



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 09:22 PM GMT

PDB ID : 3OI5
Title : Structure of the *Thermus thermophilus* 70S ribosome complexed with telithromycin. This file contains the 50S subunit of one 70S ribosome. The entire crystal structure contains two 70S ribosomes.
Authors : Bulkley, D.P.; Innis, C.A.; Blaha, G.; Steitz, T.A.
Deposited on : 2010-08-18
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>

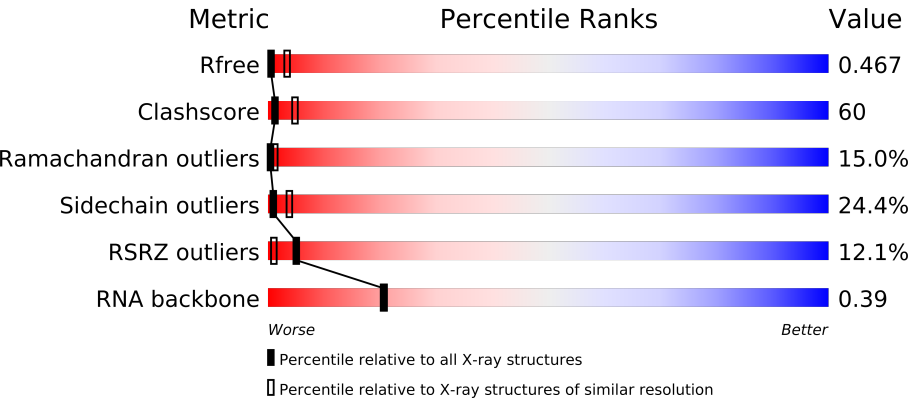
The following versions of software and data (see [references](#)) were used in the production of this report:

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.



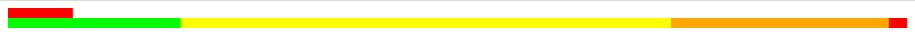
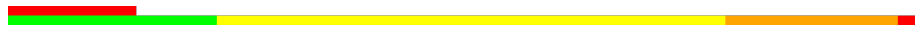
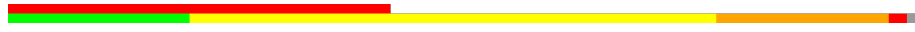
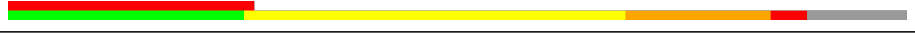
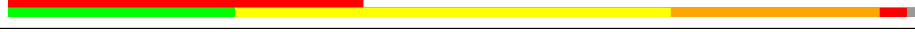

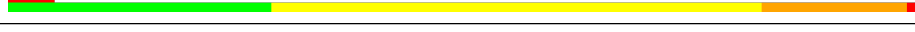


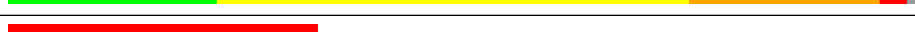

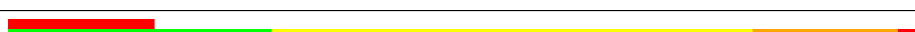
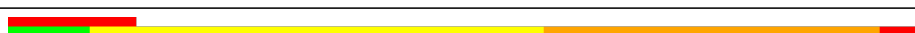
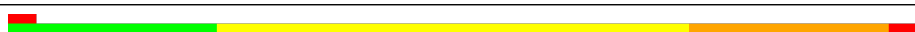
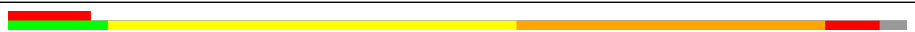

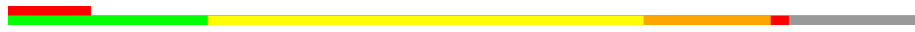

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)
RNA backbone	1838	1047 (3.60-2.60)

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	A	2787	
11	B	122	
12	D	276	

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Mol	Chain	Length	Quality of chain
13	E	206	
14	F	210	
15	G	182	
16	H	180	
17	I	148	
18	N	140	
19	O	122	
20	P	150	
21	Q	141	
22	R	118	
23	S	112	
24	T	146	
25	U	118	
26	V	101	
27	W	113	
28	X	96	
29	Y	110	
30	Z	206	

2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 87522 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	85	Total	C	N	O	S	0	0	0
			650	401	137	111	1			

- Molecule 2 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	1	89	Total	C	N	O	0	0	1
			693	435	140	118			

- Molecule 3 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	2	51	Total	C	N	O	S	0	0	1
			421	263	85	72	1			

- Molecule 4 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	3	60	Total	C	N	O	S	0	0	1
			468	298	91	78	1			

- Molecule 5 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	4	32	Total	C	N	O	0	0	0
			157	93	32	32			

- 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	9	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	45	Total	C	N	O	S	0	0	1
			381	235	78	64	4			

- Molecule 8 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	7	49	Total	C	N	O	S	0	0	1
			419	257	105	55	2			

- Molecule 9 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	8	64	Total	C	N	O	S	0	0	1
			508	326	102	78	2			

- Molecule 10 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	A	2725	Total	C	N	O	P	0	0	0
			58698	26124	10986	18864	2724			

- Molecule 11 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 12 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	D	272	Total	C	N	O	S	0	0	1
			2105	1329	417	356	3			

- Molecule 13 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	E	205	Total	C	N	O	S	0	0	1
			1564	988	300	270	6			

- Molecule 14 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	F	208	Total	C	N	O	S	0	0	1
			1624	1035	304	282	3			

- Molecule 15 is a protein called 50S ribosomal protein L5.

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

- Molecule 16 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	H	160	Total	C	N	O	S	0	0	1
			1223	773	229	220	1			

- Molecule 17 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	I	146	Total	C	N	O	S	0	0	1
			1132	723	201	207	1			

- Molecule 18 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	N	139	Total	C	N	O	S	0	0	1
			1105	712	207	182	4			

- Molecule 19 is a protein called 50S ribosomal protein L14.

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

- Molecule 20 is a protein called 50S ribosomal protein L15.

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

- Molecule 21 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	Q	136	Total	C	N	O	S	0	0	0
			1080	688	204	183	5			

- Molecule 22 is a protein called 50S ribosomal protein L17.

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

- Molecule 23 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	S	99	Total	C	N	O		0	0	1
			771	486	155	130				

- Molecule 24 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	T	132	Total	C	N	O	S	0	0	0
			1100	686	227	186	1			

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

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

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

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

- Molecule 27 is a protein called 50S ribosomal protein L22.

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

- Molecule 28 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
28	X	93	Total	C	N	O	0	0	1
			726	471	132	123			

- Molecule 29 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	Y	101	Total	C	N	O	S	0	0	1
			776	500	149	123	4			

- Molecule 30 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	Z	177	Total	C	N	O	S	0	0	1
			1404	897	253	252	2			

- Molecule 31 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
31	P	1	Total	Mg	0	0
			1	1		
31	Q	1	Total	Mg	0	0
			1	1		
31	D	2	Total	Mg	0	0
			2	2		
31	E	1	Total	Mg	0	0
			1	1		
31	B	3	Total	Mg	0	0
			3	3		
31	U	1	Total	Mg	0	0
			1	1		
31	7	1	Total	Mg	0	0
			1	1		
31	X	1	Total	Mg	0	0
			1	1		
31	A	318	Total	Mg	0	0
			318	318		
31	5	1	Total	Mg	0	0
			1	1		
31	8	1	Total	Mg	0	0
			1	1		
31	R	2	Total	Mg	0	0
			2	2		

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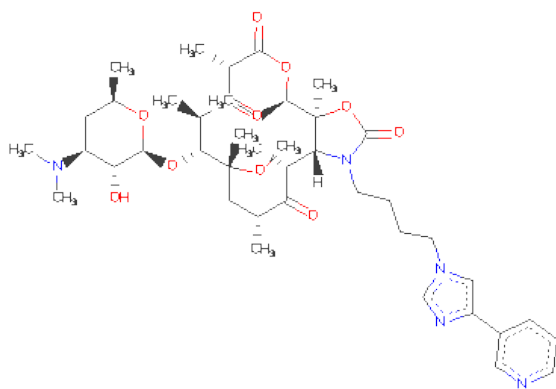
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
31	F	1	Total	Mg	0	0
			1	1		

- Molecule 32 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	A	1	Total	K	0	0
			1	1		

- Molecule 33 is TELITHROMYCIN (three-letter code: TEL) (formula: C₄₃H₆₅N₅O₁₀).

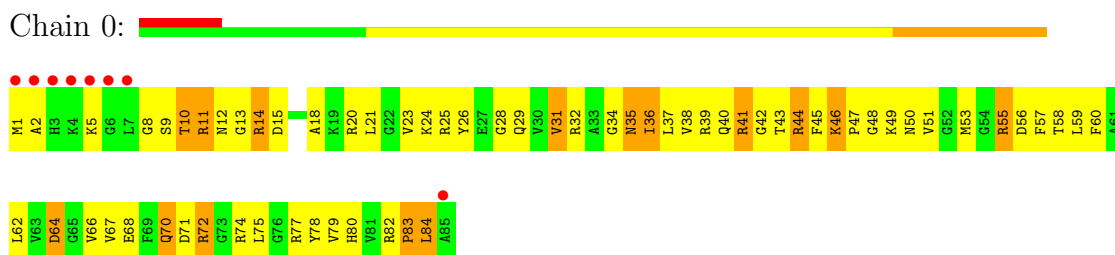


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
33	A	1	Total	C	N	O	0	0
			58	43	5	10		

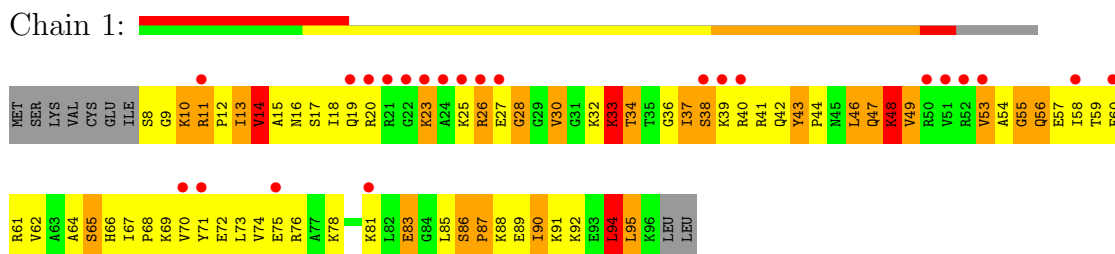
3 Residue-property plots

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.

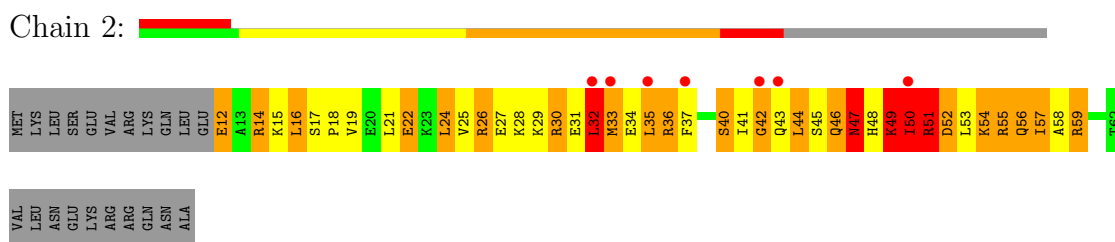
- Molecule 1: 50S ribosomal protein L27



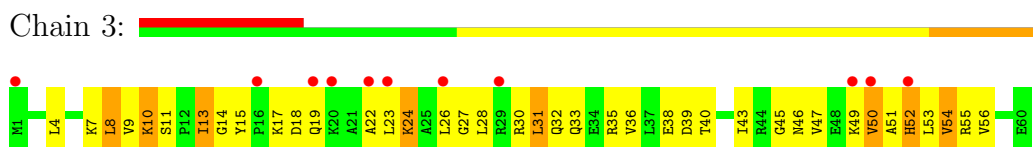
- Molecule 2: 50S ribosomal protein L28



- Molecule 3: 50S ribosomal protein L29

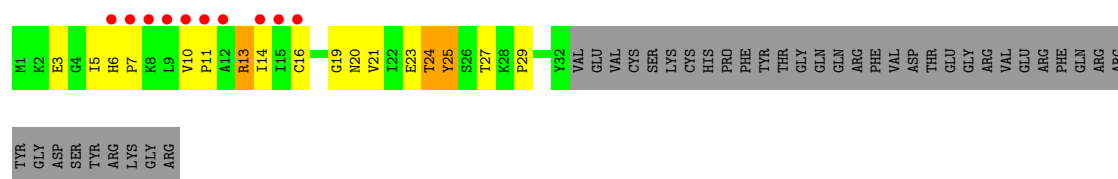


- Molecule 4: 50S ribosomal protein L30



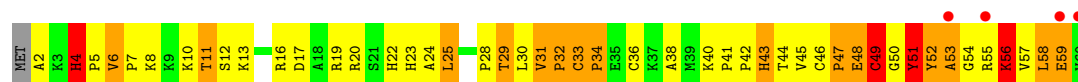
- Molecule 5: 50S ribosomal protein L31





- Molecule 6: 50S ribosomal protein L32

Chain 5:



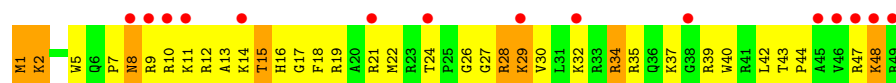
- Molecule 7: 50S ribosomal protein L33

Chain 6:



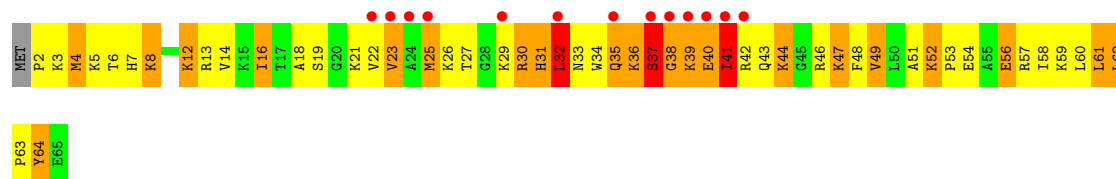
- Molecule 8: 50S ribosomal protein L34

Chain 7:



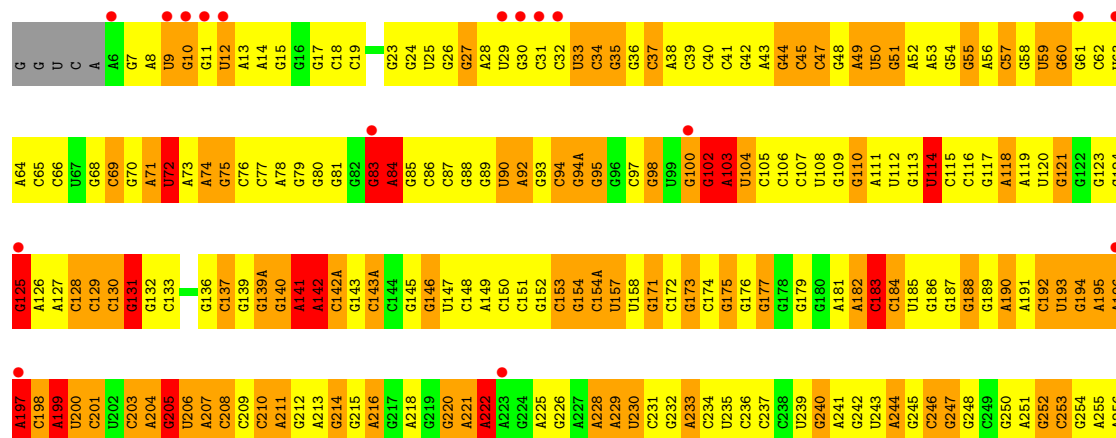
- Molecule 9: 50S ribosomal protein L35

Chain 8:



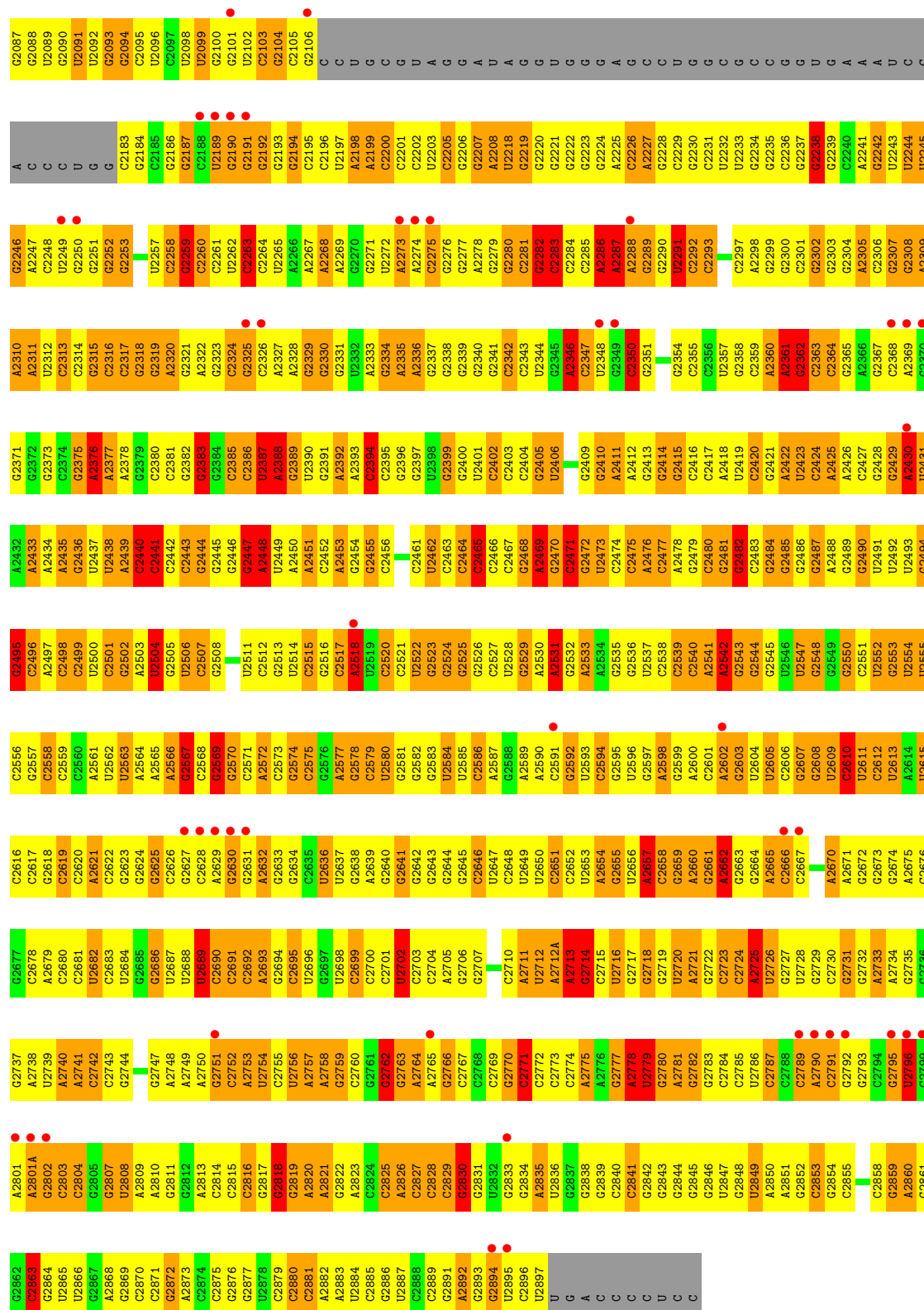
- Molecule 10: 23S ribosomal RNA

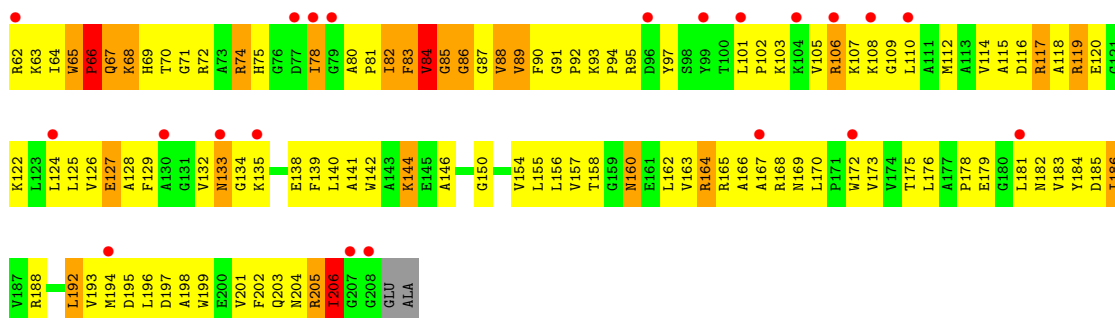
Chain A:



A1143	G1030	C971	G843	A782	A722	C658	U597	A532	A470	G407	G349	C287	A257
G1144	G1031	G972	C844	A783	G723	C659	G598	G533	A471	G408	U350	C288	G288
C1145	A1032	G973	G845	A784	U724	C660	G599	U534	A472	C409	G351	C289	G289
C1146	U1033	G974	C846	G785	G725	C661	G600	C535	G473	G410	G352	G290	G290
C1147	G1034	G975	U847	G786	G726	C662	G601	C536	G474	G411	G353	G291	G291
A1148	U1035	G976	G848	G787	A727	G663	G602	C537	U475	A412	G354	A262	A262
G1149	G1036	G977	A849	A788	G728	C664	A603	G538	G476	C413	G355	C263	C263
C1150	G1037	G978	C850	A789	G729	C665	G604	G539	A477	C414	G356	C264	C264
G1151	U1038	G979	U851	G790	C730	C666	C605	C540	A478	A415	G357	A265	A265
C1152	G1039	G980	C852	G791	C731	U667	U606	C541	A479	C416	U358	C266	C266
C1153	C1040	G981	G853	G792	C732	G668	U607	C542	A480	C417	U359	C267	C267
G1154	U1041	G982	G854	G793	G733	G669	A608	C543	G481	G418	G360	C268	C268
A1155	G1042	U922	C855	G794	A734	A670	A609	C544	A482	C419	G361	A299	A299
C1156	C1043	C923	G856	G795	A735	G671	G610	C545	A483	C420	U362	A300	A300
G1157	U1044	C924	C857	G796	C736	C672	C611	C546	A484	C421	G363	G301	G301
C1158	A1045	C925	U858	G797	G737	C673	C612	C547	C485	A422	A363A	U303	U303
U1159	G1046	A926	G859	G798	G738	G674	G613	G552	C486	A423	G363B	G304	G304
G1160	U1047	G927	U860	G801	G739	A675	U614	G553	G489	C426	G363C	U305	U305
C1161	A1048	G928	A861	A802	U740	A676	U614A	U554	G491	U427	U363D	U306	U306
C1162	U1049	U930	G862	A803	G741	A677	G614B	U555	A492	U428	U363E	G307	G307
G1163	A1050	G931	C863	A804	G742	C678	A614C	G556	G493	A429	A363F	G308	G308
C1164	G1051	C932	C864	A805	G743	C679	G615	U557	G494	G430	C364	G309	G309
U1165	U1052	C933	C865	G806	G744	G680	G616	G558	G495	G431	C365	A310	A310
C1166	C1053	G934	A866	C906	G745	C681	G618	G559	G496	G432	C366	A311	A311
U1167	A106	C935	C867	U807	A746	G683	G619	C560	G497	C433	G370	C271J	C271J
G1168	G1107	C936	U868	G808	U747	G684	G620	G561	A498	U434	A371	U271K	U271K
C1169	U1108	A996	G869	G809	G748	A685	A621	U562	G499	U435	G372	U271L	U271L
G1170	G1109	G997	A870	U810	C749	G686	G622	U563	U504	C436	U373	G271M	G271M
C1171	U1110	C998	U871	U811	G750	C687	G623	C564	A501	G437	C375	G271N	G271N
G1172	A1111	U999	A872	C812	C824	U688	C624	C565	A502	G438	C376	G271O	G271O
A1174	U1112	G873	G874	U813	A752	A689	G625	U566	A503	U441	C377	G271P	G271P
C1175	U1113	G875	G876	C814	C753	C690	U626	A567	A504	U442	C378	G271Q	G271Q
G1176	G1114	G1002	C877	C815	C754	C691	A627	G570	A505	G443	C379	A320	A320
A1177	U1115	C878	U877	C816	C755	C692	G628	G571	A506	U444	C380	G271R	G271R
C1178	C1116	C1004	U878	C817	C756	C693	G629	A572	G506	C445	U380	G321	G321
G1179	U1117	C1005	A879	G818	U757	U694	G630	G573	A507	C446	G381	G322	G322
C1180	C1006	G947	C879	A819	C758	G695	A631	C574	G508	G447	G382	A324	A324
G1181	U1118	G948	G880	A820	G759	G696	A632	C574	C509	U448	U383	G325	G325
A1182	C1121	C1008	C881	A821	G760	C697	A633	A575	U511	U449	U384	G326	G326
C1183	G1122	G950	C882	U822	A761	C698	C634	U576	C510	G450	U385	G327	G327
G1184	C1123	C951	C883	G823	U762	A699	C635	G577	A513	C451	G386	U328	U328
C1185	U1124	G952	C884	A824	G763	G700	G636	A578	A514	G452	U387	G329	G329
G1186	G1125	U1012	G892	C825	A764	G701	A637	G579	A515	C453	G388	A330	A330
C1187	A1126	C1013	C893	U826	G765	G702	G638	C580	A516	C454	G389	G331	G331
U1188	A1127	U1014	C894	U827	G766	U703	U639	C581	C517	A455	A390	A332	A332
A1189	G1128	G1015	U895	U828	U767	G704	C640	G582	C518	C456	G391	G333	G333
G1190	U1129	A896	C902	A829	G768	A705	C641	G583	C519	C457	C392	C334	C334
C1191	U1130	G1017	C897	G830	U769	A706	G642	G584	U519	A458	C393	C335	C335
G1192	G1131	C1018	C898	G831	G770	G707	A643	G585	G520	G459	A394	G336	G336
C1193	A1132	U1019	A899	G832	G771	C708	A644	A586	G521	U459	U395	C337	C337
A1194	U1133	C961	A900	U833	C772	U709	C645	C587	G522	A460	U396	G338	G338
G1195	C1135	G962	A901	C834	U773	G710	A646	U588	C523	C461	G397	U339	U339
C1196	G1136	U963	C902	A835	A774	G711	G647	C589	U524	C462	G398	A340	A340
G1197	G1137	C964	C903	G836	G775	G712	G648	A590	U525	G463	G399	G341	G341
U1198	G1138	G1024	C965	C837	G776	C713	G649	C591	A526	U464	G400	G342	G342
C1199	U1139	G966	U905	C838	A777	G714	C650	G592	C527	G465	A401	C343	C343
G1200	C1140	C967	G906	U839	G778	A717	G651	G593	A528	A466	A402	A344	A344
C1201	U1141	U968	U907	C840	U779	C719	C652	U594	A529	G467	A345	A346	A346
G1202	A1028	U969	C908	A841	G780	C720	G656	C595	G530	G468	C285	U284	U284
C1203	A1142A	C970	A909	G842	A781	C721	U657	G596	C531	G469	G406	C286	C286

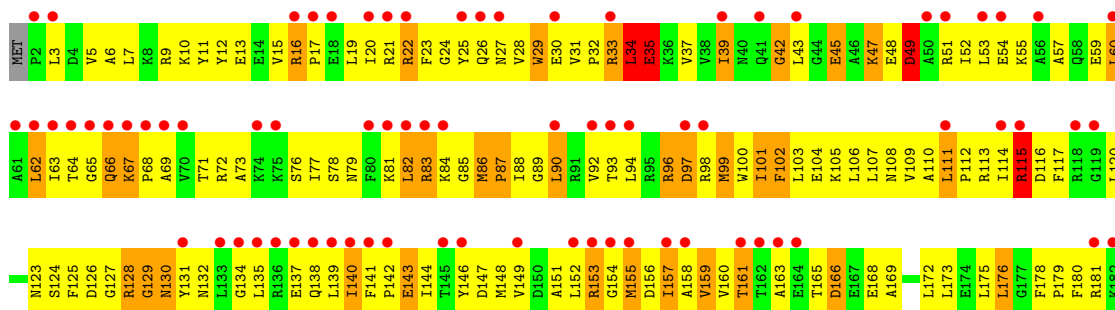
G2027	G1965	C1832	G1772	G1636	C1574	C1505	A1445	G1385	G1324	G1264	A1204
U2028	A1966	U1833	A1773	A1637	C1575	C1506	C1445A	C1386	G1325	A1265	U1205
G2029	C1967	U1834	C1774	U1698	U1576	A1507	G1446	G1387	G1326	G1266	G1206
A2030	G1968	G1835	U1775	U1699	C1577	A1508	G1447	G1388	C1327	U1267	C1207
A2031	A1969	C1836	U1776	C1640	U1578	C1509	A1448	G1389	G1328	A1268	
G2032	G1970	U1777	A1701	A1641	A1579	A1509A	A1449	U1390	U1329	A1269	A1210
A2033	C1971	G1837	G1702	G1642	A1580	A1509B	G1450	U1391	C1330	U1270	U1211
G2034	A1972	G1838	U1778	G1643	G1581	G1510	C1450A	A1392	A1331	G1271	A1212
G2035	G1973	U1911	U1779	G1644	C1582	U1512	C1451	A1393	G1332	U1272	A1213
C2036	A1974	C1843	C1780	C1645	C1584	U1513	A1452	C1333	C1334	A1273	A1214
G2037	G1975	G1844	C1782	G1646	C1584	C1513	U1453	A1394	G1335	A1274	G1215
G2038	A1976	G1845	U1706	C1647	U1514	G1514	G1455	A1395	A1336	A1275	
C2039	A1977	G1846	G1708	G1648	A1587	C1515	G1456	U1396	A1337	G1276	
C2040		A1847	U1709	G1649	C1588	C1516	A1457	U1397	G1338	G1277	
U2041	G1980	A1848	C1710	G1650	U1589	G1517	G1458	C1398	G1339	G1278	
A2042	A1981	G1849	G1711	G1651	U1590	U1518	G1459	G1399	G1340	G1279	
C2043	C1982	U1918	A1787	G1652	C1591	G1519	A1460	G1401	U1341	G1280	C1221
C2044	G1983	G1850	C1789	A1652	C1592	G1520	G1461	C1402	G1342	G1281	C1221A
C2045	U1984	U1851	U1713	A1653	G1593		C1462	C1403	A1343	U1282	C1222
		C1852	G1714	A1654	G1594	G1525		C1404	G1344	G1283	G1223
G2046		A1853	G1717	A1655	G1595	G1526	C1463	U1405	G1345	G1284	C1224
U2047	G1987	A1854	G1718	C1656	G1596	G1527	C1464	U1406	C1346	G1285	G1225
G2048	C1988	G1855	G1719	C1657	A1596	G1528	G1465	C1407	G1347	A1286	A1226
G2049	G1989	G1856	U1720	C1658	A1597	A1528A	G1466	C1408	G1347	G1287	G1227
C2050	C1990	G1857	G1721	U1659	C1598	G1529	C1467	C1409	U1348	U1288	G1228
A2051	U1991	G1858	U1796	C1660	C1599	C1530	C1468	G1410	A1349	G1289	G1229
G2052	G1992	A1859	C1797	G1661	G1600	C1531	A1469	G1411	C1350	C1290	
G2053	U1993	G1860	U1798	C1662	G1601	C1532	G1470	C1412	C1351	G1291	G1231
A2054	C1994	G1861	A1741	C1663	U1602	C1533	A1471	G1413	C1352	U1292	G1232
C2055	U1995	G1862	G1742	A1664	C1603	G1534	G1472	G1414	C1353	G1293	C1233
G2056	C1996	G1863	C1743	A1665	C1604	C1544	A1473	U1415	A1354	U1294	U1234
A2057	G1997	U1864	G1744	G1666	C1605	A1545	C1474	G1416	G1355	G1295	G1235
A2058	C1998	G1865	C1745	G1667	G1606	A1546	G1475	C1417	G1356	G1296	G1236
A2059	G1999	A1866	G1746	C1668	C1607	C1547	C1476	G1418	U1357	C1297	A1237
A2060	G2000	A1876	U1805	A1669	A1608	C1548	A1477	A1419	G1358	G1298	G1238
G2061	A2001	G1877	G1747	C1670	C1609	G1549	G1478	U1420	A1359	G1299	U1239
A2062	G2002	C1878	G1748	U1671	A1610	C1550	G1479	G1421	U1360	U1300	G1240
G2063	G2003	G1879	G1749	C1672	C1611	C1551	G1480	G1422	A1301	A1241	A1241
C2064	G2004	A1880	A1749	U1673	G1612	G1552	U1481	G1423	G1302	A1302	A1242
C2065	A2005	C1881	G1750	G1674	G1613	A1553	G1482	G1424	G1303	G1243	G1243
A2066	G2006	G1882	C1751	C1675	A1614	A1554	G1485	G1425	C1304	C1244	G1244
G2067	C2007	G1883	C1752	A1676	C1615	C1555	A1486	G1426	C1305	G1245	G1245
U2068	G2008	A1884	G1753	A1677	A1616	C1556	G1487	A1427	G1306	A1246	A1246
G2069	G2009	G1885	C1754	G1678	C1617	C1557	G1488	C1428	G1307	A1307	G1247
G2070	G2010	C1886	A1755	U1679	A1618	A1558	U1489	G1429	G1308	G1248	G1248
A2071	U2011	C1887	G1756	U1680		G1559	A1490	C1430	A1309	U1249	U1249
G2072	G2012	G1888	U1757	G1681	G1622	G1560	G1491	U1431	G1310	G1250	G1250
C2073	A2013	U1817	G1758	C1682	G1623	G1561	G1492	C1432	G1311	C1251	C1251
U2074	G1950	A1819	A1759	C1683	G1624	A1562	G1493	U1433	A1372	G1252	G1252
A2075	A2015	G1891	A1760	C1684	C1625	G1563	A1494	A1434	G1373	A1253	A1253
U2076	U2016	C1892	G1761	C1685	G1626	C1564	A1495	G1435	C1374	A1254	A1254
A2077	U2017	G1893	A1762	C1686	G1627	C1565	A1496	G1436	C1375	G1314	G1314
G2078	G2018	C1894	G1763	C1687	G1628	C1566	U1497	C1437	G1376	C1315	G1315
A2079	A2019	G1895	C1764	U1688	U1629	A1567	C1498	U1438	G1377	G1256	G1256
G2080	U1955	G1896	A1825	A1689	G1630	A1568	U1499	A1439	A1378	C1257	C1257
C2081	A2020	G1897	G1765	A1690	G1631	G1569	C1500	A1439	A1379	G1258	G1258
G2082	C2021	U1897	U1766	C1691	A1631A	A1570	G1501	G1440	G1380	G1259	G1259
U2083	U2022	G1898	G1767	C1692	A1632	A1571	C1502	G1441	G1381	G1260	G1260
G2083	G2023	G1899	U1768	U1692	A1633	A1572	G1503	G1442	G1382	C1261	C1261
C2084	G2024	A1900	A1829	C1693	G1634	A1573	U1504	G1443	A1384	A1262	A1262
C2085	U1963	C1901	G1770	C1694	A1634	G1573		G1444		U1263	U1263
U2086	C2026	G1964	G1771	G1695	G1635						





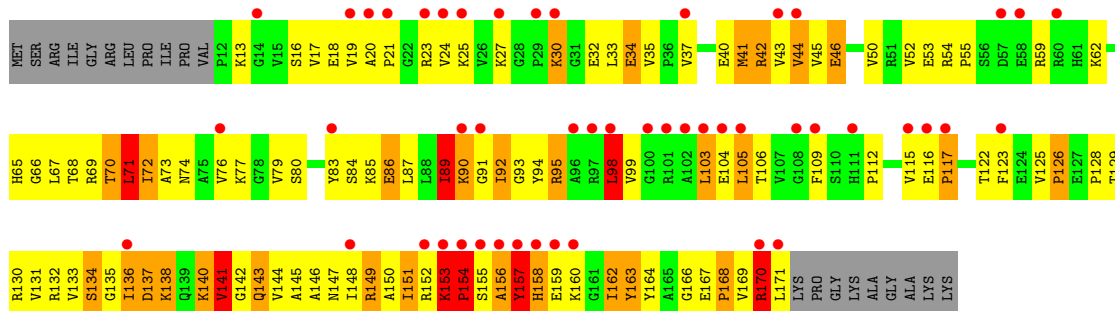
• Molecule 15: 50S ribosomal protein L5

Chain G:



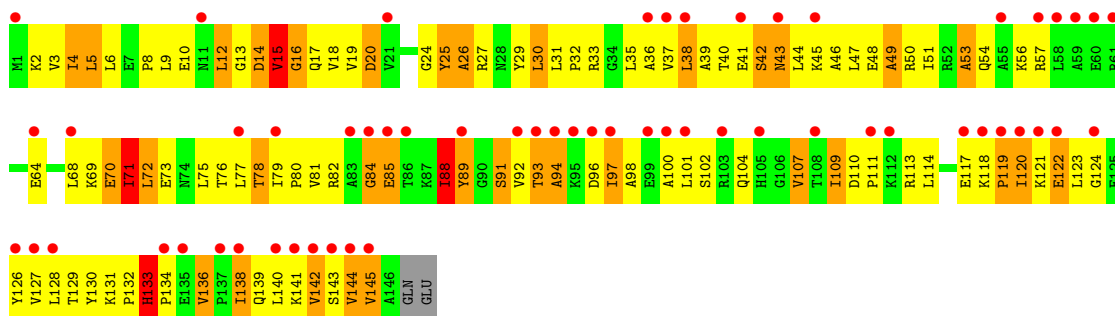
• Molecule 16: 50S ribosomal protein L6

Chain H:



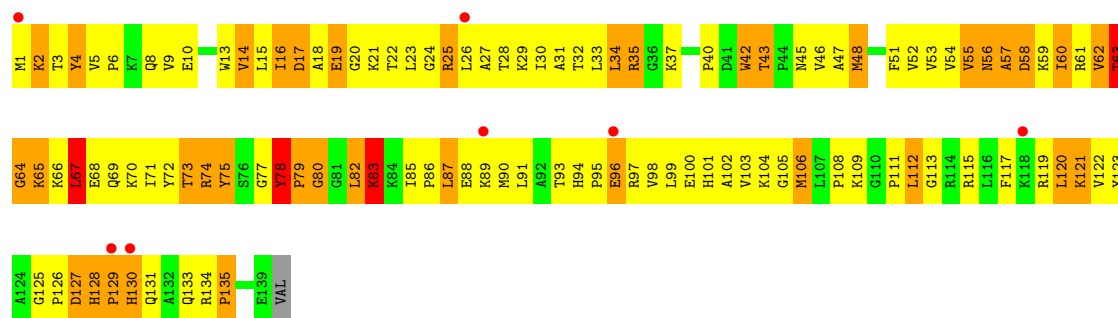
• Molecule 17: 50S ribosomal protein L9

Chain I:



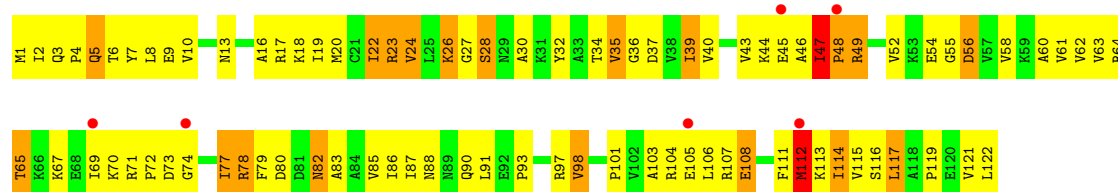
• Molecule 18: 50S ribosomal protein L13

Chain N:



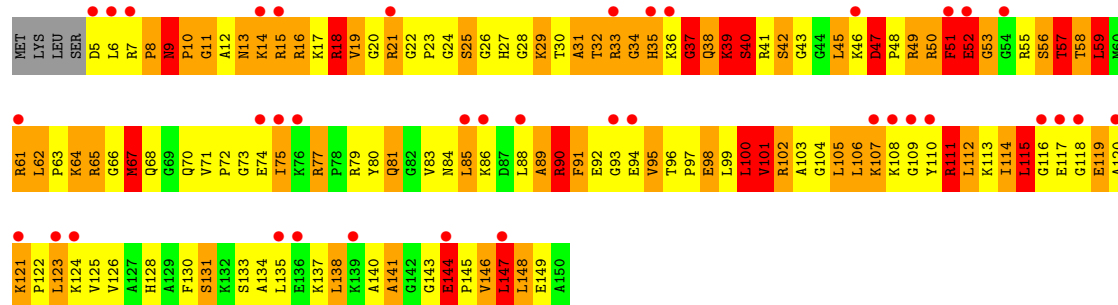
- Molecule 19: 50S ribosomal protein L14

Chain O:



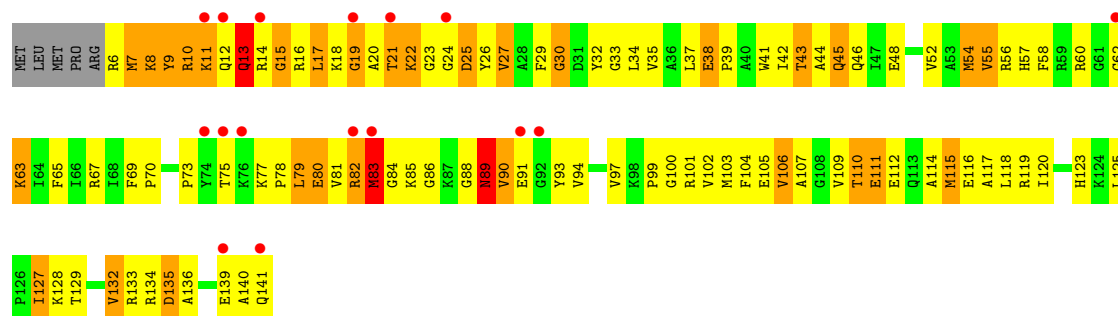
- Molecule 20: 50S ribosomal protein L15

Chain P:



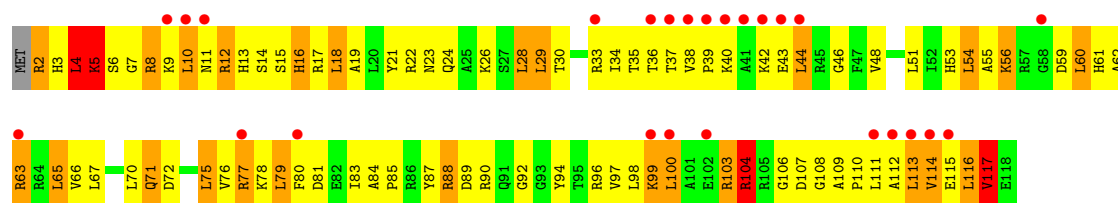
- Molecule 21: 50S ribosomal protein L16

Chain Q:



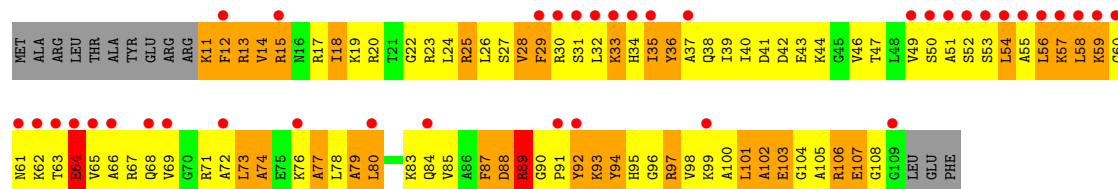
- Molecule 22: 50S ribosomal protein L17

Chain R:



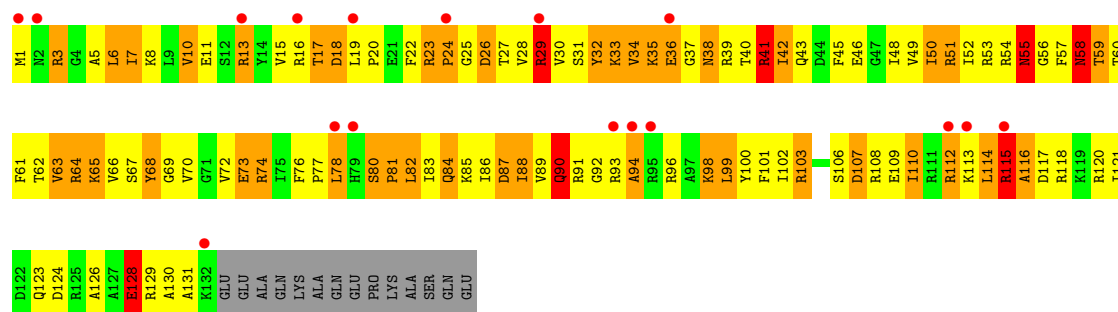
• Molecule 23: 50S ribosomal protein L18

Chain S:



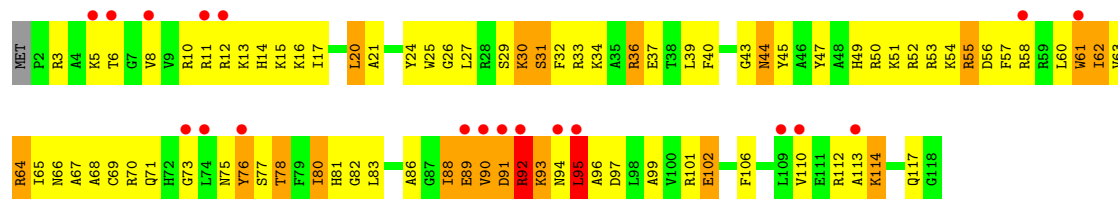
• Molecule 24: 50S ribosomal protein L19

Chain T:



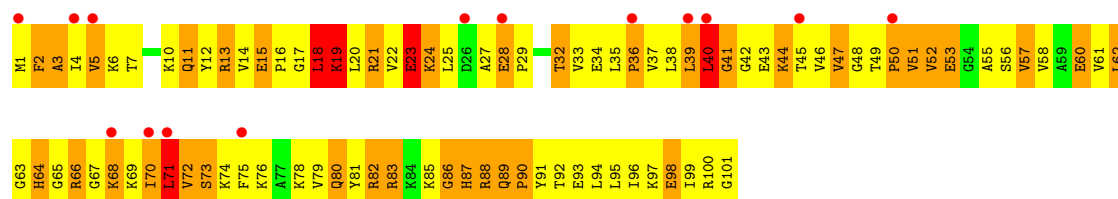
• Molecule 25: 50S ribosomal protein L20

Chain U:



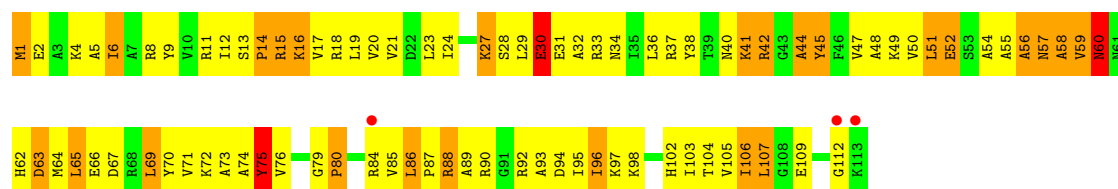
• Molecule 26: 50S ribosomal protein L21

Chain V:



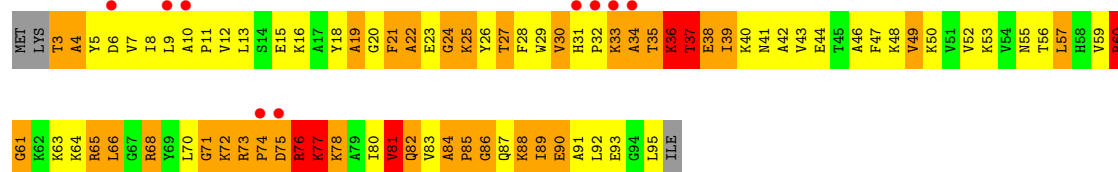
• Molecule 27: 50S ribosomal protein L22

Chain W:



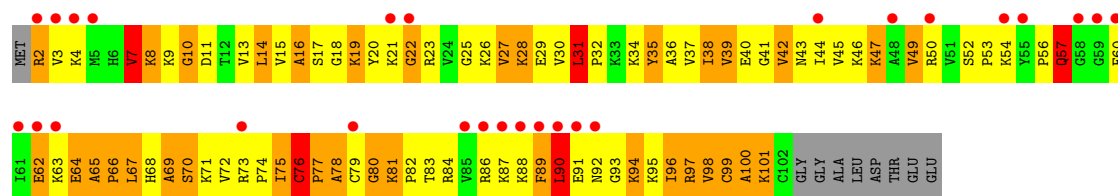
- Molecule 28: 50S ribosomal protein L23

Chain X:



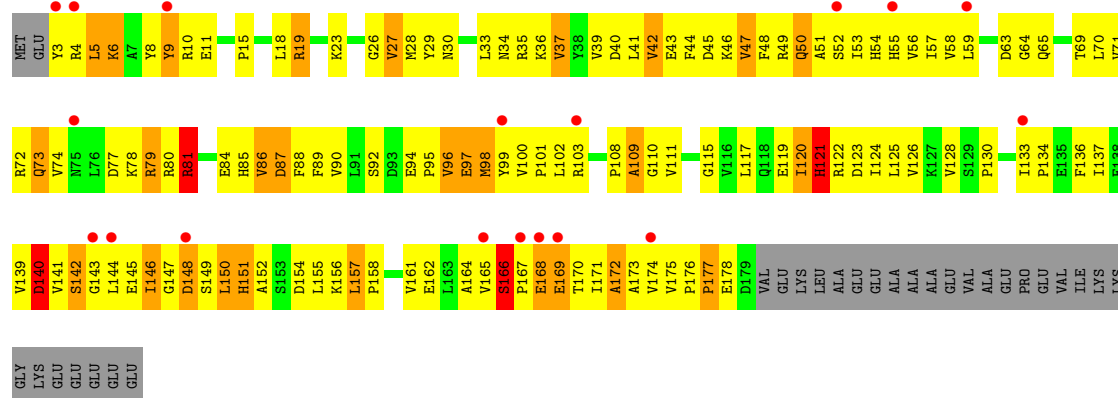
- Molecule 29: 50S ribosomal protein L24

Chain Y:



- Molecule 30: 50S ribosomal protein L25

Chain Z:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	207.32Å 437.99Å 614.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.97 – 3.10 48.97 – 3.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (48.97-3.10) 91.4 (48.97-3.10)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 3.12Å)	Xtriage
Refinement program	Phenix	Depositor
R, R_{free}	0.246 , 0.284 0.461 , 0.467	Depositor DCC
R_{free} test set	45871 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	88.4	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 62.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 914156 reflections	Xtriage
F_o, F_c correlation	0.62	EDS
Total number of atoms	87522	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: K, TEL, MG

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	0.54	0/658	0.73	0/878
2	1	0.61	0/700	0.92	1/931 (0.1%)
3	2	0.55	0/423	0.88	1/560 (0.2%)
4	3	0.45	0/473	0.66	0/636
5	4	0.28	0/156	0.52	0/215
6	5	0.67	0/473	1.01	3/639 (0.5%)
7	6	0.60	0/387	0.85	1/517 (0.2%)
8	7	0.61	0/427	0.81	0/563
9	8	0.61	0/516	0.94	1/681 (0.1%)
10	A	0.89	28/65745 (0.0%)	1.45	1209/102639 (1.2%)
11	B	0.63	0/2853	1.18	25/4451 (0.6%)
12	D	0.58	0/2155	0.82	2/2907 (0.1%)
13	E	0.58	0/1597	0.83	0/2155
14	F	0.53	1/1659 (0.1%)	0.74	0/2246
15	G	0.35	0/1498	0.59	1/2013 (0.0%)
16	H	0.41	0/1246	0.66	0/1684
17	I	0.43	0/1147	0.66	1/1553 (0.1%)
18	N	0.56	0/1132	0.76	0/1527
19	O	0.53	0/943	0.73	0/1269
20	P	0.56	0/1131	0.94	4/1504 (0.3%)
21	Q	0.55	0/1100	0.74	0/1470
22	R	0.57	0/974	0.80	2/1302 (0.2%)
23	S	0.43	0/779	0.72	0/1038
24	T	0.52	0/1114	0.79	0/1488
25	U	0.56	0/975	0.74	1/1297 (0.1%)
26	V	0.54	0/789	0.84	1/1054 (0.1%)
27	W	0.61	0/907	0.88	0/1216
28	X	0.63	0/740	0.90	0/995
29	Y	0.53	0/789	0.81	0/1053
30	Z	0.40	0/1436	0.61	1/1951 (0.1%)
All	All	0.80	29/94922 (0.0%)	1.31	1254/142432 (0.9%)

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	0	0	1
2	1	0	1
3	2	0	1
6	5	0	1
10	A	18	0
12	D	0	2
13	E	0	2
16	H	0	1
20	P	0	3
21	Q	0	1
22	R	0	1
24	T	0	1
26	V	0	2
28	X	0	3
All	All	18	20

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	1142(A)	A	N9-C4	-9.23	1.32	1.37
10	A	1694	C	C4'-C3'	-9.11	1.43	1.53
10	A	669	G	C4'-C3'	-8.53	1.43	1.53
10	A	1332	G	N9-C4	-8.29	1.31	1.38
10	A	774	A	N9-C4	-7.36	1.33	1.37

The worst 5 of 1254 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	1332	G	N3-C4-C5	15.46	136.33	128.60
10	A	1332	G	N3-C4-N9	-14.37	117.38	126.00
10	A	1779	U	C5-C6-N1	-13.74	115.83	122.70
10	A	679	C	N1-C2-O2	-12.95	111.13	118.90
10	A	2828	C	C6-N1-C2	12.89	125.46	120.30

5 of 18 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
10	A	472	A	C3'

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Mol	Chain	Res	Type	Atom
10	A	669	G	C4',C3',C1'
10	A	945	A	C1'
10	A	1300	U	C4',C3'
10	A	1379	A	C1'

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	11	ARG	Peptide
2	1	30	VAL	Peptide
3	2	54	LYS	Peptide
6	5	51	TYR	Peptide
12	D	47	GLY	Peptide

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	650	0	654	95	0
2	1	693	0	764	156	0
3	2	421	0	461	136	0
4	3	468	0	523	54	0
5	4	157	0	69	8	0
6	5	459	0	480	99	0
7	6	381	0	390	95	0
8	7	419	0	467	57	0
9	8	508	0	576	151	0
10	A	58698	0	29591	4381	0
11	B	2551	0	1295	231	0
12	D	2105	0	2182	406	0
13	E	1564	0	1629	278	0
14	F	1624	0	1677	209	0
15	G	1474	0	1534	223	0
16	H	1223	0	1282	162	0
17	I	1132	0	1218	158	0
18	N	1105	0	1180	231	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	O	933	0	996	133	0
20	P	1114	0	1187	345	0
21	Q	1080	0	1127	195	0
22	R	960	0	1021	146	0
23	S	771	0	832	172	0
24	T	1100	0	1164	209	0
25	U	958	0	1015	177	0
26	V	779	0	851	258	0
27	W	896	0	953	128	0
28	X	726	0	777	199	0
29	Y	776	0	870	191	0
30	Z	1404	0	1432	196	0
31	5	1	0	0	0	0
31	7	1	0	0	0	0
31	8	1	0	0	0	0
31	A	318	0	0	0	0
31	B	3	0	0	0	0
31	D	2	0	0	0	0
31	E	1	0	0	0	0
31	F	1	0	0	0	0
31	P	1	0	0	0	0
31	Q	1	0	0	0	0
31	R	2	0	0	0	0
31	U	1	0	0	0	0
31	X	1	0	0	0	0
32	A	1	0	0	0	0
33	A	58	0	65	34	0
All	All	87522	0	58262	8614	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 60.

The worst 5 of 8614 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
33:A:3206:TEL:H11	33:A:3206:TEL:C14	1.64	1.28
10:A:1722:A:H2	10:A:1740:G:H5'	1.08	1.18
10:A:2287:A:N6	10:A:2344:U:H3	1.42	1.17
28:X:77:LYS:HG2	28:X:78:LYS:HG3	1.25	1.16
26:V:2:PHE:HB2	26:V:42:GLY:HA3	1.25	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	83/85 (98%)	62 (75%)	14 (17%)	7 (8%)	1	9
2	1	87/98 (89%)	44 (51%)	26 (30%)	17 (20%)	0	0
3	2	49/72 (68%)	26 (53%)	13 (26%)	10 (20%)	0	0
4	3	58/60 (97%)	44 (76%)	13 (22%)	1 (2%)	14	54
5	4	30/71 (42%)	6 (20%)	11 (37%)	13 (43%)	0	0
6	5	57/60 (95%)	36 (63%)	8 (14%)	13 (23%)	0	0
7	6	41/54 (76%)	18 (44%)	11 (27%)	12 (29%)	0	0
8	7	47/49 (96%)	45 (96%)	1 (2%)	1 (2%)	11	48
9	8	62/65 (95%)	38 (61%)	13 (21%)	11 (18%)	0	0
12	D	270/276 (98%)	202 (75%)	52 (19%)	16 (6%)	2	17
13	E	203/206 (98%)	136 (67%)	39 (19%)	28 (14%)	0	2
14	F	206/210 (98%)	137 (66%)	45 (22%)	24 (12%)	1	4
15	G	177/182 (97%)	109 (62%)	47 (27%)	21 (12%)	1	4
16	H	158/180 (88%)	97 (61%)	37 (23%)	24 (15%)	0	1
17	I	144/148 (97%)	83 (58%)	38 (26%)	23 (16%)	0	1
18	N	137/140 (98%)	97 (71%)	25 (18%)	15 (11%)	1	5
19	O	120/122 (98%)	98 (82%)	17 (14%)	5 (4%)	4	27
20	P	144/150 (96%)	72 (50%)	29 (20%)	43 (30%)	0	0
21	Q	134/141 (95%)	91 (68%)	29 (22%)	14 (10%)	1	5
22	R	115/118 (98%)	71 (62%)	34 (30%)	10 (9%)	1	9
23	S	97/112 (87%)	41 (42%)	29 (30%)	27 (28%)	0	0
24	T	130/146 (89%)	80 (62%)	26 (20%)	24 (18%)	0	0
25	U	115/118 (98%)	82 (71%)	24 (21%)	9 (8%)	1	11
26	V	97/101 (96%)	47 (48%)	25 (26%)	25 (26%)	0	0
27	W	111/113 (98%)	78 (70%)	15 (14%)	18 (16%)	0	0
28	X	91/96 (95%)	45 (50%)	21 (23%)	25 (28%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	Y	99/110 (90%)	41 (41%)	27 (27%)	31 (31%)	0	0
30	Z	175/206 (85%)	116 (66%)	41 (23%)	18 (10%)	1	6
All	All	3237/3489 (93%)	2042 (63%)	710 (22%)	485 (15%)	0	1

5 of 485 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	44	ARG
2	1	11	ARG
2	1	14	VAL
2	1	48	LYS
2	1	65	SER

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	61/67 (91%)	48 (79%)	13 (21%)	1	7
2	1	73/83 (88%)	53 (73%)	20 (27%)	0	1
3	2	46/67 (69%)	28 (61%)	18 (39%)	0	0
4	3	51/52 (98%)	42 (82%)	9 (18%)	3	10
6	5	51/52 (98%)	41 (80%)	10 (20%)	2	8
7	6	43/52 (83%)	28 (65%)	15 (35%)	0	0
8	7	41/42 (98%)	31 (76%)	10 (24%)	1	4
9	8	53/55 (96%)	35 (66%)	18 (34%)	0	0
12	D	213/218 (98%)	157 (74%)	56 (26%)	1	2
13	E	165/166 (99%)	126 (76%)	39 (24%)	1	5
14	F	165/166 (99%)	132 (80%)	33 (20%)	2	8
15	G	155/156 (99%)	126 (81%)	29 (19%)	2	9
16	H	132/148 (89%)	107 (81%)	25 (19%)	2	9
17	I	122/124 (98%)	100 (82%)	22 (18%)	2	10
18	N	117/119 (98%)	81 (69%)	36 (31%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	O	100/100 (100%)	80 (80%)	20 (20%)	2	8
20	P	112/116 (97%)	67 (60%)	45 (40%)	0	0
21	Q	106/111 (96%)	82 (77%)	24 (23%)	1	5
22	R	100/101 (99%)	76 (76%)	24 (24%)	1	4
23	S	77/88 (88%)	59 (77%)	18 (23%)	1	5
24	T	116/127 (91%)	77 (66%)	39 (34%)	0	0
25	U	92/94 (98%)	71 (77%)	21 (23%)	1	5
26	V	82/82 (100%)	57 (70%)	25 (30%)	0	1
27	W	91/92 (99%)	69 (76%)	22 (24%)	1	4
28	X	74/78 (95%)	54 (73%)	20 (27%)	1	2
29	Y	84/91 (92%)	66 (79%)	18 (21%)	1	7
30	Z	155/179 (87%)	131 (84%)	24 (16%)	4	14
All	All	2677/2826 (95%)	2024 (76%)	653 (24%)	1	4

5 of 653 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	I	4	ILE
19	O	78	ARG
28	X	57	LEU
17	I	71	ILE
18	N	43	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
14	F	160	ASN
18	N	94	HIS
27	W	61	ASN
14	F	169	ASN
17	I	43	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	2723/2787 (97%)	827 (30%)	75 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	B	118/122 (96%)	42 (35%)	0
All	All	2841/2909 (97%)	869 (30%)	75 (2%)

5 of 869 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	A	9	U
10	A	10	G
10	A	12	U
10	A	15	G
10	A	23	G

5 of 75 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	A	1420	U
10	A	1558	A
10	A	2662	A
10	A	1427	A
10	A	1494	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 ⓘ

Of 336 ligands modelled in this entry, 335 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
33	TEL	A	3206	-	62,62,62	1.79	9 (14%)	92,92,92	3.04	30 (32%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	TEL	A	3206	-	1/1/19/19	0/73/108/108	0/3/5/5

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	A	3206	TEL	C43-C40	-6.79	1.37	1.48
33	A	3206	TEL	C37-N31	-4.58	1.29	1.36
33	A	3206	TEL	O5-C2	-4.47	1.40	1.47
33	A	3206	TEL	C36-N31	-3.88	1.32	1.37
33	A	3206	TEL	O32-C28	-3.76	1.36	1.44

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	A	3206	TEL	C8-C4-C2	-16.53	92.52	115.53
33	A	3206	TEL	O9-C15-C21	9.87	121.11	110.84
33	A	3206	TEL	C2-O5-C10	-9.22	102.95	108.91
33	A	3206	TEL	C28-C34-C30	-6.74	99.95	113.72
33	A	3206	TEL	O20-C15-C21	-5.11	117.88	124.86

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
33	A	3206	TEL	C21

There are no torsion outliers.

There are no ring outliers.

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	85/85 (100%)	0.97	8 (9%) 9 2	62, 82, 179, 199	0
2	1	89/98 (90%)	1.27	23 (25%) 1 0	57, 88, 162, 191	0
3	2	51/72 (70%)	0.66	7 (13%) 4 1	68, 110, 167, 192	0
4	3	60/60 (100%)	1.10	11 (18%) 2 0	54, 79, 145, 186	0
5	4	32/71 (45%)	1.55	10 (31%) 1 0	139, 180, 199, 201	0
6	5	58/60 (96%)	0.46	4 (6%) 17 3	42, 69, 186, 197	0
7	6	45/54 (83%)	2.00	22 (48%) 1 0	57, 102, 169, 189	0
8	7	49/49 (100%)	1.58	15 (30%) 1 0	45, 54, 132, 180	0
9	8	64/65 (98%)	1.09	13 (20%) 1 0	55, 79, 140, 168	0
10	A	2725/2787 (97%)	0.26	163 (5%) 21 3	44, 71, 181, 203	0
11	B	119/122 (97%)	0.37	8 (6%) 17 3	64, 127, 194, 203	0
12	D	272/276 (98%)	0.58	23 (8%) 11 2	47, 73, 128, 175	0
13	E	205/206 (99%)	0.50	14 (6%) 17 3	46, 78, 169, 195	0
14	F	208/210 (99%)	0.76	29 (13%) 4 1	44, 89, 182, 199	0
15	G	181/182 (99%)	2.31	76 (41%) 1 0	119, 188, 200, 203	0
16	H	160/180 (88%)	1.45	49 (30%) 1 0	87, 142, 186, 195	0
17	I	146/148 (98%)	1.79	58 (39%) 1 0	76, 180, 198, 201	0
18	N	139/140 (99%)	0.57	7 (5%) 28 4	56, 90, 155, 190	0
19	O	122/122 (100%)	0.40	6 (4%) 28 4	54, 84, 136, 173	0
20	P	146/150 (97%)	1.30	38 (26%) 1 0	42, 109, 168, 198	0
21	Q	136/141 (96%)	0.76	16 (11%) 5 1	59, 90, 160, 191	0
22	R	117/118 (99%)	0.91	25 (21%) 1 0	47, 68, 136, 182	0
23	S	99/112 (88%)	2.02	38 (38%) 1 0	83, 136, 192, 198	0
24	T	132/146 (90%)	0.69	17 (12%) 4 1	65, 107, 179, 195	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	U	117/118 (99%)	1.14	19 (16%) 2 1	48, 76, 145, 194	0
26	V	101/101 (100%)	0.71	14 (13%) 4 1	49, 120, 186, 197	0
27	W	113/113 (100%)	0.15	3 (2%) 52 8	43, 62, 130, 191	0
28	X	93/96 (96%)	0.53	9 (9%) 8 2	57, 84, 153, 186	0
29	Y	101/110 (91%)	1.69	27 (26%) 1 0	68, 121, 195, 199	0
30	Z	177/206 (85%)	0.70	18 (10%) 7 2	80, 133, 185, 196	0
All	All	6142/6398 (95%)	0.66	770 (12%) 5 1	42, 82, 190, 203	0

The worst 5 of 770 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
15	G	63	ILE	16.2
10	A	2802	G	16.0
10	A	1051	G	15.6
15	G	138	GLN	13.2
15	G	137	GLU	12.2

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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
31	MG	A	3155	1/1	0.45	-	64,64,64,64	0
31	MG	A	2964	1/1	0.41	-	42,42,42,42	0
31	MG	A	3110	1/1	0.25	-	68,68,68,68	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
31	MG	A	2909	1/1	0.55	-	41,41,41,41	0
31	MG	A	3202	1/1	0.40	-	75,75,75,75	0
31	MG	A	3014	1/1	0.55	-	46,46,46,46	0
31	MG	A	3149	1/1	0.82	-	73,73,73,73	0
31	MG	A	276	1/1	0.13	-	38,38,38,38	0
31	MG	A	278	1/1	0.47	-	55,55,55,55	0
31	MG	A	3183	1/1	0.57	-	93,93,93,93	0
31	MG	A	3043	1/1	0.52	-	46,46,46,46	0
31	MG	A	3181	1/1	0.23	-	65,65,65,65	0
31	MG	A	3123	1/1	0.21	-	57,57,57,57	0
31	MG	A	3052	1/1	0.49	-	51,51,51,51	0
31	MG	A	3013	1/1	0.65	-	60,60,60,60	0
31	MG	A	155	1/1	0.93	-	80,80,80,80	0
31	MG	A	2940	1/1	0.24	-	63,63,63,63	0
31	MG	A	3186	1/1	0.80	-	58,58,58,58	0
31	MG	A	3112	1/1	0.20	-	72,72,72,72	0
31	MG	A	3085	1/1	0.14	-	62,62,62,62	0
31	MG	A	3073	1/1	0.99	-	80,80,80,80	0
31	MG	A	3094	1/1	0.13	-	48,48,48,48	0
31	MG	A	3045	1/1	0.30	-	69,69,69,69	0
31	MG	A	3051	1/1	0.32	-	61,61,61,61	0
31	MG	A	2981	1/1	0.19	-	50,50,50,50	0
31	MG	A	3140	1/1	0.40	-	62,62,62,62	0
31	MG	5	105	1/1	0.17	-	51,51,51,51	0
31	MG	A	3131	1/1	0.23	-	48,48,48,48	0
31	MG	A	3037	1/1	0.38	-	31,31,31,31	0
31	MG	A	2921	1/1	0.49	-	76,76,76,76	0
31	MG	A	2938	1/1	0.39	-	61,61,61,61	0
31	MG	B	175	1/1	0.17	-	80,80,80,80	0
31	MG	A	3156	1/1	0.60	-	92,92,92,92	0
31	MG	A	101	1/1	0.16	-	57,57,57,57	0
31	MG	A	2941	1/1	0.26	-	51,51,51,51	0
31	MG	U	263	1/1	0.66	-	75,75,75,75	0
31	MG	A	3082	1/1	0.73	-	71,71,71,71	0
31	MG	A	2978	1/1	0.16	-	42,42,42,42	0
31	MG	A	160	1/1	0.57	-	66,66,66,66	0
31	MG	A	2972	1/1	0.61	-	52,52,52,52	0
31	MG	A	169	1/1	0.27	-	77,77,77,77	0
31	MG	A	3003	1/1	0.20	-	38,38,38,38	0
31	MG	R	141	1/1	0.43	-	45,45,45,45	0
31	MG	A	3190	1/1	0.15	-	67,67,67,67	0
31	MG	A	2934	1/1	0.26	-	43,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
31	MG	A	3109	1/1	0.51	-	49,49,49,49	0
31	MG	A	3107	1/1	0.49	-	55,55,55,55	0
31	MG	A	3124	1/1	0.34	-	73,73,73,73	0
31	MG	A	3141	1/1	0.41	-	91,91,91,91	0
31	MG	A	2926	1/1	0.34	-	42,42,42,42	0
31	MG	A	3044	1/1	0.43	-	65,65,65,65	0
31	MG	A	2983	1/1	0.44	-	46,46,46,46	0
31	MG	A	2966	1/1	0.28	-	50,50,50,50	0
31	MG	A	3004	1/1	0.19	-	56,56,56,56	0
31	MG	A	3064	1/1	0.19	-	35,35,35,35	0
31	MG	A	2956	1/1	0.30	-	39,39,39,39	0
31	MG	A	3034	1/1	0.31	-	83,83,83,83	0
31	MG	A	3099	1/1	0.65	-	58,58,58,58	0
31	MG	A	3115	1/1	0.50	-	81,81,81,81	0
31	MG	A	3195	1/1	0.14	-	76,76,76,76	0
31	MG	A	3143	1/1	0.12	-	51,51,51,51	0
31	MG	A	2950	1/1	0.21	-	43,43,43,43	0
31	MG	A	2948	1/1	0.30	-	55,55,55,55	0
31	MG	A	3093	1/1	0.45	-	55,55,55,55	0
31	MG	D	278	1/1	0.52	-	38,38,38,38	0
31	MG	A	2935	1/1	0.32	-	68,68,68,68	0
31	MG	A	2930	1/1	0.12	-	39,39,39,39	0
31	MG	A	3067	1/1	0.33	-	48,48,48,48	0
31	MG	A	3103	1/1	0.20	-	44,44,44,44	0
31	MG	A	3189	1/1	0.44	-	57,57,57,57	0
31	MG	A	3025	1/1	0.80	-	64,64,64,64	0
31	MG	A	2987	1/1	0.56	-	58,58,58,58	0
31	MG	A	3118	1/1	0.11	-	57,57,57,57	0
31	MG	A	91	1/1	0.46	-	44,44,44,44	0
31	MG	A	2998	1/1	0.69	-	49,49,49,49	0
31	MG	A	3165	1/1	0.17	-	55,55,55,55	0
31	MG	A	2974	1/1	0.46	-	80,80,80,80	0
31	MG	A	2937	1/1	0.15	-	66,66,66,66	0
31	MG	A	3203	1/1	0.38	-	60,60,60,60	0
31	MG	A	3192	1/1	0.57	-	63,63,63,63	0
31	MG	A	3007	1/1	0.46	-	58,58,58,58	0
31	MG	A	3166	1/1	0.17	-	67,67,67,67	0
31	MG	A	3133	1/1	0.09	-	94,94,94,94	0
31	MG	A	3065	1/1	0.55	-	68,68,68,68	0
31	MG	A	3128	1/1	0.10	-	80,80,80,80	0
31	MG	A	3020	1/1	0.37	-	65,65,65,65	0
31	MG	A	3053	1/1	0.60	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
31	MG	A	3197	1/1	0.48	-	86,86,86,86	0
31	MG	A	3011	1/1	0.14	-	42,42,42,42	0
31	MG	A	2996	1/1	0.39	-	53,53,53,53	0
31	MG	A	3040	1/1	0.27	-	49,49,49,49	0
31	MG	B	211	1/1	0.35	-	47,47,47,47	0
31	MG	A	3170	1/1	0.40	-	70,70,70,70	0
31	MG	A	3138	1/1	0.89	-	72,72,72,72	0
31	MG	A	3012	1/1	0.29	-	56,56,56,56	0
31	MG	A	2913	1/1	0.43	-	40,40,40,40	0
31	MG	A	3173	1/1	0.33	-	64,64,64,64	0
31	MG	A	3134	1/1	0.46	-	69,69,69,69	0
31	MG	A	2932	1/1	0.48	-	61,61,61,61	0
31	MG	A	2962	1/1	0.43	-	51,51,51,51	0
31	MG	A	2945	1/1	0.83	-	68,68,68,68	0
31	MG	F	211	1/1	0.84	-	83,83,83,83	0
31	MG	A	2929	1/1	0.18	-	38,38,38,38	0
31	MG	A	3057	1/1	0.32	-	45,45,45,45	0
31	MG	A	3174	1/1	0.46	-	32,32,32,32	0
31	MG	A	2991	1/1	0.34	-	62,62,62,62	0
31	MG	A	170	1/1	0.41	-	50,50,50,50	0
31	MG	A	3179	1/1	0.42	-	60,60,60,60	0
31	MG	A	3150	1/1	0.30	-	87,87,87,87	0
31	MG	A	2943	1/1	0.29	-	54,54,54,54	0
31	MG	A	3154	1/1	0.62	-	72,72,72,72	0
31	MG	A	3120	1/1	0.64	-	69,69,69,69	0
31	MG	A	3049	1/1	0.22	-	59,59,59,59	0
31	MG	A	2922	1/1	0.35	-	40,40,40,40	0
31	MG	A	3153	1/1	1.16	-	57,57,57,57	0
31	MG	A	3015	1/1	0.32	-	56,56,56,56	0
33	TEL	A	3206	58/58	0.34	-	110,110,110,110	0
31	MG	A	3023	1/1	0.23	-	56,56,56,56	0
31	MG	A	2916	1/1	0.18	-	52,52,52,52	0
31	MG	A	3021	1/1	0.16	-	59,59,59,59	0
31	MG	A	3016	1/1	0.30	-	76,76,76,76	0
31	MG	A	3130	1/1	0.13	-	47,47,47,47	0
31	MG	A	165	1/1	0.52	-	39,39,39,39	0
31	MG	A	3160	1/1	0.13	-	68,68,68,68	0
31	MG	A	3108	1/1	0.23	-	53,53,53,53	0
31	MG	A	3074	1/1	0.16	-	96,96,96,96	0
31	MG	A	3072	1/1	0.67	-	54,54,54,54	0
31	MG	A	2924	1/1	0.20	-	55,55,55,55	0
31	MG	A	2954	1/1	0.54	-	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
31	MG	A	3000	1/1	0.26	-	56,56,56,56	0
31	MG	A	3146	1/1	0.17	-	77,77,77,77	0
31	MG	A	3162	1/1	1.03	-	87,87,87,87	0
31	MG	A	3193	1/1	0.81	-	65,65,65,65	0
31	MG	A	3102	1/1	0.19	-	71,71,71,71	0
31	MG	A	3042	1/1	0.49	-	48,48,48,48	0
31	MG	A	2989	1/1	0.32	-	43,43,43,43	0
31	MG	A	2942	1/1	0.29	-	41,41,41,41	0
31	MG	A	3122	1/1	0.90	-	56,56,56,56	0
31	MG	A	3050	1/1	0.45	-	35,35,35,35	0
31	MG	A	2925	1/1	0.42	-	34,34,34,34	0
31	MG	A	3077	1/1	0.51	-	53,53,53,53	0
31	MG	A	3159	1/1	1.47	-	80,80,80,80	0
31	MG	A	3172	1/1	0.75	-	63,63,63,63	0
31	MG	A	2910	1/1	0.82	-	61,61,61,61	0
31	MG	A	2982	1/1	0.12	-	56,56,56,56	0
31	MG	A	2986	1/1	0.43	-	59,59,59,59	0
31	MG	A	3152	1/1	0.51	-	55,55,55,55	0
31	MG	A	164	1/1	0.40	-	71,71,71,71	0
31	MG	A	3182	1/1	0.15	-	104,104,104,104	0
31	MG	A	2999	1/1	0.36	-	75,75,75,75	0
31	MG	A	3002	1/1	0.28	-	51,51,51,51	0
31	MG	A	3070	1/1	0.69	-	56,56,56,56	0
31	MG	A	3062	1/1	0.34	-	59,59,59,59	0
31	MG	A	3001	1/1	0.20	-	42,42,42,42	0
31	MG	A	2912	1/1	0.18	-	69,69,69,69	0
31	MG	A	3080	1/1	0.73	-	49,49,49,49	0
31	MG	A	2936	1/1	0.25	-	36,36,36,36	0
31	MG	A	3126	1/1	0.40	-	76,76,76,76	0
31	MG	A	3200	1/1	2.06	-	54,54,54,54	0
31	MG	A	3098	1/1	0.29	-	43,43,43,43	0
31	MG	A	3145	1/1	1.07	-	91,91,91,91	0
31	MG	A	2952	1/1	0.47	-	51,51,51,51	0
31	MG	A	2919	1/1	0.53	-	29,29,29,29	0
31	MG	A	3198	1/1	0.59	-	53,53,53,53	0
31	MG	A	3142	1/1	0.90	-	55,55,55,55	0
31	MG	A	168	1/1	0.85	-	80,80,80,80	0
31	MG	A	3148	1/1	0.75	-	60,60,60,60	0
31	MG	A	3187	1/1	0.77	-	67,67,67,67	0
31	MG	A	3058	1/1	0.32	-	64,64,64,64	0
31	MG	A	2928	1/1	0.35	-	42,42,42,42	0
31	MG	A	3033	1/1	0.06	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
31	MG	A	3039	1/1	0.40	-	74,74,74,74	0
31	MG	B	174	1/1	0.39	-	59,59,59,59	0
31	MG	A	2993	1/1	0.43	-	53,53,53,53	0
31	MG	A	3031	1/1	0.12	-	40,40,40,40	0
31	MG	A	2946	1/1	1.06	-	69,69,69,69	0
31	MG	A	3180	1/1	0.11	-	50,50,50,50	0
31	MG	A	2931	1/1	0.38	-	54,54,54,54	0
31	MG	A	3018	1/1	0.28	-	75,75,75,75	0
31	MG	A	2977	1/1	0.51	-	85,85,85,85	0
31	MG	A	2990	1/1	0.22	-	27,27,27,27	0
31	MG	A	3078	1/1	0.54	-	81,81,81,81	0
31	MG	A	3029	1/1	0.24	-	54,54,54,54	0
31	MG	A	3164	1/1	1.09	-	83,83,83,83	0
31	MG	X	244	1/1	0.26	-	76,76,76,76	0
31	MG	A	3026	1/1	0.21	-	61,61,61,61	0
31	MG	A	3116	1/1	0.46	-	73,73,73,73	0
31	MG	A	3204	1/1	0.17	-	83,83,83,83	0
31	MG	A	3111	1/1	0.60	-	62,62,62,62	0
31	MG	A	3017	1/1	0.31	-	75,75,75,75	0
31	MG	A	3136	1/1	0.09	-	70,70,70,70	0
31	MG	A	3191	1/1	0.20	-	80,80,80,80	0
31	MG	A	3009	1/1	0.30	-	74,74,74,74	0
31	MG	A	163	1/1	0.67	-	72,72,72,72	0
31	MG	A	3106	1/1	0.55	-	78,78,78,78	0
31	MG	A	3063	1/1	0.23	-	48,48,48,48	0
31	MG	A	2908	1/1	0.49	-	66,66,66,66	0
31	MG	A	2958	1/1	0.29	-	44,44,44,44	0
31	MG	A	2997	1/1	0.21	-	61,61,61,61	0
31	MG	A	3030	1/1	0.36	-	57,57,57,57	0
31	MG	A	3022	1/1	0.43	-	72,72,72,72	0
31	MG	A	3032	1/1	0.41	-	62,62,62,62	0
31	MG	A	2994	1/1	0.34	-	53,53,53,53	0
31	MG	A	3028	1/1	0.42	-	63,63,63,63	0
31	MG	A	3087	1/1	0.35	-	59,59,59,59	0
31	MG	A	2971	1/1	0.72	-	70,70,70,70	0
31	MG	A	3151	1/1	0.41	-	61,61,61,61	0
31	MG	A	3194	1/1	0.58	-	75,75,75,75	0
31	MG	A	2911	1/1	0.33	-	39,39,39,39	0
31	MG	A	3104	1/1	0.29	-	33,33,33,33	0
31	MG	A	3095	1/1	0.33	-	64,64,64,64	0
31	MG	D	277	1/1	0.41	-	56,56,56,56	0
31	MG	A	3184	1/1	0.30	-	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
31	MG	A	2980	1/1	0.34	-	56,56,56,56	0
31	MG	A	3158	1/1	0.65	-	78,78,78,78	0
31	MG	A	2973	1/1	0.81	-	57,57,57,57	0
31	MG	A	3096	1/1	1.60	-	74,74,74,74	0
31	MG	A	3055	1/1	0.76	-	53,53,53,53	0
31	MG	E	207	1/1	0.15	-	34,34,34,34	0
31	MG	A	3008	1/1	0.37	-	85,85,85,85	0
31	MG	A	46	1/1	0.24	-	49,49,49,49	0
31	MG	A	161	1/1	0.36	-	59,59,59,59	0
31	MG	A	3119	1/1	0.29	-	78,78,78,78	0
31	MG	A	3048	1/1	0.29	-	57,57,57,57	0
31	MG	A	3079	1/1	0.13	-	45,45,45,45	0
31	MG	A	2939	1/1	0.37	-	51,51,51,51	0
31	MG	A	273	1/1	0.65	-	70,70,70,70	0
31	MG	A	3175	1/1	0.12	-	71,71,71,71	0
31	MG	A	3083	1/1	0.49	-	54,54,54,54	0
31	MG	A	3036	1/1	0.37	-	72,72,72,72	0
31	MG	A	2975	1/1	0.24	-	54,54,54,54	0
31	MG	A	3090	1/1	0.27	-	47,47,47,47	0
31	MG	A	3127	1/1	0.52	-	56,56,56,56	0
31	MG	A	3060	1/1	0.44	-	76,76,76,76	0
31	MG	A	3139	1/1	0.39	-	69,69,69,69	0
31	MG	A	3147	1/1	0.40	-	72,72,72,72	0
31	MG	A	3010	1/1	0.26	-	50,50,50,50	0
31	MG	A	167	1/1	0.56	-	72,72,72,72	0
31	MG	A	277	1/1	0.43	-	55,55,55,55	0
31	MG	A	3178	1/1	0.83	-	60,60,60,60	0
31	MG	A	3144	1/1	0.48	-	61,61,61,61	0
31	MG	A	2984	1/1	0.52	-	62,62,62,62	0
31	MG	A	2918	1/1	0.28	-	43,43,43,43	0
31	MG	A	2988	1/1	0.20	-	50,50,50,50	0
31	MG	A	2963	1/1	0.18	-	60,60,60,60	0
31	MG	A	3185	1/1	0.17	-	64,64,64,64	0
31	MG	A	3100	1/1	0.36	-	49,49,49,49	0
31	MG	A	3056	1/1	0.23	-	55,55,55,55	0
31	MG	A	138	1/1	1.33	-	81,81,81,81	0
31	MG	A	3069	1/1	0.21	-	67,67,67,67	0
31	MG	A	3038	1/1	0.47	-	61,61,61,61	0
31	MG	A	3091	1/1	0.24	-	46,46,46,46	0
31	MG	A	2933	1/1	0.20	-	32,32,32,32	0
31	MG	A	3041	1/1	0.26	-	35,35,35,35	0
31	MG	A	3088	1/1	0.32	-	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
31	MG	A	3076	1/1	0.47	-	58,58,58,58	0
31	MG	A	3168	1/1	0.13	-	59,59,59,59	0
31	MG	A	3161	1/1	0.73	-	72,72,72,72	0
31	MG	A	2923	1/1	0.38	-	54,54,54,54	0
31	MG	A	3092	1/1	0.58	-	73,73,73,73	0
31	MG	A	3114	1/1	0.37	-	47,47,47,47	0
31	MG	A	3167	1/1	0.81	-	87,87,87,87	0
31	MG	A	3089	1/1	0.60	-	74,74,74,74	0
31	MG	A	3086	1/1	0.12	-	41,41,41,41	0
31	MG	A	2951	1/1	0.24	-	39,39,39,39	0
31	MG	A	3117	1/1	1.08	-	79,79,79,79	0
31	MG	R	207	1/1	0.33	-	50,50,50,50	0
31	MG	A	3071	1/1	0.61	-	62,62,62,62	0
31	MG	A	3177	1/1	0.97	-	88,88,88,88	0
31	MG	A	2965	1/1	0.16	-	55,55,55,55	0
31	MG	A	3035	1/1	0.62	-	66,66,66,66	0
31	MG	A	2961	1/1	0.40	-	38,38,38,38	0
31	MG	A	3046	1/1	0.23	-	43,43,43,43	0
31	MG	7	293	1/1	1.15	-	58,58,58,58	0
31	MG	A	2995	1/1	0.12	-	54,54,54,54	0
31	MG	A	3075	1/1	0.95	-	65,65,65,65	0
31	MG	A	2979	1/1	0.57	-	55,55,55,55	0
31	MG	A	3132	1/1	0.53	-	84,84,84,84	0
31	MG	A	3059	1/1	0.42	-	49,49,49,49	0
31	MG	A	2960	1/1	0.33	-	47,47,47,47	0
31	MG	A	3005	1/1	0.25	-	59,59,59,59	0
31	MG	A	2927	1/1	0.40	-	74,74,74,74	0
31	MG	A	3084	1/1	0.65	-	56,56,56,56	0
31	MG	A	3157	1/1	0.40	-	67,67,67,67	0
31	MG	A	3024	1/1	0.34	-	84,84,84,84	0
31	MG	A	2967	1/1	0.13	-	40,40,40,40	0
31	MG	P	261	1/1	0.23	-	42,42,42,42	0
31	MG	A	159	1/1	0.16	-	80,80,80,80	0
31	MG	A	3019	1/1	0.22	-	58,58,58,58	0
31	MG	A	3196	1/1	0.15	-	54,54,54,54	0
31	MG	A	3113	1/1	0.12	-	62,62,62,62	0
31	MG	8	179	1/1	0.69	-	66,66,66,66	0
31	MG	A	3081	1/1	0.15	-	48,48,48,48	0
31	MG	A	2959	1/1	0.39	-	90,90,90,90	0
31	MG	A	2957	1/1	0.39	-	53,53,53,53	0
31	MG	A	3047	1/1	0.40	-	65,65,65,65	0
31	MG	A	2920	1/1	0.59	-	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
31	MG	A	3137	1/1	0.40	-	61,61,61,61	0
31	MG	A	2968	1/1	0.67	-	76,76,76,76	0
32	K	A	3205	1/1	0.17	-	82,82,82,82	0
31	MG	A	2949	1/1	0.24	-	48,48,48,48	0
31	MG	A	3188	1/1	0.63	-	64,64,64,64	0
31	MG	A	3121	1/1	0.28	-	42,42,42,42	0
31	MG	A	2985	1/1	0.40	-	39,39,39,39	0
31	MG	A	2955	1/1	0.43	-	54,54,54,54	0
31	MG	A	3068	1/1	0.17	-	52,52,52,52	0
31	MG	A	3163	1/1	0.63	-	66,66,66,66	0
31	MG	A	3201	1/1	0.24	-	69,69,69,69	0
31	MG	A	162	1/1	0.98	-	44,44,44,44	0
31	MG	A	2969	1/1	0.72	-	72,72,72,72	0
31	MG	A	2917	1/1	0.36	-	45,45,45,45	0
31	MG	A	2970	1/1	0.24	-	46,46,46,46	0
31	MG	A	3027	1/1	0.28	-	67,67,67,67	0
31	MG	A	3171	1/1	0.54	-	70,70,70,70	0
31	MG	A	3105	1/1	0.24	-	61,61,61,61	0
31	MG	A	2914	1/1	0.53	-	40,40,40,40	0
31	MG	A	2953	1/1	0.19	-	28,28,28,28	0
31	MG	A	3101	1/1	0.41	-	62,62,62,62	0
31	MG	A	3176	1/1	0.22	-	74,74,74,74	0
31	MG	A	3006	1/1	0.56	-	54,54,54,54	0
31	MG	A	2976	1/1	0.21	-	52,52,52,52	0
31	MG	A	2992	1/1	0.23	-	61,61,61,61	0
31	MG	A	2915	1/1	0.25	-	50,50,50,50	0
31	MG	A	3135	1/1	0.53	-	44,44,44,44	0
31	MG	A	3169	1/1	0.44	-	57,57,57,57	0
31	MG	A	3061	1/1	0.18	-	73,73,73,73	0
31	MG	A	3125	1/1	0.21	-	48,48,48,48	0
31	MG	A	3129	1/1	0.14	-	65,65,65,65	0
31	MG	A	3066	1/1	0.65	-	41,41,41,41	0
31	MG	A	3199	1/1	0.86	-	64,64,64,64	0
31	MG	A	2944	1/1	0.18	-	39,39,39,39	0
31	MG	Q	194	1/1	0.75	-	63,63,63,63	0
31	MG	A	166	1/1	0.32	-	51,51,51,51	0
31	MG	A	3054	1/1	0.42	-	66,66,66,66	0
31	MG	A	2947	1/1	0.29	-	36,36,36,36	0
31	MG	A	3097	1/1	0.26	-	53,53,53,53	0

6.5 Other polymers ⓘ

There are no such residues in this entry.