



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:33 PM GMT

PDB ID : 4WT8  
Title : Crystal Structure of bactobolin A bound to 70S ribosome-tRNA complex  
Authors : Amunts, A.; Fiedorczuk, K.; Ramakrishnan, V.  
Deposited on : 2014-10-29  
Resolution : 3.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

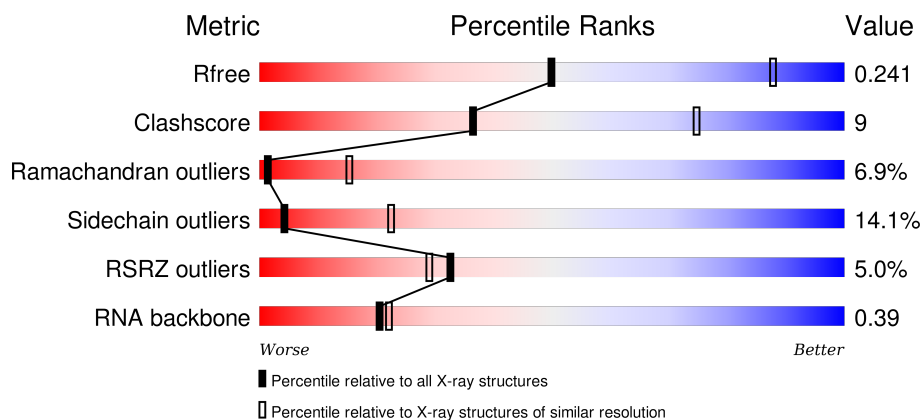
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 Å.

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





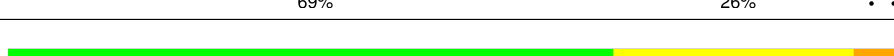

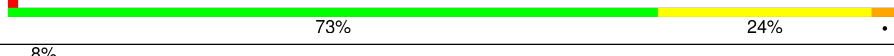
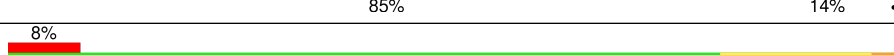

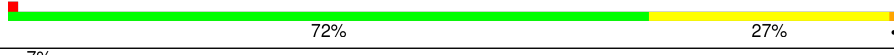
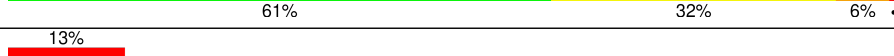
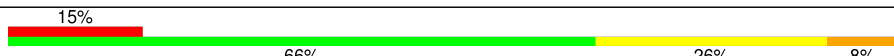

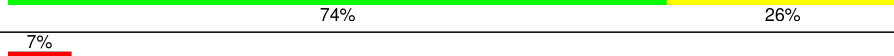
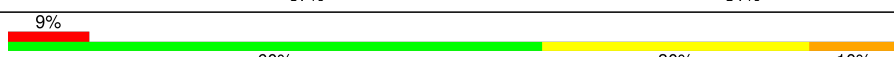





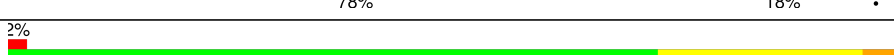



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	1476 (3.50-3.30)
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)
RNA backbone	2183	1041 (4.00-2.80)

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

Mol	Chain	Length	Quality of chain
1	A2	9	
2	AA	234	
2	BA	234	
3	AC	238	

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Mol	Chain	Length	Quality of chain
4	AD	208	
4	BD	208	
5	AE	150	
5	BE	150	
6	AF	101	
6	BF	101	
7	AG	155	
7	BG	155	
8	AH	138	
8	BH	138	
9	AI	127	
9	BI	127	
10	AJ	98	
10	BJ	98	
11	AK	119	
11	BK	119	
12	AL	124	
12	BL	124	
13	AM	124	
13	BM	124	
14	AN	60	
14	BN	60	
15	AO	88	
15	BO	88	
16	AP	83	

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Mol	Chain	Length	Quality of chain
16	BP	83	
17	AR	99	
17	BR	99	
18	AS	70	
18	BS	70	
19	AT	78	
19	BT	78	
20	AU	99	
20	BU	99	
21	AW	24	
21	BW	24	
22	Ab	1504	
22	Bb	1504	
23	B2	10	
24	BC	206	
25	C2	76	
25	C3	76	
25	D3	76	
26	C4	77	
27	CA	206	
28	CB	271	
28	DB	271	
29	CC	204	
29	DC	204	
30	CD	207	

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Mol	Chain	Length	Quality of chain
30	DD	207	
31	CE	181	
31	DE	181	
32	CF	159	
32	DF	159	
33	CI	145	
33	DI	145	
34	CJ	130	
34	DJ	130	
35	CM	138	
35	DM	138	
36	CN	122	
36	DN	122	
37	CO	146	
37	DO	146	
38	CP	141	
38	DP	141	
39	CQ	117	
39	DQ	117	
40	CR	98	
40	DR	98	
41	CS	137	
41	DS	137	
42	CT	117	
42	DT	117	

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Mol	Chain	Length	Quality of chain
43	CU	101	
43	DU	101	
44	CW	113	
45	CX	92	
45	DX	92	
46	CY	100	
46	DY	100	
47	CZ	176	
47	DZ	176	
48	Ca	84	
48	Da	84	
49	CH	93	
49	DH	93	
50	CK	71	
50	DK	71	
51	CL	59	
51	DL	59	
52	C5	30	
52	D5	30	
53	C6	59	
53	D6	59	
54	C7	44	
54	D7	44	
55	C8	48	
55	D8	48	

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Mol	Chain	Length	Quality of chain
56	C9	63	
56	D9	63	
57	C0	36	
57	D0	36	
58	C1	2899	
58	D1	2899	
59	Cs	119	
59	Ds	119	
60	D2	20	
61	D4	76	
62	DA	206	
63	DW	113	
64	DV	55	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
65	PAR	Ab	1601	-	-	-	X
65	PAR	Bb	1601	-	-	-	X
66	3V6	C1	3001	-	-	-	X
66	3V6	D1	3001	-	-	X	X
67	MG	C1	3002	-	-	-	X
67	MG	D1	3002	-	-	X	-

## 2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 295910 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A2	9	Total	C	N	O	P	0	0	0
			173	76	29	59	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AA	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			
2	BA	234	Total	C	N	O	S	0	0	0
			1901	1213	341	342	5			

- 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
			1612	1016	314	281	1			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			
5	BE	150	Total	C	N	O	S	0	0	0
			1147	724	217	202	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			
6	BF	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			
7	BG	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			
8	BH	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	AI	127	Total	C	N	O	0	0	0
			1011	639	198	174			
9	BI	127	Total	C	N	O	0	0	0
			1011	639	198	174			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	58	ARG	HIS	conflict	UNP P80374

- 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
			795	499	156	139	1			
10	BJ	98	Total	C	N	O	S	0	0	0
			795	499	156	139	1			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			
12	BL	124	Total	C	N	O	S	0	0	0
			971	611	195	164	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AM	124	Total	C	N	O	S	0	0	0
			988	611	205	170	2			
13	BM	124	Total	C	N	O	S	0	0	0
			988	611	205	170	2			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			
16	BP	83	Total	C	N	O	S	0	0	0
			701	443	139	118	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AR	99	Total	C	N	O	S	0	0	0
			824	528	151	143	2			
17	BR	99	Total	C	N	O	S	0	0	0
			824	528	151	143	2			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AT	78	Total	C	N	O	S	0	0	0
			630	403	114	111	2			
19	BT	78	Total	C	N	O	S	0	0	0
			630	403	114	111	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AU	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			
20	BU	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	AW	24	Total	C	N	O	0	0	0
			209	128	50	31			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	BW	24	Total	C	N	O	0	0	0
			209	128	50	31			

- Molecule 22 is a RNA chain called RNA (1504-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	Ab	1504	Total	C	N	O	P	0	0	0
			32329	14390	5992	10444	1503			
22	Bb	1504	Total	C	N	O	P	0	0	0
			32329	14390	5992	10444	1503			

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	B2	10	Total	C	N	O	P	0	0	0
			194	86	34	64	10			

- Molecule 24 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	BC	206	Total	C	N	O	S	0	0	0
			1613	1016	314	282	1			

- Molecule 25 is a RNA chain called A site tNA, E site tNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	C2	75	Total	C	N	O	P	0	0	0
			1597	713	285	525	74			
25	C3	76	Total	C	N	O	P	0	0	0
			1619	723	290	531	75			
25	D3	76	Total	C	N	O	P	0	0	0
			1619	723	290	531	75			

- Molecule 26 is a RNA chain called P site trNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	C4	77	Total	C	N	O	P	0	0	0
			1640	732	297	535	76			

- Molecule 27 is a protein called 50S ribosomal protein L1.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
27	CA	190	Total	C	N	O	0	0	0
			1156	706	220	230			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CA	106	ALA	GLY	conflict	UNP Q5SLP7

- Molecule 28 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	CB	271	Total	C	N	O	S	0	0	0
			2105	1329	416	357	3			
28	DB	271	Total	C	N	O	S	0	0	0
			2105	1329	416	357	3			

- Molecule 29 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	CC	204	Total	C	N	O	S	0	0	0
			1564	988	299	271	6			
29	DC	204	Total	C	N	O	S	0	0	0
			1564	988	299	271	6			

- Molecule 30 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	CD	207	Total	C	N	O	S	0	0	0
			1624	1035	303	283	3			
30	DD	207	Total	C	N	O	S	0	0	0
			1624	1035	303	283	3			

- Molecule 31 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	CE	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			
31	DE	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			

- Molecule 32 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	CF	159	Total	C	N	O	S	0	0	0
			1223	773	228	221	1			
32	DF	159	Total	C	N	O	S	0	0	0
			1223	773	228	221	1			

- Molecule 33 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	CI	145	Total	C	N	O	S	0	0	0
			1132	723	200	208	1			
33	DI	145	Total	C	N	O	S	0	0	0
			1132	723	200	208	1			

- Molecule 34 is a protein called ribosomal L10 protein.

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

- Molecule 35 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	CM	138	Total	C	N	O	S	0	0	0
			1105	712	206	183	4			
35	DM	138	Total	C	N	O	S	0	0	0
			1105	712	206	183	4			

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	CN	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			
36	DN	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	CO	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	DO	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	CP	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			
38	DP	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	CQ	117	Total	C	N	O		0	0	0
			960	599	202	159				
39	DQ	117	Total	C	N	O		0	0	0
			960	599	202	159				

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	CR	98	Total	C	N	O		0	0	0
			771	486	154	131				
40	DR	98	Total	C	N	O		0	0	0
			771	486	154	131				

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	CS	137	Total	C	N	O	S	0	0	0
			1142	710	234	197	1			
41	DS	137	Total	C	N	O	S	0	0	0
			1142	710	234	197	1			

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	CT	117	Total	C	N	O	S	0	0	0
			958	604	202	151	1			
42	DT	117	Total	C	N	O	S	0	0	0
			958	604	202	151	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CT	32	ALA	PHE	conflict	UNP P60491
DT	32	ALA	PHE	conflict	UNP P60491

- Molecule 43 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	CU	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			
43	DU	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 44 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
44	CW	113	Total	C	N	O	S	0	0	0
			896	563	176	155	2			

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
45	CX	92	Total	C	N	O	0	0	0
			726	471	131	124			
45	DX	92	Total	C	N	O	0	0	0
			726	471	131	124			

- Molecule 46 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	CY	100	Total	C	N	O	S	0	0	0
			776	500	148	124	4			
46	DY	100	Total	C	N	O	S	0	0	0
			776	500	148	124	4			

- Molecule 47 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	CZ	176	Total	C	N	O	S	0	0	0
			1404	897	252	253	2			
47	DZ	176	Total	C	N	O	S	0	0	0
			1404	897	252	253	2			

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	Ca	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			
48	Da	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			

- Molecule 49 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	CH	93	Total	C	N	O	S	0	0	0
			734	460	147	126	1			
49	DH	93	Total	C	N	O	S	0	0	0
			734	460	147	126	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DH	81	ARG	LYS	conflict	UNP P60494

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	CK	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			
50	DK	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			

- Molecule 51 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	CL	59	Total	C	N	O	S	0	0	0
			468	298	90	79	1			
51	DL	59	Total	C	N	O	S	0	0	0
			468	298	90	79	1			

- Molecule 52 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	C5	30	Total	C	N	O	S	0	0	0
			226	142	36	44	4			
52	D5	30	Total	C	N	O	S	0	0	0
			226	142	36	44	4			

- Molecule 53 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	C6	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			
53	D6	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

- Molecule 54 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	C7	44	Total	C	N	O	S	0	0	0
			381	235	77	65	4			
54	D7	44	Total	C	N	O	S	0	0	0
			381	235	77	65	4			

- Molecule 55 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	C8	48	Total	C	N	O	S	0	0	0
			419	257	104	56	2			
55	D8	48	Total	C	N	O	S	0	0	0
			419	257	104	56	2			

- Molecule 56 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	C9	63	Total	C	N	O	S	0	0	0
			508	326	101	79	2			
56	D9	63	Total	C	N	O	S	0	0	0
			508	326	101	79	2			

- Molecule 57 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
57	C0	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			
57	D0	36	Total	C	N	O	S	0	0	0
			299	183	67	46	3			

- Molecule 58 is a RNA chain called 23S rRNA (2899-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
58	C1	2807	Total	C	N	O	P	0	0	0
			60459	26907	11311	19435	2806			
58	D1	2807	Total	C	N	O	P	0	0	0
			60459	26907	11311	19435	2806			

- Molecule 59 is a RNA chain called 5S rRNA (119-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
59	Cs	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			
59	Ds	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			

- Molecule 60 is a RNA chain called tRNA (5'-D(\*AP\*UP\*CP\*CP\*CP\*CP\*GP\*UP\*GP\*UP\*CP\*CP\*UP\*UP\*GP\*GP\*UP\*UP\*CP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
60	D2	20	Total	C	N	O	P	0	0	0
			416	186	65	146	19			

- Molecule 61 is a RNA chain called tRNA (76-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
61	D4	76	Total	C	N	O	P	0	0	0
			1623	723	294	530	76			

- Molecule 62 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
62	DA	190	Total	C	N	O	0	0	0
			1155	705	220	230			

- Molecule 63 is a protein called 50S ribosomal protein L22.

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

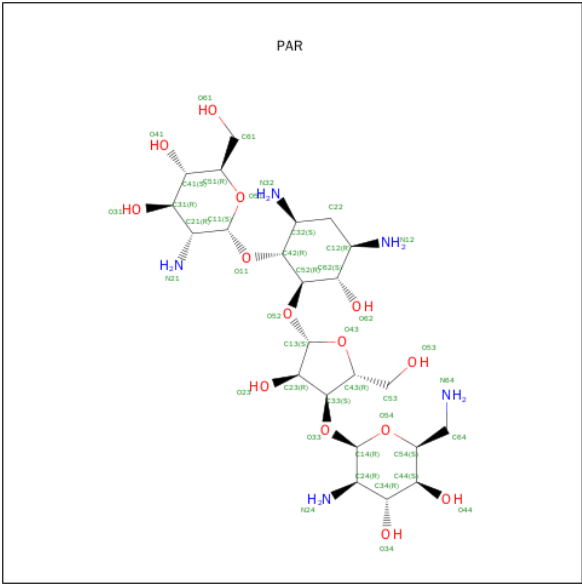
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DW	113	ALA	-	expression tag	UNP Q5SHP3

- Molecule 64 is a RNA chain called DNA (55-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
64	DV	55	Total	C	N	O	P	0	0	0
			1167	527	220	379	41			

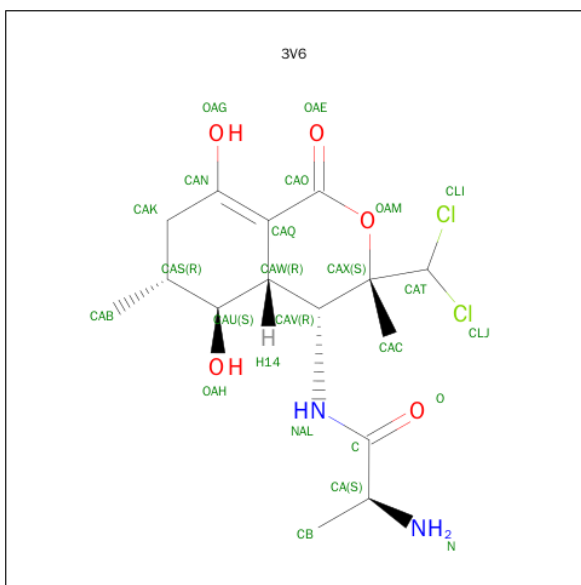
- Molecule 65 is PAROMOMYCIN (three-letter code: PAR) (formula: C<sub>23</sub>H<sub>45</sub>N<sub>5</sub>O<sub>14</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
65	Ab	1	Total	C	N	O	0	0
			42	23	5	14		
65	Bb	1	Total	C	N	O	0	0
			42	23	5	14		

- Molecule 66 is Bactobolin A (three-letter code: 3V6) (formula: C<sub>15</sub>H<sub>22</sub>Cl<sub>2</sub>N<sub>2</sub>O<sub>5</sub>).



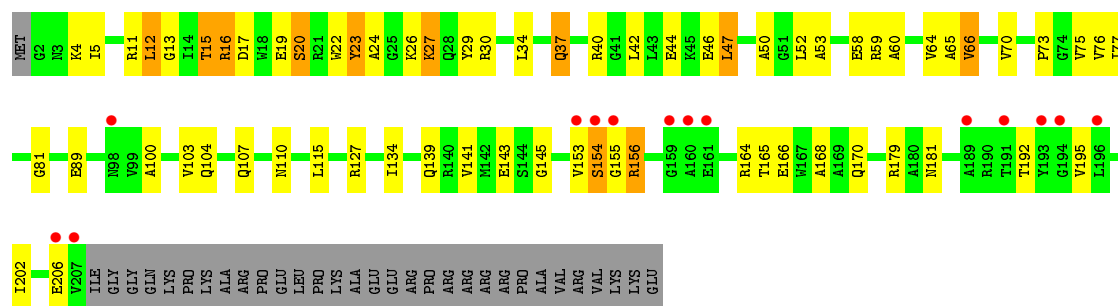


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
66	C1	1	Total 24	C 15	Cl 2	N 2	O 5	0	0
66	D1	1	Total 24	C 15	Cl 2	N 2	O 5	0	0

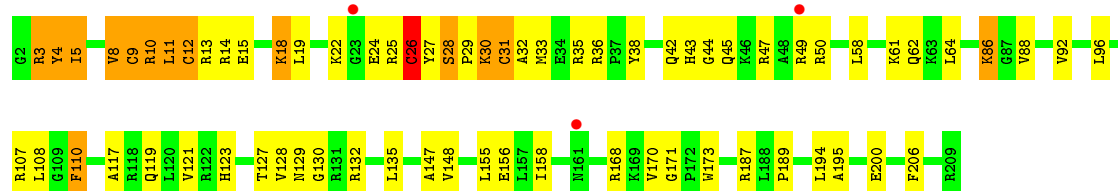
- Molecule 67 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
67	C1	1	Total Mg 1 1	0	0
67	D1	1	Total Mg 1 1	0	0

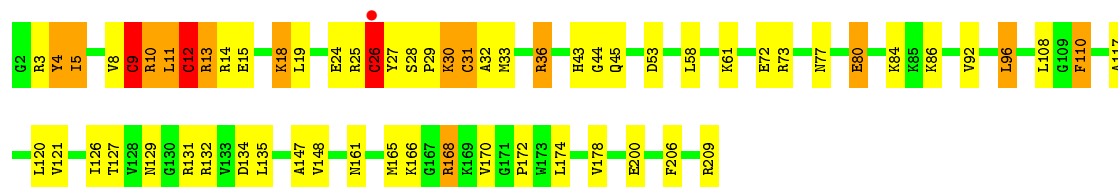




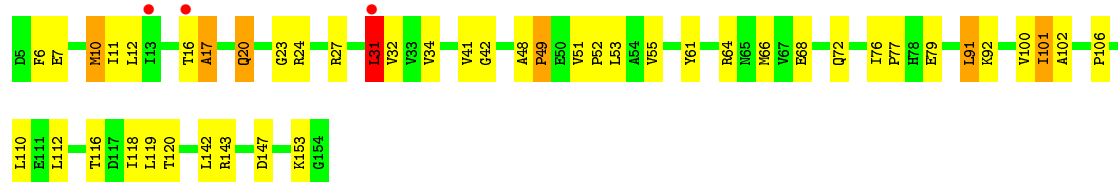
- Molecule 4: 30S ribosomal protein S4



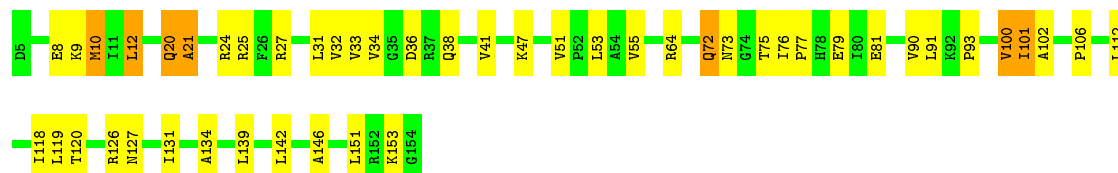
- Molecule 4: 30S ribosomal protein S4



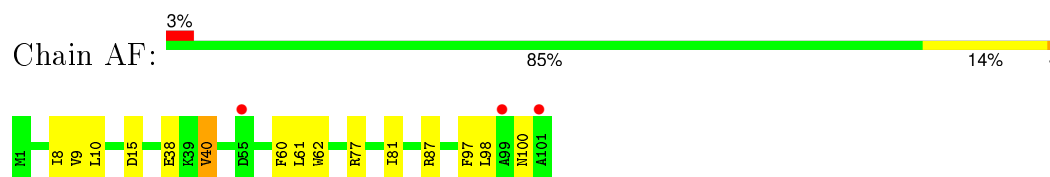
- Molecule 5: 30S ribosomal protein S5



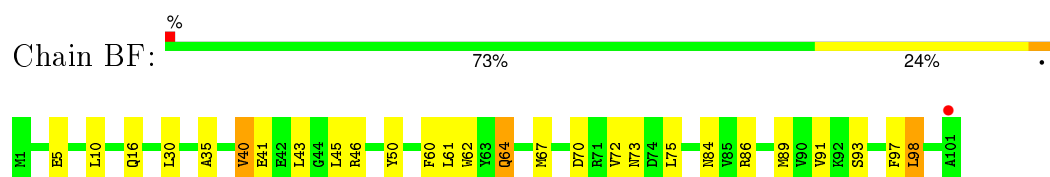
- Molecule 5: 30S ribosomal protein S5



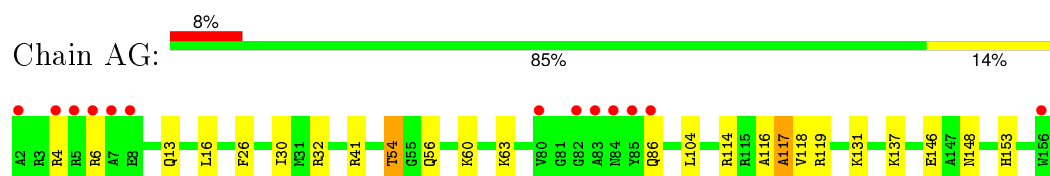
- Molecule 6: 30S ribosomal protein S6



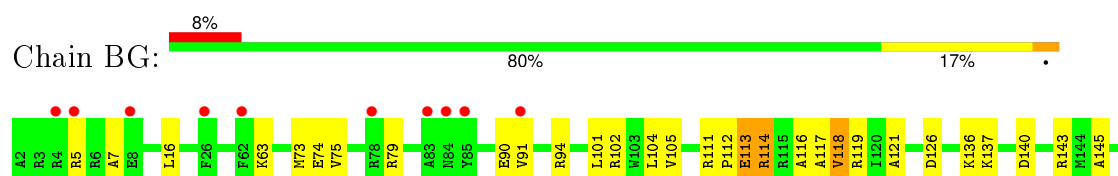
- Molecule 6: 30S ribosomal protein S6



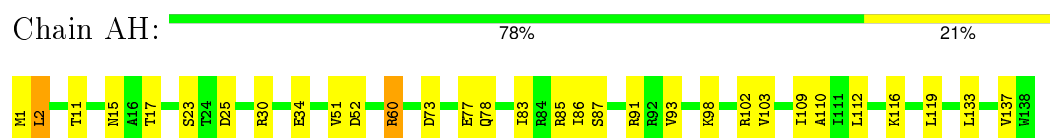
- Molecule 7: 30S ribosomal protein S7



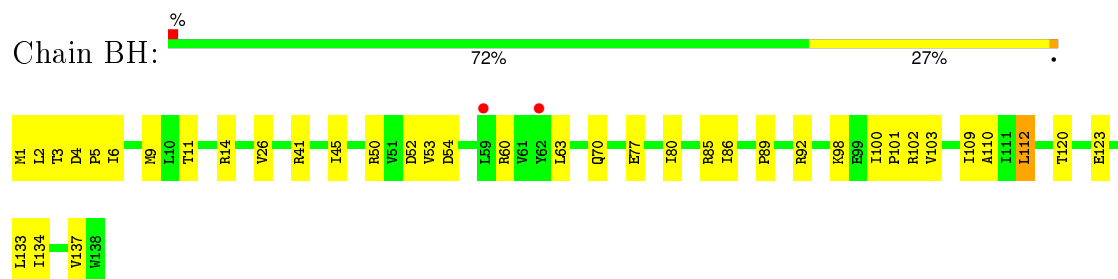
- Molecule 7: 30S ribosomal protein S7



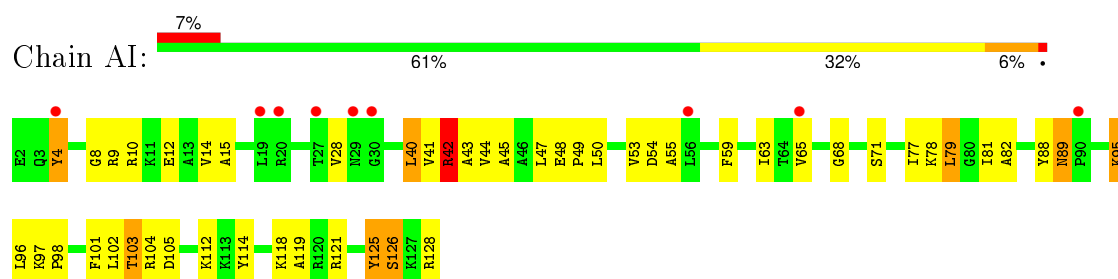
- Molecule 8: 30S ribosomal protein S8



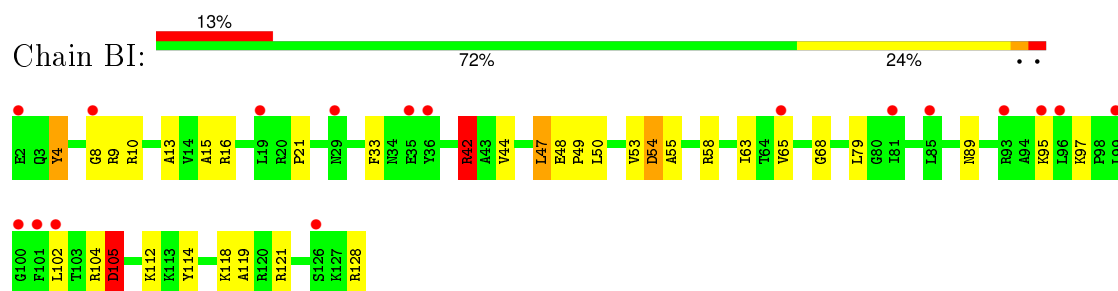
- Molecule 8: 30S ribosomal protein S8



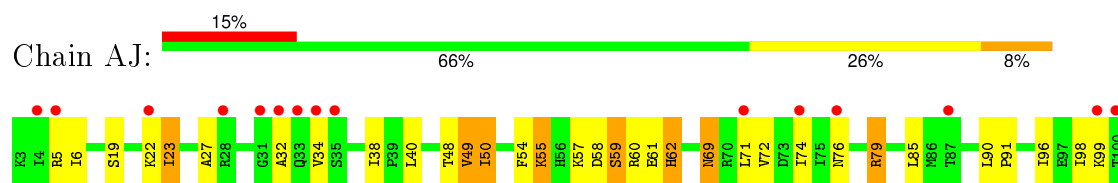
- Molecule 9: 30S ribosomal protein S9



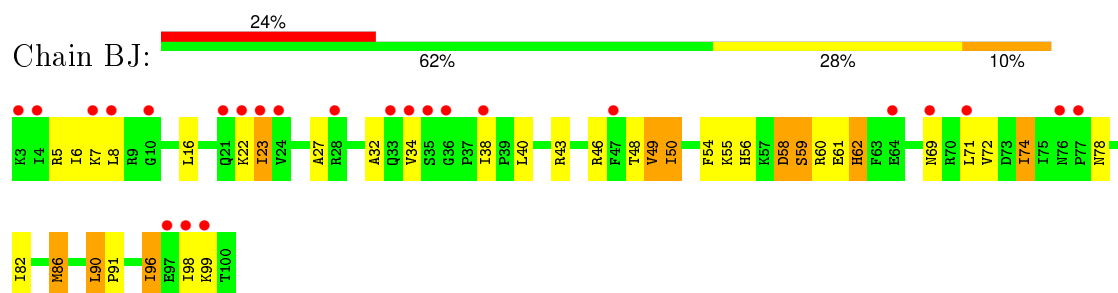
- Molecule 9: 30S ribosomal protein S9



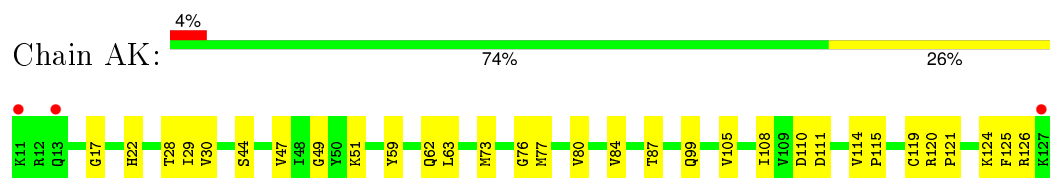
- Molecule 10: 30S ribosomal protein S10



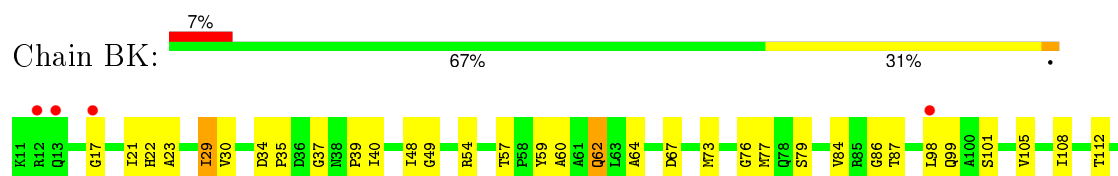
- Molecule 10: 30S ribosomal protein S10

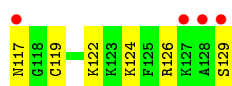


- Molecule 11: 30S ribosomal protein S11



- Molecule 11: 30S ribosomal protein S11





- Molecule 12: 30S ribosomal protein S12



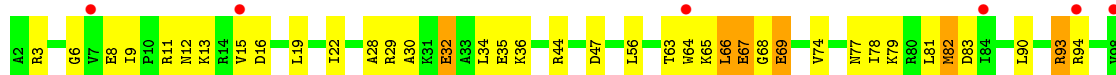
- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13

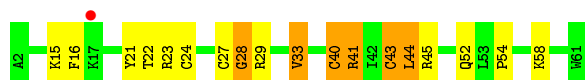


- Molecule 13: 30S ribosomal protein S13

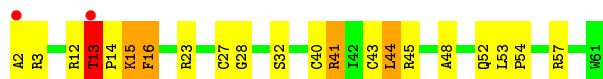


- Molecule 14: 30S ribosomal protein S14 type Z

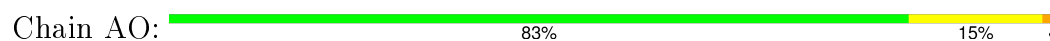




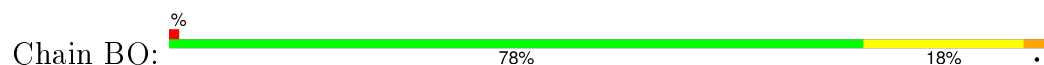
- Molecule 14: 30S ribosomal protein S14 type Z



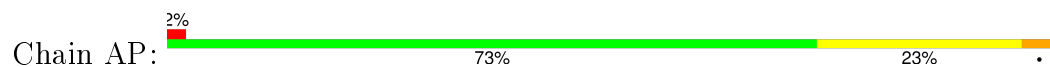
- Molecule 15: 30S ribosomal protein S15



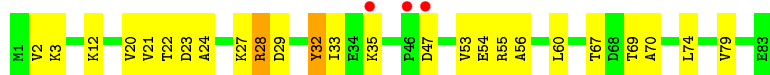
- Molecule 15: 30S ribosomal protein S15



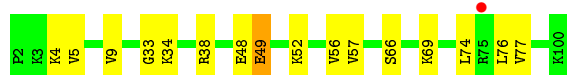
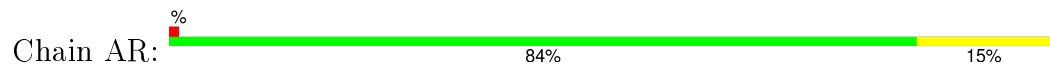
- Molecule 16: 30S ribosomal protein S16



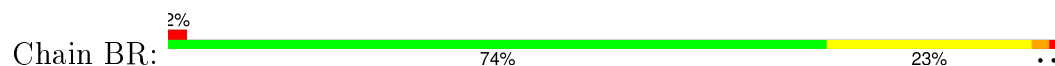
- Molecule 16: 30S ribosomal protein S16

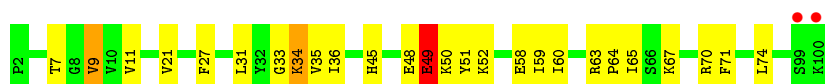


- Molecule 17: 30S ribosomal protein S17

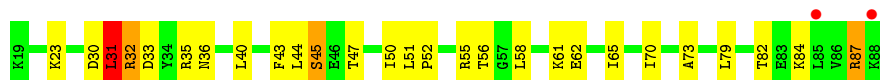


- Molecule 17: 30S ribosomal protein S17





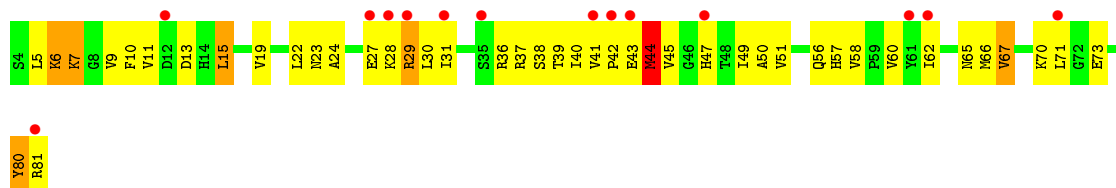
- Molecule 18: 30S ribosomal protein S18



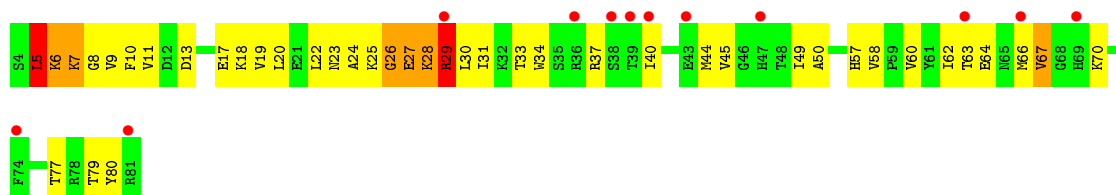
- Molecule 18: 30S ribosomal protein S18



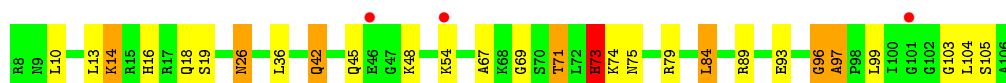
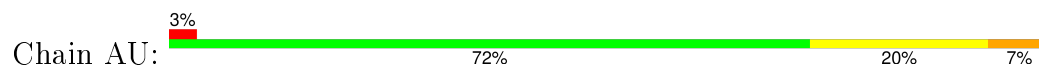
- Molecule 19: 30S ribosomal protein S19



- Molecule 19: 30S ribosomal protein S19



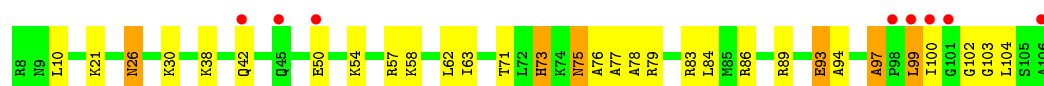
- Molecule 20: 30S ribosomal protein S20



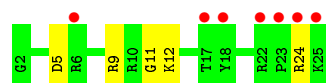
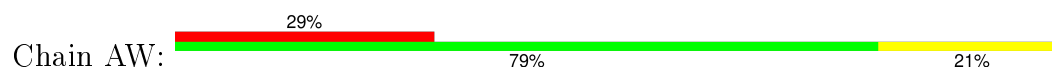
- Molecule 20: 30S ribosomal protein S20







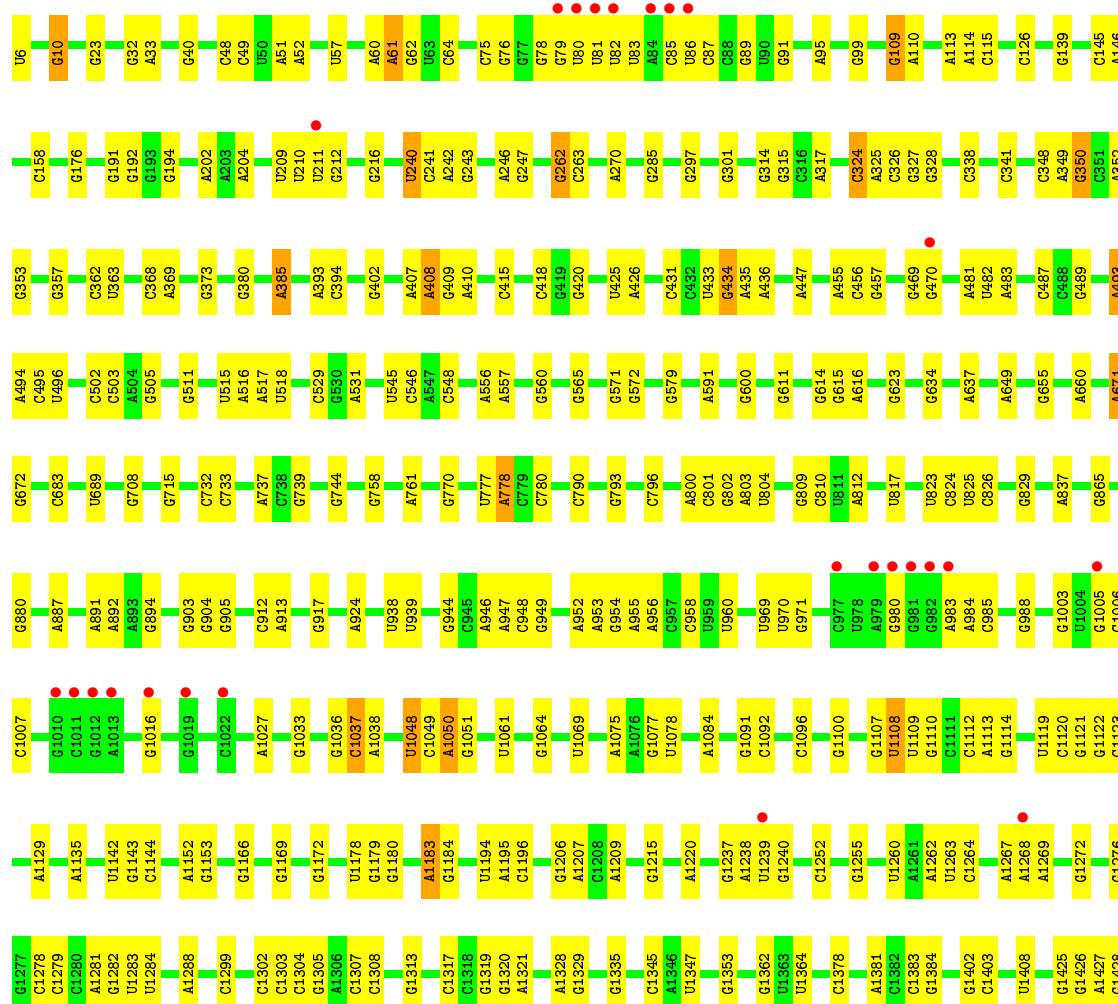
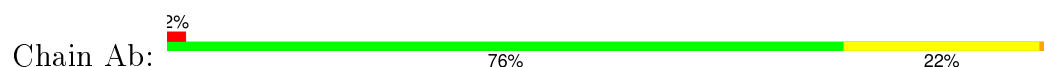
- Molecule 21: 30S ribosomal protein Thx



- Molecule 21: 30S ribosomal protein Thx

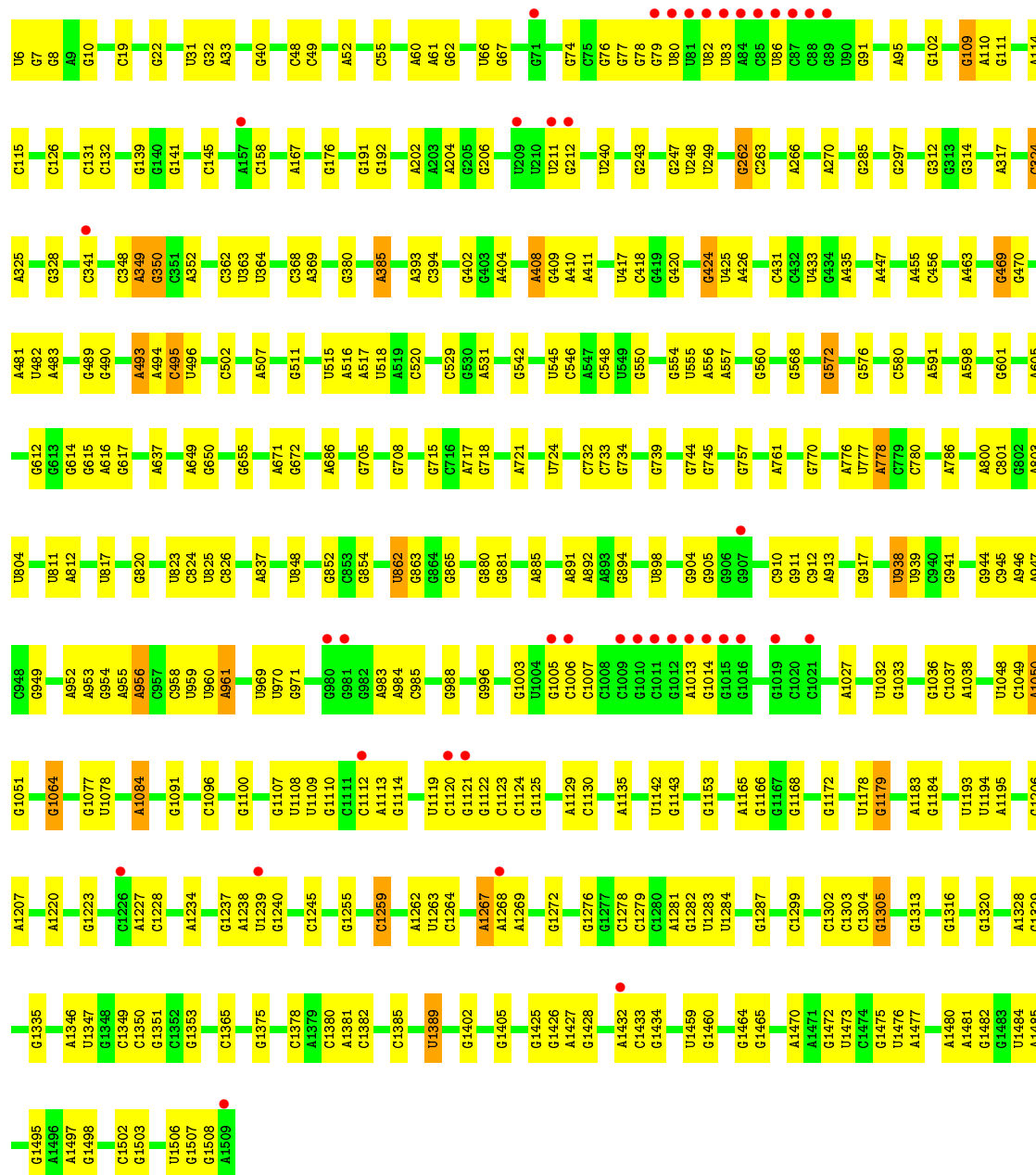
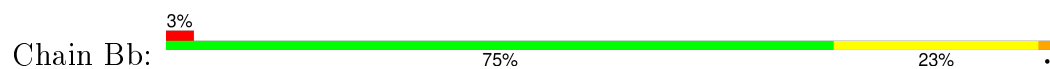


- Molecule 22: RNA (1504-MER)

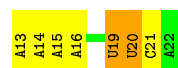




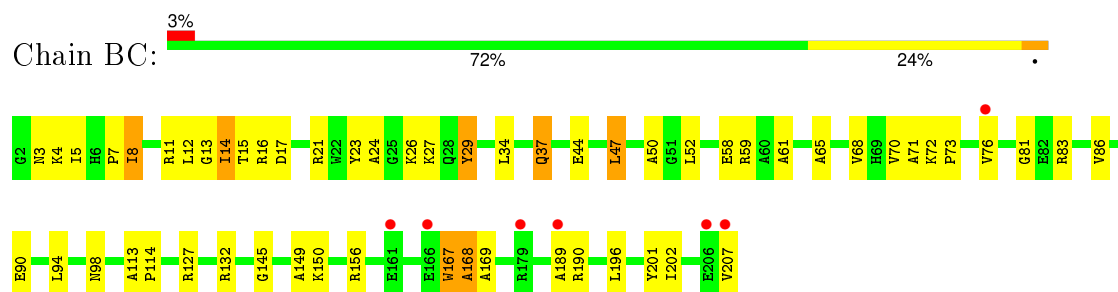
• Molecule 22: RNA (1504-MER)



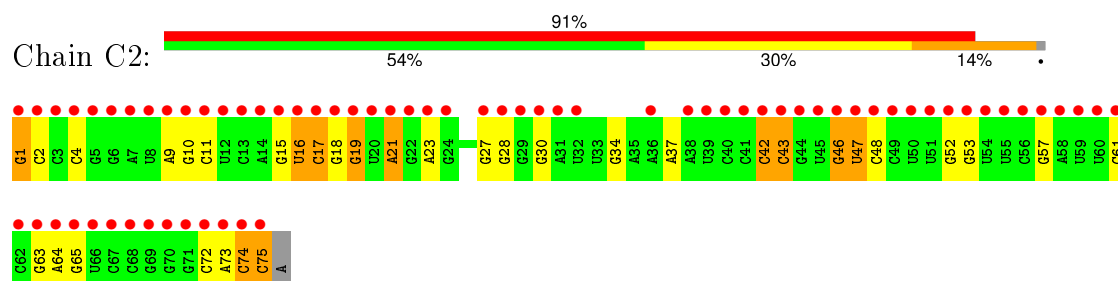
• Molecule 23: mRNA



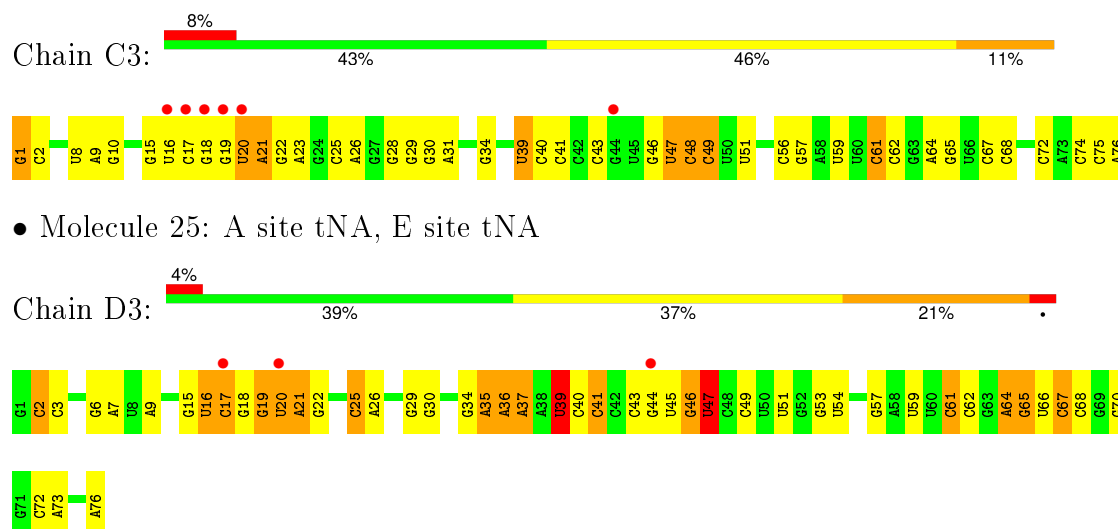
- Molecule 24: 30S ribosomal protein S3



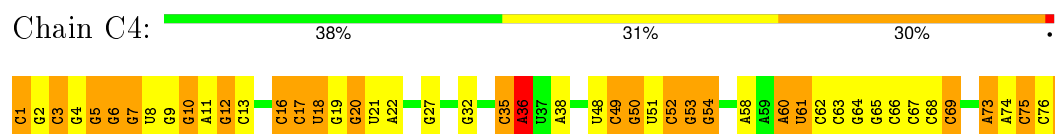
- Molecule 25: A site tNA, E site tNA



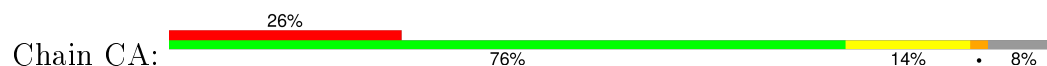
- Molecule 25: A site tNA, E site tNA



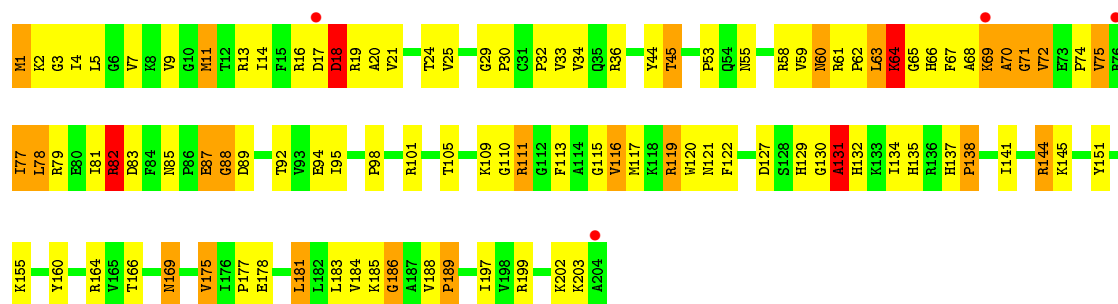
- Molecule 26: P site trNA



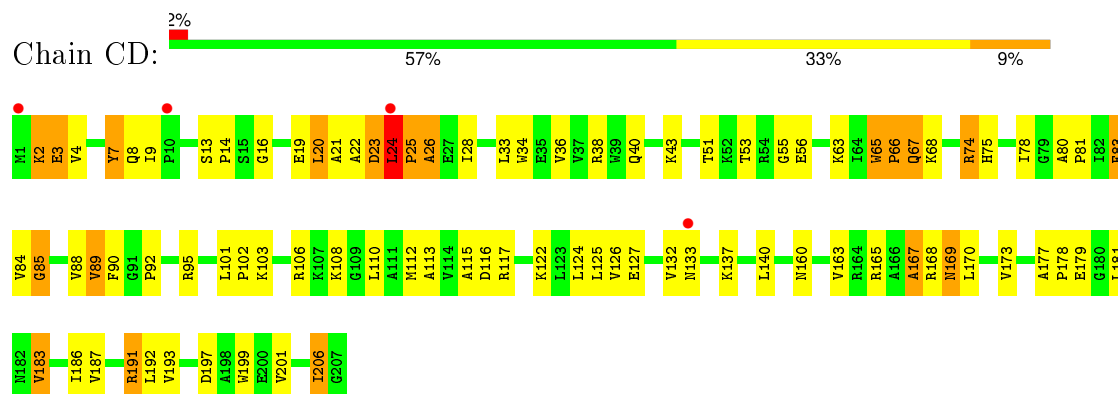
- Molecule 27: 50S ribosomal protein L1



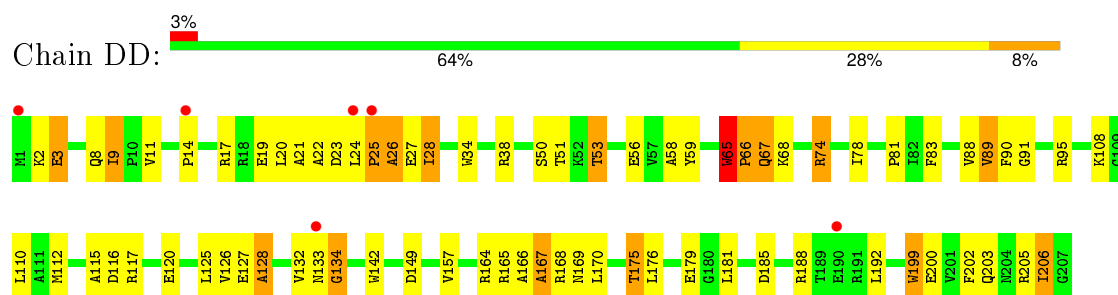




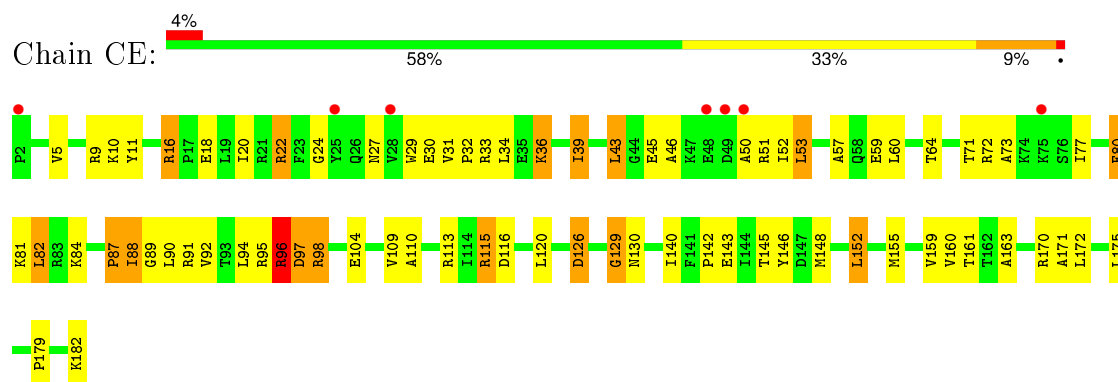
- Molecule 30: 50S ribosomal protein L4



- Molecule 30: 50S ribosomal protein L4

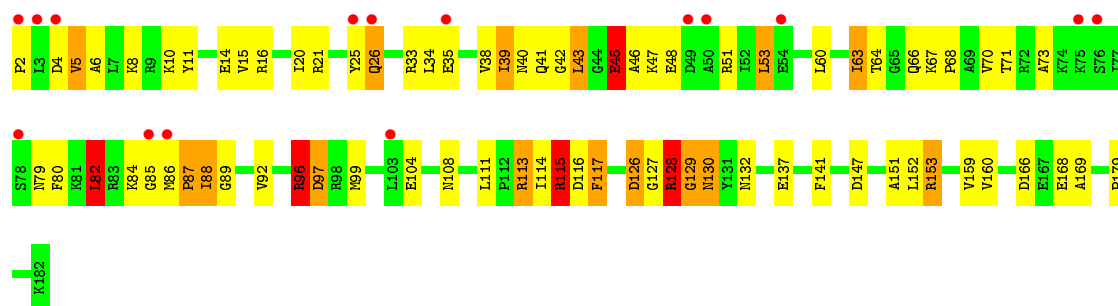


- Molecule 31: 50S ribosomal protein L5

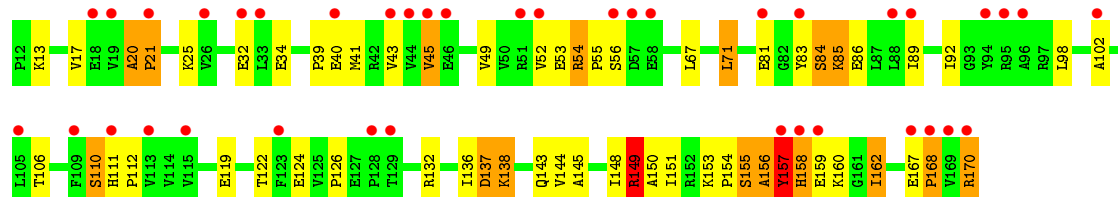


- Molecule 31: 50S ribosomal protein L5

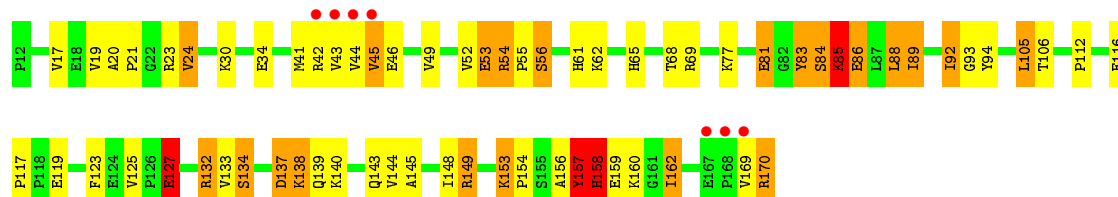




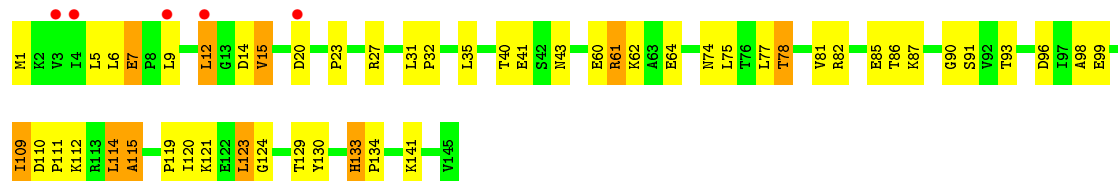
- Molecule 32: 50S ribosomal protein L6



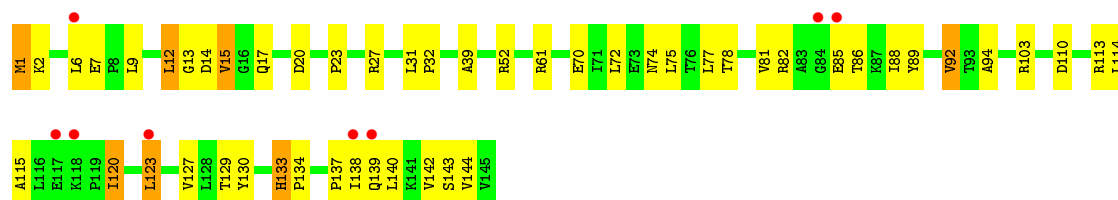
- Molecule 32: 50S ribosomal protein L6



- Molecule 33: 50S ribosomal protein L9



- Molecule 33: 50S ribosomal protein L9



- Molecule 34: ribosomal L10 protein

Chain CJ:  100%

There are no outlier residues recorded for this chain.

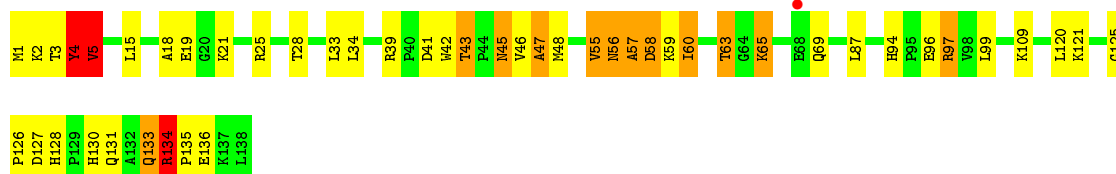
- Molecule 34: ribosomal L10 protein

Chain DJ:  95% 5%



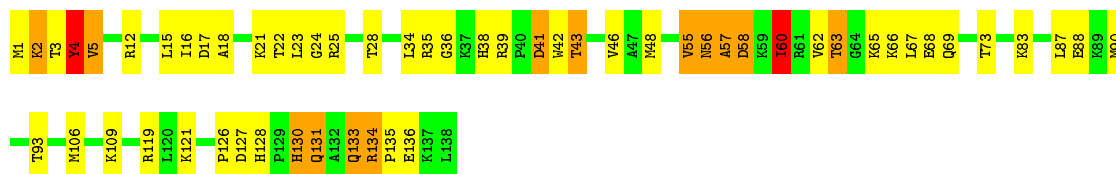
- Molecule 35: 50S ribosomal protein L13

Chain CM:  % 65% 24% 9%



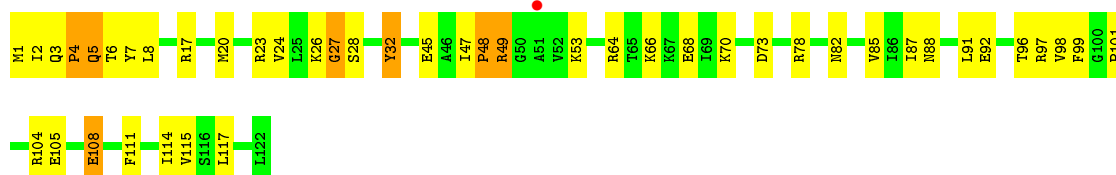
- Molecule 35: 50S ribosomal protein L13

Chain DM:  59% 30% 9%




- Molecule 36: 50S ribosomal protein L14

Chain CN:  % 63% 31% 6%

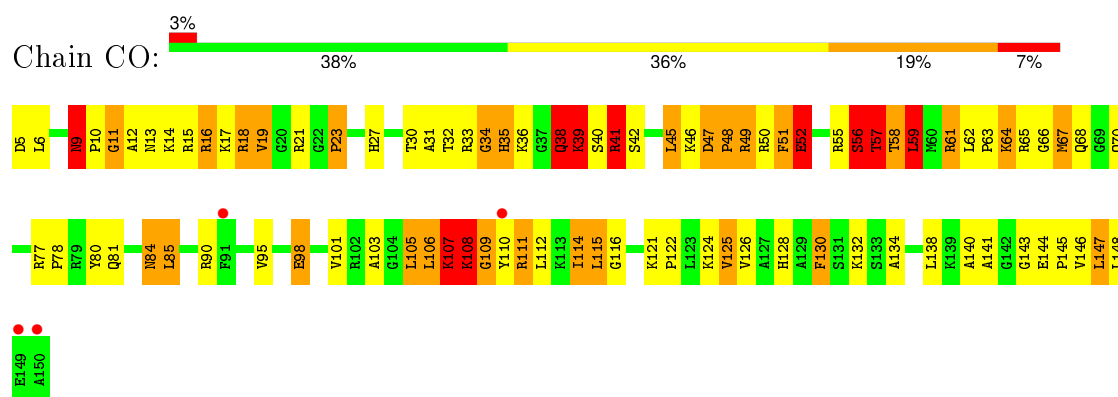


- Molecule 36: 50S ribosomal protein L14

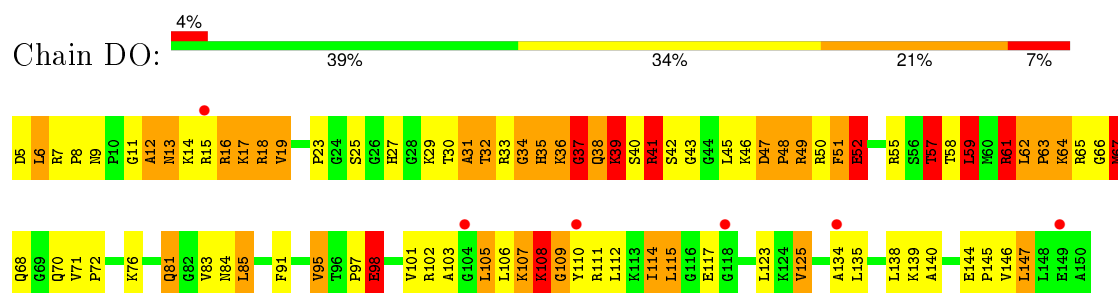
Chain DN:  75% 19% 7%



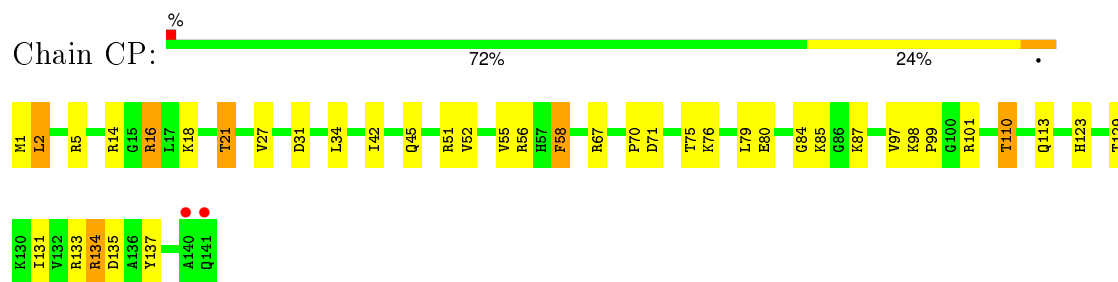
- Molecule 37: 50S ribosomal protein L15



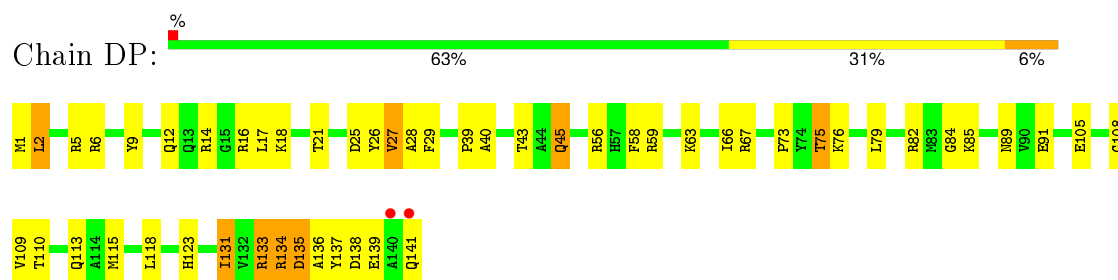
• Molecule 37: 50S ribosomal protein L15



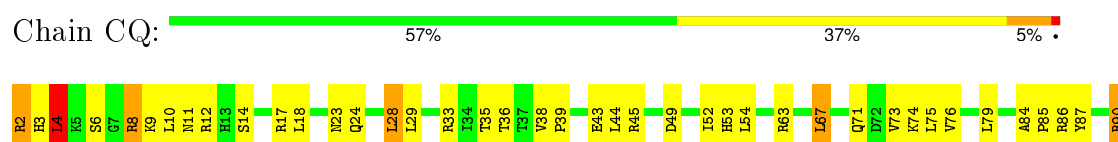
• Molecule 38: 50S ribosomal protein L16



• Molecule 38: 50S ribosomal protein L16



• Molecule 39: 50S ribosomal protein L17

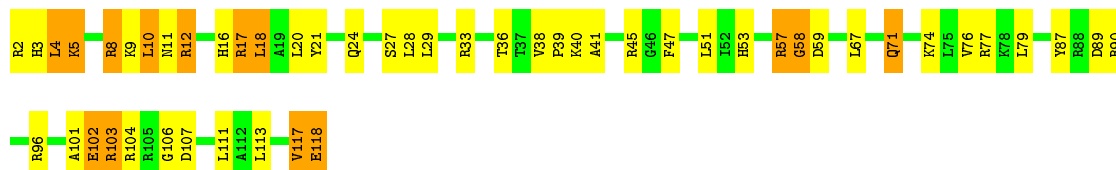






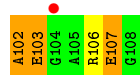
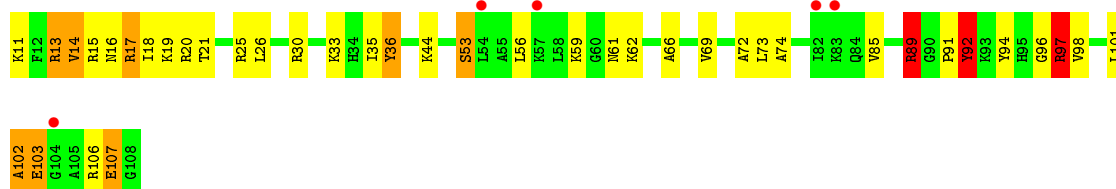
- Molecule 39: 50S ribosomal protein L17

Chain DQ: 56% 32% 12%



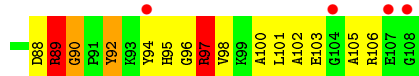
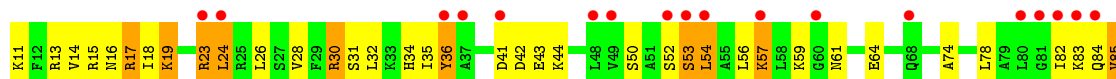
- Molecule 40: 50S ribosomal protein L18

Chain CR: 5% 59% 30% 8%



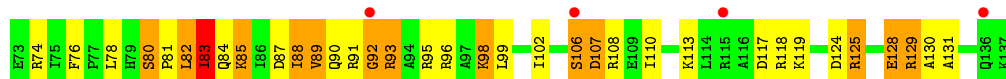
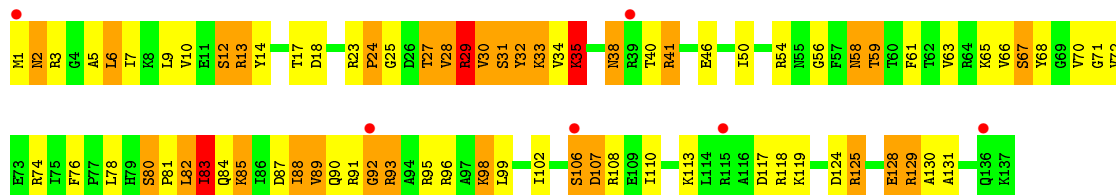
- Molecule 40: 50S ribosomal protein L18

Chain DR: 22% 47% 39% 12%



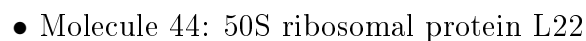
- Molecule 41: 50S ribosomal protein L19

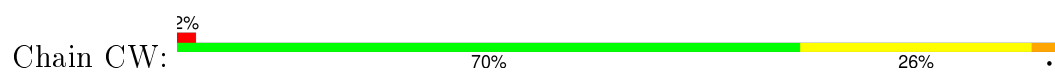
Chain CS: 4% 43% 34% 21%



- Molecule 41: 50S ribosomal protein L19

Chain DS: 3% 45% 37% 12% 5%

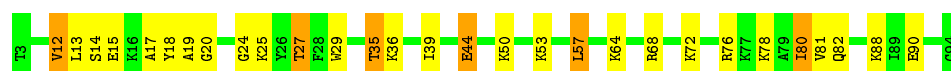




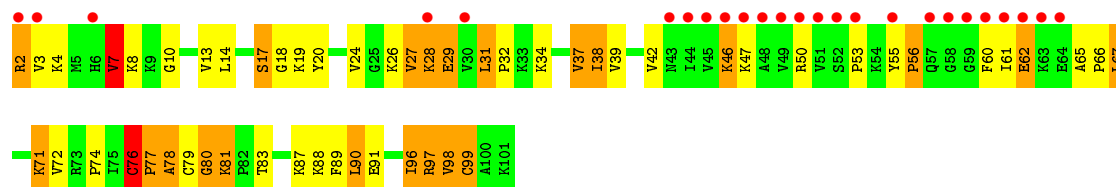
- Molecule 45: 50S ribosomal protein L23



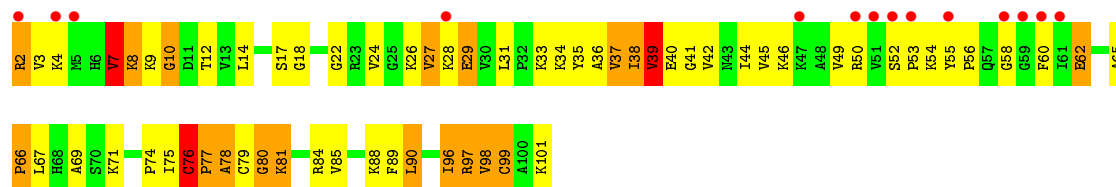
- Molecule 45: 50S ribosomal protein L23



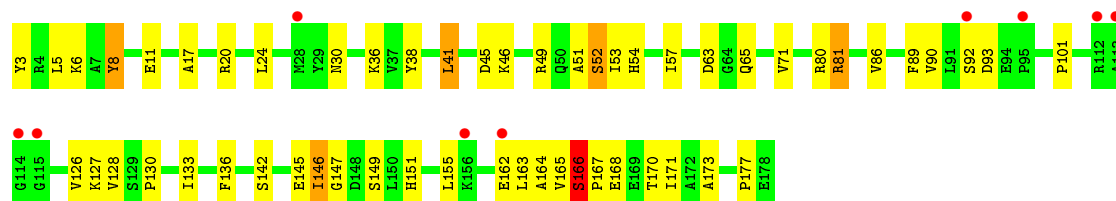
- Molecule 46: 50S ribosomal protein L24




- Molecule 46: 50S ribosomal protein L24

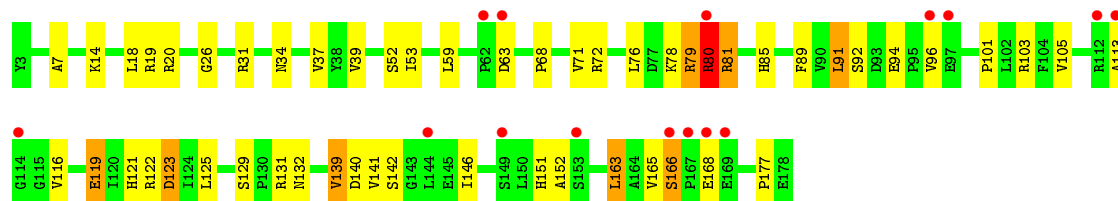


- Molecule 47: 50S ribosomal protein L25




- Molecule 47: 50S ribosomal protein L25

Chain DZ: 




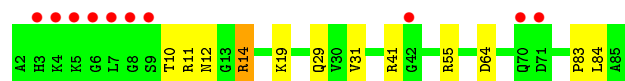
- Molecule 48: 50S ribosomal protein L27

Chain Ca: 



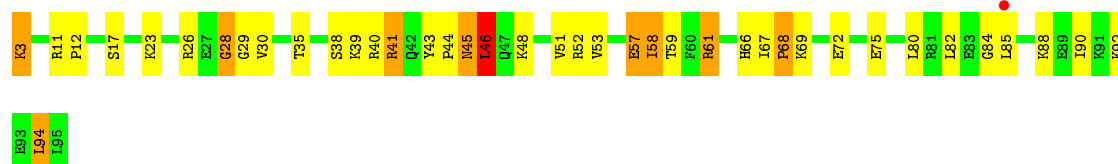
- Molecule 48: 50S ribosomal protein L27

Chain Da: 



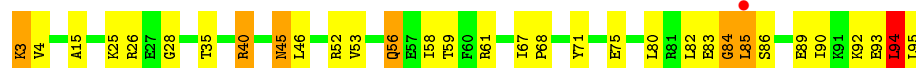
- Molecule 49: 50S ribosomal protein L28

Chain CH: 



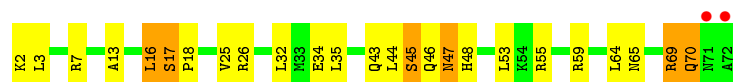
- Molecule 49: 50S ribosomal protein L28

Chain DH: 



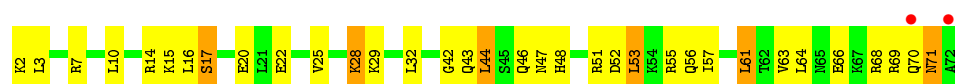
- Molecule 50: 50S ribosomal protein L29

Chain CK: 

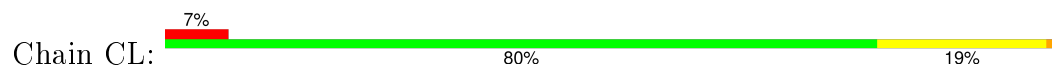


- Molecule 50: 50S ribosomal protein L29

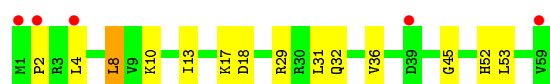
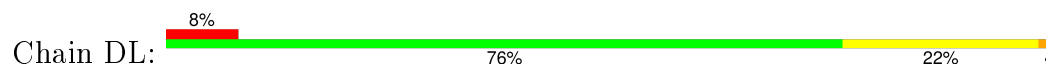
Chain DK: 



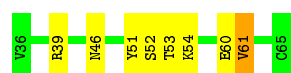
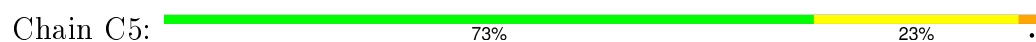
- Molecule 51: 50S ribosomal protein L30



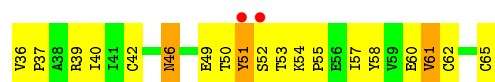
- Molecule 51: 50S ribosomal protein L30



- Molecule 52: 50S ribosomal protein L31



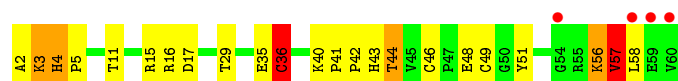
- Molecule 52: 50S ribosomal protein L31



- Molecule 53: 50S ribosomal protein L32

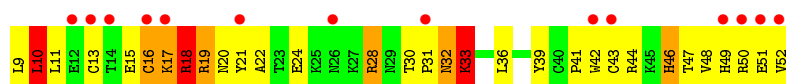


- Molecule 53: 50S ribosomal protein L32

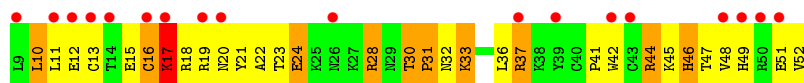


- Molecule 54: 50S ribosomal protein L33

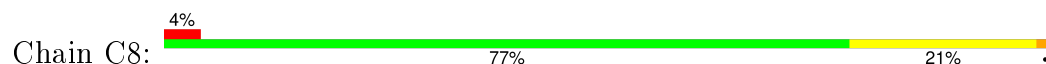




- Molecule 54: 50S ribosomal protein L33



- Molecule 55: 50S ribosomal protein L34



- Molecule 55: 50S ribosomal protein L34



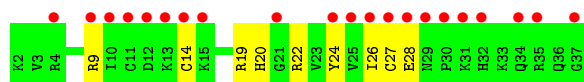
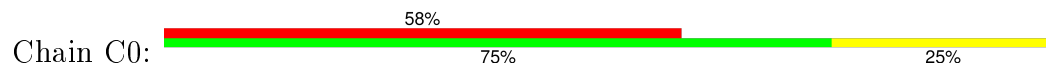
- Molecule 56: 50S ribosomal protein L35



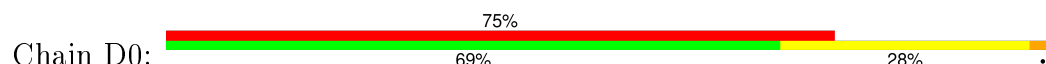
- Molecule 56: 50S ribosomal protein L35



- Molecule 57: 50S ribosomal protein L36



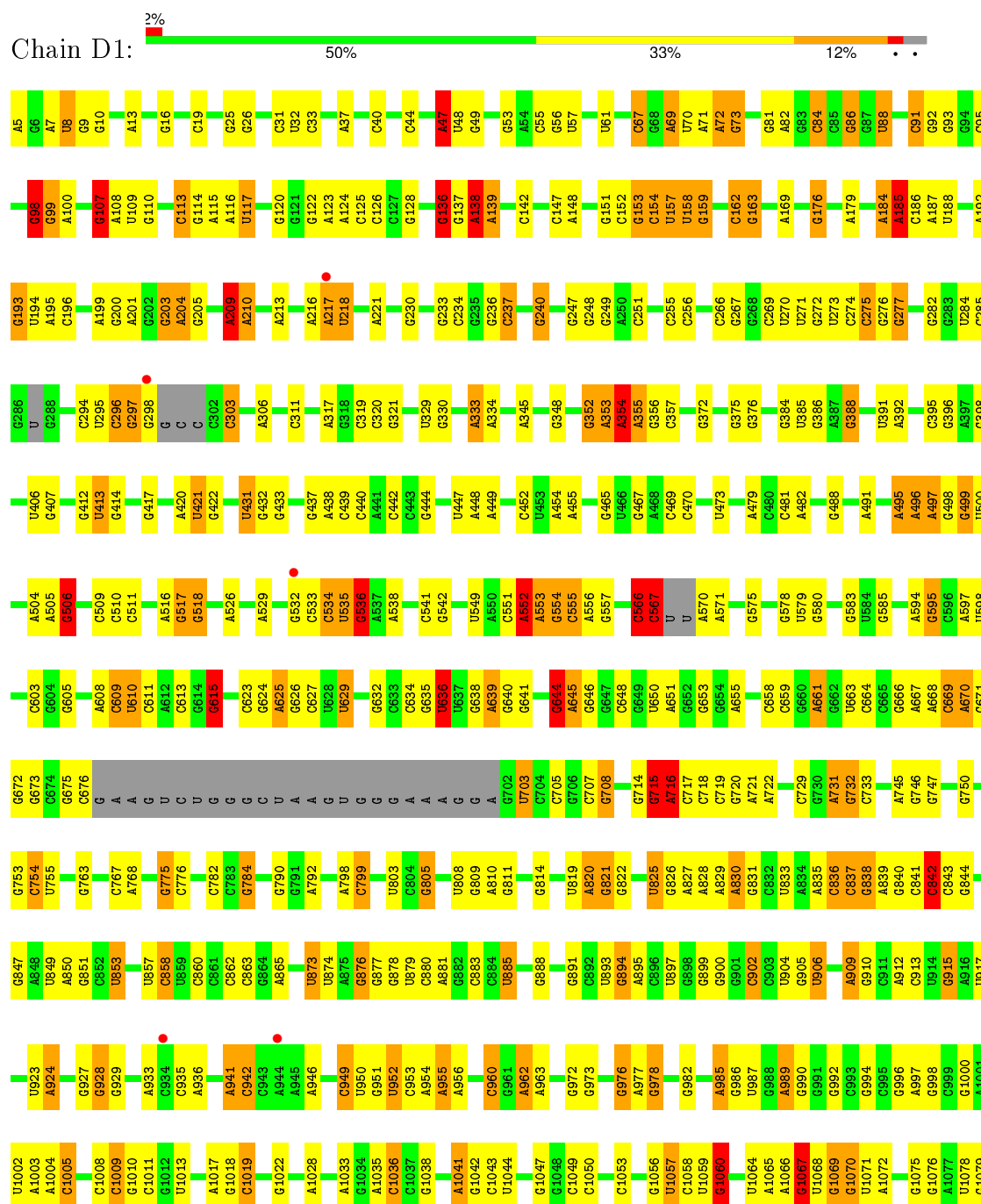
- Molecule 57: 50S ribosomal protein L36



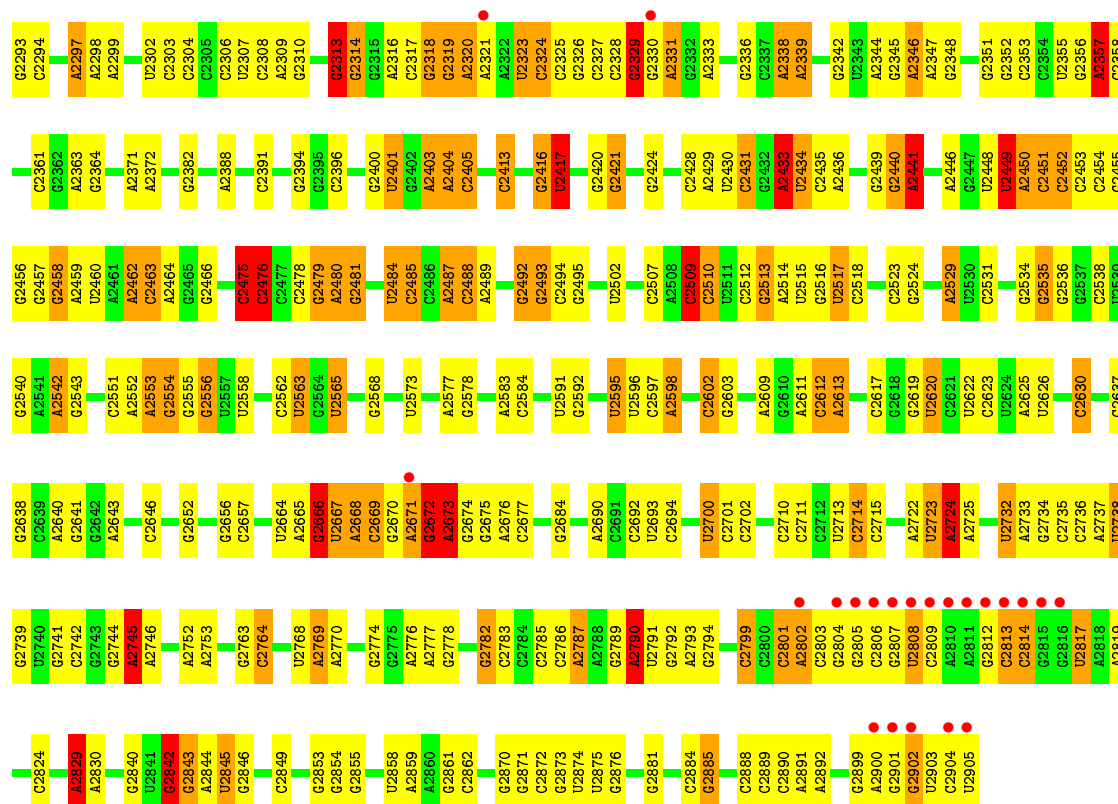


G2535	C2451	C2353	C2259	G2175	G2090	C2003	A1921	G1829	U1734	G1637	A1553	U1465	C1396
G2540	C2462	C2354	U2260	G2176	G2091	C2004	A1922	C1830	U1740	G1638	C1554	G1466	G1297
G2541	G2455	U2355	C2269	G2177	G2092	G2008	C1923	A1831	G1741	G1639	A1555	C1375	A1298
A2542	G2456	C2356	G2270	G2178	G2093	G2010	C1926	A1832	G1742	G1640	U1565	A1472	G1301
U2548	U2460	C2357	G2271	G2179	C2094	U2012	G1927	A1833	G1743	C1643	U1566	C1473	C1302
C2549	C2463	C2358	A2279	G2180	U2095	G2013	C1928	A1842	A1744	U1647	U1567	C1474	
A2553	G2464	G2359	A2280	G2181	U2096	G2014	C1929	G1846	G1745	A1648	U1568	U1476	C1306
G2554	G2465	C2361	C2286	G2182	U2100	U2018	C1930	A1847	A1746	A1649	G1569	C1477	A1307
G2555	G2466	A2371	C2287	G2183	G2101	G2019	C1931	U1848	G1747	A1650	G1570	U1478	U1308
G2556	G2467	C2375	A2289	G2189	U2107	G2020	A1933	A1849	G1748	C1652	U1573	G1383	G1309
U2557	A2470	G2376	C2290	A2192	G2108	G2021	A1934	U1850	A1749	A1653	A1574	U1385	A1310
U2558	C2472	G2377	C2291	U2193	G2109	G2022	C1935	A1851	A1766	A1654	U1575	U1387	U1312
U2565	C2473	G2378	C2292	A2194	U2110	C2028	U1936		A1767	A1655	C1576	C1482	A1313
U2566	C2474	G2379	C2293	G2198	G2114	G2029	A1937	G1854	U1768	G1659	C1577	G1488	A1314
U2574	C2475	A2389	A2287	C2199	G2115	G2030	U1938	A1855	G1769	C1660	C1578	G1489	A1315
A2575	C2476	G2402	A2298	C2200	G2116	G2031	A1939	G1856	A1770	A1661	C1579	A1490	C1316
A2576	G2477	A2403	C2300	G2201	C2117	U2032	C1941	C1857	C1771	A1662	G	G1391	G1317
A2577	A2480	C2404	U2302	C2198	U2120	G2033	U1944	G1858	G1775	A1663	C	G1494	U1318
G2578	G2481	C2405	C2303	C2199	G2121	A2036	G1950	G1859	G1776	U1666	C	A1495	A1319
G2580	G2482	G2406	G2304	G2202	G2122	U2043	G1951	G1865	G1777	G1667	A	G1496	A1323
G2581	C2485	G2407	G2310	G2203	U2123	G2044	U1952	C1868	A1778	G1670	G	C1497	G1326
C2582	C2486	G2408	G2311	U2210	G2124	C2047	A1953	G1869	G1779	G1671	G	U1500	A1404
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C2584	C2488	A2403	G2315	G2212	U2130	U2049	G1955	C1874	C1784	U1679	C	G1502	A1331
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G2587	G2493	C2415	G2318	A2219	U2133	G2053	U1959	A1877	G1793	C1684	C1593	U1507	C1335
A2588	C2494	G2416	A2319	C2221	G2134	A2054	U1960	U1878	A1794	U1685	U1594	U1513	C1336
C2590	G2495	U2417	A2320	C2222	A2138	U2055	U1961	G1879	G1794	C1686	C1595	G1413	C1337
U2591	U2502	G2420	A2321	C2223	U2139	G2056	G1966	G1888	G1799	U1693	A1600	A1517	C1338
U2592	G2505	A2421	C2324	U2224	A2140	C2057	U1967	A1889	G1800	G1694	G1601	G1521	U1339
U2595	C2508	C2423	C2327	G2225	G2146	C2060	U1976	G1893	A1802	G1697	A1604	G1524	C1342
C2597	C2509	G2424	G2328	G2226	A2147	U2062	U1977	A1894	C1803	A1698	G1605	U1527	C1343
A2598	G2513	G2425	G2329	G2227	A2148	A2063	C1978	G1895	C1804	A1699	U1528	G1429	U1345
C2602	G2516	U2426	G2330	U2228	C2149	C2064	C1979	A1896	U1805	A1700	G1528	G1430	A1346
G2603	U2604	U2430	A2331	G2229	G2152	G2073	C1983	A1897	G1806	C1702	G1614	G1530	A1347
C2605	C2517	A2433	G2332	A2236	U2153	C2076	U1984	A1898	U1809	C1703	A1615	U1436	C1351
A2609	C2518	U2434	G2336	G2237	G2154	G2077	G1985	A1899	A1810	C1704	A1535	A1535	A1352
G2610	G2519	C2435	C2337	G2238	A2155	A2078	C1986	C1900	C1811	U1709	G1537	U1441	G1354
A2611	C2521	A2436	A2338	C2240	A2156	G2079	A1987	C1902	A1813	C1713	C1538	U1448	C1355
C2612	U2522	G2440	G2339	G2246	C2157	A2080	C1988	C1903	A1814	G1720	A1539	C1449	U1358
G2613	G2527	U2442	A2341	G2249	C2160	A2081	G1989	A1906	A1815	G1724	A1540	U1450	C1359
A2614	C2528	U2443	G2345	G2250	C2161	G2082	U1990	C1907	A1816	U1725	A1541	U1451	U1360
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G2619	U2620	U2449	A2347	U2256	C2167	C2085	A1992	G1909	C1820	U1726	C1453	C1453	C1362
C2621	C2532	G2450	G2352	A2258	G2168	C2086	C1995	A1910	A1821	G1727	C1547	U1548	C1363
					G2170	C2087	G2001	G1917	C1826	C1732	U1549	C1462	C1364
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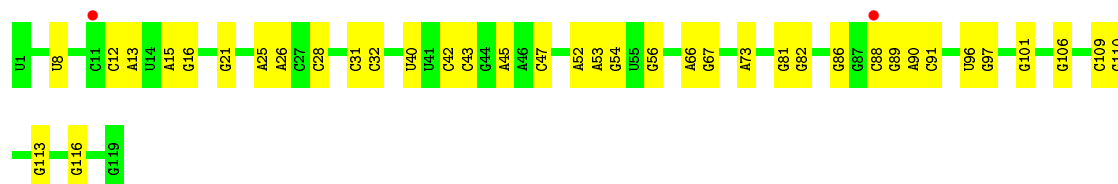




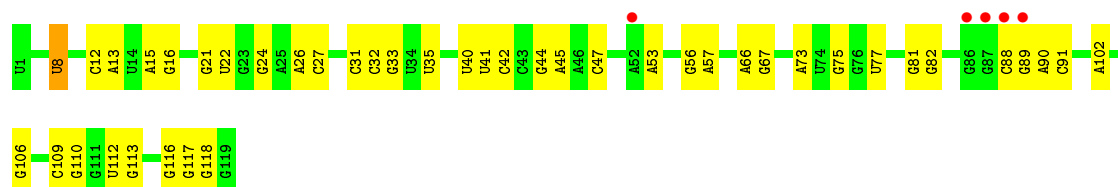




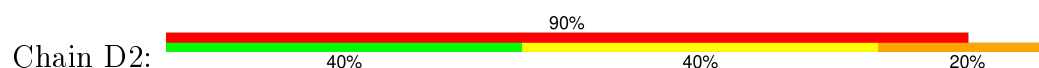
• Molecule 59: 5S rRNA (119-MER)

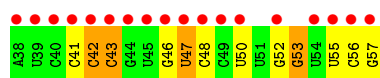


• Molecule 59: 5S rRNA (119-MER)



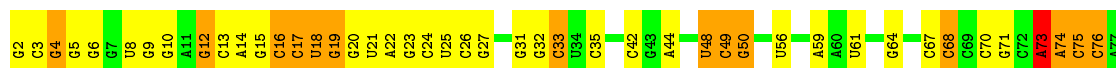
• Molecule 60: tRNA (5'-D(\*AP\*UP\*CP\*CP\*CP\*GP\*UP\*GP\*UP\*CP\*CP\*UP\*UP\*GP\*GP\*UP\*UP\*CP\*G)-3')





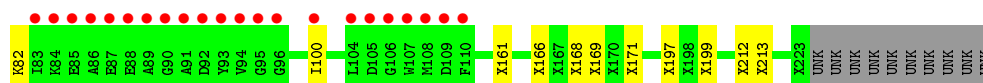
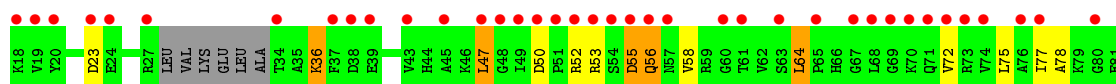
• Molecule 61: tRNA (76-MER)

Chain D4: 41% 39% 18%



• Molecule 62: 50S ribosomal protein L1

Chain DA: 29% 80% 10% 8%



• Molecule 63: 50S ribosomal protein L22

Chain DW: 2% 69% 27%



• Molecule 64: DNA (55-MER)

Chain DV: 91% 49% 42% 9%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	214.21Å 457.45Å 639.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.91 – 3.40 49.91 – 3.40	Depositor EDS
% Data completeness (in resolution range)	98.5 (49.91-3.40) 98.6 (49.91-3.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.28	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.46 (at 3.40Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.204 , 0.241 0.207 , 0.241	Depositor DCC
$R_{free}$ test set	42005 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	74.2	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 78.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 840382 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	295910	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.91% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3V6, PAR, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A2	0.48	0/192	0.82	0/297
2	AA	0.51	0/1936	0.74	0/2609
2	BA	0.50	0/1936	0.72	0/2609
3	AC	0.62	0/1636	0.82	2/2205 (0.1%)
4	AD	0.64	1/1733 (0.1%)	0.88	2/2318 (0.1%)
4	BD	0.68	2/1733 (0.1%)	0.98	9/2318 (0.4%)
5	AE	0.56	0/1163	0.82	1/1564 (0.1%)
5	BE	0.52	0/1163	0.78	0/1564
6	AF	0.52	0/856	0.78	0/1154
6	BF	0.56	0/856	0.81	0/1154
7	AG	0.51	0/1276	0.75	0/1709
7	BG	0.56	0/1276	0.78	2/1709 (0.1%)
8	AH	0.52	0/1136	0.75	0/1527
8	BH	0.52	0/1136	0.79	0/1527
9	AI	0.57	0/1029	0.82	0/1378
9	BI	0.54	0/1029	0.77	0/1378
10	AJ	0.58	0/808	0.84	0/1085
10	BJ	0.60	0/808	0.81	0/1085
11	AK	0.59	0/900	0.81	0/1213
11	BK	0.54	0/900	0.74	0/1213
12	AL	0.61	0/987	0.86	0/1320
12	BL	0.65	0/987	0.91	1/1320 (0.1%)
13	AM	0.57	0/999	0.86	1/1336 (0.1%)
13	BM	0.59	0/999	0.88	0/1336
14	AN	0.60	0/501	0.91	1/664 (0.2%)
14	BN	0.64	0/501	1.00	2/664 (0.3%)
15	AO	0.51	0/745	0.70	0/992
15	BO	0.53	0/745	0.80	0/992
16	AP	0.59	0/717	0.83	0/963
16	BP	0.56	0/717	0.81	0/963
17	AR	0.55	0/837	0.81	0/1117
17	BR	0.49	0/837	0.75	0/1117

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
18	AS	0.52	0/579	0.75	0/768
18	BS	0.54	0/579	0.73	0/768
19	AT	0.60	0/643	0.78	1/865 (0.1%)
19	BT	0.55	0/643	0.79	1/865 (0.1%)
20	AU	0.55	0/765	0.85	1/1007 (0.1%)
20	BU	0.50	0/765	0.80	0/1007
21	AW	0.61	0/213	0.90	0/277
21	BW	0.72	0/213	0.88	0/277
22	Ab	0.47	4/36190 (0.0%)	0.82	64/56486 (0.1%)
22	Bb	0.47	3/36190 (0.0%)	0.82	66/56486 (0.1%)
23	B2	0.42	0/216	0.86	0/334
24	BC	0.53	0/1637	0.76	1/2205 (0.0%)
25	C2	0.31	0/1784	0.72	1/2780 (0.0%)
25	C3	0.40	0/1809	0.77	3/2819 (0.1%)
25	D3	0.38	1/1809 (0.1%)	0.74	1/2819 (0.0%)
26	C4	0.49	0/1832	0.95	5/2855 (0.2%)
27	CA	0.55	0/646	0.72	0/869
28	CB	0.73	0/2155	0.99	3/2905 (0.1%)
28	DB	0.80	2/2155 (0.1%)	1.01	6/2905 (0.2%)
29	CC	0.70	1/1597 (0.1%)	0.93	2/2153 (0.1%)
29	DC	0.74	2/1597 (0.1%)	0.96	4/2153 (0.2%)
30	CD	0.65	0/1659	0.89	0/2244
30	DD	0.71	1/1659 (0.1%)	0.93	0/2244
31	CE	0.57	0/1499	0.84	0/2016
31	DE	0.58	0/1499	0.80	0/2016
32	CF	0.59	1/1246 (0.1%)	0.77	1/1682 (0.1%)
32	DF	0.69	1/1246 (0.1%)	0.92	2/1682 (0.1%)
33	CI	0.57	0/1147	0.84	1/1551 (0.1%)
33	DI	0.57	0/1147	0.81	0/1551
35	CM	0.60	0/1132	0.86	1/1525 (0.1%)
35	DM	0.63	0/1132	0.87	0/1525
36	CN	0.64	0/943	0.89	0/1269
36	DN	0.64	0/943	0.87	0/1269
37	CO	0.82	0/1131	1.17	4/1504 (0.3%)
37	DO	0.87	0/1131	1.16	2/1504 (0.1%)
38	CP	0.57	0/1143	0.80	0/1527
38	DP	0.63	0/1143	0.89	0/1527
39	CQ	0.67	0/974	0.99	2/1302 (0.2%)
39	DQ	0.74	0/974	1.08	6/1302 (0.5%)
40	CR	0.64	0/779	0.96	2/1036 (0.2%)
40	DR	0.71	0/779	1.04	2/1036 (0.2%)
41	CS	0.69	0/1156	1.04	0/1542
41	DS	0.73	0/1156	1.12	4/1542 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
42	CT	0.64	0/975	0.92	1/1297 (0.1%)
42	DT	0.75	0/975	1.07	4/1297 (0.3%)
43	CU	0.56	0/790	0.88	0/1057
43	DU	0.63	0/790	0.96	1/1057 (0.1%)
44	CW	0.64	0/907	0.89	0/1216
45	CX	0.63	0/740	0.85	0/993
45	DX	0.69	1/740 (0.1%)	1.01	2/993 (0.2%)
46	CY	0.75	0/789	0.98	0/1051
46	DY	0.80	0/789	1.00	1/1051 (0.1%)
47	CZ	0.51	0/1436	0.77	0/1949
47	DZ	0.53	0/1436	0.77	1/1949 (0.1%)
48	Ca	0.61	0/671	0.87	1/892 (0.1%)
48	Da	0.67	0/671	0.96	1/892 (0.1%)
49	CH	0.65	0/741	0.95	1/984 (0.1%)
49	DH	0.60	0/741	0.89	0/984
50	CK	0.54	0/600	0.83	0/793
50	DK	0.59	0/600	0.84	0/793
51	CL	0.54	0/473	0.80	0/634
51	DL	0.60	0/473	0.83	0/634
52	C5	0.63	0/229	0.86	0/309
52	D5	0.61	0/229	0.80	0/309
53	C6	0.67	0/473	0.91	1/639 (0.2%)
53	D6	0.64	0/473	0.94	1/639 (0.2%)
54	C7	0.89	0/387	1.06	1/515 (0.2%)
54	D7	0.71	0/387	1.01	1/515 (0.2%)
55	C8	0.72	0/427	1.01	1/561 (0.2%)
55	D8	0.78	0/427	0.99	1/561 (0.2%)
56	C9	0.74	0/516	1.08	0/679
56	D9	0.73	0/516	1.04	1/679 (0.1%)
57	C0	0.53	0/302	0.70	0/397
57	D0	0.59	0/302	0.87	0/397
58	C1	0.55	15/67709 (0.0%)	0.91	250/105690 (0.2%)
58	D1	0.58	32/67709 (0.0%)	0.96	353/105690 (0.3%)
59	Cs	0.45	0/2853	0.80	3/4451 (0.1%)
59	Ds	0.49	0/2853	0.85	4/4451 (0.1%)
60	D2	0.34	0/459	0.74	0/712
61	D4	0.48	0/1813	0.86	7/2825 (0.2%)
62	DA	0.55	0/645	0.73	0/867
63	DW	0.66	0/907	0.95	1/1216 (0.1%)
64	DV	0.28	0/1269	0.65	0/1956
All	All	0.56	67/318931 (0.0%)	0.89	845/476973 (0.2%)

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
2	AA	0	1
3	AC	0	1
12	AL	0	1
13	AM	0	1
13	BM	0	1
14	BN	0	1
18	BS	0	1
19	AT	0	1
20	AU	0	1
22	Ab	1	0
22	Bb	1	0
25	C3	1	0
25	D3	1	0
28	CB	0	4
28	DB	0	3
29	DC	0	2
30	CD	0	1
31	CE	0	2
32	DF	0	1
33	CI	0	1
34	DJ	0	1
37	CO	0	6
37	DO	0	6
39	DQ	0	1
41	CS	0	1
41	DS	0	3
42	CT	0	1
42	DT	0	1
46	CY	0	1
46	DY	0	2
47	DZ	0	1
48	Da	0	1
53	C6	0	1
54	C7	0	1
54	D7	0	1
56	D9	0	1
58	C1	20	0
58	D1	21	0
All	All	45	52

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	C1	296	C	O3'-P	8.28	1.71	1.61
28	DB	237	GLU	CG-CD	8.11	1.64	1.51
29	DC	127	ASP	CB-CG	8.00	1.68	1.51
58	D1	1346	A	O3'-P	7.44	1.70	1.61
58	D1	1429	A	O3'-P	-7.22	1.52	1.61

The worst 5 of 845 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	C4	36	A	O5'-P-OP2	-17.36	89.87	110.70
58	D1	2028	C	O5'-P-OP2	-16.34	90.99	105.70
58	D1	2603	G	O5'-P-OP2	-16.16	91.15	105.70
58	D1	598	U	O5'-P-OP2	-13.61	93.45	105.70
58	C1	2613	A	O5'-P-OP1	-12.83	94.15	105.70

5 of 45 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
22	Ab	408	A	C1'
22	Bb	408	A	C1'
25	C3	47	U	C1'
58	C1	98	G	C1'
58	C1	715	G	C4',C1',C3'

5 of 52 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AA	23	ARG	Peptide
3	AC	26	LYS	Peptide
12	AL	91	LYS	Peptide
13	AM	69	GLU	Peptide
19	AT	28	LYS	Peptide

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A2	173	0	85	16	0
2	AA	1901	0	1951	33	0
2	BA	1901	0	1951	32	0
3	AC	1612	0	1677	30	0
4	AD	1703	0	1763	41	0
4	BD	1703	0	1763	43	0
5	AE	1147	0	1207	27	0
5	BE	1147	0	1207	23	0
6	AF	843	0	857	6	0
6	BF	843	0	857	19	0
7	AG	1257	0	1296	8	0
7	BG	1257	0	1296	15	0
8	AH	1116	0	1177	11	0
8	BH	1116	0	1177	17	0
9	AI	1011	0	1043	29	0
9	BI	1011	0	1043	18	0
10	AJ	795	0	840	22	0
10	BJ	795	0	840	21	0
11	AK	885	0	904	13	0
11	BK	885	0	904	21	0
12	AL	971	0	1057	24	0
12	BL	971	0	1057	17	0
13	AM	988	0	1059	35	0
13	BM	988	0	1059	27	0
14	AN	492	0	529	20	0
14	BN	492	0	529	13	0
15	AO	734	0	771	7	0
15	BO	734	0	771	8	0
16	AP	701	0	720	10	0
16	BP	701	0	720	14	0
17	AR	824	0	891	5	0
17	BR	824	0	891	14	0
18	AS	574	0	644	17	0
18	BS	574	0	644	15	0
19	AT	630	0	652	24	0
19	BT	630	0	652	26	0
20	AU	763	0	861	16	0
20	BU	763	0	861	13	0
21	AW	209	0	221	1	0
21	BW	209	0	221	3	0
22	Ab	32329	0	16318	0	0
22	Bb	32329	0	16318	0	1
23	B2	194	0	95	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	BC	1613	0	1677	26	0
25	C2	1597	0	811	18	0
25	C3	1619	0	822	28	0
25	D3	1619	0	822	46	0
26	C4	1640	0	837	56	0
27	CA	1156	0	755	15	0
28	CB	2105	0	2182	95	0
28	DB	2105	0	2182	88	0
29	CC	1564	0	1629	60	0
29	DC	1564	0	1629	79	0
30	CD	1624	0	1677	61	0
30	DD	1624	0	1677	47	0
31	CE	1474	0	1535	44	0
31	DE	1474	0	1535	57	0
32	CF	1223	0	1282	26	0
32	DF	1223	0	1282	49	0
33	CI	1132	0	1218	25	1
33	DI	1132	0	1218	29	0
34	CJ	651	0	155	0	0
34	DJ	651	0	155	4	0
35	CM	1105	0	1180	34	0
35	DM	1105	0	1180	37	0
36	CN	933	0	996	23	0
36	DN	933	0	996	21	0
37	CO	1114	0	1187	84	0
37	DO	1114	0	1187	103	0
38	CP	1122	0	1179	26	0
38	DP	1122	0	1179	37	0
39	CQ	960	0	1021	30	0
39	DQ	960	0	1021	34	0
40	CR	771	0	832	29	0
40	DR	771	0	832	29	0
41	CS	1142	0	1202	79	0
41	DS	1142	0	1202	80	0
42	CT	958	0	1018	45	0
42	DT	958	0	1018	44	0
43	CU	779	0	852	44	0
43	DU	779	0	852	45	0
44	CW	896	0	953	22	0
45	CX	726	0	778	17	0
45	DX	726	0	778	19	0
46	CY	776	0	870	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	DY	776	0	868	60	0
47	CZ	1404	0	1432	34	0
47	DZ	1404	0	1432	23	0
48	Ca	662	0	688	0	0
48	Da	662	0	688	0	0
49	CH	734	0	808	16	0
49	DH	734	0	808	17	0
50	CK	598	0	653	11	0
50	DK	598	0	653	17	0
51	CL	468	0	523	9	0
51	DL	468	0	523	8	0
52	C5	226	0	229	2	0
52	D5	226	0	229	11	0
53	C6	459	0	478	13	0
53	D6	459	0	477	15	0
54	C7	381	0	390	17	0
54	D7	381	0	390	21	0
55	C8	419	0	467	8	0
55	D8	419	0	467	5	0
56	C9	508	0	576	36	0
56	D9	508	0	576	33	0
57	C0	299	0	326	4	0
57	D0	299	0	324	5	0
58	C1	60459	0	30486	641	0
58	D1	60459	0	30488	729	0
59	Cs	2551	0	1295	0	0
59	Ds	2551	0	1295	0	0
60	D2	416	0	215	8	0
61	D4	1623	0	825	46	0
62	DA	1155	0	757	14	0
63	DW	896	0	956	19	0
64	DV	1167	0	624	15	0
65	Ab	42	0	45	0	0
65	Bb	42	0	45	0	0
66	C1	24	0	20	5	0
66	D1	24	0	21	11	0
67	C1	1	0	0	0	0
67	D1	1	0	0	2	0
All	All	295910	0	199849	3935	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 3935 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
61:D4:2:G:C2	61:D4:73:A:N3	1.85	1.31
58:C1:1331:A:O2'	58:C1:1333:U:OP2	1.54	1.25
58:D1:927:G:O2'	64:DV:19:G:C6	1.93	1.22
58:C1:2492:G:O2'	58:C1:2493:G:OP2	1.60	1.17
29:DC:132:HIS:ND1	58:D1:1704:C:OP1	1.79	1.16

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	Interatomic distance (Å)	Clash overlap (Å)
22:Bb:364:U:OP1	33:CI:91:SER:OG[4_455]	2.14	0.06

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AA	232/234 (99%)	174 (75%)	47 (20%)	11 (5%)	3	26
2	BA	232/234 (99%)	180 (78%)	41 (18%)	11 (5%)	3	26
3	AC	204/238 (86%)	145 (71%)	42 (21%)	17 (8%)	1	11
4	AD	206/208 (99%)	161 (78%)	33 (16%)	12 (6%)	2	20
4	BD	206/208 (99%)	168 (82%)	27 (13%)	11 (5%)	2	22
5	AE	148/150 (99%)	130 (88%)	15 (10%)	3 (2%)	9	48
5	BE	148/150 (99%)	130 (88%)	14 (10%)	4 (3%)	6	41
6	AF	99/101 (98%)	92 (93%)	5 (5%)	2 (2%)	9	48
6	BF	99/101 (98%)	89 (90%)	9 (9%)	1 (1%)	19	63
7	AG	153/155 (99%)	124 (81%)	26 (17%)	3 (2%)	9	48
7	BG	153/155 (99%)	135 (88%)	17 (11%)	1 (1%)	26	70

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AH	136/138 (99%)	110 (81%)	24 (18%)	2 (2%)	13	54
8	BH	136/138 (99%)	116 (85%)	19 (14%)	1 (1%)	26	70
9	AI	125/127 (98%)	97 (78%)	23 (18%)	5 (4%)	4	31
9	BI	125/127 (98%)	98 (78%)	22 (18%)	5 (4%)	4	31
10	AJ	96/98 (98%)	79 (82%)	13 (14%)	4 (4%)	3	29
10	BJ	96/98 (98%)	76 (79%)	15 (16%)	5 (5%)	2	23
11	AK	117/119 (98%)	102 (87%)	14 (12%)	1 (1%)	21	65
11	BK	117/119 (98%)	93 (80%)	20 (17%)	4 (3%)	5	36
12	AL	122/124 (98%)	92 (75%)	20 (16%)	10 (8%)	1	11
12	BL	122/124 (98%)	94 (77%)	16 (13%)	12 (10%)	1	8
13	AM	122/124 (98%)	83 (68%)	26 (21%)	13 (11%)	0	6
13	BM	122/124 (98%)	83 (68%)	26 (21%)	13 (11%)	0	6
14	AN	58/60 (97%)	43 (74%)	12 (21%)	3 (5%)	2	23
14	BN	58/60 (97%)	41 (71%)	14 (24%)	3 (5%)	2	23
15	AO	86/88 (98%)	73 (85%)	9 (10%)	4 (5%)	3	26
15	BO	86/88 (98%)	72 (84%)	13 (15%)	1 (1%)	16	59
16	AP	81/83 (98%)	63 (78%)	15 (18%)	3 (4%)	4	33
16	BP	81/83 (98%)	67 (83%)	14 (17%)	0	100	100
17	AR	97/99 (98%)	89 (92%)	5 (5%)	3 (3%)	5	39
17	BR	97/99 (98%)	84 (87%)	10 (10%)	3 (3%)	5	39
18	AS	68/70 (97%)	57 (84%)	5 (7%)	6 (9%)	1	10
18	BS	68/70 (97%)	54 (79%)	10 (15%)	4 (6%)	2	19
19	AT	76/78 (97%)	61 (80%)	7 (9%)	8 (10%)	1	7
19	BT	76/78 (97%)	55 (72%)	13 (17%)	8 (10%)	1	7
20	AU	97/99 (98%)	77 (79%)	14 (14%)	6 (6%)	2	18
20	BU	97/99 (98%)	75 (77%)	19 (20%)	3 (3%)	5	39
21	AW	22/24 (92%)	19 (86%)	2 (9%)	1 (4%)	3	27
21	BW	22/24 (92%)	17 (77%)	3 (14%)	2 (9%)	1	9
24	BC	204/206 (99%)	153 (75%)	41 (20%)	10 (5%)	3	25
27	CA	83/206 (40%)	56 (68%)	22 (26%)	5 (6%)	2	19
28	CB	269/271 (99%)	210 (78%)	39 (14%)	20 (7%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	DB	269/271 (99%)	209 (78%)	38 (14%)	22 (8%)	1	11
29	CC	202/204 (99%)	143 (71%)	43 (21%)	16 (8%)	1	12
29	DC	202/204 (99%)	145 (72%)	32 (16%)	25 (12%)	0	4
30	CD	205/207 (99%)	162 (79%)	30 (15%)	13 (6%)	2	18
30	DD	205/207 (99%)	166 (81%)	24 (12%)	15 (7%)	1	14
31	CE	179/181 (99%)	132 (74%)	32 (18%)	15 (8%)	1	11
31	DE	179/181 (99%)	139 (78%)	28 (16%)	12 (7%)	1	16
32	CF	157/159 (99%)	112 (71%)	25 (16%)	20 (13%)	0	4
32	DF	157/159 (99%)	113 (72%)	26 (17%)	18 (12%)	0	5
33	CI	143/145 (99%)	112 (78%)	22 (15%)	9 (6%)	2	18
33	DI	143/145 (99%)	104 (73%)	29 (20%)	10 (7%)	1	15
35	CM	136/138 (99%)	103 (76%)	24 (18%)	9 (7%)	1	16
35	DM	136/138 (99%)	96 (71%)	30 (22%)	10 (7%)	1	14
36	CN	120/122 (98%)	106 (88%)	10 (8%)	4 (3%)	5	37
36	DN	120/122 (98%)	110 (92%)	8 (7%)	2 (2%)	11	51
37	CO	144/146 (99%)	84 (58%)	29 (20%)	31 (22%)	0	1
37	DO	144/146 (99%)	86 (60%)	26 (18%)	32 (22%)	0	1
38	CP	139/141 (99%)	118 (85%)	17 (12%)	4 (3%)	6	40
38	DP	139/141 (99%)	117 (84%)	17 (12%)	5 (4%)	4	34
39	CQ	115/117 (98%)	93 (81%)	14 (12%)	8 (7%)	1	15
39	DQ	115/117 (98%)	98 (85%)	11 (10%)	6 (5%)	2	23
40	CR	96/98 (98%)	62 (65%)	23 (24%)	11 (12%)	0	5
40	DR	96/98 (98%)	66 (69%)	15 (16%)	15 (16%)	0	2
41	CS	135/137 (98%)	92 (68%)	24 (18%)	19 (14%)	0	3
41	DS	135/137 (98%)	89 (66%)	28 (21%)	18 (13%)	0	4
42	CT	115/117 (98%)	103 (90%)	10 (9%)	2 (2%)	11	51
42	DT	115/117 (98%)	93 (81%)	15 (13%)	7 (6%)	2	18
43	CU	99/101 (98%)	75 (76%)	11 (11%)	13 (13%)	0	4
43	DU	99/101 (98%)	72 (73%)	13 (13%)	14 (14%)	0	3
44	CW	111/113 (98%)	92 (83%)	12 (11%)	7 (6%)	2	18
45	CX	90/92 (98%)	77 (86%)	7 (8%)	6 (7%)	1	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	DX	90/92 (98%)	79 (88%)	9 (10%)	2 (2%)	8	46
46	CY	98/100 (98%)	60 (61%)	17 (17%)	21 (21%)	0	1
46	DY	98/100 (98%)	60 (61%)	18 (18%)	20 (20%)	0	1
47	CZ	174/176 (99%)	121 (70%)	42 (24%)	11 (6%)	2	18
47	DZ	174/176 (99%)	136 (78%)	28 (16%)	10 (6%)	2	20
48	Ca	82/84 (98%)	72 (88%)	9 (11%)	1 (1%)	16	59
48	Da	82/84 (98%)	74 (90%)	7 (8%)	1 (1%)	16	59
49	CH	91/93 (98%)	73 (80%)	10 (11%)	8 (9%)	1	10
49	DH	91/93 (98%)	73 (80%)	12 (13%)	6 (7%)	1	16
50	CK	69/71 (97%)	50 (72%)	12 (17%)	7 (10%)	1	7
50	DK	69/71 (97%)	54 (78%)	11 (16%)	4 (6%)	2	20
51	CL	57/59 (97%)	51 (90%)	5 (9%)	1 (2%)	11	50
51	DL	57/59 (97%)	52 (91%)	3 (5%)	2 (4%)	4	35
52	C5	28/30 (93%)	20 (71%)	5 (18%)	3 (11%)	0	6
52	D5	28/30 (93%)	18 (64%)	7 (25%)	3 (11%)	0	6
53	C6	57/59 (97%)	48 (84%)	5 (9%)	4 (7%)	1	15
53	D6	57/59 (97%)	46 (81%)	7 (12%)	4 (7%)	1	15
54	C7	40/44 (91%)	22 (55%)	9 (22%)	9 (22%)	0	1
54	D7	40/44 (91%)	21 (52%)	8 (20%)	11 (28%)	0	0
55	C8	46/48 (96%)	42 (91%)	4 (9%)	0	100	100
55	D8	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
56	C9	61/63 (97%)	47 (77%)	11 (18%)	3 (5%)	3	25
56	D9	61/63 (97%)	41 (67%)	15 (25%)	5 (8%)	1	11
57	C0	34/36 (94%)	32 (94%)	2 (6%)	0	100	100
57	D0	34/36 (94%)	32 (94%)	2 (6%)	0	100	100
62	DA	83/206 (40%)	52 (63%)	28 (34%)	3 (4%)	4	34
63	DW	111/113 (98%)	94 (85%)	11 (10%)	6 (5%)	2	22
All	All	11440/11918 (96%)	8901 (78%)	1752 (15%)	787 (7%)	1	15

5 of 787 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AA	83	MET

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Mol	Chain	Res	Type
2	AA	165	VAL
3	AC	4	LYS
3	AC	12	LEU
3	AC	47	LEU

### 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	AA	202/202 (100%)	180 (89%)	22 (11%)	8	34
2	BA	202/202 (100%)	181 (90%)	21 (10%)	9	37
3	AC	160/187 (86%)	142 (89%)	18 (11%)	7	32
4	AD	180/180 (100%)	162 (90%)	18 (10%)	9	38
4	BD	180/180 (100%)	160 (89%)	20 (11%)	8	33
5	AE	115/115 (100%)	101 (88%)	14 (12%)	6	28
5	BE	115/115 (100%)	102 (89%)	13 (11%)	7	32
6	AF	90/90 (100%)	85 (94%)	5 (6%)	26	66
6	BF	90/90 (100%)	86 (96%)	4 (4%)	35	73
7	AG	126/126 (100%)	113 (90%)	13 (10%)	9	37
7	BG	126/126 (100%)	114 (90%)	12 (10%)	11	41
8	AH	119/119 (100%)	104 (87%)	15 (13%)	5	27
8	BH	119/119 (100%)	104 (87%)	15 (13%)	5	27
9	AI	98/98 (100%)	82 (84%)	16 (16%)	3	16
9	BI	98/98 (100%)	88 (90%)	10 (10%)	9	38
10	AJ	88/88 (100%)	77 (88%)	11 (12%)	6	27
10	BJ	88/88 (100%)	77 (88%)	11 (12%)	6	27
11	AK	90/90 (100%)	82 (91%)	8 (9%)	12	45
11	BK	90/90 (100%)	82 (91%)	8 (9%)	12	45
12	AL	104/104 (100%)	87 (84%)	17 (16%)	3	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	BL	104/104 (100%)	88 (85%)	16 (15%)	3	18
13	AM	99/99 (100%)	87 (88%)	12 (12%)	6	28
13	BM	99/99 (100%)	82 (83%)	17 (17%)	2	13
14	AN	49/49 (100%)	45 (92%)	4 (8%)	14	50
14	BN	49/49 (100%)	43 (88%)	6 (12%)	6	28
15	AO	79/79 (100%)	75 (95%)	4 (5%)	29	69
15	BO	79/79 (100%)	72 (91%)	7 (9%)	12	45
16	AP	72/72 (100%)	65 (90%)	7 (10%)	10	40
16	BP	72/72 (100%)	62 (86%)	10 (14%)	4	23
17	AR	94/94 (100%)	90 (96%)	4 (4%)	35	74
17	BR	94/94 (100%)	87 (93%)	7 (7%)	17	55
18	AS	61/61 (100%)	56 (92%)	5 (8%)	14	50
18	BS	61/61 (100%)	53 (87%)	8 (13%)	5	25
19	AT	69/69 (100%)	55 (80%)	14 (20%)	1	7
19	BT	69/69 (100%)	54 (78%)	15 (22%)	1	6
20	AU	76/76 (100%)	68 (90%)	8 (10%)	8	36
20	BU	76/76 (100%)	63 (83%)	13 (17%)	2	14
21	AW	19/19 (100%)	17 (90%)	2 (10%)	8	36
21	BW	19/19 (100%)	17 (90%)	2 (10%)	8	36
24	BC	160/160 (100%)	141 (88%)	19 (12%)	6	29
27	CA	61/74 (82%)	53 (87%)	8 (13%)	5	25
28	CB	213/213 (100%)	179 (84%)	34 (16%)	3	16
28	DB	213/213 (100%)	179 (84%)	34 (16%)	3	16
29	CC	165/165 (100%)	137 (83%)	28 (17%)	2	14
29	DC	165/165 (100%)	142 (86%)	23 (14%)	4	23
30	CD	165/165 (100%)	139 (84%)	26 (16%)	3	17
30	DD	165/165 (100%)	139 (84%)	26 (16%)	3	17
31	CE	155/155 (100%)	140 (90%)	15 (10%)	10	40
31	DE	155/155 (100%)	123 (79%)	32 (21%)	1	7
32	CF	132/132 (100%)	113 (86%)	19 (14%)	4	21
32	DF	132/132 (100%)	110 (83%)	22 (17%)	3	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	CI	122/122 (100%)	109 (89%)	13 (11%)	8	35
33	DI	122/122 (100%)	110 (90%)	12 (10%)	10	40
35	CM	117/117 (100%)	96 (82%)	21 (18%)	2	11
35	DM	117/117 (100%)	95 (81%)	22 (19%)	2	9
36	CN	100/100 (100%)	84 (84%)	16 (16%)	3	16
36	DN	100/100 (100%)	88 (88%)	12 (12%)	6	29
37	CO	112/112 (100%)	82 (73%)	30 (27%)	0	3
37	DO	112/112 (100%)	83 (74%)	29 (26%)	0	3
38	CP	111/111 (100%)	99 (89%)	12 (11%)	8	35
38	DP	111/111 (100%)	97 (87%)	14 (13%)	5	27
39	CQ	100/100 (100%)	81 (81%)	19 (19%)	2	9
39	DQ	100/100 (100%)	83 (83%)	17 (17%)	2	14
40	CR	77/77 (100%)	60 (78%)	17 (22%)	1	5
40	DR	77/77 (100%)	58 (75%)	19 (25%)	1	4
41	CS	120/120 (100%)	92 (77%)	28 (23%)	1	4
41	DS	120/120 (100%)	100 (83%)	20 (17%)	3	14
42	CT	92/92 (100%)	79 (86%)	13 (14%)	4	22
42	DT	92/92 (100%)	81 (88%)	11 (12%)	6	29
43	CU	82/82 (100%)	69 (84%)	13 (16%)	3	17
43	DU	82/82 (100%)	61 (74%)	21 (26%)	0	3
44	CW	91/92 (99%)	82 (90%)	9 (10%)	10	39
45	CX	74/74 (100%)	63 (85%)	11 (15%)	4	20
45	DX	74/74 (100%)	60 (81%)	14 (19%)	2	9
46	CY	84/84 (100%)	67 (80%)	17 (20%)	1	7
46	DY	84/84 (100%)	68 (81%)	16 (19%)	2	9
47	CZ	155/155 (100%)	142 (92%)	13 (8%)	14	49
47	DZ	155/155 (100%)	136 (88%)	19 (12%)	6	28
48	Ca	66/66 (100%)	57 (86%)	9 (14%)	5	24
48	Da	66/66 (100%)	56 (85%)	10 (15%)	3	19
49	CH	78/78 (100%)	56 (72%)	22 (28%)	0	2
49	DH	78/78 (100%)	62 (80%)	16 (20%)	1	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	CK	66/66 (100%)	55 (83%)	11 (17%)	3	14
50	DK	66/66 (100%)	53 (80%)	13 (20%)	1	8
51	CL	51/51 (100%)	49 (96%)	2 (4%)	39	76
51	DL	51/51 (100%)	48 (94%)	3 (6%)	24	64
52	C5	27/27 (100%)	24 (89%)	3 (11%)	8	33
52	D5	27/27 (100%)	21 (78%)	6 (22%)	1	5
53	C6	51/51 (100%)	43 (84%)	8 (16%)	3	18
53	D6	51/51 (100%)	42 (82%)	9 (18%)	2	12
54	C7	43/43 (100%)	36 (84%)	7 (16%)	3	16
54	D7	43/43 (100%)	35 (81%)	8 (19%)	2	10
55	C8	41/41 (100%)	37 (90%)	4 (10%)	10	40
55	D8	41/41 (100%)	32 (78%)	9 (22%)	1	5
56	C9	53/53 (100%)	40 (76%)	13 (24%)	1	4
56	D9	53/53 (100%)	43 (81%)	10 (19%)	2	9
57	C0	33/33 (100%)	30 (91%)	3 (9%)	12	44
57	D0	33/33 (100%)	27 (82%)	6 (18%)	2	11
62	DA	61/74 (82%)	53 (87%)	8 (13%)	5	25
63	DW	91/91 (100%)	86 (94%)	5 (6%)	27	66
All	All	9654/9708 (99%)	8293 (86%)	1361 (14%)	4	22

5 of 1361 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	CN	7	TYR
43	CU	95	LEU
47	DZ	39	VAL
37	CO	16	ARG
39	CQ	105	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 195 such sidechains are listed below:

Mol	Chain	Res	Type
35	CM	45	ASN
42	CT	81	HIS
47	DZ	132	ASN

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Mol	Chain	Res	Type
36	CN	5	GLN
39	CQ	24	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A2	8/9 (88%)	4 (50%)	2 (25%)
22	Ab	1503/1504 (99%)	324 (21%)	0
22	Bb	1503/1504 (99%)	339 (22%)	0
23	B2	8/10 (80%)	4 (50%)	1 (12%)
25	C2	74/76 (97%)	24 (32%)	4 (5%)
25	C3	75/76 (98%)	19 (25%)	1 (1%)
25	D3	75/76 (98%)	31 (41%)	3 (4%)
26	C4	76/77 (98%)	36 (47%)	4 (5%)
58	C1	2800/2899 (96%)	802 (28%)	155 (5%)
58	D1	2800/2899 (96%)	818 (29%)	149 (5%)
59	Cs	118/119 (99%)	35 (29%)	0
59	Ds	118/119 (99%)	40 (33%)	0
60	D2	19/20 (95%)	8 (42%)	1 (5%)
61	D4	75/76 (98%)	23 (30%)	5 (6%)
64	DV	41/55 (74%)	14 (34%)	1 (2%)
All	All	9293/9519 (97%)	2521 (27%)	326 (3%)

5 of 2521 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A2	15	A
1	A2	17	U
1	A2	18	G
1	A2	19	U
22	Ab	10	G

5 of 326 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
58	C1	2553	A
58	D1	99	G
58	D1	2475	C
58	C1	2622	U
58	C1	2843	G

## 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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
65	PAR	Ab	1601	-	45,45,45	1.39	4 (8%)	59,67,67	1.40	10 (16%)
65	PAR	Bb	1601	-	45,45,45	1.49	6 (13%)	59,67,67	2.00	17 (28%)
66	3V6	C1	3001	67	22,25,25	2.02	8 (36%)	23,39,39	2.25	7 (30%)
66	3V6	D1	3001	67	22,25,25	2.26	9 (40%)	23,39,39	3.16	9 (39%)

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
65	PAR	Ab	1601	-	-	1/18/94/94	2/4/4/4
65	PAR	Bb	1601	-	-	1/18/94/94	0/4/4/4
66	3V6	C1	3001	67	-	0/12/53/53	0/2/2/2
66	3V6	D1	3001	67	-	0/12/53/53	0/2/2/2

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
66	D1	3001	3V6	CAK-CAN	-5.23	1.42	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	Ab	1601	PAR	C34-C24	-5.12	1.47	1.53
65	Ab	1601	PAR	O33-C33	-3.38	1.35	1.43
66	C1	3001	3V6	CAK-CAN	-3.37	1.44	1.49
66	D1	3001	3V6	CAW-CAQ	-2.92	1.45	1.50

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	Bb	1601	PAR	O54-C54-C64	-7.83	90.80	106.10
66	D1	3001	3V6	OAG-CAN-CAQ	-6.30	114.56	123.25
66	D1	3001	3V6	OAE-CAO-CAQ	-5.28	118.86	125.58
66	D1	3001	3V6	CAX-CAV-NAL	-4.73	105.80	112.34
66	D1	3001	3V6	CLI-CAT-CLJ	-4.64	100.97	108.59

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
65	Ab	1601	PAR	C52-O52-C13-C23
65	Bb	1601	PAR	C42-O11-C11-C21

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
65	Ab	1601	PAR	C14-C24-C34-C44-C54-O54
65	Ab	1601	PAR	C12-C22-C32-C42-C52-C62

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
66	C1	3001	3V6	5	0
66	D1	3001	3V6	11	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

The following chains have linkage breaks:



Mol	Chain	Number of breaks
27	CA	2
62	DA	2
58	D1	1
54	C7	1
58	C1	1
54	D7	1

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	DA	110:PHE	C	119:UNK	N	14.86
1	CA	110:PHE	C	119:UNK	N	12.87
1	CA	136:UNK	C	139:UNK	N	8.88
1	D7	46:HIS	C	47:THR	N	7.64
1	C7	46:HIS	C	47:THR	N	7.62

## 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, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A2	9/9 (100%)	0.03	0 100 100	50, 89, 111, 114	0
2	AA	234/234 (100%)	0.27	10 (4%) 39 34	78, 124, 168, 197	0
2	BA	234/234 (100%)	0.38	19 (8%) 15 14	80, 130, 179, 209	0
3	AC	206/238 (86%)	0.26	14 (6%) 20 19	65, 108, 148, 173	0
4	AD	208/208 (100%)	-0.05	3 (1%) 78 73	51, 86, 123, 147	0
4	BD	208/208 (100%)	-0.12	1 (0%) 91 89	48, 78, 117, 144	0
5	AE	150/150 (100%)	0.02	3 (2%) 68 62	66, 91, 124, 144	0
5	BE	150/150 (100%)	0.06	0 100 100	57, 83, 122, 141	0
6	AF	101/101 (100%)	-0.27	3 (2%) 54 49	55, 85, 109, 170	0
6	BF	101/101 (100%)	-0.15	1 (0%) 84 79	52, 96, 130, 158	0
7	AG	155/155 (100%)	0.09	13 (8%) 14 13	58, 86, 125, 181	0
7	BG	155/155 (100%)	0.50	12 (7%) 16 16	78, 112, 154, 184	0
8	AH	138/138 (100%)	0.02	0 100 100	60, 90, 117, 184	0
8	BH	138/138 (100%)	0.30	2 (1%) 78 73	63, 95, 123, 145	0
9	AI	127/127 (100%)	0.50	9 (7%) 19 18	62, 108, 150, 175	0
9	BI	127/127 (100%)	0.93	17 (13%) 4 4	77, 131, 179, 215	0
10	AJ	98/98 (100%)	0.82	15 (15%) 3 3	77, 121, 176, 188	0
10	BJ	98/98 (100%)	1.20	24 (24%) 1 1	65, 134, 173, 202	0
11	AK	119/119 (100%)	-0.00	5 (4%) 40 35	39, 76, 110, 158	0
11	BK	119/119 (100%)	0.52	8 (6%) 21 20	47, 94, 141, 193	0
12	AL	124/124 (100%)	0.38	11 (8%) 12 11	49, 82, 125, 180	0
12	BL	124/124 (100%)	0.10	5 (4%) 42 37	41, 60, 105, 158	0
13	AM	124/124 (100%)	0.33	7 (5%) 28 25	66, 98, 144, 197	0
13	BM	124/124 (100%)	0.77	11 (8%) 12 11	66, 113, 164, 204	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
14	AN	60/60 (100%)	0.28	1 (1%) 73 67	65, 103, 130, 142	0
14	BN	60/60 (100%)	0.33	2 (3%) 50 45	59, 94, 119, 134	0
15	AO	88/88 (100%)	-0.04	0 100 100	46, 76, 112, 123	0
15	BO	88/88 (100%)	0.09	1 (1%) 82 77	55, 94, 120, 132	0
16	AP	83/83 (100%)	0.14	2 (2%) 62 57	52, 73, 101, 136	0
16	BP	83/83 (100%)	0.44	3 (3%) 46 41	59, 89, 135, 152	0
17	AR	99/99 (100%)	0.06	1 (1%) 84 79	59, 80, 108, 115	0
17	BR	99/99 (100%)	0.19	2 (2%) 68 62	65, 94, 126, 135	0
18	AS	70/70 (100%)	0.29	2 (2%) 55 50	56, 88, 119, 156	0
18	BS	70/70 (100%)	0.62	5 (7%) 19 18	66, 94, 142, 180	0
19	AT	78/78 (100%)	0.89	14 (17%) 2 2	67, 110, 164, 180	0
19	BT	78/78 (100%)	1.08	12 (15%) 3 3	79, 118, 161, 184	0
20	AU	99/99 (100%)	0.33	3 (3%) 54 49	62, 86, 125, 146	0
20	BU	99/99 (100%)	0.64	8 (8%) 15 14	64, 107, 146, 154	0
21	AW	24/24 (100%)	1.73	7 (29%) 1 1	63, 80, 112, 138	0
21	BW	24/24 (100%)	1.28	7 (29%) 1 1	64, 91, 132, 163	0
22	Ab	1504/1504 (100%)	-0.15	27 (1%) 71 65	30, 75, 154, 300	0
22	Bb	1504/1504 (100%)	-0.01	40 (2%) 58 53	31, 81, 165, 318	0
23	B2	10/10 (100%)	0.33	0 100 100	60, 107, 138, 172	0
24	BC	206/206 (100%)	0.16	7 (3%) 49 44	64, 105, 149, 169	0
25	C2	75/76 (98%)	7.55	69 (92%) 0 0	99, 250, 345, 377	0
25	C3	76/76 (100%)	0.37	6 (7%) 15 14	60, 130, 198, 227	0
25	D3	76/76 (100%)	0.53	3 (3%) 43 38	59, 147, 212, 228	0
26	C4	77/77 (100%)	-0.29	0 100 100	44, 79, 132, 159	0
27	CA	87/206 (42%)	3.20	53 (60%) 0 0	98, 186, 221, 241	0
28	CB	271/271 (100%)	-0.31	0 100 100	23, 48, 83, 150	0
28	DB	271/271 (100%)	-0.22	4 (1%) 76 71	20, 52, 86, 159	0
29	CC	204/204 (100%)	0.13	7 (3%) 49 44	31, 68, 123, 150	0
29	DC	204/204 (100%)	0.03	4 (1%) 68 62	24, 61, 124, 169	0
30	CD	207/207 (100%)	-0.25	4 (1%) 70 64	29, 64, 133, 194	0
30	DD	207/207 (100%)	-0.07	6 (2%) 55 50	20, 65, 146, 223	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
31	CE	181/181 (100%)	0.07	7 (3%) 43 38	59, 92, 137, 213	0
31	DE	181/181 (100%)	0.54	15 (8%) 14 13	76, 117, 154, 198	0
32	CF	159/159 (100%)	1.15	39 (24%) 1 1	82, 134, 175, 219	0
32	DF	159/159 (100%)	0.14	7 (4%) 38 34	45, 85, 126, 178	0
33	CI	145/145 (100%)	0.31	5 (3%) 49 44	40, 88, 128, 150	0
33	DI	145/145 (100%)	0.32	8 (5%) 29 26	60, 108, 139, 165	0
34	CJ	0/130	-	-	-	-
34	DJ	0/130	-	-	-	-
35	CM	138/138 (100%)	0.06	1 (0%) 89 85	47, 78, 118, 130	0
35	DM	138/138 (100%)	-0.03	0 100 100	36, 73, 121, 151	0
36	CN	122/122 (100%)	-0.08	1 (0%) 87 83	35, 66, 89, 111	0
36	DN	122/122 (100%)	-0.33	0 100 100	27, 51, 75, 107	0
37	CO	146/146 (100%)	0.28	4 (2%) 58 53	34, 77, 127, 168	0
37	DO	146/146 (100%)	0.31	6 (4%) 41 36	31, 87, 123, 165	0
38	CP	141/141 (100%)	-0.00	2 (1%) 78 73	44, 75, 111, 192	0
38	DP	141/141 (100%)	-0.08	2 (1%) 78 73	42, 71, 106, 219	0
39	CQ	117/117 (100%)	-0.18	0 100 100	38, 63, 94, 127	0
39	DQ	117/117 (100%)	-0.02	0 100 100	27, 61, 99, 130	0
40	CR	98/98 (100%)	0.42	5 (5%) 32 28	47, 89, 130, 176	0
40	DR	98/98 (100%)	1.29	22 (22%) 1 1	68, 113, 143, 163	0
41	CS	137/137 (100%)	0.06	6 (4%) 38 34	45, 79, 142, 200	0
41	DS	137/137 (100%)	0.07	4 (2%) 55 50	43, 71, 148, 192	0
42	CT	117/117 (100%)	-0.07	2 (1%) 73 67	37, 66, 116, 138	0
42	DT	117/117 (100%)	-0.14	1 (0%) 85 81	31, 68, 111, 153	0
43	CU	101/101 (100%)	0.08	3 (2%) 54 49	35, 92, 122, 134	0
43	DU	101/101 (100%)	0.25	5 (4%) 32 29	26, 86, 123, 196	0
44	CW	113/113 (100%)	-0.13	2 (1%) 71 65	38, 54, 90, 182	0
45	CX	92/92 (100%)	-0.26	0 100 100	39, 65, 89, 109	0
45	DX	92/92 (100%)	-0.27	0 100 100	33, 55, 88, 115	0
46	CY	100/100 (100%)	1.21	25 (25%) 1 1	58, 94, 168, 214	0
46	DY	100/100 (100%)	0.87	14 (14%) 4 4	48, 81, 193, 251	0
47	CZ	176/176 (100%)	0.36	9 (5%) 32 28	76, 118, 157, 233	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
47	DZ	176/176 (100%)	0.51	15 (8%) 13 13	69, 119, 173, 203	0
48	Ca	84/84 (100%)	0.66	9 (10%) 8 7	44, 67, 127, 170	0
48	Da	84/84 (100%)	0.64	10 (11%) 6 6	49, 82, 137, 167	0
49	CH	93/93 (100%)	-0.08	1 (1%) 82 77	30, 54, 102, 140	0
49	DH	93/93 (100%)	0.10	1 (1%) 82 77	29, 66, 121, 179	0
50	CK	71/71 (100%)	0.03	2 (2%) 56 52	42, 85, 125, 180	0
50	DK	71/71 (100%)	0.01	2 (2%) 56 52	37, 68, 124, 179	0
51	CL	59/59 (100%)	0.66	4 (6%) 20 19	45, 72, 111, 223	0
51	DL	59/59 (100%)	0.39	5 (8%) 13 13	48, 79, 120, 213	0
52	C5	30/30 (100%)	-0.29	0 100 100	76, 99, 130, 155	0
52	D5	30/30 (100%)	0.42	2 (6%) 21 20	99, 128, 155, 167	0
53	C6	59/59 (100%)	0.37	5 (8%) 13 13	34, 63, 160, 206	0
53	D6	59/59 (100%)	0.09	4 (6%) 20 19	28, 65, 172, 205	0
54	C7	44/44 (100%)	1.62	14 (31%) 1 1	54, 101, 146, 183	0
54	D7	44/44 (100%)	2.23	18 (40%) 0 0	84, 125, 165, 181	0
55	C8	48/48 (100%)	-0.11	2 (4%) 40 35	26, 40, 79, 139	0
55	D8	48/48 (100%)	-0.15	2 (4%) 40 35	21, 34, 77, 135	0
56	C9	63/63 (100%)	0.01	1 (1%) 74 69	34, 54, 90, 123	0
56	D9	63/63 (100%)	0.11	2 (3%) 51 47	39, 66, 102, 136	0
57	C0	36/36 (100%)	3.14	21 (58%) 0 0	93, 125, 175, 177	0
57	D0	36/36 (100%)	2.97	27 (75%) 0 0	73, 106, 141, 145	0
58	C1	2807/2899 (96%)	-0.23	32 (1%) 82 77	21, 54, 148, 279	0
58	D1	2807/2899 (96%)	-0.19	44 (1%) 74 69	16, 52, 155, 267	0
59	Cs	119/119 (100%)	-0.23	2 (1%) 73 67	58, 83, 138, 197	0
59	Ds	119/119 (100%)	0.23	5 (4%) 40 35	62, 104, 147, 172	0
60	D2	20/20 (100%)	4.00	18 (90%) 0 0	133, 235, 281, 283	0
61	D4	76/76 (100%)	-0.22	0 100 100	37, 79, 120, 201	0
62	DA	87/206 (42%)	3.33	60 (68%) 0 0	118, 190, 257, 309	0
63	DW	113/113 (100%)	-0.16	2 (1%) 71 65	33, 51, 100, 159	0
64	DV	55/55 (100%)	6.77	50 (90%) 0 0	110, 248, 297, 345	0
All	All	20982/21697 (96%)	0.14	1048 (4%) 32 29	16, 77, 159, 377	0

The worst 5 of 1048 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
25	C2	70	G	24.2
25	C2	71	G	22.4
64	DV	50	G	22.4
25	C2	17	C	21.1
25	C2	3	C	20.8

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
66	3V6	C1	3001	24/24	0.92	0.25	5.02	46,63,76,91	0
66	3V6	D1	3001	24/24	0.94	0.24	4.89	32,55,75,86	0
67	MG	C1	3002	1/1	0.95	0.22	2.84	41,41,41,41	0
65	PAR	Bb	1601	42/42	0.96	0.20	2.78	42,50,56,67	0
65	PAR	Ab	1601	42/42	0.93	0.20	2.12	51,65,75,91	0
67	MG	D1	3002	1/1	0.93	0.24	-	40,40,40,40	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.