



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 02:41 am BST

PDB ID : 4V4P  
Title : Crystal structure of 70S ribosome with thrS operator and tRNAs.  
Authors : Jenner, L.; Romby, P.; Rees, B.; Schulze-Bries, C.; Springer, M.; Ehresmann, C.; Ehresmann, B.; Moras, D.; Yusupova, G.; Yusupov, M.  
Deposited on : 2005-01-19  
Resolution : 5.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

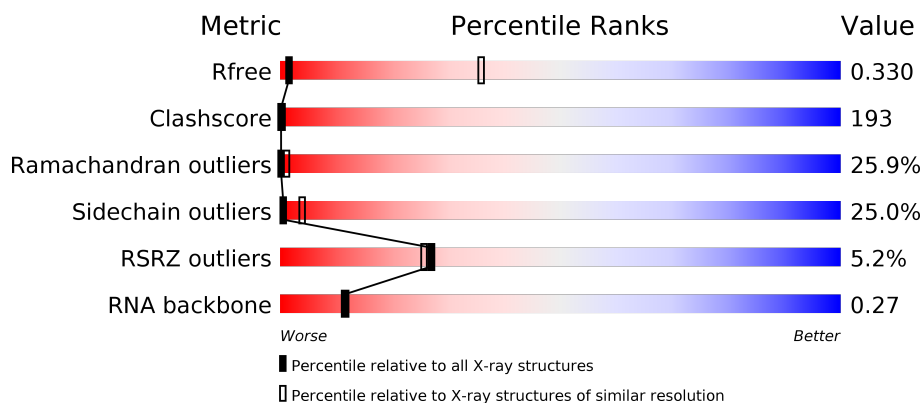
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 5.50 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))
$R_{free}$	130704	1019 (7.12-3.82)
Clashscore	141614	1010 (7.10-3.90)
Ramachandran outliers	138981	1014 (7.12-3.82)
Sidechain outliers	138945	1191 (7.20-3.80)
RSRZ outliers	127900	1023 (7.08-3.76)
RNA backbone	3102	1074 (7.80-3.00)

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

Mol	Chain	Length	Quality of chain
1	AB	123	<div> <div>52%</div> <div>41%</div> <div>7%</div> </div>
2	AA	2915	<div> <div>41%</div> <div>39%</div> <div>18%</div> <div>•</div> </div>
3	AC	228	<div> <div>2%</div> <div>9%</div> <div>64%</div> <div>19%</div> <div>• •</div> </div>
4	AD	178	<div> <div>6%</div> <div>39%</div> <div>40%</div> <div>16%</div> <div>•</div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	AE	338	
6	AF	246	
7	AG	176	
8	AH	177	
9	AI	128	
9	AJ	128	
10	AK	149	
11	AL	141	
12	AM	145	
13	AN	122	
14	AO	164	
15	AP	138	
16	AQ	186	
17	AR	66	
18	AS	113	
19	AT	84	
20	AU	119	
21	AV	253	
22	AW	70	
23	AX	60	
24	A0	118	
25	A1	118	
26	A2	100	
27	A3	91	
28	A4	73	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	A5	60	
30	A6	82	
31	A7	47	
32	A8	64	
33	A9	36	
34	BA	1522	
35	BB	76	
35	BC	76	
36	B1	78	
37	BE	256	
38	BF	239	
39	BG	209	
40	BH	162	
41	BI	101	
42	BJ	156	
43	BK	138	
44	BL	128	
45	BM	105	
46	BN	129	
47	BO	135	
48	BP	126	
49	BQ	61	
50	BR	89	
51	BS	88	
52	BT	105	

Continued on next page...

Mol	Chain	Length	Quality of chain
53	BU	88	
54	BV	93	
55	BW	106	
56	BX	27	

## 2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 148539 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AB	123	Total	C	N	O	P	0	0	0
			2641	1175	488	855	123			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AB	-1	A	-	INSERTION	GB 48271
AB	120	U	-	INSERTION	GB 48271

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AA	2872	Total	C	N	O	P	0	0	0
			61847	27526	11556	19893	2872			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	494	G	-	INSERTION	GB 48268

- Molecule 3 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	221	Total	C	N	O	S	0	0	0
			1687	1066	306	312	3			

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	AD	173	Total	C	N	O	S	0	0	0
			1308	820	246	236	6			

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	191	Total	C	N	O	S	0	0	0
			1507	940	290	273	4			

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	189	Total	C	N	O	S	0	0	0
			1430	872	255	302	1			

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	122	Total	C	N	O	S	0	0	0
			957	597	176	180	4			

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	164	Total	C	N	O	S	0	0	0
			1251	787	225	237	2			

- Molecule 9 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AI	128	Total	C	N	O	S	0	0	0
			945	599	152	193	1			
9	AJ	128	Total	C	N	O	S	0	0	0
			945	599	152	193	1			

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AK	148	Total	C	N	O	S	0	0	0
			1145	727	205	212	1			

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AL	133	Total	C	N	O	S	0	0	0
			999	642	169	182	6			

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AM	117	Total	C	N	O	S	0	0	0
			917	570	164	180	3			

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AN	122	Total	C	N	O	S	0	0	0
			937	585	180	169	3			

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	AO	84	Total	C	N	O	0	0	0
			639	391	109	139			

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AP	138	Total	C	N	O	S	0	0	0
			1081	678	208	192	3			

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AQ	113	Total	C	N	O	S	0	0	0
			866	536	165	164	1			

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AR	52	Total	C	N	O	S	0	0	0
			406	242	74	85	5			

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	AS	108	Total	C	N	O	0	0	0
			860	542	169	149			

- Molecule 19 is a protein called 50S ribosomal protein L23.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AT	76	Total	C	N	O	S	0	0	0
			602	366	102	131	3			

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AU	110	Total	C	N	O	S	0	0	0
			879	531	166	182				

- Molecule 21 is a protein called 50S general stress protein CTC (L25).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	AV	177	Total	C	N	O	S	0	0	0
			1360	859	238	257	6			

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AW	64	Total	C	N	O	S	0	0	0
			494	301	93	99	1			

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AX	60	Total	C	N	O	S	0	0	0
			477	303	91	82	1			

- Molecule 24 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	A0	105	Total	C	N	O	S	0	0	0
			855	536	174	145				

- Molecule 25 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	A1	117	Total	C	N	O	S	0	0	0
			978	608	210	159	1			

- Molecule 26 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	A2	100	Total	C	N	O	S	0	0	0
			787	495	146	145	1			

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	A3	86	Total	C	N	O	S	0	0	0
			641	402	124	114	1			

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	A4	73	Total	C	N	O	S	0	0	0
			604	382	110	108	4			

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	A5	58	Total	C	N	O	S	0	0	0
			457	281	94	77	5			

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	A6	53	Total	C	N	O	S	0	0	0
			431	274	80	76	1			

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	A7	46	Total	C	N	O	S	0	0	0
			383	230	91	60	2			

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	A8	63	Total	C	N	O	S	0	0	0
			496	312	101	78	5			

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	A9	35	Total	C	N	O	S	0	0	0
			285	172	64	45	4			

- Molecule 34 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	BA	1515	Total	C	N	O	P	0	0	0
			32554	14490	6022	10527	1515			

- Molecule 35 is a RNA chain called tRNA Phe (unmodified bases).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	BB	76	Total	C	N	O	P	0	0	0
			1626	725	293	532	76			
35	BC	76	Total	C	N	O	P	0	0	0
			1626	725	293	532	76			

- Molecule 36 is a RNA chain called thrS mRNA operator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	B1	66	Total	C	N	O	P	0	0	0
			1405	629	247	463	66			

- Molecule 37 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
37	BE	234	Total	C	N	O	S	0	0	0
			1900	1213	341	341	5			

- Molecule 38 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
38	BF	206	Total	C	N	O	S	0	0	0
			1612	1016	314	281	1			

- Molecule 39 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
39	BG	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 40 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
40	BH	150	Total	C	N	O	S	0	0	0
			1146	724	217	201	4			

- Molecule 41 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
41	BI	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
42	BJ	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 43 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
43	BK	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BK	25	ASP	GLU	CONFLICT	UNP Q5SHQ2
BK	37	ARG	LYS	CONFLICT	UNP Q5SHQ2
BK	52	ASP	GLU	CONFLICT	UNP Q5SHQ2
BK	61	VAL	ILE	CONFLICT	UNP Q5SHQ2
BK	62	TYR	HIS	CONFLICT	UNP Q5SHQ2
BK	81	HIS	LYS	CONFLICT	UNP Q5SHQ2
BK	88	LYS	ARG	CONFLICT	UNP Q5SHQ2
BK	115	SER	PRO	CONFLICT	UNP Q5SHQ2

- Molecule 44 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
44	BL	127	Total	C	N	O	0	0	0
			1011	639	198	174			

- Molecule 45 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
45	BM	98	Total	C	N	O	S	0	0	0
			794	499	156	138	1			

- Molecule 46 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
46	BN	119	Total	C	N	O	S	0	0	0
			885	549	168	165	3			

- Molecule 47 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
47	BO	124	Total	C	N	O	S	0	0	0
			970	611	195	163	1			

- Molecule 48 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
48	BP	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			

- Molecule 49 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
49	BQ	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 50 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
50	BR	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

- Molecule 51 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
51	BS	83	Total	C	N	O	S	0	0	0
			700	443	139	117	1			

- Molecule 52 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
52	BT	104	Total	C	N	O	S	0	0	0
			857	547	161	147	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BT	96	GLN	GLU	CONFLICT	UNP Q5SHP7

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
53	BU	73	Total	C	N	O	S	0	0	0
			597	380	118	99				

- Molecule 54 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
54	BV	80	Total	C	N	O	S	0	0	0
			647	414	119	112	2			

- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
55	BW	99	Total	C	N	O	S	0	0	0
			762	469	162	129	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BW	41	VAL	ILE	CONFLICT	UNP Q5SIH2

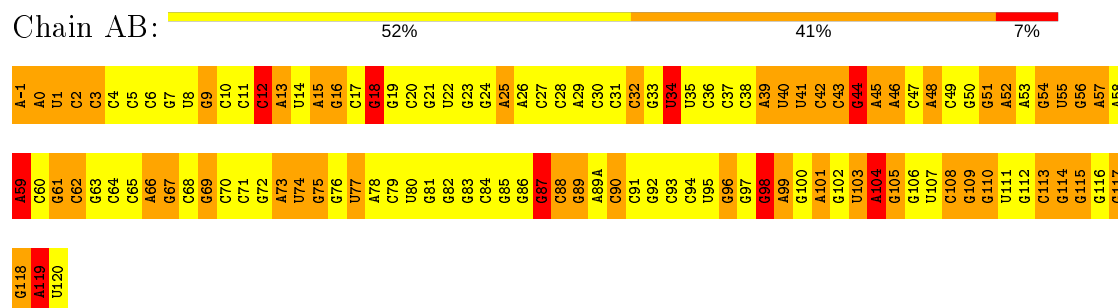
- Molecule 56 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
56	BX	24	Total	C	N	O	S	0	0	0
			208	128	50	30				

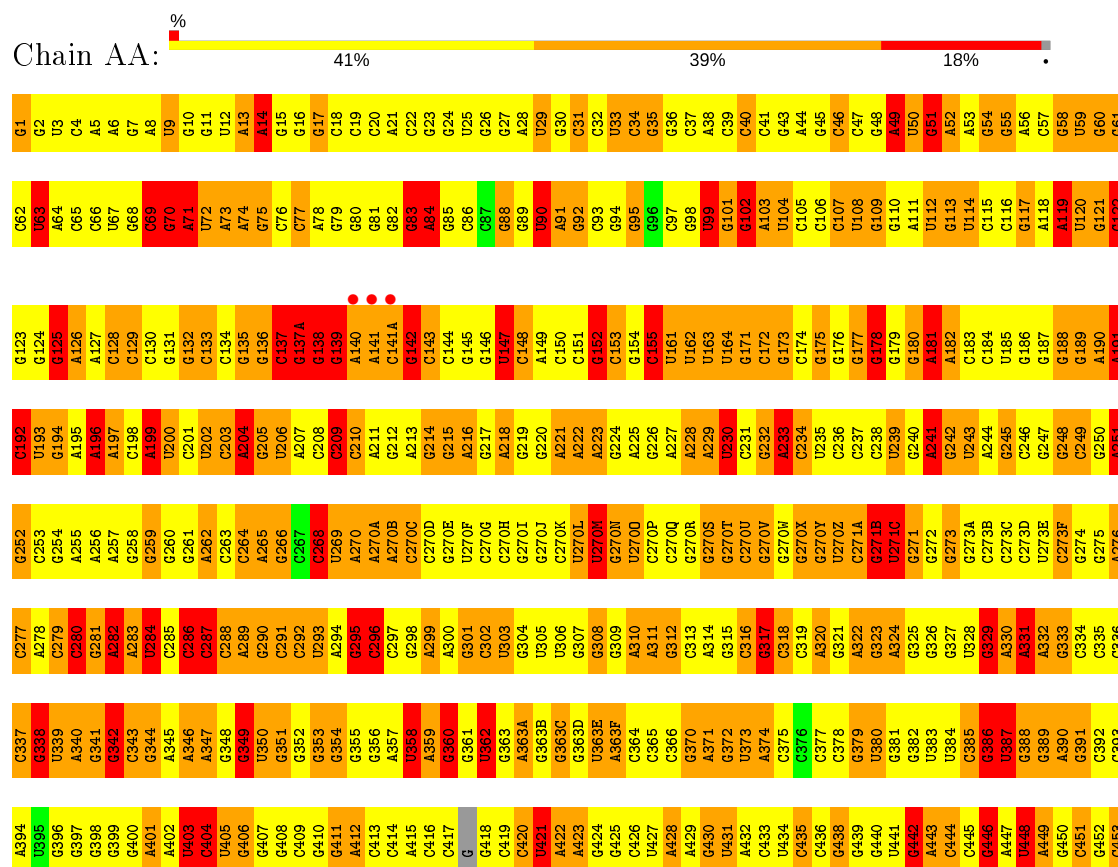
### 3 Residue-property plots

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 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 ( $\text{RSRZ} > 2$ ). 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: 5S ribosomal RNA



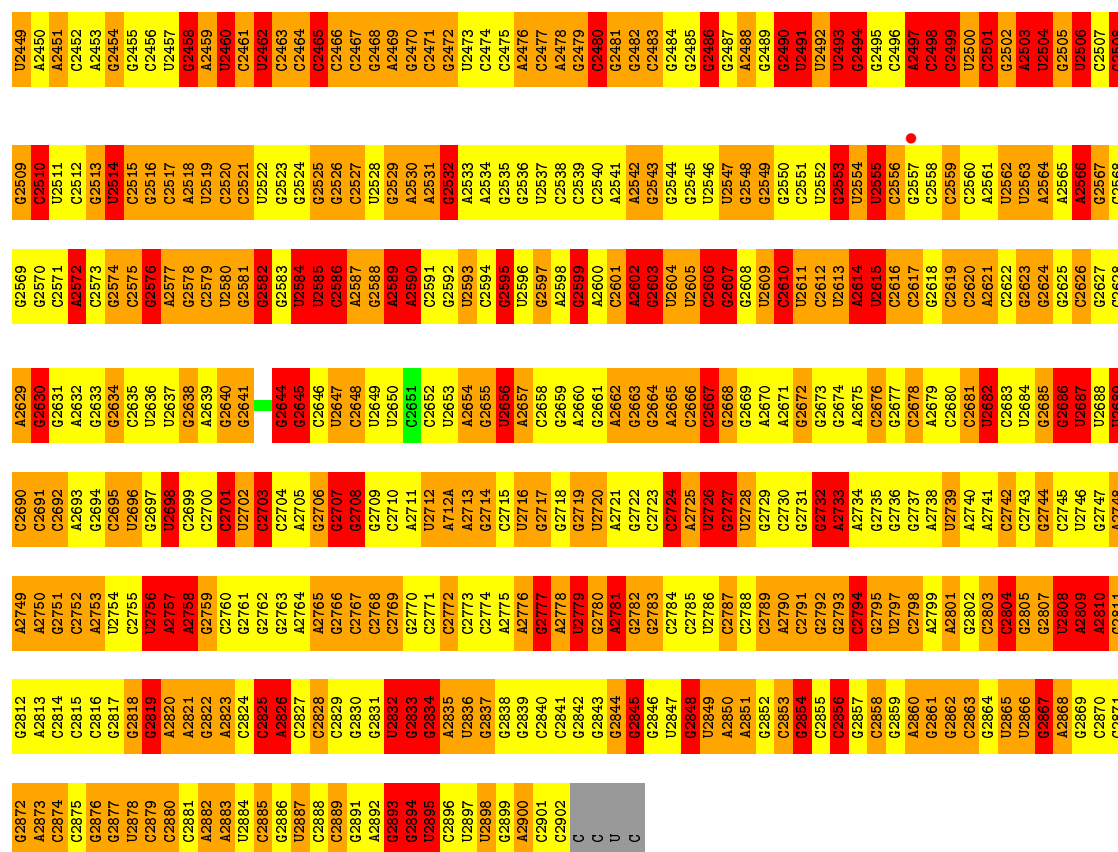
#### • Molecule 2: 23S ribosomal RNA



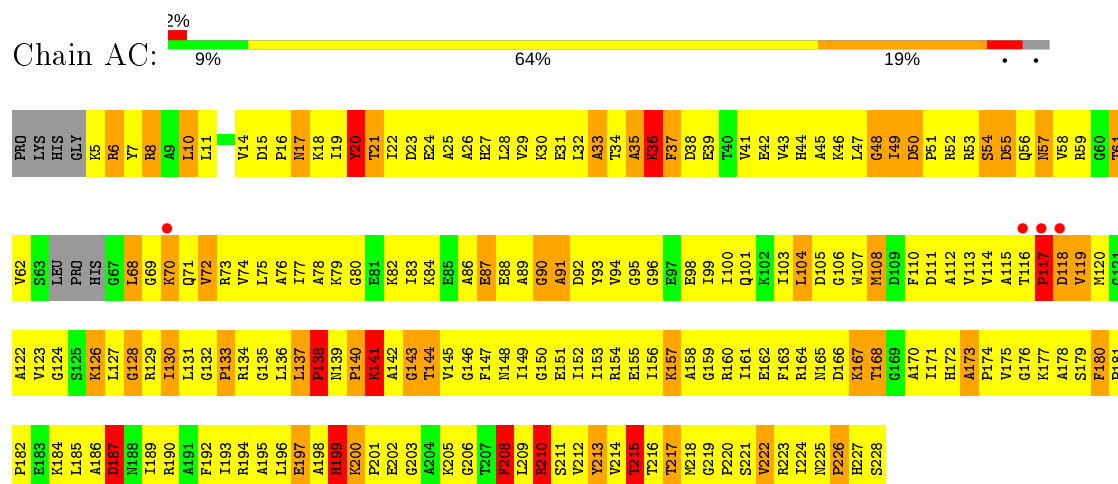
A1395	U1335	A1275	G1215	G1154	A1095	U1035	C975	C915	G854	G794	A734	G674	C635	G577	A515	A454
A1396	A1336	A1276	G1216	A1155	A1096	G1036	C976	G916	G855	C795	A735	A675	G636	A578	C516	C485
U1397	G1337	G1277	C1217	A1156	U1097	G1037	G977	A917	C856	C796	C736	A676	A637	G579	G517	C486
G1398	G1338	A1278	G1218	A1157	A1098	C1038	G978	A918	C857	C797	C737	A677	G638	C580	G518	A457
G1399	G1339	G1279	G1219	C1158	G1099	G1039	G979	G920	U858	G798	G738	C678	U639	C581	U519	G458
G1400	U1340	G1280	A1220	U1159	C1100	C1040	A980	G921	G859	G799	G739	C679	C640	G582	G520	U459
G1401	U1341	G1281	C1221	G1160	U1101	C1041	A981	G922	U860	A800	U740	G680	C641	G583	G521	A460
C1402	A1342	U1282	C1222	C1161	A1102	G1042	C982	U922	G861	G801	G741	G681	G642	C584	G522	C461
G1403	G1343	G1283	C1223	A1162	C1103	C1043	A983	C923	G862	A802	G742	G682	A643	C585	G523	C462
G1404	G1344	A1284	G1224	G1163	A1104	G1044	A984	C924	A863	U803	G743	C683	A644	A586	U524	G463
U1405	G1345	G1285	C1225	G1164	U1105	A1045	C985	C925	G864	A804	G744	G684	C645	C587	U525	U464
U1406	G1346	A1286	G1226	U1165	G1106	A1046	C986	A926	G865	G805	G745	A685	A646	U588	A526	G465
G1407	G1347	G1287	C1227	C1166	G1107	G1047	G987	G928	A866	C806	A746	G686	G647	C589	C527	A466
G1408	G1348	U1288	G1228	U1167	U1108	A1048	A988	G929	C867	U807	U747	C687	G648	A590	A528	G467
G1409	G1349	C1289	G1229	G1168	C1109	A1049	G989	U930	U868	G808	G748	U688	G649	C591	A529	G468
G1410	C1350	C1290	G1230	G1169	A1110	A1050	A990	G931	G869	G809	C749	A689	C	G592	A530	G469
C1411	C1351	C1291	G1231	G1170	A1111	G1051	C991	G932	A870	U810	A750	G690	G	G593	C531	A470
A1412	U1352	U1292	G1232	G1171	G1112	C1052	C992	A933	U871	U811	A751	C691	C	U594	A532	A471
G1413	A1353	C1293	C1233	G1173	U1113	C1053	G993	G934	A872	C812	A752	C692	A	C595	G533	A472
G1414	A1354	U1294	U1234	A1174	G1114	A1054	C994	C935	G873	U813	C753	C693	A	G596	U534	G473
U1415	G1355	C1295	G1235	U1175	G1115	G1055	C995	C936	G874	C814	C754	U694	G	U597	G535	G474
G1416	G1356	G1296	G1236	G1176	C1116	A1056	A996	U937	G875	C815	C755	G695	C	G598	A536	U475
C1417	U1357	C1297	A1237	A1177	G1117	A1057	G997	G938	C876	C816	C756	G696	G	G599	C537	G476
G1418	G1358	C1298	G1238	C1178	G1118	G1058	C998	G939	U877	C817	U757	C697	G	G600	G539	A477
U1419	A1359	G1299	G1239	C1179	C1119	G1059	U999	G940	A878	G818	C758	C698	G	C601	G540	A478
U1420	A1360	U1300	U1240	C1180	G1120	U1060	A1000	A941	G879	A819	G759	A699	C	G602	C541	A479
G1421	G1361	A1301	A1241	C1181	C1121	U1061	A1001	G942	G880	A820	G760	G700	C	A603	C542	A480
G1422	C1362	A1302	A1242	A1182	G1122	G1062	G1002	U943	G881	A821	A761	G701	G	G604	C543	G481
G1423	C1363	G1303	G1243	G1183	C1123	G1063	G1003	G944	G882	U822	U762	G702	C	C605	C544	A482
G1424	G1364	C1304	G1244	G1184	C1124	C1064	G1004	A945	G883	G823	G763	G703	A	U606	G545	A483
G1425	A1365	C1305	G1245	C1185	G1125	U1065	C1005	G946	C884	A824	A764	G704	C	U607	C546	C484
G1426	A1366	C1306	A1246	G1186	A1126	U1066	C1006	G947	C885	C825	G765	A705	G	A608	A547	C485
A1427	A1367	A1307	A1247	G1187	A1127	A1067	C1007	G948	C886	U826	C766	A706	C	A609	A548	C486
C1428	G1368	A1308	G1248	U1188	A1128	G1068	C1008	C949	A887	U827	U767	G707	G	G609A	G549	C487
G1429	G1369	G1309	U1249	A1189	A1129	A1069	A1009	G950	C888	U828	G768	C708	G	C610	G550	G488
C1430	C1370	G1310	G1250	G1190	U1130	A1070	A1010	C951	C889	A829	G769	U709	C	C611	G551	G489
U1431	G1371	G1311	C1251	G1191	G1131	G1071	G1011	G952	A890	G830	G770	G710	C	G612	G552	G491
C1432	U1372	U1312	G1252	G1192	A1132	C1072	U1012	A953	G892	G831	G771	G711	G650	U613	U553	A492
U1433	A1373	U1313	A1253	G1193	U1133	A1073	C1013	G954	C893	G832	C772	G712	C	G614	U554	G493
A1434	G1374	C1314	A1254	A1194	G1134	G1074	U1014	C955	C894	U833	U773	G713	G652	U615	G556	G494
G1435	C1375	C1315	U1255	G1195	C1135	C1075	U895	G956	U895	C834	A774	G714	A654	A616	U557	G495
G1436	C1376	U1316	G1256	C1196	G1136	C1076	G1016	A957	A896	A835	G775	G715	A655	G617	G558	G496
G1437	G1377	A1317	C1257	G1197	G1137	A1077	G1017	U958	C897	G836	G776	A716	G656	G618	G559	A497
U1438	U1378	C1318	C1258	U1198	G1138	U1078	C1018	U959	C898	C837	A777	G717	U657	C618A	C560	G498
A1439	A1379	C1319	G1259	U1199	G1139	C1079	A999	A960	A899	C838	G778	A718	C658	G619	G561	U499
G1440	G1380	C1320	G1260	C1200	U1140	C1080	A1020	C961	A900	U839	U779	C719	G659	G620	U562	G500
G1441	G1381	A1321	C1261	C1201	U1141	U1081	A1021	G962	A901	C840	G780	C720	G660	A621	G563	A501
G1442	G1382	C1322	A1262	C1202	U1142	U1082	U1022	U963	C902	A841	A781	C721	C661	G622	C564	A502
G1443	C1383	U1323	U1263	G1203	A1424	U1083	U1023	C964	C903	G842	A782	A722	G662	G623	C565	A503
G1444	A1384	G1324	G1264	A1204	A1143	A1084	C904	C965	C904	G843	A783	G723	G663	C624	U566	U504
A4444	G1385	G1325	A1265	U1205	G1144	A1085	G1025	G966	U905	C844	A784	U724	C664	G625	A567	A505
C1445	C1386	U1326	G1266	G1206	C1145	A1086	U1026	C967	G906	G845	G785	G725	C665	U626	U568	G506
G1446	C1387	C1327	U1267	C1207	G1146	G1087	A1027	U968	U907	C846	C786	A726	G666	U627	U569	A507
G1447	G1388	G1328	A1268	C1208	C1147	A1088	U969	U969	C908	U847	U787	U627	U667	G628	G570	G508
A1448	G1389	U1329	A1269	G1209	A1148	U1089	A1029	C970	A848	G848	A788	G728	G668	G629	A571	C509
U1449	U1390	C1330	C1270	A1210	G1149	U1090	C971	C971	A910	A849	A789	G729	G669	G630	A572	C510
G449A	U1391	A1331	G1271	U1211	C1150	G1091	G1031	G972	A911	C850	C790	C730	A670	A631	G573	U511
C1450	A1392	G1332	A1272	G1212	G1151	G1092	U1032	A973	C912	U851	C791	C731	C671	A632	C574	G512
G1451	A1393	C1333	U1273	A1213	G1152	G1093	U1033	G974	U913	G852	G792	C732	C672	A633	A575	G513
A1453	U1394	G1334	A1274	A1214	C1153	U1094	G1034	C974A	C914	G853	A793	G733	C673	C634	U576	A514



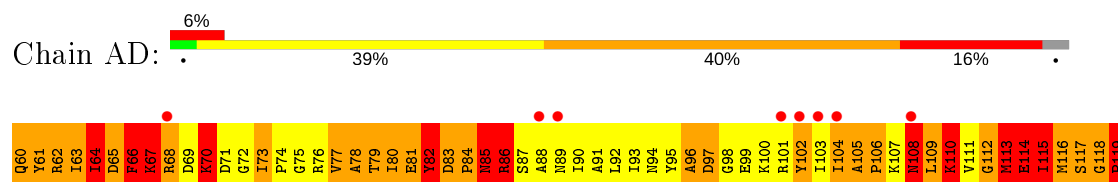




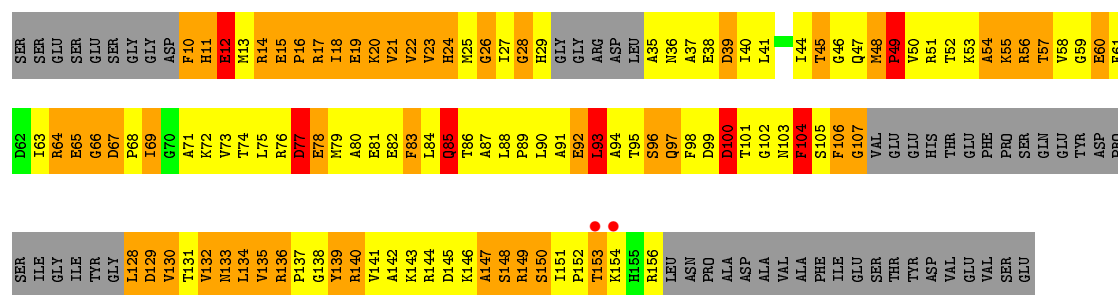
### • Molecule 3: 50S ribosomal protein L1



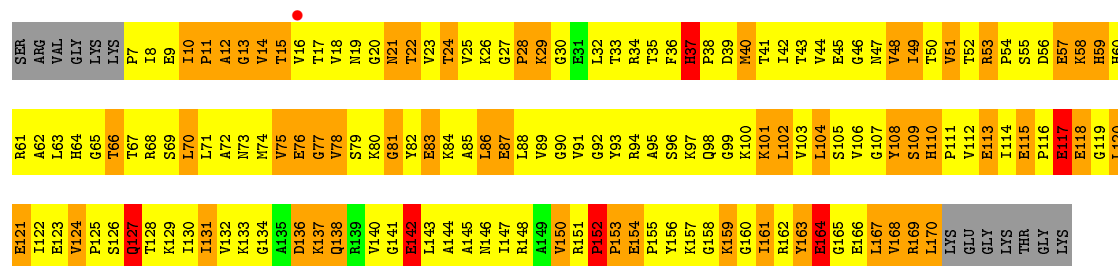
### • Molecule 4: 50S ribosomal protein L2



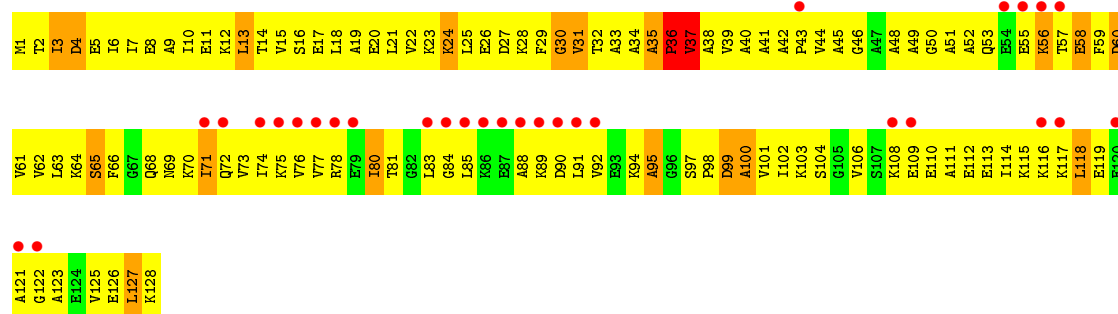




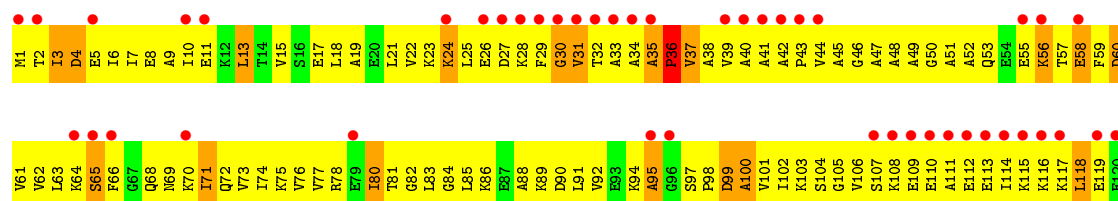
• Molecule 8: 50S ribosomal protein L6

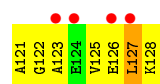


• Molecule 9: 50S ribosomal protein L7/L12

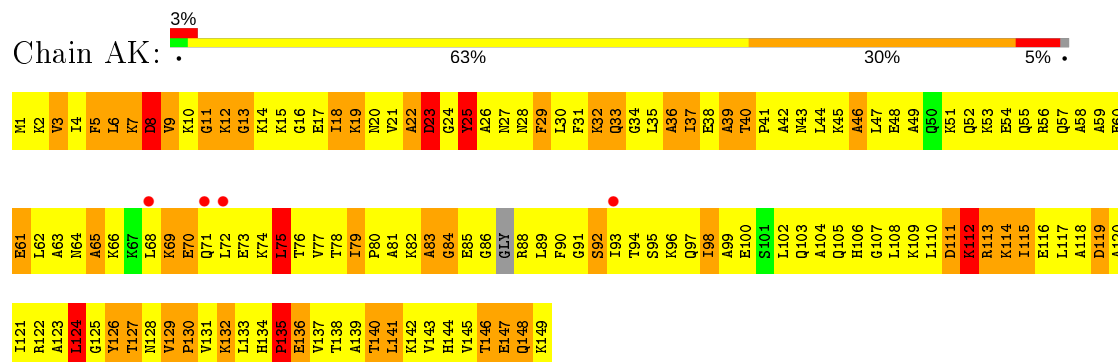


• Molecule 9: 50S ribosomal protein L7/L12

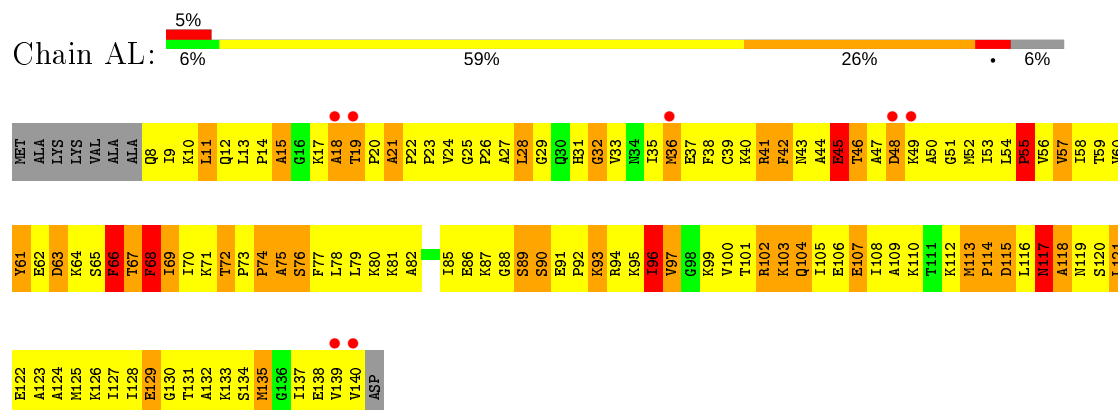




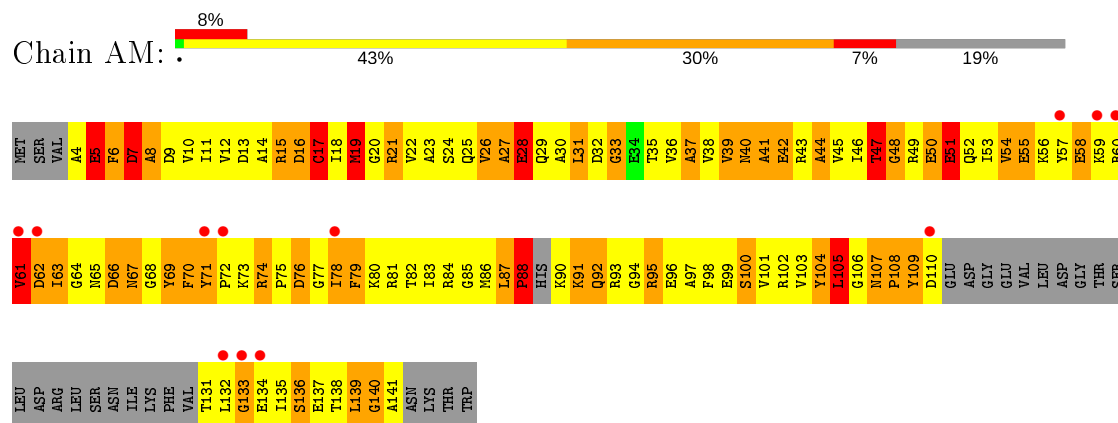
• Molecule 10: 50S ribosomal protein L9



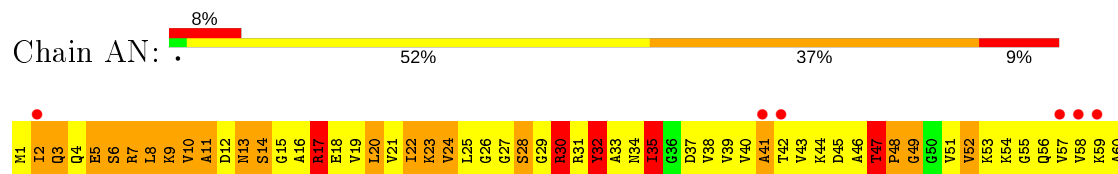
• Molecule 11: 50S ribosomal protein L11

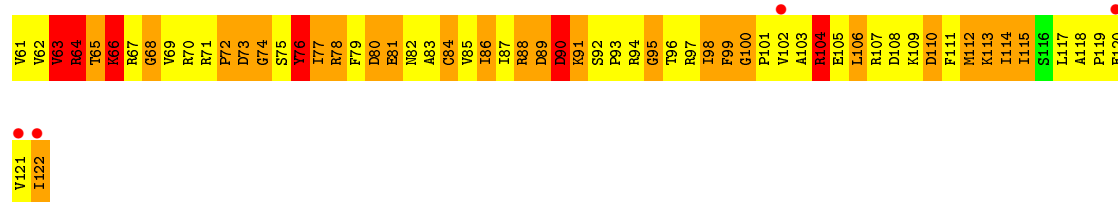


• Molecule 12: 50S ribosomal protein L13

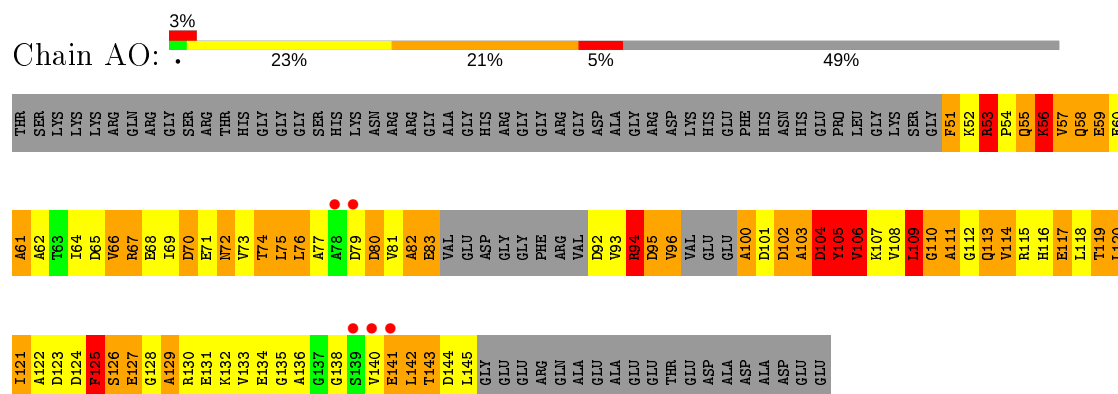


• Molecule 13: 50S ribosomal protein L14

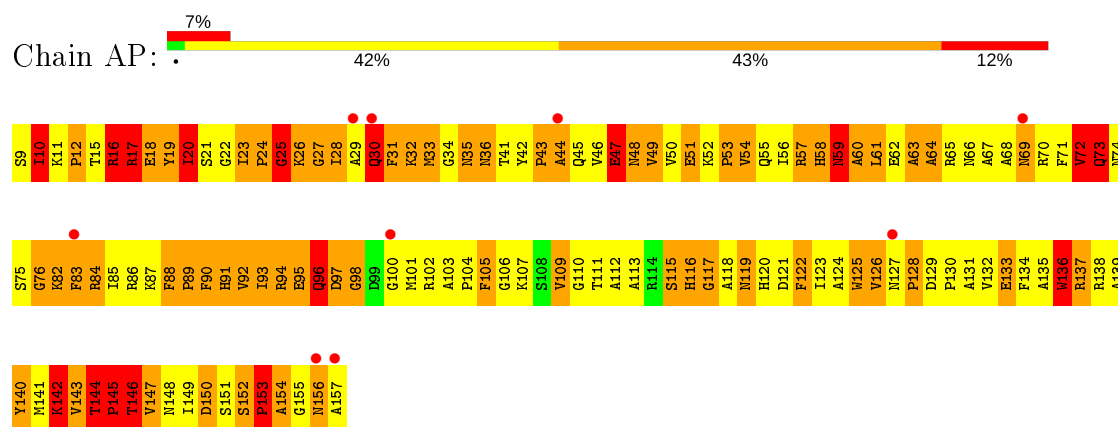




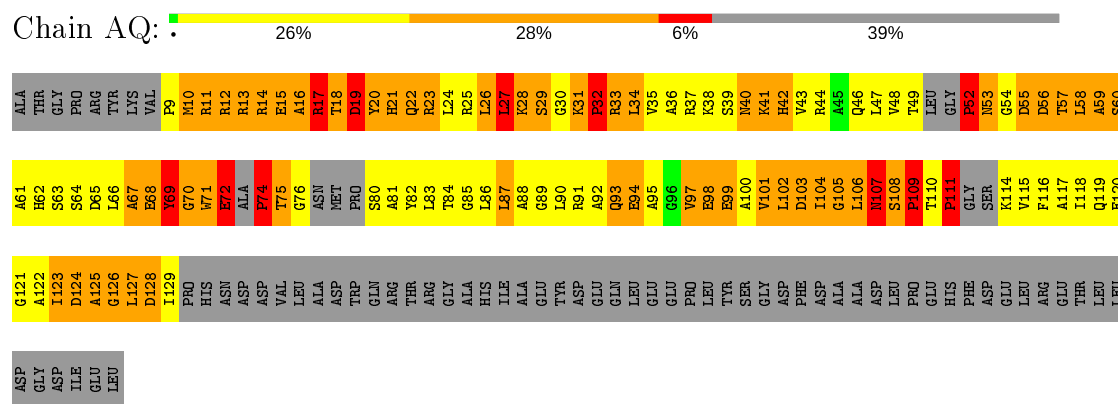
• Molecule 14: 50S ribosomal protein L15



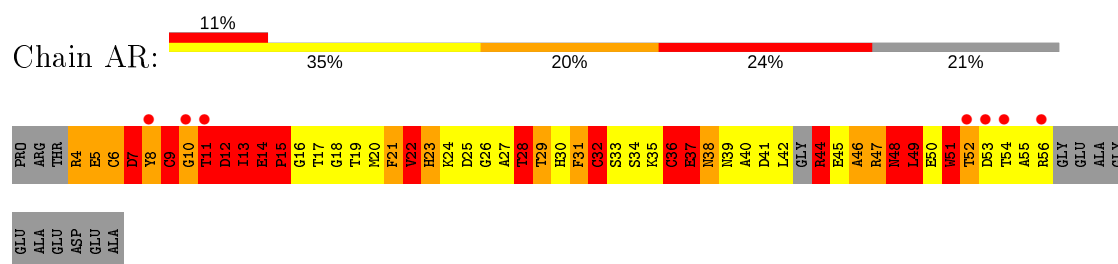
• Molecule 15: 50S ribosomal protein L16



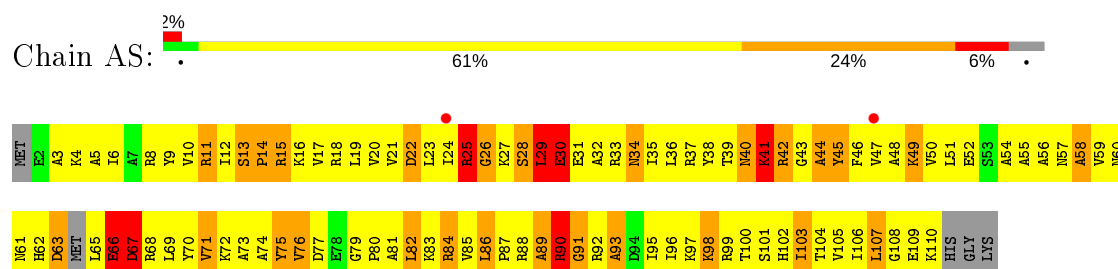
• Molecule 16: 50S ribosomal protein L18



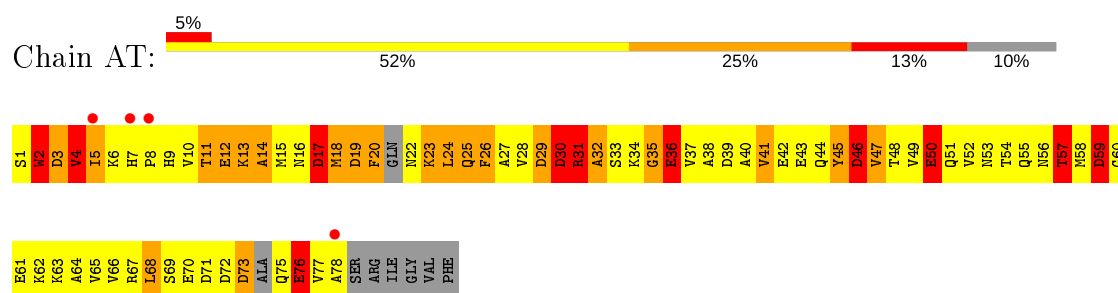
• Molecule 17: 50S ribosomal protein L19



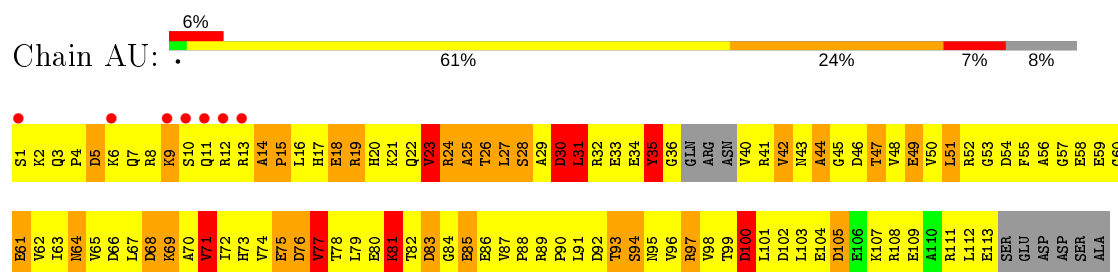
• Molecule 18: 50S ribosomal protein L22



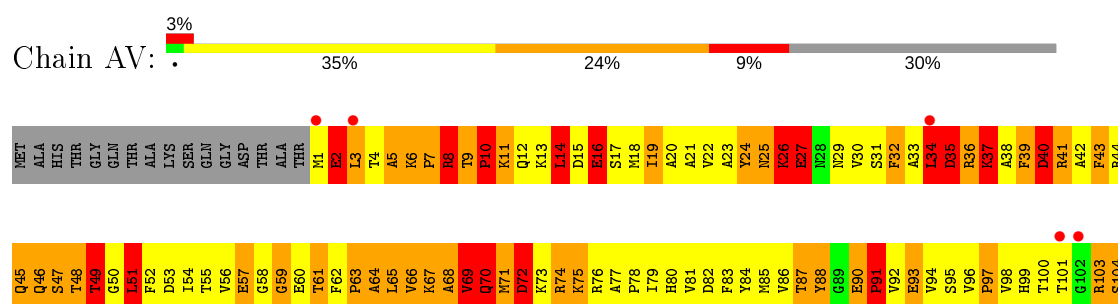
• Molecule 19: 50S ribosomal protein L23

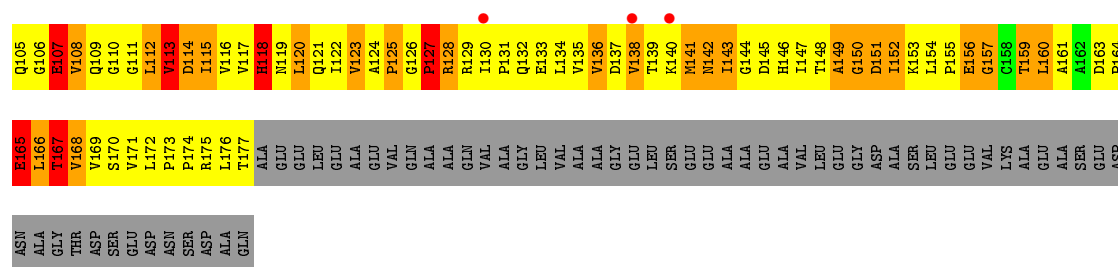


• Molecule 20: 50S ribosomal protein L24

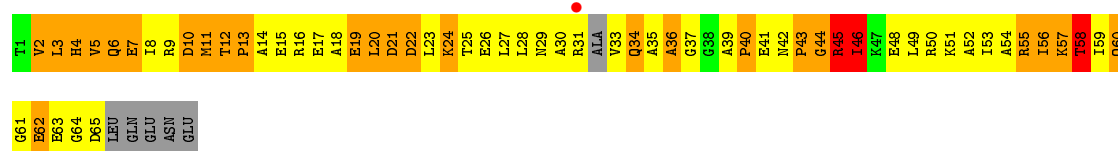


• Molecule 21: 50S general stress protein CTC (L25)





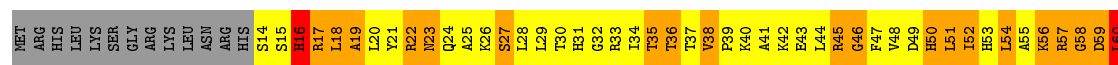
- Molecule 22: 50S ribosomal protein L29



- Molecule 23: 50S ribosomal protein L30



- Molecule 24: 50S ribosomal protein L17



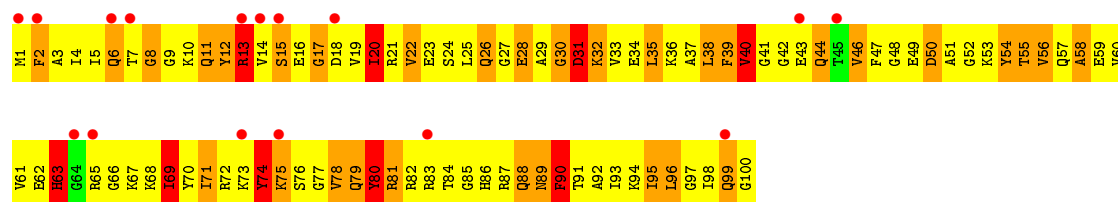
- Molecule 25: 50S ribosomal protein L20



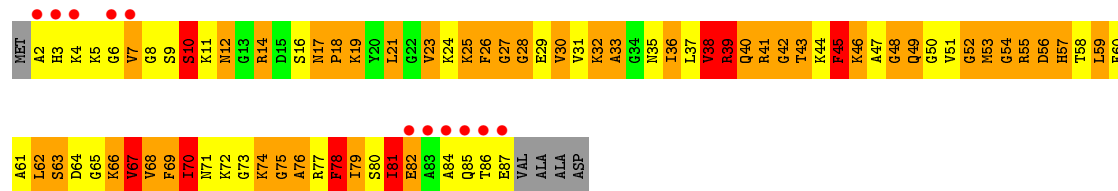
- Molecule 26: 50S ribosomal protein L21







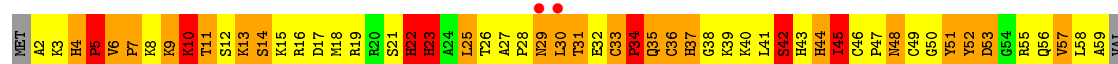
• Molecule 27: 50S ribosomal protein L27



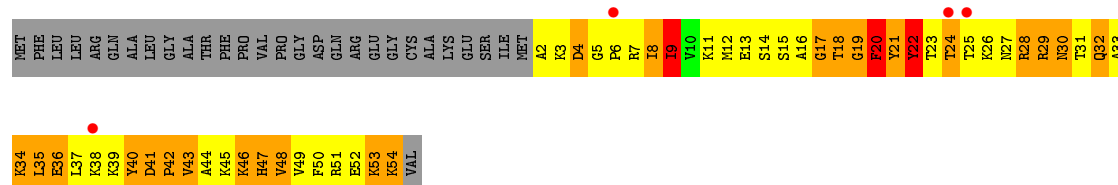
• Molecule 28: 50S ribosomal protein L31



• Molecule 29: 50S ribosomal protein L32



• Molecule 30: 50S ribosomal protein L33



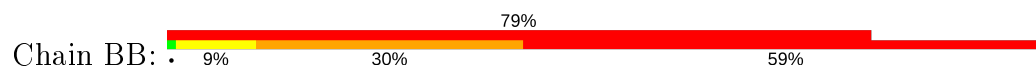
• Molecule 31: 50S ribosomal protein L34

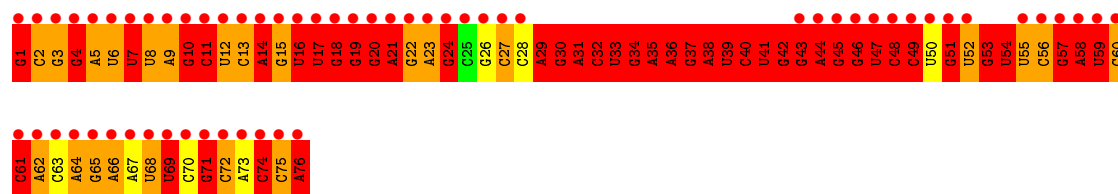




G1523	C1463	A1398	A1339	A1279	U1219	C1098	C1038	A983	A923	U863	C797	A737	U677	G617
G1524	G1464	C1399	A1340	A1280	G1220	G1099	C1039	C984	C924	A864	G798	C738	U678	G618
G1525	G1465	C1400	U1341	U1281	G1221	G1099	U1040	C985	C925	A865	G799	C739	U679	G619
G1526	C1466	G1401	C1342	U1282	G1222	A1100	A1041	C986	G926	C866	G800	U740	C679	G620
C1527	G1467	C1402	G1343	G1283	G1223	A1102	G1042	C987	G927	C867	U801	G741	C681	A621
A1468	C1403	C1403	G1344	C1284	G1224	C1103	C1043	G988	G928	C868	A802	G742	C682	A622
G1469	U1345	A1285	U1345	A1285	A1225	G1104	A1044	C989	G929	C869	G803	U743	G683	G623
G1470	A1346	A1286	A1346	A1286	G1226	G1105	C1045	C990	G930	U870	U804	C744	A684	C624
G1471	U1406	A1287	G1347	A1287	A1227	A1106	A1046	C991	C931	U871	C805	C745	G695	G625
C1532	A1472	A1288	U1348	A1288	C1228	G1107	G1047	U992	C932	A872	C806	C746	U686	U626
A1534	A1473	A1408	A1349	A1289	G1229	G1108	G1048	G993	G933	A873	A807	C747	A687	G627
C1535	G1474	C1409	A1350	G1290	G1230	G1109	U1049	A994	C934	G874	C808	C748	G688	G628
C1536	G1475	G1410	U1351	G1291	G1231	A1110	C1050	C995	A935	C875	G809	C749	G689	G629
U1537	G1476	C1411	C1352	U1292	U1232	A1111	C1051	A996	C936	G876	C810	G750	G690	G630
U1538	C1477	C1412	G1353	G1293	G1233	C1112	U1052	U997	A937	C877	C811	G751	G691	G631
U1539	C1478	C1413	C1354	G1294	C1234	C1113	G1053	G998	A938	G878	C812	G752	U692	A632
U1540	C1479	U1414	G1355	G1295	U1235	C1114	C1054	C999	G939	C879	U813	A753	G693	G633
U1541	G1480	G1415	G1356	C1296	A1236	C1115	A1055	U1000	C940	C880	A814	C754	A694	C634
U1542	U1481	G1416	A1357	G1297	C1237	C1116	U1056	A1001	G941	G881	A815	G755	A695	G635
C	G1482	G1417	U1358	C1298	A1238	G1117	G1057	G1002	G942	C882	A816	C756	A696	U636
U	A1483	A1418	C1359	A1299	A1239	C1118	G1058	C1003	C943	C883	C817	C757	U697	G637
	C1484	G1419	A1360	G1300	U1240	C1119	C1059	G3A	G944	U884	G818	G758	G698	G638
	U1485	C1420	G1361	U1301	G1241	G1120	C1060	A1094	G945	G885	A819	A759	C699	G639
	G1486	G1421	C361A	U1302	G1242	A1121	G1061	A1005	A946	G886	U820	G760	G700	A640
	G1487	G1422	C1362	C1303	C1243	U1122	U1062	C1006	G947	G887	G821	C761	C701	U641
	G1488	G1423	A1363	G1304	C1244	A1123	C1063	C1007	C948	G888	C822	C762	A702	A642
	G1489	C1424	U1364	G1305	A1245	G1124	G1064	C1008	A949	A889	G823	G763	G703	C643
	C1490	U1425	G1365	A1306	C1246	U1125	U1065	C1009	U950	C890	C824	C764	A704	G644
	G1491	C1426	C1366	U1307	U1247	U1126	C1066	G1010	G951	U891	G825	G765	U705	C645
	A1492	U1427	C1367	U1308	A1248	G1127	A1067	G1011	U952	A892	C826	A766	A706	U646
	A1493	A1428	G1368	G1309	C1249	C1128	G1068	U1012	G953	C893	U827	C767	C707	C647
	G1494	C1429	C1369	G1310	A1250	C1129	C1069	G1013	G954	C894	A828	A768	C708	A648
	U1495	C1430	G1370	G1311	A1251	A1130	U1070	A1014	U955	G895	G829	G769	G709	G649
	G1496	C1431	G1371	G1312	A1252	G1131	C1071	A1015	U956	C896	G830	C770	G710	G650
	G1497	A1432	G1372	C1313	G1253	C1132	G1072	A1016	U957	C897	U831	G771	G711	C651
	U1498	A1433	G1373	C1314	C1254	G1133	U1073	G1017	A958	G898	C832	U772	A712	U652
	A1499	A1434	A1374	U1315	G1255	G1134	G1074	C1018	A959	C899	U833	G773	G713	A653
	A1500	G1435	A1375	G1316	A1256	U1135	C1075	C1019	U960	A900	C834	G774	G714	G654
	C1501	U1436	U1376	C1317	U1257	U1136	C1076	U1020	G961	A901	U835	G775	A715	A655
	A1502	C1437	A1377	A1318	G1258	C1137	G1077	G1021	C962	G902	G836	G776	A716	C656
	G1503	C1438	C1378	A1319	C1259	G1138	U1078	G1022	G963	G903	G837	U777	C717	G657
	G1504	A1439	G1379	C1320	C1260	G1139	G1079	G1023	A964	C904	G838	G778	G718	G658
	U1505	U1440	U1380	C1321	A1261	C1140	A1080	G1024	A965	U905	U839	C779	C719	U659
	U1506	G1441	U1381	C1322	C1262	C1141	G1081	U1035	G966	G906	C840	A780	C720	G660
	A1507	G1442	C1382	G1323	C1263	G1142	G1082	G1026	C967	A907	U841	A781	G721	G661
	G1508	C1383	C1383	A1324	C1264	G1143	U1083	C1027	A968	A908	C848	A782	A722	G662
	C1509	A1446	C1384	C1325	G1265	G1144	G1084	C1028	A969	A909	C849	C783	U723	A663
	U1510	G1447	G1385	C1326	G1266	C1145	U1085	C1029	C970	C910	U850	C784	G724	G664
	G1511	C1448	G1386	C1327	C1267	A1146	U1086	G1030	G971	U911	G851	G785	G725	A665
	U1512	C1449	G1387	C1328	A1268	C1147	G1087	G30A	C972	C912	G852	G786	C726	G666
	A1513	C1388	C1388	A1329	A1269	U1148	G1088	C30B	G973	A913	G853	A787	G727	G667
	C1514	U1450	C1389	U1330	G1270	C1149	G1089	G30C	A974	A914	G854	A788	A728	G668
	U1515	A1451	C1452	G1331	G1271	C1150	U1090	A30D	A975	A915	G855	A789	A729	U669
	G1516	G1453	U1391	A1332	G1272	A1151	U1091	G1031	G976	G916	C856	A790	G730	G670
	G1517	G1454	G1392	A1333	G1273	A1152	A1092	G1032	A977	G917	C857	A791	G731	G671
	A1518	G1455	U1393	G1334	G1274	C1153	A1093	G1033	A978	A918	G858	A792	G732	U672
	U1519	C1459	A1394	C1335	A1275	G1154	G1094	G1034	C979	A919	A859	U793	A733	G673
	G1520	A1460	C1395	G1336	G1276	G1155	U1095	A1035	C980	U920	A860	A794	G734	G674
	U1521	G1461	A1396	G1337	G1277	G1156	C1096	G1036	U981	U921	G861	C795	A675	A675
	U1522	G1462	C1397	G1338	U1278	A1157	C1097	C1037	U982	G922	C862	C796	C736	A676

• Molecule 35: tRNA Phe (unmodified bases)





• Molecule 35: tRNA Phe (unmodified bases)

Chain BC: . 42% 38% 18%



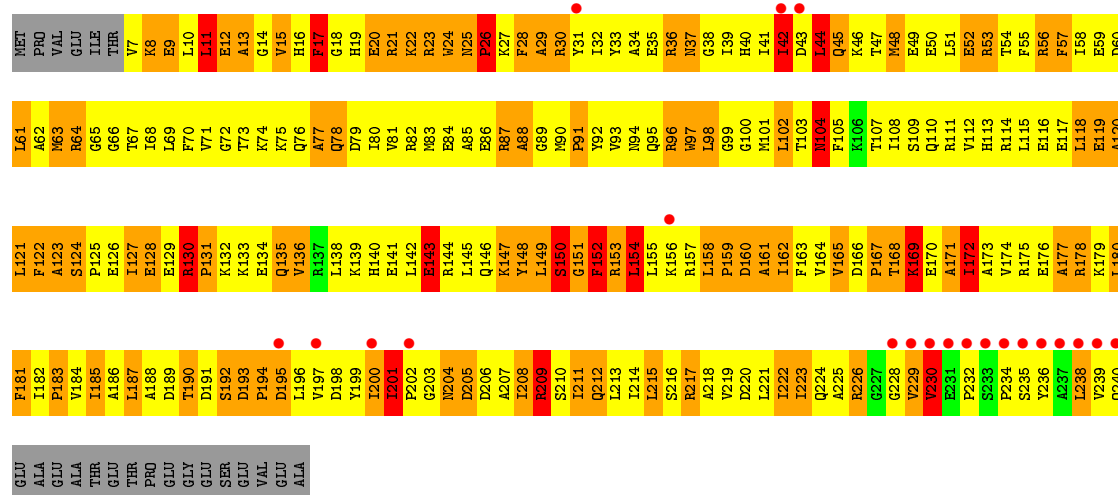
• Molecule 36: thrS mRNA operator

Chain B1: . 55% 50% 26% 6% 15%



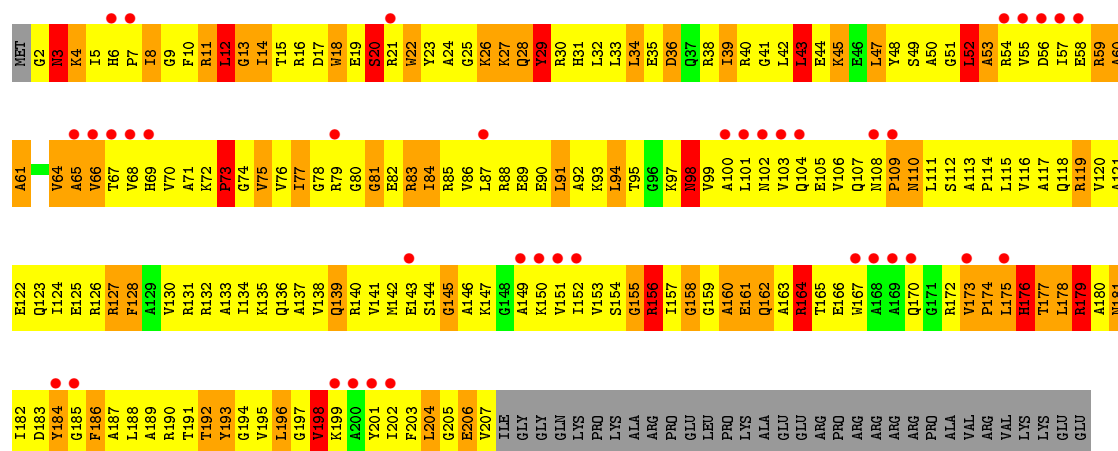
• Molecule 37: 30S ribosomal protein S2

Chain BE: . 8% 50% 33% 6% 9%

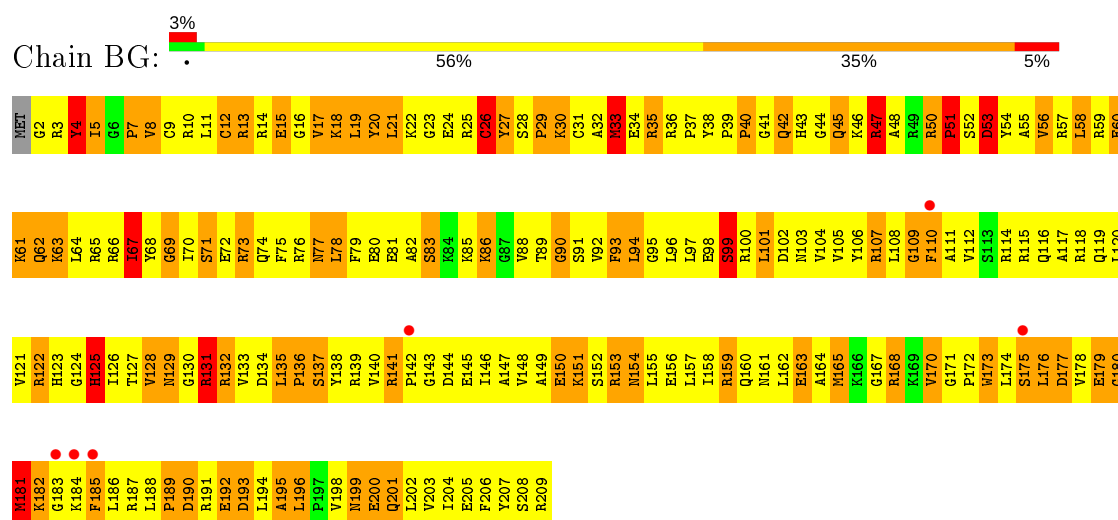


• Molecule 38: 30S ribosomal protein S3

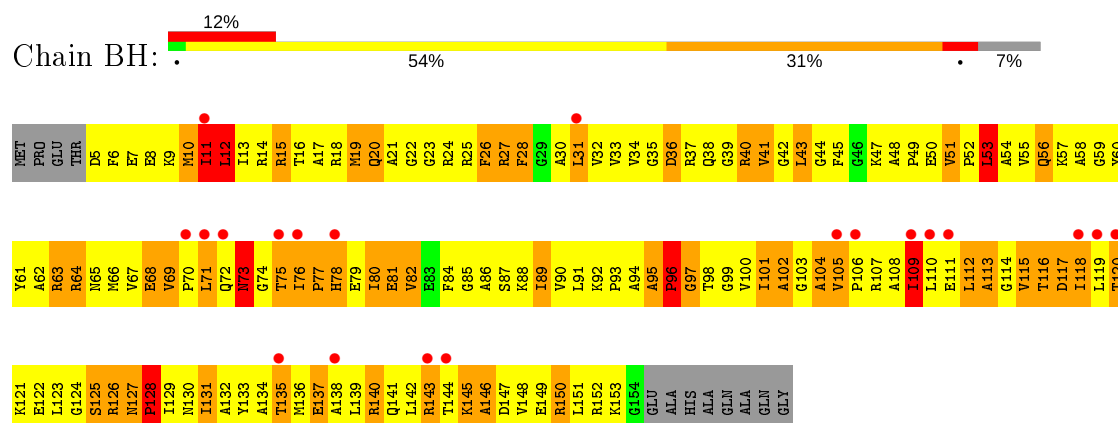
Chain BF: . 16% 5% 54% 23% 5% 14%



• Molecule 39: 30S ribosomal protein S4

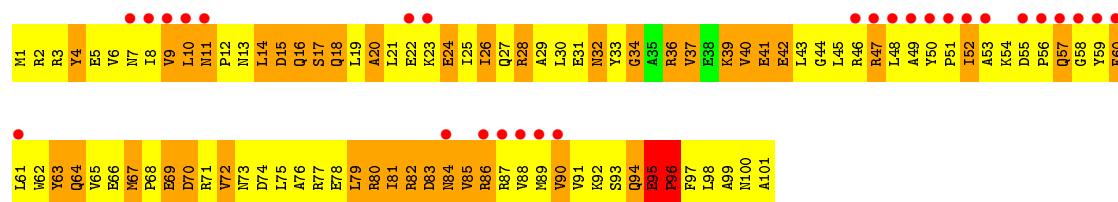


• Molecule 40: 30S ribosomal protein S5

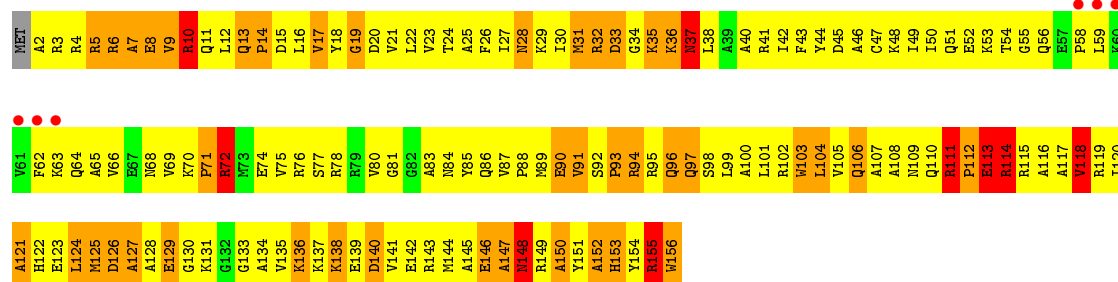
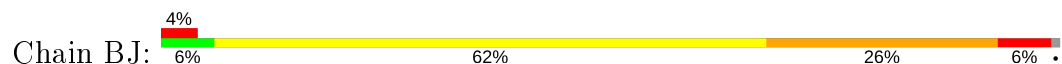


• Molecule 41: 30S ribosomal protein S6

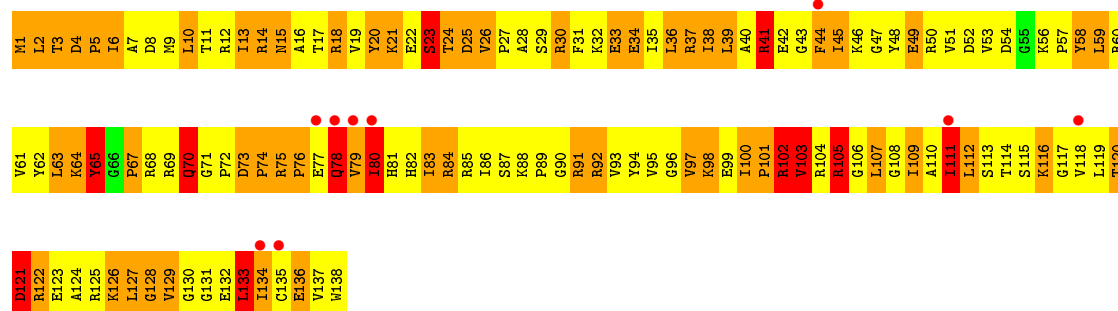




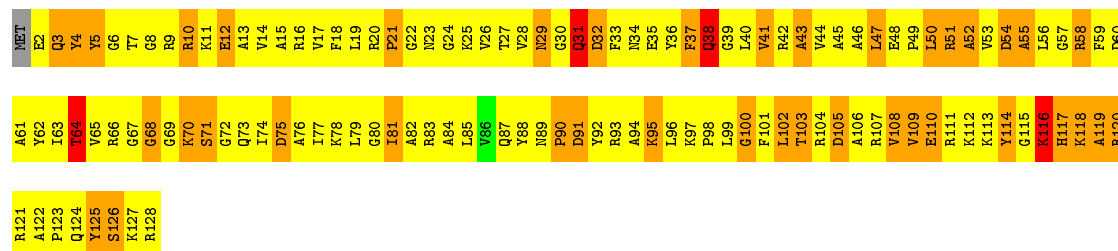
- Molecule 42: 30S ribosomal protein S7



- Molecule 43: 30S ribosomal protein S8



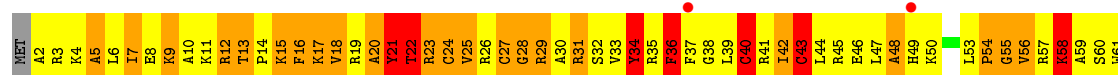
- Molecule 44: 30S ribosomal protein S9



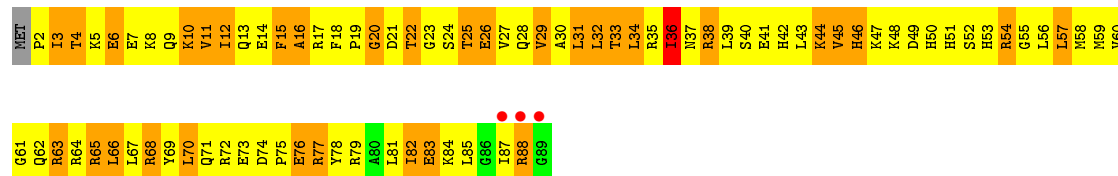
- Molecule 45: 30S ribosomal protein S10



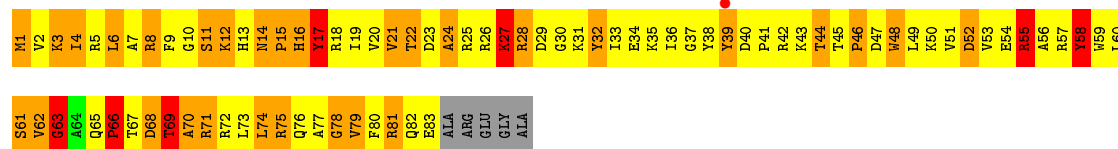




- Molecule 50: 30S ribosomal protein S15



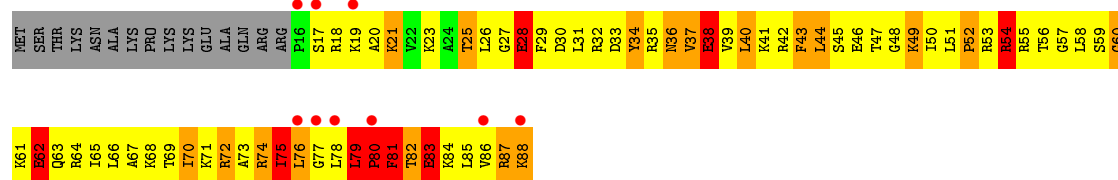
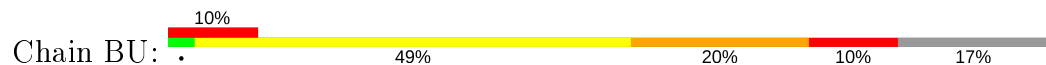
- Molecule 51: 30S ribosomal protein S16



- Molecule 52: 30S ribosomal protein S17



- Molecule 53: 30S ribosomal protein S18



- Molecule 54: 30S ribosomal protein S19







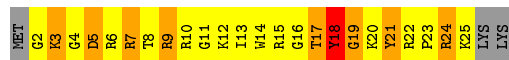
- Molecule 55: 30S ribosomal protein S20

Chain BW: 56% 32% 6% 7%



- Molecule 56: 30S ribosomal protein Thx

Chain BX: 56% 30% • 11%



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	508.64Å 508.64Å 806.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	300.00 – 5.50 268.38 – 5.50	Depositor EDS
% Data completeness (in resolution range)	94.6 (300.00-5.50) 97.5 (268.38-5.50)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 5.42Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.307 , 0.356 0.288 , 0.330	Depositor DCC
$R_{free}$ test set	7724 reflections (4.56%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	206.2	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.11 , 178.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	148539	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	338.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.74% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 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	AB	0.95	1/2954 (0.0%)	1.06	7/4606 (0.2%)
2	AA	1.16	181/69267 (0.3%)	1.22	549/108130 (0.5%)
3	AC	0.62	0/1715	0.94	2/2310 (0.1%)
4	AD	1.11	6/1329 (0.5%)	1.52	22/1787 (1.2%)
5	AE	1.04	3/1542 (0.2%)	1.41	21/2084 (1.0%)
6	AF	0.82	0/1446	1.26	14/1960 (0.7%)
7	AG	0.83	0/972	1.20	6/1307 (0.5%)
8	AH	0.76	0/1272	1.13	1/1721 (0.1%)
9	AI	0.48	0/950	0.72	0/1275
9	AJ	0.43	0/950	0.68	0/1275
10	AK	0.73	0/1157	1.17	8/1547 (0.5%)
11	AL	0.48	0/1015	0.91	4/1366 (0.3%)
12	AM	1.04	2/928 (0.2%)	1.23	2/1248 (0.2%)
13	AN	1.06	2/946 (0.2%)	1.43	14/1269 (1.1%)
14	AO	0.67	0/643	1.30	9/870 (1.0%)
15	AP	1.04	1/1109 (0.1%)	1.43	16/1499 (1.1%)
16	AQ	0.71	0/880	1.23	5/1189 (0.4%)
17	AR	1.37	4/413 (1.0%)	2.01	18/557 (3.2%)
18	AS	0.81	0/869	1.19	3/1166 (0.3%)
19	AT	0.76	0/609	1.05	0/823
20	AU	0.46	0/887	0.89	0/1195
21	AV	0.71	0/1385	1.10	7/1883 (0.4%)
22	AW	0.73	0/497	1.05	1/668 (0.1%)
23	AX	0.81	0/482	1.18	2/646 (0.3%)
24	A0	0.86	0/867	1.24	3/1162 (0.3%)
25	A1	1.03	0/994	1.33	6/1323 (0.5%)
26	A2	0.71	0/797	1.14	4/1061 (0.4%)
27	A3	0.72	0/649	1.14	3/860 (0.3%)
28	A4	0.97	1/620 (0.2%)	1.18	4/831 (0.5%)
29	A5	0.79	0/469	1.41	5/629 (0.8%)
30	A6	0.93	0/438	1.25	4/583 (0.7%)
31	A7	0.78	0/387	1.05	0/509
32	A8	0.98	2/503 (0.4%)	1.48	8/657 (1.2%)
33	A9	1.36	1/286 (0.3%)	1.44	4/375 (1.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
34	BA	1.03	30/36438 (0.1%)	1.17	167/56869 (0.3%)
35	BB	2.33	76/1818 (4.2%)	2.48	157/2831 (5.5%)
35	BC	1.09	5/1818 (0.3%)	1.11	7/2831 (0.2%)
36	B1	1.14	7/1571 (0.4%)	0.96	7/2445 (0.3%)
37	BE	0.75	0/1935	1.06	3/2609 (0.1%)
38	BF	0.62	0/1636	0.99	5/2205 (0.2%)
39	BG	0.86	2/1733 (0.1%)	1.16	4/2318 (0.2%)
40	BH	0.85	0/1162	1.12	1/1564 (0.1%)
41	BI	0.78	0/856	1.06	1/1154 (0.1%)
42	BJ	0.70	1/1276 (0.1%)	1.00	6/1709 (0.4%)
43	BK	0.81	0/1136	1.18	5/1527 (0.3%)
44	BL	0.52	0/1029	0.86	1/1378 (0.1%)
45	BM	0.58	0/807	0.94	2/1085 (0.2%)
46	BN	0.75	0/900	1.04	0/1213
47	BO	0.78	0/986	1.22	3/1320 (0.2%)
48	BP	0.59	0/1008	0.98	0/1347
49	BQ	0.83	1/501 (0.2%)	1.09	2/664 (0.3%)
50	BR	0.74	0/745	1.05	2/992 (0.2%)
51	BS	0.81	0/716	1.10	3/963 (0.3%)
52	BT	0.82	0/870	1.11	2/1159 (0.2%)
53	BU	0.72	0/603	1.18	2/799 (0.3%)
54	BV	0.59	0/661	0.98	1/890 (0.1%)
55	BW	0.84	0/764	1.12	2/1006 (0.2%)
56	BX	0.45	0/212	0.81	0/277
All	All	1.05	326/161408 (0.2%)	1.21	1135/241526 (0.5%)

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	AB	0	14
2	AA	0	527
4	AD	0	1
5	AE	0	1
6	AF	0	1
7	AG	0	2
12	AM	0	2
13	AN	0	2
14	AO	0	2
16	AQ	0	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
23	AX	0	1
25	A1	0	3
26	A2	0	1
28	A4	0	1
30	A6	0	1
34	BA	0	220
35	BB	0	35
35	BC	0	12
36	B1	0	4
38	BF	0	1
39	BG	0	1
41	BI	0	1
43	BK	0	1
48	BP	0	1
51	BS	0	2
All	All	0	838

The worst 5 of 326 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AA	142	G	C5-C6	27.73	1.70	1.42
36	B1	48	A	C5-C6	27.45	1.65	1.41
35	BB	37	G	C2-N2	18.34	1.52	1.34
34	BA	1541	U	C4-C5	17.23	1.59	1.43
2	AA	142	G	C2-N3	16.69	1.46	1.32

The worst 5 of 1135 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	BA	1064	G	N1-C2-N2	-65.61	57.15	116.20
34	BA	1064	G	N3-C2-N2	63.69	164.48	119.90
34	BA	1064	G	N1-C2-N3	-27.38	107.47	123.90
2	AA	1084	A	O5'-P-OP2	-26.59	78.79	110.70
35	BB	36	A	OP1-P-O3'	-18.47	64.57	105.20

There are no chirality outliers.

5 of 838 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AB	12	C	Sidechain
1	AB	18	G	Sidechain

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Group
1	AB	34	U	Sidechain
1	AB	39	A	Sidechain
1	AB	44	G	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	AB	2641	0	1337	635	1
2	AA	61847	0	31165	17729	1
3	AC	1687	0	1737	723	0
4	AD	1308	0	1355	898	0
5	AE	1507	0	1494	986	0
6	AF	1430	0	1386	832	0
7	AG	957	0	959	519	0
8	AH	1251	0	1298	612	0
9	AI	945	0	999	497	0
9	AJ	945	0	999	362	0
10	AK	1145	0	1227	630	0
11	AL	999	0	1071	497	0
12	AM	917	0	904	616	0
13	AN	937	0	1000	549	0
14	AO	639	0	615	373	0
15	AP	1081	0	1062	743	0
16	AQ	866	0	875	512	0
17	AR	406	0	361	160	0
18	AS	860	0	919	442	0
19	AT	602	0	563	332	0
20	AU	879	0	868	477	0
21	AV	1360	0	1390	788	0
22	AW	494	0	506	240	0
23	AX	477	0	529	309	0
24	A0	855	0	906	492	0
25	A1	978	0	1020	685	0
26	A2	787	0	804	571	0
27	A3	641	0	668	421	0
28	A4	604	0	595	365	0
29	A5	457	0	462	294	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	A6	431	0	456	224	0
31	A7	383	0	414	260	0
32	A8	496	0	549	296	0
33	A9	285	0	312	125	0
34	BA	32554	0	16429	7563	1
35	BB	1626	0	817	629	0
35	BC	1626	0	820	429	0
36	B1	1405	0	706	258	1
37	BE	1900	0	1951	930	0
38	BF	1612	0	1677	662	0
39	BG	1703	0	1763	719	0
40	BH	1146	0	1207	489	1
41	BI	843	0	857	398	0
42	BJ	1257	0	1296	527	0
43	BK	1116	0	1177	677	0
44	BL	1011	0	1043	442	0
45	BM	794	0	840	332	0
46	BN	885	0	904	409	0
47	BO	970	0	1057	459	0
48	BP	997	0	1072	493	0
49	BQ	492	0	529	258	0
50	BR	734	0	771	330	0
51	BS	700	0	720	318	0
52	BT	857	0	930	423	0
53	BU	597	0	668	334	0
54	BV	647	0	673	254	0
55	BW	762	0	859	366	0
56	BX	208	0	221	103	0
All	All	148539	0	99792	47710	3

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 193.

The worst 5 of 47710 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)
2:AA:2515:C:N4	2:AA:2569:G:H1	1.08	1.45
34:BA:292:G:H1	34:BA:308:C:N4	1.08	1.45
34:BA:144:G:H1	34:BA:178:C:N4	1.13	1.45
2:AA:447:A:H1'	2:AA:449:A:N6	1.28	1.44
33:A9:11:CYS:SG	33:A9:11:CYS:CB	2.06	1.44

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:-1:A:O2'	1:AB:-1:A:O2'[15_545]	1.59	0.61
2:AA:2153:G:O2'	34:BA:423:G:OP2[3_655]	2.16	0.04
36:B1:29:G:O3'	40:BH:5:ASP:OD2[3_655]	2.17	0.03

## 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	
3	AC	217/228 (95%)	143 (66%)	36 (17%)	38 (18%)	0	3
4	AD	171/178 (96%)	71 (42%)	38 (22%)	62 (36%)	0	0
5	AE	187/338 (55%)	89 (48%)	41 (22%)	57 (30%)	0	0
6	AF	183/246 (74%)	83 (45%)	40 (22%)	60 (33%)	0	0
7	AG	118/176 (67%)	57 (48%)	29 (25%)	32 (27%)	0	0
8	AH	162/177 (92%)	89 (55%)	39 (24%)	34 (21%)	0	2
9	AI	126/128 (98%)	87 (69%)	24 (19%)	15 (12%)	0	6
9	AJ	126/128 (98%)	86 (68%)	25 (20%)	15 (12%)	0	6
10	AK	146/149 (98%)	83 (57%)	34 (23%)	29 (20%)	0	2
11	AL	131/141 (93%)	66 (50%)	33 (25%)	32 (24%)	0	1
12	AM	113/145 (78%)	48 (42%)	26 (23%)	39 (34%)	0	0
13	AN	120/122 (98%)	60 (50%)	33 (28%)	27 (22%)	0	1
14	AO	82/164 (50%)	40 (49%)	17 (21%)	25 (30%)	0	0
15	AP	136/138 (99%)	50 (37%)	43 (32%)	43 (32%)	0	0
16	AQ	111/186 (60%)	41 (37%)	32 (29%)	38 (34%)	0	0
17	AR	50/66 (76%)	19 (38%)	17 (34%)	14 (28%)	0	0
18	AS	104/113 (92%)	70 (67%)	18 (17%)	16 (15%)	0	3

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	AT	74/84 (88%)	33 (45%)	17 (23%)	24 (32%)	0	0
20	AU	108/119 (91%)	60 (56%)	25 (23%)	23 (21%)	0	2
21	AV	175/253 (69%)	69 (39%)	46 (26%)	60 (34%)	0	0
22	AW	62/70 (89%)	21 (34%)	25 (40%)	16 (26%)	0	1
23	AX	58/60 (97%)	29 (50%)	13 (22%)	16 (28%)	0	0
24	A0	103/118 (87%)	50 (48%)	33 (32%)	20 (19%)	0	2
25	A1	115/118 (98%)	48 (42%)	40 (35%)	27 (24%)	0	1
26	A2	98/100 (98%)	54 (55%)	18 (18%)	26 (26%)	0	0
27	A3	84/91 (92%)	32 (38%)	16 (19%)	36 (43%)	0	0
28	A4	71/73 (97%)	21 (30%)	19 (27%)	31 (44%)	0	0
29	A5	56/60 (93%)	25 (45%)	11 (20%)	20 (36%)	0	0
30	A6	51/82 (62%)	26 (51%)	8 (16%)	17 (33%)	0	0
31	A7	44/47 (94%)	14 (32%)	12 (27%)	18 (41%)	0	0
32	A8	61/64 (95%)	24 (39%)	16 (26%)	21 (34%)	0	0
33	A9	33/36 (92%)	19 (58%)	8 (24%)	6 (18%)	0	3
37	BE	232/256 (91%)	107 (46%)	58 (25%)	67 (29%)	0	0
38	BF	204/239 (85%)	113 (55%)	46 (22%)	45 (22%)	0	1
39	BG	206/209 (99%)	97 (47%)	63 (31%)	46 (22%)	0	1
40	BH	148/162 (91%)	90 (61%)	38 (26%)	20 (14%)	0	4
41	BI	99/101 (98%)	55 (56%)	24 (24%)	20 (20%)	0	2
42	BJ	153/156 (98%)	63 (41%)	49 (32%)	41 (27%)	0	0
43	BK	136/138 (99%)	67 (49%)	39 (29%)	30 (22%)	0	1
44	BL	125/128 (98%)	64 (51%)	27 (22%)	34 (27%)	0	0
45	BM	96/105 (91%)	54 (56%)	19 (20%)	23 (24%)	0	1
46	BN	117/129 (91%)	54 (46%)	33 (28%)	30 (26%)	0	1
47	BO	122/135 (90%)	65 (53%)	28 (23%)	29 (24%)	0	1
48	BP	123/126 (98%)	59 (48%)	30 (24%)	34 (28%)	0	0
49	BQ	58/61 (95%)	22 (38%)	10 (17%)	26 (45%)	0	0
50	BR	86/89 (97%)	36 (42%)	35 (41%)	15 (17%)	0	3
51	BS	81/88 (92%)	42 (52%)	24 (30%)	15 (18%)	0	2
52	BT	102/105 (97%)	62 (61%)	20 (20%)	20 (20%)	0	2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	BU	71/88 (81%)	29 (41%)	24 (34%)	18 (25%)	0	1
54	BV	78/93 (84%)	35 (45%)	17 (22%)	26 (33%)	0	0
55	BW	97/106 (92%)	27 (28%)	46 (47%)	24 (25%)	0	1
56	BX	22/27 (82%)	9 (41%)	5 (23%)	8 (36%)	0	0
All	All	5832/6739 (86%)	2857 (49%)	1467 (25%)	1508 (26%)	0	1

5 of 1508 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	17	ASN
3	AC	35	ALA
3	AC	54	SER
3	AC	68	LEU
3	AC	87	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	
3	AC	174/180 (97%)	144 (83%)	30 (17%)	2	12
4	AD	135/139 (97%)	90 (67%)	45 (33%)	0	2
5	AE	156/284 (55%)	114 (73%)	42 (27%)	0	3
6	AF	152/193 (79%)	121 (80%)	31 (20%)	1	7
7	AG	102/147 (69%)	74 (72%)	28 (28%)	0	3
8	AH	137/147 (93%)	99 (72%)	38 (28%)	0	3
9	AI	98/98 (100%)	89 (91%)	9 (9%)	9	30
9	AJ	98/98 (100%)	89 (91%)	9 (9%)	9	30
10	AK	119/119 (100%)	96 (81%)	23 (19%)	1	9
11	AL	108/113 (96%)	91 (84%)	17 (16%)	2	14
12	AM	95/121 (78%)	71 (75%)	24 (25%)	0	4
13	AN	101/101 (100%)	74 (73%)	27 (27%)	0	3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	AO	67/126 (53%)	51 (76%)	16 (24%)	0	4
15	AP	110/110 (100%)	73 (66%)	37 (34%)	0	2
16	AQ	89/149 (60%)	58 (65%)	31 (35%)	0	1
17	AR	44/52 (85%)	24 (54%)	20 (46%)	0	0
18	AS	88/92 (96%)	65 (74%)	23 (26%)	0	3
19	AT	67/73 (92%)	48 (72%)	19 (28%)	0	2
20	AU	97/105 (92%)	75 (77%)	22 (23%)	1	5
21	AV	151/203 (74%)	109 (72%)	42 (28%)	0	3
22	AW	51/56 (91%)	36 (71%)	15 (29%)	0	2
23	AX	52/52 (100%)	34 (65%)	18 (35%)	0	1
24	A0	89/101 (88%)	59 (66%)	30 (34%)	0	2
25	A1	96/97 (99%)	67 (70%)	29 (30%)	0	2
26	A2	79/79 (100%)	60 (76%)	19 (24%)	0	4
27	A3	64/67 (96%)	46 (72%)	18 (28%)	0	3
28	A4	66/66 (100%)	50 (76%)	16 (24%)	0	4
29	A5	51/53 (96%)	38 (74%)	13 (26%)	0	4
30	A6	46/69 (67%)	35 (76%)	11 (24%)	0	4
31	A7	39/40 (98%)	30 (77%)	9 (23%)	1	5
32	A8	50/51 (98%)	33 (66%)	17 (34%)	0	1
33	A9	34/35 (97%)	30 (88%)	4 (12%)	5	21
37	BE	202/220 (92%)	152 (75%)	50 (25%)	0	4
38	BF	160/188 (85%)	127 (79%)	33 (21%)	1	7
39	BG	180/181 (99%)	136 (76%)	44 (24%)	0	4
40	BH	115/123 (94%)	66 (57%)	49 (43%)	0	0
41	BI	90/90 (100%)	64 (71%)	26 (29%)	0	2
42	BJ	126/127 (99%)	106 (84%)	20 (16%)	2	14
43	BK	119/119 (100%)	73 (61%)	46 (39%)	0	0
44	BL	98/99 (99%)	81 (83%)	17 (17%)	2	12
45	BM	88/92 (96%)	70 (80%)	18 (20%)	1	7
46	BN	90/99 (91%)	70 (78%)	20 (22%)	1	6
47	BO	104/111 (94%)	85 (82%)	19 (18%)	1	10

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	BP	100/101 (99%)	80 (80%)	20 (20%)	1	8
49	BQ	49/50 (98%)	41 (84%)	8 (16%)	2	13
50	BR	79/80 (99%)	59 (75%)	20 (25%)	0	4
51	BS	72/74 (97%)	44 (61%)	28 (39%)	0	0
52	BT	96/97 (99%)	74 (77%)	22 (23%)	1	5
53	BU	64/77 (83%)	47 (73%)	17 (27%)	0	3
54	BV	71/80 (89%)	59 (83%)	12 (17%)	2	12
55	BW	76/82 (93%)	53 (70%)	23 (30%)	0	2
56	BX	19/22 (86%)	17 (90%)	2 (10%)	7	26
All	All	4903/5528 (89%)	3677 (75%)	1226 (25%)	0	4

5 of 1226 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	AX	23	LEU
29	A5	31	THR
51	BS	27	LYS
24	A0	27	SER
25	A1	113	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 187 such sidechains are listed below:

Mol	Chain	Res	Type
26	A2	79	GLN
31	A7	29	ASN
50	BR	62	GLN
27	A3	17	ASN
28	A4	32	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AB	122/123 (99%)	47 (38%)	5 (4%)
2	AA	2870/2915 (98%)	1226 (42%)	290 (10%)
34	BA	1515/1522 (99%)	452 (29%)	161 (10%)
35	BB	76/76 (100%)	34 (44%)	16 (21%)
35	BC	75/76 (98%)	31 (41%)	9 (12%)

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
36	B1	65/78 (83%)	24 (36%)	4 (6%)
All	All	4723/4790 (98%)	1814 (38%)	485 (10%)

5 of 1814 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AB	0	A
1	AB	1	U
1	AB	2	C
1	AB	3	C
1	AB	9	G

5 of 485 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	AA	1992	G
2	AA	2542	A
34	BA	1498	U
2	AA	2035	G
2	AA	2320	A

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	AB	123/123 (100%)	-0.47	0 100 100	308, 357, 402, 412	0
2	AA	2872/2915 (98%)	-0.48	15 (0%) 91 85	232, 307, 404, 474	0
3	AC	221/228 (96%)	-0.06	4 (1%) 68 60	384, 428, 464, 467	0
4	AD	173/178 (97%)	0.47	11 (6%) 19 17	243, 279, 292, 298	0
5	AE	191/338 (56%)	0.54	36 (18%) 1 3	258, 311, 397, 403	0
6	AF	189/246 (76%)	-0.37	2 (1%) 80 73	233, 399, 427, 434	0
7	AG	122/176 (69%)	-0.35	2 (1%) 72 63	350, 366, 443, 447	0
8	AH	164/177 (92%)	-0.37	1 (0%) 89 84	320, 351, 366, 370	0
9	AI	128/128 (100%)	1.33	30 (23%) 0 2	580, 591, 602, 603	0
9	AJ	128/128 (100%)	1.93	49 (38%) 0 1	569, 582, 594, 596	0
10	AK	148/149 (99%)	-0.12	4 (2%) 54 46	305, 329, 353, 361	0
11	AL	133/141 (94%)	0.11	7 (5%) 26 25	455, 504, 541, 543	0
12	AM	117/145 (80%)	0.25	12 (10%) 6 8	286, 310, 364, 368	0
13	AN	122/122 (100%)	0.29	10 (8%) 11 12	245, 262, 277, 293	0
14	AO	84/164 (51%)	0.22	5 (5%) 21 20	330, 452, 471, 473	0
15	AP	138/138 (100%)	0.42	9 (6%) 18 17	283, 324, 364, 379	0
16	AQ	113/186 (60%)	-0.77	0 100 100	317, 367, 386, 390	0
17	AR	52/66 (78%)	0.62	7 (13%) 3 5	251, 267, 285, 288	0
18	AS	108/113 (95%)	0.15	2 (1%) 66 58	280, 311, 324, 332	0
19	AT	76/84 (90%)	-0.09	4 (5%) 26 25	329, 344, 360, 363	0
20	AU	110/119 (92%)	-0.08	7 (6%) 19 17	647, 661, 722, 724	0
21	AV	177/253 (69%)	-0.07	8 (4%) 33 29	295, 365, 416, 424	0
22	AW	64/70 (91%)	0.11	1 (1%) 72 63	346, 364, 373, 375	0
23	AX	60/60 (100%)	-0.22	0 100 100	291, 306, 315, 316	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
24	A0	105/118 (88%)	-0.16	2 (1%) 66 58	263, 281, 304, 308	0
25	A1	117/118 (99%)	-0.52	1 (0%) 84 77	267, 297, 311, 317	0
26	A2	100/100 (100%)	0.72	16 (16%) 1 4	416, 430, 462, 470	0
27	A3	86/91 (94%)	0.53	11 (12%) 3 6	359, 389, 475, 486	0
28	A4	73/73 (100%)	-0.00	6 (8%) 11 12	319, 354, 373, 378	0
29	A5	58/60 (96%)	0.04	2 (3%) 45 38	259, 314, 361, 373	0
30	A6	53/82 (64%)	0.17	4 (7%) 14 14	287, 316, 332, 340	0
31	A7	46/47 (97%)	0.19	1 (2%) 62 53	316, 339, 352, 357	0
32	A8	63/64 (98%)	-0.02	1 (1%) 72 63	262, 282, 294, 306	0
33	A9	35/36 (97%)	-0.58	0 100 100	281, 303, 316, 319	0
34	BA	1515/1522 (99%)	-0.49	4 (0%) 94 90	251, 312, 419, 609	0
35	BB	76/76 (100%)	7.38	60 (78%) 0 0	631, 651, 667, 669	0
35	BC	76/76 (100%)	-0.66	0 100 100	273, 310, 328, 337	0
36	B1	66/78 (84%)	5.89	43 (65%) 0 0	337, 829, 918, 922	0
37	BE	234/256 (91%)	0.16	21 (8%) 9 10	293, 321, 364, 385	0
38	BF	206/239 (86%)	0.73	39 (18%) 1 3	301, 349, 377, 382	0
39	BG	208/209 (99%)	0.05	6 (2%) 51 43	276, 299, 318, 329	0
40	BH	150/162 (92%)	0.64	20 (13%) 3 5	277, 295, 315, 324	0
41	BI	101/101 (100%)	1.10	28 (27%) 0 2	299, 318, 330, 336	0
42	BJ	155/156 (99%)	0.02	6 (3%) 39 33	326, 357, 370, 373	0
43	BK	138/138 (100%)	0.17	9 (6%) 18 17	266, 284, 297, 306	0
44	BL	127/128 (99%)	-0.37	0 100 100	385, 487, 499, 500	0
45	BM	98/105 (93%)	0.83	11 (11%) 5 8	337, 394, 423, 424	0
46	BN	119/129 (92%)	0.20	9 (7%) 13 14	288, 307, 330, 334	0
47	BO	124/135 (91%)	0.20	4 (3%) 47 39	265, 282, 319, 328	0
48	BP	125/126 (99%)	-0.90	0 100 100	350, 370, 412, 415	0
49	BQ	60/61 (98%)	-0.09	2 (3%) 46 39	322, 352, 360, 365	0
50	BR	88/89 (98%)	-0.39	3 (3%) 45 38	277, 288, 315, 318	0
51	BS	83/88 (94%)	-0.41	1 (1%) 79 70	271, 284, 303, 316	0
52	BT	104/105 (99%)	-0.21	3 (2%) 51 43	249, 268, 323, 344	0
53	BU	73/88 (82%)	0.27	9 (12%) 4 7	259, 296, 323, 348	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
54	BV	80/93 (86%)	0.17	5 (6%) 20 17	353, 369, 395, 399	0
55	BW	99/106 (93%)	-0.54	0 100 100	264, 281, 292, 300	0
56	BX	24/27 (88%)	-1.09	0 100 100	475, 489, 493, 496	0
All	All	10678/11529 (92%)	-0.05	553 (5%) 27 26	232, 322, 533, 922	0

The worst 5 of 553 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
36	B1	15	A	20.7
35	BB	4	G	18.9
36	B1	42	G	18.3
36	B1	17	G	17.4
35	BB	5	A	17.2

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.