



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 12:28 pm GMT

PDB ID : 4V66
EMDB ID: : EMD-1055
Title : Structure of the E. coli ribosome and the tRNAs in Post-accommodation state
Authors : Devkota, B.; Caulfield, T.R.; Tan, R.-Z.; Harvey, S.C.
Deposited on : 2008-08-03
Resolution : 9.00 Å(reported)
Based on PDB ID : 2I2P, 1EHZ

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

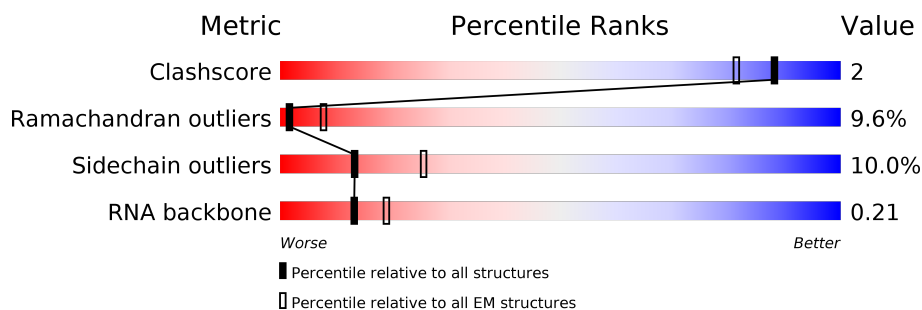
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 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.








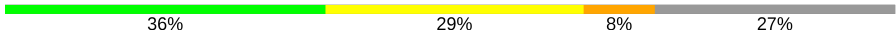



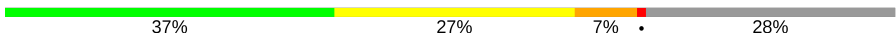


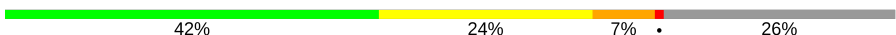












Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	AA	76	22% 41% 36% .
1	AE	76	25% 61% 14%
1	AP	76	25% 55% 18% .
2	AM	20	20% 35% 45%
3	A1	1530	17% 48% 35%
4	AB	241	61% 23% 5% 10%
5	AC	129	57% 26% 5% . 9%
6	AD	124	56% 31% 10% . .









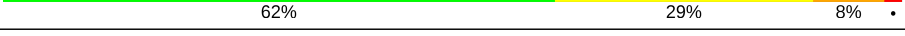

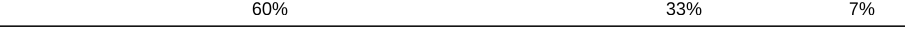






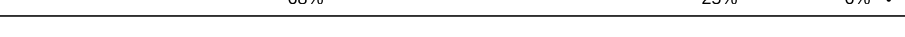
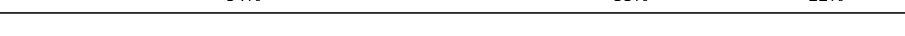
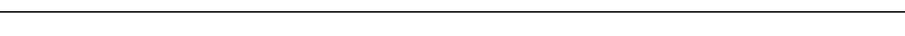
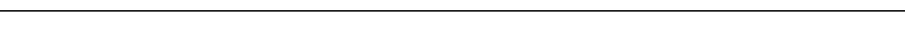
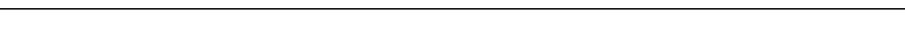
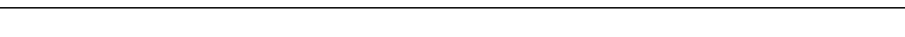

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Mol	Chain	Length	Quality of chain
7	AF	118	
8	AG	101	
9	AH	89	
10	AI	82	
11	AJ	84	
12	AK	75	
13	AL	92	
14	AN	87	
15	AO	233	
16	AQ	71	
17	AR	206	
18	AS	159	
19	AT	135	
20	AU	179	
21	AV	130	
22	AW	130	
23	AX	103	
24	BA	117	
25	BB	2903	
26	BC	94	
27	BD	123	
28	BE	144	
29	BF	136	
30	BG	127	
31	BH	117	

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Mol	Chain	Length	Quality of chain
32	BI	115	
33	BJ	118	
34	BK	103	
35	BL	110	
36	BM	99	
37	BN	270	
38	BO	103	
39	BP	85	
40	BQ	63	
41	BR	59	
42	BS	70	
43	BT	57	
44	BU	54	
45	BV	46	
46	BW	64	
47	BX	38	
48	BY	209	
49	BZ	213	
50	B1	201	
51	B2	178	
52	B3	177	
53	B4	149	
54	B5	142	
55	B6	140	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 149248 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 A/T, P and E-site tRNAs.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	75	Total	C	N	O	P	0	0
			1600	715	288	523	74		
1	AP	75	Total	C	N	O	P	0	0
			1600	715	288	523	74		
1	AE	76	Total	C	N	O	P	0	0
			1622	725	293	529	75		

- Molecule 2 is a RNA chain called mRNA model.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AM	20	Total	C	N	O	P	0	0
			397	180	40	158	19		

- Molecule 3 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A1	1530	Total	C	N	O	P	0	0
			32828	14642	6024	10633	1529		

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AB	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 5 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AC	117	Total	C	N	O	S	0	0
			876	540	174	159	3		

- Molecule 6 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AD	123	Total	C	N	O	S	0	0
			954	590	196	164	4		

- Molecule 7 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AF	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 8 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AG	96	Total	C	N	O	S	0	0
			773	483	160	127	3		

- Molecule 9 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AH	88	Total	C	N	O	S	0	0
			715	440	146	128	1		

- Molecule 10 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AI	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AJ	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 12 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	AK	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AL	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

- Molecule 15 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 16 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 17 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AR	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 18 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 19 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AT	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 20 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AU	150	Total	C	N	O	S	0	0
			1174	730	226	214	4		

- Molecule 21 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AV	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 22 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AW	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

- Molecule 23 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AX	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 24 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BA	117	Total	C	N	O	P	0	0
			2504	1116	459	813	116		

- Molecule 25 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BB	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BC	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 27 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BD	121	Total	C	N	O	S	0	0
			930	582	179	164	5		

- Molecule 28 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BE	144	Total	C	N	O	S	0	0
			1052	654	207	189	2		

- Molecule 29 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BF	136	Total	C	N	O	S	0	0
			1073	686	205	176	6		

- Molecule 30 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BG	127	Total	C	N	O	S	0	0
			1007	621	204	177	5		

- Molecule 31 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BH	117	Total	C	N	O	S	0	0
			899	557	179	162	1		

- Molecule 32 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BI	114	Total	C	N	O	S	0	0
			916	574	179	162	1		

- Molecule 33 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	BJ	117	Total	C	N	O	0	0
			946	604	192	150		

- Molecule 34 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BK	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 35 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BL	110	Total	C	N	O	S	0	0
			856	532	166	155	3		

- Molecule 36 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BM	99	Total	C	N	O	S	0	0
			777	491	145	139	2		

- Molecule 37 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BN	267	Total	C	N	O	S	0	0
			2053	1271	416	359	7		

- Molecule 38 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BO	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 39 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BP	84	Total	C	N	O	S	0	0
			633	391	129	112	1		

- Molecule 40 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BQ	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 41 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BR	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 42 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BS	70	Total	C	N	O	S	0	0
			548	339	104	99	6		

- Molecule 43 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BT	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

- Molecule 44 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BU	54	Total	C	N	O	S	0	0
			440	284	81	75			

- Molecule 45 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BV	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 46 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BW	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 47 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BX	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 48 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BY	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 49 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BZ	213	Total	C	N	O	S	0	0
			1687	1078	300	308	1		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BZ	1	MET	-	INSERTION	UNP P35024
BZ	?	-	MET	DELETION	UNP P35024
BZ	70	SER	PHE	CONFLICT	UNP P35024
BZ	82	LYS	ASN	CONFLICT	UNP P35024
BZ	?	-	MET	DELETION	UNP P35024
BZ	?	-	MET	DELETION	UNP P35024
BZ	?	-	MET	DELETION	UNP P35024

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B1	201	Total	C	N	O	S	0	0
			1551	974	283	289	5		

- Molecule 51 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B2	178	Total	C	N	O	S	0	0
			1419	905	251	257	6		

- Molecule 52 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B3	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 53 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B4	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 54 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B5	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

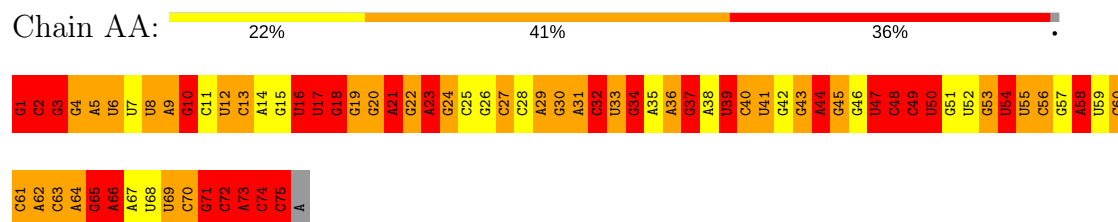
- Molecule 55 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B6	140	Total	C	N	O	S	0	0
			1112	704	210	194	4		

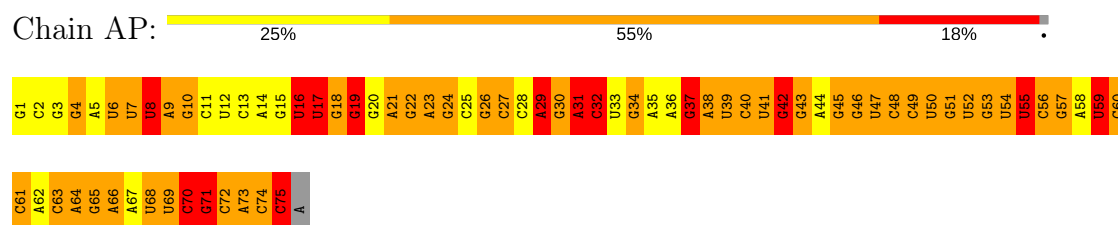
3 Residue-property plots

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

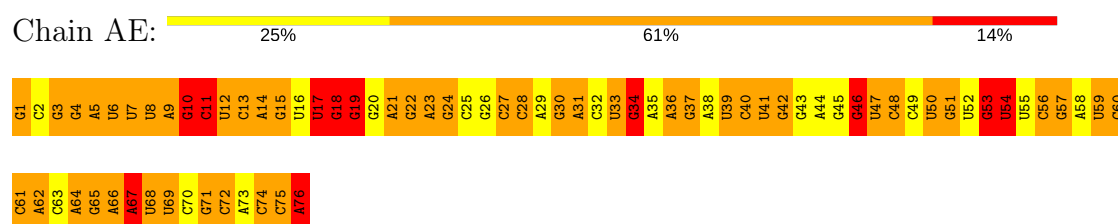
- Molecule 1: A/T, P and E-site tRNAs



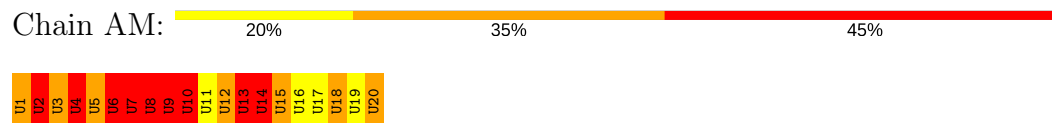
- Molecule 1: A/T, P and E-site tRNAs



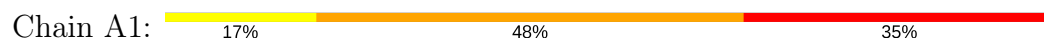
- Molecule 1: A/T, P and E-site tRNAs



- Molecule 2: mRNA model

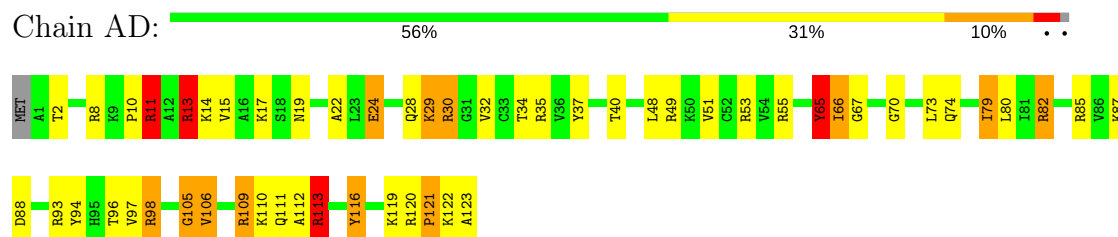


- Molecule 3: 16S rRNA

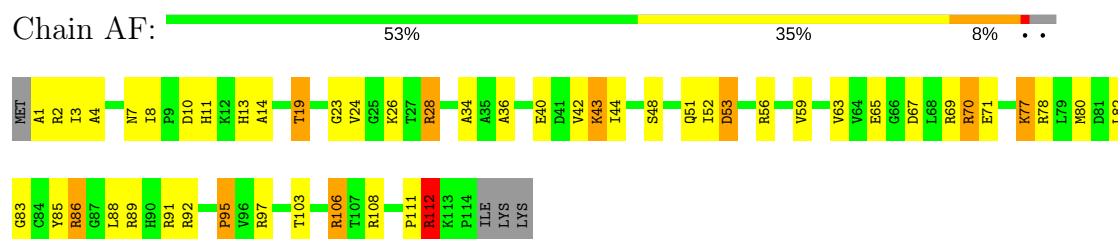


U965	U966	U905	A845	G785	G725	A865	U605	C545	U485	G425	U365	G305	U245	U185	U125	A65	U5
G866	G867	A906	G846	G786	C726	G665	G606	A546	U486	U426	A366	A306	A246	C186	G126	A66	G6
G907	G847	A907	G847	A787	G727	G667	A607	A547	A487	U427	U367	C307	G247	C187	G127	A67	A7
A968	C848	A908	G848	U788	A728	G668	A608	A548	C488	G428	U368	C308	C248	C188	G128	G68	A8
A969	A969	A909	A969	A789	A729	G669	A609	C549	C489	U429	G369	A309	U249	A189	A129	G69	G9
C970	C970	C910	U850	A790	G730	G670	U610	C550	C490	U430	C370	G310	A250	A190	A130	U70	A10
G971	C851	U911	C851	G791	G731	G671	C611	U551	C491	A431	A371	C311	G251	G191	A131	A71	G11
C972	G852	C912	G852	A792	G732	U672	C612	U552	C492	A432	C372	C312	U252	A192	C132	A72	U12
G973	G853	A913	G853	U793	G733	A673	C613	U553	A493	G433	A373	A313	U253	C193	U133	C73	U13
A974	U854	A914	U854	A794	G734	G674	C614	A554	C494	U434	A374	C314	G254	C194	U134	A74	U14
A975	U855	A915	U855	C795	C735	A675	C615	U555	A495	U435	U375	A315	G255	C195	U135	A75	G15
G976	C856	U916	C856	C796	G736	A676	C616	C556	A496	C436	G376	C316	U256	A196	C136	G76	A16
A977	G857	C917	C857	C797	C737	U677	C617	G557	G497	U437	G377	U317	G257	A197	U137	A77	U17
A978	G858	A918	G858	U798	C738	U678	C618	G558	A498	U438	G378	G318	G258	G198	G138	A78	C18
C979	G859	A919	G859	C799	C739	C679	U619	A559	A499	U439	C379	G319	G259	A199	A139	G79	A19
C980	U860	U920	A860	G800	U740	C680	C620	U560	C500	C440	G380	A320	G260	G200	U140	A80	U20
U981	C861	U921	C861	A801	G741	A881	A621	U561	C501	A441	C381	A321	U261	G201	G141	A81	G21
U982	C982	G922	C982	A802	G742	G882	A622	U562	A502	G442	A382	C322	G262	G202	G142	G82	G22
A983	U883	A923	U883	G803	A743	G883	C623	A563	C503	C443	A383	U323	G263	G203	A143	C83	C23
C984	A864	C924	A864	U804	G744	U884	C624	C564	C504	G444	C384	G324	G264	G204	G144	U84	U24
C985	A865	G925	A865	C805	G745	G885	U625	C565	G505	G445	C385	A325	G265	G205	G145	U85	C25
U986	C866	G926	C866	C806	A746	U886	G626	G566	C506	G446	C386	G326	G266	G206	G146	G86	A26
G987	G987	G927	G867	A807	A747	A887	G627	G567	C507	G447	U387	A327	G267	C207	G147	C87	G27
G988	C988	G928	C988	C808	G748	G888	G628	G568	U508	A448	G388	C328	U268	U208	G148	U88	A28
U989	G869	G929	C869	G809	A749	C889	A629	C569	A509	G449	A389	A329	C269	U209	A149	U89	U29
C990	U870	C930	U870	C810	C750	G890	A630	G570	A510	G450	U390	C330	A270	C210	U150	C90	U30
U991	U871	C931	U871	C811	U751	G891	C631	U571	C511	A451	G391	G331	C271	G211	A151	U91	G31
U992	A872	G932	A872	G812	G752	U892	U632	A572	U512	A452	C392	G332	C272	G212	A152	U92	A32
G993	A873	C933	A873	C813	A753	G893	G633	A573	C513	G453	A393	U333	U273	G213	C153	U93	C34
A994	C874	A934	C874	A814	C754	A894	C634	A574	C514	G454	G394	C334	A274	G214	U154	G94	C34
C995	U875	A935	U875	A815	G755	A895	A635	G575	G515	G455	C395	C335	G275	C215	A155	C95	C35
A996	C876	C936	C876	A816	C756	A896	U636	C576	U516	A456	C396	A336	G276	U216	C156	U96	C36
G997	G877	G937	G877	C817	U757	U897	G637	G577	G517	A457	A397	G337	C277	G217	U157	G97	U37
C998	A878	C938	A878	G818	C758	G898	U638	A578	C518	U458	U398	A338	G278	U218	G158	A98	G38
C999	C879	G939	C879	A819	A759	C899	G639	C579	C519	G459	G399	U339	A279	U219	C159	C99	G39
A1000	C880	C940	C880	U820	G760	G700	A640	C580	A520	A460	C400	U340	G280	G220	A160	G100	C40
C1001	G881	G941	G881	G821	G761	U701	U641	G581	G521	A461	C401	G341	G281	G221	A161	A101	G41
G1002	C882	G942	C882	U822	U762	A702	A642	C582	C522	G462	C402	C342	A282	G222	A162	G102	G42
G1003	C883	U943	C883	G823	G763	G703	C643	A583	A523	U463	C403	U343	U283	A223	C163	U103	C43
A1004	U884	G944	U884	G824	C764	A704	U644	G584	G524	U464	G404	A344	C284	U224	G164	G104	A44
A1005	G885	G945	G885	A825	G765	G705	C645	G585	C525	A465	U405	C345	C285	G225	G165	G105	G45
G1006	C886	A946	C886	C826	A766	A706	C646	C586	C526	A466	G406	G346	G286	G226	U166	C106	G46
U1007	G887	G947	G887	U827	G767	U707	C647	G587	C527	U467	U407	G347	U287	G227	A167	G107	C47
U1008	C888	C948	C888	U828	A768	C708	A648	G588	C528	A468	A408	G348	A288	A228	G168	G108	C48
U1009	A889	A949	A889	G829	G769	U709	A649	U589	G529	C469	U409	A349	G289	U229	C169	A109	U49
U1010	G890	U950	G890	G830	C770	G710	G650	U590	G530	C470	G410	G350	C290	G230	U170	C110	A50
C1011	U891	G951	U891	A831	G771	G711	C651	U591	U531	U471	A411	G351	U291	U231	A171	G111	A51
A1012	A892	U952	A892	G832	U772	A712	U652	G592	A532	U472	A412	C352	G292	G232	A172	G112	C52
G1013	C893	G953	C893	G833	G773	G713	U653	U593	A533	U473	G413	A353	G293	C233	U173	G113	A53
A1014	G894	G954	G894	U834	G774	G714	G654	U594	U534	G474	A414	G354	U294	C234	A174	U114	C54
G1015	G895	U955	G895	U835	G775	A715	A655	A595	A535	C475	A415	C355	C295	C235	C175	G115	A55
A1016	C896	U956	C896	G836	G776	U716	G656	A596	C536	U476	A356	A356	U296	A236	C176	A116	U56
U1017	G897	U957	G897	U837	A777	U717	U657	G597	G537	C477	G417	G357	G297	G237	G177	G117	G57
G1018	U898	G958	U898	G838	G778	A718	C658	U598	C538	A478	C418	U358	A298	G238	C178	U118	C58
A1019	C899	A959	C899	C839	C779	C719	U659	C599	A539	U479	G419	G359	G299	U239	A179	A119	A59
G1020	U900	U960	U900	C840	A780	C720	C660	A600	G540	U480	U420	G360	A300	G240	U180	A120	A60
U1021	A901	U961	A901	C841	A781	G721	C661	G601	G541	G481	U421	G361	G301	G241	A181	U121	G61
A1022	G902	C962	G902	U842	A782	G722	U662	A602	G542	A482	C422	G362	G302	G242	A182	G122	U62
U1023	G903	G963	U903	U843	C783	U723	A663	U603	U543	C483	G423	A363	A303	G243	C183	U123	C63
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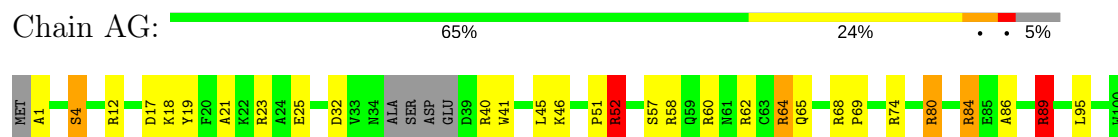
- Molecule 6: 30S ribosomal protein S12



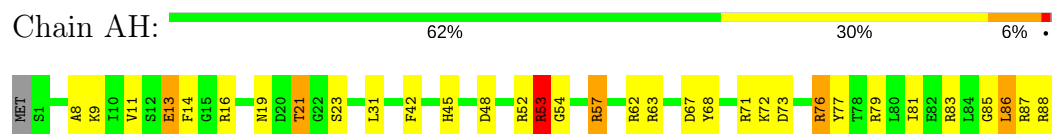
- Molecule 7: 30S ribosomal protein S13



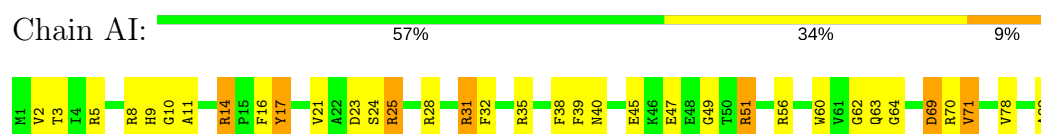
- Molecule 8: 30S ribosomal protein S14



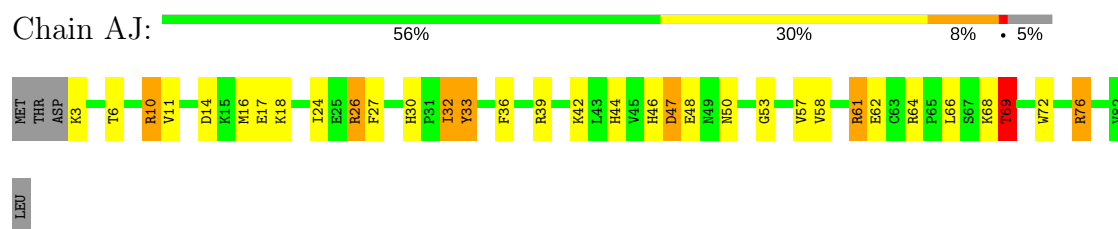
- Molecule 9: 30S ribosomal protein S15



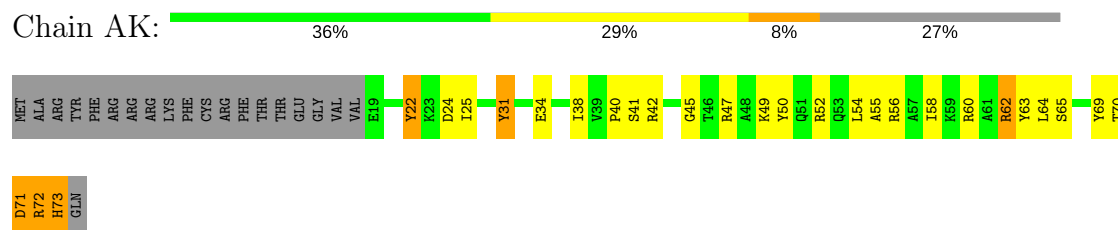
- Molecule 10: 30S ribosomal protein S16



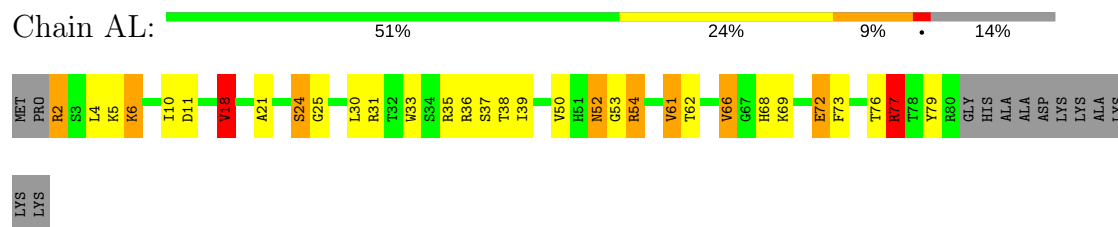
- Molecule 11: 30S ribosomal protein S17



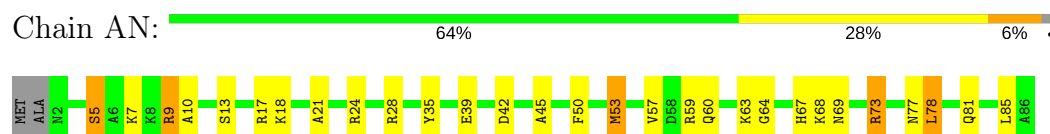
- Molecule 12: 30S ribosomal protein S18



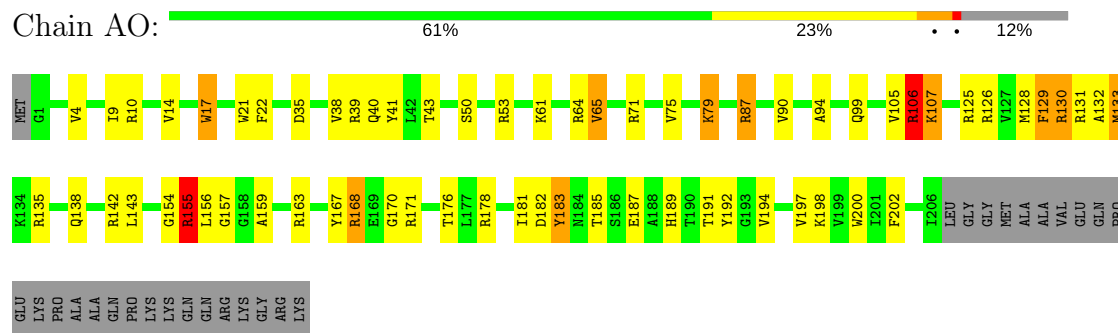
- Molecule 13: 30S ribosomal protein S19



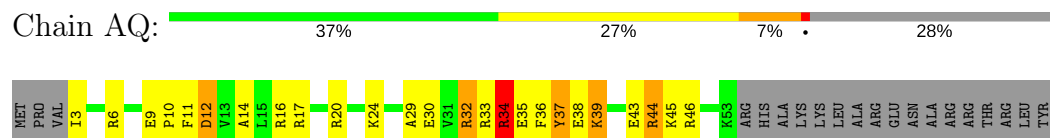
- Molecule 14: 30S ribosomal protein S20



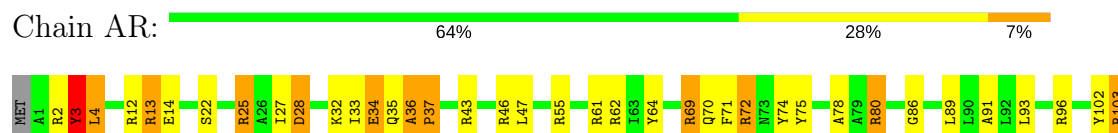
- Molecule 15: 30S ribosomal protein S3

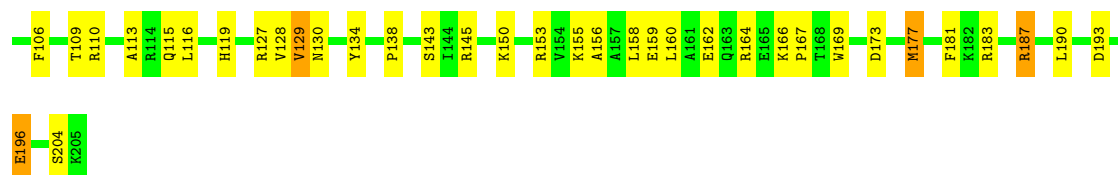


- Molecule 16: 30S ribosomal protein S21



- Molecule 17: 30S ribosomal protein S4





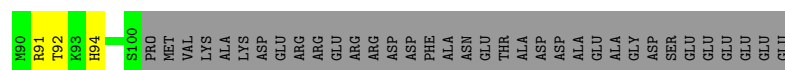
- Molecule 18: 30S ribosomal protein S5

Chain AS: 62% 25% 8% 6%



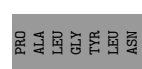
- Molecule 19: 30S ribosomal protein S6

Chain AT: 42% 24% 7% 26%



- Molecule 20: 30S ribosomal protein S7

Chain AU: 48% 29% 6% 16%



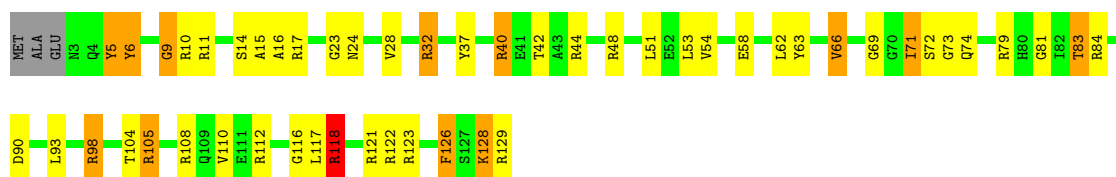
- Molecule 21: 30S ribosomal protein S8

Chain AV: 62% 31% 5% 2%



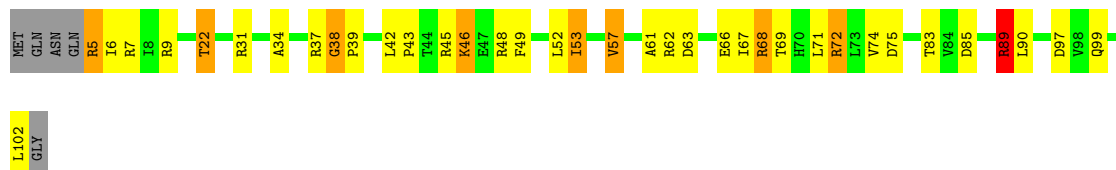
- Molecule 22: 30S ribosomal protein S9

Chain AW: 58% 29% 9% 4%



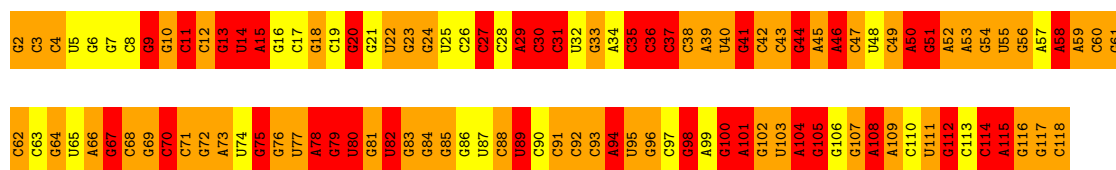
- Molecule 23: 30S ribosomal protein S10

Chain AX: 59% 27% 8% • 5%




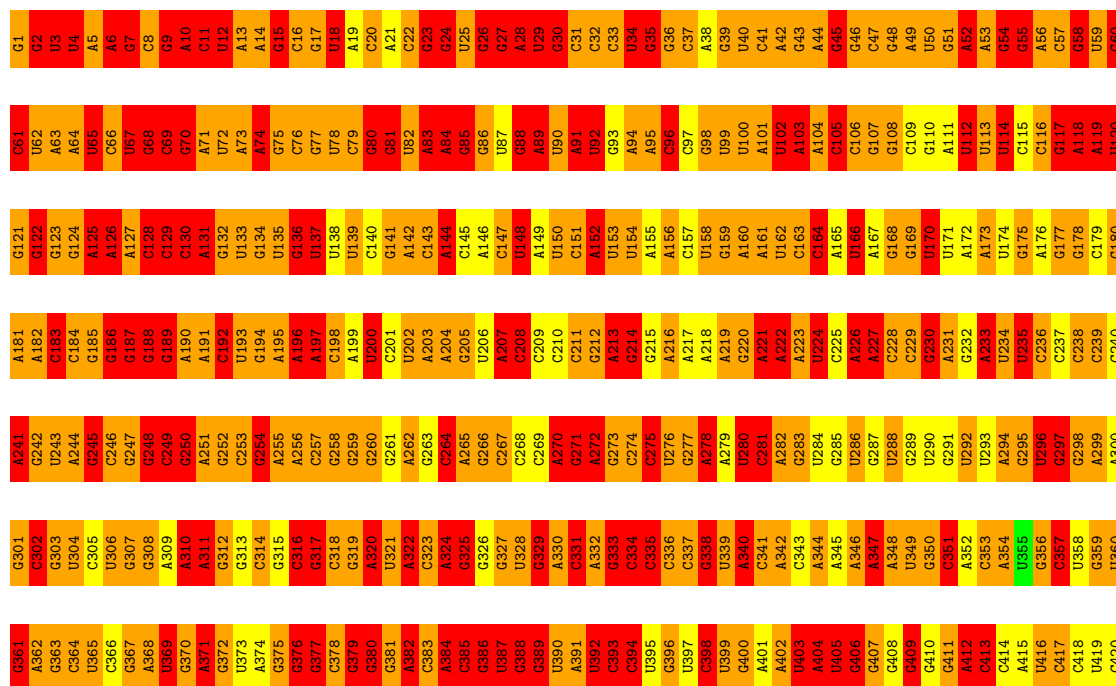
- Molecule 24: 5S rRNA

Chain BA:  22% 46% 32%



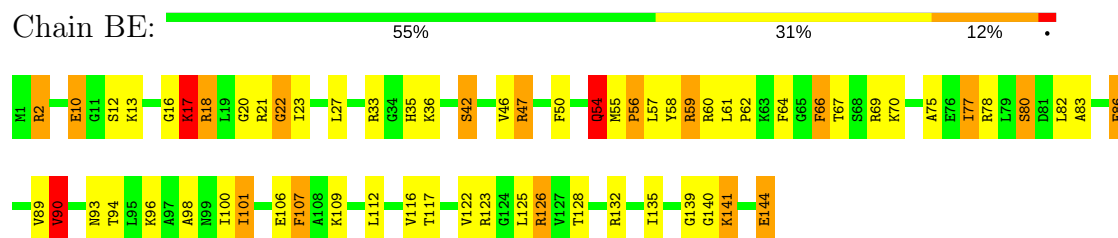
- Molecule 25: 23S rRNA

Chain BB: 

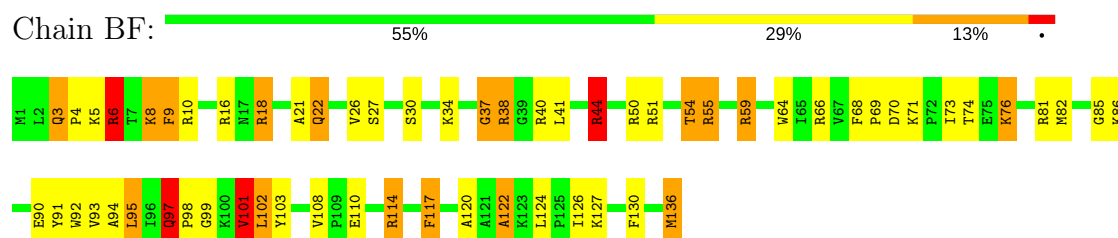


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A1322	A1262	G1202	A1142	U1082	G1022	G962	C902	U842	A782	A722	A662	A602	A542	A482	A422
C1323	U1263	A1203	A1143	U1083	G1023	U963	C903	G843	A783	A723	A663	A603	A543	A483	A423
G1324	A1264	A1204	A1144	U1084	G1024	C964	G904	A844	A784	A724	A664	G604	A544	C484	G424
U1325	C1265	A1205	C1145	A1085	G1025	C965	A905	U845	A785	A725	A665	U605	U545	C485	G425
U1326	A1266	A1206	C1146	U1086	G1026	G966	U906	U846	A786	A726	A666	U606	U546	C486	C426
A1327	U1267	C1207	A1147	G1087	A1027	U967	G907	U847	A787	A727	U667	U607	A547	C487	U427
A1328	A1268	U1208	U1148	A1088	A1028	C968	C908	C848	A788	A728	A668	A608	G548	C488	A428
U1329	C1269	C1209	G1149	U1089	A1029	G969	A909	A849	A789	G729	A669	A609	G549	C489	A429
G1330	A1270	A1210	A1150	U1090	C1030	U970	A910	U850	A790	A730	A670	C610	C550	C490	A430
G1331	C1271	C1211	A1151	G1091	G1031	G971	A911	C851	A791	A731	C871	C611	C551	C491	U431
G1332	A1272	G1212	C1152	C1092	A1032	A972	C912	U852	A792	G732	C872	G612	U552	A492	A432
G1333	U1273	A1213	C1153	U1093	U1033	A973	C913	C853	A793	G733	C873	A613	C653	C493	C433
A1334	A1274	A1214	G1154	U1094	G1034	G974	G914	C854	A794	A734	G874	A614	U554	C494	U434
C1335	G1275	G1215	A1155	A1095	U1035	A975	C915	G855	A795	A735	A675	U615	G555	G495	U435
A1336	A1276	A1216	A1156	A1096	G1036	G976	G916	G856	A796	G736	A676	A616	A556	C496	C436
G1337	U1277	U1217	G1157	U1097	G1037	G977	A917	C857	A797	G737	C877	G617	C557	A497	U437
C1338	C1278	G1218	C1158	A1098	G1038	G978	A918	G858	A798	G738	C878	G618	U558	C498	G438
G1339	A1279	U1219	U1159	G1099	A1039	A979	U919	G859	A799	A739	C879	G619	G559	U499	A439
U1340	G1280	G1220	G1160	C1100	A1040	A980	A920	U860	A800	A740	C880	G620	C560	G500	C440
A1341	C1281	C1221	C1161	U1101	G1041	A981	C921	A861	A801	G741	C881	A621	A561	A501	U441
U1342	U1282	U1222	G1162	C1102	G1042	C982	C922	A862	A802	A742	G882	G622	U562	A502	G442
G1343	G1283	G1223	G1163	A1103	C1043	A983	G923	A863	U803	A743	U683	C623	A563	A503	A443
U1344	A1284	U1224	C1164	C1104	A1044	A984	G924	G864	A804	A744	G884	G624	C564	A504	C444
A1345	A1285	G1225	A1165	U1105	C1045	C985	A925	G865	G805	G745	A685	G625	C565	C445	C445
G1346	A1286	A1226	G1166	G1106	A1046	C986	G926	A866	C806	U746	U686	A626	U566	G506	G446
A1347	U1287	G1227	C1167	U1107	G1047	C987	A927	U867	A807	A747	C887	A627	U567	A507	U447
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C1350	C1290	A1230	C1170	G1110	A1050	A990	G930	U870	U810	A750	G890	G630	C570	C510	U450
G1351	U1291	U1231	G1171	U1111	C1051	C991	U931	U871	U811	A751	C691	A631	U571	U511	U451
U1352	G1292	G1232	C1172	G1112	C1052	C992	U932	U872	C812	A752	C692	A632	A572	G512	G452
A1353	C1293	C1233	U1173	U1113	G1053	G993	A933	C873	A813	A753	A693	A633	U573	A513	A453
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A1367	A1307	A1247	U1187	C1127	A1067	C1007	A947	U887	U827	U767	G707	G647	C587	C527	G467
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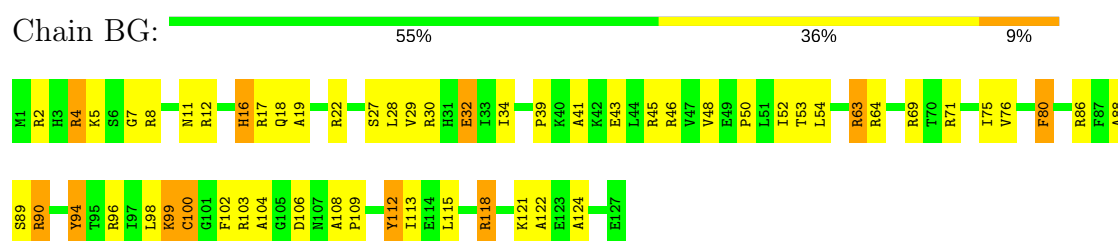
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G2282	C2222	G2162	A2042	U1982	G1922	G1862	A1802	U1742	G1682	G1622	U1562	A1502	U1442	G1382
C2283	G2223	A2163	C2043	G1983	U1923	G1863	A1803	G1743	U1683	G1623	U1563	A1503	U1443	A1383
A2284	G2224	C2164	C2044	G1984	U1924	U1864	C1804	A1744	U1684	U1624	C1564	A1504	G1444	A1384
C2285	A2225	G2165	C2045	G1985	G1925	U1865	A1805	A1745	C1685	C1625	C1565	U1505	G1445	A1385
G2286	G2046	U2106	G2047	C1986	U1926	A1866	C1806	A1746	C1686	A1626	U1566	U1506	C1446	C1386
A2287	G2047	G2107	C2047	U1987	A1927	G1867	A1807	U1747	G1687	G1627	G1567	C1507	G1447	A1387
G2288	G2048	A2108	G2048	G1988	A1928	C1868	A1808	C1748	U1688	G1628	G1568	A1508	G1448	G1388
G2289	U2229	C2169	G2049	U1989	G1929	G1869	A1809	A1749	A1689	U1629	A1569	A1509	G1449	G1389
G2290	G2230	G2110	C2050	C1990	G1930	A1870	A1810	U1750	A1690	A1630	U1570	G1510	G1450	U1390
A2291	U2231	A2171	A2051	U1991	G1931	A1871	A1811	U1751	C1691	A1571	G1511	G1511	C1451	U1391
G2292	C2232	U2172	A2052	G1992	A1932	A1872	A1812	G1752	U1692	A1572	C1512	G1512	G1452	A1392
C2293	G2233	G2113	G2053	U1993	G1933	G1873	G1813	G1753	U1693	G1633	U1513	G1513	A1453	A1393
G2294	G2234	A2114	A2054	C1994	C1934	C1874	G1814	A1754	C1694	A1634	C1574	G1514	C1454	U1394
C2295	G2235	G2115	C2055	U1995	G1935	A1875	A1815	A1755	G1695	A1635	U1575	A1515	G1455	A1395
U2296	U2236	A2176	G2056	C1996	A1936	A1876	C1816	G1756	G1696	U1636	U1576	G1516	G1456	U1396
A2297	G2237	C2177	G2057	U1997	A1937	A1877	A1817	A1757	G1697	U1637	U1577	G1517	U1457	U1397
G2298	G2238	U2118	A2058	A1998	A1938	G1878	U1818	U1758	A1698	C1638	U1578	C1518	U1458	C1398
U2299	G2239	C2179	A2059	G1999	U1939	C1879	A1819	A1759	G1699	C1639	A1579	G1519	G1459	C1399
G2300	U2240	U2180	A2060	C2000	U1940	U1880	A1820	C1760	A1700	A1640	A1580	U1520	U1460	U1400
C2301	A2241	G2121	G2061	C2001	G1941	C1881	A1821	C1761	A1701	A1641	A1581	U1521	G1461	G1401
U2302	G2242	U2182	A2062	G2002	C1942	U1882	C1822	A1762	G1702	G1642	C1582	A1522	C1462	U1402
G2303	U2243	A2183	C2063	A2003	U1943	U1883	G1823	G1763	C1703	G1643	A1583	U1523	C1463	A1403
U2304	U2244	A2184	C2064	G2004	U1944	G1884	G1824	C1764	C1704	C1644	U1584	G1524	G1464	C1404
G2305	U2245	U2185	C2065	A2005	G1945	A1885	U1825	U1765	A1705	G1645	C1585	A1525	G1465	U1405
C2306	G2246	G2186	C2066	C2006	U1946	U1886	G1826	G1766	C1706	C1646	A1586	C1526	U1466	U1406
G2307	A2247	U2187	G2067	U2007	C1947	C1887	G1827	G1767	U1707	U1647	G1587	G1527	U1467	G1407
U2308	C2248	C2188	U2068	C2008	G1948	G1888	G1828	C1768	C1708	A1648	A1528	U1528	U1468	G1408
A2309	U2249	U2189	C2069	A2009	G1949	A1889	A1829	U1769	U1709	G1649	U1589	G1529	A1469	U1409
C2310	G2250	G2190	A2070	G2010	U1950	A1890	G1830	G1770	G1710	A1650	A1590	G1530	A1470	G1410
A2311	G2251	A2191	A2071	U2011	U1951	G1891	G1831	C1771	U1711	G1651	A1591	C1531	G1471	U1411
U2312	G2252	U2192	C2072	G2012	A1952	C1892	C1832	A1772	U1712	A1652	C1592	A1532	G1472	U1412
C2313	G2253	G2193	C2073	A2013	A1953	C1893	C1833	A1773	U1713	G1653	A1593	C1533	G1473	U1413
A2314	C2254	U2194	U2074	A2014	G1954	C1894	A1834	C1774	U1714	A1654	U1594	U1534	U1474	C1414
G2315	G2255	A2135	U2075	A2015	U1955	C1895	G1835	U1775	G1715	A1655	C1595	A1535	G1475	U1415
C2316	G2256	G2136	U2076	U2016	U1956	G1896	C1836	G1776	U1716	C1656	A1596	C1536	U1476	G1416
U2317	U2257	U2197	A2077	U2017	C1957	G1897	G1837	U1777	A1717	U1657	A1597	G1537	A1477	C1417
G2318	C2258	G2198	C2078	G2018	C1958	U1898	C1838	U1778	G1718	C1658	A1598	G1538	G1478	G1418
G2319	U2259	U2139	U2079	A2019	G1959	A1899	G1839	U1779	G1719	G1659	U1599	U1539	G1479	A1419
U2320	C2260	G2140	A2080	A2020	A1960	G1900	G1840	A1780	U1720	G1660	C1600	G1540	G1480	A1420
A2321	C2261	G2201	U2081	C2021	C1961	A1901	U1841	U1781	G1721	G1661	G1601	C1541	U1481	G1421
U2322	A2262	U2202	A2082	U2022	C1962	C1902	G1842	U1782	U1722	U1662	U1542	U1542	G1482	G1422
G2323	C2263	G2203	G2083	C2023	U1963	G1903	C1843	A1783	G1723	G1663	A1603	G1543	G1483	G1423
U2324	C2264	G2204	C2084	G2024	G1964	G1904	C1844	A1784	G1724	A1664	C1604	A1544	U1484	G1424
G2325	U2265	C2145	U2085	C2025	C1965	C1905	G1845	A1785	U1725	A1665	C1605	A1545	U1485	G1425
A2326	A2266	C2146	U2086	U2026	A1966	G1906	G1846	A1786	G1726	G1666	C1606	G1546	U1486	G1426
U2327	A2267	A2147	G2087	G2027	C1967	G1907	A1847	A1787	G1727	G1667	C1607	C1547	U1487	A1427
A2328	A2268	G2148	A2088	U2028	G1968	C1908	A1848	C1788	U1728	A1668	A1608	A1548	C1488	C1428
G2329	G2269	G2209	C2089	G2029	A1969	C1909	G1849	A1789	U1729	A1669	A1609	A1549	C1489	G1429
U2330	A2270	U2210	A2090	A2030	A1970	G1910	G1850	C1790	U1730	C1670	A1610	C1550	A1490	G1430
G2331	G2271	A2211	C2091	A2031	U1971	U1911	U1851	A1791	G1731	U1671	C1611	A1551	G1491	A1431
C2332	U2272	G2152	G2092	G2032	G1972	A1912	U1852	G1792	C1732	A1672	A1552	A1552	G1492	G1432
A2333	A2273	C2153	G2093	A2033	G1973	A1913	A1853	C1793	G1733	G1673	C1613	A1553	C1493	A1433
U2334	A2274	A2154	A2094	U2034	C1974	A1914	A1854	A1794	G1734	G1674	A1614	U1554	A1494	A1434
G2335	G2275	G2155	A2095	G2035	G1975	U1915	U1855	A1795	A1735	C1675	G1615	G1555	A1495	G1435
A2336	G2276	G2156	C2096	C2036	U1976	A1916	U1856	U1796	U1736	A1676	A1616	C1556	A1496	G1436
G2337	G2277	G2157	A2097	A2037	A1977	U1917	G1857	G1797	G1737	A1677	C1617	C1557	U1497	C1437
C2338	A2278	A2158	U2098	G2038	A1978	A1918	A1858	U1798	A1738	A1678	A1618	C1558	C1498	U1438
U2339	G2279	G2159	U2099	U2039	A1979	A1919	U1859	G1799	A1739	A1679	G1619	U1559	C1499	A1439
A2340	G2280	G2160	G2100	G2040	G1980	C1920	G1860	C1800	G1740	U1680	G1620	G1560	G1500	U1440



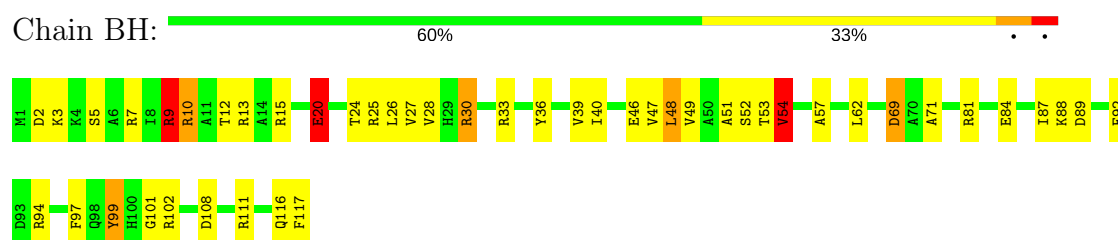
• Molecule 29: 50S ribosomal protein L16



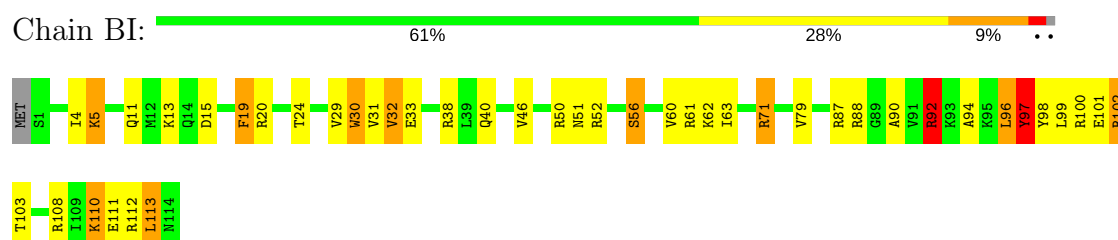
• Molecule 30: 50S ribosomal protein L17



• Molecule 31: 50S ribosomal protein L18

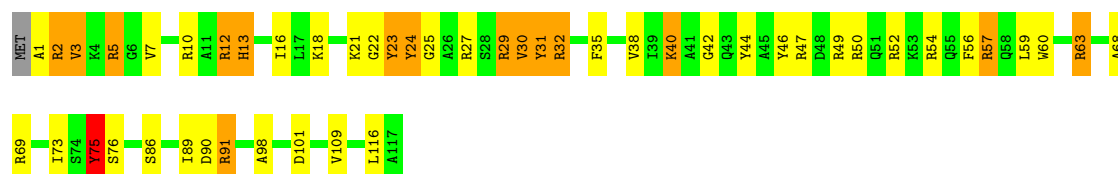


• Molecule 32: 50S ribosomal protein L19



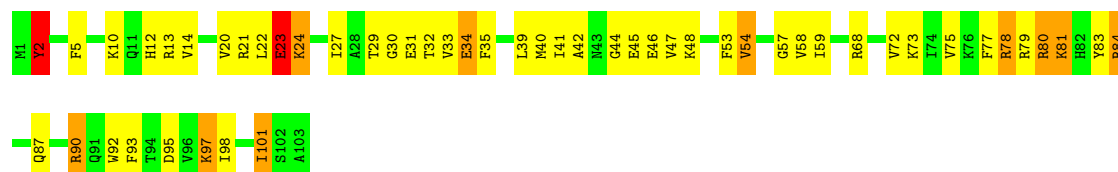
• Molecule 33: 50S ribosomal protein L20





• Molecule 34: 50S ribosomal protein L21

Chain BK: 50% 39% 10%



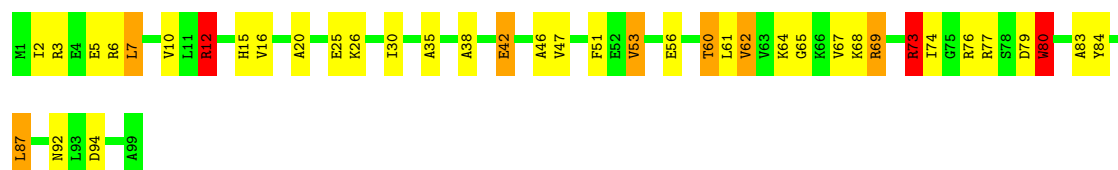
• Molecule 35: 50S ribosomal protein L22

Chain BL: 59% 30% 10%



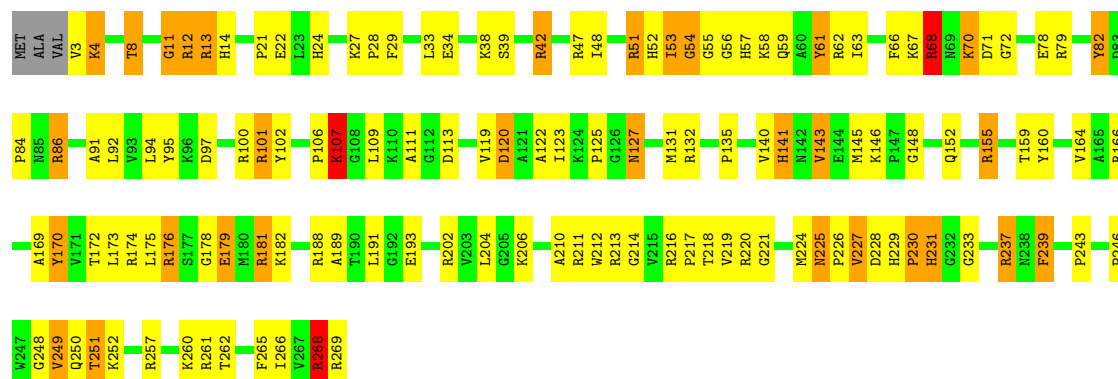
• Molecule 36: 50S ribosomal protein L23

Chain BM: 60% 30% 7%

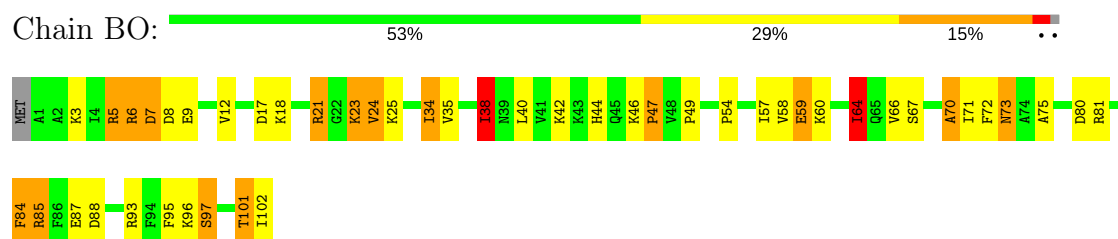


• Molecule 37: 50S ribosomal protein L2

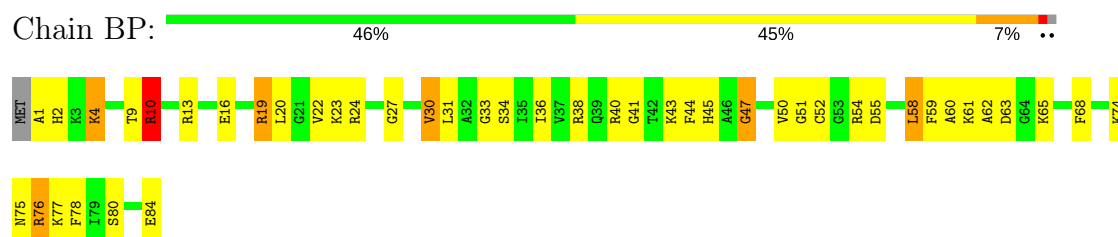
Chain BN: 50% 36% 11%



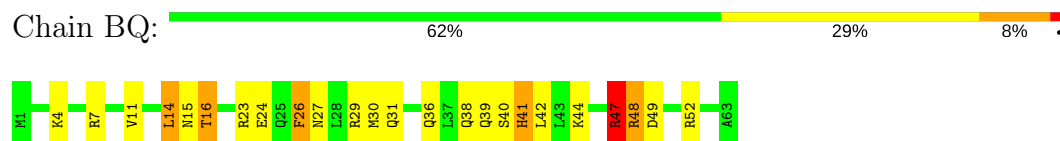
- Molecule 38: 50S ribosomal protein L24



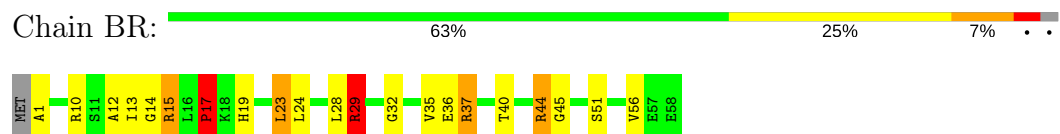
- Molecule 39: 50S ribosomal protein L27



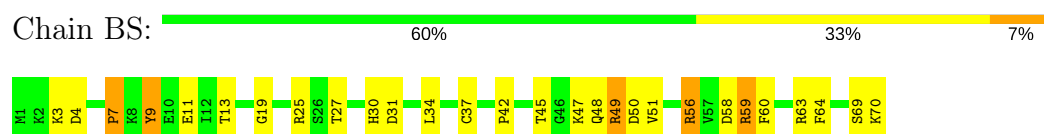
- Molecule 40: 50S ribosomal protein L29



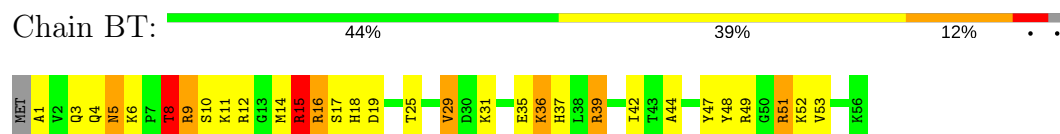
- Molecule 41: 50S ribosomal protein L30



- Molecule 42: 50S ribosomal protein L31



- Molecule 43: 50S ribosomal protein L32



- Molecule 44: 50S ribosomal protein L33





- Molecule 45: 50S ribosomal protein L34



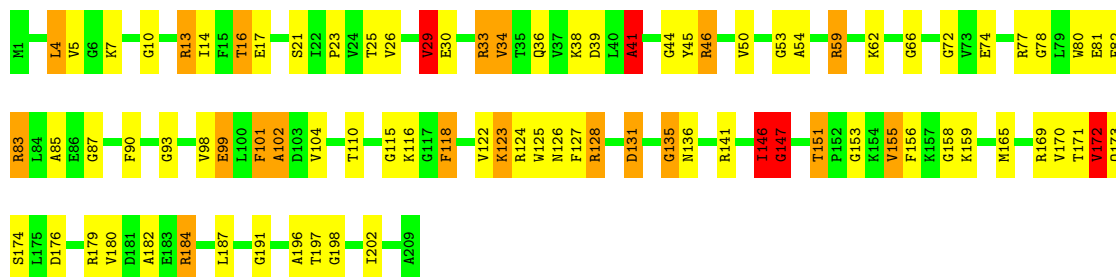
- Molecule 46: 50S ribosomal protein L35



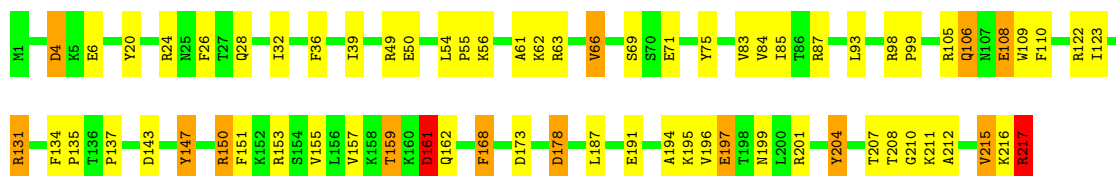
- Molecule 47: 50S ribosomal protein L36



- Molecule 48: 50S ribosomal protein L3

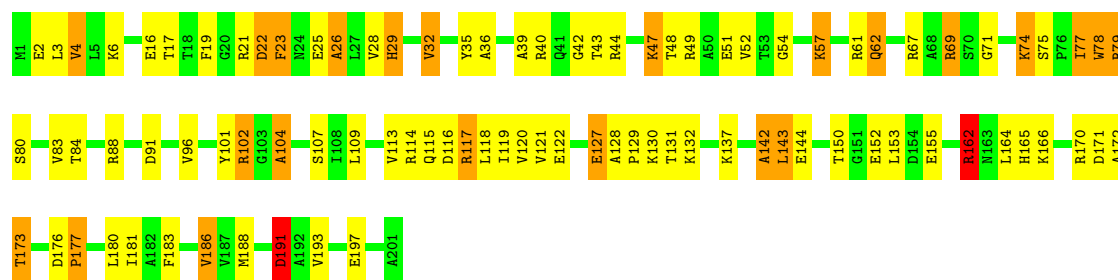


- Molecule 49: 50S ribosomal protein L1P



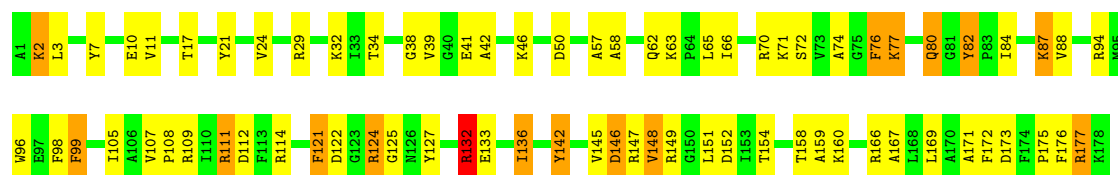
- Molecule 50: 50S ribosomal protein L4





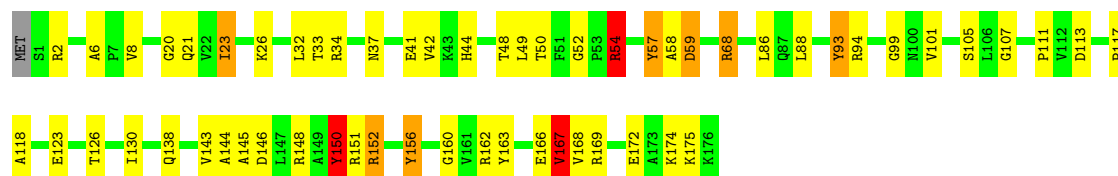
- Molecule 51: 50S ribosomal protein L5

Chain B2: 58% 33% 8%



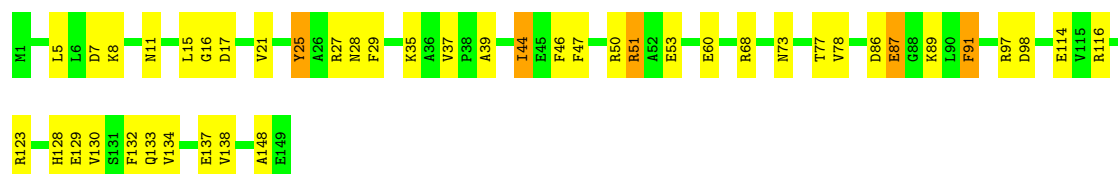
- Molecule 52: 50S ribosomal protein L6

Chain B3: 67% 27%



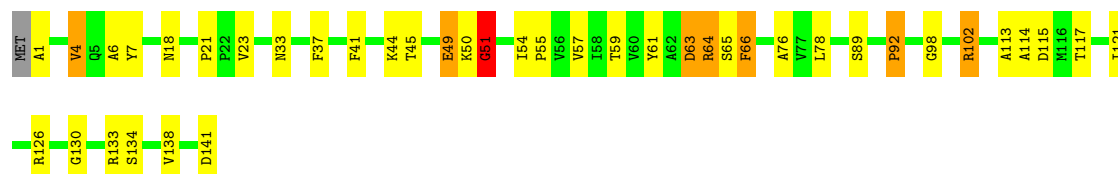
- Molecule 53: 50S ribosomal protein L9

Chain B4: 70% 26%

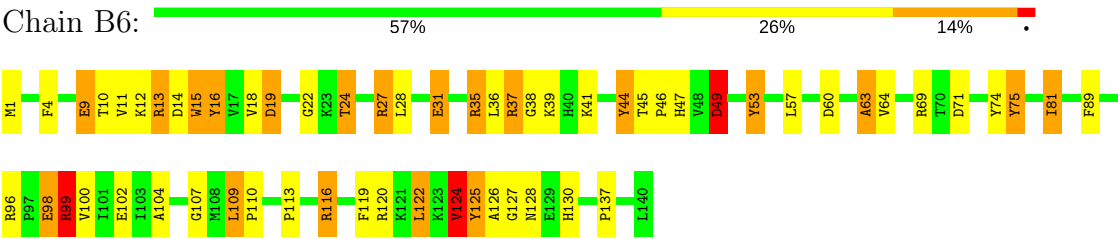


- Molecule 54: 50S ribosomal protein L11

Chain B5: 70% 23% 5%



- Molecule 55: 50S ribosomal protein L13



4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	Not provided	Depositor
Voltage (kV)	Not provided	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	AA	3.40	236/1789 (13.2%)	4.38	561/2788 (20.1%)
1	AE	3.39	235/1814 (13.0%)	4.16	549/2827 (19.4%)
1	AP	4.04	200/1789 (11.2%)	4.62	517/2788 (18.5%)
10	AI	1.65	6/658 (0.9%)	2.62	33/884 (3.7%)
11	AJ	1.59	5/657 (0.8%)	2.37	33/881 (3.7%)
12	AK	1.77	5/462 (1.1%)	2.48	33/621 (5.3%)
13	AL	1.63	3/652 (0.5%)	2.09	19/877 (2.2%)
14	AN	1.53	3/670 (0.4%)	2.09	21/888 (2.4%)
15	AO	1.66	19/1651 (1.2%)	2.22	58/2225 (2.6%)
16	AQ	1.74	6/430 (1.4%)	2.77	30/570 (5.3%)
17	AR	1.65	17/1664 (1.0%)	2.37	81/2227 (3.6%)
18	AS	1.67	10/1118 (0.9%)	2.31	38/1504 (2.5%)
19	AT	1.63	5/835 (0.6%)	2.30	36/1128 (3.2%)
2	AM	2.83	38/436 (8.7%)	3.84	119/672 (17.7%)
20	AU	1.68	10/1187 (0.8%)	2.46	56/1591 (3.5%)
21	AV	1.64	7/988 (0.7%)	2.27	43/1326 (3.2%)
22	AW	1.78	14/1033 (1.4%)	2.59	48/1375 (3.5%)
23	AX	1.57	4/796 (0.5%)	2.46	38/1077 (3.5%)
24	BA	3.32	357/2800 (12.8%)	4.36	854/4367 (19.6%)
25	BB	15.87	8884/69795 (12.7%)	4.40	21260/108884 (19.5%)
26	BC	1.63	10/765 (1.3%)	2.11	24/1025 (2.3%)
27	BD	1.69	7/939 (0.7%)	2.47	44/1258 (3.5%)
28	BE	1.68	9/1061 (0.8%)	2.33	37/1413 (2.6%)
29	BF	1.62	6/1092 (0.5%)	2.24	37/1460 (2.5%)
3	A1	3.49	4705/36759 (12.8%)	4.27	10939/57346 (19.1%)
30	BG	1.70	10/1020 (1.0%)	2.53	58/1364 (4.3%)
31	BH	1.69	11/909 (1.2%)	2.40	43/1219 (3.5%)
32	BI	1.71	8/928 (0.9%)	2.37	36/1242 (2.9%)
33	BJ	1.71	15/959 (1.6%)	2.50	62/1278 (4.9%)
34	BK	1.62	5/828 (0.6%)	2.36	35/1107 (3.2%)
35	BL	1.52	4/863 (0.5%)	2.38	33/1156 (2.9%)
36	BM	1.54	4/784 (0.5%)	2.16	28/1048 (2.7%)
37	BN	1.74	26/2092 (1.2%)	2.34	97/2813 (3.4%)
38	BO	1.59	2/787 (0.3%)	2.39	37/1051 (3.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	BP	1.71	7/641 (1.1%)	2.42	28/848 (3.3%)
4	AB	1.61	8/1735 (0.5%)	2.18	57/2338 (2.4%)
40	BQ	1.67	5/509 (1.0%)	2.16	15/677 (2.2%)
41	BR	1.60	5/452 (1.1%)	2.10	15/605 (2.5%)
42	BS	1.65	8/558 (1.4%)	2.43	20/745 (2.7%)
43	BT	1.77	7/449 (1.6%)	2.34	22/599 (3.7%)
44	BU	1.61	3/447 (0.7%)	2.19	18/594 (3.0%)
45	BV	1.74	3/379 (0.8%)	2.64	22/498 (4.4%)
46	BW	1.55	3/512 (0.6%)	2.18	20/676 (3.0%)
47	BX	1.56	2/302 (0.7%)	2.90	18/397 (4.5%)
48	BY	1.69	11/1585 (0.7%)	2.23	58/2134 (2.7%)
49	BZ	1.57	8/1711 (0.5%)	2.13	57/2305 (2.5%)
5	AC	1.67	7/892 (0.8%)	2.45	47/1205 (3.9%)
50	B1	1.66	15/1570 (1.0%)	2.30	70/2113 (3.3%)
51	B2	1.67	11/1443 (0.8%)	2.29	62/1937 (3.2%)
52	B3	1.60	9/1342 (0.7%)	2.13	50/1816 (2.8%)
53	B4	1.61	11/1121 (1.0%)	2.08	27/1515 (1.8%)
54	B5	1.51	4/1045 (0.4%)	2.16	35/1410 (2.5%)
55	B6	1.69	9/1135 (0.8%)	2.39	60/1529 (3.9%)
6	AD	1.69	12/968 (1.2%)	2.37	39/1300 (3.0%)
7	AF	1.58	5/892 (0.6%)	2.47	46/1193 (3.9%)
8	AG	1.66	9/785 (1.1%)	2.56	33/1046 (3.2%)
9	AH	1.80	12/723 (1.7%)	2.44	37/966 (3.8%)
All	All	10.61	15060/162206 (9.3%)	3.93	36793/242726 (15.2%)

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
1	AA	0	52
1	AE	0	46
1	AP	2	51
10	AI	0	9
11	AJ	0	4
12	AK	0	3
13	AL	0	8
14	AN	1	0
15	AO	0	9
16	AQ	0	5
17	AR	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
18	AS	0	2
19	AT	0	9
2	AM	0	12
20	AU	0	8
21	AV	0	4
22	AW	0	9
23	AX	0	2
24	BA	0	81
25	BB	3	1853
26	BC	0	2
27	BD	0	4
28	BE	0	5
29	BF	0	9
3	A1	4	995
30	BG	0	5
31	BH	0	7
32	BI	0	6
33	BJ	0	3
34	BK	0	11
35	BL	0	4
36	BM	0	3
37	BN	0	12
38	BO	0	4
39	BP	0	7
4	AB	0	8
41	BR	0	4
42	BS	0	7
43	BT	0	3
44	BU	0	3
45	BV	0	4
46	BW	0	7
47	BX	0	1
48	BY	0	8
49	BZ	0	9
5	AC	0	4
50	B1	0	9
51	B2	0	7
52	B3	0	7
53	B4	0	3
54	B5	0	3
55	B6	0	12
6	AD	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	AF	0	8
8	AG	0	3
9	AH	0	2
All	All	10	3370

The worst 5 of 15060 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BB	995	C	C4-C5	2385.00	20.50	1.43
25	BB	995	C	C2-N3	2363.63	20.26	1.35
25	BB	995	C	C4-N4	2355.33	22.53	1.33
3	A1	1429	A	P-O5'	178.05	3.37	1.59
3	A1	1340	A	C3'-O3'	103.07	2.86	1.42

The worst 5 of 36793 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	BB	995	C	C5-C4-N4	-167.42	3.01	120.20
25	BB	995	C	C4-C5-C6	-165.92	34.44	117.40
25	BB	995	C	N1-C2-N3	-110.87	41.59	119.20
1	AP	74	C	P-O3'-C3'	-90.94	10.58	119.70
25	BB	995	C	N3-C4-C5	-73.62	92.45	121.90

5 of 10 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AP	31	A	C2',C1'
3	A1	13	U	C2',C1'
3	A1	1198	G	C4'
3	A1	1483	A	C2'
14	AN	13	SER	CA

5 of 3370 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	G	Sidechain
1	AA	3	G	Sidechain
1	AA	4	G	Sidechain
1	AA	5	A	Sidechain
1	AA	6	U	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1600	0	754	13	0
1	AE	1622	0	773	5	0
1	AP	1600	0	756	42	0
2	AM	397	0	202	4	0
3	A1	32828	0	15398	147	0
4	AB	1704	0	1732	7	0
5	AC	876	0	887	5	0
6	AD	954	0	1019	5	0
7	AF	883	0	944	5	0
8	AG	773	0	824	4	0
9	AH	715	0	742	3	0
10	AI	648	0	666	0	0
11	AJ	648	0	691	2	0
12	AK	455	0	478	1	0
13	AL	637	0	665	5	0
14	AN	664	0	714	5	0
15	AO	1624	0	1699	2	0
16	AQ	425	0	449	1	0
17	AR	1642	0	1710	6	0
18	AS	1105	0	1148	3	0
19	AT	817	0	808	2	0
20	AU	1174	0	1230	0	0
21	AV	978	0	1034	3	0
22	AW	1021	0	1070	0	0
23	AX	786	0	828	7	0
24	BA	2504	0	1160	13	0
25	BB	62317	0	29301	262	0
26	BC	752	0	780	2	0
27	BD	930	0	1000	1	0
28	BE	1052	0	1129	6	0
29	BF	1073	0	1157	8	0
30	BG	1007	0	1045	5	0
31	BH	899	0	935	2	0
32	BI	916	0	965	6	0
33	BJ	946	0	1022	3	0
34	BK	815	0	839	5	0
35	BL	856	0	922	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	BM	777	0	840	5	0
37	BN	2053	0	2122	10	0
38	BO	779	0	834	8	0
39	BP	633	0	656	0	0
40	BQ	508	0	543	5	0
41	BR	448	0	491	0	0
42	BS	548	0	552	0	0
43	BT	443	0	461	1	0
44	BU	440	0	485	1	0
45	BV	376	0	418	5	0
46	BW	503	0	574	3	0
47	BX	301	0	343	0	0
48	BY	1564	0	1616	7	0
49	BZ	1687	0	1814	4	0
50	B1	1551	0	1619	6	0
51	B2	1419	0	1460	6	0
52	B3	1322	0	1374	4	0
53	B4	1110	0	1148	1	0
54	B5	1031	0	1088	2	0
55	B6	1112	0	1147	1	0
All	All	149248	0	97061	544	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 544 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)
25:BB:1687:G:C2'	25:BB:1687:G:C3'	1.94	1.42
25:BB:1687:G:C2'	25:BB:1687:G:C1'	1.98	1.40
1:AP:31:A:C2'	3:A1:1340:A:H3'	1.50	1.40
25:BB:1687:G:C4'	25:BB:1687:G:C3'	1.99	1.37
1:AP:31:A:C1'	1:AP:31:A:C2'	2.04	1.35

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AB	216/241 (90%)	173 (80%)	35 (16%)	8 (4%)	4	33
5	AC	115/129 (89%)	85 (74%)	26 (23%)	4 (4%)	4	34
6	AD	121/124 (98%)	71 (59%)	35 (29%)	15 (12%)	0	7
7	AF	112/118 (95%)	76 (68%)	27 (24%)	9 (8%)	1	17
8	AG	94/101 (93%)	71 (76%)	18 (19%)	5 (5%)	2	26
9	AH	86/89 (97%)	67 (78%)	14 (16%)	5 (6%)	2	24
10	AI	80/82 (98%)	56 (70%)	15 (19%)	9 (11%)	0	8
11	AJ	78/84 (93%)	51 (65%)	22 (28%)	5 (6%)	1	22
12	AK	53/75 (71%)	40 (76%)	9 (17%)	4 (8%)	1	18
13	AL	77/92 (84%)	57 (74%)	13 (17%)	7 (9%)	1	15
14	AN	83/87 (95%)	68 (82%)	12 (14%)	3 (4%)	4	33
15	AO	204/233 (88%)	157 (77%)	33 (16%)	14 (7%)	1	20
16	AQ	49/71 (69%)	38 (78%)	7 (14%)	4 (8%)	1	16
17	AR	203/206 (98%)	165 (81%)	29 (14%)	9 (4%)	3	29
18	AS	148/159 (93%)	111 (75%)	26 (18%)	11 (7%)	1	18
19	AT	98/135 (73%)	76 (78%)	15 (15%)	7 (7%)	1	19
20	AU	148/179 (83%)	118 (80%)	20 (14%)	10 (7%)	1	20
21	AV	127/130 (98%)	102 (80%)	17 (13%)	8 (6%)	1	22
22	AW	125/130 (96%)	96 (77%)	22 (18%)	7 (6%)	2	25
23	AX	96/103 (93%)	73 (76%)	15 (16%)	8 (8%)	1	16
26	BC	92/94 (98%)	70 (76%)	16 (17%)	6 (6%)	1	22
27	BD	119/123 (97%)	84 (71%)	25 (21%)	10 (8%)	1	15
28	BE	142/144 (99%)	90 (63%)	27 (19%)	25 (18%)	0	3
29	BF	134/136 (98%)	74 (55%)	37 (28%)	23 (17%)	0	4
30	BG	125/127 (98%)	82 (66%)	32 (26%)	11 (9%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	BH	115/117 (98%)	78 (68%)	27 (24%)	10 (9%)	1	15
32	BI	112/115 (97%)	67 (60%)	32 (29%)	13 (12%)	0	8
33	BJ	115/118 (98%)	84 (73%)	19 (16%)	12 (10%)	0	10
34	BK	101/103 (98%)	57 (56%)	32 (32%)	12 (12%)	0	7
35	BL	108/110 (98%)	71 (66%)	18 (17%)	19 (18%)	0	3
36	BM	97/99 (98%)	70 (72%)	19 (20%)	8 (8%)	1	16
37	BN	265/270 (98%)	167 (63%)	49 (18%)	49 (18%)	0	3
38	BO	100/103 (97%)	51 (51%)	31 (31%)	18 (18%)	0	3
39	BP	82/85 (96%)	42 (51%)	26 (32%)	14 (17%)	0	4
40	BQ	61/63 (97%)	44 (72%)	13 (21%)	4 (7%)	1	21
41	BR	56/59 (95%)	39 (70%)	10 (18%)	7 (12%)	0	7
42	BS	68/70 (97%)	47 (69%)	14 (21%)	7 (10%)	0	11
43	BT	54/57 (95%)	37 (68%)	11 (20%)	6 (11%)	0	9
44	BU	52/54 (96%)	35 (67%)	14 (27%)	3 (6%)	2	24
45	BV	44/46 (96%)	33 (75%)	9 (20%)	2 (4%)	3	29
46	BW	62/64 (97%)	31 (50%)	16 (26%)	15 (24%)	0	2
47	BX	36/38 (95%)	23 (64%)	6 (17%)	7 (19%)	0	3
48	BY	207/209 (99%)	120 (58%)	54 (26%)	33 (16%)	0	4
49	BZ	211/213 (99%)	169 (80%)	33 (16%)	9 (4%)	3	29
50	B1	199/201 (99%)	117 (59%)	53 (27%)	29 (15%)	0	5
51	B2	176/178 (99%)	125 (71%)	35 (20%)	16 (9%)	1	15
52	B3	174/177 (98%)	145 (83%)	19 (11%)	10 (6%)	2	24
53	B4	147/149 (99%)	109 (74%)	31 (21%)	7 (5%)	2	28
54	B5	139/142 (98%)	116 (84%)	17 (12%)	6 (4%)	3	29
55	B6	138/140 (99%)	78 (56%)	40 (29%)	20 (14%)	0	5
All	All	5844/6172 (95%)	4106 (70%)	1175 (20%)	563 (10%)	2	13

5 of 563 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AB	21	TYR
4	AB	97	GLY
4	AB	169	HIS

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Mol	Chain	Res	Type
5	AC	118	ASN
6	AD	15	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AB	180/199 (90%)	167 (93%)	13 (7%)	17	49
5	AC	90/99 (91%)	81 (90%)	9 (10%)	9	33
6	AD	103/104 (99%)	91 (88%)	12 (12%)	6	27
7	AF	92/96 (96%)	82 (89%)	10 (11%)	7	30
8	AG	79/84 (94%)	76 (96%)	3 (4%)	38	67
9	AH	76/77 (99%)	71 (93%)	5 (7%)	19	52
10	AI	65/65 (100%)	61 (94%)	4 (6%)	21	54
11	AJ	74/78 (95%)	69 (93%)	5 (7%)	18	51
12	AK	48/66 (73%)	42 (88%)	6 (12%)	5	26
13	AL	70/79 (89%)	62 (89%)	8 (11%)	7	28
14	AN	65/66 (98%)	58 (89%)	7 (11%)	7	31
15	AO	170/190 (90%)	158 (93%)	12 (7%)	17	49
16	AQ	44/61 (72%)	39 (89%)	5 (11%)	7	28
17	AR	172/173 (99%)	156 (91%)	16 (9%)	10	37
18	AS	113/119 (95%)	97 (86%)	16 (14%)	4	22
19	AT	87/116 (75%)	78 (90%)	9 (10%)	8	32
20	AU	123/147 (84%)	109 (89%)	14 (11%)	7	28
21	AV	104/105 (99%)	98 (94%)	6 (6%)	23	56
22	AW	105/107 (98%)	95 (90%)	10 (10%)	10	36
23	AX	86/90 (96%)	81 (94%)	5 (6%)	23	56
26	BC	78/78 (100%)	76 (97%)	2 (3%)	51	75
27	BD	102/104 (98%)	94 (92%)	8 (8%)	15	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	BE	103/103 (100%)	84 (82%)	19 (18%)	2	12
29	BF	109/109 (100%)	94 (86%)	15 (14%)	4	23
30	BG	103/103 (100%)	94 (91%)	9 (9%)	12	40
31	BH	87/87 (100%)	82 (94%)	5 (6%)	24	56
32	BI	99/100 (99%)	95 (96%)	4 (4%)	36	65
33	BJ	89/90 (99%)	79 (89%)	10 (11%)	7	29
34	BK	84/84 (100%)	73 (87%)	11 (13%)	5	24
35	BL	93/93 (100%)	83 (89%)	10 (11%)	7	31
36	BM	83/83 (100%)	71 (86%)	12 (14%)	4	21
37	BN	213/215 (99%)	188 (88%)	25 (12%)	6	27
38	BO	83/84 (99%)	74 (89%)	9 (11%)	7	31
39	BP	62/63 (98%)	53 (86%)	9 (14%)	4	21
40	BQ	55/55 (100%)	45 (82%)	10 (18%)	2	12
41	BR	48/49 (98%)	45 (94%)	3 (6%)	21	53
42	BS	62/62 (100%)	58 (94%)	4 (6%)	20	52
43	BT	47/48 (98%)	34 (72%)	13 (28%)	0	3
44	BU	48/48 (100%)	43 (90%)	5 (10%)	8	32
45	BV	38/38 (100%)	32 (84%)	6 (16%)	3	18
46	BW	51/51 (100%)	41 (80%)	10 (20%)	1	10
47	BX	34/34 (100%)	32 (94%)	2 (6%)	23	55
48	BY	164/164 (100%)	150 (92%)	14 (8%)	12	42
49	BZ	187/187 (100%)	172 (92%)	15 (8%)	14	45
50	B1	165/165 (100%)	143 (87%)	22 (13%)	4	24
51	B2	149/149 (100%)	133 (89%)	16 (11%)	8	31
52	B3	137/138 (99%)	123 (90%)	14 (10%)	8	33
53	B4	114/114 (100%)	104 (91%)	10 (9%)	12	39
54	B5	109/110 (99%)	100 (92%)	9 (8%)	13	43
55	B6	114/114 (100%)	102 (90%)	12 (10%)	8	32
All	All	4856/5043 (96%)	4368 (90%)	488 (10%)	13	33

5 of 488 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	BG	32	GLU
36	BM	42	GLU
52	B3	68	ARG
30	BG	121	LYS
34	BK	23	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
30	BG	16	HIS
30	BG	73	ASN
37	BN	162	GLN
27	BD	90	ASN
28	BE	99	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	74/76 (97%)	21 (28%)	0
1	AE	75/76 (98%)	12 (16%)	0
1	AP	74/76 (97%)	10 (13%)	0
2	AM	19/20 (95%)	10 (52%)	0
24	BA	116/117 (99%)	36 (31%)	0
25	BB	2901/2903 (99%)	1500 (51%)	0
3	A1	1529/1530 (99%)	730 (47%)	0
All	All	4788/4798 (99%)	2319 (48%)	0

5 of 2319 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	C
1	AA	3	G
1	AA	10	G
1	AA	16	U
1	AA	17	U

There are no RNA pucker outliers to report.

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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
25	BB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	1959:G	O3'	1960:A	P	3.49