



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:54 PM BST

PDB ID : 4V65
EMDB ID: : EMD-1055
Title : Structure of the E. coli ribosome in the Pre-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 EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

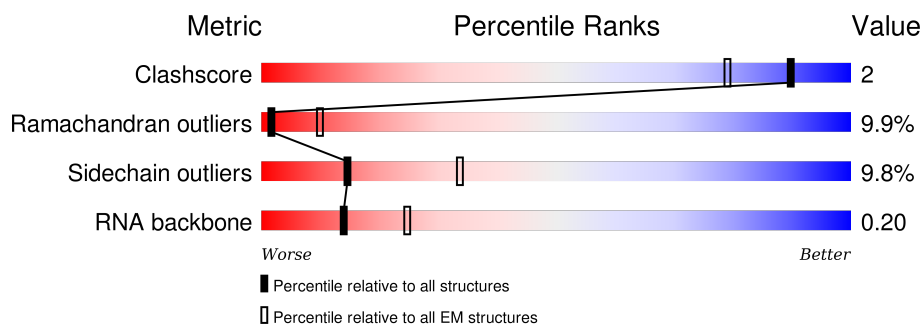
1 Overall quality at a glance

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.














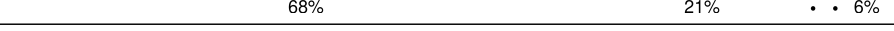





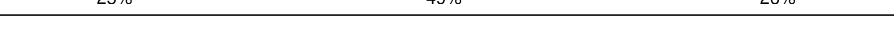

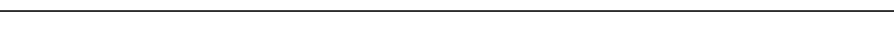

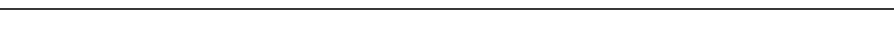
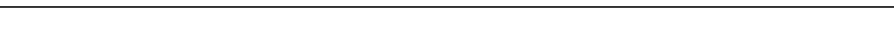


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	11% 51% 37% .
1	AE	76	30% 49% 21%
1	AP	76	18% 46% 34% .
2	AM	20	15% 50% 35%
3	A1	1530	17% 45% 39%
4	AB	241	69% 17% . 10%
5	AC	129	66% 22% . . 9%
6	AD	124	59% 30% 9% . .














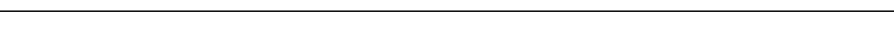


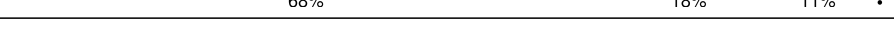
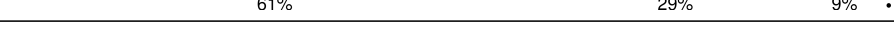






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Mol	Chain	Length	Quality of chain
7	AF	118	
8	AG	101	
9	AH	89	
10	AI	82	
11	AJ	84	
12	AK	75	
13	AL	92	
14	AN	87	
15	AO	233	
16	AQ	71	
17	AR	206	
18	AS	159	
19	AT	135	
20	AU	179	
21	AV	130	
22	AW	130	
23	AX	103	
24	BA	117	
25	BB	2903	
26	BC	94	
27	BD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

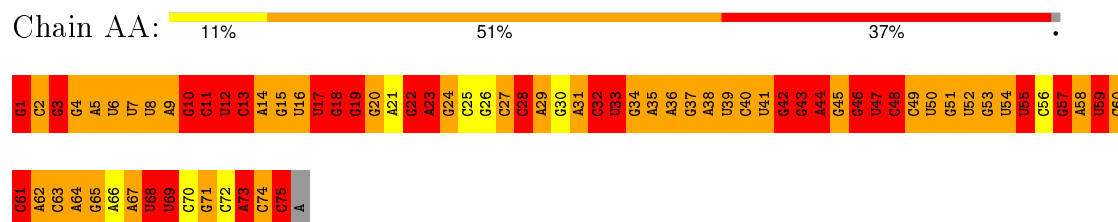
- Molecule 55 is a protein called 50S ribosomal protein L13.

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

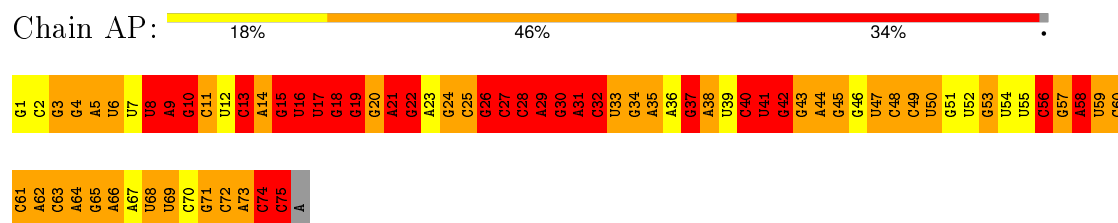
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

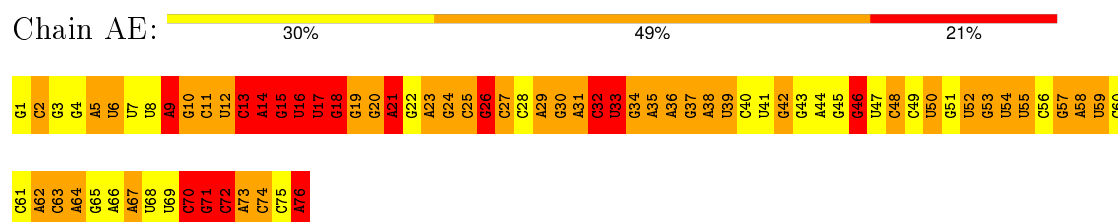
- Molecule 1: A/T, P and E-site tRNAs



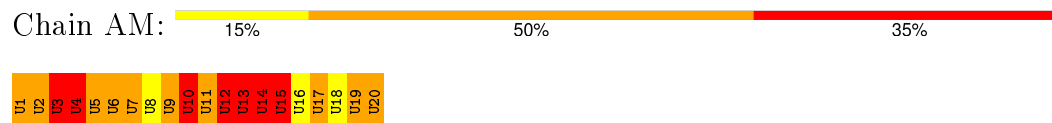
- Molecule 1: A/T, P and E-site tRNAs



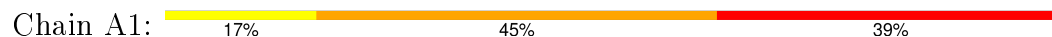
- Molecule 1: A/T, P and E-site tRNAs



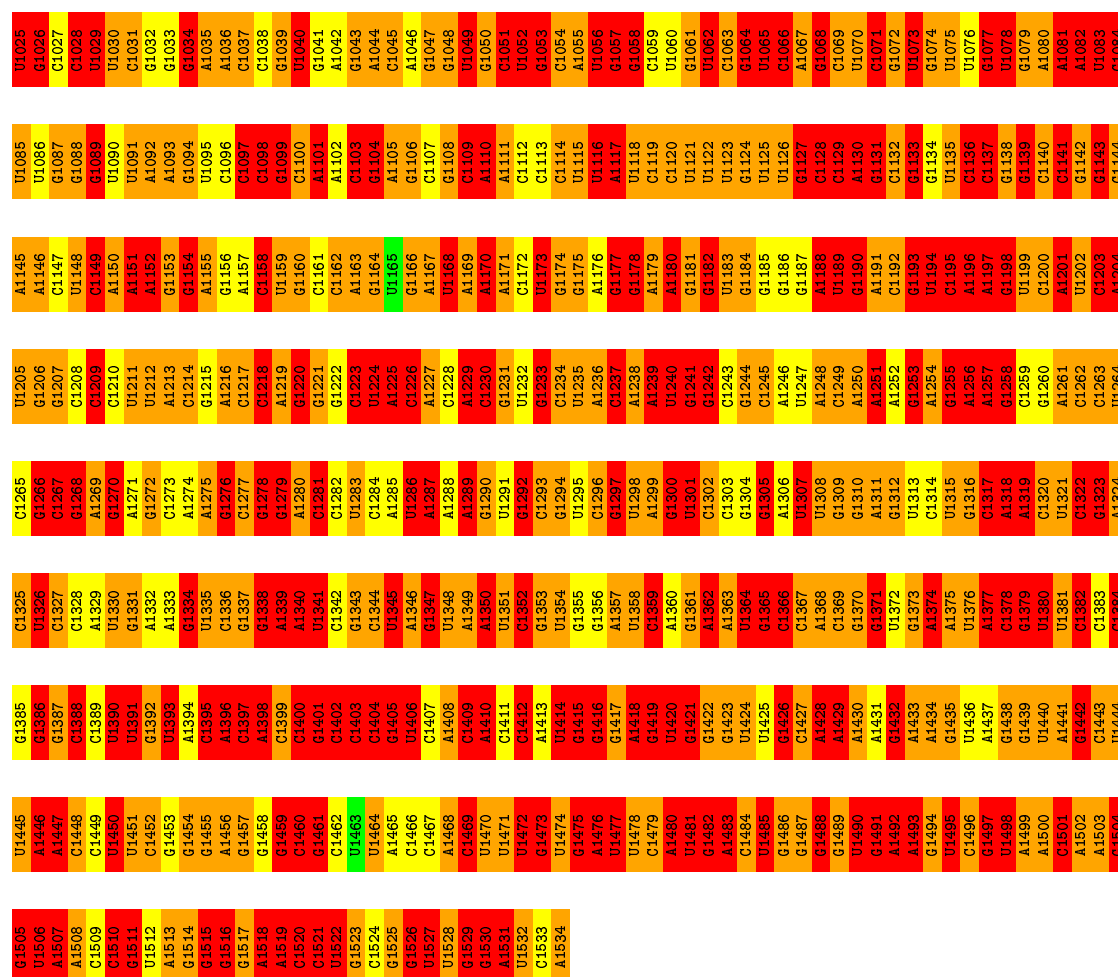
- Molecule 2: mRNA model



- Molecule 3: 16S rRNA

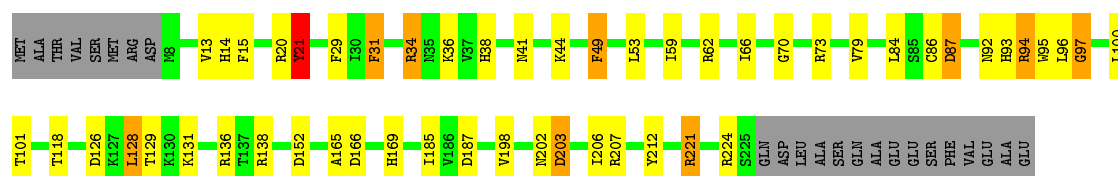


U985	G986	A987	A988	A989	C990	U991	C992	C993	A994	C995	A996	U997	A998	C999	A1000	G1001	G1002	G1003	A1004	A1005	G1006	U1007	U1008	U1009	U1010	C1011	A1012	G1013	A1014	G1015	A1016	U1017	G1018	A1019	G1020	A1021	A1022	U1023	G1024																														
U905	A906	G907	C908	U909	C910	U911	C912	C913	A914	A915	C916	C917	C918	A919	U920	U921	G922	A923	C924	C925	G926	G927	C928	U929	C930	C931	U932	G933	A934	C935	A936	A937	A938	C939	C940	G941	G942	C943	U944	G945	A946	U947	C948	A949	U950	C951	U952	G953	A954	U955	G956	U957	A958	U959	U960	U961	C962	G963	A964										
A845	G786	G787	C788	C789	U790	G791	U792	C793	A794	U795	C796	C797	U798	C799	A800	U801	A802	U803	A804	A805	C806	A807	C808	U809	U810	C811	U812	A813	U814	C815	C816	C817	C818	C819	C820	U821	U822	C823	U824	C825	C826	U827	A828	U829	C830	U831	U832	C833	U834	C835	C836	U837	U838	U839	C840														
G725	C726	G727	A728	A729	G730	G731	C732	G733	A734	C735	C736	U737	C738	U739	U740	G741	C742	A743	U744	C745	G746	A747	C748	U749	C750	U751	G752	A753	C754	U755	A756	C757	U758	C759	U760	G761	U762	C763	U764	C765	A766	U767	A768	U769	C770	G771	U772	U773	G774	G775	A776	U777	U778	C779	U780	A781	U782	C783	A784										
A665	G666	G667	A668	A669	U670	G671	U672	C673	A674	G675	A676	U677	U678	C679	U680	C681	G682	U683	U684	C685	U686	A687	C688	U689	C690	U691	G692	C693	A694	U695	A696	C697	U698	C699	U700	G701	U702	A703	C704	U705	A706	U707	C708	U709	A710	G711	U712	U713	G714	A715	U716	U717	U718	C719	U720	G721	U722	U723	A724										
U605	C545	U485	G425	U385	G305	U245	U185	U125	A65	G66	A66	C67	G68	A69	C70	G71	U72	C73	A74	U75	C76	U77	A78	C79	U80	A81	U82	C83	A84	U85	C86	U87	A88	C89	U90	A91	U92	C93	A94	U95	C96	U97	A98	C99	U100	A101	U102	C103	A104	U105	C106	U107	A108	U109	C110	A111	U112	C113	A114	U115	C116	U117	A118	U119	C120	A121	U122	C123	A124
U5	G6	A7	A8	G9	A10	C11	U12	C13	U14	G15	A16	U17	C18	A19	U20	G21	A22	C23	U24	C25	A26	G27	U28	U29	C30	G31	A32	U33	A34	C35	C36	U37	G38	C39	G40	G41	G42	C43	A44	G45	C46	G47	C48	U49	A50	A51	C52	A53	U54	C55	A56	U57	C58	A59	A60	G61	U62	C63	G64										



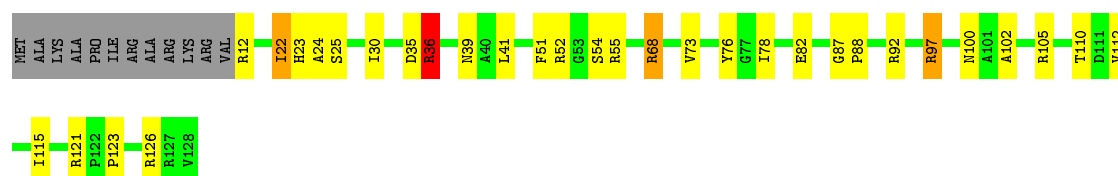
• Molecule 4: 30S ribosomal protein S2

Chain AB: 69% 17% 10%

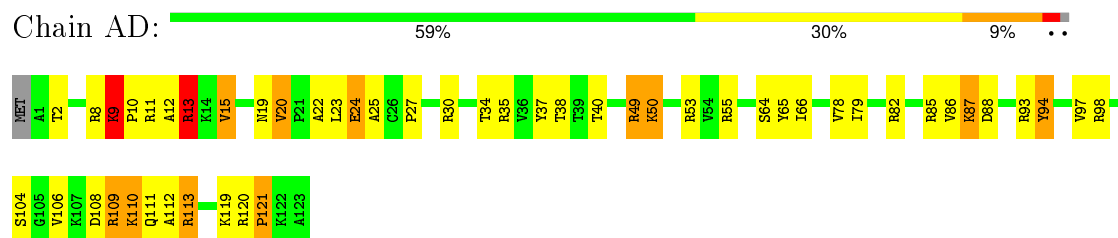


• Molecule 5: 30S ribosomal protein S11

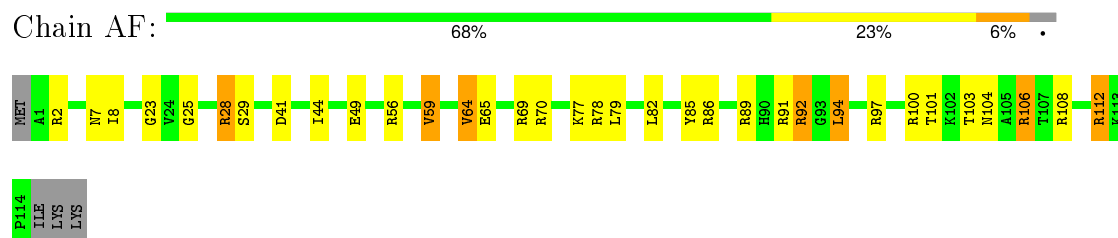
Chain AC: 66% 22% 9%



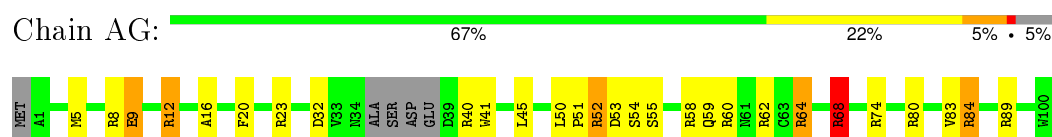
• Molecule 6: 30S ribosomal protein S12



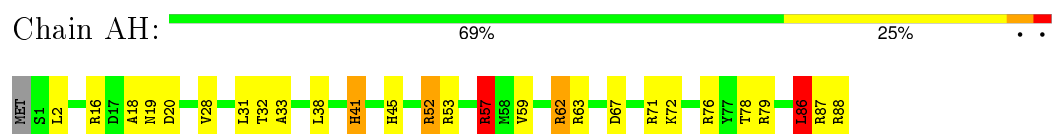
- Molecule 7: 30S ribosomal protein S13



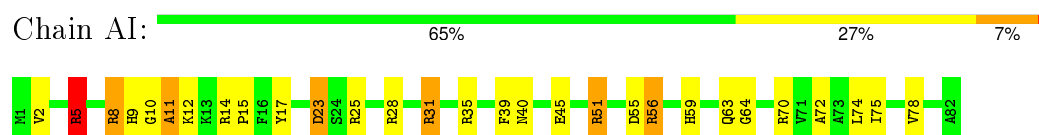
- Molecule 8: 30S ribosomal protein S14



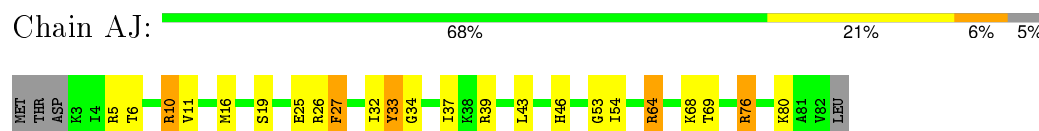
- Molecule 9: 30S ribosomal protein S15



- Molecule 10: 30S ribosomal protein S16

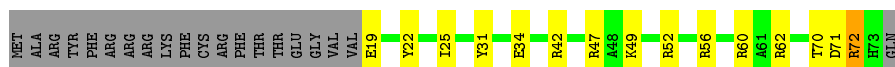


- Molecule 11: 30S ribosomal protein S17



- Molecule 12: 30S ribosomal protein S18

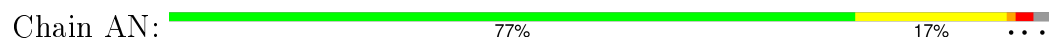




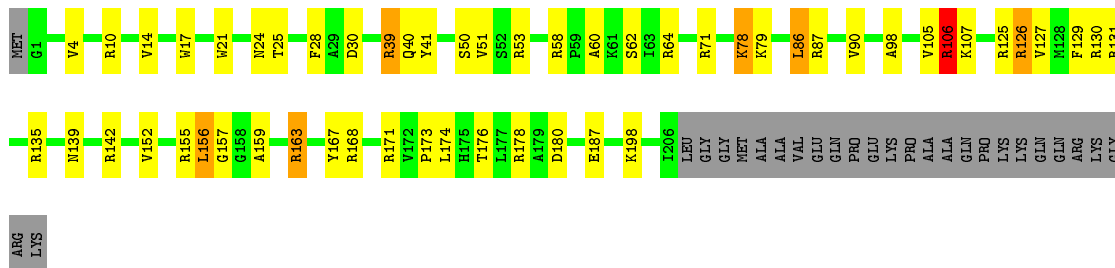
- Molecule 13: 30S ribosomal protein S19



- Molecule 14: 30S ribosomal protein S20



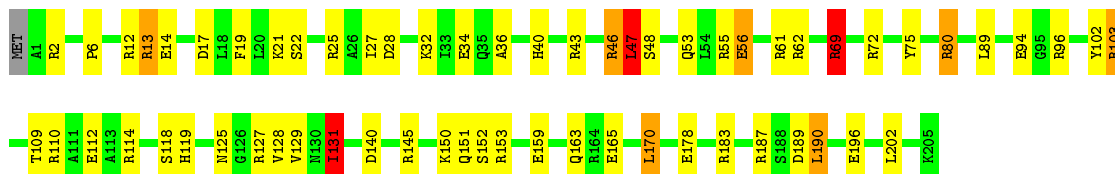
- Molecule 15: 30S ribosomal protein S3



- Molecule 16: 30S ribosomal protein S21

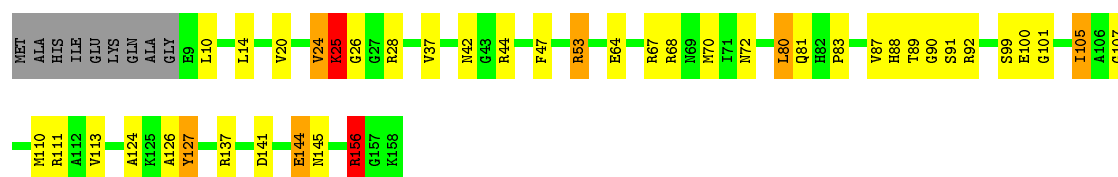


- Molecule 17: 30S ribosomal protein S4



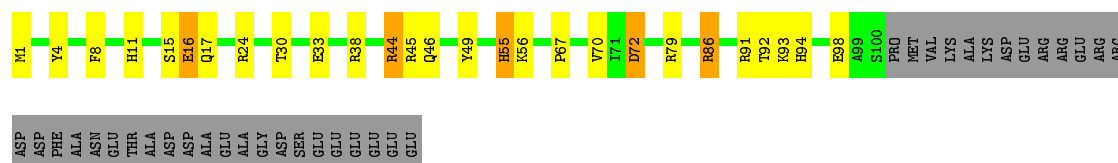
- Molecule 18: 30S ribosomal protein S5





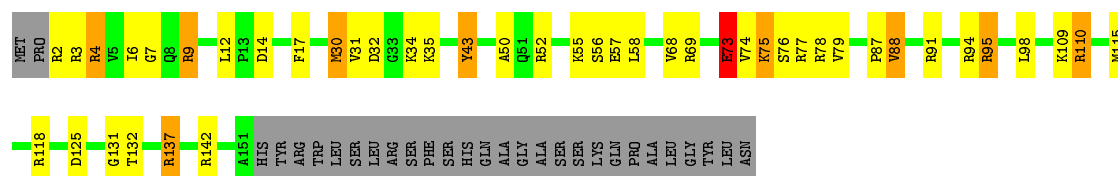
- Molecule 19: 30S ribosomal protein S6

Chain AT: 




- Molecule 20: 30S ribosomal protein S7

Chain AU: 




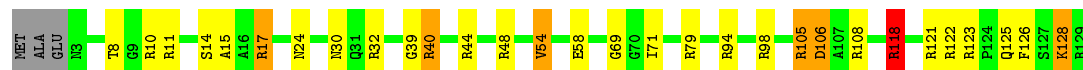
- Molecule 21: 30S ribosomal protein S8

Chain AV: 



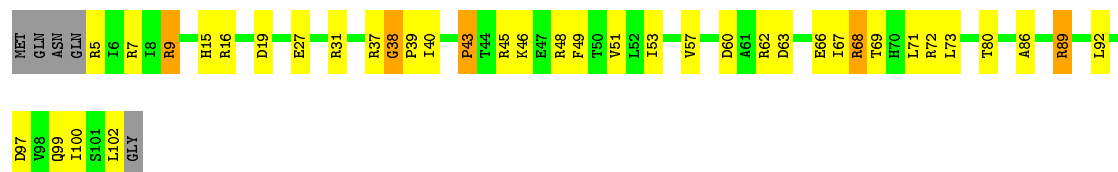
- Molecule 22: 30S ribosomal protein S9

Chain AW: 



- Molecule 23: 30S ribosomal protein S10

Chain AX: 



- Molecule 24: 5S rRNA

Chain BA:

25%

49%

26%

G2	C62	G62	C63	G63	C64	U6	U64	U65	A66	G67	C68	G69	G70	C71	C11	C12	G13	U14	A15	G16	G17	C17	G18	C19	G20	G21	U22	G23	G24	G25	C26	G27	C28	A29	C30	C31	U32	G33	A34	C35	G36	C37	G38	A39	U40	G41	G42	U103	C43	A44	A45	G46	G47	U48	C49	A50	G51	A52	A53	G54	U55	G56	G57	A58	A59	G60	G61
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• Molecule 25: 23S rRNA

Chain BB:

17%

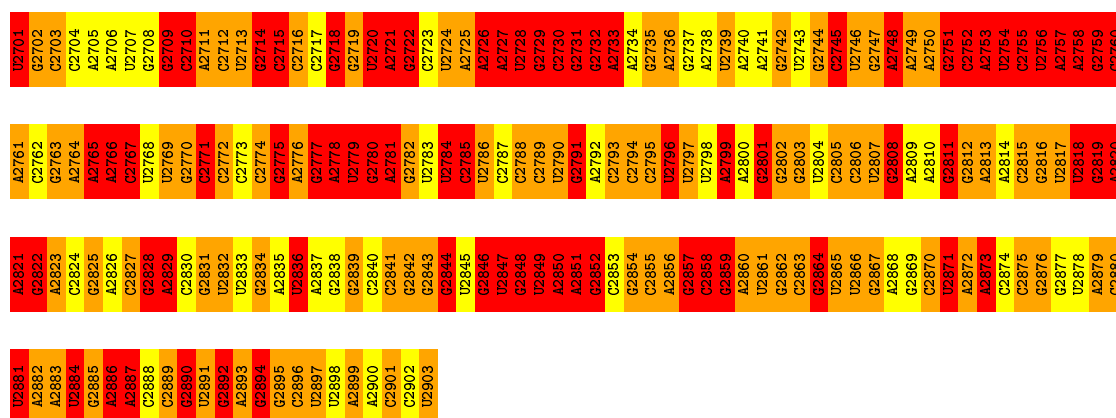
44%

39%

A721	A661	C601	A541	G481	C421	G361	G301	A241	G121	C61	G1
A722	G662	A602	C542	A482	A422	A362	C302	G242	A182	U62	G2
G723	G663	A603	G543	A483	A423	G363	G303	U243	G123	A63	U3
U724	G664	G604	C544	A484	G424	G364	U304	A244	G124	A64	U4
G725	G665	G605	U545	C485	G425	U365	C305	G245	G125	U65	A5
G726	A666	U606	U546	C486	C426	C366	U306	C246	A126	C66	A6
A727	U667	U607	A547	C487	U427	G367	G307	G247	G127	U67	G7
G728	A608	G608	G548	A488	A428	A368	C308	G248	C128	G68	C8
G729	G669	A609	G549	C489	A429	U369	A309	C249	G129	C69	C9
U730	A610	C610	C550	C490	A430	G370	A310	G250	G130	G70	A10
G731	G671	C611	G551	C491	U431	A371	A311	A251	A131	A71	C11
C732	G672	G612	U552	A492	A432	G372	G312	G252	G132	U72	U12
G733	G673	A613	G553	C493	C433	U373	G313	C253	U133	A73	A13
A734	G674	U614	U554	A494	U434	A374	C314	G254	G134	A74	A14
A735	A675	U615	G555	C495	C435	G375	G315	A255	U135	G75	A15
G736	G736	A616	A556	A496	C436	G376	C316	A256	G136	C76	C16
A737	A677	G617	C557	A497	U437	G377	G317	C257	U137	G77	G17
G738	C678	G618	U558	C498	A438	C378	C318	G258	U138	U78	U18
A739	G679	G619	G559	A499	A439	G379	G319	G259	U139	C79	A19
G740	C680	G620	C560	U500	C440	G380	A320	G260	U140	G80	C20
U741	G681	A621	G561	A501	U441	C381	U321	G261	G141	A81	A21
A742	G682	G622	U562	A502	A442	A382	A322	A262	U142	U82	C22
U743	U683	C623	A563	A503	A443	C383	C323	G263	C143	A83	G23
U744	G684	C624	C564	A504	C444	A384	A324	C264	A144	A84	G24
G745	A685	G625	C565	A505	C445	C385	A325	A265	C145	G85	U25
U746	U686	A626	U566	U506	A446	G386	G326	G266	U146	G86	U26
U747	C687	A627	U567	A507	A447	U387	U327	C267	C147	U87	G27
G748	U688	G628	U568	A508	U448	G388	U328	C268	U148	G88	A28
A749	A689	G629	U569	C509	U449	G389	G329	C269	A149	A89	U29
U750	C690	G630	C570	C510	A450	U390	A330	A270	U150	U90	G30
A751	G691	A631	U571	U511	A451	A391	C331	G271	C211	A91	C31
G752	C692	A632	A572	U512	A452	U392	A332	A272	A152	U92	C32
U753	A693	C633	U573	A513	A453	C393	G333	G273	U153	G93	C33
U754	U694	C634	A574	A514	A454	C394	C334	C274	G154	A94	U34
U755	G695	C635	A575	A515	C455	U395	C335	C275	A155	A95	G35
A756	G696	G636	U576	C516	C456	G396	C336	U276	A156	C96	G36
G757	G697	A637	C577	G517	A457	U397	C337	G277	C157	C97	C37
C758	U698	G638	G578	U518	A458	C398	G338	A278	U158	G98	A38
U759	A699	U639	G579	U519	U459	U399	U339	A279	G159	U99	G39
G760	G700	C640	U580	U520	A460	A400	A340	G280	A160	U100	U40
U761	C701	U641	C581	U521	C461	A401	C341	C281	G161	A101	C41
U762	U702	U642	A582	A522	C462	A402	A342	A282	U162	U102	A42
G763	G703	A643	G583	C523	C463	U403	C343	G283	A223	A103	G43
A764	U704	A644	C584	U524	U464	A404	A344	U284	C164	A104	A44
C765	A705	C645	G585	U525	C465	U405	A345	G285	A225	C105	G45
U766	A706	U646	A586	A526	A466	G406	A346	U286	U166	C106	G46
G767	U707	G647	C587	C527	G467	G407	A347	G287	A227	G107	C47
U768	G708	C648	U588	A528	C468	G408	U348	U288	G168	U108	C48
U769	U709	G649	U589	A529	A469	G409	U349	G289	C229	C109	A49
G770	U710	C650	A590	U530	A470	G410	G350	U290	G230	U110	U50
U771	G711	U651	U591	C531	A471	G411	C351	G291	U171	A111	G51
G772	U712	U652	A592	A532	A472	A412	A352	U292	G232	U112	A52
U773	G713	U653	U593	C533	G473	C413	C353	G293	A173	U113	A53
C774	U714	A554	U594	U534	C474	C414	A354	A294	U174	U114	G54
G775	A715	C595	G595	G535	C475	C415	U355	G295	G175	C115	G55
U776	U716	G596	U596	A536	C476	U416	G356	U296	A176	C116	A56
G777	C717	U657	A597	U537	A477	C417	C357	G297	G177	G117	C57
U778	A718	U598	U598	A538	A478	C418	U358	G298	G178	A118	G58
G779	C719	G599	A599	C539	A479	U419	G359	A299	C179	A119	U59
U780	U720	C600	A600	U540	C480	C420	U360	A200	G180	C120	C60

G1681	U1621	C1561	G1501	G1381	A1321	C1261	U1201	U1141	U1081	A1021	C961	C901	G841	A781
G1682	G1622	U1562	A1502	G1382	A1322	A1262	G1202	A1142	U1082	G1022	G962	C902	U842	A782
G1683	G1623	U1563	A1503	A1383	A1323	U1263	U1203	A1143	U1083	U1023	U963	C903	G843	A783
G1684	U1624	C1564	A1504	A1384	G1324	A1264	A1204	A1144	A1084	G1024	G964	C904	A844	G784
G1685	C1625	C1565	A1505	G1385	U1325	A1265	A1205	C1145	A1085	G1025	G965	A905	A845	G785
G1686	A1626	A1566	U1506	C1386	U1326	G1266	G1206	C1146	A1086	G1026	G966	U906	U846	G786
G1687	G1627	G1567	C1507	A1387	A1327	U1267	C1207	A1147	G1087	A1027	U967	G907	U847	C787
G1688	G1628	G1568	A1508	G1388	A1328	A1268	C1208	U1148	A1088	A1028	G968	C908	C848	A788
A1689	U1629	A1569	A1509	G1389	U1329	A1269	U1209	G1149	A1089	A1029	G969	A909	A849	A789
A1690	A1630	G1510	G1510	U1390	C1330	C1270	G1210	C1150	A1090	C1030	U970	A910	U850	U790
C1691	G1631	A1571	G1511	U1391	G1331	G1271	G1211	A1151	G1091	G1031	G971	A911	C851	C791
U1692	A1632	A1572	C1512	A1392	G1332	A1272	G1212	C1152	G1092	A1032	A972	C912	U852	A792
U1693	G1633	G1573	U1513	G1393	G1333	U1273	A1213	C1153	G1093	U1033	A973	C913	C853	A793
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G1695	A1635	C1575	A1515	A1395	C1335	A1275	G1215	A1155	A1095	U1035	A975	C915	G855	C795
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G1697	A1637	C1577	U1517	U1397	G1337	G1277	U1217	G1157	U1097	G1037	G977	A917	G857	G797
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G1699	G1639	A1579	G1519	C1399	G1339	G1279	U1219	U1159	G1099	A1039	A979	U919	G859	G799
A1700	A1640	U1580	U1520	U1400	U1340	G1280	G1220	G1160	C1100	A1040	A980	A920	U860	A800
A1701	A1641	G1581	G1521	G1401	G1341	G1281	C1221	C1161	U1101	G1041	A981	C921	A861	A801
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C1706	C1646	A1586	C1526	U1406	G1346	A1286	A1226	G1166	G1106	A1046	C986	G926	A866	G806
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C1708	U1648	G1588	A1528	U1468	C1348	G1408	G1228	G1168	A1108	A1048	A988	A928	U868	G808
U1709	G1649	U1589	G1529	U1469	C1349	C1289	C1229	A1169	C1109	C1049	A989	U929	G869	A809
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A1711	G1651	C1591	C1531	U1471	C1351	C1291	U1231	G1171	A1111	G1051	C991	U931	U871	U811
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G1715	A1655	C1595	G1535	U1475	U1355	U1295	G1235	G1175	G1115	G1055	C995	C935	G875	C815
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G1719	U1659	U1599	U1539	A1479	A1359	G1299	G1239	G1179	U1119	G1059	U999	G939	G879	A819
U1720	G1660	C1600	G1540	C1480	A1420	G1300	U1240	U1180	G1120	U1060	A1000	G940	G880	A820
G1721	G1661	G1601	C1541	G1481	G1421	A1301	A1241	U1181	C1121	U1061	A1001	A941	G881	A821
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C1728	A1668	A1608	A1548	C1488	G1368	A1308	G1248	U1188	G1128	G1068	A1008	C948	C888	U828
U1729	U1669	A1609	A1549	G1489	G1369	G1309	U1249	A1189	A1129	A1069	A1009	G949	C889	A829
C1730	C1670	A1610	C1550	G1490	C1370	G1310	G1250	G1190	U1130	A1070	A1010	G950	C890	G830
G1731	U1671	C1611	A1551	G1491	G1371	G1311	C1251	G1191	G1131	G1071	G1011	C951	G891	G831
C1732	A1672	C1612	A1552	G1492	G1372	U1312	G1252	G1192	U1132	U1072	U1012	G952	A892	U832
G1733	G1673	G1613	A1553	A1493	A1373	U1313	A1253	G1193	A1133	A1073	C1013	G953	C893	A833
G1734	G1674	A1614	U1554	A1494	G1374	C1314	A1254	A1194	A1134	G1074	A1014	G954	U894	G834
A1735	C1675	G1615	G1555	A1495	U1375	C1315	U1255	G1195	C1135	C1075	U1015	U955	U895	C835
U1736	A1676	C1556	C1556	A1496	G1376	U1316	G1256	C1196	G1136	C1076	G1016	G956	A896	G836
G1737	A1677	U1497	C1557	C1437	G1377	G1317	C1257	G1197	G1137	A1077	G1017	C957	C897	C837
G1738	A1678	A1618	C1558	U1438	A1378	U1318	U1258	U1198	G1138	U1078	U1018	U958	C898	C838
A1739	U1679	G1619	U1559	C1499	A1379	G1319	G1259	U1199	G1139	C1079	U1019	A959	A899	U839
G1740	U1680	G1620	G1560	U1440	G1380	C1320	A1260	C1200	C1140	A1080	A1020	C960	A900	C840

G2641	G2642	G2643	G2644	G2645	G2646	G2647	G2648	G2649	G2650	G2651	G2652	G2653	G2654	G2655	G2656	G2657	G2658	G2659	G2660	G2661	G2662	G2663	G2664	G2665	G2666	G2667	G2668	G2669	G2670	G2671	G2672	G2673	G2674	G2675	G2676	G2677	G2678	G2679	G2680	G2681	G2682	G2683	G2684	G2685	G2686	G2687	G2688	G2689	G2690	G2691	G2692	G2693	G2694	G2695	G2696	G2697	G2698	G2699	A2700
G2581	G2582	G2583	G2584	G2585	G2586	G2587	G2588	G2589	G2590	G2591	G2592	G2593	G2594	G2595	G2596	G2597	G2598	G2599	G2600	G2601	G2602	G2603	G2604	G2605	G2606	G2607	G2608	G2609	G2610	G2611	G2612	G2613	G2614	G2615	G2616	G2617	G2618	G2619	G2620	G2621	G2622	G2623	G2624	G2625	G2626	G2627	G2628	G2629	G2630	G2631	G2632	G2633	G2634	G2635	G2636	G2637	G2638	G2639	G2640
C2521	C2522	C2523	C2524	C2525	C2526	C2527	C2528	C2529	C2530	C2531	C2532	C2533	C2534	C2535	C2536	C2537	C2538	C2539	C2540	C2541	C2542	C2543	C2544	C2545	C2546	C2547	C2548	C2549	C2550	C2551	C2552	C2553	C2554	C2555	C2556	C2557	C2558	C2559	C2560	C2561	C2562	C2563	C2564	C2565	C2566	C2567	C2568	C2569	C2570	C2571	C2572	C2573	C2574	C2575	C2576	C2577	C2578	C2579	C2580
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U2401	U2402	U2403	U2404	U2405	U2406	U2407	U2408	U2409	U2410	U2411	U2412	U2413	U2414	U2415	U2416	U2417	U2418	U2419	U2420	U2421	U2422	U2423	U2424	U2425	U2426	U2427	U2428	U2429	U2430	U2431	U2432	U2433	U2434	U2435	U2436	U2437	U2438	U2439	U2440	U2441	U2442	U2443	U2444	U2445	U2446	U2447	U2448	U2449	U2450	U2451	U2452	U2453	U2454	U2455	U2456	U2457	U2458	U2459	U2460
G2341	G2342	G2343	G2344	G2345	G2346	G2347	G2348	G2349	G2350	G2351	G2352	G2353	G2354	G2355	G2356	G2357	G2358	G2359	G2360	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2368	G2369	G2370	G2371	G2372	G2373	G2374	G2375	G2376	G2377	G2378	G2379	G2380	G2381	G2382	G2383	G2384	G2385	G2386	G2387	G2388	G2389	G2390	G2391	G2392	G2393	G2394	G2395	G2396	G2397	G2398	G2399	G2400
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G2221	G2222	G2223	G2224	G2225	G2226	G2227	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	G2239	G2240	G2241	G2242	G2243	G2244	G2245	G2246	G2247	G2248	G2249	G2250	G2251	G2252	G2253	G2254	G2255	G2256	G2257	G2258	G2259	G2260	G2261	G2262	G2263	G2264	G2265	G2266	G2267	G2268	G2269	G2270	G2271	G2272	G2273	G2274	G2275	G2276	G2277	G2278	G2279	G2280
C2161	C2162	C2163	C2164	C2165	C2166	C2167	C2168	C2169	C2170	C2171	C2172	C2173	C2174	C2175	C2176	C2177	C2178	C2179	C2180	C2181	C2182	C2183	C2184	C2185	C2186	C2187	C2188	C2189	C2190	C2191	C2192	C2193	C2194	C2195	C2196	C2197	C2198	C2199	C2200	C2201	C2202	C2203	C2204	C2205	C2206	C2207	C2208	C2209	C2210	C2211	C2212	C2213	C2214	C2215	C2216	C2217	C2218	C2219	C2220
A2101	A2102	A2103	A2104	A2105	A2106	A2107	A2108	A2109	A2110	A2111	A2112	A2113	A2114	A2115	A2116	A2117	A2118	A2119	A2120	A2121	A2122	A2123	A2124	A2125	A2126	A2127	A2128	A2129	A2130	A2131	A2132	A2133	A2134	A2135	A2136	A2137	A2138	A2139	A2140	A2141	A2142	A2143	A2144	A2145	A2146	A2147	A2148	A2149	A2150	A2151	A2152	A2153	A2154	A2155	A2156	A2157	A2158	A2159	A2160
U2041	U2042	U2043	U2044	U2045	U2046	U2047	U2048	U2049	U2050	U2051	U2052	U2053	U2054	U2055	U2056	U2057	U2058	U2059	U2060	U2061	U2062	U2063	U2064	U2065	U2066	U2067	U2068	U2069	U2070	U2071	U2072	U2073	U2074	U2075	U2076	U2077	U2078	U2079	U2080	U2081	U2082	U2083	U2084	U2085	U2086	U2087	U2088	U2089	U2090	U2091	U2092	U2093	U2094	U2095	U2096	U2097	U2098	U2099	U2100
A1981	A1982	A1983	A1984	A1985	A1986	A1987	A1988	A1989	A1990	A1991	A1992	A1993	A1994	A1995	A1996	A1997	A1998	A1999	C2000	C2001	C2002	C2003	C2004	C2005	C2006	C2007	C2008	A2009	A2010	A2011	A2012	A2013	A2014	A2015	A2016	U2017	G2018	A2019	A2020	C2021	C2022	C2023	C2024	C2025	U2026	G2027	C2028	C2029	A2030	A2031	C2032	A2033	U2034	C2035	C2036	A2037	C2038	U2039	G2040
G1921	G1922	G1923	G1924	G1925	G1926	G1927	G1928	G1929	G1930	G1931	G1932	G1933	G1934	G1935	G1936	G1937	G1938	G1939	U1940	C1941	C1942	C1943	C1944	C1945	C1946	C1947	C1948	G1949	G1950	G1951	A1952	A1953	C1954	C1955	C1956	C1957	C1958	G1959	G1960	A1961	G1962	C1963	C1964	C1965	A1966	G1967	C1968	A1969	A1970	U1971	C1972	A1973	C1974	C1975	U1976	A1977	A1978	C1979	G1980
G1861	G1862	G1863	G1864	G1865	G1866	G1867	G1868	G1869	G1870	G1871	G1872	G1873	G1874	G1875	G1876	G1877	G1878	C1879	U1880	C1881	C1882	C1883	C1884	C1885	C1886	C1887	C1888	A1889	A1890	A1891	C1892	C1893	C1894	C1895	C1896	G1897	U1898	C1899	A1900	U1901	C1902	C1903	C1904	C1905	G1906	G1907	C1908	A1909	G1910	U1911	C1912	A1913	C1914	C1915	U1916	U1917	A1918	C1919	G1920
A1801	A1802	A1803	A1804	A1805	A1806	A1807	A1808	A1809	A1810	A1811	A1812	A1813	A1814	A1815	A1816	A1817	A1818	A1819	U1820	C1821	C1822	C1823	C1824	C1825	C1826	C1827	C1828	A1829	C1830	C1831	C1832	C1833	C1834	C1835	C1836	C1837	C1838	G1839	A1840	U1841	C1842	C1843	C1844	C1845	A1846	A1847	C1848	A1849	U1850	U1851	C1852	A1853	C1854	C1855	U1856	G1857	A1858	C1859	G1860
C1741	C1742	C1743	C1744	C1745	C1746	C1747	C1748	C1749	C1750	C1751	C1752	C1753	C1754	C1755	C1756	C1757	C1758	C1759	C1760	C1761	C1762	C1763	C1764	C1765	C1766	C1767	C1768	C1769	C1770	C1771	C1772	C1773	C1774	C1775	C1776	C1777	C1778	C1779	A1780	U1781	C1782	C1783	C1784	A1785	A1786	C1787	C1788	A1789	C1790	A1791	C1792	C1793	C1794	C1795	U1796	G1797	C1798	C1799	C1800



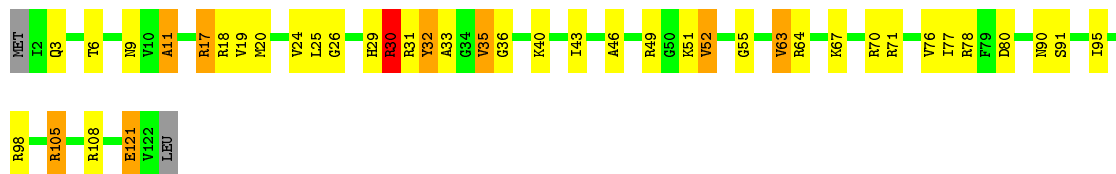
- Molecule 26: 50S ribosomal protein L25

Chain BC: 76% 21% .



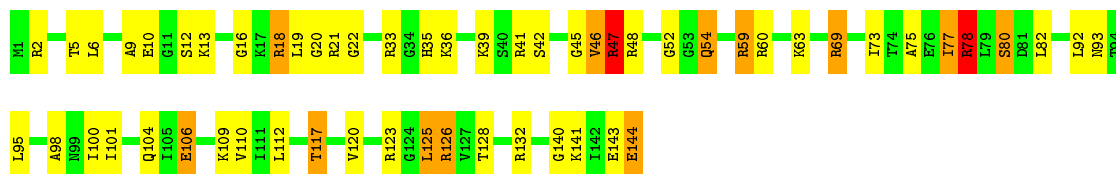
- Molecule 27: 50S ribosomal protein L14

Chain BD: 65% 26% 7% ..



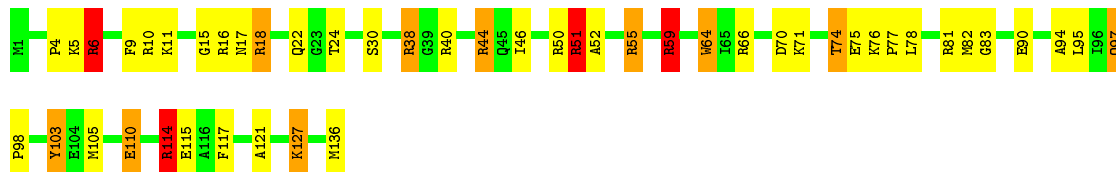
- Molecule 28: 50S ribosomal protein L15

Chain BE: 60% 30% 8% .

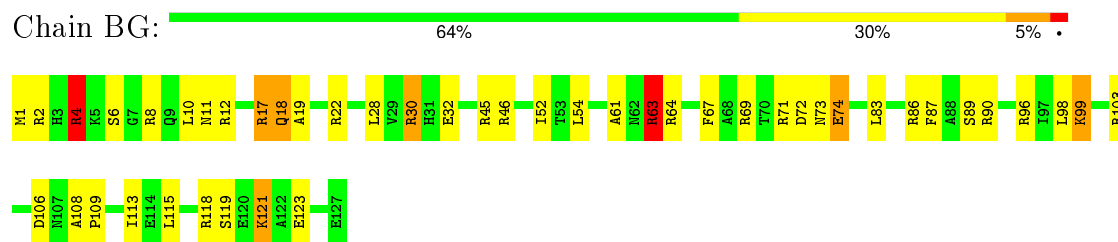


- Molecule 29: 50S ribosomal protein L16

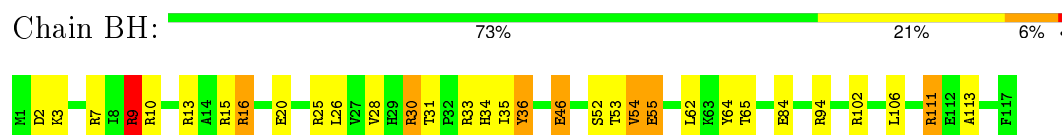
Chain BF: 65% 25% 7% .



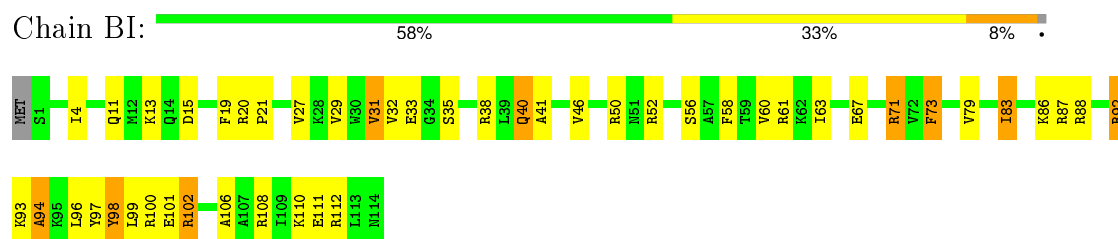
- Molecule 30: 50S ribosomal protein L17



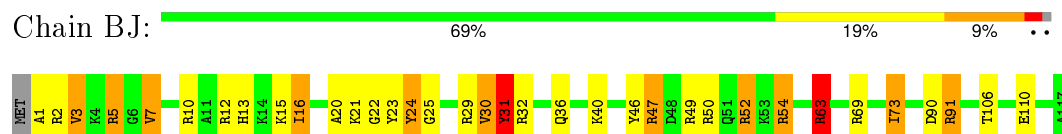
- Molecule 31: 50S ribosomal protein L18



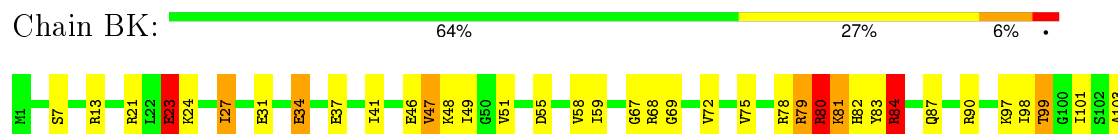
- Molecule 32: 50S ribosomal protein L19



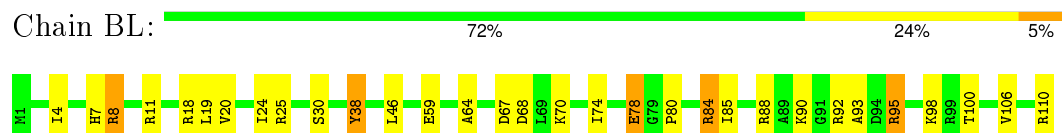
- Molecule 33: 50S ribosomal protein L20



- Molecule 34: 50S ribosomal protein L21

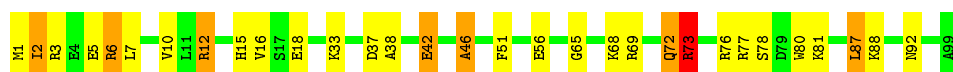


- Molecule 35: 50S ribosomal protein L22



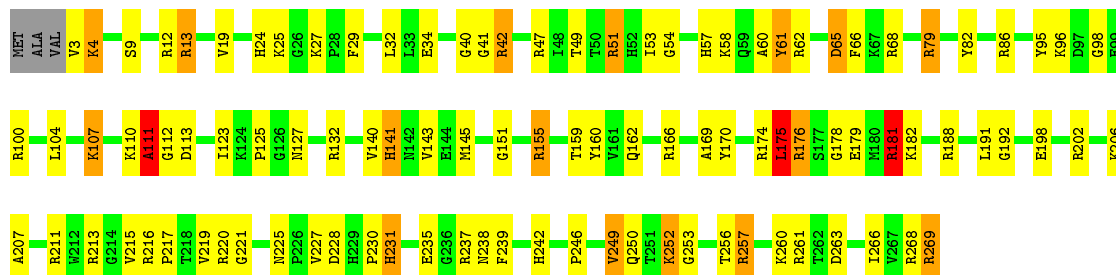
- Molecule 36: 50S ribosomal protein L23





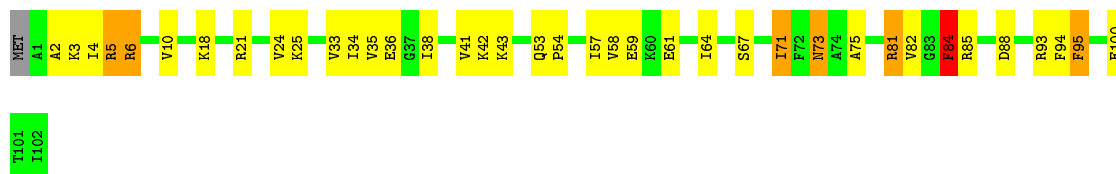
- Molecule 37: 50S ribosomal protein L2

Chain BN: 61% 31% 6% ..



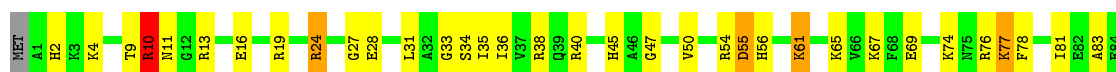
- Molecule 38: 50S ribosomal protein L24

Chain BO: 62% 30% 6% ..



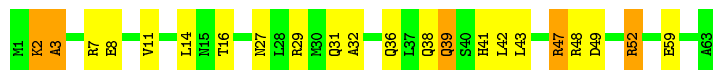
- Molecule 39: 50S ribosomal protein L27

Chain BP: 59% 34% 5% ..



- Molecule 40: 50S ribosomal protein L29

Chain BQ: 65% 27% 8%



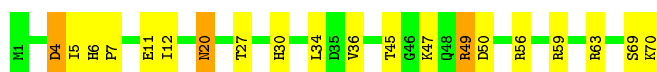
- Molecule 41: 50S ribosomal protein L30

Chain BR: 71% 20% 5% ..



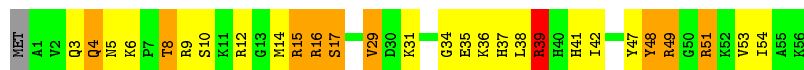
- Molecule 42: 50S ribosomal protein L31

Chain BS: 71% 24% .



- Molecule 43: 50S ribosomal protein L32

Chain BT: 49% 32% 16% . .



- Molecule 44: 50S ribosomal protein L33

Chain BU: 65% 30% 6%



- Molecule 45: 50S ribosomal protein L34

Chain BV: 67% 22% 9% .



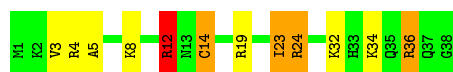
- Molecule 46: 50S ribosomal protein L35

Chain BW: 66% 19% 16%



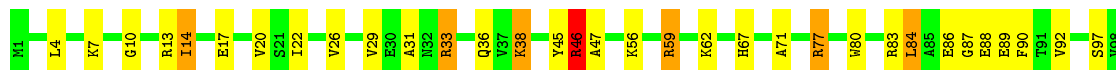
- Molecule 47: 50S ribosomal protein L36

Chain BX: 68% 18% 11% .

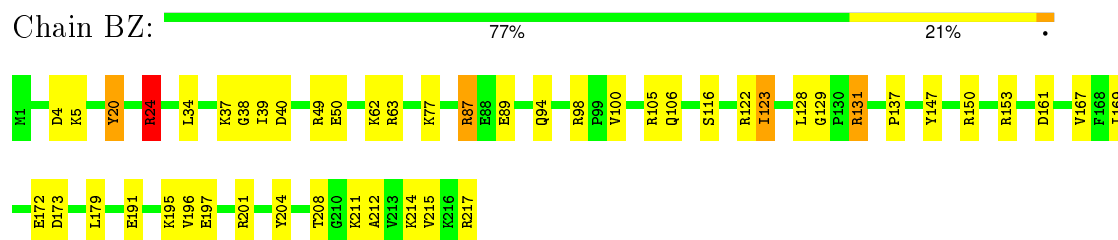


- Molecule 48: 50S ribosomal protein L3

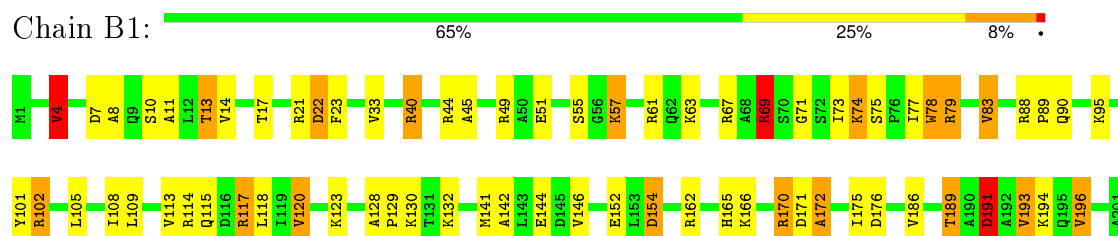
Chain BY: 61% 29% 9% .



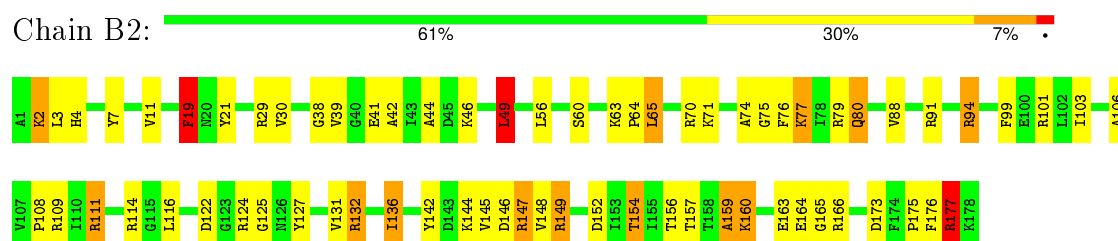
- Molecule 49: 50S ribosomal protein L1P



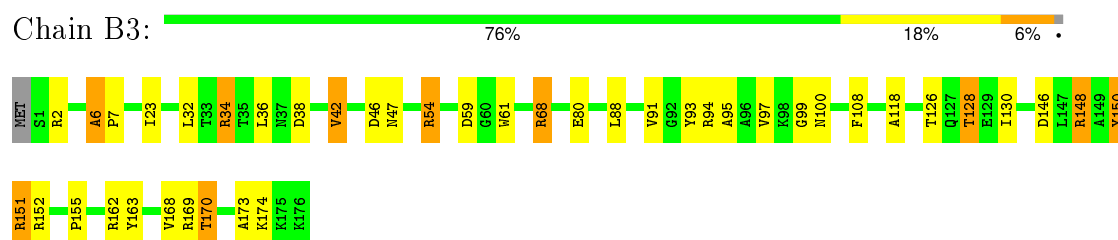
- Molecule 50: 50S ribosomal protein L4



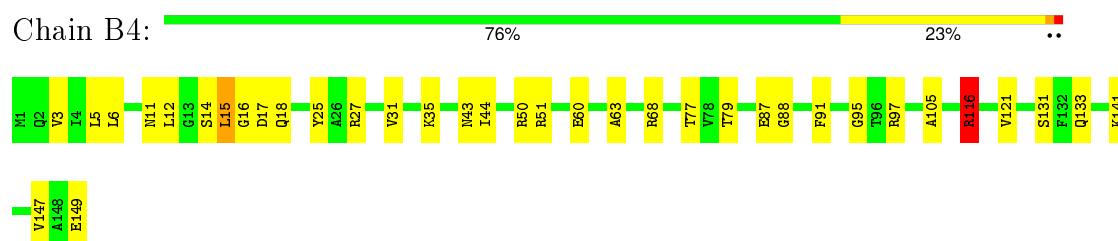
- Molecule 51: 50S ribosomal protein L5



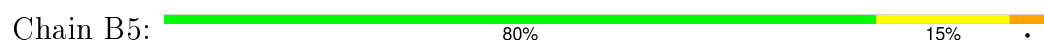
- Molecule 52: 50S ribosomal protein L6

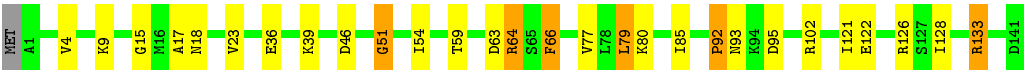


- Molecule 53: 50S ribosomal protein L9



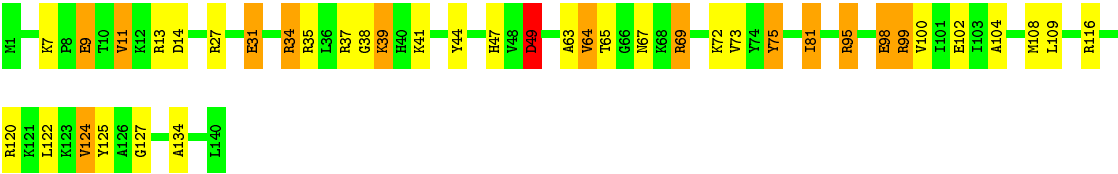
- Molecule 54: 50S ribosomal protein L11





● Molecule 55: 50S ribosomal protein L13

Chain B6: 71% 19% 9%



4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	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	2.55	109/1789 (6.1%)	3.85	439/2788 (15.7%)
1	AE	2.27	78/1814 (4.3%)	3.60	403/2827 (14.3%)
1	AP	3.55	99/1789 (5.5%)	3.96	389/2788 (14.0%)
10	AI	1.17	4/658 (0.6%)	2.16	20/884 (2.3%)
11	AJ	0.99	2/657 (0.3%)	1.87	11/881 (1.2%)
12	AK	1.19	5/462 (1.1%)	1.98	15/621 (2.4%)
13	AL	1.08	2/652 (0.3%)	1.96	14/877 (1.6%)
14	AN	1.03	4/670 (0.6%)	1.87	14/888 (1.6%)
15	AO	1.08	6/1651 (0.4%)	1.94	43/2225 (1.9%)
16	AQ	1.23	2/430 (0.5%)	2.26	19/570 (3.3%)
17	AR	1.08	2/1664 (0.1%)	1.94	46/2227 (2.1%)
18	AS	1.02	2/1118 (0.2%)	1.70	19/1504 (1.3%)
19	AT	1.03	1/835 (0.1%)	1.81	13/1128 (1.2%)
2	AM	2.44	19/436 (4.4%)	3.59	99/672 (14.7%)
20	AU	1.12	4/1187 (0.3%)	1.97	33/1591 (2.1%)
21	AV	0.95	1/988 (0.1%)	1.65	14/1326 (1.1%)
22	AW	1.13	1/1033 (0.1%)	1.98	27/1375 (2.0%)
23	AX	1.03	2/796 (0.3%)	2.11	28/1077 (2.6%)
24	BA	2.22	97/2800 (3.5%)	3.50	592/4367 (13.6%)
25	BB	2.24	2712/69795 (3.9%)	3.62	15539/108884 (14.3%)
26	BC	1.01	1/765 (0.1%)	1.78	11/1025 (1.1%)
27	BD	1.11	4/939 (0.4%)	2.36	28/1258 (2.2%)
28	BE	1.13	2/1061 (0.2%)	1.97	25/1413 (1.8%)
29	BF	1.09	3/1092 (0.3%)	2.16	36/1460 (2.5%)
3	A1	2.55	1627/36759 (4.4%)	3.68	8418/57346 (14.7%)
30	BG	1.16	6/1020 (0.6%)	2.13	43/1364 (3.2%)
31	BH	1.11	1/909 (0.1%)	2.12	33/1219 (2.7%)
32	BI	1.15	4/928 (0.4%)	2.04	30/1242 (2.4%)
33	BJ	1.18	4/959 (0.4%)	1.97	27/1278 (2.1%)
34	BK	1.05	1/828 (0.1%)	2.02	23/1107 (2.1%)
35	BL	0.98	0/863	1.86	17/1156 (1.5%)
36	BM	0.99	2/784 (0.3%)	1.93	18/1048 (1.7%)
37	BN	1.10	9/2092 (0.4%)	1.99	65/2813 (2.3%)
38	BO	1.03	1/787 (0.1%)	1.87	18/1051 (1.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	BP	1.05	1/641 (0.2%)	2.02	17/848 (2.0%)
4	AB	0.97	2/1735 (0.1%)	1.84	41/2338 (1.8%)
40	BQ	1.02	0/509	2.09	13/677 (1.9%)
41	BR	0.99	2/452 (0.4%)	2.05	14/605 (2.3%)
42	BS	1.04	0/558	1.99	13/745 (1.7%)
43	BT	1.10	0/449	2.22	16/599 (2.7%)
44	BU	1.08	0/447	1.81	8/594 (1.3%)
45	BV	1.16	0/379	2.33	18/498 (3.6%)
46	BW	0.99	0/512	1.74	9/676 (1.3%)
47	BX	1.07	1/302 (0.3%)	2.23	8/397 (2.0%)
48	BY	0.99	3/1585 (0.2%)	1.98	42/2134 (2.0%)
49	BZ	0.98	3/1711 (0.2%)	1.64	26/2305 (1.1%)
5	AC	1.10	5/892 (0.6%)	1.74	19/1205 (1.6%)
50	B1	1.01	0/1570	1.86	35/2113 (1.7%)
51	B2	1.07	2/1443 (0.1%)	1.88	40/1937 (2.1%)
52	B3	1.01	0/1342	1.81	32/1816 (1.8%)
53	B4	0.97	1/1121 (0.1%)	1.74	16/1515 (1.1%)
54	B5	0.94	0/1045	1.71	11/1410 (0.8%)
55	B6	1.02	1/1135 (0.1%)	1.95	28/1529 (1.8%)
6	AD	1.14	2/968 (0.2%)	2.24	38/1300 (2.9%)
7	AF	1.16	7/892 (0.8%)	2.21	32/1193 (2.7%)
8	AG	1.13	3/785 (0.4%)	2.22	33/1046 (3.2%)
9	AH	1.13	5/723 (0.7%)	2.18	30/966 (3.1%)
All	All	2.08	4855/162206 (3.0%)	3.29	27108/242726 (11.2%)

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	55
1	AE	0	49
1	AP	2	50
10	AI	0	3
11	AJ	0	4
13	AL	0	8
14	AN	1	1
15	AO	0	3
16	AQ	0	4
17	AR	0	7
18	AS	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
19	AT	0	4
2	AM	0	9
20	AU	0	4
21	AV	0	2
22	AW	0	4
23	AX	0	4
24	BA	0	66
25	BB	3	1717
26	BC	0	3
27	BD	0	6
28	BE	0	6
29	BF	0	4
3	A1	4	945
30	BG	0	4
31	BH	0	1
32	BI	0	4
33	BJ	0	4
34	BK	0	5
35	BL	0	5
36	BM	0	1
37	BN	0	12
38	BO	0	4
39	BP	0	3
4	AB	0	3
40	BQ	0	3
41	BR	0	3
42	BS	0	3
43	BT	0	2
44	BU	0	5
45	BV	0	2
46	BW	0	4
47	BX	0	2
48	BY	0	9
49	BZ	0	2
5	AC	0	3
50	B1	0	9
51	B2	0	6
52	B3	0	5
53	B4	0	4
54	B5	0	3
55	B6	0	8
6	AD	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	AF	0	5
8	AG	0	4
9	AH	0	5
All	All	10	3101

The worst 5 of 4855 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A1	1429	A	P-O5'	178.16	3.38	1.59
3	A1	1340	A	C3'-O3'	99.95	2.82	1.42
1	AP	31	A	C4'-C3'	53.26	2.11	1.53
1	AP	31	A	C2'-C1'	45.01	2.02	1.53
1	AP	31	A	C4'-O4'	44.63	2.03	1.45

The worst 5 of 27108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AP	74	C	P-O3'-C3'	-78.58	25.40	119.70
1	AP	74	C	O3'-P-O5'	-40.02	27.95	104.00
25	BB	2376	A	N1-C6-N6	-29.09	101.15	118.60
3	A1	1225	A	N1-C6-N6	-28.97	101.22	118.60
3	A1	1250	A	N1-C6-N6	-27.68	101.99	118.60

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 3101 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	760	11	0
1	AE	1622	0	769	7	0
1	AP	1600	0	755	42	0
2	AM	397	0	202	6	0
3	A1	32828	0	15511	162	0
4	AB	1704	0	1732	9	0
5	AC	876	0	887	3	0
6	AD	954	0	1019	4	0
7	AF	883	0	944	1	0
8	AG	773	0	825	2	0
9	AH	715	0	742	2	0
10	AI	648	0	666	5	0
11	AJ	648	0	691	3	0
12	AK	455	0	478	0	0
13	AL	637	0	665	0	0
14	AN	664	0	714	4	0
15	AO	1624	0	1699	5	0
16	AQ	425	0	449	1	0
17	AR	1642	0	1710	9	0
18	AS	1105	0	1148	4	0
19	AT	817	0	808	2	0
20	AU	1174	0	1230	3	0
21	AV	978	0	1034	0	0
22	AW	1021	0	1070	1	0
23	AX	786	0	828	4	0
24	BA	2504	0	1208	11	0
25	BB	62317	0	29633	224	0
26	BC	752	0	780	4	0
27	BD	930	0	1000	5	0
28	BE	1052	0	1129	9	0
29	BF	1073	0	1157	8	0
30	BG	1007	0	1045	4	0
31	BH	899	0	935	2	0
32	BI	916	0	965	6	0
33	BJ	946	0	1022	8	0
34	BK	815	0	839	4	0
35	BL	856	0	922	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	BM	777	0	840	2	0
37	BN	2053	0	2122	9	0
38	BO	779	0	834	2	0
39	BP	633	0	656	1	0
40	BQ	508	0	543	3	0
41	BR	448	0	491	2	0
42	BS	548	0	552	2	0
43	BT	443	0	461	2	0
44	BU	440	0	485	2	0
45	BV	376	0	418	2	0
46	BW	503	0	574	7	0
47	BX	301	0	343	1	0
48	BY	1564	0	1616	7	0
49	BZ	1687	0	1814	3	0
50	B1	1551	0	1619	7	0
51	B2	1419	0	1460	8	0
52	B3	1322	0	1374	3	0
53	B4	1110	0	1148	2	0
54	B5	1031	0	1088	4	0
55	B6	1112	0	1147	2	0
All	All	149248	0	97556	534	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 534 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'	1.91	1.47
25:BB:1687:G:C1'	25:BB:1687:G:C2'	1.93	1.45
1:AP:31:A:C2'	3:A1:1340:A:H3'	1.45	1.44
25:BB:1687:G:C4'	25:BB:1687:G:C3'	1.96	1.43
1:AP:31:A:C3'	1:AP:31:A:C2'	2.01	1.39

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%)	178 (82%)	33 (15%)	5 (2%)	8	48
5	AC	115/129 (89%)	91 (79%)	17 (15%)	7 (6%)	2	26
6	AD	121/124 (98%)	78 (64%)	28 (23%)	15 (12%)	0	8
7	AF	112/118 (95%)	80 (71%)	24 (21%)	8 (7%)	1	22
8	AG	94/101 (93%)	69 (73%)	20 (21%)	5 (5%)	2	29
9	AH	86/89 (97%)	73 (85%)	11 (13%)	2 (2%)	8	48
10	AI	80/82 (98%)	55 (69%)	15 (19%)	10 (12%)	0	8
11	AJ	78/84 (93%)	52 (67%)	18 (23%)	8 (10%)	1	12
12	AK	53/75 (71%)	44 (83%)	7 (13%)	2 (4%)	4	37
13	AL	77/92 (84%)	51 (66%)	19 (25%)	7 (9%)	1	17
14	AN	83/87 (95%)	66 (80%)	13 (16%)	4 (5%)	3	32
15	AO	204/233 (88%)	151 (74%)	38 (19%)	15 (7%)	1	21
16	AQ	49/71 (69%)	35 (71%)	8 (16%)	6 (12%)	0	8
17	AR	203/206 (98%)	161 (79%)	29 (14%)	13 (6%)	2	25
18	AS	148/159 (93%)	114 (77%)	20 (14%)	14 (10%)	1	15
19	AT	98/135 (73%)	80 (82%)	13 (13%)	5 (5%)	2	30
20	AU	148/179 (83%)	118 (80%)	19 (13%)	11 (7%)	1	21
21	AV	127/130 (98%)	103 (81%)	19 (15%)	5 (4%)	4	36
22	AW	125/130 (96%)	95 (76%)	23 (18%)	7 (6%)	2	28
23	AX	96/103 (93%)	78 (81%)	9 (9%)	9 (9%)	1	16
26	BC	92/94 (98%)	74 (80%)	14 (15%)	4 (4%)	3	34
27	BD	119/123 (97%)	90 (76%)	16 (13%)	13 (11%)	0	11
28	BE	142/144 (99%)	91 (64%)	30 (21%)	21 (15%)	0	5
29	BF	134/136 (98%)	73 (54%)	40 (30%)	21 (16%)	0	5
30	BG	125/127 (98%)	84 (67%)	32 (26%)	9 (7%)	1	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	BH	115/117 (98%)	72 (63%)	32 (28%)	11 (10%)	1	15
32	BI	112/115 (97%)	63 (56%)	32 (29%)	17 (15%)	0	5
33	BJ	115/118 (98%)	77 (67%)	27 (24%)	11 (10%)	1	15
34	BK	101/103 (98%)	59 (58%)	33 (33%)	9 (9%)	1	17
35	BL	108/110 (98%)	72 (67%)	27 (25%)	9 (8%)	1	18
36	BM	97/99 (98%)	69 (71%)	18 (19%)	10 (10%)	1	12
37	BN	265/270 (98%)	165 (62%)	61 (23%)	39 (15%)	0	6
38	BO	100/103 (97%)	60 (60%)	22 (22%)	18 (18%)	0	4
39	BP	82/85 (96%)	44 (54%)	21 (26%)	17 (21%)	0	3
40	BQ	61/63 (97%)	42 (69%)	14 (23%)	5 (8%)	1	18
41	BR	56/59 (95%)	38 (68%)	13 (23%)	5 (9%)	1	17
42	BS	68/70 (97%)	38 (56%)	22 (32%)	8 (12%)	0	9
43	BT	54/57 (95%)	32 (59%)	11 (20%)	11 (20%)	0	3
44	BU	52/54 (96%)	33 (64%)	14 (27%)	5 (10%)	1	15
45	BV	44/46 (96%)	33 (75%)	6 (14%)	5 (11%)	0	10
46	BW	62/64 (97%)	35 (56%)	20 (32%)	7 (11%)	0	10
47	BX	36/38 (95%)	23 (64%)	8 (22%)	5 (14%)	0	6
48	BY	207/209 (99%)	113 (55%)	54 (26%)	40 (19%)	0	3
49	BZ	211/213 (99%)	163 (77%)	33 (16%)	15 (7%)	1	22
50	B1	199/201 (99%)	111 (56%)	53 (27%)	35 (18%)	0	4
51	B2	176/178 (99%)	123 (70%)	26 (15%)	27 (15%)	0	5
52	B3	174/177 (98%)	149 (86%)	20 (12%)	5 (3%)	6	43
53	B4	147/149 (99%)	103 (70%)	33 (22%)	11 (8%)	1	21
54	B5	139/142 (98%)	113 (81%)	17 (12%)	9 (6%)	1	25
55	B6	138/140 (99%)	79 (57%)	41 (30%)	18 (13%)	0	7
All	All	5844/6172 (95%)	4093 (70%)	1173 (20%)	578 (10%)	2	14

5 of 578 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AB	36	LYS
4	AB	97	GLY
4	AB	169	HIS

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Mol	Chain	Res	Type
6	AD	9	LYS
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%)	164 (91%)	16 (9%)	12	44
5	AC	90/99 (91%)	81 (90%)	9 (10%)	9	38
6	AD	103/104 (99%)	87 (84%)	16 (16%)	3	22
7	AF	92/96 (96%)	84 (91%)	8 (9%)	13	45
8	AG	79/84 (94%)	75 (95%)	4 (5%)	29	66
9	AH	76/77 (99%)	73 (96%)	3 (4%)	39	72
10	AI	65/65 (100%)	61 (94%)	4 (6%)	23	60
11	AJ	74/78 (95%)	69 (93%)	5 (7%)	20	57
12	AK	48/66 (73%)	44 (92%)	4 (8%)	14	49
13	AL	70/79 (89%)	59 (84%)	11 (16%)	3	21
14	AN	65/66 (98%)	59 (91%)	6 (9%)	11	43
15	AO	170/190 (90%)	158 (93%)	12 (7%)	18	55
16	AQ	44/61 (72%)	40 (91%)	4 (9%)	12	43
17	AR	172/173 (99%)	156 (91%)	16 (9%)	11	42
18	AS	113/119 (95%)	98 (87%)	15 (13%)	5	28
19	AT	87/116 (75%)	77 (88%)	10 (12%)	7	32
20	AU	123/147 (84%)	108 (88%)	15 (12%)	6	31
21	AV	104/105 (99%)	98 (94%)	6 (6%)	25	61
22	AW	105/107 (98%)	98 (93%)	7 (7%)	20	57
23	AX	86/90 (96%)	78 (91%)	8 (9%)	11	42
26	BC	78/78 (100%)	74 (95%)	4 (5%)	29	66
27	BD	102/104 (98%)	98 (96%)	4 (4%)	39	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	BE	103/103 (100%)	84 (82%)	19 (18%)	2	14
29	BF	109/109 (100%)	95 (87%)	14 (13%)	5	29
30	BG	103/103 (100%)	90 (87%)	13 (13%)	5	29
31	BH	87/87 (100%)	81 (93%)	6 (7%)	19	56
32	BI	99/100 (99%)	96 (97%)	3 (3%)	48	77
33	BJ	89/90 (99%)	78 (88%)	11 (12%)	6	30
34	BK	84/84 (100%)	73 (87%)	11 (13%)	5	28
35	BL	93/93 (100%)	83 (89%)	10 (11%)	8	35
36	BM	83/83 (100%)	69 (83%)	14 (17%)	2	18
37	BN	213/215 (99%)	189 (89%)	24 (11%)	7	33
38	BO	83/84 (99%)	76 (92%)	7 (8%)	14	48
39	BP	62/63 (98%)	55 (89%)	7 (11%)	7	33
40	BQ	55/55 (100%)	47 (86%)	8 (14%)	4	24
41	BR	48/49 (98%)	46 (96%)	2 (4%)	36	70
42	BS	62/62 (100%)	58 (94%)	4 (6%)	21	58
43	BT	47/48 (98%)	35 (74%)	12 (26%)	1	6
44	BU	48/48 (100%)	45 (94%)	3 (6%)	22	59
45	BV	38/38 (100%)	34 (90%)	4 (10%)	8	36
46	BW	51/51 (100%)	43 (84%)	8 (16%)	3	21
47	BX	34/34 (100%)	30 (88%)	4 (12%)	6	32
48	BY	164/164 (100%)	145 (88%)	19 (12%)	7	32
49	BZ	187/187 (100%)	174 (93%)	13 (7%)	19	56
50	B1	165/165 (100%)	147 (89%)	18 (11%)	8	35
51	B2	149/149 (100%)	130 (87%)	19 (13%)	5	29
52	B3	137/138 (99%)	125 (91%)	12 (9%)	12	45
53	B4	114/114 (100%)	104 (91%)	10 (9%)	12	45
54	B5	109/110 (99%)	102 (94%)	7 (6%)	22	58
55	B6	114/114 (100%)	107 (94%)	7 (6%)	23	60
All	All	4856/5043 (96%)	4380 (90%)	476 (10%)	14	39

5 of 476 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	BF	95	LEU
35	BL	38	TYR
51	B2	177	ARG
30	BG	10	LEU
32	BI	99	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
23	AX	58	ASN
31	BH	34	HIS
48	BY	148	GLN
27	BD	5	GLN
33	BJ	36	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	75/76 (98%)	20 (26%)	8 (10%)
1	AE	75/76 (98%)	11 (14%)	1 (1%)
1	AP	74/76 (97%)	15 (20%)	6 (8%)
2	AM	20/20 (100%)	9 (45%)	7 (35%)
24	BA	116/117 (99%)	37 (31%)	11 (9%)
25	BB	2901/2903 (99%)	1516 (52%)	511 (17%)
3	A1	1529/1530 (99%)	753 (49%)	280 (18%)
All	All	4790/4798 (99%)	2361 (49%)	824 (17%)

5 of 2361 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	C
1	AA	3	G
1	AA	10	G
1	AA	13	C
1	AA	17	U

5 of 824 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	BB	444	C
25	BB	899	A

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Mol	Chain	Res	Type
25	BB	2521	C
25	BB	475	C
25	BB	683	U

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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
1	AP	1
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	3.50
1	AP	74:C	O3'	75:C	P	1.08