



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 05:00 PM GMT

PDB ID : 2Y0X
Title : THE CRYSTAL STRUCTURE OF EF-TU AND A9C-TRNA-TRP BOUND
TO A NEAR-COGNATE CODON ON THE 70S RIBOSOME
Authors : Schmeing, T.M.; Voorhees, R.M.; Ramakrishnan, V.
Deposited on : 2010-12-07
Resolution : 3.10 Å(reported)

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

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

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

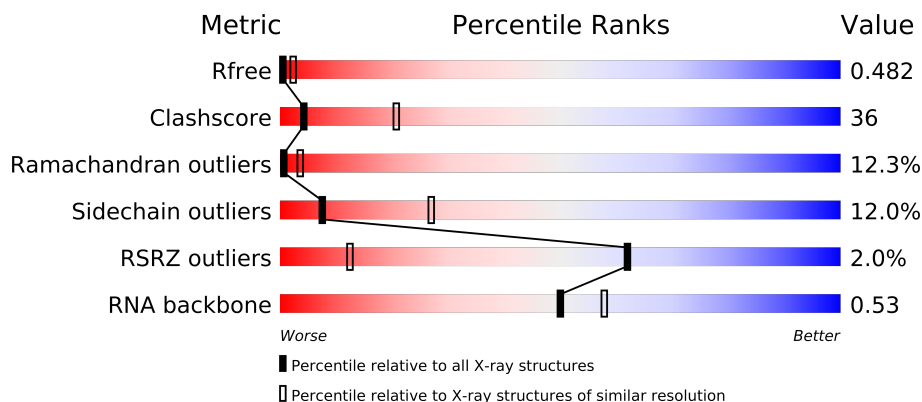
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.10 Å.

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



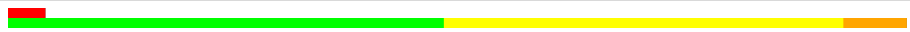
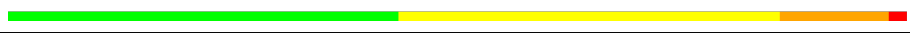
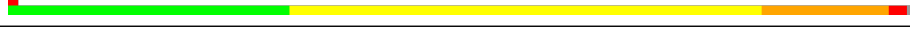

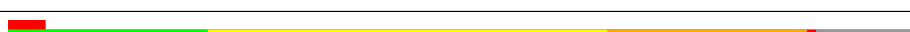


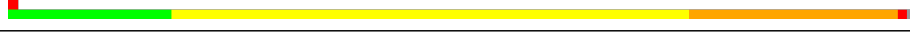
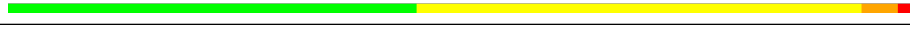

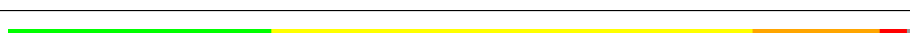
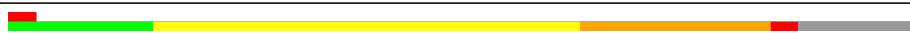
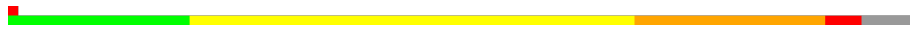
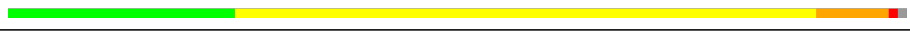
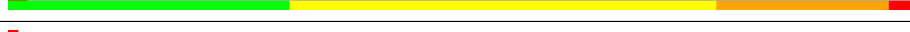

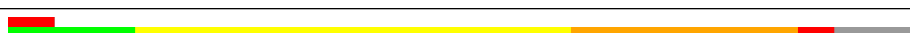
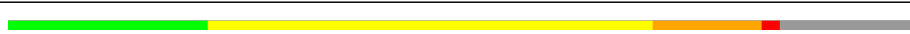



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)
RNA backbone	1838	1047 (3.60-2.60)

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

Mol	Chain	Length	Quality of chain
1	0	85	
2	1	98	
3	2	72	
4	3	60	
5	4	71	
6	5	60	
7	6	54	
8	7	49	
9	8	65	
10	9	37	
11	A	2915	
12	B	122	

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Mol	Chain	Length	Quality of chain
13	C	229	
14	D	276	
15	E	206	
16	F	210	
17	G	182	
18	H	180	
19	J	173	
20	K	147	
21	N	140	
22	O	122	
23	P	150	
24	Q	141	
25	R	118	
26	S	112	
27	T	146	
28	U	118	
29	V	101	
30	W	113	
31	X	96	
32	Y	110	
33	Z	206	

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 93750 atoms, of which 0 are hydrogen and 0 are deuterium.

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

- Molecule 1 is a protein called 50S RIBOSOMAL PROTEIN L27.

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

- Molecule 2 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1	93	Total	C	N	O	S	0	0	0
			731	460	145	125	1			

- Molecule 3 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	2	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			

- Molecule 4 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	3	59	Total	C	N	O	S	0	0	0
			467	298	90	78	1			

- Molecule 5 is a protein called 50S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	4	44	Total	C	N	O	S	0	0	0
			340	218	57	61	4			

- Molecule 6 is a protein called 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

- Molecule 7 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	6	50	Total	C	N	O	S	0	0	0
			433	270	88	71	4			

- Molecule 8 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	7	48	Total	C	N	O	S	0	0	0
			418	257	104	55	2			

- Molecule 9 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	8	63	Total	C	N	O	S	0	0	0
			507	326	101	78	2			

- Molecule 10 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 11 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	A	2901	Total	C	N	O	P	0	0	0
			62477	27807	11683	20087	2900			

- Molecule 12 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	B	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			

- Molecule 13 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	C	228	Total	C	N	O	S	0	0	0
			1742	1101	319	319	3			

- Molecule 14 is a protein called 50S RIBOSOMAL PROTEIN L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	D	275	Total	C	N	O	S	0	0	0
			2145	1353	428	361	3			

- Molecule 15 is a protein called 50S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	E	204	Total	C	N	O	S	0	0	0
			1563	988	299	270	6			

- Molecule 16 is a protein called 50S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	F	207	Total	C	N	O	S	0	0	0
			1623	1035	303	282	3			

- Molecule 17 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	G	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			

- Molecule 18 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	H	159	Total	C	N	O	S	0	0	0
			1222	773	228	220	1			

- Molecule 19 is a protein called 50S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	J	130	Total	C	N	O		0	0	0
			651	391	130	130				

- Molecule 20 is a protein called 50S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	K	140	Total	C	N	O		0	0	0
			700	420	140	140				

- Molecule 21 is a protein called 50S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	N	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			

- Molecule 22 is a protein called 50S RIBOSOMAL PROTEIN L14.

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

- Molecule 23 is a protein called 50S RIBOSOMAL PROTEIN L15.

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

- Molecule 24 is a protein called 50S RIBOSOMAL PROTEIN L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	Q	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	R	117	Total	C	N	O	0	0	0
			960	599	202	159			

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
26	S	98	Total	C	N	O	0	0	0
			770	486	154	130			

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	T	137	Total	C	N	O	S	0	0	0
			1141	710	234	196	1			

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	U	117	Total	C	N	O	S	0	0	0
			958	604	202	151	1			

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	V	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L22.

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

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	X	92	Total	C	N	O	S	0	0	0
			725	471	131	123				

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	Y	100	Total	C	N	O	S	0	0	0
			775	500	148	123	4			

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L25.

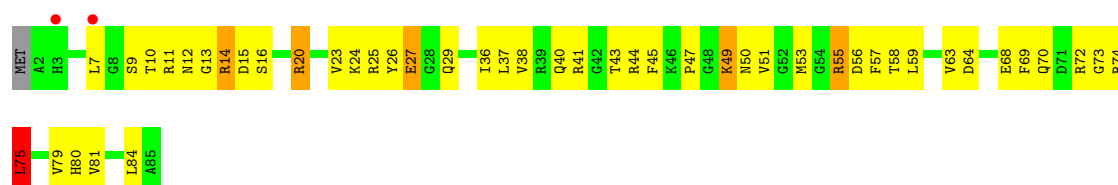
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	Z	176	Total	C	N	O	S	0	0	0
			1403	897	252	252	2			

3 Residue-property plots

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

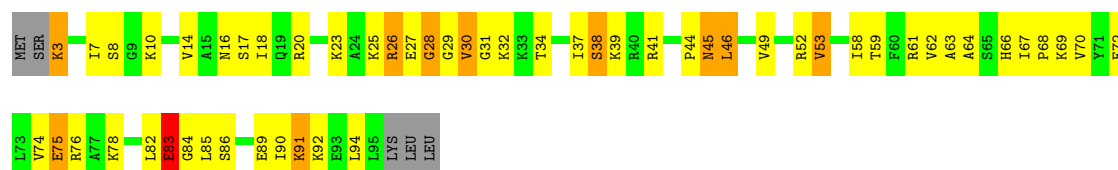
- Molecule 1: 50S RIBOSOMAL PROTEIN L27

Chain 0: 



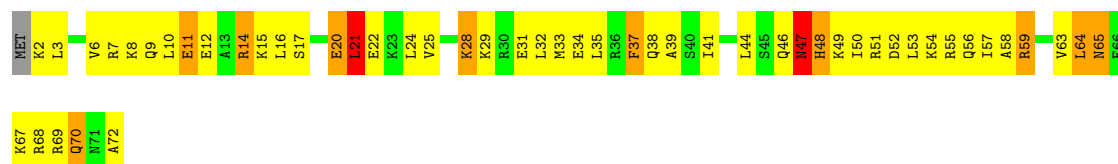
- Molecule 2: 50S RIBOSOMAL PROTEIN L28

Chain 1: 



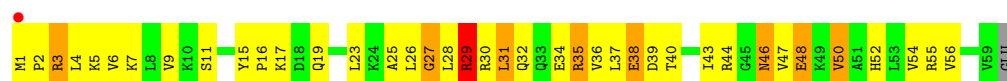
- Molecule 3: 50S RIBOSOMAL PROTEIN L29

Chain 2: 



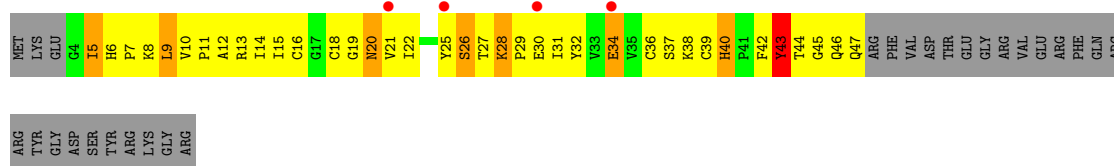
- Molecule 4: 50S RIBOSOMAL PROTEIN L30

Chain 3: 



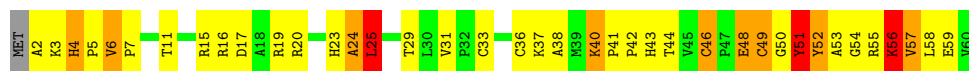
- Molecule 5: 50S RIBOSOMAL PROTEIN L31

Chain 4: 



• Molecule 6: 50S RIBOSOMAL PROTEIN L32

Chain 5:



• Molecule 7: 50S RIBOSOMAL PROTEIN L33

Chain 6:



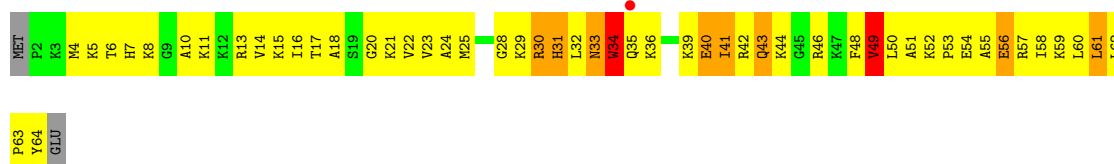
• Molecule 8: 50S RIBOSOMAL PROTEIN L34

Chain 7:



• Molecule 9: 50S RIBOSOMAL PROTEIN L35

Chain 8:



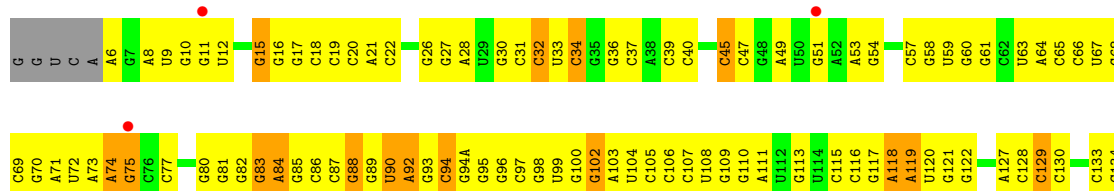
• Molecule 10: 50S RIBOSOMAL PROTEIN L36

Chain 9:



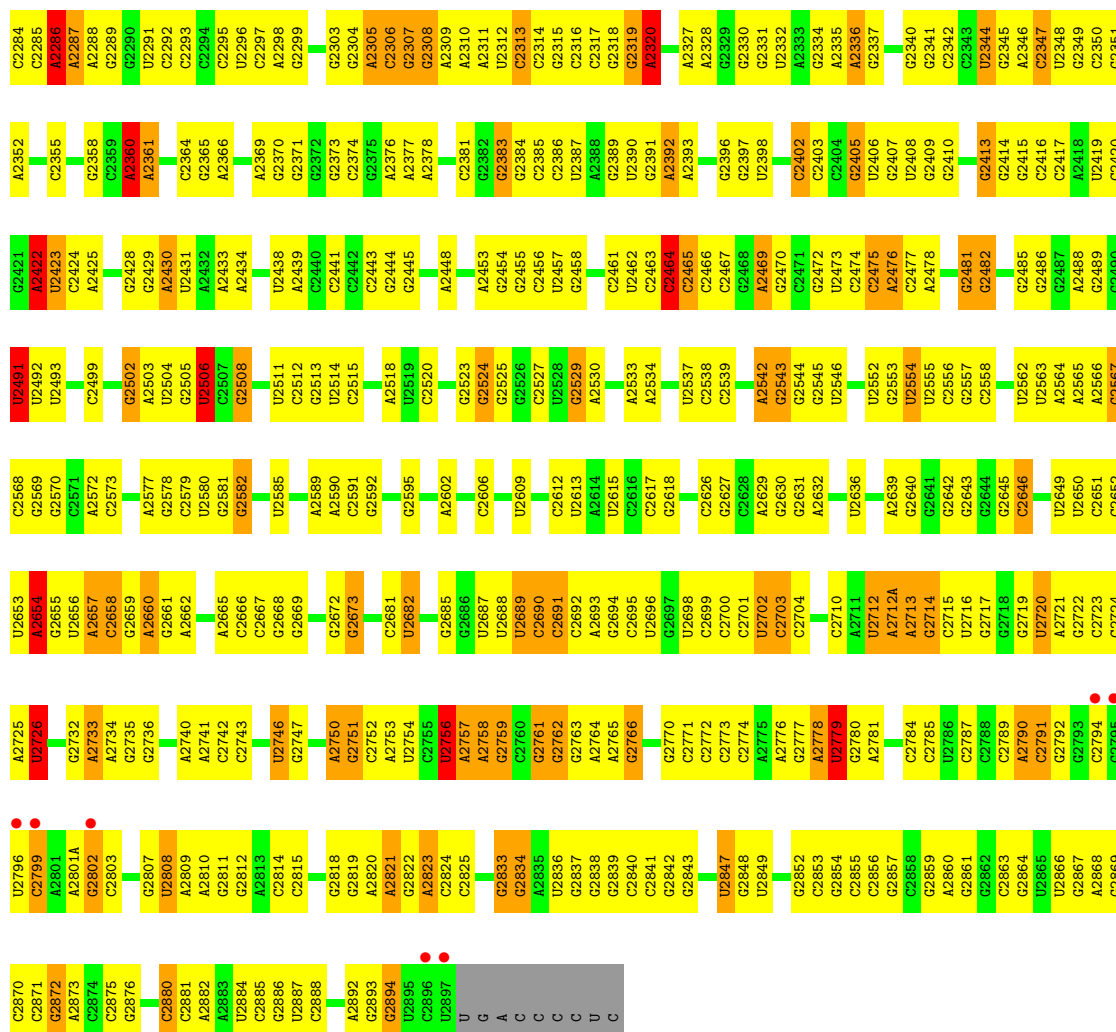
• Molecule 11: 23S RIBOSOMAL RNA

Chain A:



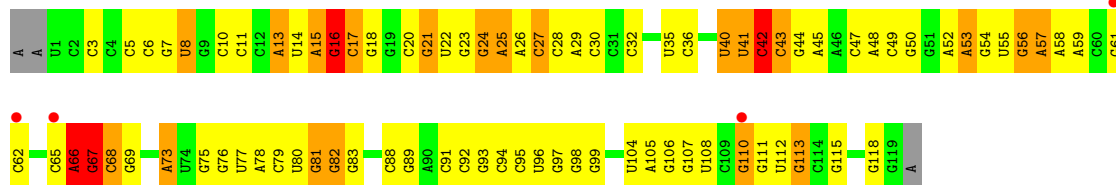
A1073	A1074	C1075	C1076	C1077	H1078	C1079	G1080	U1081	A1082	A1083	A1084	A1085	A1086	A1087	A1088	A1089	A1090	A1091	C1092	G1093	U1094	A1095	A1096	A1097	A1098	G1099	C1100	U1101	C1102	A1103	U1104	U1105	C1106	G1107	U1108	C1109	G1110	A1111	C1112	U1113	G1114	G1115	C1116	G1120	G1131	A1132	U1133	C1135	G1136	G1137	G1138	C1139	C1140	U1141	U1142	A1143	A1144	A1145	C1146	C1147	A1148																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
G135	G136	C137	G138	G139A	G140	A141	A142	C142A	G143	C143A	G144	G145	G146	A149	C150	C151	G152	C153	G154	U158	C171	G172	G173	C174	G175	G176	G177	G178	A181	A182	C183	C184	U185	G186	G189	A190	A191	C192	U193	G194	A196	A197	C198	A199	U200	U202	C203	A204	G205	C208	C209	C210																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
A211	G212	A213	G214	G215	A216	G220	A221	A222	A225	A228	A229	U230	C231	G232	A233	C234	U235	C236	C237	C238	U239	G242	U243	G244	G245	G248	C249	G250	A251	G252	C253	G254	A257	G258	G259	G260	G261	A265	G266	C267	C268	U269	A270	C271C	G271D	U271E	C271F	C271G	G271H	G271I																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
C271J	U271K	G271L	G271M	U271N	C271O	C271P	G271Q	G271R	G271S	C271T	G271U	G271V	G271W	G271X	U271Y	G271Z	U272A	G272B	G272C	G272D	C272E	U272F	C272G	C272H	C272I	C272J	G272K	C272L	C272M	C272N	C272O	C272P	C272Q	C272R	C272S	C272T	C272U	C272V	C272W	C272X	C272Y	C272Z	C273A	C273B	C273C	C273D	C273E	C273F	C273G	C273H	C273I	C273J	C273K	C273L	C273M	C273N	C273O	C273P	C273Q	C273R	C273S	C273T	C273U	C273V	C273W	C273X	C273Y	C273Z	C274A	C274B	C274C	C274D	C274E	C274F	C274G	C274H	C274I	C274J	C274K	C274L	C274M	C274N	C274O	C274P	C274Q	C274R	C274S	C274T	C274U	C274V	C274W	C274X	C274Y	C274Z	C275A	C275B	C275C	C275D	C275E	C275F	C275G	C275H	C275I	C275J	C275K	C275L	C275M	C275N	C275O	C275P	C275Q	C275R	C275S	C275T	C275U	C275V	C275W	C275X	C275Y	C275Z	C276A	C276B	C276C	C276D	C276E	C276F	C276G	C276H	C276I	C276J	C276K	C276L	C276M	C276N	C276O	C276P	C276Q	C276R	C276S	C276T	C276U	C276V	C276W	C276X	C276Y	C276Z	C277A	C277B	C277C	C277D	C277E	C277F	C277G	C277H	C277I	C277J	C277K	C277L	C277M	C277N	C277O	C277P	C277Q	C277R	C277S	C277T	C277U	C277V	C277W	C277X	C277Y	C277Z	C278A	C278B	C278C	C278D	C278E	C278F	C278G	C278H	C278I	C278J	C278K	C278L	C278M	C278N	C278O	C278P	C278Q	C278R	C278S	C278T	C278U	C278V	C278W	C278X	C278Y	C278Z	C279A	C279B	C279C	C279D	C279E	C279F	C279G	C279H	C279I	C279J	C279K	C279L	C279M	C279N	C279O	C279P	C279Q	C279R	C279S	C279T	C279U	C279V	C279W	C279X	C279Y	C279Z	C280A	C280B	C280C	C280D	C280E	C280F	C280G	C280H	C280I	C280J	C280K	C280L	C280M	C280N	C280O	C280P	C280Q	C280R	C280S	C280T	C280U	C280V	C280W	C280X	C280Y	C280Z	C281A	C281B	C281C	C281D	C281E	C281F	C281G	C281H	C281I	C281J	C281K	C281L	C281M	C281N	C281O	C281P	C281Q	C281R	C281S	C281T	C281U	C281V	C281W	C281X	C281Y	C281Z	C282A	C282B	C282C	C282D	C282E	C282F	C282G	C282H	C282I	C282J	C282K	C282L	C282M	C282N	C282O	C282P	C282Q	C282R	C282S	C282T	C282U	C282V	C282W	C282X	C282Y	C282Z	C283A	C283B	C283C	C283D	C283E	C283F	C283G	C283H	C283I	C283J	C283K	C283L	C283M	C283N	C283O	C283P	C283Q	C283R	C283S	C283T	C283U	C283V	C283W	C283X	C283Y	C283Z	C284A	C284B	C284C	C284D	C284E	C284F	C284G	C284H	C284I	C284J	C284K	C284L	C284M	C284N	C284O	C284P	C284Q	C284R	C284S	C284T	C284U	C284V	C284W	C284X	C284Y	C284Z	C285A	C285B	C285C	C285D	C285E	C285F	C285G	C285H	C285I	C285J	C285K	C285L	C285M	C285N	C285O	C285P	C285Q	C285R	C285S	C285T	C285U	C285V	C285W	C285X	C285Y	C285Z	C286A	C286B	C286C	C286D	C286E	C286F	C286G	C286H	C286I	C286J	C286K	C286L	C286M	C286N	C286O	C286P	C286Q	C286R	C286S	C286T	C286U	C286V	C286W	C286X	C286Y	C286Z	C287A	C287B	C287C	C287D	C287E	C287F	C287G	C287H	C287I	C287J	C287K	C287L	C287M	C287N	C287O	C287P	C287Q	C287R	C287S	C287T	C287U	C287V	C287W	C287X	C287Y	C287Z	C288A	C288B	C288C	C288D	C288E	C288F	C288G	C288H	C288I	C288J	C288K	C288L	C288M	C288N	C288O	C288P	C288Q	C288R	C288S	C288T	C288U	C288V	C288W	C288X	C288Y	C288Z	C289A	C289B	C289C	C289D	C289E	C289F	C289G	C289H	C289I	C289J	C289K	C289L	C289M	C289N	C289O	C289P	C289Q	C289R	C289S	C289T	C289U	C289V	C289W	C289X	C289Y	C289Z	C290A	C290B	C290C	C290D	C290E	C290F	C290G	C290H	C290I	C290J	C290K	C290L	C290M	C290N	C290O	C290P	C290Q	C290R	C290S	C290T	C290U	C290V	C290W	C290X	C290Y	C290Z	C291A	C291B	C291C	C291D	C291E	C291F	C291G	C291H	C291I	C291J	C291K	C291L	C291M	C291N	C291O	C291P	C291Q	C291R	C291S	C291T	C291U	C291V	C291W	C291X	C291Y	C291Z	C292A	C292B	C292C	C292D	C292E	C292F	C292G	C292H	C292I	C292J	C292K	C292L	C292M	C292N	C292O	C292P	C292Q	C292R	C292S	C292T	C292U	C292V	C292W	C292X	C292Y	C292Z	C293A	C293B	C293C	C293D	C293E	C293F	C293G	C293H	C293I	C293J	C293K	C293L	C293M	C293N	C293O	C293P	C293Q	C293R	C293S	C293T	C293U	C293V	C293W	C293X	C293Y	C293Z	C294A	C294B	C294C	C294D	C294E	C294F	C294G	C294H	C294I	C294J	C294K	C294L	C294M	C294N	C294O	C294P	C294Q	C294R	C294S	C294T	C294U	C294V	C294W	C294X	C294Y	C294Z	C295A	C295B	C295C	C295D	C295E	C295F	C295G	C295H	C295I	C295J	C295K	C295L	C295M	C295N	C295O	C295P	C295Q	C295R	C295S	C295T	C295U	C295V	C295W	C295X	C295Y	C295Z	C296A	C296B	C296C	C296D	C296E	C296F	C296G	C296H	C296I	C296J	C296K	C296L	C296M	C296N	C296O	C296P	C296Q	C296R	C296S	C296T	C296U	C296V	C296W	C296X	C296Y	C296Z	C297A	C297B	C297C	C297D	C297E	C297F	C297G	C297H	C297I	C297J	C297K	C297L	C297M	C297N	C297O	C297P	C297Q	C297R	C297S	C297T	C297U	C297V	C297W	C297X	C297Y	C297Z	C298A	C298B	C298C	C298D	C298E	C298F	C298G	C298H	C298I	C298J	C298K	C298L	C298M	C298N	C298O	C298P	C298Q	C298R	C298S	C298T	C298U	C298V	C298W	C298X	C298Y	C298Z	C299A	C299B	C299C	C299D	C299E	C299F	C299G	C299H	C299I	C299J	C299K	C299L	C299M	C299N	C299O	C299P	C299Q	C299R	C299S	C299T	C299U	C299V	C299W	C299X	C299Y	C299Z	C300A	C300B	C300C	C300D	C300E	C300F	C300G	C300H	C300I	C300J	C300K	C300L	C300M	C300N	C300O	C300P	C300Q	C300R	C300S	C300T	C300U	C300V	C300W	C300X	C300Y	C300Z	C301A	C301B	C301C	C301D	C301E	C301F	C301G	C301H	C301I	C301J	C301K	C301L	C301M	C301N	C301O	C301P	C301Q	C301R	C301S	C301T	C301U	C301V	C301W	C301X	C301Y	C301Z	C302A	C302B	C302C	C302D	C302E	C302F	C302G	C302H	C302I	C302J	C302K	C302L	C302M	C302N	C302O	C302P	C302Q	C302R	C302S	C302T	C302U	C302V	C302W	C302X	C302Y	C302Z	C303A	C303B	C303C	C303D	C303E	C303F	C303G	C303H	C303I	C303J	C3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U2197	G2133	G1989	G1811	G1719	G1642	C1498	U1431	G1355	G1285	G1216	G1149
A2198	A2134	C1908	A1812	U1720	G1643	C1499	C1432	G1359	A1286	G1216	C1150
A2199	A2135	C1909	G1813	G1721	G1647	A1567	A1433	A1359	A1287	C1221A	C1151
C2200	G1910	G1991	A1722	A1722	C1648	A1568	A1434	A1360	U1288	G1222	G1152
C2201	U1911	U1993	G1816	U1739	G1651	A1570	G1437	G1361	C1289	G1223	C1153
C2138	C2073	G1997	G1817	G1740	A1652	A1571	G1437	C1362	C1290	C1224	G1154
C2139	U2074	G1998	U1818	G1743	G1653	A1572	G1441	C1363	C1291	A1155	A1155
C2140	U2075	U1915	U1819	C1743	A1654	A1573	G1442	G1364	U1292	A1156	A1156
C2145	C2078	A1916	U1820	C1745A	G1657	C1574	G1442	A1365	C1293	U1159	U1159
C2146	U2079	A1917	G1826	G1746	C1657	C1577	A1445	A1366	C1297	G1229	G1160
G2219	G2080	G2001	G1827	G1747	C1658	A1578	C1445A	A1367	C1298	G1230	C1161
G2220	A2001	G2002	C1827	G1747A	U1659	A1580	C1446	G1368	G1231	G1231	G1162
G2221	A2082	G2007	G1828	G1748	C1660	G1581	G1447	G1369	G1232	G1232	G1163
G2222	C2008	C2008	G1831	A1749	C1661	G1582	G1448	A1378	G1236	G1236	G1164
G2223	C2009	U1926	G1835	G1750	G1662	A1586	G1449	A1379	A1237	A1237	U1165
G2224	G2010	U1926	G1835	C1751	C1663	C1584	G1450	G1380	G1238	G1238	G1166
G2225	U2011	G1929	U1841	G1752	A1664	A1587	G1450A	G1384	G1239	G1239	U1167
G2226	G2012	G1930	G1842	G1753	A1665	A1588	C1451	A1384	U1240	U1240	G1168
G2227	A2013	U1931	G1843	G1754	G1666	C1589	A1452	A1385	A1241	A1241	G1169
G2228	A2014	A1932	C1844	A1755	G1667	U1590	G1455	G1386	A1242	A1242	G1170
G2229	A2015	G1933	C1844	A1762	A1668	G1591	G1310	C1387	G1243	G1243	G1171
G2230	U2016	G1936	A1847	G1763	A1669	G1592	G1311	G1388	G1244	G1244	G1172
G2231	U2096	A1937	A1847	G1764	C1670	C1593	G1459	U1390	G1245	G1245	A1174
G2232	C2097	A1938	A1853	C1765	G1674	G1594	G1460	U1390	A1246	A1246	U1175
G2233	U2098	U1939	A1854	U1766	G1675	G1595	G1461	U1391	A1247	A1247	G1176
G2234	U2099	U1940	G1858	C1771	C1676	A1596	G1462	A1395	G1248	G1248	A1177
G2235	G2023	U1946	G1858	G1772	A1676	A1597	C1463	U1396	U1249	U1249	C1178
G2236	G2024	C1947	G1860	A1773	A1677	A1598	C1464	C1397	G1250	G1250	C1179
G2237	C2025	G1948	G1861	C1774	G1678	C1599	C1465	U1398	C1251	C1251	C1180
G2238	C2026	G1949	G1862	U1775	G1681	C1600	G1466	C1399	G1252	G1252	C1181
G2239	G2031	A1952	G1863	G1776	C1682	C1601	C1467	G1400	A1253	A1253	A1182
G2240	G2032	A1953	G1864	U1777	C1683	G1602	C1469	C1402	G1256	G1256	G1183
G2241	U2033	G1954	G1865	U1778	C1684	U1533	A1471	C1403	C1257	C1257	G1184
G2242	U2034	U1955	C1866	A1780	C1685	U1534	A1472	C1404	G1258	G1258	G1186
G2243	G2035	C1958	A1876	C1781	U1688	C1607	C1473	U1405	G1259	G1259	G1187
G2244	A2036	G1959	A1877	C1782	A1689	A1608	C1474	U1406	G1260	G1260	U1188
G2245	G2037	G1959	G1878	A1783	C1692	A1609	C1475	C1407	C1261	C1261	A1189
G2246	G2038	G1963	C1879	U1784	U1692	G1610	C1476	C1408	A1262	A1262	G1191
G2247	G2039	U1963	G1880	A1785	U1693	C1611	C1477	G1410	G1263	G1263	G1192
G2248	C2040	C1967	C1881	A1786	G1694	G1612	C1478	C1411	A1265	A1265	G1193
G2249	U2041	C1967	C1882	A1787	G1695	A1614	C1479	A1412	U1268	U1268	U1198
G2250	G2042	G1968	G1883	C1790	G1696	C1617	U1481	G1413	A1269	A1269	U1199
G2251	C2043	A1969	A1884	C1791	A1697	A1618	G1482	G1416	C1270	C1270	G1203
G2252	G2052	A1971	C1886	A1796	G1699	A1618	G1485	C1417	U1340	U1340	A1204
G2253	C2055	A1972	C1887	U1796	A1700	C1625	G1486	G1418	A1272	A1272	U1205
G2254	G2056	G1980	A1889	C1797	A1701	G1626	G1487	U1420	U1273	U1273	G1206
G2255	A1981	A1981	G1899	U1799	C1708	A1632	U1488	G1424	A1275	A1275	C1207
G2256	C1982	C1982	G1899	C1800	U1709	G1633	A1490	G1425	A1278	A1278	C1208
G2257	A1983	A1983	A1901	G1801	C1710	A1634	G1490	G1426	G1279	G1279	G1209
G2258	G1984	G1984	A1901	G1801	C1710	A1634	G1490	G1426	G1280	G1280	A1210
G2259	G1985	G1985	C1902	G1807	U1713	C1638	G1493	A1427	G1281	G1281	G1212
G2260	C2064	C2064	G1903	U1808	G1714	U1639	A1494	G1428	U1282	U1282	A1213
G2261	G1987	G1987	G1906	A1810	G1718	C1640	A1495	C1429	G1283	G1283	A1214
G2262	C1988	C1988	G1906	A1810	G1718	C1641	U1497	C1430	A1354	A1354	G1215



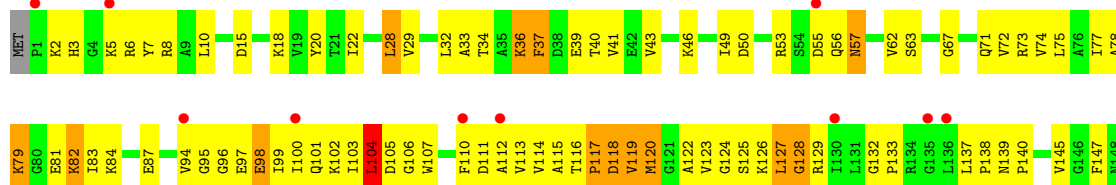
• Molecule 12: 5S RIBOSOMAL RNA

Chain B:



• Molecule 13: 50S RIBOSOMAL PROTEIN L1

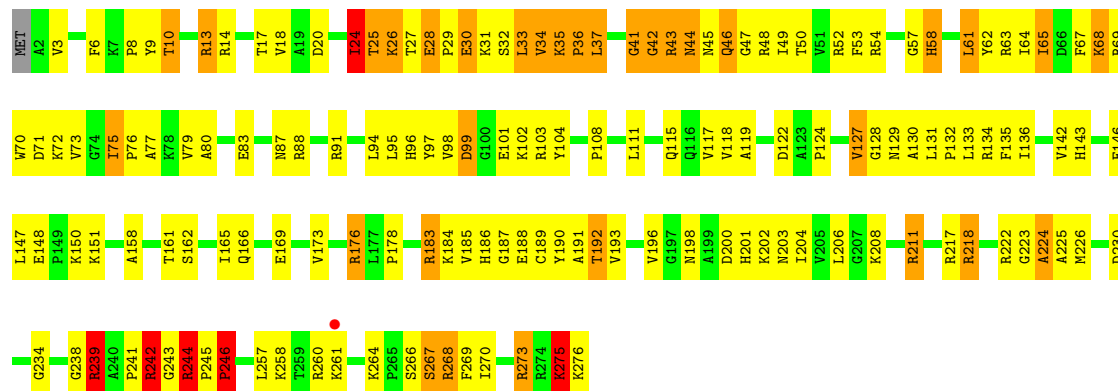
Chain C:





• Molecule 14: 50S RIBOSOMAL PROTEIN L2

Chain D:



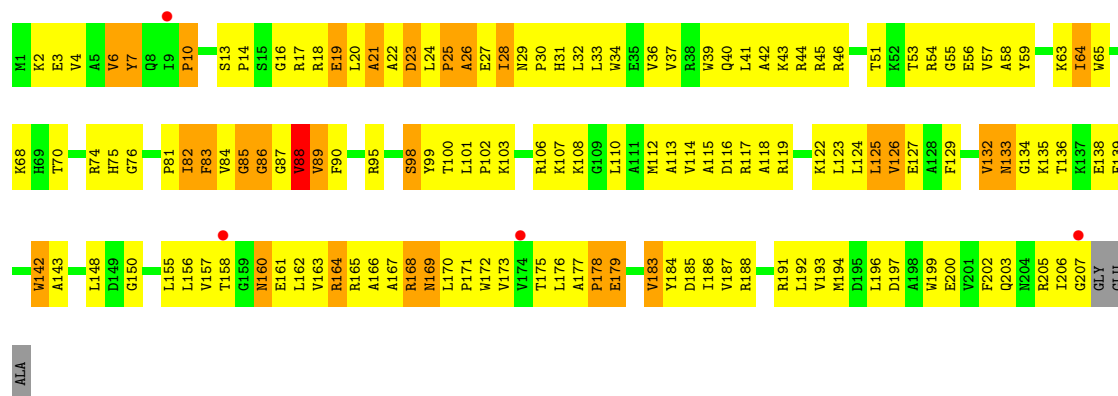
• Molecule 15: 50S RIBOSOMAL PROTEIN L3

Chain E:



• Molecule 16: 50S RIBOSOMAL PROTEIN L4

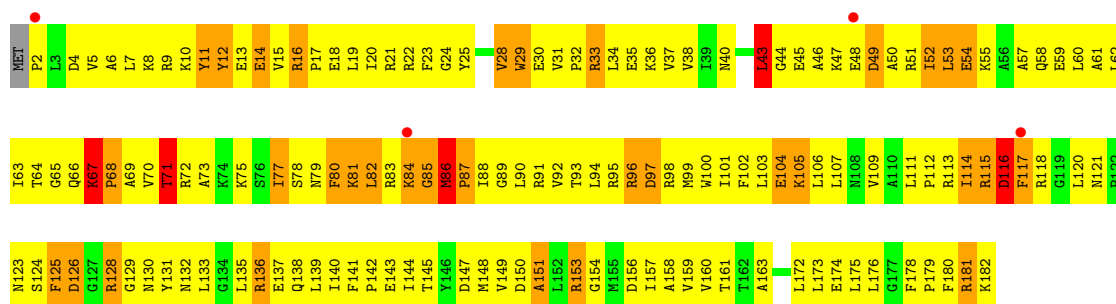
Chain F:



• Molecule 17: 50S RIBOSOMAL PROTEIN L5

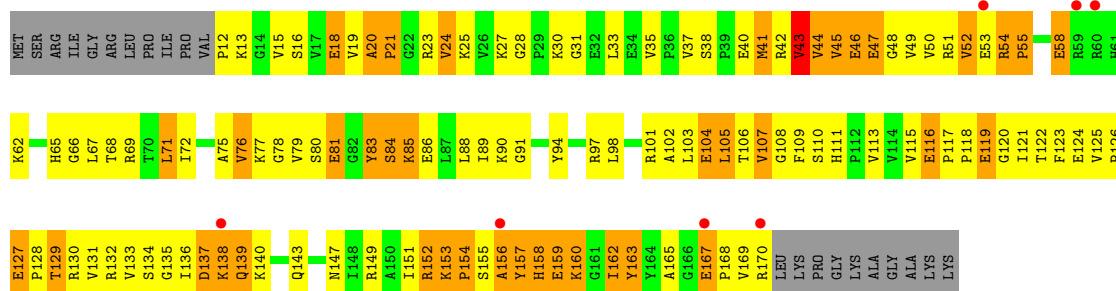
Chain G:





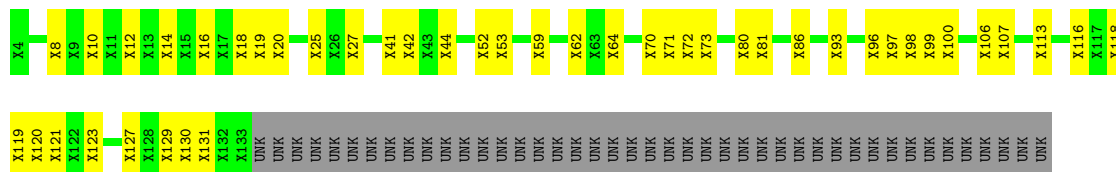
• Molecule 18: 50S RIBOSOMAL PROTEIN L6

Chain H:



• Molecule 19: 50S RIBOSOMAL PROTEIN L10

Chain J:



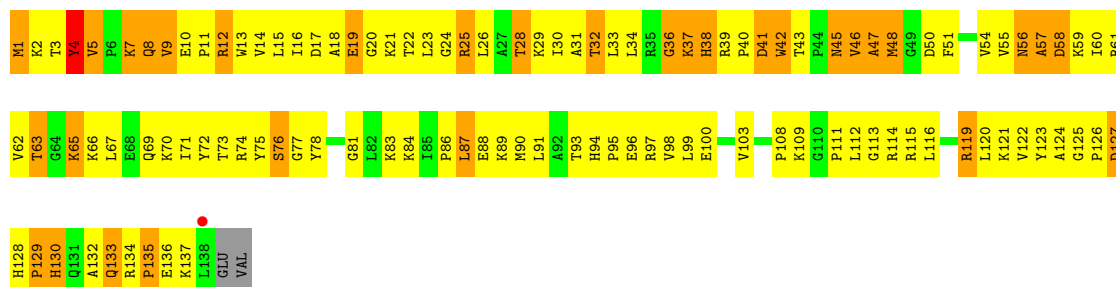
• Molecule 20: 50S RIBOSOMAL PROTEIN L11

Chain K:



• Molecule 21: 50S RIBOSOMAL PROTEIN L13

Chain N:



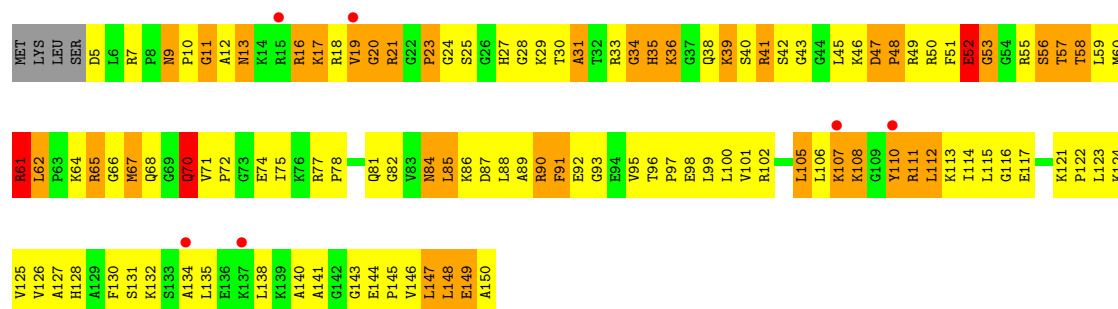
- Molecule 22: 50S RIBOSOMAL PROTEIN L14

Chain O:



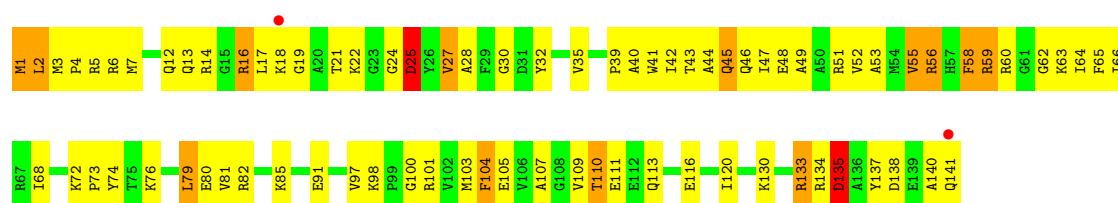
- Molecule 23: 50S RIBOSOMAL PROTEIN L15

Chain P:



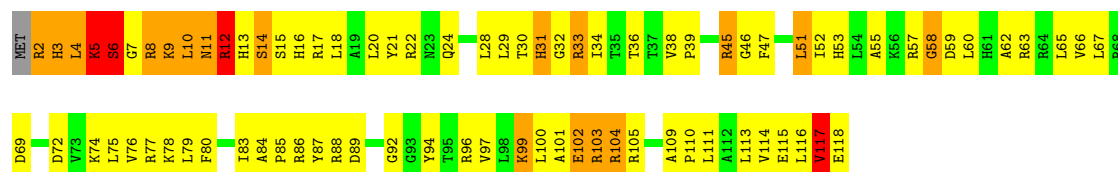
- Molecule 24: 50S RIBOSOMAL PROTEIN L16

Chain Q:



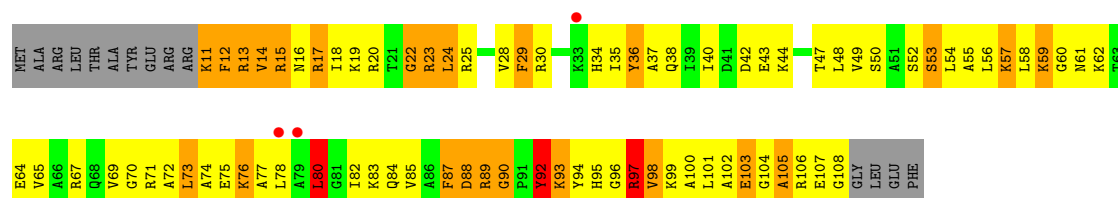
- Molecule 25: 50S RIBOSOMAL PROTEIN L17

Chain R:

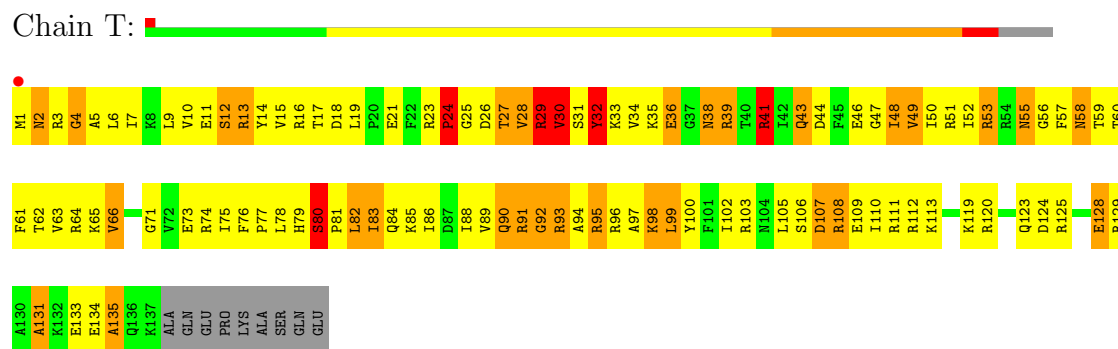


- Molecule 26: 50S RIBOSOMAL PROTEIN L18

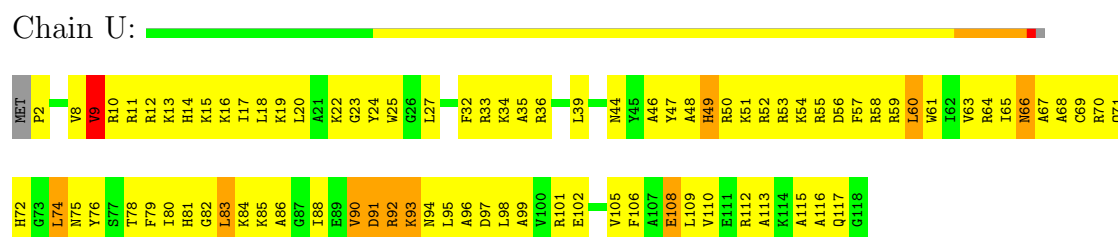
Chain S:



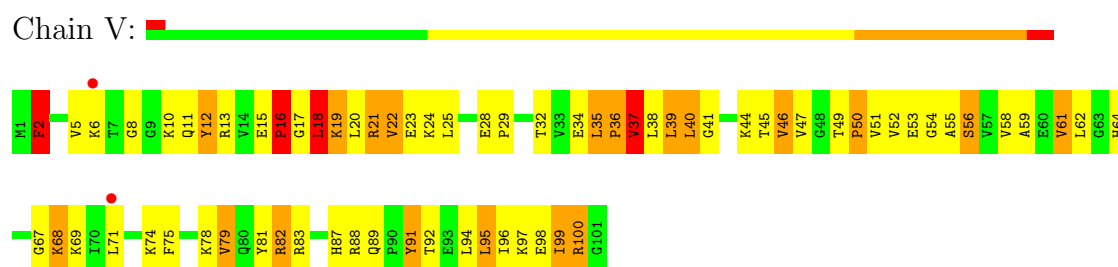
- Molecule 27: 50S RIBOSOMAL PROTEIN L19



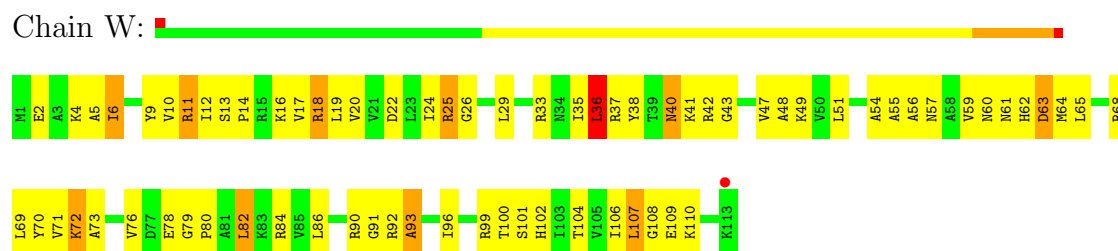
- Molecule 28: 50S RIBOSOMAL PROTEIN L20



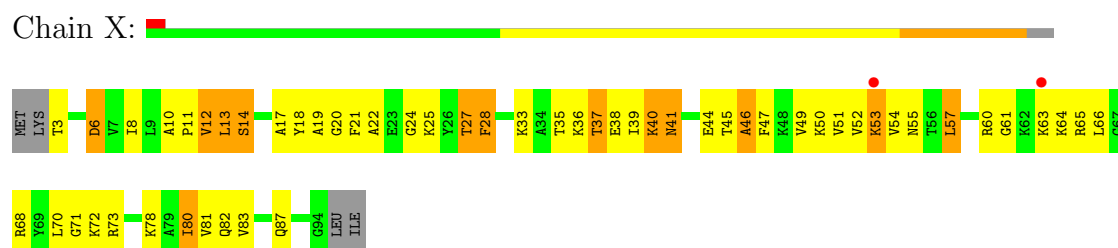
- Molecule 29: 50S RIBOSOMAL PROTEIN L21



- Molecule 30: 50S RIBOSOMAL PROTEIN L22

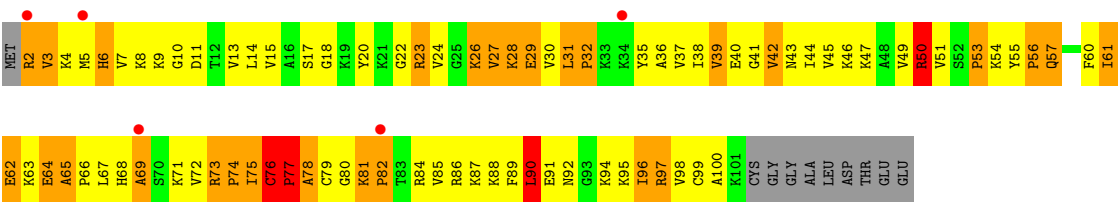


- Molecule 31: 50S RIBOSOMAL PROTEIN L23



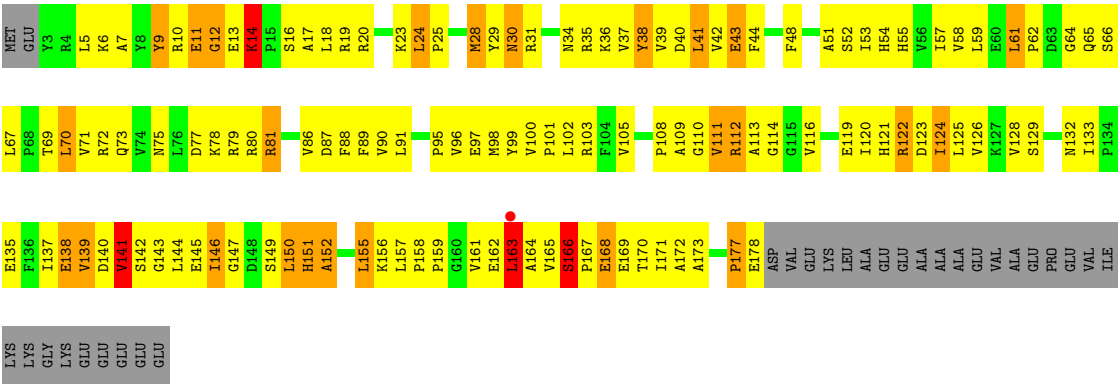
- Molecule 32: 50S RIBOSOMAL PROTEIN L24

Chain Y: 



• Molecule 33: 50S RIBOSOMAL PROTEIN L25

Chain Z: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	289.90Å 268.50Å 403.60Å 90.00° 91.62° 90.00°	Depositor
Resolution (Å)	50.00 – 3.10 49.92 – 2.93	Depositor EDS
% Data completeness (in resolution range)	98.0 (50.00-3.10) 90.5 (49.92-2.93)	Depositor EDS
R_{merge}	0.02	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.91Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.243 , 0.267 0.477 , 0.482	Depositor DCC
R_{free} test set	59600 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	59.1	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 59.4	EDS
Estimated twinning fraction	0.018 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 1195890 reflections	Xtriage
F_o, F_c correlation	0.52	EDS
Total number of atoms	93750	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.41	0/671	0.70	0/892
2	1	0.40	0/738	0.68	0/981
3	2	0.33	0/600	0.64	1/793 (0.1%)
4	3	0.35	0/472	0.61	0/634
5	4	0.37	0/349	0.65	0/474
6	5	0.38	0/473	0.71	0/639
7	6	0.54	0/440	0.80	0/586
8	7	0.42	0/426	0.69	0/561
9	8	0.53	0/515	0.87	1/679 (0.1%)
10	9	0.41	0/310	0.65	0/407
11	A	0.49	2/69976 (0.0%)	0.72	32/109244 (0.0%)
12	B	0.46	0/2853	0.75	2/4451 (0.0%)
13	C	0.40	2/1774 (0.1%)	0.60	0/2391
14	D	0.50	0/2195	0.80	1/2955 (0.0%)
15	E	0.43	0/1596	0.74	0/2153
16	F	0.37	0/1658	0.65	0/2244
17	G	0.38	0/1499	0.68	0/2016
18	H	0.32	0/1245	0.66	0/1682
21	N	0.37	0/1131	0.69	0/1525
22	O	0.46	0/943	0.67	0/1269
23	P	0.42	0/1131	0.91	2/1504 (0.1%)
24	Q	0.49	0/1143	0.72	0/1527
25	R	0.38	0/974	0.70	1/1302 (0.1%)
26	S	0.37	0/778	0.75	0/1036
27	T	0.41	0/1155	0.76	2/1542 (0.1%)
28	U	0.43	0/975	0.68	0/1297
29	V	0.39	0/790	0.68	0/1057
30	W	0.36	0/907	0.67	0/1216
31	X	0.40	0/739	0.65	0/993
32	Y	0.36	0/788	0.73	1/1051 (0.1%)
33	Z	0.44	0/1435	0.74	0/1949
All	All	0.47	4/100679 (0.0%)	0.72	43/151050 (0.0%)

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
11	A	2	67
12	B	0	6
All	All	2	73

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	761	A	C5-C6	-10.14	1.31	1.41
11	A	2506	U	N1-C2	8.34	1.46	1.38
13	C	218	MET	CG-SD	6.24	1.97	1.81
13	C	120	MET	CG-SD	5.48	1.95	1.81

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	D	244	ARG	C-N-CD	-10.91	96.59	120.60
11	A	1820	U	C2'-C3'-O3'	9.56	130.53	109.50
11	A	1786	A	N9-C1'-C2'	8.61	125.20	114.00
11	A	1819	A	C2'-C3'-O3'	8.49	128.18	109.50
11	A	1992	G	C2'-C3'-O3'	8.28	127.73	109.50

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
11	A	1819	A	C3'
11	A	1820	U	C3'

5 of 73 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	A	140	G	Sidechain
11	A	15	G	Sidechain
11	A	202	U	Sidechain
11	A	463	G	Sidechain
11	A	532	A	Sidechain

5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	662	0	688	60	0
2	1	731	0	808	67	0
3	2	598	0	653	67	0
4	3	467	0	523	47	0
5	4	340	0	339	52	0
6	5	459	0	480	65	0
7	6	433	0	461	131	0
8	7	418	0	467	28	0
9	8	507	0	576	123	0
10	9	307	0	338	42	0
11	A	62477	0	31497	2205	0
12	B	2551	0	1295	97	0
13	C	1742	0	1800	131	0
14	D	2145	0	2234	234	0
15	E	1563	0	1629	222	0
16	F	1623	0	1677	197	0
17	G	1474	0	1535	228	0
18	H	1222	0	1282	184	0
19	J	651	0	164	31	0
20	K	700	0	173	15	0
21	N	1104	0	1180	171	0
22	O	933	0	996	77	0
23	P	1114	0	1187	265	0
24	Q	1122	0	1179	106	0
25	R	960	0	1021	128	0
26	S	770	0	832	150	0
27	T	1141	0	1202	217	0
28	U	958	0	1015	130	0
29	V	779	0	852	120	0
30	W	896	0	953	86	0
31	X	725	0	778	84	0
32	Y	775	0	870	156	0
33	Z	1403	0	1432	200	0
All	All	93750	0	62116	5634	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 36.

The worst 5 of 5634 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:C:123:VAL:CG2	13:C:127:LEU:HD23	1.33	1.53
13:C:123:VAL:HG23	13:C:127:LEU:CD2	1.50	1.42
11:A:1899:G:N2	11:A:1902:C:H41	1.34	1.24
11:A:2645:G:H3'	11:A:2646:C:H5'	1.21	1.18
27:T:33:LYS:HE3	27:T:43:GLN:HE21	1.06	1.16

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 X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	82/85 (96%)	69 (84%)	10 (12%)	3 (4%)	5	31
2	1	91/98 (93%)	71 (78%)	14 (15%)	6 (7%)	2	15
3	2	69/72 (96%)	44 (64%)	18 (26%)	7 (10%)	1	6
4	3	57/60 (95%)	47 (82%)	5 (9%)	5 (9%)	1	8
5	4	42/71 (59%)	20 (48%)	17 (40%)	5 (12%)	1	4
6	5	57/60 (95%)	39 (68%)	8 (14%)	10 (18%)	0	0
7	6	48/54 (89%)	24 (50%)	8 (17%)	16 (33%)	0	0
8	7	46/49 (94%)	42 (91%)	3 (6%)	1 (2%)	10	46
9	8	61/65 (94%)	34 (56%)	21 (34%)	6 (10%)	1	6
10	9	35/37 (95%)	24 (69%)	8 (23%)	3 (9%)	1	9
13	C	226/229 (99%)	171 (76%)	43 (19%)	12 (5%)	3	21
14	D	273/276 (99%)	217 (80%)	31 (11%)	25 (9%)	1	7
15	E	202/206 (98%)	134 (66%)	39 (19%)	29 (14%)	0	2
16	F	205/210 (98%)	149 (73%)	34 (17%)	22 (11%)	1	5
17	G	179/182 (98%)	119 (66%)	31 (17%)	29 (16%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	H	157/180 (87%)	94 (60%)	33 (21%)	30 (19%)	0	0
21	N	136/140 (97%)	93 (68%)	20 (15%)	23 (17%)	0	0
22	O	120/122 (98%)	106 (88%)	8 (7%)	6 (5%)	3	22
23	P	144/150 (96%)	77 (54%)	37 (26%)	30 (21%)	0	0
24	Q	139/141 (99%)	114 (82%)	20 (14%)	5 (4%)	5	31
25	R	115/118 (98%)	83 (72%)	17 (15%)	15 (13%)	0	3
26	S	96/112 (86%)	49 (51%)	23 (24%)	24 (25%)	0	0
27	T	135/146 (92%)	82 (61%)	30 (22%)	23 (17%)	0	0
28	U	115/118 (98%)	83 (72%)	25 (22%)	7 (6%)	2	16
29	V	99/101 (98%)	62 (63%)	22 (22%)	15 (15%)	0	1
30	W	111/113 (98%)	85 (77%)	14 (13%)	12 (11%)	1	5
31	X	90/96 (94%)	65 (72%)	19 (21%)	6 (7%)	2	14
32	Y	98/110 (89%)	43 (44%)	29 (30%)	26 (26%)	0	0
33	Z	174/206 (84%)	109 (63%)	47 (27%)	18 (10%)	1	6
All	All	3402/3607 (94%)	2349 (69%)	634 (19%)	419 (12%)	1	3

5 of 419 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	75	LEU
2	1	30	VAL
2	1	83	GLU
2	1	85	LEU
3	2	11	GLU

5.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	66/67 (98%)	56 (85%)	10 (15%)	4	16
2	1	78/83 (94%)	71 (91%)	7 (9%)	14	47
3	2	66/67 (98%)	60 (91%)	6 (9%)	14	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	51/52 (98%)	44 (86%)	7 (14%)	5	21
5	4	39/63 (62%)	32 (82%)	7 (18%)	2	10
6	5	51/52 (98%)	43 (84%)	8 (16%)	4	14
7	6	49/52 (94%)	37 (76%)	12 (24%)	1	4
8	7	41/42 (98%)	35 (85%)	6 (15%)	5	18
9	8	53/55 (96%)	45 (85%)	8 (15%)	4	16
10	9	34/34 (100%)	31 (91%)	3 (9%)	14	49
13	C	180/181 (99%)	171 (95%)	9 (5%)	34	75
14	D	217/218 (100%)	186 (86%)	31 (14%)	5	19
15	E	165/166 (99%)	148 (90%)	17 (10%)	10	36
16	F	165/166 (99%)	150 (91%)	15 (9%)	14	45
17	G	155/156 (99%)	138 (89%)	17 (11%)	9	34
18	H	132/148 (89%)	116 (88%)	16 (12%)	7	27
21	N	117/119 (98%)	102 (87%)	15 (13%)	6	24
22	O	100/100 (100%)	95 (95%)	5 (5%)	34	75
23	P	112/116 (97%)	97 (87%)	15 (13%)	6	22
24	Q	111/111 (100%)	97 (87%)	14 (13%)	7	24
25	R	100/101 (99%)	90 (90%)	10 (10%)	11	38
26	S	77/88 (88%)	68 (88%)	9 (12%)	8	29
27	T	120/127 (94%)	98 (82%)	22 (18%)	2	10
28	U	92/94 (98%)	84 (91%)	8 (9%)	15	49
29	V	82/82 (100%)	66 (80%)	16 (20%)	2	8
30	W	91/92 (99%)	86 (94%)	5 (6%)	30	71
31	X	74/78 (95%)	64 (86%)	10 (14%)	6	22
32	Y	84/91 (92%)	70 (83%)	14 (17%)	3	11
33	Z	155/179 (87%)	135 (87%)	20 (13%)	6	24
All	All	2857/2980 (96%)	2515 (88%)	342 (12%)	7	27

5 of 342 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	G	77	ILE
21	N	87	LEU

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Mol	Chain	Res	Type
32	Y	73	ARG
17	G	125	PHE
18	H	143	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
16	F	133	ASN
21	N	133	GLN
30	W	57	ASN
16	F	160	ASN
18	H	139	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	2900/2915 (99%)	508 (17%)	46 (1%)
12	B	118/122 (96%)	25 (21%)	2 (1%)
All	All	3018/3037 (99%)	533 (17%)	48 (1%)

5 of 533 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	10	G
11	A	32	C
11	A	34	C
11	A	45	C
11	A	71	A

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	1300	U
11	A	1558	A
11	A	2750	A
11	A	1301	A
11	A	1427	A

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	84/85 (98%)	0.34	2 (2%) 56 9	50, 66, 95, 108	0
2	1	93/98 (94%)	0.20	0 100 100	54, 71, 121, 129	0
3	2	71/72 (98%)	0.21	0 100 100	88, 107, 126, 142	0
4	3	59/60 (98%)	0.10	1 (1%) 67 15	51, 72, 91, 116	0
5	4	44/71 (61%)	0.89	4 (9%) 9 2	110, 148, 172, 176	0
6	5	59/60 (98%)	0.16	0 100 100	46, 73, 130, 148	0
7	6	50/54 (92%)	0.33	2 (4%) 36 5	54, 82, 106, 114	0
8	7	48/49 (97%)	0.37	3 (6%) 19 3	47, 55, 89, 110	0
9	8	63/65 (96%)	0.21	1 (1%) 68 15	51, 65, 80, 101	0
10	9	37/37 (100%)	0.40	1 (2%) 52 8	61, 77, 96, 98	0
11	A	2901/2915 (99%)	0.12	58 (1%) 62 12	26, 67, 173, 200	0
12	B	119/122 (97%)	0.10	4 (3%) 43 6	55, 82, 104, 123	0
13	C	228/229 (99%)	0.32	10 (4%) 33 5	51, 80, 152, 167	0
14	D	275/276 (99%)	-0.04	1 (0%) 90 45	29, 46, 71, 96	0
15	E	204/206 (99%)	0.07	3 (1%) 70 16	41, 65, 114, 124	0
16	F	207/210 (98%)	0.34	4 (1%) 64 13	45, 97, 152, 159	0
17	G	181/182 (99%)	0.23	4 (2%) 59 11	78, 100, 124, 135	0
18	H	159/180 (88%)	0.38	7 (4%) 33 5	83, 119, 144, 151	0
19	J	0/173	-	-	-	-
20	K	0/147	-	-	-	-
21	N	138/140 (98%)	0.07	1 (0%) 84 32	51, 75, 118, 123	0
22	O	122/122 (100%)	-0.20	0 100 100	35, 50, 62, 65	0
23	P	146/150 (97%)	0.55	6 (4%) 35 5	49, 95, 118, 139	0
24	Q	141/141 (100%)	-0.02	2 (1%) 72 17	39, 54, 76, 117	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	R	117/118 (99%)	0.11	0 100 100	52, 71, 89, 93	0
26	S	98/112 (87%)	0.35	3 (3%) 47 7	71, 90, 114, 117	0
27	T	137/146 (93%)	0.06	1 (0%) 84 32	51, 72, 134, 164	0
28	U	117/118 (99%)	0.13	0 100 100	52, 69, 89, 112	0
29	V	101/101 (100%)	0.23	2 (1%) 62 12	52, 98, 113, 116	0
30	W	113/113 (100%)	0.27	1 (0%) 81 25	56, 72, 103, 134	0
31	X	92/96 (95%)	0.29	2 (2%) 59 11	65, 84, 102, 112	0
32	Y	100/110 (90%)	0.63	5 (5%) 28 4	93, 114, 151, 160	0
33	Z	176/206 (85%)	0.10	1 (0%) 86 36	56, 78, 111, 119	0
All	All	6480/6964 (93%)	0.17	129 (1%) 62 12	26, 73, 146, 200	0

The worst 5 of 129 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
11	A	2802	G	5.9
11	A	2795	G	4.4
11	A	2796	U	4.4
11	A	1090	U	4.3
11	A	654(E)	G	4.2

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.