



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 12:25 pm GMT

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/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.

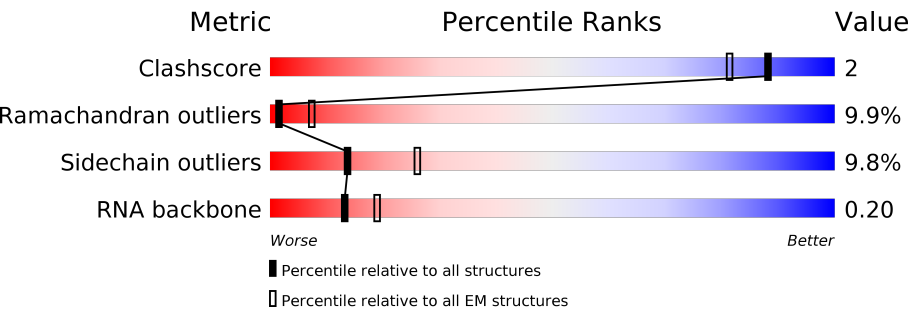
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

1 Overall quality at a glance i

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.












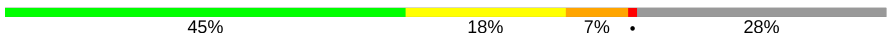







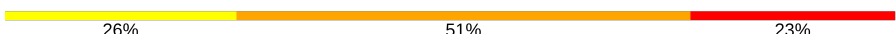







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026
RNA backbone	3398	335

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 <=5%

Mol	Chain	Length	Quality of chain
1	AA	76	11% 57% 32% .
1	AE	76	30% 50% 20%
1	AP	76	21% 47% 30% .
2	AM	20	30% 35% 35%
3	A1	1530	18% 47% 36%
4	AB	241	69% 17% . 10%
5	AC	129	66% 22% . . 9%
6	AD	124	59% 30% 9% . .

























Continued on next page...

Continued from previous page...

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	

Continued on next page...

Continued from previous page...

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	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		

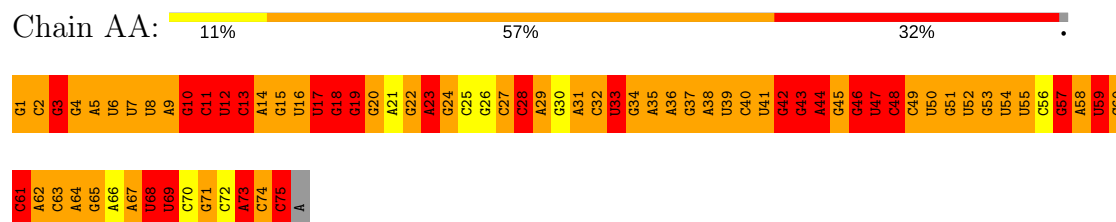
- Molecule 55 is a protein called 50S ribosomal protein L13.

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

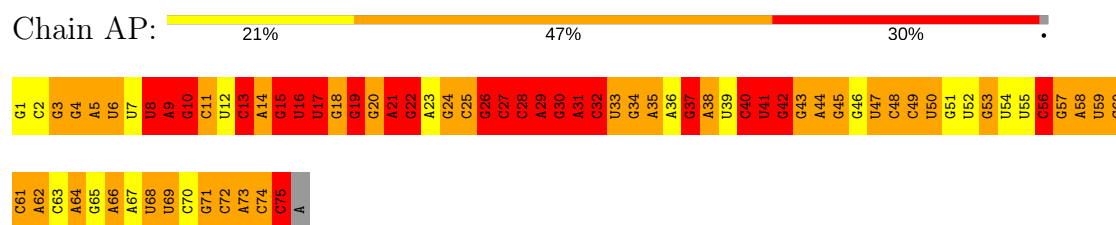
3 Residue-property plots

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.

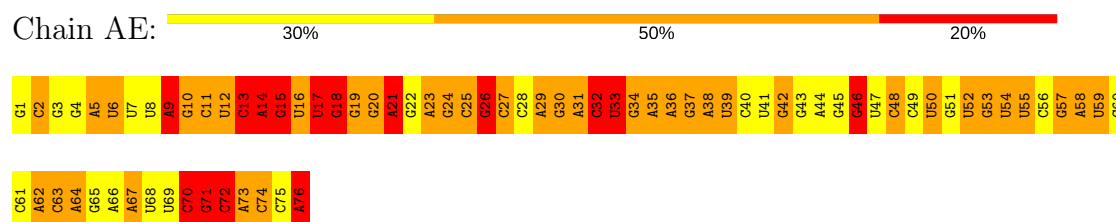
- Molecule 1: A/T, P and E-site tRNAs



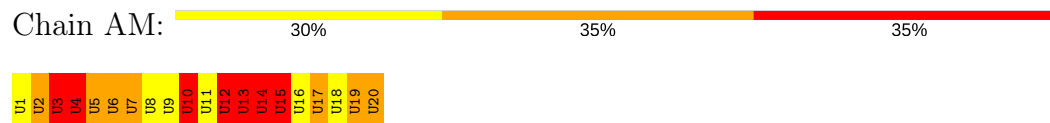
- Molecule 1: A/T, P and E-site tRNAs



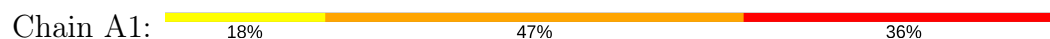
- Molecule 1: A/T, P and E-site tRNAs



- Molecule 2: mRNA model



- Molecule 3: 16S rRNA



U985	G966	A846	G785	G725	A665	U605	C545	U485	G425	U365	G305	U245	U185	U125	A65	U5
G967	A847	G847	G786	G726	G666	G606	A546	U486	G426	U366	A306	A346	C186	U126	A66	G6
A968	G848	G848	G787	G727	G667	A607	A547	U487	U427	U367	G307	A247	G187	G127	A67	A7
A969	G849	G849	G788	A728	G668	A608	G548	C488	G428	U368	A308	C248	C188	G128	G68	G8
C910	U850	G849	A790	G730	G670	U610	G550	C490	U430	C370	G310	A250	A190	A130	U70	A10
U911	G851	G851	G791	G731	G671	C511	U551	C491	A431	A371	C311	G251	G191	A131	A71	G11
C912	G852	G852	A792	G732	U672	C512	U552	C492	A432	C372	C312	U252	A192	A132	A72	U12
G913	G853	G853	G793	G733	A673	C513	A553	C493	G433	A373	A313	A253	C193	A133	C73	U13
A914	U854	G854	A794	G734	G674	C514	A554	C494	U434	A374	C314	G254	C194	G134	A74	U14
G915	U855	G855	G795	C735	A675	G515	U555	C495	A435	U375	A315	G255	A195	C135	G75	G15
U916	C856	G856	G796	C736	A676	G516	C556	C496	C436	C376	C316	U256	A196	C136	G76	A16
G917	C857	G857	G797	C737	U677	G517	G557	C497	U437	G377	U317	G257	A197	U137	A77	U17
A918	G858	G858	U798	C738	U678	C518	G558	C498	U438	G378	G318	G258	G198	G138	A78	C18
G919	G859	G859	G799	C739	U679	U519	A559	C499	U439	G379	G319	G259	A199	A139	G79	A19
C980	U860	G860	U800	U740	C680	C520	G560	C500	C440	G380	A320	G260	G200	U140	A80	U20
U921	G861	G861	G801	G741	A681	C521	U561	C501	A441	C381	A321	U261	G201	G141	A81	G21
G922	C862	G862	A802	G742	G682	A622	U562	C502	G442	A382	C322	A262	G202	G142	G82	G22
A923	U863	G863	G803	A743	G683	C523	A563	C503	G443	A383	U323	A263	G203	A143	C83	C23
C984	C924	A864	U804	C744	U684	C524	C564	C504	G444	C384	G324	G264	G204	G144	U84	U24
G925	A865	G865	C805	G745	G685	U625	U565	C505	G445	C385	A325	G265	A205	G145	U85	C25
U926	C866	G866	C806	A746	U686	G626	G566	C506	G446	C386	G326	G266	G206	G146	G86	A26
G927	G867	G867	A807	A747	A687	G627	G567	C507	G447	U387	A327	C267	G207	G147	C87	G27
C988	C868	G868	C808	G748	G688	G628	C568	C508	A448	C388	C328	U268	U208	G148	U88	A28
U929	G869	G869	G809	A749	C689	A629	C569	C509	G449	A389	C329	C269	U209	A149	U89	U29
C990	U870	G870	C910	C750	G690	A630	G570	A510	G450	U390	C330	A270	G210	U150	C90	U30
U931	U871	G871	C911	U751	G691	C631	U571	C511	A451	C391	G331	C271	G211	A151	U91	G31
G932	A872	G872	G812	G752	U692	U632	A572	U512	A452	C392	G332	C272	G212	A152	U92	A32
C933	C873	G873	U813	A753	G693	G633	A573	C513	G453	C393	U333	U273	G213	C153	U93	A33
A934	C874	G874	A914	C754	A694	C634	A574	C514	G454	C394	C334	A274	C214	U154	G94	C34
G935	U875	A895	A915	G755	A695	A635	G575	C515	G455	C395	C335	G275	C215	A155	C95	C35
A936	C876	G876	A916	C756	A696	U636	C576	U516	A456	C396	A336	G276	U216	C156	U96	C36
U937	G877	G877	C917	U757	U697	C637	G577	C517	G457	A397	G337	C277	G217	U157	G97	U37
C938	A878	G878	G818	C758	U698	G638	C578	C518	U458	U398	A338	G278	U218	G158	A98	G38
U939	C879	G879	A919	A759	C699	G639	A579	C519	A459	G399	C339	A279	U219	C159	C99	G39
C940	C880	G880	U820	G760	G700	A640	C860	C520	A460	C400	U340	C280	G220	A160	G100	C40
U941	G881	G881	G821	G761	U701	A641	G861	G521	A461	C401	C341	G281	C221	A161	A101	G41
G942	C882	G882	C822	G762	A702	A642	C582	C522	G462	C402	C342	U282	G222	A162	G102	G42
C943	C883	G883	G823	G763	G703	C643	A583	A523	U463	C403	U343	U283	C223	C163	G103	C43
U944	U884	G884	G824	C764	A704	U644	G584	C524	U464	U404	A344	G284	U224	G164	G104	A44
G945	A885	G885	A825	G765	G705	G645	G585	C525	A465	U405	C345	C285	C225	G165	G105	C45
A946	C886	G886	C826	A766	A706	G646	C866	C526	A466	C406	G346	C286	G226	U166	C106	C46
U1007	G887	G887	U827	A767	U707	C647	G867	C527	U467	U407	G347	U287	G227	A167	G107	C47
C948	C888	G888	G828	G768	C708	A648	G588	C528	A468	A408	C348	A288	A228	G168	G108	C48
U949	A889	G889	G829	G769	U709	A649	U589	C529	C469	U409	A349	G289	U229	C168	A109	A49
U1010	G890	G890	G830	C770	G710	G650	U590	C530	C470	G410	C350	C290	G230	U170	C110	A50
C1011	U891	G891	A831	G771	G711	C651	U591	U531	U471	A411	C351	U291	U231	A171	G111	A51
U952	A892	G892	G832	U772	A712	U652	C592	A532	U472	A412	C352	G292	G232	A172	G112	C52
G1013	C893	G893	G833	G773	G713	U653	U593	A533	U473	G413	C353	G293	C233	U173	G113	A53
A1014	G894	G894	U834	C774	G714	G654	U594	U534	C474	A414	C354	U294	C234	A174	C114	C54
U1015	U895	G895	U835	G775	A715	A655	A595	A535	C475	A415	C355	C295	C235	G175	G115	A55
A1016	C896	G896	G836	G776	U716	G656	G596	C536	U476	G416	A356	U296	A236	C176	A116	C56
U1017	U897	C897	U837	A777	U717	U657	G597	G537	C477	G417	G357	G297	G237	G177	G117	G57
A958	G898	G898	G838	G778	A718	C558	U898	C538	A478	C418	U358	A298	A238	C178	U118	C58
U959	C899	G899	C839	C779	U719	U659	C599	C539	U479	C419	G359	G299	G239	A179	A119	A59
U1020	A900	G900	C940	G780	C720	C660	A600	A540	U480	U420	C360	A300	G240	A180	A120	A60
C1021	G901	A901	C941	A781	G721	G661	G601	G541	G481	U421	C361	G301	G241	A181	U121	G61
U1022	U962	G902	U942	A782	U662	U602	A602	C542	A482	C422	C362	G302	G242	A182	G122	U62
C1023	G963	G903	U943	G783	U723	U663	U603	U543	C483	G423	A363	A303	G243	C183	U123	C63
U1024	A964	G964	C944	A784	C724	G664	C604	C544	C484	G424	C364	A304	G244	C184	C124	G64

U1025	G1026	U1085	U1086	A1145	U1205	C1265	C1325	G1385	U1445	G1505
G1027	C1028	U1087	G1088	A1146	G1206	G1266	U1326	G1386	A1446	U1506
C1029	U1030	C1089	G1089	A1147	G1207	G1267	C1327	G1387	A1447	U1507
C1031	U1091	G1090	U1091	U1148	C1208	G1268	C1328	C1388	A1448	A1508
G1032	A1092	U1092	A1092	C1149	C1209	A1269	A1329	C1389	C1449	C1509
G1033	A1093	G1093	A1093	A1150	C1210	G1270	U1330	U1390	U1450	C1510
G1034	U1094	G1094	U1094	A1151	U1211	A1271	G1331	U1391	U1451	G1511
A1035	G1095	G1095	A1095	A1152	U1212	G1272	A1332	C1392	C1452	U1512
A1036	C1096	G1096	C1096	G1153	U1213	C1273	A1333	U1393	G1453	A1513
C1037	U1097	C1097	U1097	G1154	C1214	A1274	U1334	C1394	G1454	G1514
C1038	C1098	C1098	C1098	G1155	G1215	G1275	U1335	C1395	G1455	G1515
G1039	U1099	C1099	U1099	G1156	A1216	G1276	C1336	A1396	A1456	G1516
U1040	C1099	C1099	C1099	A1157	C1217	C1277	G1337	C1397	G1457	G1517
U1041	A1101	C1101	A1101	C1158	C1218	G1278	G1338	A1398	G1458	A1518
A1042	U1102	G1102	U1102	U1159	A1219	U1279	A1339	C1399	G1459	A1519
G1043	G1103	C1103	G1103	G1160	U1220	A1280	A1340	C1400	C1460	C1520
A1044	C1104	G1104	C1104	C1161	G1221	C1281	U1341	G1401	G1461	U1521
U1045	G1105	A1105	U1105	C1162	C1222	C1282	C1342	C1402	C1462	C1522
A1046	U1106	G1106	U1106	G1163	G1223	U1283	G1343	C1403	C1463	G1523
G1047	C1107	G1107	C1107	G1164	U1224	C1284	C1344	C1404	U1464	C1524
U1048	G1108	C1108	G1108	U1165	A1225	A1285	U1345	G1405	A1465	G1525
U1049	U1109	C1109	U1109	A1166	C1226	U1286	A1346	U1406	C1466	U1526
G1050	A1110	C1110	A1110	A1167	G1227	A1287	G1347	C1407	C1467	G1527
C1051	C1111	C1111	C1111	U1168	C1228	A1288	U1348	A1408	A1468	U1528
G1052	C1112	C1112	C1112	A1169	U1229	A1289	A1349	C1409	C1469	G1529
C1053	C1113	C1113	C1113	A1170	C1230	G1290	A1350	A1410	U1470	C1530
C1054	U1114	C1114	U1114	C1171	G1231	U1291	C1351	C1411	U1471	A1531
A1055	U1115	U1115	U1115	U1172	U1232	C1292	C1352	C1412	U1472	U1532
U1056	U1116	U1116	U1116	U1173	C1233	C1293	C1353	C1413	C1473	C1533
G1057	C1117	C1117	C1117	C1174	G1234	G1294	U1354	U1414	U1474	A1534
G1058	U1118	U1118	U1118	G1175	U1235	U1295	C1355	G1415	G1475	
C1059	C1119	C1119	C1119	A1176	A1236	C1296	C1356	G1416	A1476	
U1060	U1120	C1120	U1120	U1177	C1237	G1297	A1357	G1417	U1477	
G1061	U1121	U1121	U1121	U1178	U1238	U1298	U1358	U1418	U1478	
U1062	U1122	U1122	U1122	A1179	A1239	A1299	C1359	G1419	C1479	
C1063	C1123	C1123	C1123	U1180	U1240	G1300	A1360	U1420	A1480	
G1064	G1124	G1124	G1124	G1181	G1241	U1301	G1361	G1421	U1481	
U1065	U1125	U1125	U1125	C1182	C1242	C1302	A1362	G1422	G1482	
C1066	U1126	U1126	C1066	U1183	C1243	C1303	A1363	G1423	A1483	
A1067	U1127	U1127	A1067	G1184	G1244	G1304	U1364	U1424	C1484	
G1068	C1128	C1128	G1068	G1185	C1245	G1305	C1365	U1425	U1485	
C1069	U1129	U1129	C1069	G1186	A1246	A1306	C1366	G1426	G1486	
U1070	U1130	U1130	U1070	U1187	U1247	U1307	C1367	G1427	G1487	
C1071	G1131	C1131	C1071	A1188	A1248	U1308	A1368	A1428	G1488	
G1072	C1132	C1132	G1072	U1189	C1249	G1309	C1369	A1429	G1489	
C1073	U1133	U1133	C1073	G1190	A1250	G1310	G1370	U1430	U1490	
G1074	G1134	G1134	G1074	A1191	A1251	A1311	A1371	A1431	G1491	
U1075	U1135	U1135	U1075	C1192	A1252	G1312	U1372	G1432	A1492	
U1076	C1136	C1136	U1076	G1193	G1253	U1313	G1373	A1433	A1493	
G1077	U1136	U1136	G1077	U1194	A1254	C1314	A1374	A1434	G1494	
U1078	U1137	U1137	U1078	C1195	G1255	U1315	A1375	G1435	U1495	
G1079	C1138	C1138	G1079	A1197	A1256	G1316	U1376	U1436	C1496	
U1080	U1139	U1139	U1080	U1198	C1257	C1317	A1377	A1437	G1497	
A1081	C1140	C1140	A1081	G1199	G1258	C1318	C1378	G1438	U1498	
U1082	U1200	U1200	U1082	C1259	C1260	A1319	G1379	U1439	A1499	
C1083	A1201	A1201	C1083	U1261	A1261	C1320	U1380	U1440	A1500	
G1084	U1202	U1202	G1084	C1262	C1262	U1321	U1381	A1441	C1501	
	G1142	G1142		C1263	C1263	C1322	C1382	G1442	A1502	
	G1143	G1143		G1263	G1263	C1323	C1383	C1443	A1503	
	G1144	G1144		U1264	U1264	A1324	C1384	U1444	G1504	

• Molecule 4: 30S ribosomal protein S2

Chain AB:  69% 17% 10%

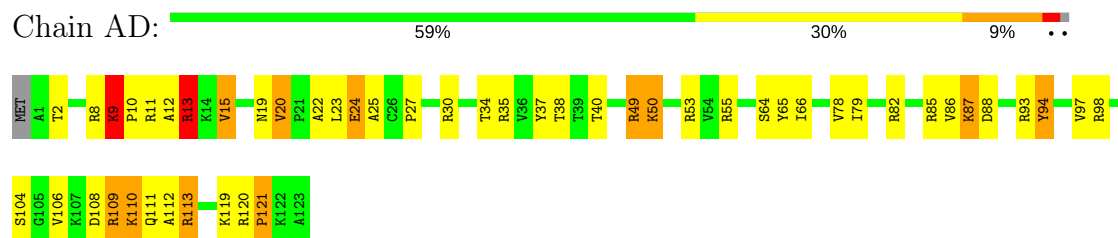
MET	ALA	THR	VAL	SER	MET	ARG	ASP	PRO	ILE	ARG	ALA	ARG	LYS	VAL	R12	I22	H23	A24	S25	I30	D35	R36	N39	A40	L41	F51	R52	G53	S54	R55	R68	V73	Y76	G77	I78	E82	G87	P88	R92	R97	N100	A101	A102	R105	T110	D111	V112			

• Molecule 5: 30S ribosomal protein S11

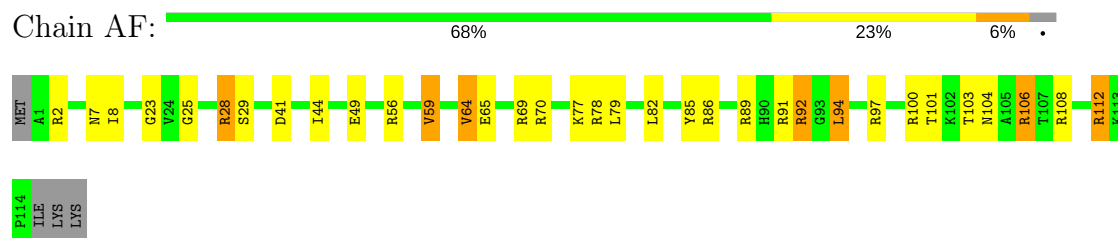
Chain AC:  66% 22% 9%

MET	ALA	LYS	ALA	PRO	ILE	ARG	ALA	ARG	LYS	ARG	VAL	R12	I22	H23	A24	S25	I30	D35	R36	N39	A40	L41	F51	R52	G53	S54	R55	R68	V73	Y76	G77	I78	E82	G87	P88	R92	R97	N100	A101	A102	R105	T110	D111	V112	
																</																													

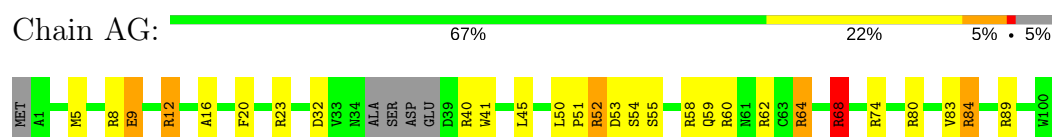
• Molecule 6: 30S ribosomal protein S12



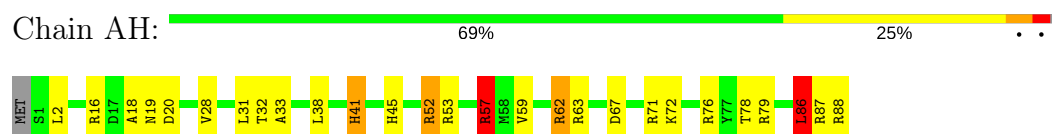
- Molecule 7: 30S ribosomal protein S13



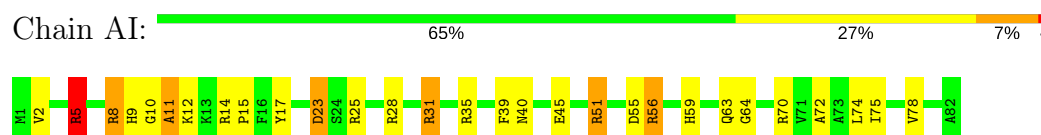
- Molecule 8: 30S ribosomal protein S14



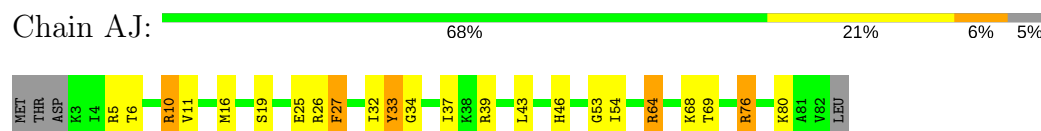
- Molecule 9: 30S ribosomal protein S15



- Molecule 10: 30S ribosomal protein S16



- Molecule 11: 30S ribosomal protein S17



- Molecule 12: 30S ribosomal protein S18

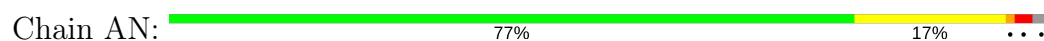




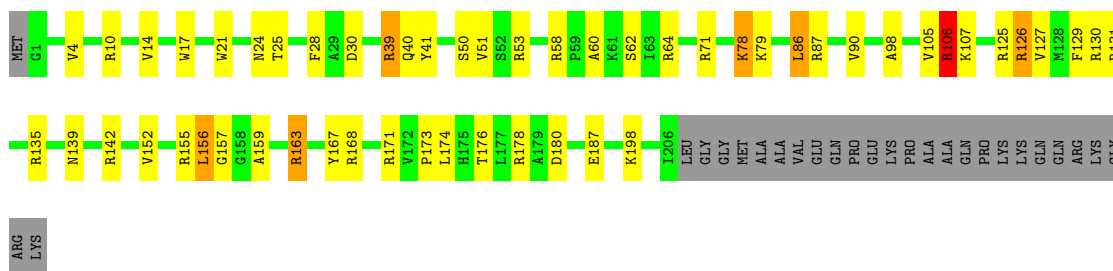
- Molecule 13: 30S ribosomal protein S19



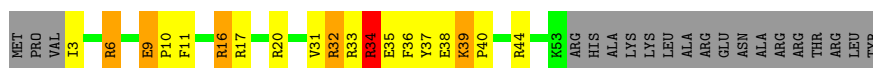
- Molecule 14: 30S ribosomal protein S20



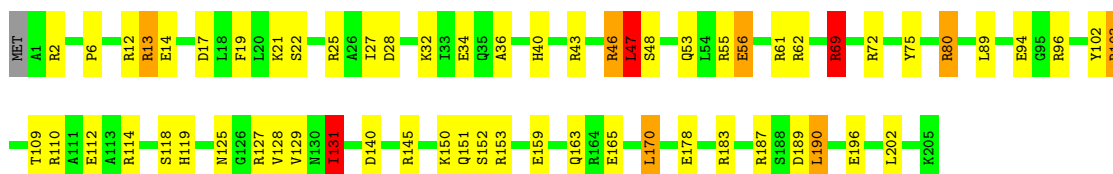
- Molecule 15: 30S ribosomal protein S3



- Molecule 16: 30S ribosomal protein S21

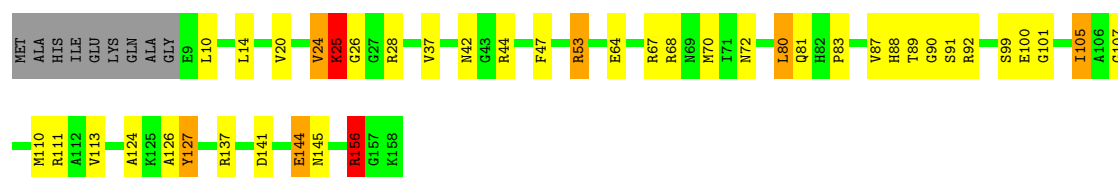


- Molecule 17: 30S ribosomal protein S4

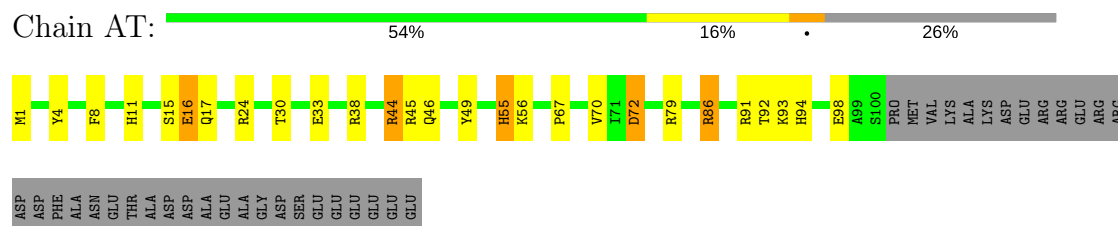


- Molecule 18: 30S ribosomal protein S5

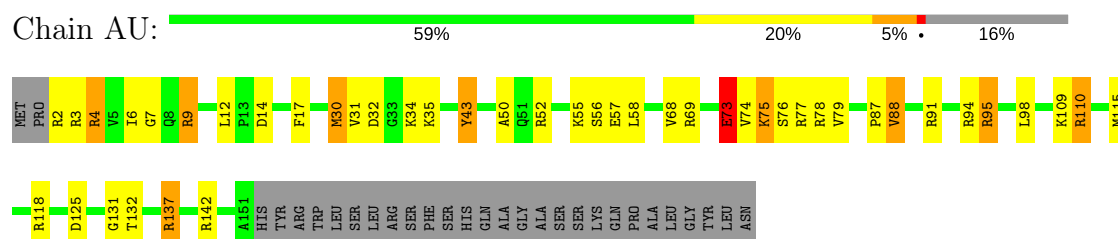




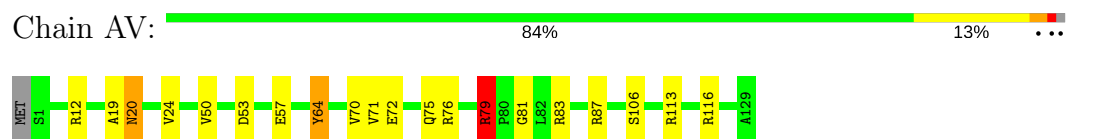
- Molecule 19: 30S ribosomal protein S6



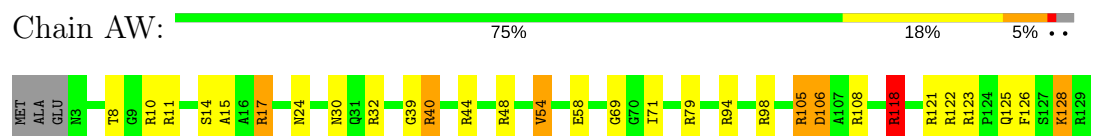
- Molecule 20: 30S ribosomal protein S7



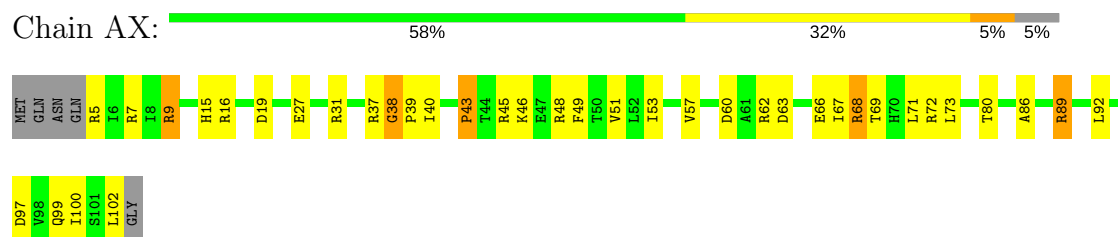
- Molecule 21: 30S ribosomal protein S8



- Molecule 22: 30S ribosomal protein S9



- Molecule 23: 30S ribosomal protein S10



- Molecule 24: 5S rRNA

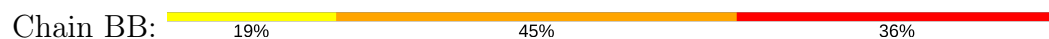
Chain BA:



G62	C63	G64	U65	A66	G67	C68	G69	C70	G71	C72	A73	U74	G75	G76	U77	A78	G79	U80	G81	U82	G83	G84	G85	G86	U87	C88	C89	C90	C91	C92	C93	A94	U95	G96	C97	G98	A99	G100	A101	G102	U103	A104	G105	G106	G107	A108	C109	C110	U111	G112	C113	A114	U115	G116	G117	C118			
G2	C3	C4	U5	G6	G7	C8	G9	G10	C11	C12	G13	U14	A15	G16	C17	G18	C19	G20	G21	U22	G23	G24	U25	C26	C27	C28	A29	C30	C31	U32	G33	A34	C35	C36	C37	C38	A39	U40	G41	C42	C43	G44	A45	A46	G47	U48	C49	A50	G51	A52	A53	G54	U55	G56	A57	A58	A59	C60	G61

• Molecule 25: 23S rRNA

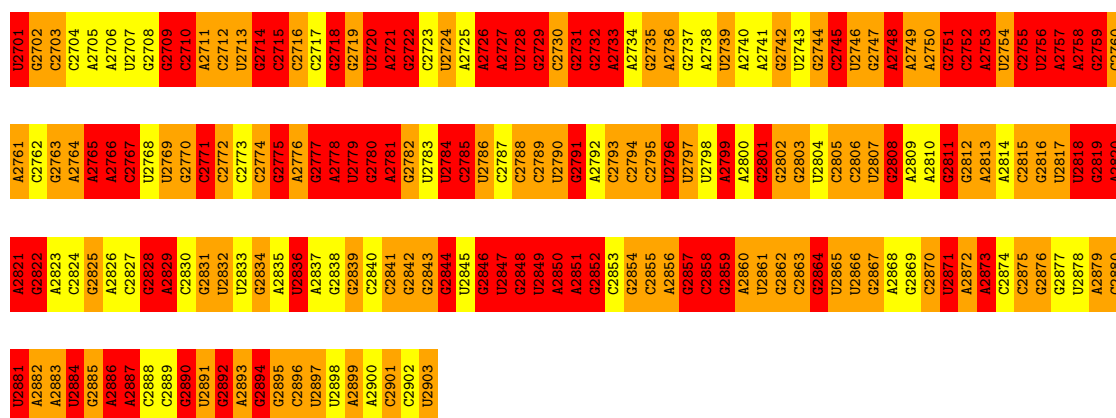
Chain BB:




A721	A661	C601	A541	G481	C421	G361	G301	A241	A181	G121	C61	G1
A722	G662	A602	C542	A482	A422	A362	C302	G242	G187	G122	C62	G2
A723	G663	A603	C543	A483	A423	A363	G303	G243	C183	G123	A63	U3
A724	G664	G604	C544	A484	G424	C364	U304	A244	C184	A124	A64	U4
G725	U665	G605	U545	C485	G425	U365	C305	G245	G185	A125	U65	A5
G726	A666	U606	U546	C486	C426	C366	U306	C246	G186	A126	C66	A6
A727	U667	U607	A547	C487	U427	G367	G307	G247	G187	A127	U67	C7
A728	A668	A608	G548	A488	A428	A368	G308	G248	C188	C128	G68	C8
G729	G669	A609	G549	C489	A429	U369	A309	C249	G189	C129	C69	G9
A730	A670	C610	C550	C490	A430	G370	A310	G250	A190	C130	G70	A10
C731	C671	C611	G551	C491	U431	A371	A311	A251	A191	A131	A71	C11
C732	C672	G612	U552	A492	A432	C372	G312	G252	C192	G132	U72	U12
G733	C673	A613	G553	C493	C433	U373	G313	C253	U193	U133	A73	A13
A734	G674	A614	U554	C494	U434	A374	C314	G254	G194	G134	A74	A14
A735	A675	U615	G555	C495	C435	G375	G315	A255	A195	U135	G75	G15
C736	A676	A616	A556	C496	C436	G376	C316	A256	A196	G136	C76	C16
A737	A677	G617	C557	A497	U437	G377	G317	C257	A197	U137	G77	G17
G738	C678	G618	U558	C498	C438	C378	C318	G258	C198	U138	U78	U18
A739	C679	G619	G559	U499	A439	G379	G319	G259	A199	U139	C79	A19
C740	G680	G620	C560	U500	C440	G380	A320	G260	U200	C140	G80	C20
U741	G681	A621	U561	A501	U441	G381	U321	G261	C201	G141	G81	A21
A742	G682	G622	U562	A502	G442	A382	A322	A262	U202	A142	U82	C22
A743	U683	C623	A563	A503	A443	C383	C323	G263	A203	C143	A83	G23
U744	G684	C624	C564	A504	C444	A384	A324	C264	A204	A144	A84	G24
A745	A685	G625	C565	A505	C445	C385	G325	A265	G205	C145	G85	U25
U746	U686	A626	U566	U506	G446	G386	G326	G266	U206	A146	G86	U26
A747	C687	G627	U567	A507	A447	U387	U327	C267	A207	C147	U87	G27
G748	U688	G628	U568	A508	U448	G388	U328	C268	C208	U148	G88	A28
A749	A689	G629	U569	C509	U449	G389	U329	C269	C209	A149	A89	U29
U750	G690	C630	C570	C510	C450	U390	A330	A270	C210	U150	U90	G30
A751	C691	A631	U571	U511	U451	A391	C331	G271	C211	C151	A91	C31
A752	C692	A632	A572	U512	A452	U392	A332	A272	G212	A152	U92	C32
A753	A693	U573	C573	U513	A453	C393	G333	G273	A213	U153	G93	C33
U754	U694	C634	A574	A514	A454	C394	C334	C274	G214	U154	A94	U34
A755	G695	C635	A575	A515	C455	U395	C335	C275	G215	A155	A95	G35
U756	C696	G636	U576	C516	C456	C396	C336	U276	A216	A156	C96	G36
G757	A697	A637	C577	C517	A457	U397	C337	G277	A217	C157	C97	C37
A758	C698	G638	G578	U518	A458	C398	U338	A278	A218	U158	G98	A38
U759	U699	U539	G579	U519	U459	U399	U339	G279	A219	G159	U99	G39
G760	G700	C640	U580	U520	A460	A400	A340	G280	G220	A160	U100	U40
A761	G701	U641	C581	U521	C461	A401	C341	C281	A221	A161	A101	C41
U762	U702	U642	A582	A522	C462	A402	A342	A282	A222	U162	U102	A42
G763	U703	A643	C583	C523	G463	U403	C343	G283	C223	C163	A103	A43
A764	G704	A644	C584	U524	U464	A404	A344	U284	U224	C164	A104	A44
C765	A705	C645	G585	U525	G465	U405	A345	G285	C225	A165	C105	A45
U766	A706	U646	A586	A526	A466	G406	A346	U286	A226	U166	C106	G46
G767	G707	G647	C587	C527	G467	G407	A347	G287	A227	A167	G107	C47
U768	U708	C648	U588	A528	G468	G408	U348	U288	C228	G168	U108	G48
A769	G709	U649	U589	A529	C469	A409	U349	G289	C229	G169	C109	A49
G770	U710	C650	A590	U530	A470	G410	U350	G290	A230	U170	G110	U50
U771	G711	G651	U591	C531	A471	G411	C351	G291	A231	U171	A111	G51
C772	U712	U652	A592	A532	A472	A412	A352	U292	G232	A172	U112	A52
U773	G713	U653	U593	C533	G473	C413	C353	U293	A233	A173	U113	A53
A774	U714	A654	U594	U534	G474	C414	A354	A294	U234	U174	U114	G54
G775	A715	A655	C595	A535	C475	C415	U355	G295	U235	G175	C115	G55
U776	A716	G656	U596	U536	G476	U416	U356	U296	C236	A176	C116	A56
C777	C717	U657	G597	U537	A477	C417	C357	G297	C237	G177	A117	C57
G778	A718	U658	U598	A538	A478	C418	U358	G298	C238	G178	A118	G58
U779	C719	G659	A599	C539	A479	U419	G359	A299	C239	C179	U119	U59
A780	U720	C660	C600	U540	A480	C420	U360	A240	C180	G120	C60	G0

G1681	G1682	G1683	G1684	G1685	G1686	G1687	G1688	G1689	G1690	G1691	G1692	G1693	G1694	G1695	G1696	G1697	G1698	G1699	A1700	A1701	G1702	G1703	C1704	A1705	C1706	G1707	G1708	G1709	G1710	G1711	G1712	G1713	G1714	G1715	G1716	A1717	G1718	G1719	G1720	G1721	A1722	G1723	G1724	G1725	C1726	C1727	G1728	G1729	G1730	G1731	C1732	G1733	G1734	A1735	G1736	G1737	G1738	A1739	G1740	
G1501	A1502	G1503	A1504	A1505	U1506	G1507	A1508	A1509	G1510	G1511	C1512	C1513	A1514	G1515	G1516	G1517	G1518	G1519	U1520	G1521	A1522	G1523	G1524	A1525	C1526	G1527	A1528	G1529	G1530	C1531	A1532	G1533	A1534	G1535	A1536	G1537	G1538	U1539	G1540	C1541	G1542	G1543	A1544	A1545	C1546	C1547	A1548	A1549	C1550	C1551	A1552	G1553	A1554	G1555	C1556	C1557	C1558	G1559	G1560	
C1561	G1562	C1563	G1564	C1565	A1566	G1567	G1568	A1569	A1570	A1571	A1572	G1573	C1574	C1575	G1576	C1577	G1578	A1579	U1580	G1581	A1582	A1583	G1584	C1585	A1586	G1587	G1588	A1589	A1590	A1591	C1592	A1593	A1594	C1595	A1596	A1597	A1598	U1599	G1600	G1601	A1602	G1603	C1604	C1605	C1606	G1607	A1608	A1609	C1610	C1611	G1612	G1613	A1614	G1615	A1616	C1617	A1618	G1619	G1620	
U1621	G1622	G1623	U1624	C1625	A1626	G1627	G1628	G1629	G1630	G1631	G1632	G1633	A1634	A1635	U1636	A1637	C1638	C1639	A1640	A1641	G1642	G1643	C1644	G1645	C1646	U1647	U1648	G1649	A1650	G1651	A1652	G1653	A1654	A1655	C1656	U1657	C1658	G1659	G1660	G1661	U1662	G1663	A1664	A1665	G1666	G1667	A1668	U1669	C1670	U1671	A1672	G1673	G1674	A1675	U1676	A1677	A1678	A1679	U1680	
G1441	U1442	A1443	G1444	G1445	C1446	C1447	G1448	G1449	G1450	G1451	G1452	A1453	C1454	A1455	G1456	U1457	G1458	G1459	U1460	G1461	C1462	G1463	G1464	G1465	U1466	U1467	G1468	A1469	A1470	G1471	C1472	G1473	C1474	G1475	G1476	A1477	G1478	G1479	C1480	G1481	G1482	G1483	U1484	U1485	U1486	U1487	C1488	C1489	A1490	G1491	G1492	C1493	A1494	A1495	C1496	U1497	C1498	U1499	G1500	
G1381	G1382	A1383	G1384	C1385	A1386	A1387	G1388	G1389	U1390	U1391	G1392	A1393	U1394	A1395	U1396	U1397	C1398	C1399	U1400	G1401	U1402	G1403	C1404	A1405	U1406	G1407	G1408	U1409	G1410	U1411	U1412	A1413	C1414	U1415	G1416	C1417	G1418	A1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	A1427	C1428	G1429	G1430	A1431	G1432	A1433	A1434	A1435	G1436	C1437	U1438	A1439	U1440	
C1321	A1322	C1323	G1324	A1325	U1326	A1327	A1328	U1329	C1330	G1331	G1332	A1333	G1334	C1335	A1336	G1337	C1338	G1339	U1340	G1341	G1342	G1343	C1344	A1345	G1346	A1347	G1348	U1349	C1350	C1351	U1352	A1353	C1354	G1355	G1356	C1357	G1358	A1359	G1360	G1361	C1362	C1363	G1364	A1365	A1366	A1367	G1368	G1369	C1370	G1371	U1372	A1373	G1374	A1375	C1376	G1377	A1378	U1379	U1380	
C1261	A1262	U1263	A1264	A1265	G1266	U1267	A1268	U1269	G1270	G1271	G1272	A1273	A1274	G1275	A1276	G1277	G1278	G1279	G1280	G1281	U1282	G1283	A1284	A1285	U1286	G1287	G1288	C1289	C1290	C1291	G1292	C1293	U1294	G1295	G1296	C1297	C1298	G1299	G1300	A1301	A1302	G1303	A1304	C1305	A1306	A1307	A1308	G1309	G1310	G1311	U1312	G1313	C1314	C1315	U1316	G1317	U1318	C1319	C1320	
U1201	G1202	U1203	A1204	A1205	G1206	C1207	U1208	U1209	G1210	C1211	G1212	A1213	A1214	G1215	A1216	U1217	G1218	U1219	G1220	C1221	U1222	G1223	U1224	G1225	A1226	G1227	G1228	C1229	A1230	U1231	G1232	C1233	U1234	G1235	G1236	A1237	G1238	G1239	U1240	A1241	U1242	G1243	A1244	C1245	A1246	U1247	G1248	U1249	G1250	C1251	G1252	G1253	A1254	U1255	G1256	C1257	U1258	U1259	A1260	
U1141	A1142	A1143	A1144	C1145	G1146	A1147	U1148	G1149	C1150	A1151	C1152	C1153	G1154	A1155	A1156	G1157	G1158	U1159	G1160	C1161	G1162	G1163	C1164	A1165	G1166	G1167	G1168	C1169	G1170	G1171	C1172	U1173	U1174	A1175	U1176	G1177	C1178	G1179	U1180	U1181	U1182	U1183	U1184	G1185	G1186	G1187	U1188	U1189	G1190	G1191	G1192	G1193	A1194	G1195	C1196	G1197	U1198	G1199	U1200	
U1081	U1082	U1083	A1084	A1085	A1086	G1087	A1088	A1089	A1090	G1091	C1092	U1093	U1094	A1095	A1096	U1097	A1098	A1099	C1100	U1101	C1102	A1103	C1104	U1105	G1106	G1107	U1108	C1109	G1110	A1111	G1112	U1113	C1114	G1115	G1116	C1117	U1118	U1119	G1120	C1121	G1122	C1123	G1124	G1125	A1126	A1127	G1128	A1129	U1130	G1131	U1132	A1133	A1134	G1135	G1136	G1137	G1138	C1139	C1140	
A1021	G1022	U1023	G1024	A1025	G1026	A1027	A1028	A1029	C1030	G1031	A1032	U1033	G1034	U1035	A1036	G1037	G1038	A1039	C1100	C1101	G1042	C1043	A1044	C1045	A1046	G1047	A1048	C1049	A1050	G1051	C1052	G1053	A1054	G1055	G1056	A1057	U1058	G1059	U1060	A1061	U1062	G1063	C1064	U1065	U1066	A1067	G1068	A1069	U1070	G1071	G1072	A1073	G1074	C1075	C1076	A1077	U1078	A1080		
C961	G962	U963	C964	A965	G966	U967	C968	A969	U970	G971	A972	A973	G974	A975	G976	G977	G978	A979	A980	C921	A981	G982	A983	A984	C985	C986	G987	A988	G989	A990	C991	C992	G993	C994	A995	G996	G997	C998	U999	A1000	A1001	G1002	G1003	U1004	C1005	C1006	A1007	A1008	A1009	U1010	G1011	G1012	C1013	A1014	U1015	G1016	G1017	U1018	U1019	A1020
C901	C902	C903	A904	A905	U906	G907	C908	C909	A910	A911	C912	U913	G914	C915	G916	A917	A918	U919	A920	C922	G923	A924	A925	G926	A927	U928	G929	A930	U931	U932	A933	U934	C935	A936	C937	G938	G939	G940	A941	G942	A943	C944	A945	C946	C947	C948	G949	G950	C951	G952	G953	A954	U955	G956	C957	U958	A959	A960		
G841	U842	G843	A844	A845	U846	U847	C848	A849	U850	C851	U852	C853	C854	G855	G856	G857	G858	G859	U860	A861	G862	A863	G864	C865	A866	C867	U868	G869	U870	U871	U872	C873	G874	C875	C876	A877	A878	G879	G880	G881	G882	G883	U884	C885	A886	U887	C888	C889	C890	G891	A892	A893	U894	U895	A896	C897	C898	U899	A900	
A781	A782	A783	G784	G785	C786	C787	A788	A789	U790	C791	U792	A793	A794	C795	C796	G797	G798	G799	U800	A801	G802	A803	A804	C805	A806	C807	U808	G809	U810	U811	U812	U813	C814	C815	C816	C817	A818	A819	G820	A821	G822	G823	U824	A825	U826	U827	C828	A829	G830	G831	U832	A833	U834	U835	A836	C837	C838	U839	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	G2700													
C2581	C2582	C2583	C2584	C2585	C2586	C2587	C2588	C2589	C2590	C2591	C2592	C2593	C2594	C2595	C2596	C2597	C2598	C2599	C2600	C2601	C2602	C2603	C2604	C2605	C2606	C2607	C2608	C2609	C2610	C2611	C2612	C2613	C2614	C2615	C2616	C2617	C2618	C2619	C2620	G2621	G2622	G2623	G2624	G2625	G2626	G2627	G2628	G2629	G2630	G2631	G2632	G2633	G2634	G2635	G2636	G2637	G2638	G2639	G2640			
A2461	A2462	A2463	A2464	A2465	A2466	A2467	A2468	A2469	A2470	A2471	A2472	A2473	A2474	A2475	A2476	A2477	A2478	A2479	A2480	A2481	A2482	A2483	A2484	A2485	A2486	A2487	A2488	A2489	A2490	A2491	A2492	A2493	A2494	A2495	A2496	A2497	A2498	A2499	A2500	A2501	A2502	A2503	A2504	A2505	A2506	A2507	A2508	A2509	A2510	A2511	A2512	A2513	A2514	A2515	A2516	A2517	A2518	A2519	A2520			
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			
A2281	A2282	A2283	A2284	A2285	A2286	A2287	A2288	A2289	A2290	A2291	A2292	A2293	A2294	A2295	A2296	A2297	A2298	A2299	A2300	C2301	C2302	C2303	C2304	C2305	C2306	C2307	C2308	A2309	A2310	A2311	A2312	C2313	A2314	C2315	C2316	C2317	A2318	A2319	A2320	U2321	U2322	C2323	C2324	C2325	C2326	A2327	A2328	A2329	C2330	C2331	C2332	C2333	A2334	U2335	C2336	C2337	C2338	C2339	C2340			
G2221	G2222	G2223	G2224	A2225	C2226	A2227	G2228	G2229	G2230	C2231	C2232	C2233	G2234	G2235	C2236	G2237	C2238	G2239	U2240	C2241	G2242	C2243	U2244	U2245	G2246	A2247	C2248	C2249	G2250	C2251	C2252	C2253	G2254	C2255	C2256	C2257	C2258	A2259	C2260	C2261	U2262	C2263	G2264	C2265	C2266	A2267	C2268	C2269	C2270	C2271	C2272	C2273	C2274	C2275	C2276	C2277	C2278	C2279	C2280			
C2161	C2162	C2163	C2164	C2165	C2166	C2167	C2168	C2169	C2170	A2171	C2172	C2173	C2174	C2175	C2176	C2177	C2178	C2179	U2180	C2181	U2182	C2183	A2184	C2185	C2186	C2187	C2188	C2189	C2190	C2191	C2192	C2193	C2194	C2195	C2196	C2197	C2198	A2199	C2200	C2201	C2202	C2203	C2204	C2205	C2206	C2207	C2208	C2209	C2210	C2211	C2212	C2213	C2214	C2215	C2216	C2217	C2218	C2219	C2220			
A201	A202	C2003	C2004	C2005	U2006	C2007	C2008	C2009	C2010	C2011	C2012	C2013	C2014	C2015	C2016	C2017	C2018	C2019	C2020	C2021	C2022	C2023	C2024	C2025	C2026	C2027	C2028	C2029	C2030	C2031	C2032	C2033	C2034	C2035	C2036	C2037	C2038	C2039	C2040	C2041	C2042	C2043	C2044	C2045	C2046	C2047	C2048	C2049	C2050	C2051	C2052	C2053	C2054	C2055	C2056	C2057	C2058	C2059	C2060			
G1921	G1922	G1923	C1924	C1925	U1926	C1927	A1928	G1929	G1930	C1931	C1932	C1933	C1934	C1935	C1936	C1937	C1938	C1939	U1940	C1941	C1942	C2003	C2004	U1944	C1945	C1946	C1947	C1948	C2008	C1949	C2009	C2010	C2011	C1952	C1953	C1954	C1955	C1956	C1957	C1958	C1959	C1960	C1961	C1962	C1963	C1964	C1965	C1966	C1967	C1968	C1969	C1970	U1971	C1972	C1973	C1974	C1975	C1976	C1977	C1978	C1979	G1980
G1861	G1862	G1863	C1864	U1865	C1866	C1867	C1868	G1869	C1870	C1871	C1872	C1873	C1874	C1875	C1876	C1877	C1878	C1879	U1880	C1881	C1882	C1883	C1884	C1885	C1886	C1887	C1888	C2008	C1889	C1890	C1891	C1892	C1893	C1894	C1895	C1896	C1897	C1898	C1899	C1900	C1901	C1902	C1903	C1904	C1905	C1906	C1907	C1908	C1909	C1910	U1911	C1912	C1913	C1914	C1915	C1916	C1917	C1918	C1919	C1920		
G1801	A1802	A1803	C1804	A1805	C1806	C1807	C1808	C1809	A1810	C1811	C1812	C1813	C1814	C1815	C1816	C1817	U1818	C1819	U1820	C1821	C1822	C1823	C1824	U1825	C1826	C1827	C1828	C1829	C1830	C1831	C1832	C1833	C1834	C1835	C1836	C1837	C1838	C1839	A1840	U1841	C1842	C1843	C1844	C1845	C1846	C1847	C1848	C1849	U1850	U1851	C1852	C1853	C1854	C1855	U1856	C1857	C1858	C1859	C1860			
G1741	U1742	G1743	A1744	A1745	A1746	U1747	C1748	A1749	G1750	U1751	C1752	C1753	A1754	A1755	C1756	A1757	U1758	A1759	C1760	C1761	A1762	C1763	C1764	U1765	C1766	C1767	C1768	C1769	C1770	C1771	A1772	A1773	C1774	C1775	C1776	C1777	U1778	U1779	A1780	U1781	U1782	C1783	A1784	A1785	C1786	A1787	C1788	A1789	C1790	A1791	C1792	C1793	C1794	A1795	C1796	C1797	U1798	C1799	G1800			



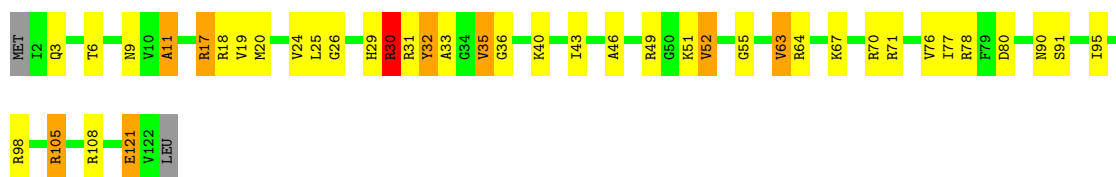
- Molecule 26: 50S ribosomal protein L25

Chain BC:  76% 21% •



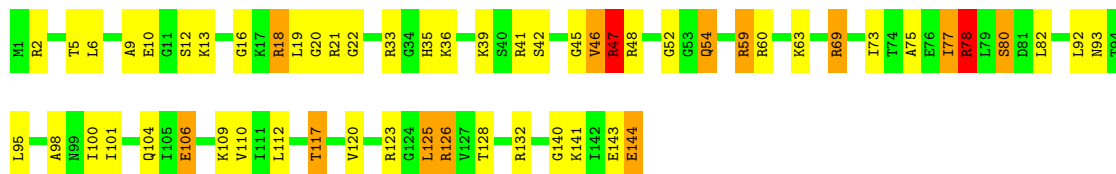
- Molecule 27: 50S ribosomal protein L14

Chain BD:  65% 26% 7% ••



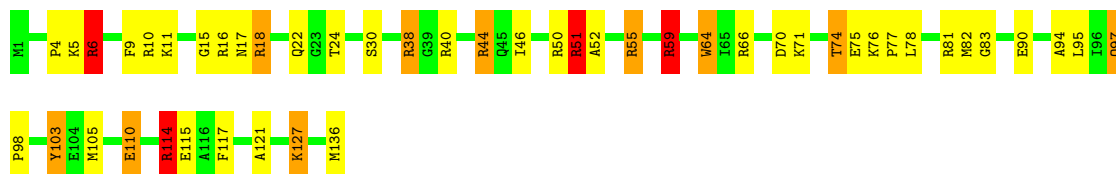
- Molecule 28: 50S ribosomal protein L15

Chain BE:  60% 30% 8% •

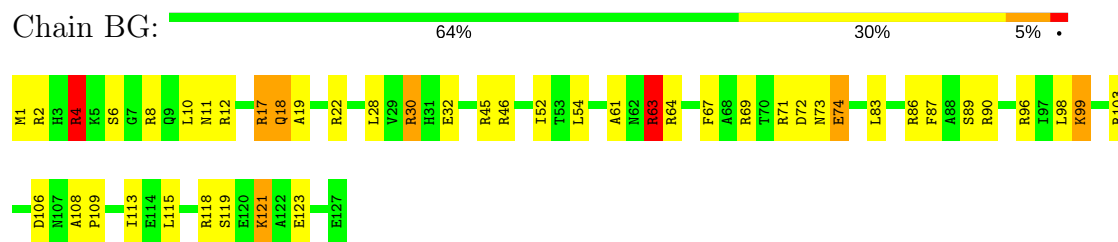


- Molecule 29: 50S ribosomal protein L16

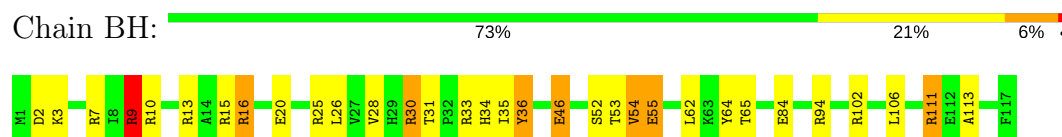
Chain BF:  65% 25% 7% •



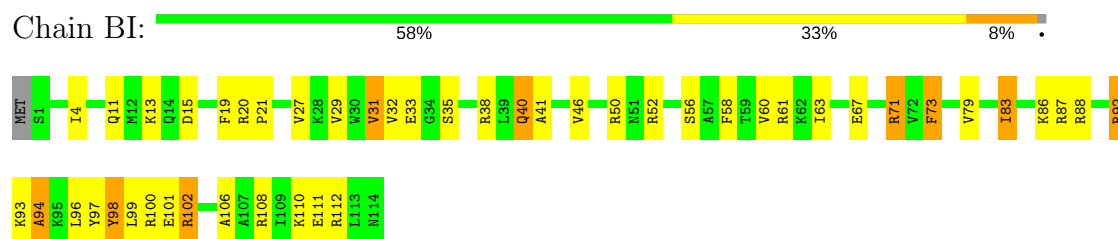
- Molecule 30: 50S ribosomal protein L17



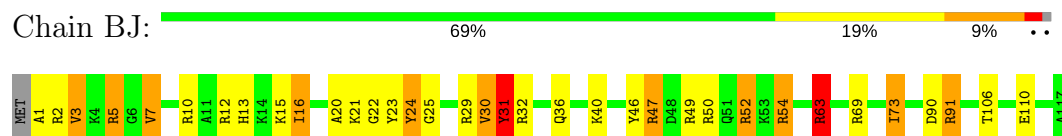
- Molecule 31: 50S ribosomal protein L18



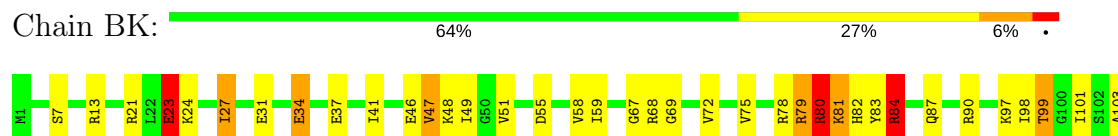
- Molecule 32: 50S ribosomal protein L19



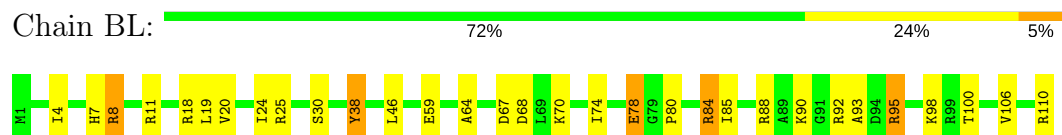
- Molecule 33: 50S ribosomal protein L20



- Molecule 34: 50S ribosomal protein L21

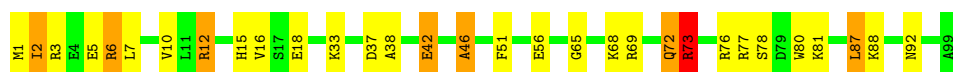


- Molecule 35: 50S ribosomal protein L22



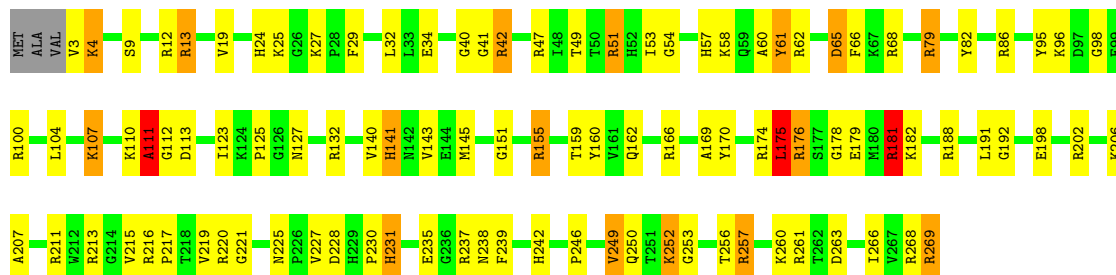
- Molecule 36: 50S ribosomal protein L23





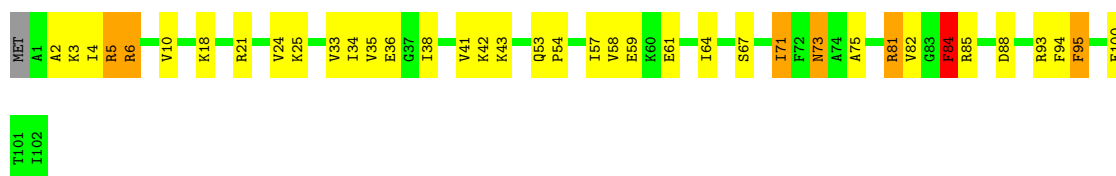
• Molecule 37: 50S ribosomal protein L2

Chain BN: 61% 31% 6% ..



• Molecule 38: 50S ribosomal protein L24

Chain BO: 62% 30% 6% ..



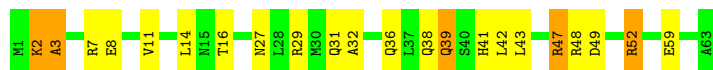
• Molecule 39: 50S ribosomal protein L27

Chain BP: 59% 34% 5% ..



• Molecule 40: 50S ribosomal protein L29

Chain BQ: 65% 27% 8%



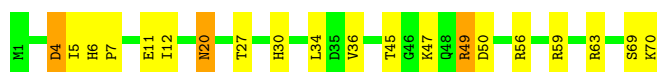
• Molecule 41: 50S ribosomal protein L30

Chain BR: 71% 20% 5% ..



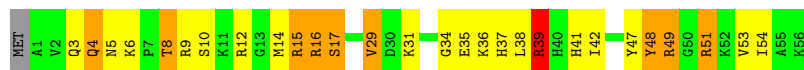
• Molecule 42: 50S ribosomal protein L31

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%



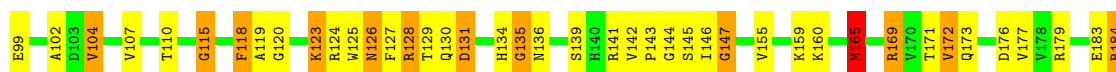
- Molecule 47: 50S ribosomal protein L36

Chain BX: 68% 18% 11% .

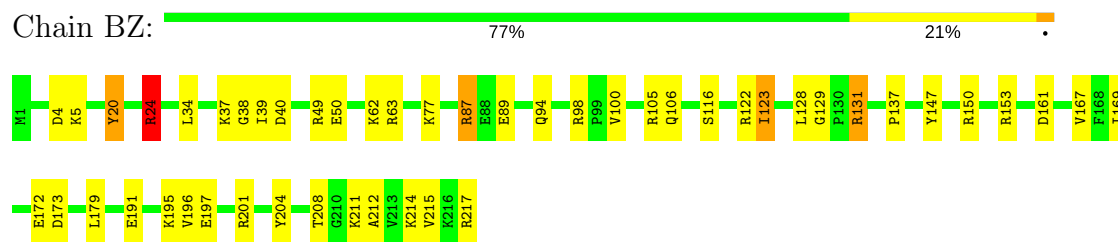


- Molecule 48: 50S ribosomal protein L3

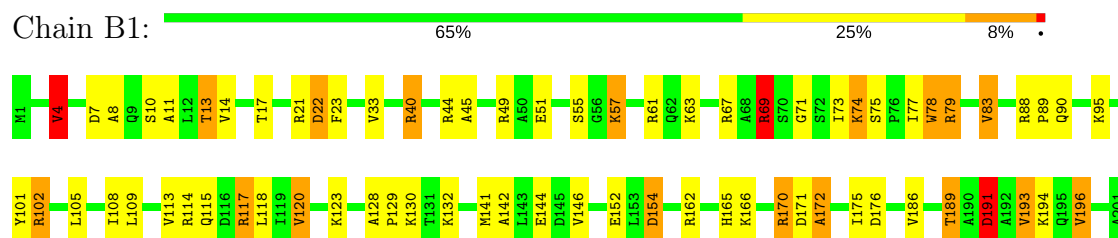
Chain BY: 61% 29% 9% .



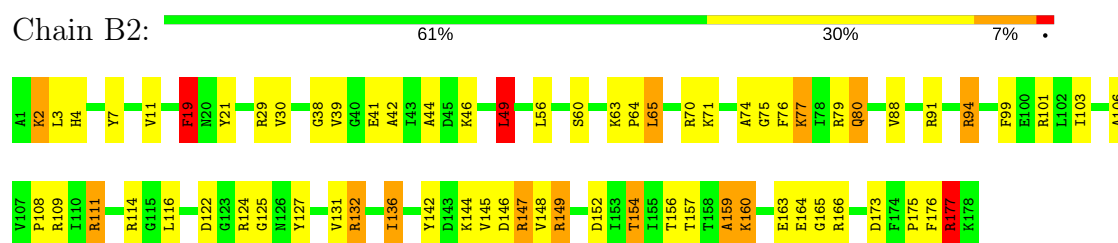
- Molecule 49: 50S ribosomal protein L1P



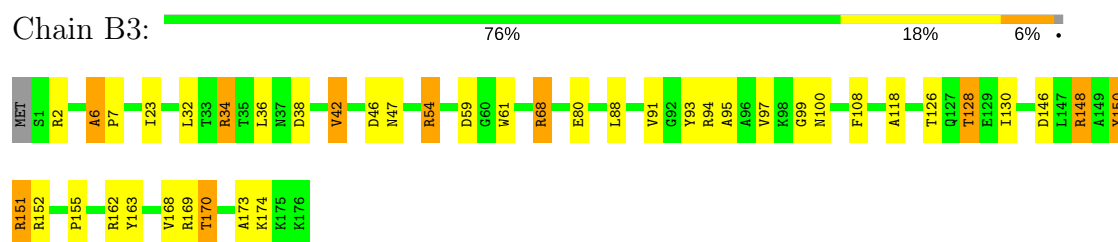
- Molecule 50: 50S ribosomal protein L4



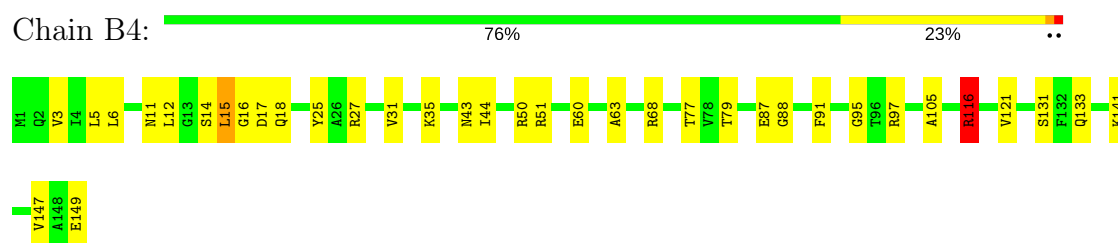
- Molecule 51: 50S ribosomal protein L5



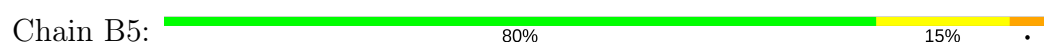
- Molecule 52: 50S ribosomal protein L6

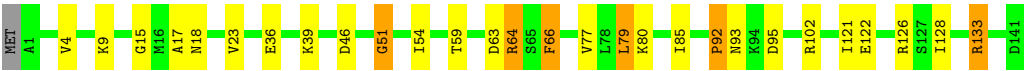


- Molecule 53: 50S ribosomal protein L9



- Molecule 54: 50S ribosomal protein L11





• Molecule 55: 50S ribosomal protein L13



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	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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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%)	7	43
5	AC	115/129 (89%)	91 (79%)	17 (15%)	7 (6%)	2	22
6	AD	121/124 (98%)	78 (64%)	28 (23%)	15 (12%)	0	7
7	AF	112/118 (95%)	80 (71%)	24 (21%)	8 (7%)	1	19
8	AG	94/101 (93%)	69 (73%)	20 (21%)	5 (5%)	2	26
9	AH	86/89 (97%)	73 (85%)	11 (13%)	2 (2%)	7	43
10	AI	80/82 (98%)	55 (69%)	15 (19%)	10 (12%)	0	7
11	AJ	78/84 (93%)	52 (67%)	18 (23%)	8 (10%)	0	11
12	AK	53/75 (71%)	44 (83%)	7 (13%)	2 (4%)	4	32
13	AL	77/92 (84%)	51 (66%)	19 (25%)	7 (9%)	1	15
14	AN	83/87 (95%)	66 (80%)	13 (16%)	4 (5%)	2	28
15	AO	204/233 (88%)	151 (74%)	38 (19%)	15 (7%)	1	18
16	AQ	49/71 (69%)	35 (71%)	8 (16%)	6 (12%)	0	7
17	AR	203/206 (98%)	161 (79%)	29 (14%)	13 (6%)	1	22
18	AS	148/159 (93%)	114 (77%)	20 (14%)	14 (10%)	1	14
19	AT	98/135 (73%)	80 (82%)	13 (13%)	5 (5%)	2	26
20	AU	148/179 (83%)	118 (80%)	19 (13%)	11 (7%)	1	18
21	AV	127/130 (98%)	103 (81%)	19 (15%)	5 (4%)	3	31
22	AW	125/130 (96%)	95 (76%)	23 (18%)	7 (6%)	2	25
23	AX	96/103 (93%)	78 (81%)	9 (9%)	9 (9%)	1	14
26	BC	92/94 (98%)	74 (80%)	14 (15%)	4 (4%)	3	29
27	BD	119/123 (97%)	90 (76%)	16 (13%)	13 (11%)	0	10
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	4
30	BG	125/127 (98%)	84 (67%)	32 (26%)	9 (7%)	1	19

Continued on next page...

Continued from previous page...

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

5 of 578 Ramachandran outliers are listed below:

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

Continued on next page...

Continued from previous page...

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%)	11	39
5	AC	90/99 (91%)	81 (90%)	9 (10%)	9	33
6	AD	103/104 (99%)	87 (84%)	16 (16%)	3	19
7	AF	92/96 (96%)	84 (91%)	8 (9%)	12	40
8	AG	79/84 (94%)	75 (95%)	4 (5%)	28	60
9	AH	76/77 (99%)	73 (96%)	3 (4%)	37	66
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%)	44 (92%)	4 (8%)	13	43
13	AL	70/79 (89%)	59 (84%)	11 (16%)	3	18
14	AN	65/66 (98%)	59 (91%)	6 (9%)	11	37
15	AO	170/190 (90%)	158 (93%)	12 (7%)	17	49
16	AQ	44/61 (72%)	40 (91%)	4 (9%)	11	38
17	AR	172/173 (99%)	156 (91%)	16 (9%)	10	37
18	AS	113/119 (95%)	98 (87%)	15 (13%)	4	24
19	AT	87/116 (75%)	77 (88%)	10 (12%)	6	28
20	AU	123/147 (84%)	108 (88%)	15 (12%)	6	26
21	AV	104/105 (99%)	98 (94%)	6 (6%)	23	56
22	AW	105/107 (98%)	98 (93%)	7 (7%)	19	51
23	AX	86/90 (96%)	78 (91%)	8 (9%)	10	37
26	BC	78/78 (100%)	74 (95%)	4 (5%)	28	60
27	BD	102/104 (98%)	98 (96%)	4 (4%)	37	66

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	BE	103/103 (100%)	84 (82%)	19 (18%)	2	12
29	BF	109/109 (100%)	95 (87%)	14 (13%)	5	25
30	BG	103/103 (100%)	90 (87%)	13 (13%)	5	26
31	BH	87/87 (100%)	81 (93%)	6 (7%)	18	51
32	BI	99/100 (99%)	96 (97%)	3 (3%)	46	72
33	BJ	89/90 (99%)	78 (88%)	11 (12%)	5	26
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%)	69 (83%)	14 (17%)	2	16
37	BN	213/215 (99%)	189 (89%)	24 (11%)	7	29
38	BO	83/84 (99%)	76 (92%)	7 (8%)	13	43
39	BP	62/63 (98%)	55 (89%)	7 (11%)	7	29
40	BQ	55/55 (100%)	47 (86%)	8 (14%)	4	21
41	BR	48/49 (98%)	46 (96%)	2 (4%)	34	64
42	BS	62/62 (100%)	58 (94%)	4 (6%)	20	52
43	BT	47/48 (98%)	35 (74%)	12 (26%)	0	5
44	BU	48/48 (100%)	45 (94%)	3 (6%)	21	53
45	BV	38/38 (100%)	34 (90%)	4 (10%)	8	32
46	BW	51/51 (100%)	43 (84%)	8 (16%)	3	18
47	BX	34/34 (100%)	30 (88%)	4 (12%)	6	27
48	BY	164/164 (100%)	145 (88%)	19 (12%)	6	28
49	BZ	187/187 (100%)	174 (93%)	13 (7%)	18	50
50	B1	165/165 (100%)	147 (89%)	18 (11%)	7	30
51	B2	149/149 (100%)	130 (87%)	19 (13%)	5	25
52	B3	137/138 (99%)	125 (91%)	12 (9%)	12	39
53	B4	114/114 (100%)	104 (91%)	10 (9%)	12	39
54	B5	109/110 (99%)	102 (94%)	7 (6%)	20	53
55	B6	114/114 (100%)	107 (94%)	7 (6%)	22	55
All	All	4856/5043 (96%)	4380 (90%)	476 (10%)	14	34

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	74/76 (97%)	20 (27%)	0
1	AE	75/76 (98%)	11 (14%)	0
1	AP	74/76 (97%)	15 (20%)	0
2	AM	19/20 (95%)	9 (47%)	0
24	BA	116/117 (99%)	37 (31%)	0
25	BB	2901/2903 (99%)	1516 (52%)	0
3	A1	1529/1530 (99%)	753 (49%)	0
All	All	4788/4798 (99%)	2361 (49%)	0

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

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
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