



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 06:02 AM UTC

PDB ID : 4YLP / pdb_00004ylp
Title : E. coli Transcription Initiation Complex - 16-bp spacer and 5-nt RNA
Authors : Zuo, Y.; Steitz, T.A.
Deposited on : 2015-03-05
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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

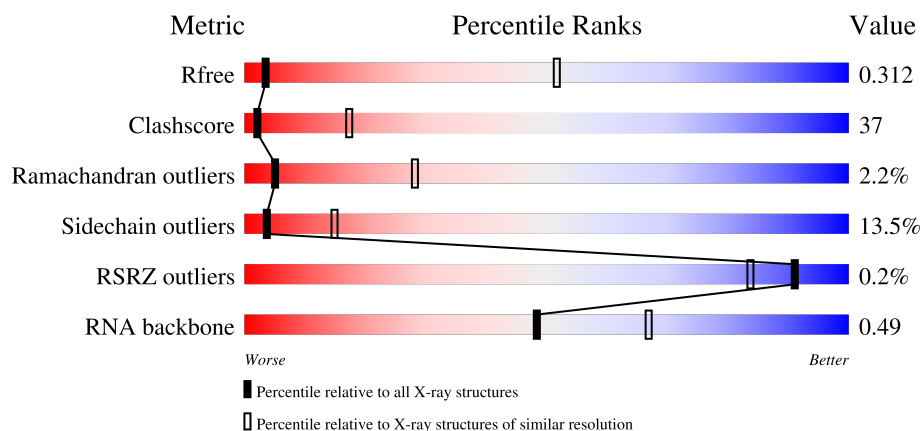
1 Overall quality at a glance

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}	180053	1088 (7.00-4.00)
Clashscore	190562	1147 (7.00-4.00)
Ramachandran outliers	187476	1012 (7.02-3.98)
Sidechain outliers	187428	1023 (7.04-3.96)
RSRZ outliers	180081	1081 (7.00-4.00)
RNA backbone	3983	1052 (7.80-3.10)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	A	242	39% 45% 10% 5%
1	B	242	37% 40% 17% 6%
1	G	242	47% 40% 7% 5%
1	H	242	48% 35% 11% 6%

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Mol	Chain	Length	Quality of chain
1	M	242	
1	N	242	
2	C	1342	
2	I	1342	
2	O	1342	
3	D	1407	
3	J	1407	
3	P	1407	
4	E	90	
4	K	90	
4	Q	90	
5	F	628	
5	L	628	
5	R	628	
6	1	49	
6	4	49	
6	7	49	
7	2	49	
7	5	49	
7	8	49	
8	3	5	
8	6	5	
8	9	5	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
9	ZN	P	1501	-	-	X	-
9	ZN	P	1502	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 94668 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 protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1787	1112	317	352	6			
1	B	228	Total	C	N	O	S	0	0	0
			1767	1100	312	349	6			
1	G	230	Total	C	N	O	S	0	0	0
			1787	1112	317	352	6			
1	H	228	Total	C	N	O	S	0	0	0
			1767	1100	312	349	6			
1	M	230	Total	C	N	O	S	0	0	0
			1787	1112	317	352	6			
1	N	228	Total	C	N	O	S	0	0	0
			1767	1100	312	349	6			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	ALA	-	expression tag	UNP A7ZSI4
A	-5	HIS	-	expression tag	UNP A7ZSI4
A	-4	HIS	-	expression tag	UNP A7ZSI4
A	-3	HIS	-	expression tag	UNP A7ZSI4
A	-2	HIS	-	expression tag	UNP A7ZSI4
A	-1	HIS	-	expression tag	UNP A7ZSI4
A	0	HIS	-	expression tag	UNP A7ZSI4
B	-6	ALA	-	expression tag	UNP A7ZSI4
B	-5	HIS	-	expression tag	UNP A7ZSI4
B	-4	HIS	-	expression tag	UNP A7ZSI4
B	-3	HIS	-	expression tag	UNP A7ZSI4
B	-2	HIS	-	expression tag	UNP A7ZSI4
B	-1	HIS	-	expression tag	UNP A7ZSI4
B	0	HIS	-	expression tag	UNP A7ZSI4
G	-6	ALA	-	expression tag	UNP A7ZSI4
G	-5	HIS	-	expression tag	UNP A7ZSI4
G	-4	HIS	-	expression tag	UNP A7ZSI4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-3	HIS	-	expression tag	UNP A7ZSI4
G	-2	HIS	-	expression tag	UNP A7ZSI4
G	-1	HIS	-	expression tag	UNP A7ZSI4
G	0	HIS	-	expression tag	UNP A7ZSI4
H	-6	ALA	-	expression tag	UNP A7ZSI4
H	-5	HIS	-	expression tag	UNP A7ZSI4
H	-4	HIS	-	expression tag	UNP A7ZSI4
H	-3	HIS	-	expression tag	UNP A7ZSI4
H	-2	HIS	-	expression tag	UNP A7ZSI4
H	-1	HIS	-	expression tag	UNP A7ZSI4
H	0	HIS	-	expression tag	UNP A7ZSI4
M	-6	ALA	-	expression tag	UNP A7ZSI4
M	-5	HIS	-	expression tag	UNP A7ZSI4
M	-4	HIS	-	expression tag	UNP A7ZSI4
M	-3	HIS	-	expression tag	UNP A7ZSI4
M	-2	HIS	-	expression tag	UNP A7ZSI4
M	-1	HIS	-	expression tag	UNP A7ZSI4
M	0	HIS	-	expression tag	UNP A7ZSI4
N	-6	ALA	-	expression tag	UNP A7ZSI4
N	-5	HIS	-	expression tag	UNP A7ZSI4
N	-4	HIS	-	expression tag	UNP A7ZSI4
N	-3	HIS	-	expression tag	UNP A7ZSI4
N	-2	HIS	-	expression tag	UNP A7ZSI4
N	-1	HIS	-	expression tag	UNP A7ZSI4
N	0	HIS	-	expression tag	UNP A7ZSI4

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1341	Total	C	N	O	S	0	0	0
			10576	6636	1842	2055	43			
2	I	1341	Total	C	N	O	S	0	0	0
			10576	6636	1842	2055	43			
2	O	1341	Total	C	N	O	S	0	0	0
			10576	6636	1842	2055	43			

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1362	Total	C	N	O	S	0	0	0
			10568	6633	1887	1998	50			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	J	1362	Total	C	N	O	S	0	0	0
			10568	6633	1887	1998	50			
3	P	1362	Total	C	N	O	S	0	0	0
			10568	6633	1887	1998	50			

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	90	Total	C	N	O	S	0	0	0
			708	430	136	141	1			
4	K	90	Total	C	N	O	S	0	0	0
			708	430	136	141	1			
4	Q	90	Total	C	N	O	S	0	0	0
			708	430	136	141	1			

- Molecule 5 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	497	Total	C	N	O	S	0	0	0
			4022	2512	719	768	23			
5	L	497	Total	C	N	O	S	0	0	0
			4022	2512	719	768	23			
5	R	497	Total	C	N	O	S	0	0	0
			4022	2512	719	768	23			

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-14	MET	-	expression tag	UNP P00579
F	-13	ARG	-	expression tag	UNP P00579
F	-12	GLY	-	expression tag	UNP P00579
F	-11	SER	-	expression tag	UNP P00579
F	-10	HIS	-	expression tag	UNP P00579
F	-9	HIS	-	expression tag	UNP P00579
F	-8	HIS	-	expression tag	UNP P00579
F	-7	HIS	-	expression tag	UNP P00579
F	-6	HIS	-	expression tag	UNP P00579
F	-5	HIS	-	expression tag	UNP P00579
F	-4	THR	-	expression tag	UNP P00579
F	-3	ASP	-	expression tag	UNP P00579
F	-2	GLN	-	expression tag	UNP P00579
F	-1	PHE	-	expression tag	UNP P00579

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Chain	Residue	Modelled	Actual	Comment	Reference
F	0	THR	-	expression tag	UNP P00579
L	-14	MET	-	expression tag	UNP P00579
L	-13	ARG	-	expression tag	UNP P00579
L	-12	GLY	-	expression tag	UNP P00579
L	-11	SER	-	expression tag	UNP P00579
L	-10	HIS	-	expression tag	UNP P00579
L	-9	HIS	-	expression tag	UNP P00579
L	-8	HIS	-	expression tag	UNP P00579
L	-7	HIS	-	expression tag	UNP P00579
L	-6	HIS	-	expression tag	UNP P00579
L	-5	HIS	-	expression tag	UNP P00579
L	-4	THR	-	expression tag	UNP P00579
L	-3	ASP	-	expression tag	UNP P00579
L	-2	GLN	-	expression tag	UNP P00579
L	-1	PHE	-	expression tag	UNP P00579
L	0	THR	-	expression tag	UNP P00579
R	-14	MET	-	expression tag	UNP P00579
R	-13	ARG	-	expression tag	UNP P00579
R	-12	GLY	-	expression tag	UNP P00579
R	-11	SER	-	expression tag	UNP P00579
R	-10	HIS	-	expression tag	UNP P00579
R	-9	HIS	-	expression tag	UNP P00579
R	-8	HIS	-	expression tag	UNP P00579
R	-7	HIS	-	expression tag	UNP P00579
R	-6	HIS	-	expression tag	UNP P00579
R	-5	HIS	-	expression tag	UNP P00579
R	-4	THR	-	expression tag	UNP P00579
R	-3	ASP	-	expression tag	UNP P00579
R	-2	GLN	-	expression tag	UNP P00579
R	-1	PHE	-	expression tag	UNP P00579
R	0	THR	-	expression tag	UNP P00579

- Molecule 6 is a DNA chain called NT strand DNA (49-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	1	49	Total	C	N	O	P	0	0	0
			996	476	178	294	48			
6	4	49	Total	C	N	O	P	0	0	0
			996	476	178	294	48			
6	7	49	Total	C	N	O	P	0	0	0
			996	476	178	294	48			

- Molecule 7 is a DNA chain called T strand DNA (49-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	2	49	Total	C	N	O	P	0	0	0
			1012	481	191	292	48			
7	5	49	Total	C	N	O	P	0	0	0
			1012	481	191	292	48			
7	8	49	Total	C	N	O	P	0	0	0
			1012	481	191	292	48			

- Molecule 8 is a RNA chain called RNA (5'-R(*(GTP))-R(P*AP*GP*UP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	3	5	Total	C	N	O	P	0	0	0
			117	48	20	42	7			
8	6	5	Total	C	N	O	P	0	0	0
			117	48	20	42	7			
8	9	5	Total	C	N	O	P	0	0	0
			117	48	20	42	7			

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	2	Total	Zn	0	0
			2	2		
9	J	2	Total	Zn	0	0
			2	2		
9	P	2	Total	Zn	0	0
			2	2		

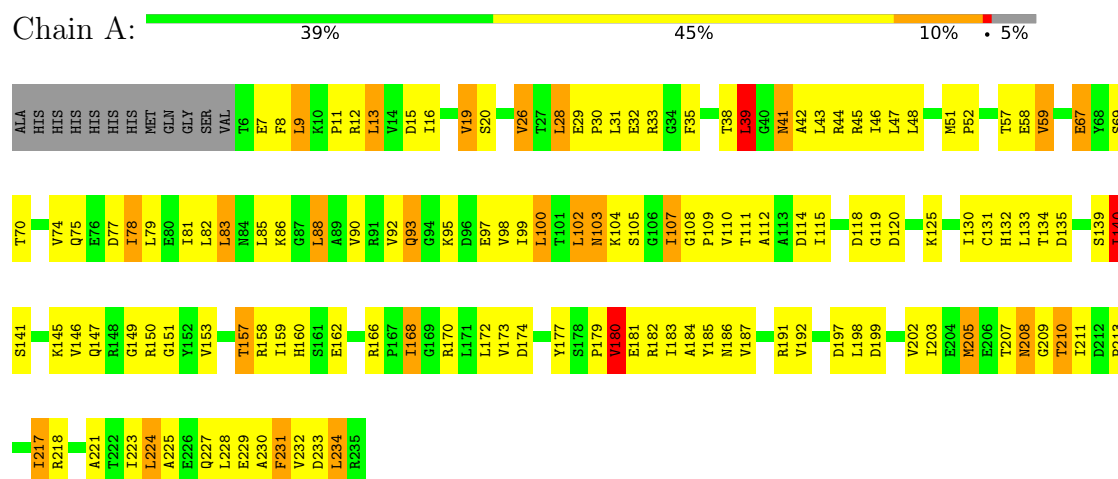
- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	D	1	Total	Mg	0	0
			1	1		
10	J	1	Total	Mg	0	0
			1	1		
10	P	1	Total	Mg	0	0
			1	1		

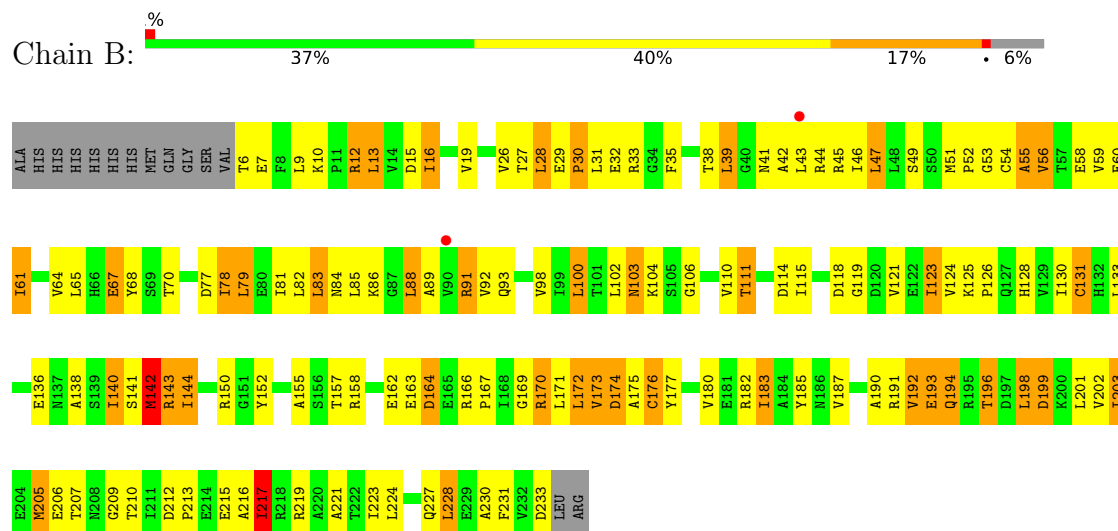
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 ($RSRZ > 2$). 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: DNA-directed RNA polymerase subunit alpha

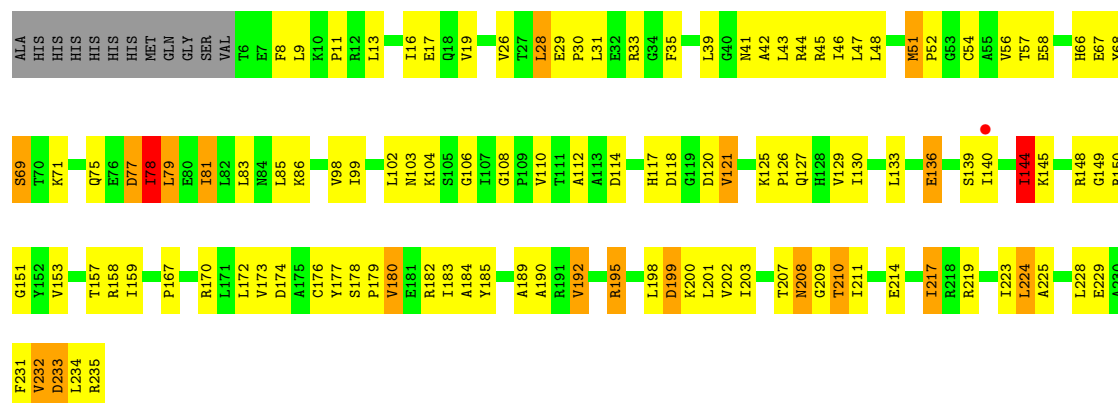


• Molecule 1: DNA-directed RNA polymerase subunit alpha



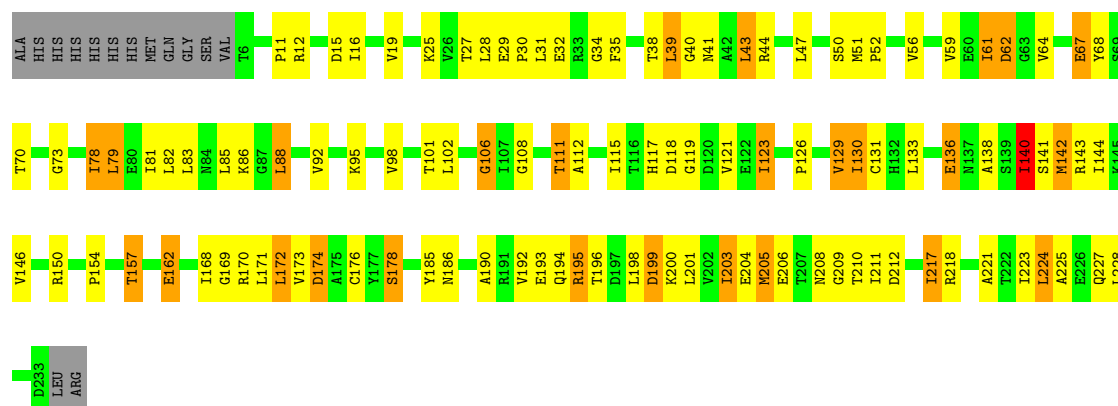
• Molecule 1: DNA-directed RNA polymerase subunit alpha





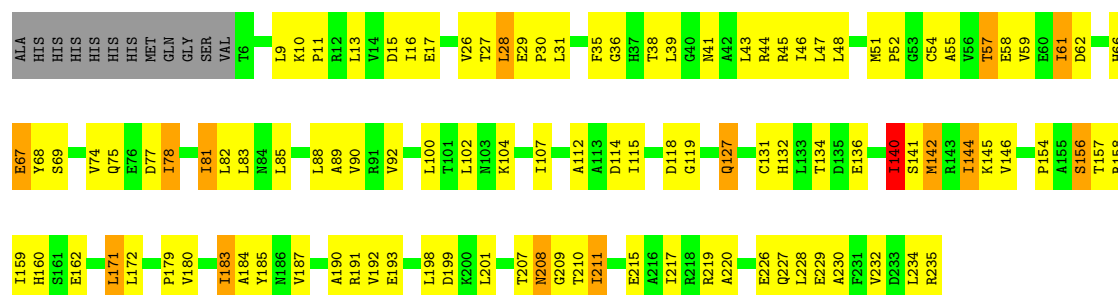
• Molecule 1: DNA-directed RNA polymerase subunit alpha

Chain H: 48% 35% 11% 6%



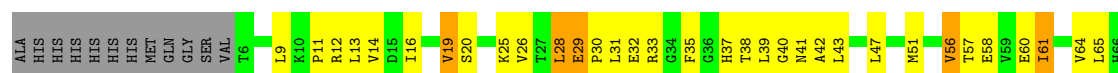
• Molecule 1: DNA-directed RNA polymerase subunit alpha

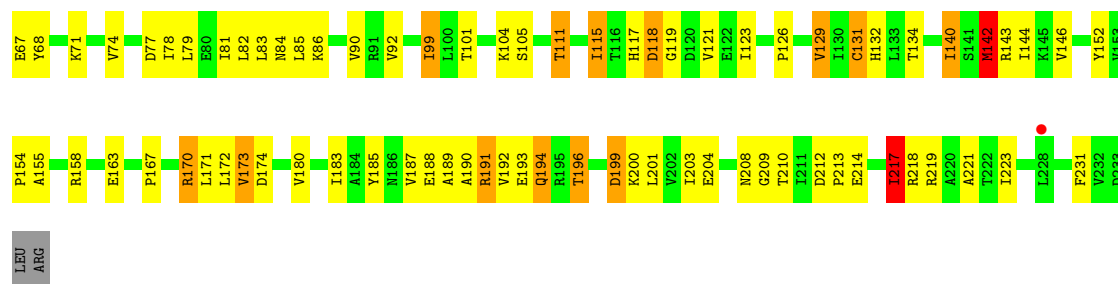
Chain M: 50% 38% 6% 5%



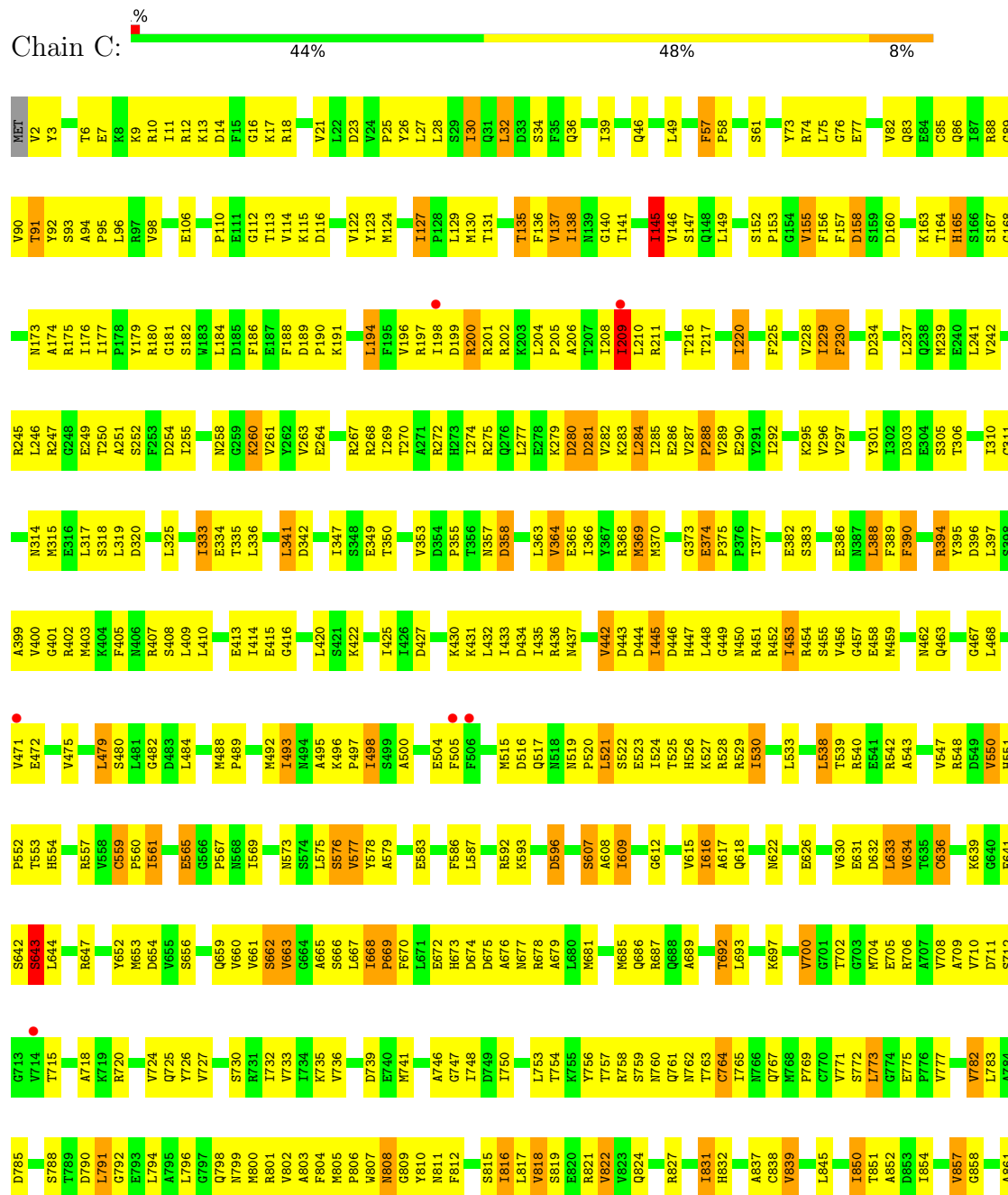
• Molecule 1: DNA-directed RNA polymerase subunit alpha

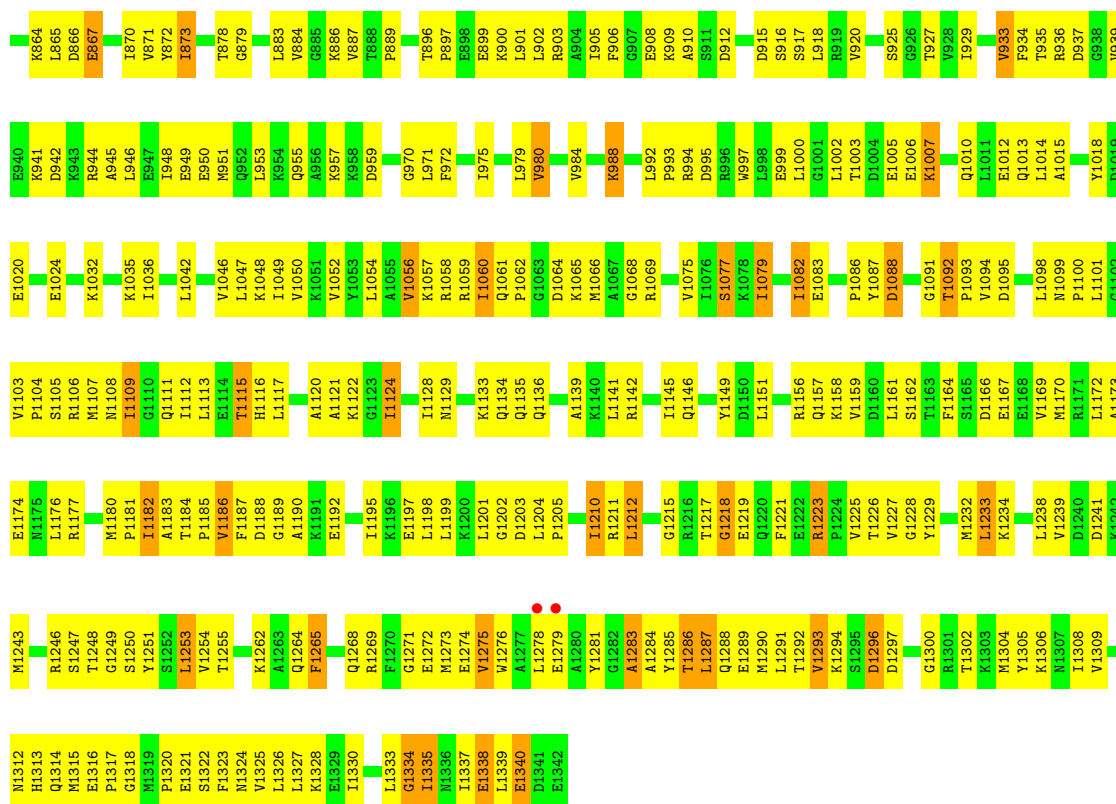
Chain N: 49% 37% 7% 6%





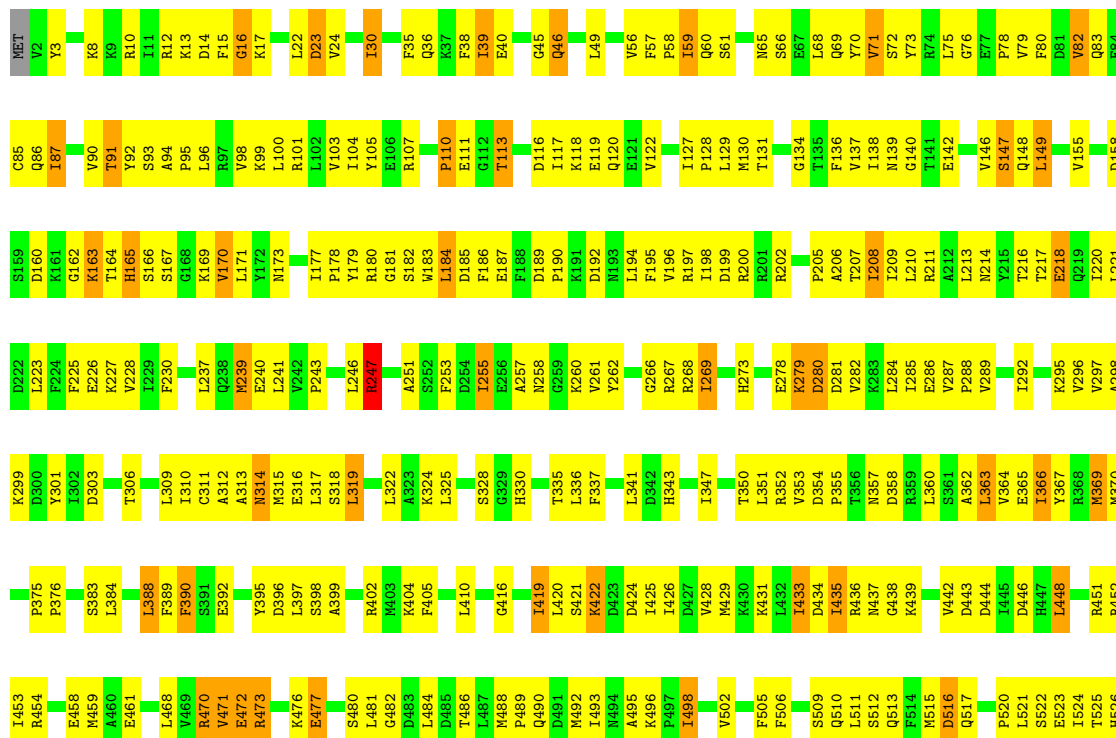
• Molecule 2: DNA-directed RNA polymerase subunit beta

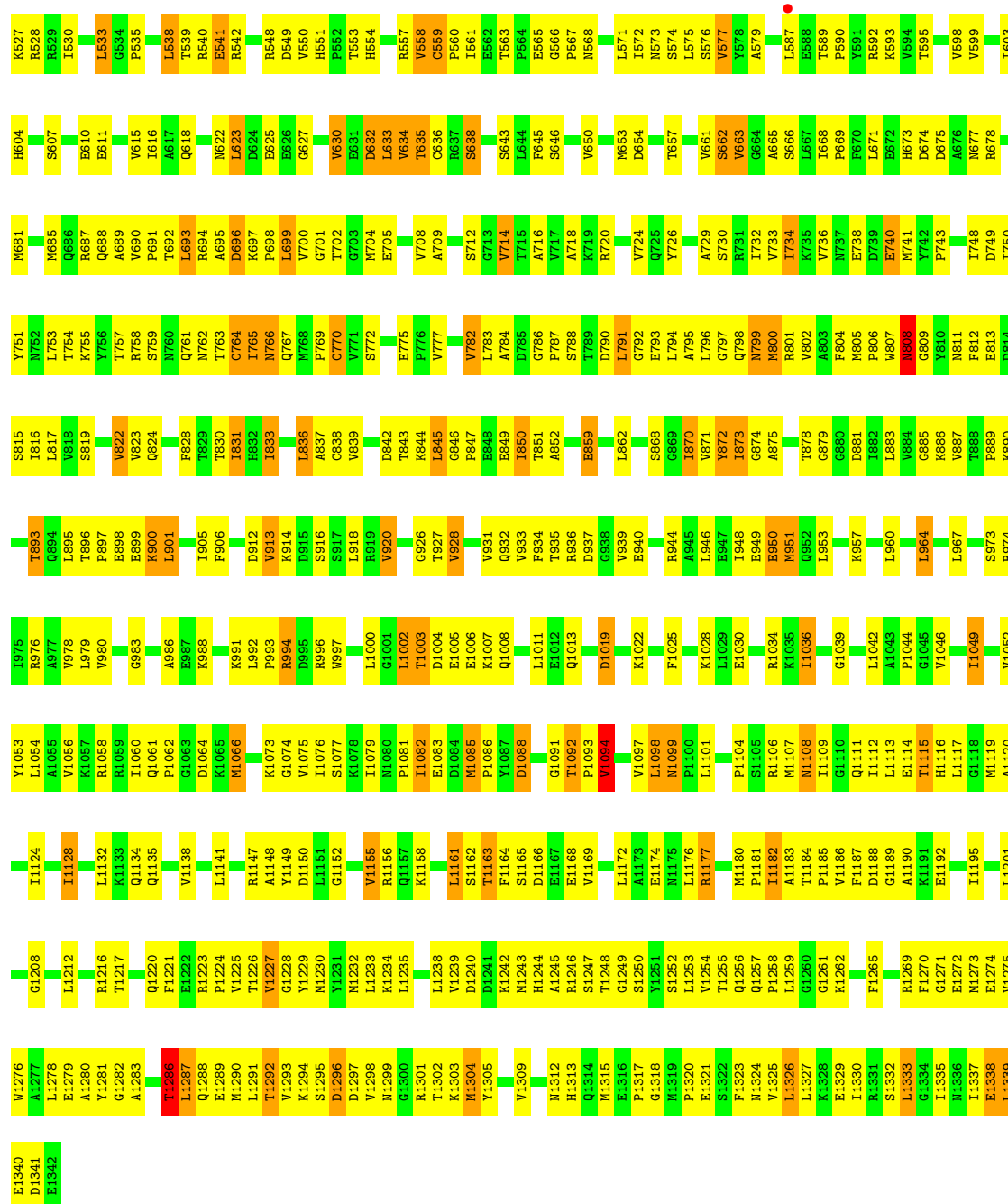




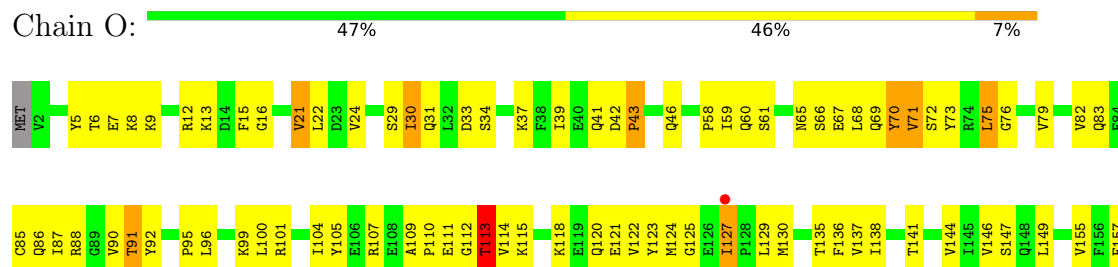
● Molecule 2: DNA-directed RNA polymerase subunit beta

Chain I: 42% 48% 9%





• Molecule 2: DNA-directed RNA polymerase subunit beta

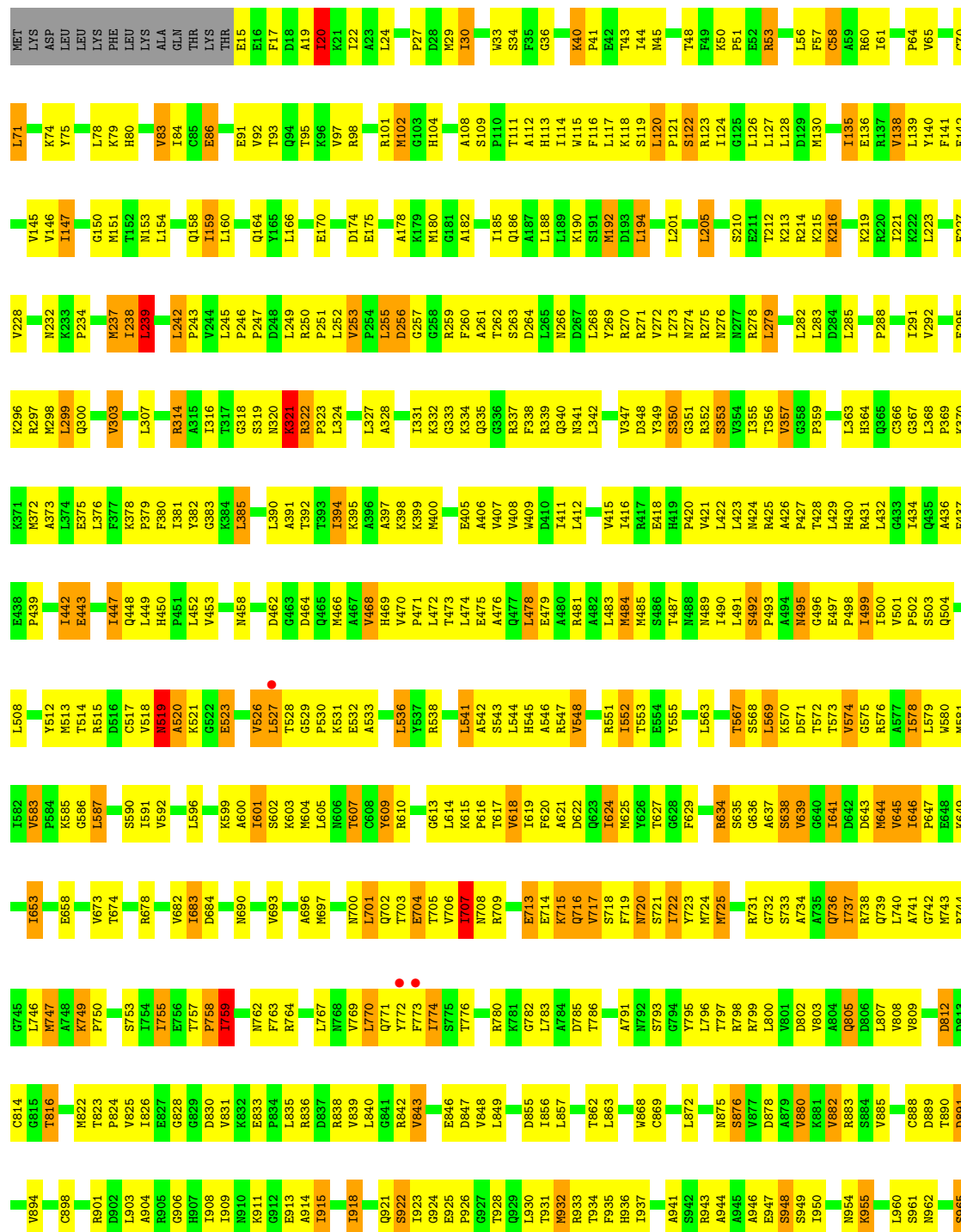


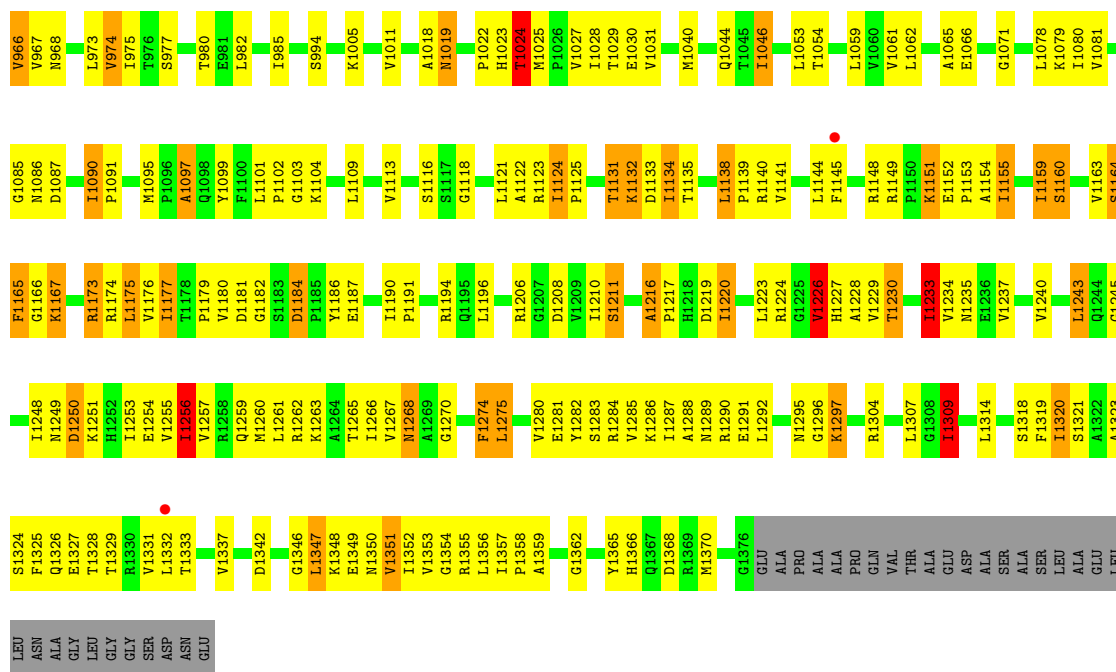
G1266	L1198	L1042	E949	L794	Q725	D654	T563	D485	V400	L322	V228	D158
G1267	L1199	A1043	E950	A795	Y726	V655	F564	T486	G401	L326	V229	S159
G1268	L1200	P1044	M951	L796	Y727	S656	E585	L487	R402	S326	L232	D160
R1269	G1202	G1045	Q952	G797	D728	M488	G566	M489	F405	S328	T232	K163
G1270	L1203	L1046	L953	W799	A729	Q659	I569	P489	R406	S328	T233	T164
G1271	L1204	L1047	A956	W800	S730	V660	V569	T493	R407	S331	E240	H165
G1272	L1205	Q1048	Q956	W801	R731	V661	V570	L493	R408	S332	L241	S166
M1273	L1206	V1049	D959	R801	L732	S662	L575	V502	S408	S333	V242	S167
V1274	L1207	V1050	L960	M805	W733	V663	S576	V503	E415	L334	P243	V170
G1275	L1208	Y1053	L961	W806	K735	G664	A679	K496	G416	T335	R245	Y171
L1276	L1209	L1054	L962	W807	W736	A665	Q580	L498	S417	L336	L246	L172
L1277	L1210	Q1061	Q957	W808	W737	S666	T581	V504	G418	F337	R247	M173
L1278	L1211	P1062	L963	W809	E738	L668	H582	V505	L419	D340	S252	L177
L1279	L1212	G1063	L964	W810	M741	L671	E583	F506	L420	L341	T253	P178
L1280	L1213	P1064	L965	W811	Y742	S672	L587	S509	S421	D342	T254	Y179
L1281	L1214	D1065	L966	W812	P743	H673	E588	S510	K422	H343	T255	L182
L1282	L1215	E1066	L967	W813	A746	D674	T589	Q513	L425	G344	A257	L183
L1283	L1216	M1067	R974	W814	W747	D675	P590	F514	V428	F346	K260	L184
L1284	L1217	Q1068	L968	W815	G747	L676	F591	M515	V429	T347	V261	F186
L1285	L1218	H1070	L969	W816	L748	A678	R592	N518	K431	S348	Y262	F187
L1286	L1219	K1071	R970	W817	D749	L680	K593	N519	L432	E349	R267	F188
L1287	L1220	G1072	L971	W818	W750	L681	T595	P520	L433	T350	R268	D189
L1288	L1221	L1073	L972	W819	Y751	M681	D596	L521	L434	L351	R269	P190
L1289	L1222	Q1074	L973	W820	W752	M682	G597	L522	L435	F352	R270	K191
L1290	L1223	P1075	L974	W821	L753	M683	F598	L523	L436	V353	L274	L193
L1291	L1224	E1076	L975	W822	T754	A689	V599	L524	G440	N357	L275	L194
L1292	L1225	L1077	L976	W823	W755	V690	S607	L525	V441	D358	L276	R197
L1293	L1226	Q1078	L977	W824	K756	L691	T603	R528	V442	R359	E277	D199
L1294	L1227	P1079	L978	W825	W757	L692	L606	L530	L448	S361	K279	L198
L1295	L1228	E1080	L979	W826	W758	L693	R607	L531	R451	L363	D281	L199
L1296	L1229	L1081	L980	W827	W759	L694	S608	L532	R452	V364	V289	R200
L1297	L1230	Q1082	L981	W828	W760	L695	E610	L533	R453	E365	V290	R201
L1298	L1231	E1083	L982	W829	W761	L696	E611	L534	L454	L366	T292	R202
L1299	L1232	L1084	L983	W830	W762	L697	T616	L535	V456	T293	A293	K203
L1300	L1233	Q1085	L984	W831	W763	L698	A617	L536	G457	M369	G294	L204
L1301	L1234	D1086	L985	W832	W764	L699	Q618	L537	R458	K295	V296	P205
L1302	L1235	E1087	L986	W833	W765	L700	L623	L538	R459	G373	V297	T207
L1303	L1236	L1088	L987	W834	W766	L701	G627	L539	R460	E379	L208	L208
L1304	L1237	Q1089	L988	W835	W767	L702	V634	L540	R461	E380	L209	L210
L1305	L1238	E1090	L989	W836	W768	L703	V635	L541	R462	E381	R211	R211
L1306	L1239	L1091	L990	W837	W769	L704	C636	L542	R463	E382	A212	A212
L1307	L1240	Q1092	L991	W838	W770	L705	R637	L543	F464	E383	L213	L213
L1308	L1241	E1093	L992	W839	W771	L706	V637	L544	R465	E384	N214	N214
L1309	L1242	L1094	L993	W840	W772	L707	V638	L545	R466	E385	Y215	Y215
L1310	L1243	Q1095	L994	W841	W773	L708	V639	L546	R467	E386	T216	T216
L1311	L1244	E1096	L995	W842	W774	L709	V640	L547	R468	E387	F217	F217
L1312	L1245	L1097	L996	W843	W775	L710	C637	L548	V471	E388	A312	A312
L1313	L1246	Q1098	L997	W844	W776	L711	R638	L549	R469	E389	N314	N314
L1314	L1247	E1099	L998	W845	W777	L712	V641	L550	R470	E390	L310	L310
L1315	L1248	L1099	L999	W846	W778	L713	V642	L551	R471	E391	F389	F389
L1316	L1249	Q1100	L1000	W847	W779	L714	V643	L552	R472	E392	A313	A313
L1317	L1250	E1101	L1001	W848	W780	L715	V644	L553	R473	E393	N315	N315
L1318	L1251	L1102	L1002	W849	W781	L716	V645	L554	R474	E394	L316	L316
L1319	L1252	Q1103	L1003	W850	W782	L717	V646	L555	R475	E395	A314	A314
L1320	L1253	E1104	L1004	W851	W783	L718	V647	L556	R476	E396	L317	L317
L1321	L1254	L1105	L1005	W852	W784	L719	V648	L557	R477	E397	S318	S318
L1322	L1255	Q1106	L1006	W853	W785	L720	V649	L558	R478	E398	L319	L319
L1323	L1256	E1107	L1007	W854	W786	L721	V650	L559	R479	E399	A399	A399
L1324	L1257	L1108	L1008	W855	W787	L722	V651	L560	R480	E400	L320	L320
L1325	L1258	Q1109	L1009	W856	W788	L723	V652	L561	R481	E401	D222	D222
L1326	L1259	E1110	L1010	W857	W789	L724	V653	L562	R482	E402	L221	L221
L1327	L1260	L1109	L1011	W858	W790	L725	V654	L563	R483	E403	D222	D222
L1328	L1261	Q1110	L1012	W859	W791	L726	V655	L564	R484	E404	L222	L222
L1329	L1262	E1111	L1013	W860	W792	L727	V656	L565	R485	E405	D223	D223
L1330	L1263	L1110	L1014	W861	W793	L728	V657	L566	R486	E406	L224	L224
L1331	L1264	Q1111	L1015	W862	W794	L729	V658	L567	R487	E407	D225	D225
L1332	L1265	E1112	L1016	W863	W795	L730	V659	L568	R488	E408	L226	L226
L1333	L1266	L1111	L1017	W864	W796	L731	V660	L569	R489	E409	D227	D227
L1334	L1267	Q1112	L1018	W865	W797	L732	V661	L570	R490	E410	L228	L228
L1335	L1268	E1113	L1019	W866	W798	L733	V662	L571	R491	E411	D229	D229
L1336	L1269	L1112	L1020	W867	W799	L734	V663	L572	R492	E412	L230	L230
L1337	L1270	Q1113	L1021	W868	W800	L735	V664	L573	R493	E413	D231	D231
L1338	L1271	E1114	L1022	W869	W801	L736	V665	L574	R494	E414	L232	L232
L1339	L1272	L1113	L1023	W870	W802	L737	V666	L575	R495	E415	D233	D233
L1340	L1273	Q1114	L1024	W871	W803	L738	V667	L576	R496	E416	L234	L234
L1341	L1274	E1115	L1025	W872	W804	L739	V668	L577	R497	E417	D235	D235
L1342	L1275	L1114	L1026	W873	W805	L740	V669	L578	R498	E418	L236	L236
L1343	L1276	Q1115	L1027	W874	W806	L741	V670	L579	R499	E419	D237	D237
L1344	L1277	E1116	L1028	W875	W807	L742	V671	L580	R500	E420	L238	L238
L1345	L1278	L1115	L1029	W876	W808	L743	V672	L581	R501	E421	D239	D239
L1346	L1279	Q1116	L1030	W877	W809	L744	V673	L582	R502	E422	L240	L240
L1347	L1280	E1117	L1031	W878	W810	L745	V674	L583	R503	E423	D241	D241
L1348	L1281	L1116	L1032	W879	W811	L746	V675	L584	R504	E424	L242	L242
L1349	L1282	Q1117	L1033	W880	W812	L747	V676	L585	R505	E425	D243	D243
L1350	L1283	E1118	L1034	W881	W813	L748	V677	L586	R506	E426	L244	L244
L1351	L1284	L1117	L1035	W882	W814	L749	V678	L587	R507	E427	D245	D245
L1352	L1285	Q1118	L1036	W883	W815	L750	V679	L588	R508	E428	L246	L246
L1353	L1286	E1119	L1037	W884	W816	L751	V680	L589	R509	E429	D247	D247
L1354	L1287	L1118	L1038	W885	W817	L752	V681	L590	R510	E430	L248	L248
L1355	L1288	Q1119	L1039	W886	W818	L753	V682	L591	R511	E431	D249	D249
L1356	L1289	E1120	L1040	W887	W819	L754	V683	L592	R512	E432	L250	L250
L1357	L1290	L1119	L1041	W888	W820	L755	V684	L593	R513	E433	D251	D251
L1358	L1291	Q1120	L1042	W889	W821	L756	V685	L594	R514	E434	L252	L252
L1359	L1292	E1121	L1043	W890	W822	L757	V686	L595	R515	E435	D253	D253
L1360	L1293	L1120	L1044	W891	W823	L758	V687	L596	R516	E436	L254	L254
L1361	L1294	Q1121	L1045	W892	W824	L759	V688	L597	R517	E437	D255	D255
L1362	L1295	E1122	L1046	W893	W825	L760	V689	L598	R518	E438	L256	L256
L1363	L1296	L1121	L1047	W894	W826	L761	V690	L599	R519	E439	D257	D257
L1364	L1297	Q1122	L1048	W895	W827	L762	V691	L600	R520	E440	L258	L258
L1365	L1298	E1123	L1049	W896	W828	L763	V692	L601	R521	E441	D259	D259
L1366	L1299	L1122	L1050	W897	W829	L764	V693	L602	R522	E442	L260	L260
L1367	L1300	Q1123	L1051	W898	W830	L765	V694	L603	R523	E443	D261	D261
L1368	L1301	E1124	L1052	W899	W831	L766	V695	L604	R524	E444	L262	L262
L1369	L1302	L1123	L1053	W900	W832	L767	V696	L605	R525	E445	D263	D263
L1370	L1303	Q1124	L1054	W901	W833	L768	V697	L606	R526	E446	L264	L264
L1371	L1304	E1125	L1055	W902	W834	L769	V698	L607	R527	E447	D2	

K1328
E1329
I1330
R1331
S1332
L1333
G1334
I1335
R1336
I1337
E1338
L1339
E1340
D1341
E1342

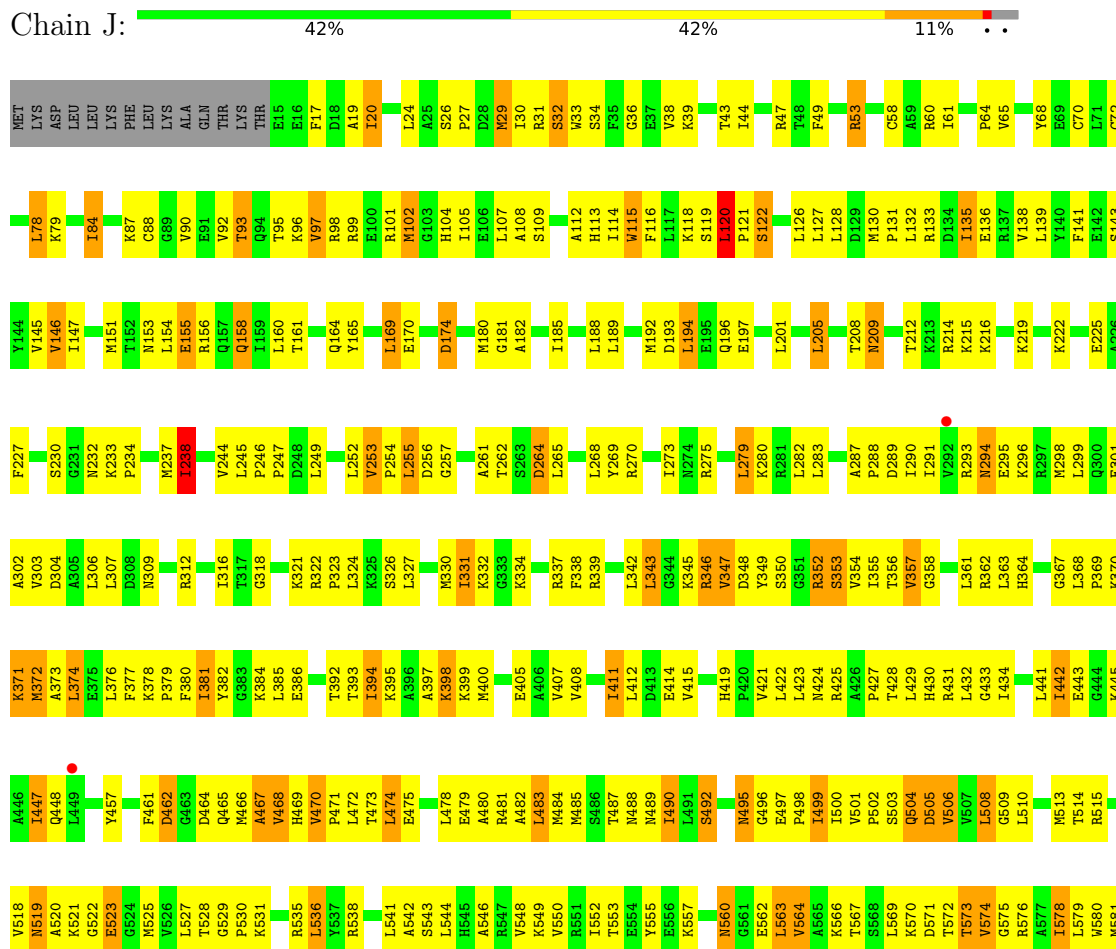
● Molecule 3: DNA-directed RNA polymerase subunit beta'

Chain D: 43% 43% 10% ..





• Molecule 3: DNA-directed RNA polymerase subunit beta'





Response	Percentage
Yes	44%
No	42%
Don't know	10%

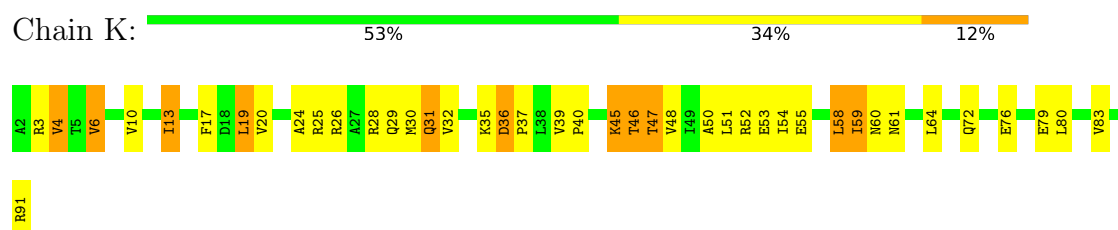




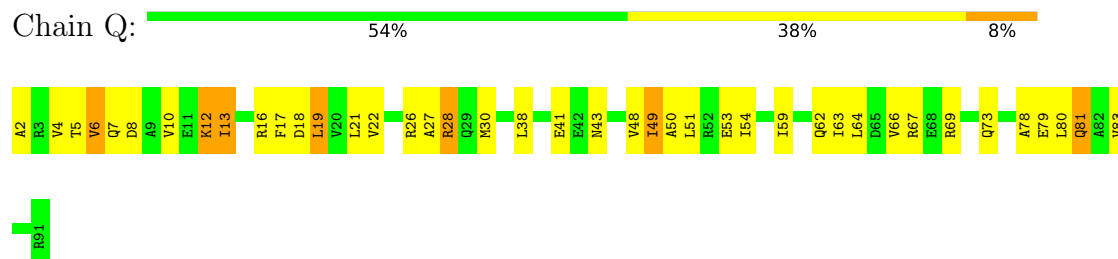
- Molecule 4: DNA-directed RNA polymerase subunit omega



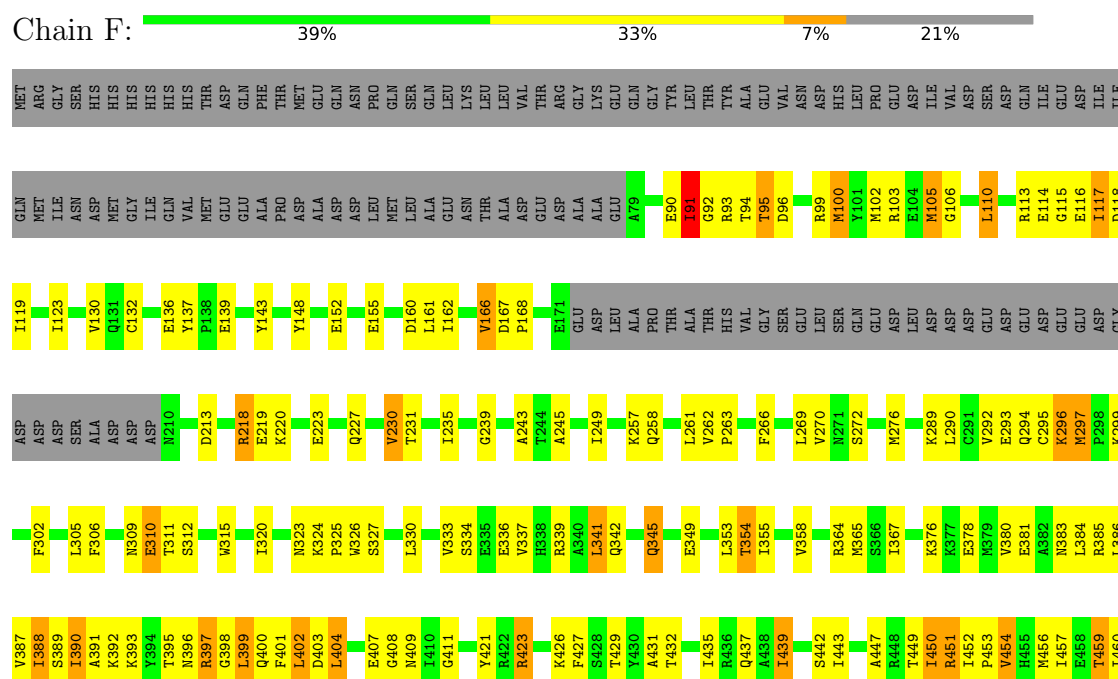
- Molecule 4: DNA-directed RNA polymerase subunit omega

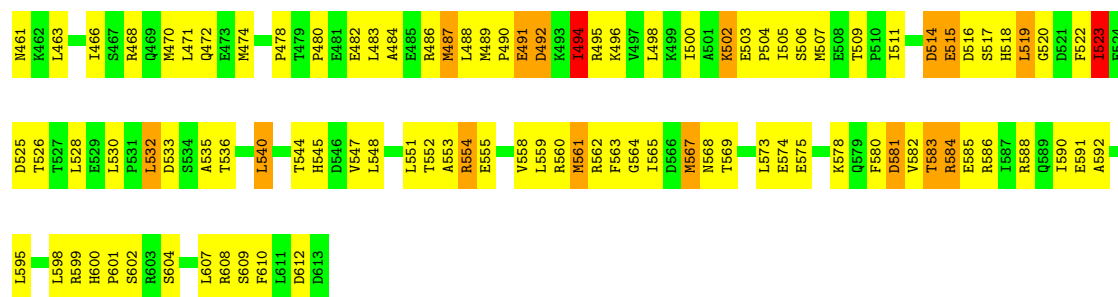


- Molecule 4: DNA-directed RNA polymerase subunit omega



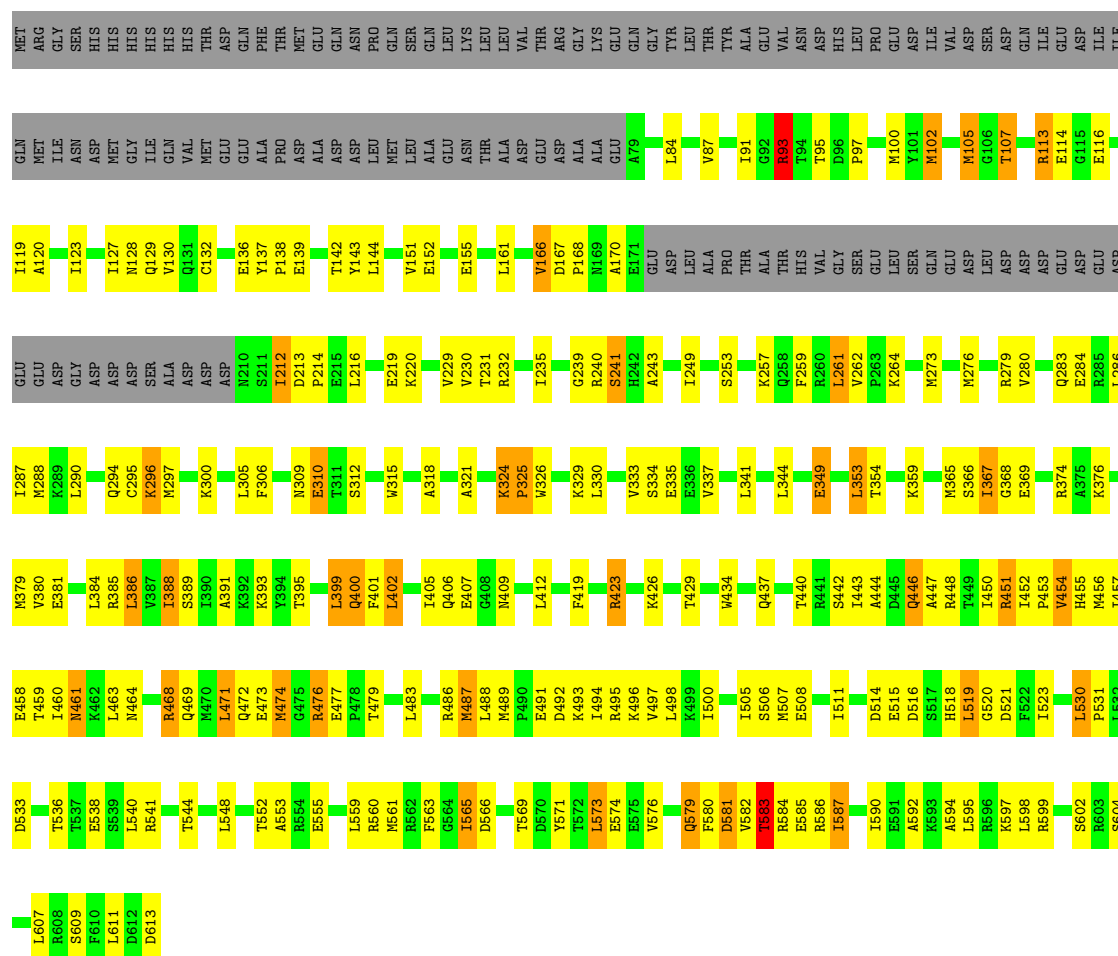
- Molecule 5: RNA polymerase sigma factor RpoD





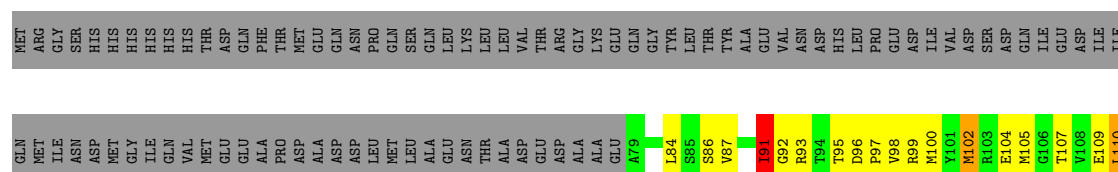
• Molecule 5: RNA polymerase sigma factor RpoD

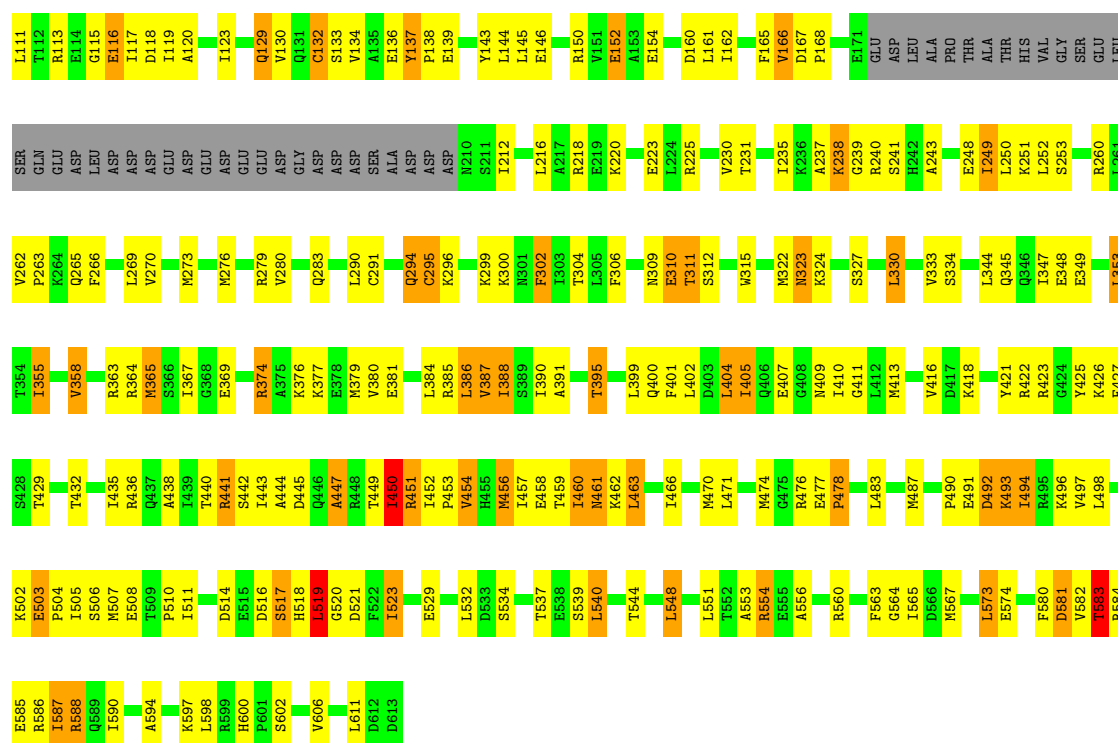
Chain L: 42% 31% 6% 21%



• Molecule 5: RNA polymerase sigma factor RpoD

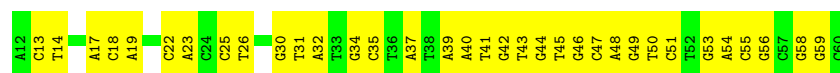
Chain R: 40% 31% 8% 21%





• Molecule 6: NT strand DNA (49-MER)

Chain 1: 31% 69%



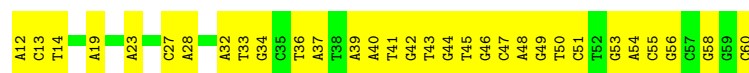
• Molecule 6: NT strand DNA (49-MER)

Chain 4: 33% 65%



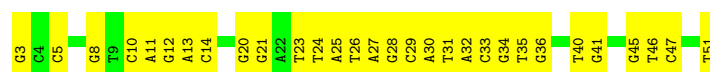
• Molecule 6: NT strand DNA (49-MER)

Chain 7: 37% 63%



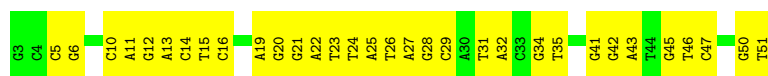
• Molecule 7: T strand DNA (49-MER)

Chain 2: 39% 61%



- Molecule 7: T strand DNA (49-MER)

Chain 5:  35% 65%



- Molecule 7: T strand DNA (49-MER)

Chain 8:  41% 57%

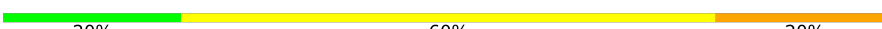


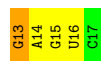
- Molecule 8: RNA (5'-R(*(GTP))-R(P*AP*GP*UP*C)-3')

Chain 3:  80% 20%



- Molecule 8: RNA (5'-R(*(GTP))-R(P*AP*GP*UP*C)-3')

Chain 6:  20% 60% 20%



- Molecule 8: RNA (5'-R(*(GTP))-R(P*AP*GP*UP*C)-3')

Chain 9:  40% 60%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	237.67Å 204.99Å 248.84Å 90.00° 116.86° 90.00°	Depositor
Resolution (Å)	39.98 – 5.50 39.98 – 5.50	Depositor EDS
% Data completeness (in resolution range)	97.9 (39.98-5.50) 97.9 (39.98-5.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 5.37Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.231 , 0.313 0.231 , 0.312	Depositor DCC
R_{free} test set	3384 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	324.1	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 171.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.055 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	94668	wwPDB-VP
Average B, all atoms (Å ²)	198.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, ZN, 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	A	0.88	0/1809	1.28	11/2450 (0.4%)
1	B	0.84	0/1789	1.29	8/2425 (0.3%)
1	G	0.82	0/1809	1.26	4/2450 (0.2%)
1	H	0.87	0/1789	1.34	14/2425 (0.6%)
1	M	0.76	0/1809	1.16	3/2450 (0.1%)
1	N	0.82	0/1789	1.21	9/2425 (0.4%)
2	C	0.76	0/10745	1.18	51/14499 (0.4%)
2	I	0.77	2/10745 (0.0%)	1.16	33/14499 (0.2%)
2	O	0.73	0/10745	1.14	36/14499 (0.2%)
3	D	0.81	1/10729 (0.0%)	1.18	56/14487 (0.4%)
3	J	0.82	4/10729 (0.0%)	1.23	60/14487 (0.4%)
3	P	0.81	2/10729 (0.0%)	1.18	47/14487 (0.3%)
4	E	0.72	0/710	1.08	2/956 (0.2%)
4	K	0.84	1/710 (0.1%)	1.23	5/956 (0.5%)
4	Q	0.76	0/710	1.08	0/956
5	F	0.70	0/4076	1.08	13/5482 (0.2%)
5	L	0.74	0/4076	1.10	6/5482 (0.1%)
5	R	0.74	1/4076 (0.0%)	1.07	12/5482 (0.2%)
6	1	0.35	0/1114	0.65	0/1714
6	4	1.03	1/1114 (0.1%)	0.83	4/1714 (0.2%)
6	7	0.39	0/1115	0.65	0/1718
7	2	0.35	0/1136	0.61	0/1752
7	5	0.35	0/1136	0.62	0/1752
7	8	0.39	0/1137	0.64	1/1756 (0.1%)
8	3	0.45	0/94	0.65	0/144
8	6	0.46	0/94	0.64	0/144
8	9	0.43	0/94	0.67	0/144
All	All	0.77	12/96608 (0.0%)	1.14	375/131735 (0.3%)

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
3	P	0	1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	4	51	DC	O3'-P	32.46	2.09	1.61
2	I	638	SER	CB-OG	10.49	1.63	1.42
3	D	955	LYS	CE-NZ	9.04	1.76	1.49
4	K	91	ARG	C-O	6.95	1.37	1.23
2	I	255	ILE	CG1-CD1	5.89	1.74	1.51

The worst 5 of 375 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	4	51	DC	O3'-P-O5'	-13.08	84.38	104.00
6	4	51	DC	P-O3'-C3'	11.98	138.17	120.20
3	D	737	ILE	CB-CA-C	-10.61	98.30	111.88
6	4	51	DC	OP1-P-O3'	10.47	139.42	108.00
3	D	529	GLY	CA-C-N	10.18	130.35	119.05

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	P	1276	GLU	Peptide

5.2 Too-close contacts [i](#)

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	A	1787	0	1813	211	0
1	B	1767	0	1789	221	0
1	G	1787	0	1813	171	0
1	H	1767	0	1789	164	0
1	M	1787	0	1813	139	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	N	1767	0	1789	119	0
2	C	10576	0	10591	839	0
2	I	10576	0	10591	941	0
2	O	10576	0	10591	759	0
3	D	10568	0	10781	955	1
3	J	10568	0	10780	1032	0
3	P	10568	0	10783	918	0
4	E	708	0	719	40	0
4	K	708	0	719	40	0
4	Q	708	0	719	49	0
5	F	4022	0	4083	294	0
5	L	4022	0	4083	229	0
5	R	4022	0	4083	308	0
6	1	996	0	555	65	1
6	4	996	0	556	71	0
6	7	996	0	554	60	1
7	2	1012	0	554	55	1
7	5	1012	0	554	52	0
7	8	1012	0	553	48	0
8	3	117	0	55	9	0
8	6	117	0	55	7	0
8	9	117	0	55	6	0
9	D	2	0	0	1	0
9	J	2	0	0	1	0
9	P	2	0	0	5	0
10	D	1	0	0	0	0
10	J	1	0	0	0	0
10	P	1	0	0	0	0
All	All	94668	0	92820	6986	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 37.

The worst 5 of 6986 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:I:255:ILE:CG1	2:I:255:ILE:CD1	1.74	1.59
3:D:955:LYS:NZ	3:D:955:LYS:CE	1.76	1.48
3:P:514:THR:HG21	3:P:596:LEU:CD1	1.48	1.42
3:J:421:VAL:CG1	3:J:469:HIS:O	1.70	1.40
3:P:1095:MET:SD	3:P:1173:ARG:NH2	1.97	1.38

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)
7:2:3:DG:O5'	7:2:51:DT:O3'[2_657]	1.64	0.56
3:D:1174:ARG:NH2	6:1:17:DA:OP1[2_657]	2.10	0.10
6:7:12:DA:O5'	6:7:60:DC:O3'[2_546]	2.13	0.07

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	A	228/242 (94%)	213 (93%)	11 (5%)	4 (2%)	6	33
1	B	226/242 (93%)	204 (90%)	14 (6%)	8 (4%)	3	20
1	G	228/242 (94%)	211 (92%)	14 (6%)	3 (1%)	9	41
1	H	226/242 (93%)	205 (91%)	17 (8%)	4 (2%)	6	33
1	M	228/242 (94%)	215 (94%)	12 (5%)	1 (0%)	30	67
1	N	226/242 (93%)	208 (92%)	12 (5%)	6 (3%)	4	25
2	C	1339/1342 (100%)	1220 (91%)	97 (7%)	22 (2%)	7	37
2	I	1339/1342 (100%)	1226 (92%)	88 (7%)	25 (2%)	6	31
2	O	1339/1342 (100%)	1235 (92%)	82 (6%)	22 (2%)	7	37
3	D	1360/1407 (97%)	1212 (89%)	120 (9%)	28 (2%)	5	29
3	J	1360/1407 (97%)	1212 (89%)	113 (8%)	35 (3%)	4	25
3	P	1360/1407 (97%)	1214 (89%)	111 (8%)	35 (3%)	4	25
4	E	88/90 (98%)	84 (96%)	4 (4%)	0	100	100
4	K	88/90 (98%)	84 (96%)	4 (4%)	0	100	100
4	Q	88/90 (98%)	84 (96%)	4 (4%)	0	100	100
5	F	493/628 (78%)	449 (91%)	30 (6%)	14 (3%)	4	24
5	L	493/628 (78%)	444 (90%)	30 (6%)	19 (4%)	2	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	R	493/628 (78%)	447 (91%)	30 (6%)	16 (3%)	3	21
All	All	11202/11853 (94%)	10167 (91%)	793 (7%)	242 (2%)	5	28

5 of 242 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	210	THR
1	B	209	GLY
2	C	165	HIS
2	C	808	ASN
2	C	812	PHE

5.3.2 Protein sidechains [i](#)

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	A	198/208 (95%)	165 (83%)	33 (17%)	2	11
1	B	196/208 (94%)	153 (78%)	43 (22%)	1	6
1	G	198/208 (95%)	173 (87%)	25 (13%)	4	16
1	H	196/208 (94%)	163 (83%)	33 (17%)	2	11
1	M	198/208 (95%)	175 (88%)	23 (12%)	5	18
1	N	196/208 (94%)	173 (88%)	23 (12%)	5	18
2	C	1156/1157 (100%)	1006 (87%)	150 (13%)	4	16
2	I	1156/1157 (100%)	1004 (87%)	152 (13%)	4	16
2	O	1156/1157 (100%)	1015 (88%)	141 (12%)	5	17
3	D	1135/1168 (97%)	981 (86%)	154 (14%)	3	14
3	J	1135/1168 (97%)	969 (85%)	166 (15%)	3	13
3	P	1135/1168 (97%)	991 (87%)	144 (13%)	4	16
4	E	74/74 (100%)	69 (93%)	5 (7%)	14	36
4	K	74/74 (100%)	62 (84%)	12 (16%)	2	11
4	Q	74/74 (100%)	63 (85%)	11 (15%)	3	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	F	439/554 (79%)	386 (88%)	53 (12%)	5	18
5	L	439/554 (79%)	381 (87%)	58 (13%)	4	15
5	R	439/554 (79%)	374 (85%)	65 (15%)	3	13
All	All	9594/10107 (95%)	8303 (86%)	1291 (14%)	4	15

5 of 1291 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	183	ILE
3	P	683	ILE
2	O	240	GLU
1	N	173	VAL
2	O	1036	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 182 such sidechains are listed below:

Mol	Chain	Res	Type
3	J	1252	HIS
2	O	1268	GLN
4	K	43	ASN
1	M	208	ASN
3	P	364	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	3	4/5 (80%)	0	1 (25%)
8	6	4/5 (80%)	0	1 (25%)
8	9	3/5 (60%)	0	0
All	All	11/15 (73%)	0	2 (18%)

There are no RNA backbone outliers to report.

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	3	13	GTP
8	6	13	GTP

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	4	2
6	1	1
7	2	1
7	5	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	4	46:DG	O3'	47:DC	P	5.33
1	1	46:DG	O3'	47:DC	P	4.95
1	2	12:DG	O3'	13:DA	P	2.74
1	5	11:DA	O3'	12:DG	P	2.33

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	4	51:DC	O3'	52:DT	P	2.09

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	A	230/242 (95%)	-0.78	0 100 100	134, 152, 183, 205	0
1	B	228/242 (94%)	-0.76	2 (0%) 81 69	136, 167, 199, 236	0
1	G	230/242 (95%)	-0.74	1 (0%) 88 78	139, 162, 198, 240	0
1	H	228/242 (94%)	-0.67	0 100 100	141, 176, 208, 242	0
1	M	230/242 (95%)	-0.73	0 100 100	159, 179, 209, 245	0
1	N	228/242 (94%)	-0.67	1 (0%) 88 78	169, 201, 249, 272	0
2	C	1341/1342 (99%)	-0.74	8 (0%) 85 75	107, 166, 250, 351	0
2	I	1341/1342 (99%)	-0.79	1 (0%) 92 87	98, 172, 227, 283	0
2	O	1341/1342 (99%)	-0.84	2 (0%) 92 87	113, 174, 222, 263	0
3	D	1362/1407 (96%)	-0.76	5 (0%) 88 78	112, 184, 269, 324	0
3	J	1362/1407 (96%)	-0.73	3 (0%) 91 84	100, 172, 322, 386	0
3	P	1362/1407 (96%)	-0.79	0 100 100	117, 182, 291, 333	0
4	E	90/90 (100%)	-0.79	0 100 100	136, 169, 350, 413	0
4	K	90/90 (100%)	-0.72	0 100 100	112, 152, 324, 363	0
4	Q	90/90 (100%)	-0.86	0 100 100	128, 171, 328, 364	0
5	F	497/628 (79%)	-0.76	0 100 100	154, 271, 387, 434	0
5	L	497/628 (79%)	-0.68	0 100 100	138, 281, 365, 402	0
5	R	497/628 (79%)	-0.76	0 100 100	146, 261, 390, 426	0
6	1	49/49 (100%)	-0.51	0 100 100	205, 265, 288, 289	0
6	4	49/49 (100%)	-0.58	0 100 100	181, 228, 278, 302	0
6	7	49/49 (100%)	-0.49	0 100 100	184, 228, 266, 277	0
7	2	49/49 (100%)	-0.44	0 100 100	192, 268, 291, 312	0
7	5	49/49 (100%)	-0.45	0 100 100	163, 232, 279, 326	0
7	8	49/49 (100%)	-0.51	0 100 100	166, 227, 262, 322	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
8	3	4/5 (80%)	-1.14	0 100 100	230, 234, 236, 245	0
8	6	4/5 (80%)	-1.16	0 100 100	220, 221, 224, 239	0
8	9	4/5 (80%)	-0.95	0 100 100	215, 221, 224, 236	0
All	All	11550/12162 (94%)	-0.76	23 (0%) 91 84	98, 182, 331, 434	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	J	449	LEU	4.0
3	D	772	TYR	4.0
2	C	1278	LEU	4.0
2	C	506	PHE	3.7
2	C	1279	GLU	3.5

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 oligosaccharides 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. 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	RSCC	RSR	B-factors(Å ²)	Q<0.9
10	MG	P	1503	1/1	0.96	0.08	170,170,170,170	0
9	ZN	J	1501	1/1	0.99	0.02	211,211,211,211	0
9	ZN	P	1501	1/1	0.99	0.02	206,206,206,206	0
9	ZN	D	1501	1/1	0.99	0.02	220,220,220,220	0
9	ZN	D	1502	1/1	1.00	0.03	181,181,181,181	0
9	ZN	P	1502	1/1	1.00	0.02	158,158,158,158	0
10	MG	D	1503	1/1	1.00	0.01	141,141,141,141	0
10	MG	J	1503	1/1	1.00	0.02	145,145,145,145	0
9	ZN	J	1502	1/1	1.00	0.04	144,144,144,144	0

6.5 Other polymers [i](#)

There are no such residues in this entry.