A802	G741	U677	U610
G1489	G1304	C1243	C1243	U1121	U1121	U1109	U1060	A994	G933	C868	G803	G742	U678	C611
U1490	C1244	G1181	G1181	U1121	U1121	U1109	U1060	A994	G933	C868	G803	G742	U678	C611
C1491	A1306	C1245	C1245	U1122	U1122	U1109	U1061	A995	C934	C869	U804	A743	C679	C612
A1492	U1307	U1246	U1246	U1123	U1123	U1109	G1061	A996	C935	U870	C805	C744	C680	C613
A1493	C1369	U1308	U1308	G1184	G1184	U1109	U1062	U997	C936	U871	C806	G745	A681	C614
G1494	G1370	U1309	U1309	U1247	U1247	U1109	C1063	C998	A937	A872	A807	A746	G682	C615
U1495	A1434	C1310	C1310	U1248	G1185	U1125	G1064	C999	A938	A873	C808	A747	G683	G616
C1496	G1435	U1372	A1311	C1248	G1186	U1126	U1065	A1000	G939	G874	G809	G748	U684	G617
				U1249	C1187	U1127	U1066	A1000	C940	C875	C810	A749	G685	C618
				A1250	U1189	C1128	A1067	G1003	G941	C876	C811	C750	U686	U619



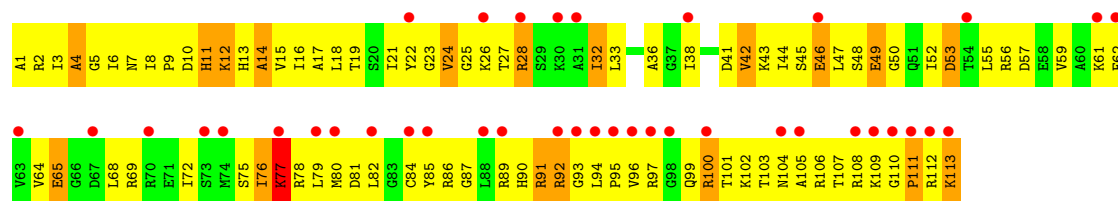
- Molecule 54: 30S ribosomal protein S7

Chain CG:



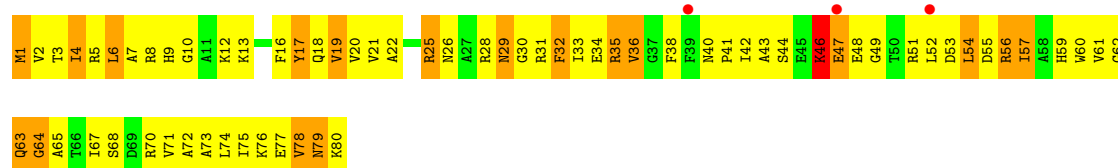
- Molecule 55: 30S ribosomal protein S13

Chain CM:



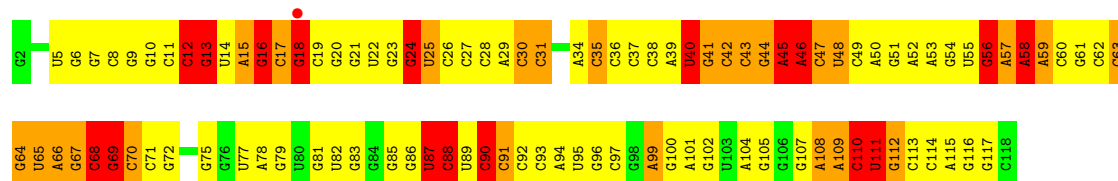
- Molecule 56: 30S ribosomal protein S16

Chain CP:



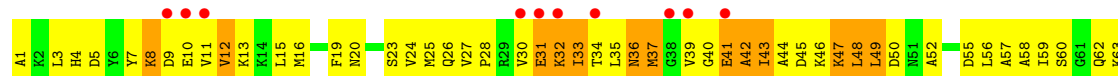
- Molecule 57: 5S rRNA

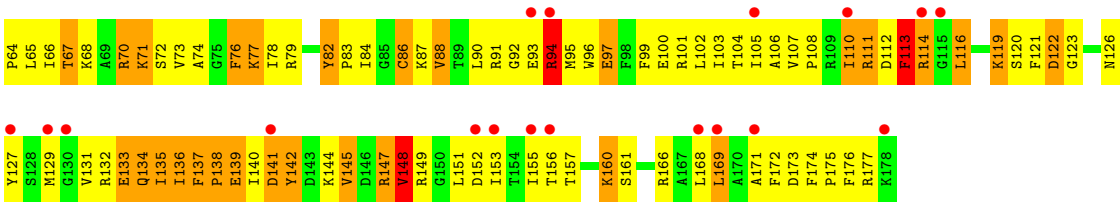
Chain DB:



- Molecule 58: 50S ribosomal protein L5

Chain DF:





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	211.96Å 434.53Å 623.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	82.40 – 3.10 82.42 – 3.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (82.40-3.10) 83.9 (82.42-3.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.13Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.205 , 0.254 0.218 , 0.264	Depositor DCC
R_{free} test set	17407 reflections (2.06%)	DCC
Wilson B-factor (Å ²)	54.4	Xtriage
Anisotropy	0.354	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 42.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 925668 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	284525	wwPDB-VP
Average B, all atoms (Å ²)	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.53	0/36834	1.32	524/57462 (0.9%)
2	AB	0.24	0/1736	0.47	0/2338
2	CB	0.22	0/1736	0.44	0/2338
3	AC	0.27	0/1652	0.50	0/2225
3	CC	0.24	0/1652	0.44	0/2225
4	AD	0.30	0/1665	0.52	0/2227
4	CD	0.37	0/1665	0.61	0/2227
5	AE	0.34	0/1119	0.61	0/1504
5	CE	0.31	0/1119	0.55	0/1504
6	AF	0.29	0/836	0.47	0/1128
6	CF	0.28	0/836	0.51	0/1128
7	AG	0.22	0/1196	0.44	0/1602
8	AH	0.32	0/989	0.56	0/1326
8	CH	0.27	0/989	0.49	0/1326
9	AI	0.23	0/1034	0.45	0/1375
9	CI	0.22	0/1034	0.41	0/1375
10	AJ	0.24	0/797	0.47	0/1077
10	CJ	0.21	0/797	0.47	0/1077
11	AK	0.27	0/893	0.53	0/1205
11	CK	0.26	0/893	0.50	0/1205
12	AL	0.38	0/969	0.69	0/1300
12	CL	0.32	0/969	0.56	0/1300
13	AM	0.23	0/893	0.49	0/1193
14	AN	0.25	0/785	0.48	0/1043
14	CN	0.21	0/780	0.38	0/1036
15	AO	0.30	0/722	0.49	0/964
15	CO	0.25	0/722	0.44	0/964
16	AP	0.31	0/659	0.51	0/884
17	AQ	0.37	0/658	0.59	0/881
17	CQ	0.26	0/658	0.50	0/881
18	AR	0.29	0/463	0.49	0/621
18	CR	0.28	0/463	0.46	0/621

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	AS	0.23	0/653	0.46	0/877
19	CS	0.21	0/653	0.41	0/877
20	AT	0.34	0/671	0.57	0/888
20	CT	0.26	0/671	0.51	0/888
21	AU	0.25	0/431	0.46	0/570
21	CU	0.31	0/431	0.58	0/570
22	BA	0.85	15/68626 (0.0%)	1.69	1674/107056 (1.6%)
22	DA	0.46	0/68314	1.26	901/106569 (0.8%)
23	BB	0.74	0/2828	1.56	46/4410 (1.0%)
24	BC	0.48	0/2122	0.74	1/2852 (0.0%)
24	DC	0.29	0/2122	0.54	0/2852
25	BD	0.61	0/1586	0.80	2/2134 (0.1%)
25	DD	0.28	0/1586	0.55	0/2134
26	BE	0.51	0/1571	0.73	0/2113
26	DE	0.25	0/1571	0.48	0/2113
27	BF	0.33	0/1435	0.55	0/1926
28	BG	0.38	0/1343	0.61	0/1816
28	DG	0.21	0/1343	0.44	0/1816
29	BH	0.28	0/1122	0.51	0/1515
29	DH	0.26	0/1122	0.48	0/1515
30	BI	0.23	0/1046	0.47	0/1410
30	DI	0.20	0/1046	0.42	0/1410
31	BJ	0.60	0/1152	0.84	1/1551 (0.1%)
31	DJ	0.27	0/1152	0.55	1/1551 (0.1%)
32	BK	0.61	1/948 (0.1%)	0.83	0/1268
32	DK	0.30	0/948	0.56	0/1268
33	BL	0.50	0/1054	0.80	2/1403 (0.1%)
33	DL	0.25	0/1054	0.51	0/1403
34	BM	0.55	0/1093	0.78	0/1460
34	DM	0.27	0/1093	0.49	0/1460
35	BN	0.55	0/974	0.82	2/1301 (0.2%)
35	DN	0.27	0/974	0.50	0/1301
36	BO	0.42	0/902	0.66	0/1209
36	DO	0.22	0/902	0.41	0/1209
37	BP	0.52	0/929	0.72	0/1242
37	DP	0.28	0/929	0.49	0/1242
38	BQ	0.72	0/960	0.89	1/1278 (0.1%)
38	DQ	0.27	0/960	0.46	0/1278
39	BR	0.67	2/829 (0.2%)	0.85	1/1107 (0.1%)
39	DR	0.27	0/829	0.48	0/1107
40	BS	0.63	0/864	0.84	0/1156
40	DS	0.26	0/864	0.51	0/1156
41	BT	0.51	0/745	0.80	0/994

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
41	DT	0.22	0/745	0.46	0/994
42	BU	0.44	0/788	0.75	0/1051
42	DU	0.23	0/788	0.45	0/1051
43	BV	0.47	0/766	0.65	0/1025
43	DV	0.23	0/766	0.43	0/1025
44	BW	0.67	0/603	0.93	1/797 (0.1%)
44	DW	0.24	0/603	0.48	0/797
45	BX	0.43	0/635	0.75	1/848 (0.1%)
45	DX	0.28	0/635	0.54	0/848
46	BY	0.39	0/510	0.63	0/677
46	DY	0.21	0/510	0.41	0/677
47	BZ	0.58	0/453	0.93	2/605 (0.3%)
47	DZ	0.25	0/453	0.49	0/605
48	B0	0.52	0/450	0.79	0/599
48	D0	0.27	0/450	0.49	0/599
49	B1	0.38	0/417	0.64	0/554
49	D1	0.23	0/417	0.46	0/554
50	B2	0.52	0/380	0.71	0/498
50	D2	0.27	0/380	0.52	0/498
51	B3	0.50	0/513	0.70	1/676 (0.1%)
51	D3	0.26	0/513	0.54	0/676
52	B4	0.41	0/303	0.64	0/397
52	D4	0.24	0/303	0.43	0/397
53	CA	0.46	0/36762	1.21	433/57350 (0.8%)
54	CG	0.22	0/1188	0.44	0/1591
55	CM	0.19	0/885	0.39	0/1181
56	CP	0.27	0/649	0.52	0/870
57	DB	0.40	0/2803	1.09	27/4371 (0.6%)
58	DF	0.21	0/1444	0.44	0/1937
All	All	0.56	18/306773 (0.0%)	1.25	3621/458565 (0.8%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
12	AL	0	1
20	AT	0	1
25	BD	0	1
31	BJ	0	1
35	BN	0	1
All	All	0	5

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	BA	1142	A	N9-C4	-8.33	1.32	1.37
22	BA	984	A	C5-C6	-7.40	1.34	1.41
39	BR	86	GLN	CB-CG	7.19	1.72	1.52
22	BA	1783	A	N7-C5	-6.87	1.35	1.39
22	BA	984	A	N9-C4	-5.90	1.34	1.37

The worst 5 of 3621 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	BA	571	U	O4'-C1'-N1	17.46	122.17	108.20
22	BA	2848	G	P-O3'-C3'	17.00	140.09	119.70
22	BA	627	A	P-O3'-C3'	16.24	139.19	119.70
22	BA	984	A	N1-C6-N6	16.11	128.26	118.60
22	BA	1603	A	P-O3'-C3'	-15.84	100.69	119.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	AL	22	ALA	Peptide
20	AT	6	ALA	Peptide
25	BD	191	GLY	Peptide
31	BJ	110	PRO	Peptide
35	BN	101	GLY	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	32895	0	16553	2319	0
2	AB	1705	0	1732	283	0
2	CB	1705	0	1732	260	0
3	AC	1625	0	1699	194	0
3	CC	1625	0	1699	238	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AD	1643	0	1710	284	0
4	CD	1643	0	1710	269	0
5	AE	1106	0	1148	203	0
5	CE	1106	0	1148	183	0
6	AF	818	0	808	113	0
6	CF	818	0	808	134	0
7	AG	1182	0	1240	150	0
8	AH	979	0	1034	162	0
8	CH	979	0	1034	140	0
9	AI	1022	0	1070	165	0
9	CI	1022	0	1070	178	0
10	AJ	787	0	828	169	0
10	CJ	787	0	828	142	0
11	AK	877	0	887	165	0
11	CK	877	0	887	138	0
12	AL	955	0	1019	132	0
12	CL	955	0	1019	173	0
13	AM	884	0	944	120	0
14	AN	774	0	827	131	0
14	CN	769	0	822	149	0
15	AO	714	0	737	93	0
15	CO	714	0	737	71	0
16	AP	649	0	666	105	0
17	AQ	649	0	691	141	0
17	CQ	649	0	691	98	0
18	AR	456	0	478	51	0
18	CR	456	0	478	95	0
19	AS	638	0	665	97	0
19	CS	638	0	665	118	0
20	AT	665	0	714	117	0
20	CT	665	0	714	99	0
21	AU	426	0	449	131	0
21	CU	426	0	449	126	0
22	BA	61274	0	30819	3116	1
22	DA	60995	0	30679	5725	1
23	BB	2529	0	1281	109	0
24	BC	2083	0	2157	313	0
24	DC	2083	0	2157	347	0
25	BD	1565	0	1616	274	0
25	DD	1565	0	1616	319	0
26	BE	1552	0	1619	199	0
26	DE	1552	0	1619	321	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	BF	1411	0	1447	210	0
28	BG	1323	0	1374	225	0
28	DG	1323	0	1374	229	0
29	BH	1111	0	1148	184	0
29	DH	1111	0	1148	208	0
30	BI	1032	0	1088	135	0
30	DI	1032	0	1088	149	0
31	BJ	1129	0	1162	214	0
31	DJ	1129	0	1162	205	0
32	BK	939	0	1012	150	0
32	DK	939	0	1012	188	0
33	BL	1045	0	1117	169	0
33	DL	1045	0	1117	224	0
34	BM	1074	0	1157	148	0
34	DM	1074	0	1157	156	0
35	BN	961	0	1000	131	0
35	DN	961	0	1000	228	0
36	BO	892	0	923	120	0
36	DO	892	0	923	118	0
37	BP	917	0	965	189	0
37	DP	917	0	965	184	0
38	BQ	947	0	1022	192	0
38	DQ	947	0	1022	203	0
39	BR	816	0	839	145	0
39	DR	816	0	839	147	0
40	BS	857	0	922	93	0
40	DS	857	0	922	125	0
41	BT	739	0	807	155	0
41	DT	739	0	807	174	0
42	BU	780	0	834	103	0
42	DU	780	0	834	147	0
43	BV	753	0	780	63	0
43	DV	753	0	780	118	0
44	BW	596	0	610	286	0
44	DW	596	0	610	180	0
45	BX	625	0	655	113	0
45	DX	625	0	655	128	0
46	BY	509	0	543	72	0
46	DY	509	0	543	114	0
47	BZ	449	0	491	44	0
47	DZ	449	0	491	69	0
48	B0	444	0	461	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	D0	444	0	461	92	0
49	B1	410	0	440	66	0
49	D1	410	0	440	55	0
50	B2	377	0	418	29	0
50	D2	377	0	418	65	0
51	B3	504	0	574	71	0
51	D3	504	0	574	105	0
52	B4	302	0	340	48	0
52	D4	302	0	343	48	0
53	CA	32831	0	16521	2706	0
54	CG	1175	0	1230	209	0
55	CM	877	0	937	176	0
56	CP	639	0	656	135	0
57	DB	2507	0	1270	238	0
58	DF	1420	0	1460	289	0
59	AA	41	0	0	0	0
59	AN	2	0	0	0	0
59	BA	135	0	0	0	0
59	BB	4	0	0	0	0
59	CA	42	0	0	0	0
59	DA	133	0	0	0	0
59	DB	1	0	0	0	0
59	DC	2	0	0	0	0
59	DJ	1	0	0	0	0
60	BA	51	0	67	4	0
61	B4	1	0	0	0	0
61	D4	1	0	0	0	0
62	AA	197	0	0	12	0
62	AE	1	0	0	0	0
62	AL	1	0	0	0	0
62	AN	7	0	0	0	0
62	AT	1	0	0	0	0
62	AU	1	0	0	0	0
62	B3	3	0	0	0	0
62	B4	2	0	0	0	0
62	BA	605	0	0	46	0
62	BB	19	0	0	0	0
62	BC	7	0	0	0	0
62	BD	3	0	0	2	0
62	BE	1	0	0	1	0
62	BL	4	0	0	1	0
62	BN	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	BR	1	0	0	0	0
62	BT	2	0	0	1	0
62	BV	1	0	0	1	0
62	CA	195	0	0	3	0
62	CE	3	0	0	1	0
62	CL	1	0	0	0	0
62	CN	3	0	0	0	0
62	CT	4	0	0	0	0
62	CU	1	0	0	0	0
62	D2	1	0	0	1	0
62	D3	1	0	0	0	0
62	D4	4	0	0	0	0
62	DA	600	0	0	30	0
62	DB	3	0	0	0	0
62	DC	13	0	0	2	0
62	DD	2	0	0	0	0
62	DE	4	0	0	0	0
62	DJ	3	0	0	0	0
62	DL	4	0	0	1	0
62	DN	2	0	0	0	0
62	DT	2	0	0	0	0
62	DU	2	0	0	0	0
62	DV	2	0	0	0	0
All	All	284525	0	190908	27236	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 58.

The worst 5 of 27236 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
37:BP:50:ARG:CG	37:BP:57:ALA:H	1.24	1.44
37:BP:50:ARG:HD2	37:BP:51:ASN:N	1.27	1.42
37:BP:50:ARG:HG2	37:BP:57:ALA:N	1.13	1.41
53:CA:238:A:C2'	53:CA:239:U:H5''	1.57	1.34
38:BQ:63:ARG:NH1	38:BQ:96:ASP:HA	1.37	1.34

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
22:BA:138:U:O4	22:DA:305:C:OP1[3_545]	2.02	0.18

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	216/218 (99%)	133 (62%)	51 (24%)	32 (15%)	0	2
2	CB	216/218 (99%)	158 (73%)	38 (18%)	20 (9%)	1	7
3	AC	204/206 (99%)	144 (71%)	36 (18%)	24 (12%)	1	4
3	CC	204/206 (99%)	138 (68%)	47 (23%)	19 (9%)	1	7
4	AD	203/205 (99%)	127 (63%)	43 (21%)	33 (16%)	0	0
4	CD	203/205 (99%)	138 (68%)	40 (20%)	25 (12%)	1	3
5	AE	148/150 (99%)	97 (66%)	28 (19%)	23 (16%)	0	1
5	CE	148/150 (99%)	111 (75%)	21 (14%)	16 (11%)	1	5
6	AF	98/100 (98%)	71 (72%)	15 (15%)	12 (12%)	1	4
6	CF	98/100 (98%)	66 (67%)	19 (19%)	13 (13%)	0	2
7	AG	149/151 (99%)	100 (67%)	37 (25%)	12 (8%)	1	10
8	AH	127/129 (98%)	101 (80%)	15 (12%)	11 (9%)	1	9
8	CH	127/129 (98%)	96 (76%)	23 (18%)	8 (6%)	2	16
9	AI	125/127 (98%)	81 (65%)	28 (22%)	16 (13%)	0	3
9	CI	125/127 (98%)	84 (67%)	32 (26%)	9 (7%)	2	12
10	AJ	96/98 (98%)	69 (72%)	10 (10%)	17 (18%)	0	0
10	CJ	96/98 (98%)	61 (64%)	21 (22%)	14 (15%)	0	2
11	AK	115/117 (98%)	80 (70%)	20 (17%)	15 (13%)	0	3
11	CK	115/117 (98%)	87 (76%)	16 (14%)	12 (10%)	1	5
12	AL	121/123 (98%)	88 (73%)	21 (17%)	12 (10%)	1	6
12	CL	121/123 (98%)	84 (69%)	24 (20%)	13 (11%)	1	5
13	AM	112/114 (98%)	83 (74%)	19 (17%)	10 (9%)	1	8
14	AN	92/100 (92%)	60 (65%)	18 (20%)	14 (15%)	0	1
14	CN	91/100 (91%)	57 (63%)	26 (29%)	8 (9%)	1	8
15	AO	86/88 (98%)	59 (69%)	19 (22%)	8 (9%)	1	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	CO	86/88 (98%)	53 (62%)	30 (35%)	3 (4%)	6	32
16	AP	80/82 (98%)	59 (74%)	12 (15%)	9 (11%)	1	4
17	AQ	78/80 (98%)	48 (62%)	24 (31%)	6 (8%)	1	11
17	CQ	78/80 (98%)	59 (76%)	11 (14%)	8 (10%)	1	6
18	AR	53/55 (96%)	40 (76%)	10 (19%)	3 (6%)	3	18
18	CR	53/55 (96%)	33 (62%)	17 (32%)	3 (6%)	3	18
19	AS	77/79 (98%)	51 (66%)	15 (20%)	11 (14%)	0	2
19	CS	77/79 (98%)	46 (60%)	24 (31%)	7 (9%)	1	8
20	AT	83/85 (98%)	57 (69%)	21 (25%)	5 (6%)	2	17
20	CT	83/85 (98%)	52 (63%)	21 (25%)	10 (12%)	1	4
21	AU	49/51 (96%)	25 (51%)	12 (24%)	12 (24%)	0	0
21	CU	49/51 (96%)	20 (41%)	13 (26%)	16 (33%)	0	0
24	BC	269/271 (99%)	197 (73%)	46 (17%)	26 (10%)	1	6
24	DC	269/271 (99%)	174 (65%)	64 (24%)	31 (12%)	1	4
25	BD	207/209 (99%)	141 (68%)	32 (16%)	34 (16%)	0	0
25	DD	207/209 (99%)	131 (63%)	41 (20%)	35 (17%)	0	0
26	BE	199/201 (99%)	144 (72%)	35 (18%)	20 (10%)	1	6
26	DE	199/201 (99%)	115 (58%)	54 (27%)	30 (15%)	0	1
27	BF	175/177 (99%)	123 (70%)	36 (21%)	16 (9%)	1	8
28	BG	174/176 (99%)	111 (64%)	38 (22%)	25 (14%)	0	2
28	DG	174/176 (99%)	99 (57%)	40 (23%)	35 (20%)	0	0
29	BH	147/149 (99%)	62 (42%)	50 (34%)	35 (24%)	0	0
29	DH	147/149 (99%)	70 (48%)	54 (37%)	23 (16%)	0	1
30	BI	139/141 (99%)	84 (60%)	41 (30%)	14 (10%)	1	6
30	DI	139/141 (99%)	75 (54%)	48 (34%)	16 (12%)	1	4
31	BJ	140/142 (99%)	104 (74%)	24 (17%)	12 (9%)	1	9
31	DJ	140/142 (99%)	92 (66%)	28 (20%)	20 (14%)	0	2
32	BK	120/122 (98%)	89 (74%)	17 (14%)	14 (12%)	1	4
32	DK	120/122 (98%)	76 (63%)	17 (14%)	27 (22%)	0	0
33	BL	141/143 (99%)	100 (71%)	30 (21%)	11 (8%)	1	11
33	DL	141/143 (99%)	77 (55%)	44 (31%)	20 (14%)	0	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	BM	134/136 (98%)	96 (72%)	18 (13%)	20 (15%)	0	1
34	DM	134/136 (98%)	90 (67%)	26 (19%)	18 (13%)	0	2
35	BN	118/120 (98%)	91 (77%)	16 (14%)	11 (9%)	1	7
35	DN	118/120 (98%)	74 (63%)	25 (21%)	19 (16%)	0	1
36	BO	114/116 (98%)	85 (75%)	18 (16%)	11 (10%)	1	7
36	DO	114/116 (98%)	74 (65%)	30 (26%)	10 (9%)	1	8
37	BP	112/114 (98%)	78 (70%)	20 (18%)	14 (12%)	1	3
37	DP	112/114 (98%)	60 (54%)	31 (28%)	21 (19%)	0	0
38	BQ	115/117 (98%)	100 (87%)	7 (6%)	8 (7%)	2	13
38	DQ	115/117 (98%)	75 (65%)	27 (24%)	13 (11%)	1	4
39	BR	101/103 (98%)	76 (75%)	14 (14%)	11 (11%)	1	5
39	DR	101/103 (98%)	64 (63%)	24 (24%)	13 (13%)	0	3
40	BS	108/110 (98%)	89 (82%)	14 (13%)	5 (5%)	4	24
40	DS	108/110 (98%)	72 (67%)	25 (23%)	11 (10%)	1	6
41	BT	91/93 (98%)	49 (54%)	26 (29%)	16 (18%)	0	0
41	DT	91/93 (98%)	41 (45%)	26 (29%)	24 (26%)	0	0
42	BU	100/102 (98%)	66 (66%)	16 (16%)	18 (18%)	0	0
42	DU	100/102 (98%)	52 (52%)	22 (22%)	26 (26%)	0	0
43	BV	92/94 (98%)	75 (82%)	15 (16%)	2 (2%)	10	46
43	DV	92/94 (98%)	60 (65%)	24 (26%)	8 (9%)	1	9
44	BW	77/79 (98%)	31 (40%)	22 (29%)	24 (31%)	0	0
44	DW	77/79 (98%)	30 (39%)	25 (32%)	22 (29%)	0	0
45	BX	75/77 (97%)	58 (77%)	10 (13%)	7 (9%)	1	7
45	DX	75/77 (97%)	44 (59%)	20 (27%)	11 (15%)	0	2
46	BY	61/63 (97%)	38 (62%)	15 (25%)	8 (13%)	0	3
46	DY	61/63 (97%)	40 (66%)	16 (26%)	5 (8%)	1	10
47	BZ	56/58 (97%)	47 (84%)	5 (9%)	4 (7%)	2	12
47	DZ	56/58 (97%)	31 (55%)	20 (36%)	5 (9%)	1	8
48	B0	54/56 (96%)	41 (76%)	9 (17%)	4 (7%)	2	11
48	D0	54/56 (96%)	33 (61%)	16 (30%)	5 (9%)	1	7
49	B1	48/50 (96%)	37 (77%)	6 (12%)	5 (10%)	1	5

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	D1	48/50 (96%)	35 (73%)	8 (17%)	5 (10%)	1	5
50	B2	44/46 (96%)	37 (84%)	7 (16%)	0	100	100
50	D2	44/46 (96%)	29 (66%)	10 (23%)	5 (11%)	1	4
51	B3	62/64 (97%)	53 (86%)	5 (8%)	4 (6%)	2	15
51	D3	62/64 (97%)	42 (68%)	12 (19%)	8 (13%)	0	3
52	B4	36/38 (95%)	24 (67%)	9 (25%)	3 (8%)	1	9
52	D4	36/38 (95%)	21 (58%)	9 (25%)	6 (17%)	0	0
54	CG	148/150 (99%)	96 (65%)	38 (26%)	14 (10%)	1	7
55	CM	111/113 (98%)	62 (56%)	36 (32%)	13 (12%)	1	4
56	CP	78/80 (98%)	48 (62%)	22 (28%)	8 (10%)	1	6
58	DF	176/178 (99%)	87 (49%)	58 (33%)	31 (18%)	0	0
All	All	11238/11447 (98%)	7411 (66%)	2418 (22%)	1409 (12%)	1	3

5 of 1409 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	21	TYR
2	AB	33	ALA
2	AB	37	VAL
2	AB	72	LYS
2	AB	75	ALA

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	180/180 (100%)	142 (79%)	38 (21%)	1	7
2	CB	180/180 (100%)	154 (86%)	26 (14%)	5	19
3	AC	170/170 (100%)	136 (80%)	34 (20%)	2	8
3	CC	170/170 (100%)	153 (90%)	17 (10%)	11	38
4	AD	172/172 (100%)	138 (80%)	34 (20%)	2	8
4	CD	172/172 (100%)	131 (76%)	41 (24%)	1	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	AE	113/113 (100%)	77 (68%)	36 (32%)	0	1
5	CE	113/113 (100%)	89 (79%)	24 (21%)	1	7
6	AF	87/87 (100%)	71 (82%)	16 (18%)	2	9
6	CF	87/87 (100%)	73 (84%)	14 (16%)	3	13
7	AG	124/124 (100%)	111 (90%)	13 (10%)	10	35
8	AH	104/104 (100%)	83 (80%)	21 (20%)	2	8
8	CH	104/104 (100%)	91 (88%)	13 (12%)	7	25
9	AI	105/105 (100%)	82 (78%)	23 (22%)	1	6
9	CI	105/105 (100%)	89 (85%)	16 (15%)	4	16
10	AJ	86/86 (100%)	70 (81%)	16 (19%)	2	9
10	CJ	86/86 (100%)	73 (85%)	13 (15%)	4	16
11	AK	90/90 (100%)	73 (81%)	17 (19%)	2	9
11	CK	90/90 (100%)	79 (88%)	11 (12%)	7	26
12	AL	103/103 (100%)	76 (74%)	27 (26%)	1	2
12	CL	103/103 (100%)	78 (76%)	25 (24%)	1	4
13	AM	92/92 (100%)	84 (91%)	8 (9%)	15	49
14	AN	79/83 (95%)	71 (90%)	8 (10%)	11	38
14	CN	79/83 (95%)	69 (87%)	10 (13%)	6	24
15	AO	76/76 (100%)	59 (78%)	17 (22%)	1	6
15	CO	76/76 (100%)	69 (91%)	7 (9%)	13	45
16	AP	65/65 (100%)	54 (83%)	11 (17%)	3	11
17	AQ	74/74 (100%)	60 (81%)	14 (19%)	2	9
17	CQ	74/74 (100%)	62 (84%)	12 (16%)	3	13
18	AR	48/48 (100%)	44 (92%)	4 (8%)	16	53
18	CR	48/48 (100%)	40 (83%)	8 (17%)	3	11
19	AS	70/70 (100%)	63 (90%)	7 (10%)	11	38
19	CS	70/70 (100%)	64 (91%)	6 (9%)	15	51
20	AT	65/65 (100%)	48 (74%)	17 (26%)	1	2
20	CT	65/65 (100%)	52 (80%)	13 (20%)	2	8
21	AU	44/44 (100%)	36 (82%)	8 (18%)	2	10
21	CU	44/44 (100%)	29 (66%)	15 (34%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	BC	216/216 (100%)	170 (79%)	46 (21%)	1	7
24	DC	216/216 (100%)	178 (82%)	38 (18%)	3	10
25	BD	164/164 (100%)	133 (81%)	31 (19%)	2	9
25	DD	164/164 (100%)	131 (80%)	33 (20%)	2	8
26	BE	165/165 (100%)	111 (67%)	54 (33%)	0	0
26	DE	165/165 (100%)	143 (87%)	22 (13%)	6	22
27	BF	148/148 (100%)	116 (78%)	32 (22%)	1	6
28	BG	137/137 (100%)	106 (77%)	31 (23%)	1	5
28	DG	137/137 (100%)	117 (85%)	20 (15%)	5	18
29	BH	114/114 (100%)	96 (84%)	18 (16%)	4	14
29	DH	114/114 (100%)	90 (79%)	24 (21%)	1	7
30	BI	109/109 (100%)	91 (84%)	18 (16%)	3	12
30	DI	109/109 (100%)	103 (94%)	6 (6%)	30	71
31	BJ	116/116 (100%)	92 (79%)	24 (21%)	2	8
31	DJ	116/116 (100%)	101 (87%)	15 (13%)	6	24
32	BK	103/103 (100%)	77 (75%)	26 (25%)	1	3
32	DK	103/103 (100%)	84 (82%)	19 (18%)	2	9
33	BL	102/102 (100%)	82 (80%)	20 (20%)	2	8
33	DL	102/102 (100%)	89 (87%)	13 (13%)	6	24
34	BM	109/109 (100%)	81 (74%)	28 (26%)	1	2
34	DM	109/109 (100%)	98 (90%)	11 (10%)	11	38
35	BN	100/100 (100%)	82 (82%)	18 (18%)	2	10
35	DN	100/100 (100%)	85 (85%)	15 (15%)	4	17
36	BO	86/86 (100%)	67 (78%)	19 (22%)	1	6
36	DO	86/86 (100%)	79 (92%)	7 (8%)	17	53
37	BP	99/99 (100%)	66 (67%)	33 (33%)	0	0
37	DP	99/99 (100%)	88 (89%)	11 (11%)	9	33
38	BQ	89/89 (100%)	68 (76%)	21 (24%)	1	5
38	DQ	89/89 (100%)	69 (78%)	20 (22%)	1	6
39	BR	84/84 (100%)	66 (79%)	18 (21%)	1	7
39	DR	84/84 (100%)	69 (82%)	15 (18%)	2	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	BS	93/93 (100%)	72 (77%)	21 (23%)	1	5
40	DS	93/93 (100%)	72 (77%)	21 (23%)	1	5
41	BT	80/80 (100%)	53 (66%)	27 (34%)	0	0
41	DT	80/80 (100%)	75 (94%)	5 (6%)	25	66
42	BU	83/83 (100%)	66 (80%)	17 (20%)	2	8
42	DU	83/83 (100%)	72 (87%)	11 (13%)	6	22
43	BV	78/78 (100%)	62 (80%)	16 (20%)	2	8
43	DV	78/78 (100%)	66 (85%)	12 (15%)	4	15
44	BW	59/59 (100%)	38 (64%)	21 (36%)	0	0
44	DW	59/59 (100%)	45 (76%)	14 (24%)	1	4
45	BX	67/67 (100%)	51 (76%)	16 (24%)	1	4
45	DX	67/67 (100%)	55 (82%)	12 (18%)	2	10
46	BY	55/55 (100%)	42 (76%)	13 (24%)	1	5
46	DY	55/55 (100%)	51 (93%)	4 (7%)	20	59
47	BZ	48/48 (100%)	35 (73%)	13 (27%)	1	2
47	DZ	48/48 (100%)	38 (79%)	10 (21%)	2	7
48	B0	47/47 (100%)	39 (83%)	8 (17%)	3	11
48	D0	47/47 (100%)	38 (81%)	9 (19%)	2	9
49	B1	45/45 (100%)	37 (82%)	8 (18%)	2	10
49	D1	45/45 (100%)	38 (84%)	7 (16%)	4	14
50	B2	38/38 (100%)	27 (71%)	11 (29%)	0	1
50	D2	38/38 (100%)	33 (87%)	5 (13%)	6	23
51	B3	51/51 (100%)	42 (82%)	9 (18%)	3	10
51	D3	51/51 (100%)	37 (72%)	14 (28%)	0	1
52	B4	34/34 (100%)	28 (82%)	6 (18%)	3	10
52	D4	34/34 (100%)	30 (88%)	4 (12%)	8	29
54	CG	123/123 (100%)	101 (82%)	22 (18%)	2	10
55	CM	91/91 (100%)	81 (89%)	10 (11%)	9	34
56	CP	65/65 (100%)	50 (77%)	15 (23%)	1	5
58	DF	149/149 (100%)	124 (83%)	25 (17%)	3	11
All	All	9331/9339 (100%)	7599 (81%)	1732 (19%)	2	9

5 of 1732 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	BQ	89	ILE
50	B2	12	ARG
39	DR	86	GLN
40	BS	1	MET
43	BV	41	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 360 such sidechains are listed below:

Mol	Chain	Res	Type
41	BT	48	GLN
3	CC	139	ASN
42	DU	39	ASN
42	BU	73	ASN
48	B0	41	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1532/1533 (99%)	518 (33%)	236 (15%)
22	BA	2850/2904 (98%)	913 (32%)	429 (15%)
22	DA	2839/2904 (97%)	1105 (38%)	498 (17%)
23	BB	117/118 (99%)	34 (29%)	17 (14%)
53	CA	1529/1530 (99%)	572 (37%)	242 (15%)
57	DB	116/117 (99%)	44 (37%)	16 (13%)
All	All	8983/9106 (98%)	3186 (35%)	1438 (16%)

5 of 3186 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	6	G
1	AA	7	A
1	AA	8	A
1	AA	9	G

5 of 1438 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	BA	2781	A

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Mol	Chain	Res	Type
53	CA	701	U
22	DA	2300	C
23	BB	25	U
53	CA	279	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 364 ligands modelled in this entry, 363 are monoatomic - leaving 1 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	$\# Z > 2$
60	ERY	BA	3136	-	53,53,53	0.73	0	82,82,82	1.65	21 (25%)

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
60	ERY	BA	3136	-	-	0/72/107/107	0/3/3/3

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	BA	3136	ERY	C25-C24-C23	-5.04	102.77	110.06
60	BA	3136	ERY	O7-C5-C6	-4.37	100.45	106.33
60	BA	3136	ERY	C3-C2-C1	-3.43	102.98	110.04
60	BA	3136	ERY	O2-C1-O1	-3.29	117.27	123.85
60	BA	3136	ERY	C15-C16-C17	-3.25	103.99	107.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	1533/1533 (100%)	-0.63	12 (0%) 83 28	21, 74, 188, 404	0
2	AB	218/218 (100%)	0.75	15 (6%) 17 3	72, 142, 202, 237	0
2	CB	218/218 (100%)	0.88	19 (8%) 10 2	98, 165, 222, 272	0
3	AC	206/206 (100%)	0.24	4 (1%) 64 13	54, 101, 149, 187	0
3	CC	206/206 (100%)	0.54	7 (3%) 43 6	80, 139, 210, 243	0
4	AD	205/205 (100%)	-0.09	3 (1%) 70 16	38, 80, 182, 310	0
4	CD	205/205 (100%)	-0.23	1 (0%) 88 39	29, 54, 103, 236	0
5	AE	150/150 (100%)	-0.05	0 100 100	37, 70, 136, 207	0
5	CE	150/150 (100%)	0.11	0 100 100	38, 87, 150, 253	0
6	AF	100/100 (100%)	-0.11	0 100 100	43, 85, 149, 174	0
6	CF	100/100 (100%)	-0.05	0 100 100	58, 109, 180, 202	0
7	AG	151/151 (100%)	0.22	1 (0%) 84 32	82, 155, 235, 286	0
8	AH	129/129 (100%)	-0.12	0 100 100	41, 69, 120, 203	0
8	CH	129/129 (100%)	0.34	2 (1%) 68 15	52, 107, 161, 197	0
9	AI	127/127 (100%)	0.59	8 (6%) 19 3	68, 153, 256, 288	0
9	CI	127/127 (100%)	0.96	17 (13%) 4 1	102, 200, 285, 325	0
10	AJ	98/98 (100%)	0.32	4 (4%) 35 5	60, 119, 200, 251	0
10	CJ	98/98 (100%)	1.53	29 (29%) 1 0	102, 192, 267, 283	0
11	AK	117/117 (100%)	0.23	2 (1%) 67 15	38, 104, 176, 222	0
11	CK	117/117 (100%)	0.16	1 (0%) 81 25	53, 102, 161, 200	0
12	AL	123/123 (100%)	-0.23	1 (0%) 83 28	16, 49, 111, 187	0
12	CL	123/123 (100%)	0.12	1 (0%) 83 28	41, 81, 128, 173	0
13	AM	114/114 (100%)	0.17	2 (1%) 65 14	69, 139, 213, 258	0
14	AN	96/100 (96%)	0.28	3 (3%) 47 7	68, 111, 199, 266	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
14	CN	95/100 (95%)	1.45	26 (27%) 1 0	112, 209, 319, 350	0
15	AO	88/88 (100%)	-0.25	0 100 100	34, 70, 111, 172	0
15	CO	88/88 (100%)	-0.18	0 100 100	68, 112, 187, 286	0
16	AP	82/82 (100%)	0.33	4 (4%) 28 4	45, 68, 174, 288	0
17	AQ	80/80 (100%)	0.28	1 (1%) 74 19	35, 71, 134, 209	0
17	CQ	80/80 (100%)	0.59	7 (8%) 10 2	47, 103, 151, 188	0
18	AR	55/55 (100%)	-0.05	2 (3%) 41 6	50, 80, 154, 211	0
18	CR	55/55 (100%)	-0.01	0 100 100	51, 87, 157, 235	0
19	AS	79/79 (100%)	0.82	7 (8%) 10 2	81, 150, 212, 259	0
19	CS	79/79 (100%)	1.69	31 (39%) 1 0	217, 411, 508, 531	0
20	AT	85/85 (100%)	-0.15	0 100 100	35, 69, 129, 176	0
20	CT	85/85 (100%)	0.75	5 (5%) 22 3	66, 130, 204, 226	0
21	AU	51/51 (100%)	1.35	12 (23%) 1 0	90, 146, 226, 252	0
21	CU	51/51 (100%)	0.38	2 (3%) 37 5	54, 109, 189, 269	0
22	BA	2854/2904 (98%)	-0.57	31 (1%) 77 22	6, 25, 148, 390	0
22	DA	2841/2904 (97%)	0.12	76 (2%) 52 8	55, 116, 270, 526	0
23	BB	118/118 (100%)	-0.69	0 100 100	12, 40, 73, 109	0
24	BC	271/271 (100%)	-0.25	1 (0%) 90 45	8, 35, 82, 192	0
24	DC	271/271 (100%)	0.30	10 (3%) 39 6	42, 95, 151, 215	0
25	BD	209/209 (100%)	-0.31	0 100 100	6, 21, 69, 179	0
25	DD	209/209 (100%)	0.40	8 (3%) 38 5	55, 115, 199, 284	0
26	BE	201/201 (100%)	-0.30	0 100 100	7, 36, 86, 151	0
26	DE	201/201 (100%)	0.96	26 (12%) 4 1	61, 235, 398, 470	0
27	BF	177/177 (100%)	-0.10	0 100 100	21, 63, 134, 167	0
28	BG	176/176 (100%)	-0.12	0 100 100	20, 61, 131, 192	0
28	DG	176/176 (100%)	0.84	20 (11%) 6 1	88, 239, 337, 389	0
29	BH	149/149 (100%)	1.46	46 (30%) 1 0	40, 171, 260, 304	0
29	DH	149/149 (100%)	1.39	40 (26%) 1 0	68, 188, 268, 298	0
30	BI	141/141 (100%)	1.44	32 (22%) 1 0	170, 245, 289, 301	0
30	DI	141/141 (100%)	1.69	50 (35%) 1 0	178, 312, 349, 370	0
31	BJ	142/142 (100%)	-0.38	0 100 100	7, 16, 60, 137	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
31	DJ	142/142 (100%)	0.25	1 (0%) 84 32	50, 106, 169, 198	0
32	BK	122/122 (100%)	-0.29	1 (0%) 83 28	11, 24, 69, 242	0
32	DK	122/122 (100%)	0.30	3 (2%) 54 9	59, 97, 147, 210	0
33	BL	143/143 (100%)	-0.32	0 100 100	6, 30, 71, 123	0
33	DL	143/143 (100%)	0.77	12 (8%) 11 2	59, 164, 279, 354	0
34	BM	136/136 (100%)	-0.38	0 100 100	7, 22, 59, 147	0
34	DM	136/136 (100%)	0.43	2 (1%) 70 16	37, 112, 192, 250	0
35	BN	120/120 (100%)	-0.32	0 100 100	8, 17, 40, 149	0
35	DN	120/120 (100%)	0.85	13 (10%) 6 1	63, 131, 211, 305	0
36	BO	116/116 (100%)	-0.26	0 100 100	21, 41, 72, 113	0
36	DO	116/116 (100%)	0.93	13 (11%) 6 1	106, 172, 240, 273	0
37	BP	114/114 (100%)	-0.30	0 100 100	12, 32, 87, 176	0
37	DP	114/114 (100%)	0.37	3 (2%) 53 8	50, 110, 175, 196	0
38	BQ	117/117 (100%)	-0.44	0 100 100	6, 15, 39, 225	0
38	DQ	117/117 (100%)	0.59	2 (1%) 67 15	65, 113, 193, 331	0
39	BR	103/103 (100%)	-0.42	0 100 100	6, 26, 67, 184	0
39	DR	103/103 (100%)	0.91	11 (10%) 6 1	73, 144, 238, 305	0
40	BS	110/110 (100%)	-0.39	0 100 100	7, 15, 48, 172	0
40	DS	110/110 (100%)	0.92	12 (10%) 6 1	71, 132, 214, 254	0
41	BT	93/93 (100%)	-0.01	2 (2%) 59 11	13, 43, 123, 233	0
41	DT	93/93 (100%)	1.52	27 (29%) 1 0	124, 265, 379, 423	0
42	BU	102/102 (100%)	-0.12	0 100 100	21, 45, 131, 240	0
42	DU	102/102 (100%)	1.85	37 (36%) 1 0	148, 305, 420, 554	0
43	BV	94/94 (100%)	-0.29	0 100 100	14, 38, 78, 135	0
43	DV	94/94 (100%)	0.56	3 (3%) 45 7	88, 136, 193, 236	0
44	BW	79/79 (100%)	-0.12	0 100 100	13, 29, 98, 213	0
44	DW	79/79 (100%)	1.33	23 (29%) 1 0	73, 169, 279, 323	0
45	BX	77/77 (100%)	-0.34	0 100 100	13, 37, 77, 108	0
45	DX	77/77 (100%)	0.57	1 (1%) 74 19	62, 118, 215, 280	0
46	BY	63/63 (100%)	-0.10	0 100 100	27, 59, 126, 209	0
46	DY	63/63 (100%)	1.10	10 (15%) 3 1	152, 379, 492, 508	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
47	BZ	58/58 (100%)	-0.39	0 100 100	9, 16, 47, 61	0
47	DZ	58/58 (100%)	0.23	2 (3%) 43 6	68, 143, 251, 271	0
48	B0	56/56 (100%)	-0.47	0 100 100	6, 18, 71, 138	0
48	D0	56/56 (100%)	0.89	6 (10%) 6 1	63, 144, 246, 262	0
49	B1	50/50 (100%)	-0.01	0 100 100	27, 47, 93, 115	0
49	D1	50/50 (100%)	1.01	7 (14%) 3 1	97, 154, 208, 231	0
50	B2	46/46 (100%)	-0.38	0 100 100	10, 19, 43, 195	0
50	D2	46/46 (100%)	0.62	1 (2%) 59 11	59, 119, 184, 211	0
51	B3	64/64 (100%)	-0.37	0 100 100	8, 22, 38, 65	0
51	D3	64/64 (100%)	0.96	9 (14%) 3 1	64, 122, 197, 255	0
52	B4	38/38 (100%)	0.21	0 100 100	25, 49, 94, 97	0
52	D4	38/38 (100%)	2.57	25 (65%) 0 0	87, 173, 235, 241	0
53	CA	1530/1530 (100%)	-0.07	33 (2%) 59 11	38, 102, 287, 422	0
54	CG	150/150 (100%)	1.37	41 (27%) 1 0	112, 196, 246, 272	0
55	CM	113/113 (100%)	1.62	39 (34%) 1 0	190, 427, 522, 545	0
56	CP	80/80 (100%)	0.47	3 (3%) 38 5	46, 97, 159, 229	0
57	DB	117/117 (100%)	-0.20	1 (0%) 81 25	88, 164, 221, 243	0
58	DF	178/178 (100%)	1.18	28 (15%) 3 1	142, 219, 259, 301	0
All	All	20431/20553 (99%)	0.09	940 (4%) 31 5	6, 93, 274, 554	0

The worst 5 of 940 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
29	DH	92	GLY	12.5
53	CA	209	U	11.8
22	BA	138	U	11.7
30	BI	2	LYS	10.6
29	DH	124	THR	10.6

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
59	MG	DA	3063	1/1	2.15	78.35	192,192,192,192	0
59	MG	DA	3109	1/1	0.71	72.43	176,176,176,176	0
59	MG	DA	3005	1/1	0.79	59.60	309,309,309,309	0
59	MG	DA	3058	1/1	0.44	54.17	235,235,235,235	0
59	MG	DA	3064	1/1	1.27	52.02	230,230,230,230	0
59	MG	BA	3055	1/1	0.37	50.55	191,191,191,191	0
59	MG	DJ	201	1/1	3.78	50.00	284,284,284,284	0
59	MG	DA	3074	1/1	0.82	45.34	240,240,240,240	0
59	MG	CA	1614	1/1	1.16	41.50	231,231,231,231	0
59	MG	BA	3025	1/1	0.44	39.05	119,119,119,119	0
59	MG	DA	3078	1/1	0.93	32.09	210,210,210,210	0
59	MG	DA	3062	1/1	0.88	31.94	193,193,193,193	0
59	MG	BA	3034	1/1	0.29	31.68	154,154,154,154	0
59	MG	DA	3033	1/1	0.66	27.71	149,149,149,149	0
59	MG	AA	1617	1/1	0.59	27.41	203,203,203,203	0
59	MG	CA	1624	1/1	0.65	27.21	179,179,179,179	0
59	MG	DA	3016	1/1	0.60	27.03	231,231,231,231	0
59	MG	BA	3060	1/1	0.48	24.44	174,174,174,174	0
59	MG	BA	3075	1/1	0.18	24.33	69,69,69,69	0
59	MG	DA	3060	1/1	0.56	23.62	161,161,161,161	0
59	MG	DA	3127	1/1	0.55	23.38	199,199,199,199	0
59	MG	BA	3118	1/1	0.42	22.70	168,168,168,168	0
59	MG	BA	3130	1/1	0.51	21.35	205,205,205,205	0
59	MG	BB	201	1/1	0.24	20.00	236,236,236,236	0
59	MG	CA	1628	1/1	1.64	19.32	236,236,236,236	0
59	MG	DA	3020	1/1	0.57	18.66	218,218,218,218	0
59	MG	DA	3045	1/1	0.53	17.88	233,233,233,233	0
59	MG	BA	3036	1/1	0.35	16.16	169,169,169,169	0
59	MG	BA	3057	1/1	0.25	15.99	161,161,161,161	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	CA	1626	1/1	0.26	15.84	29,29,29,29	0
59	MG	DA	3079	1/1	0.56	15.33	150,150,150,150	0
59	MG	BA	3110	1/1	0.19	14.76	102,102,102,102	0
59	MG	BA	3086	1/1	0.17	13.70	88,88,88,88	0
59	MG	BA	3040	1/1	0.20	13.30	8,8,8,8	0
59	MG	AA	1624	1/1	0.24	12.43	31,31,31,31	0
59	MG	BA	3056	1/1	0.30	12.26	233,233,233,233	0
59	MG	BA	3070	1/1	0.22	11.89	134,134,134,134	0
59	MG	BA	3019	1/1	0.30	11.64	10,10,10,10	0
59	MG	DA	3013	1/1	0.81	11.34	185,185,185,185	0
59	MG	DA	3082	1/1	0.35	11.11	189,189,189,189	0
59	MG	DA	3026	1/1	1.03	10.89	244,244,244,244	0
59	MG	AA	1625	1/1	0.31	10.76	121,121,121,121	0
59	MG	DA	3015	1/1	0.41	10.56	145,145,145,145	0
59	MG	BA	3059	1/1	0.22	9.30	109,109,109,109	0
59	MG	BA	3014	1/1	0.20	9.26	42,42,42,42	0
59	MG	DA	3028	1/1	1.00	9.20	262,262,262,262	0
59	MG	CA	1612	1/1	0.38	8.97	120,120,120,120	0
59	MG	BA	3100	1/1	0.20	8.96	24,24,24,24	0
59	MG	BA	3030	1/1	0.21	8.64	15,15,15,15	0
59	MG	DA	3010	1/1	0.56	8.64	171,171,171,171	0
59	MG	BA	3112	1/1	0.28	8.31	89,89,89,89	0
59	MG	BA	3135	1/1	0.44	8.31	196,196,196,196	0
59	MG	DA	3130	1/1	2.73	8.19	279,279,279,279	0
59	MG	BA	3087	1/1	0.17	7.57	125,125,125,125	0
59	MG	BA	3048	1/1	0.19	7.41	104,104,104,104	0
59	MG	DA	3125	1/1	0.30	7.25	163,163,163,163	0
59	MG	DA	3091	1/1	0.38	6.73	200,200,200,200	0
59	MG	BA	3061	1/1	0.27	6.40	223,223,223,223	0
59	MG	DA	3002	1/1	0.40	5.92	160,160,160,160	0
59	MG	BA	3097	1/1	0.14	5.86	80,80,80,80	0
59	MG	BA	3091	1/1	0.20	5.52	113,113,113,113	0
59	MG	BA	3027	1/1	0.21	5.40	109,109,109,109	0
59	MG	CA	1640	1/1	0.23	5.35	149,149,149,149	0
59	MG	BA	3123	1/1	0.36	5.32	118,118,118,118	0
59	MG	BA	3134	1/1	0.20	5.17	143,143,143,143	0
59	MG	BA	3018	1/1	0.15	5.10	40,40,40,40	0
59	MG	BA	3103	1/1	0.19	5.02	7,7,7,7	0
59	MG	BA	3083	1/1	0.18	4.83	113,113,113,113	0
59	MG	DA	3014	1/1	0.29	4.65	128,128,128,128	0
59	MG	BA	3044	1/1	0.22	4.58	14,14,14,14	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	AA	1612	1/1	0.20	4.53	104,104,104,104	0
59	MG	BA	3132	1/1	0.25	4.51	165,165,165,165	0
59	MG	BA	3063	1/1	0.18	4.49	13,13,13,13	0
59	MG	DA	3047	1/1	0.23	4.35	136,136,136,136	0
59	MG	AA	1604	1/1	0.16	4.18	120,120,120,120	0
59	MG	DA	3077	1/1	0.27	3.81	114,114,114,114	0
59	MG	CA	1627	1/1	0.23	3.76	198,198,198,198	0
59	MG	DA	3133	1/1	0.41	3.62	239,239,239,239	0
59	MG	BA	3077	1/1	0.15	3.61	121,121,121,121	0
59	MG	BA	3004	1/1	0.24	3.55	147,147,147,147	0
59	MG	BA	3082	1/1	0.16	3.52	85,85,85,85	0
59	MG	AA	1620	1/1	0.19	3.43	28,28,28,28	0
59	MG	DA	3108	1/1	0.42	3.41	172,172,172,172	0
59	MG	DA	3029	1/1	0.43	3.35	151,151,151,151	0
59	MG	BA	3108	1/1	0.17	3.19	8,8,8,8	0
59	MG	BA	3011	1/1	0.30	3.12	131,131,131,131	0
59	MG	DA	3075	1/1	0.31	3.01	140,140,140,140	0
59	MG	BA	3125	1/1	0.18	2.90	41,41,41,41	0
59	MG	DA	3049	1/1	0.27	2.84	235,235,235,235	0
59	MG	BA	3041	1/1	0.19	2.80	13,13,13,13	0
59	MG	DA	3051	1/1	0.24	2.76	124,124,124,124	0
59	MG	BA	3084	1/1	0.18	2.68	50,50,50,50	0
59	MG	BA	3104	1/1	0.18	2.63	12,12,12,12	0
59	MG	CA	1625	1/1	0.24	2.56	91,91,91,91	0
59	MG	DA	3129	1/1	0.85	2.56	203,203,203,203	0
59	MG	BA	3128	1/1	0.17	2.47	7,7,7,7	0
59	MG	BA	3020	1/1	0.15	2.39	35,35,35,35	0
59	MG	AA	1639	1/1	0.17	2.36	126,126,126,126	0
59	MG	BA	3047	1/1	0.15	2.35	152,152,152,152	0
59	MG	DA	3057	1/1	0.67	2.32	212,212,212,212	0
59	MG	BA	3107	1/1	0.18	2.27	8,8,8,8	0
59	MG	BA	3039	1/1	0.16	2.23	20,20,20,20	0
59	MG	BA	3133	1/1	0.19	2.19	10,10,10,10	0
59	MG	DA	3099	1/1	0.21	2.17	180,180,180,180	0
59	MG	DA	3059	1/1	0.22	2.15	183,183,183,183	0
59	MG	BA	3124	1/1	0.16	2.10	16,16,16,16	0
59	MG	BA	3121	1/1	0.17	2.02	10,10,10,10	0
59	MG	DA	3097	1/1	0.25	2.00	116,116,116,116	0
59	MG	CA	1605	1/1	0.20	2.00	40,40,40,40	0
59	MG	AA	1603	1/1	0.15	1.99	121,121,121,121	0
59	MG	DA	3007	1/1	0.29	1.95	253,253,253,253	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	CA	1621	1/1	0.22	1.92	55,55,55,55	0
59	MG	DA	3121	1/1	0.24	1.92	119,119,119,119	0
59	MG	BA	3111	1/1	0.17	1.78	74,74,74,74	0
59	MG	DA	3111	1/1	0.37	1.78	127,127,127,127	0
59	MG	DA	3089	1/1	0.24	1.67	69,69,69,69	0
59	MG	DC	302	1/1	0.25	1.60	121,121,121,121	0
59	MG	CA	1602	1/1	0.20	1.55	175,175,175,175	0
59	MG	AA	1610	1/1	0.10	1.50	210,210,210,210	0
59	MG	AA	1640	1/1	0.17	1.48	17,17,17,17	0
59	MG	AA	1626	1/1	0.16	1.36	106,106,106,106	0
59	MG	AA	1634	1/1	0.14	1.35	199,199,199,199	0
59	MG	CA	1603	1/1	0.28	1.25	165,165,165,165	0
59	MG	AA	1619	1/1	0.13	1.23	125,125,125,125	0
59	MG	AA	1605	1/1	0.17	1.19	35,35,35,35	0
59	MG	BA	3049	1/1	0.17	1.17	11,11,11,11	0
60	ERY	BA	3136	51/51	0.22	1.16	5,11,15,16	0
59	MG	CA	1618	1/1	0.23	1.13	139,139,139,139	0
59	MG	DA	3088	1/1	0.16	1.12	141,141,141,141	0
59	MG	AA	1638	1/1	0.13	1.11	102,102,102,102	0
59	MG	BA	3062	1/1	0.16	1.10	15,15,15,15	0
59	MG	BA	3013	1/1	0.17	1.10	9,9,9,9	0
59	MG	DA	3115	1/1	0.22	0.97	139,139,139,139	0
59	MG	AA	1614	1/1	0.19	0.86	197,197,197,197	0
59	MG	BA	3033	1/1	0.15	0.82	10,10,10,10	0
59	MG	DA	3120	1/1	0.23	0.81	76,76,76,76	0
59	MG	BA	3046	1/1	0.17	0.77	16,16,16,16	0
59	MG	DA	3076	1/1	0.20	0.61	158,158,158,158	0
59	MG	BA	3066	1/1	0.15	0.58	11,11,11,11	0
59	MG	AA	1616	1/1	0.16	0.54	78,78,78,78	0
59	MG	BA	3115	1/1	0.15	0.46	10,10,10,10	0
59	MG	BA	3001	1/1	0.14	0.43	110,110,110,110	0
59	MG	DA	3022	1/1	0.21	0.43	162,162,162,162	0
59	MG	DA	3048	1/1	0.20	0.43	132,132,132,132	0
59	MG	DA	3043	1/1	0.48	0.38	213,213,213,213	0
59	MG	BA	3114	1/1	0.17	0.32	144,144,144,144	0
59	MG	BA	3042	1/1	0.15	0.28	18,18,18,18	0
59	MG	CA	1629	1/1	0.20	0.26	217,217,217,217	0
59	MG	DA	3019	1/1	0.24	0.25	224,224,224,224	0
59	MG	DA	3036	1/1	0.14	0.19	211,211,211,211	0
59	MG	DA	3123	1/1	0.20	0.15	165,165,165,165	0
59	MG	CA	1631	1/1	0.23	0.13	88,88,88,88	0
59	MG	DA	3084	1/1	0.19	0.08	182,182,182,182	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	AA	1630	1/1	0.13	0.08	87,87,87,87	0
59	MG	DA	3065	1/1	0.22	0.02	83,83,83,83	0
59	MG	AA	1631	1/1	0.13	0.02	69,69,69,69	0
59	MG	CA	1611	1/1	0.20	-0.03	122,122,122,122	0
59	MG	DA	3006	1/1	0.23	-0.04	267,267,267,267	0
59	MG	DA	3011	1/1	0.20	-0.05	152,152,152,152	0
59	MG	DA	3128	1/1	0.28	-0.08	123,123,123,123	0
59	MG	BA	3106	1/1	0.15	-0.08	25,25,25,25	0
59	MG	DA	3071	1/1	0.19	-0.09	52,52,52,52	0
59	MG	DA	3018	1/1	0.24	-0.14	232,232,232,232	0
59	MG	AA	1608	1/1	0.15	-0.15	32,32,32,32	0
59	MG	DA	3069	1/1	0.21	-0.16	202,202,202,202	0
59	MG	BA	3073	1/1	0.22	-0.18	135,135,135,135	0
59	MG	BA	3071	1/1	0.15	-0.20	112,112,112,112	0
59	MG	DA	3035	1/1	0.19	-0.24	84,84,84,84	0
59	MG	DA	3114	1/1	0.17	-0.27	123,123,123,123	0
59	MG	BA	3008	1/1	0.13	-0.28	13,13,13,13	0
59	MG	DA	3104	1/1	0.18	-0.30	34,34,34,34	0
59	MG	DA	3103	1/1	0.17	-0.30	98,98,98,98	0
59	MG	AN	202	1/1	0.17	-0.31	169,169,169,169	0
59	MG	DA	3116	1/1	0.19	-0.31	66,66,66,66	0
59	MG	DA	3083	1/1	0.21	-0.36	224,224,224,224	0
59	MG	CA	1616	1/1	0.32	-0.41	232,232,232,232	0
59	MG	BA	3079	1/1	0.15	-0.46	30,30,30,30	0
59	MG	BA	3045	1/1	0.15	-0.50	17,17,17,17	0
59	MG	BA	3022	1/1	0.15	-0.50	9,9,9,9	0
59	MG	AA	1622	1/1	0.13	-0.51	97,97,97,97	0
59	MG	BA	3127	1/1	0.13	-0.52	15,15,15,15	0
59	MG	DA	3044	1/1	0.19	-0.54	83,83,83,83	0
59	MG	BA	3050	1/1	0.12	-0.54	37,37,37,37	0
59	MG	BA	3098	1/1	0.16	-0.55	51,51,51,51	0
59	MG	CA	1609	1/1	0.20	-0.60	80,80,80,80	0
59	MG	CA	1633	1/1	0.11	-0.64	77,77,77,77	0
59	MG	BA	3016	1/1	0.14	-0.65	7,7,7,7	0
59	MG	DA	3095	1/1	0.20	-0.65	116,116,116,116	0
59	MG	AA	1635	1/1	0.09	-0.66	88,88,88,88	0
59	MG	CA	1636	1/1	0.18	-0.66	155,155,155,155	0
59	MG	BA	3131	1/1	0.12	-0.67	140,140,140,140	0
59	MG	CA	1632	1/1	0.22	-0.68	163,163,163,163	0
59	MG	BA	3037	1/1	0.13	-0.68	17,17,17,17	0
59	MG	BA	3007	1/1	0.10	-0.68	69,69,69,69	0
59	MG	DA	3037	1/1	0.14	-0.69	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	BA	3120	1/1	0.10	-0.69	53,53,53,53	0
59	MG	CA	1638	1/1	0.15	-0.77	139,139,139,139	0
59	MG	BA	3101	1/1	0.13	-0.78	64,64,64,64	0
59	MG	BA	3015	1/1	0.13	-0.78	38,38,38,38	0
59	MG	AA	1628	1/1	0.12	-0.78	183,183,183,183	0
59	MG	DA	3021	1/1	0.18	-0.85	41,41,41,41	0
59	MG	BA	3017	1/1	0.10	-0.85	30,30,30,30	0
59	MG	CA	1617	1/1	0.17	-0.89	280,280,280,280	0
59	MG	DA	3107	1/1	0.18	-0.92	121,121,121,121	0
59	MG	DA	3100	1/1	0.19	-0.97	93,93,93,93	0
59	MG	CA	1634	1/1	0.15	-0.98	153,153,153,153	0
59	MG	DA	3080	1/1	0.15	-1.01	137,137,137,137	0
59	MG	DA	3042	1/1	0.19	-1.03	94,94,94,94	0
59	MG	AA	1633	1/1	0.09	-1.09	75,75,75,75	0
59	MG	DB	201	1/1	0.10	-1.10	114,114,114,114	0
59	MG	BA	3105	1/1	0.14	-1.10	9,9,9,9	0
59	MG	BA	3074	1/1	0.13	-1.12	18,18,18,18	0
59	MG	DA	3034	1/1	0.15	-1.16	89,89,89,89	0
59	MG	DA	3087	1/1	0.16	-1.21	164,164,164,164	0
59	MG	AA	1602	1/1	0.14	-1.21	119,119,119,119	0
59	MG	AA	1632	1/1	0.11	-1.28	31,31,31,31	0
59	MG	BA	3012	1/1	0.15	-1.31	6,6,6,6	0
59	MG	AA	1637	1/1	0.08	-1.34	104,104,104,104	0
59	MG	DA	3101	1/1	0.20	-1.38	104,104,104,104	0
59	MG	DA	3110	1/1	0.16	-1.42	183,183,183,183	0
59	MG	DA	3126	1/1	0.11	-1.43	76,76,76,76	0
59	MG	DA	3131	1/1	0.17	-1.44	70,70,70,70	0
59	MG	AA	1601	1/1	0.08	-1.46	78,78,78,78	0
59	MG	CA	1601	1/1	0.12	-1.51	179,179,179,179	0
59	MG	DA	3093	1/1	0.15	-1.55	228,228,228,228	0
59	MG	DA	3112	1/1	0.13	-1.55	66,66,66,66	0
59	MG	DA	3085	1/1	0.20	-1.56	148,148,148,148	0
59	MG	BA	3099	1/1	0.10	-1.58	18,18,18,18	0
59	MG	CA	1606	1/1	0.14	-1.58	63,63,63,63	0
59	MG	BB	203	1/1	0.11	-1.58	17,17,17,17	0
59	MG	DA	3072	1/1	0.13	-1.61	132,132,132,132	0
59	MG	BA	3003	1/1	0.13	-1.61	42,42,42,42	0
61	ZN	D4	101	1/1	0.12	-1.64	151,151,151,151	0
59	MG	DA	3105	1/1	0.16	-1.69	51,51,51,51	0
59	MG	AA	1607	1/1	0.13	-1.69	119,119,119,119	0
59	MG	AA	1618	1/1	0.09	-1.70	164,164,164,164	0
61	ZN	B4	101	1/1	0.11	-1.72	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	CA	1622	1/1	0.07	-1.72	208,208,208,208	0
59	MG	BA	3032	1/1	0.14	-1.77	16,16,16,16	0
59	MG	DA	3001	1/1	0.12	-1.79	130,130,130,130	0
59	MG	CA	1604	1/1	0.08	-1.79	60,60,60,60	0
59	MG	DC	301	1/1	0.12	-1.81	124,124,124,124	0
59	MG	CA	1610	1/1	0.09	-1.83	175,175,175,175	0
59	MG	BA	3038	1/1	0.13	-1.85	7,7,7,7	0
59	MG	AA	1606	1/1	0.08	-1.86	58,58,58,58	0
59	MG	DA	3086	1/1	0.15	-1.94	94,94,94,94	0
59	MG	CA	1608	1/1	0.15	-2.02	51,51,51,51	0
59	MG	BA	3067	1/1	0.13	-2.12	10,10,10,10	0
59	MG	DA	3113	1/1	0.07	-2.13	96,96,96,96	0
59	MG	AA	1621	1/1	0.07	-2.14	91,91,91,91	0
59	MG	BA	3113	1/1	0.09	-2.14	21,21,21,21	0
59	MG	DA	3096	1/1	0.08	-2.15	92,92,92,92	0
59	MG	DA	3038	1/1	0.14	-2.16	204,204,204,204	0
59	MG	CA	1623	1/1	0.12	-2.23	120,120,120,120	0
59	MG	CA	1619	1/1	0.12	-2.24	201,201,201,201	0
59	MG	DA	3117	1/1	0.15	-2.24	71,71,71,71	0
59	MG	DA	3009	1/1	0.14	-2.25	101,101,101,101	0
59	MG	DA	3068	1/1	0.11	-2.26	78,78,78,78	0
59	MG	DA	3132	1/1	0.13	-2.26	175,175,175,175	0
59	MG	BA	3009	1/1	0.13	-2.27	13,13,13,13	0
59	MG	DA	3024	1/1	0.17	-2.31	106,106,106,106	0
59	MG	DA	3106	1/1	0.15	-2.34	205,205,205,205	0
59	MG	BA	3078	1/1	0.08	-2.40	41,41,41,41	0
59	MG	DA	3040	1/1	0.16	-2.40	52,52,52,52	0
59	MG	AA	1641	1/1	0.11	-2.41	39,39,39,39	0
59	MG	BA	3069	1/1	0.09	-2.41	176,176,176,176	0
59	MG	CA	1607	1/1	0.16	-2.42	154,154,154,154	0
59	MG	DA	3090	1/1	0.11	-2.42	91,91,91,91	0
59	MG	DA	3067	1/1	0.10	-2.49	38,38,38,38	0
59	MG	DA	3119	1/1	0.13	-2.51	88,88,88,88	0
59	MG	BA	3085	1/1	0.13	-2.52	6,6,6,6	0
59	MG	CA	1630	1/1	0.08	-2.56	123,123,123,123	0
59	MG	DA	3032	1/1	0.13	-2.61	100,100,100,100	0
59	MG	BA	3051	1/1	0.12	-2.62	10,10,10,10	0
59	MG	DA	3053	1/1	0.11	-2.62	80,80,80,80	0
59	MG	CA	1642	1/1	0.05	-2.62	58,58,58,58	0
59	MG	DA	3061	1/1	0.10	-2.77	134,134,134,134	0
59	MG	DA	3027	1/1	0.10	-2.79	144,144,144,144	0
59	MG	BA	3064	1/1	0.11	-2.79	6,6,6,6	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	DA	3008	1/1	0.17	-2.79	142,142,142,142	0
59	MG	DA	3025	1/1	0.11	-2.86	110,110,110,110	0
59	MG	BA	3035	1/1	0.12	-2.91	11,11,11,11	0
59	MG	DA	3098	1/1	0.15	-2.97	118,118,118,118	0
59	MG	BA	3096	1/1	0.12	-3.01	45,45,45,45	0
59	MG	DA	3017	1/1	0.14	-3.10	68,68,68,68	0
59	MG	AA	1613	1/1	0.08	-3.11	57,57,57,57	0
59	MG	AA	1627	1/1	0.09	-3.19	78,78,78,78	0
59	MG	DA	3012	1/1	0.09	-3.21	51,51,51,51	0
59	MG	DA	3073	1/1	0.09	-3.22	162,162,162,162	0
59	MG	CA	1639	1/1	0.08	-3.24	226,226,226,226	0
59	MG	DA	3050	1/1	0.13	-3.25	125,125,125,125	0
59	MG	DA	3052	1/1	0.10	-3.26	49,49,49,49	0
59	MG	AN	201	1/1	0.07	-3.41	105,105,105,105	0
59	MG	BA	3002	1/1	0.10	-3.42	77,77,77,77	0
59	MG	BA	3005	1/1	0.10	-3.44	93,93,93,93	0
59	MG	DA	3023	1/1	0.12	-3.51	78,78,78,78	0
59	MG	DA	3039	1/1	0.13	-3.51	99,99,99,99	0
59	MG	DA	3070	1/1	0.10	-3.52	56,56,56,56	0
59	MG	BA	3119	1/1	0.11	-3.54	12,12,12,12	0
59	MG	AA	1623	1/1	0.09	-3.55	72,72,72,72	0
59	MG	CA	1615	1/1	0.09	-3.56	124,124,124,124	0
59	MG	BA	3029	1/1	0.09	-3.68	66,66,66,66	0
59	MG	DA	3102	1/1	0.07	-3.73	62,62,62,62	0
59	MG	DA	3056	1/1	0.12	-3.77	112,112,112,112	0
59	MG	AA	1629	1/1	0.05	-3.84	183,183,183,183	0
59	MG	BB	202	1/1	0.08	-3.90	43,43,43,43	0
59	MG	DA	3031	1/1	0.10	-4.12	79,79,79,79	0
59	MG	CA	1620	1/1	0.08	-4.12	170,170,170,170	0
59	MG	DA	3054	1/1	0.08	-4.14	71,71,71,71	0
59	MG	BA	3053	1/1	0.08	-4.17	9,9,9,9	0
59	MG	CA	1641	1/1	0.09	-4.18	80,80,80,80	0
59	MG	DA	3094	1/1	0.08	-4.24	96,96,96,96	0
59	MG	BA	3021	1/1	0.07	-4.29	43,43,43,43	0
59	MG	BA	3102	1/1	0.12	-4.31	23,23,23,23	0
59	MG	BA	3068	1/1	0.09	-4.38	20,20,20,20	0
59	MG	DA	3004	1/1	0.14	-4.39	80,80,80,80	0
59	MG	CA	1637	1/1	0.13	-4.40	63,63,63,63	0
59	MG	DA	3124	1/1	0.11	-4.44	48,48,48,48	0
59	MG	DA	3055	1/1	0.09	-4.52	84,84,84,84	0
59	MG	BA	3072	1/1	0.11	-4.59	10,10,10,10	0
59	MG	DA	3066	1/1	0.08	-4.70	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	BA	3065	1/1	0.09	-4.73	7,7,7,7	0
59	MG	BA	3095	1/1	0.09	-4.84	22,22,22,22	0
59	MG	BA	3090	1/1	0.07	-4.88	73,73,73,73	0
59	MG	BA	3129	1/1	0.10	-5.00	14,14,14,14	0
59	MG	BA	3006	1/1	0.06	-5.05	31,31,31,31	0
59	MG	DA	3118	1/1	0.11	-5.08	70,70,70,70	0
59	MG	BA	3024	1/1	0.10	-5.11	17,17,17,17	0
59	MG	AA	1609	1/1	0.07	-5.16	28,28,28,28	0
59	MG	BB	204	1/1	0.09	-5.60	20,20,20,20	0
59	MG	DA	3081	1/1	0.10	-5.74	92,92,92,92	0
59	MG	BA	3023	1/1	0.09	-5.86	7,7,7,7	0
59	MG	DA	3046	1/1	0.11	-5.96	76,76,76,76	0
59	MG	BA	3109	1/1	0.06	-6.06	57,57,57,57	0
59	MG	BA	3028	1/1	0.12	-6.11	32,32,32,32	0
59	MG	BA	3081	1/1	0.08	-6.21	39,39,39,39	0
59	MG	BA	3052	1/1	0.10	-6.29	25,25,25,25	0
59	MG	BA	3116	1/1	0.07	-6.31	17,17,17,17	0
59	MG	BA	3092	1/1	0.08	-6.57	38,38,38,38	0
59	MG	BA	3076	1/1	0.06	-6.82	32,32,32,32	0
59	MG	BA	3010	1/1	0.07	-6.87	19,19,19,19	0
59	MG	BA	3126	1/1	0.10	-7.02	18,18,18,18	0
59	MG	CA	1613	1/1	0.12	-7.09	114,114,114,114	0
59	MG	BA	3031	1/1	0.08	-7.15	34,34,34,34	0
59	MG	AA	1636	1/1	0.08	-7.28	25,25,25,25	0
59	MG	BA	3117	1/1	0.06	-8.01	83,83,83,83	0
59	MG	BA	3054	1/1	0.10	-8.37	25,25,25,25	0
59	MG	BA	3058	1/1	0.07	-8.50	35,35,35,35	0
59	MG	AA	1615	1/1	0.05	-8.56	128,128,128,128	0
59	MG	BA	3043	1/1	0.11	-9.41	29,29,29,29	0
59	MG	BA	3094	1/1	0.08	-9.57	24,24,24,24	0
59	MG	BA	3093	1/1	0.06	-9.84	45,45,45,45	0
59	MG	DA	3122	1/1	0.10	-9.85	72,72,72,72	0
59	MG	CA	1635	1/1	0.08	-9.92	85,85,85,85	0
59	MG	BA	3026	1/1	0.07	-10.71	19,19,19,19	0
59	MG	DA	3041	1/1	0.12	-12.97	122,122,122,122	0
59	MG	BA	3088	1/1	0.05	-13.57	11,11,11,11	0
59	MG	BA	3080	1/1	0.12	-13.60	11,11,11,11	0
59	MG	AA	1611	1/1	0.06	-14.56	54,54,54,54	0
59	MG	DA	3092	1/1	0.12	-18.21	121,121,121,121	0
59	MG	BA	3089	1/1	0.09	-22.04	30,30,30,30	0
59	MG	BA	3122	1/1	0.09	-30.99	21,21,21,21	0
59	MG	DA	3030	1/1	0.18	-	111,111,111,111	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
59	MG	DA	3003	1/1	1.86	-	268,268,268,268	0

6.5 Other polymers ⓘ

There are no such residues in this entry.