



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 11:21 PM GMT

PDB ID : 4YM7
Title : RNA polymerase I structure with an alternative dimer hinge
Authors : Kostrewa, D.; Kuhn, C.-D.; Engel, C.; Cramer, P.
Deposited on : 2015-03-06
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

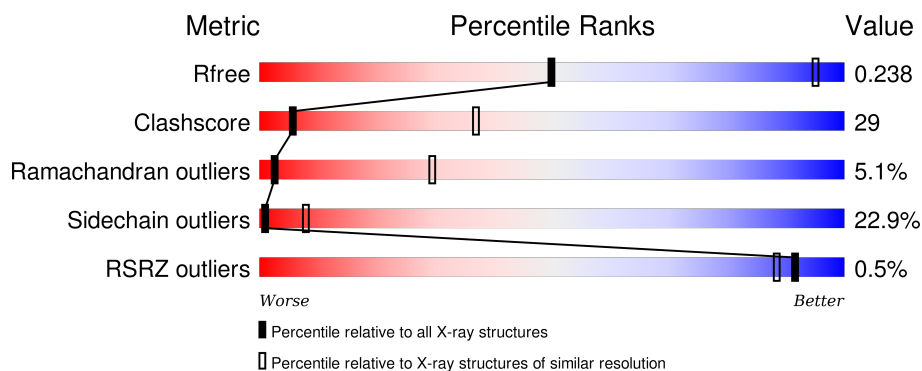
1 Overall quality at a glance ⓘ

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.




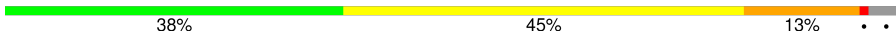
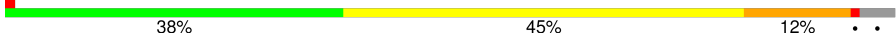



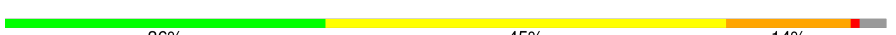
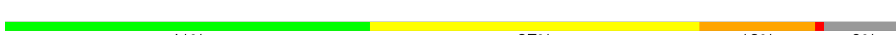



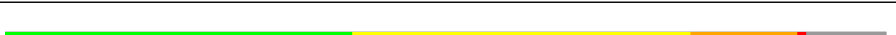

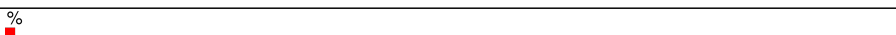
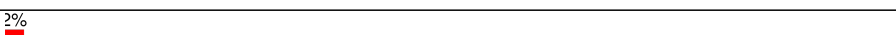
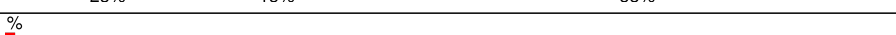

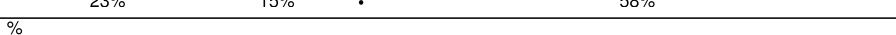







Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1015 (7.38-3.62)
Clashscore	102246	1020 (7.10-3.70)
Ramachandran outliers	100387	1014 (7.36-3.64)
Sidechain outliers	100360	1013 (7.38-3.62)
RSRZ outliers	91569	1014 (7.38-3.62)

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. 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	AA	1664	<div> <div>%</div> <div> <div></div> <div>36%</div> <div>41%</div> <div>11%</div> <div>•</div> <div>11%</div> </div> </div>
1	BA	1664	<div> <div>%</div> <div> <div></div> <div>35%</div> <div>41%</div> <div>11%</div> <div>•</div> <div>12%</div> </div> </div>
1	CA	1664	<div> <div></div> <div> <div>34%</div> <div>42%</div> <div>12%</div> <div>•</div> <div>11%</div> </div> </div>
1	DA	1664	<div> <div></div> <div> <div>34%</div> <div>42%</div> <div>12%</div> <div>•</div> <div>11%</div> </div> </div>
1	EA	1664	<div> <div></div> <div> <div>34%</div> <div>43%</div> <div>12%</div> <div>•</div> <div>11%</div> </div> </div>

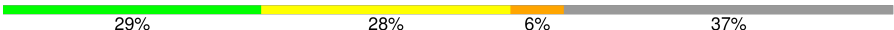


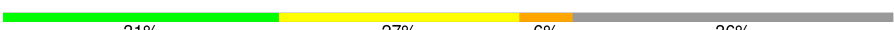
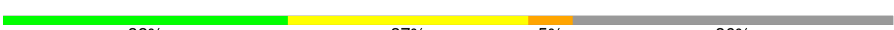
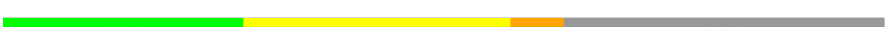




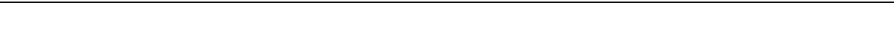

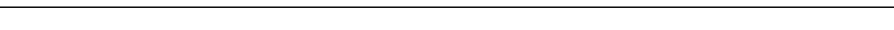
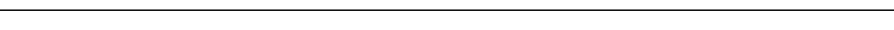







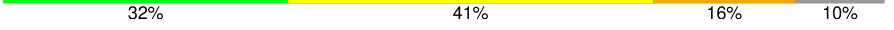


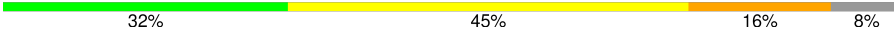
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Mol	Chain	Length	Quality of chain
1	FA	1664	
2	AB	1203	
2	BB	1203	
2	CB	1203	
2	DB	1203	
2	EB	1203	
2	FB	1203	
3	AC	335	
3	BC	335	
3	CC	335	
3	DC	335	
3	EC	335	
3	FC	335	
4	AD	137	
4	BD	137	
4	CD	137	
4	DD	137	
4	ED	137	
4	FD	137	
5	AE	215	
5	BE	215	
5	CE	215	
5	DE	215	
5	EE	215	
5	FE	215	

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Mol	Chain	Length	Quality of chain
6	AF	155	
6	BF	155	
6	CF	155	
6	DF	155	
6	EF	155	
6	FF	155	
7	AG	326	
7	AO	326	
7	BG	326	
7	BO	326	
7	CG	326	
7	CO	326	
7	DG	326	
7	DO	326	
7	EG	326	
7	EO	326	
7	FG	326	
7	FO	326	
8	AH	146	
8	BH	146	
8	CH	146	
8	DH	146	
8	EH	146	
8	FH	146	
9	AI	125	

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Mol	Chain	Length	Quality of chain
9	BI	125	
9	CI	125	
9	DI	125	
9	EI	125	
9	FI	125	
10	AJ	70	
10	BJ	70	
10	CJ	70	
10	DJ	70	
10	EJ	70	
10	FJ	70	
11	AK	142	
11	BK	142	
11	CK	142	
11	DK	142	
11	EK	142	
11	FK	142	
12	AL	70	
12	BL	70	
12	CL	70	
12	DL	70	
12	EL	70	
12	FL	70	
13	AM	415	
13	BM	415	

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Mol	Chain	Length	Quality of chain
13	CM	415	
13	DM	415	
13	EM	415	
13	FM	415	
14	AN	233	
14	BN	233	
14	CN	233	
14	DN	233	
14	EN	233	
14	FN	233	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 204233 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 I subunit RPA190.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	1484	Total	C	N	O	S	0	0	0
			11703	7385	2036	2220	62			
1	BA	1462	Total	C	N	O	S	0	0	0
			11540	7291	2003	2184	62			
1	CA	1483	Total	C	N	O	S	0	0	0
			11695	7381	2035	2217	62			
1	DA	1483	Total	C	N	O	S	0	0	0
			11697	7381	2034	2220	62			
1	EA	1484	Total	C	N	O	S	0	0	0
			11706	7390	2036	2218	62			
1	FA	1484	Total	C	N	O	S	0	0	0
			11709	7392	2036	2219	62			

- Molecule 2 is a protein called DNA-directed RNA polymerase I subunit RPA135.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AB	1154	Total	C	N	O	S	0	0	0
			9187	5822	1606	1708	51			
2	BB	1153	Total	C	N	O	S	0	0	0
			9175	5812	1603	1709	51			
2	CB	1170	Total	C	N	O	S	0	0	0
			9304	5892	1629	1732	51			
2	DB	1165	Total	C	N	O	S	0	0	0
			9269	5871	1622	1725	51			
2	EB	1164	Total	C	N	O	S	0	0	0
			9265	5871	1619	1724	51			
2	FB	1165	Total	C	N	O	S	0	0	0
			9270	5872	1622	1725	51			

- Molecule 3 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AC	304	Total	C	N	O	S	0	0	0
			2413	1534	414	457	8			
3	BC	304	Total	C	N	O	S	0	0	0
			2413	1534	414	457	8			
3	CC	304	Total	C	N	O	S	0	0	0
			2413	1534	414	457	8			
3	DC	304	Total	C	N	O	S	0	0	0
			2413	1534	414	457	8			
3	EC	304	Total	C	N	O	S	0	0	0
			2413	1534	414	457	8			
3	FC	304	Total	C	N	O	S	0	0	0
			2413	1534	414	457	8			

- Molecule 4 is a protein called DNA-directed RNA polymerase I subunit RPA14.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	AD	58	Total	C	N	O	0	0	0
			459	289	78	92			
4	BD	58	Total	C	N	O	0	0	0
			459	289	78	92			
4	CD	58	Total	C	N	O	0	0	0
			459	289	78	92			
4	DD	58	Total	C	N	O	0	0	0
			459	289	78	92			
4	ED	58	Total	C	N	O	0	0	0
			459	289	78	92			
4	FD	58	Total	C	N	O	0	0	0
			459	289	78	92			

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	AE	215	Total	C	N	O	S	0	0	0
			1760	1116	310	322	12			
5	BE	215	Total	C	N	O	S	0	0	0
			1760	1116	310	322	12			
5	CE	215	Total	C	N	O	S	0	0	0
			1760	1116	310	322	12			
5	DE	215	Total	C	N	O	S	0	0	0
			1760	1116	310	322	12			
5	EE	215	Total	C	N	O	S	0	0	0
			1760	1116	310	322	12			
5	FE	215	Total	C	N	O	S	0	0	0
			1760	1116	310	322	12			

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	AF	98	Total	C	N	O	S	0	0	0
			807	512	142	150	3			
6	BF	98	Total	C	N	O	S	0	0	0
			807	512	142	150	3			
6	CF	99	Total	C	N	O	S	0	0	0
			816	517	143	153	3			
6	DF	99	Total	C	N	O	S	0	0	0
			816	517	143	153	3			
6	EF	99	Total	C	N	O	S	0	0	0
			816	517	143	153	3			
6	FF	99	Total	C	N	O	S	0	0	0
			816	517	143	153	3			

- Molecule 7 is a protein called DNA-directed RNA polymerase I subunit RPA43.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	AG	202	Total	C	N	O	S	0	0	0
			1599	1025	276	293	5			
7	AO	52	Total	C	N	O		0	0	0
			413	253	64	96				
7	BG	195	Total	C	N	O	S	0	0	0
			1539	992	264	278	5			
7	BO	51	Total	C	N	O		0	0	0
			404	248	63	93				
7	CG	202	Total	C	N	O	S	0	0	0
			1599	1025	276	293	5			
7	CO	50	Total	C	N	O		0	0	0
			398	245	62	91				
7	DG	202	Total	C	N	O	S	0	0	0
			1599	1025	276	293	5			
7	DO	52	Total	C	N	O		0	0	0
			413	253	64	96				
7	EG	202	Total	C	N	O	S	0	0	0
			1599	1025	276	293	5			
7	EO	52	Total	C	N	O		0	0	0
			413	253	64	96				
7	FG	202	Total	C	N	O	S	0	0	0
			1599	1025	276	293	5			
7	FO	52	Total	C	N	O		0	0	0
			413	253	64	96				

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	AH	132	Total	C	N	O	S	0	0	0
			1063	670	180	209	4			
8	BH	131	Total	C	N	O	S	0	0	0
			1052	664	176	208	4			
8	CH	131	Total	C	N	O	S	0	0	0
			1052	664	176	208	4			
8	DH	134	Total	C	N	O	S	0	0	0
			1075	677	182	212	4			
8	EH	134	Total	C	N	O	S	0	0	0
			1075	677	182	212	4			
8	FH	134	Total	C	N	O	S	0	0	0
			1075	677	182	212	4			

- Molecule 9 is a protein called DNA-directed RNA polymerase I subunit RPA12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	AI	124	Total	C	N	O	S	0	0	0
			943	584	160	190	9			
9	BI	97	Total	C	N	O	S	0	0	0
			716	439	120	148	9			
9	CI	124	Total	C	N	O	S	0	0	0
			943	584	160	190	9			
9	DI	124	Total	C	N	O	S	0	0	0
			943	584	160	190	9			
9	EI	117	Total	C	N	O	S	0	0	0
			898	556	152	181	9			
9	FI	124	Total	C	N	O	S	0	0	0
			943	584	160	190	9			

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AJ	68	Total	C	N	O	S	0	0	0
			558	356	97	99	6			
10	BJ	69	Total	C	N	O	S	0	0	0
			569	362	101	100	6			
10	CJ	68	Total	C	N	O	S	0	0	0
			558	356	97	99	6			
10	DJ	69	Total	C	N	O	S	0	0	0
			569	362	101	100	6			
10	EJ	68	Total	C	N	O	S	0	0	0
			558	356	97	99	6			
10	FJ	68	Total	C	N	O	S	0	0	0
			558	356	97	99	6			

- Molecule 11 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AK	101	Total	C	N	O	S	0	0	0
			793	496	130	162	5			
11	BK	100	Total	C	N	O	S	0	0	0
			786	491	129	161	5			
11	CK	101	Total	C	N	O	S	0	0	0
			793	496	130	162	5			
11	DK	101	Total	C	N	O	S	0	0	0
			793	496	130	162	5			
11	EK	100	Total	C	N	O	S	0	0	0
			786	491	129	161	5			
11	FK	100	Total	C	N	O	S	0	0	0
			786	491	129	161	5			

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AL	44	Total	C	N	O	S	0	0	0
			352	217	70	61	4			
12	BL	44	Total	C	N	O	S	0	0	0
			352	217	70	61	4			
12	CL	44	Total	C	N	O	S	0	0	0
			352	217	70	61	4			
12	DL	44	Total	C	N	O	S	0	0	0
			352	217	70	61	4			
12	EL	44	Total	C	N	O	S	0	0	0
			352	217	70	61	4			
12	FL	44	Total	C	N	O	S	0	0	0
			352	217	70	61	4			

- Molecule 13 is a protein called DNA-directed RNA polymerase I subunit RPA49.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	AM	109	Total	C	N	O	0	0	0
			863	548	143	172			
13	BM	109	Total	C	N	O	0	0	0
			863	548	143	172			
13	CM	109	Total	C	N	O	0	0	0
			863	548	143	172			
13	DM	109	Total	C	N	O	0	0	0
			863	548	143	172			
13	EM	110	Total	C	N	O	0	0	0
			869	551	144	174			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	FM	110	Total	C	N	O	0	0	0
			869	551	144	174			

- Molecule 14 is a protein called DNA-directed RNA polymerase I subunit RPA34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AN	142	Total	C	N	O	S	0	0	0
			1127	719	183	221	4			
14	BN	143	Total	C	N	O	S	0	0	0
			1130	719	184	223	4			
14	CN	143	Total	C	N	O	S	0	0	0
			1137	728	184	221	4			
14	DN	145	Total	C	N	O	S	0	0	0
			1146	729	186	227	4			
14	EN	144	Total	C	N	O	S	0	0	0
			1140	726	186	224	4			
14	FN	145	Total	C	N	O	S	0	0	0
			1146	729	187	226	4			

- Molecule 15 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	BA	2	Total	Zn	0	0
			2	2		
15	CA	2	Total	Zn	0	0
			2	2		
15	AB	1	Total	Zn	0	0
			1	1		
15	BL	1	Total	Zn	0	0
			1	1		
15	EB	1	Total	Zn	0	0
			1	1		
15	BI	2	Total	Zn	0	0
			2	2		
15	BB	1	Total	Zn	0	0
			1	1		
15	AJ	1	Total	Zn	0	0
			1	1		
15	EI	2	Total	Zn	0	0
			2	2		
15	DL	1	Total	Zn	0	0
			1	1		

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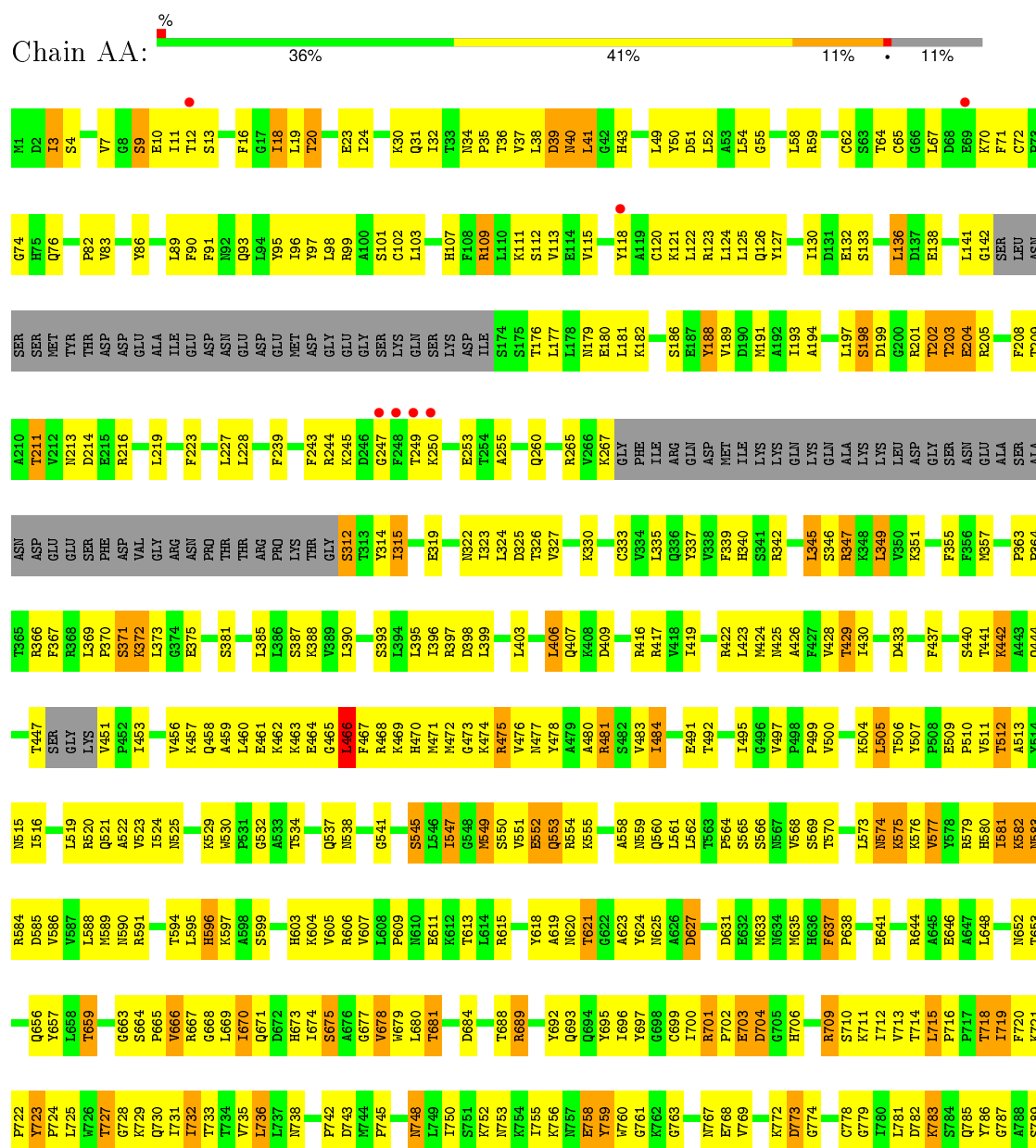
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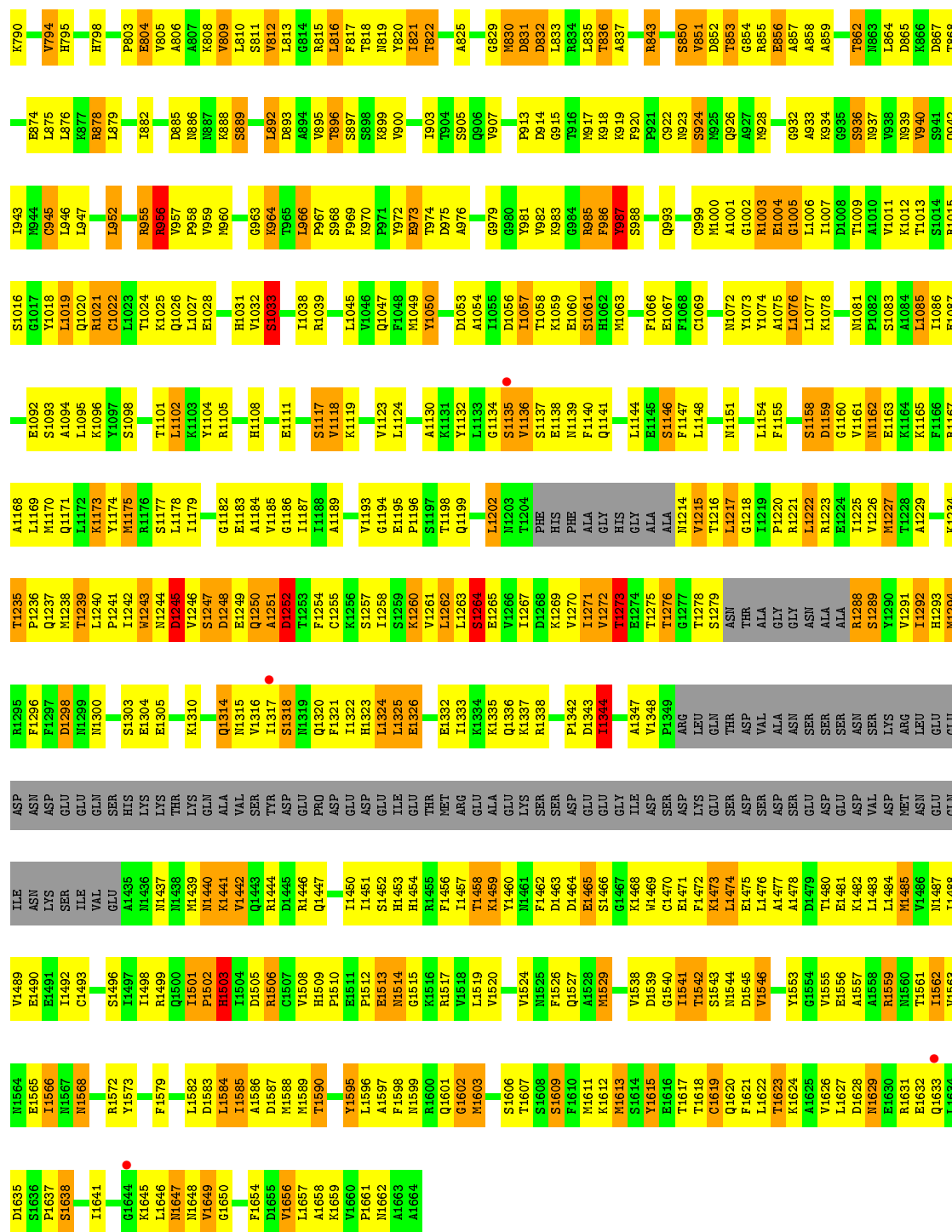
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	FL	1	Total 1	Zn 1	0	0
15	AA	2	Total 2	Zn 2	0	0
15	BJ	1	Total 1	Zn 1	0	0
15	FJ	1	Total 1	Zn 1	0	0
15	DI	2	Total 2	Zn 2	0	0
15	EA	2	Total 2	Zn 2	0	0
15	FA	2	Total 2	Zn 2	0	0
15	AI	2	Total 2	Zn 2	0	0
15	CJ	1	Total 1	Zn 1	0	0
15	DA	2	Total 2	Zn 2	0	0
15	FI	2	Total 2	Zn 2	0	0
15	AL	1	Total 1	Zn 1	0	0
15	FB	1	Total 1	Zn 1	0	0
15	EL	1	Total 1	Zn 1	0	0
15	DJ	1	Total 1	Zn 1	0	0
15	CB	1	Total 1	Zn 1	0	0
15	CI	2	Total 2	Zn 2	0	0
15	EJ	1	Total 1	Zn 1	0	0
15	CL	1	Total 1	Zn 1	0	0
15	DB	1	Total 1	Zn 1	0	0

3 Residue-property plots

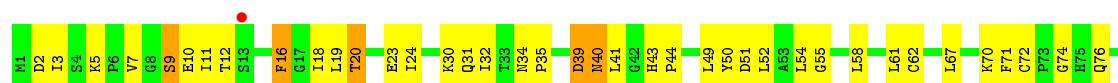
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: DNA-directed RNA polymerase I subunit RPA190

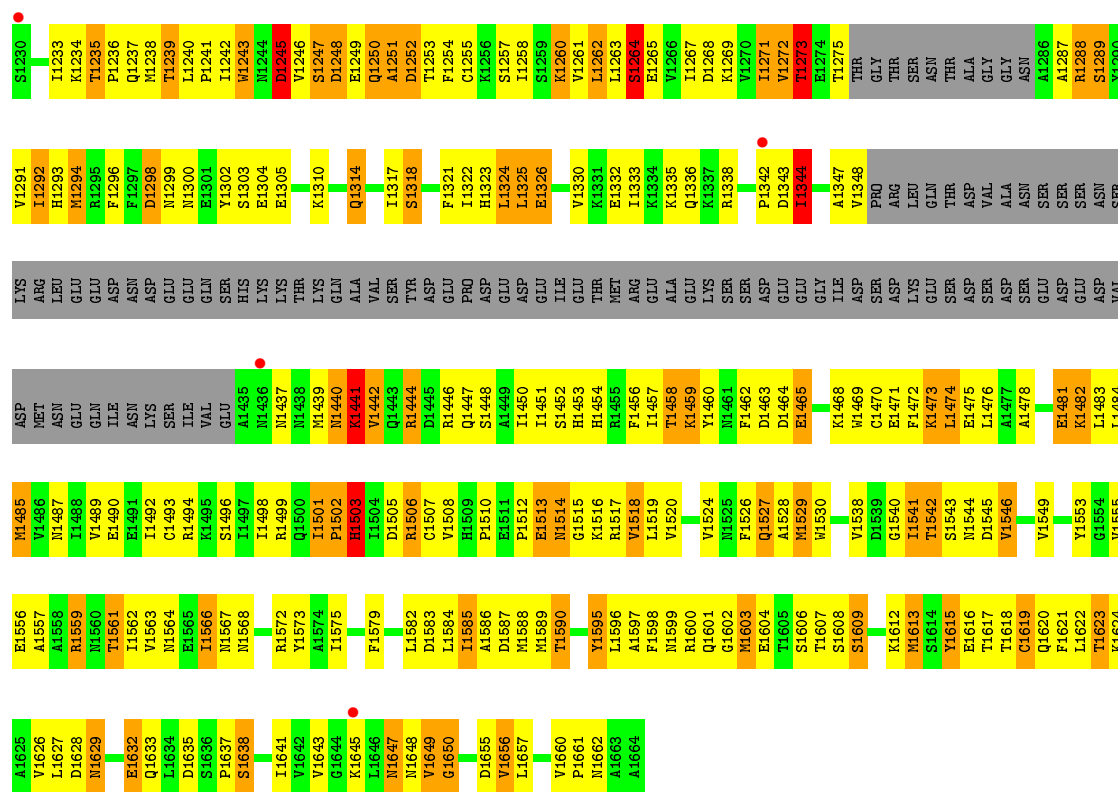




- Molecule 1: DNA-directed RNA polymerase I subunit RPA190

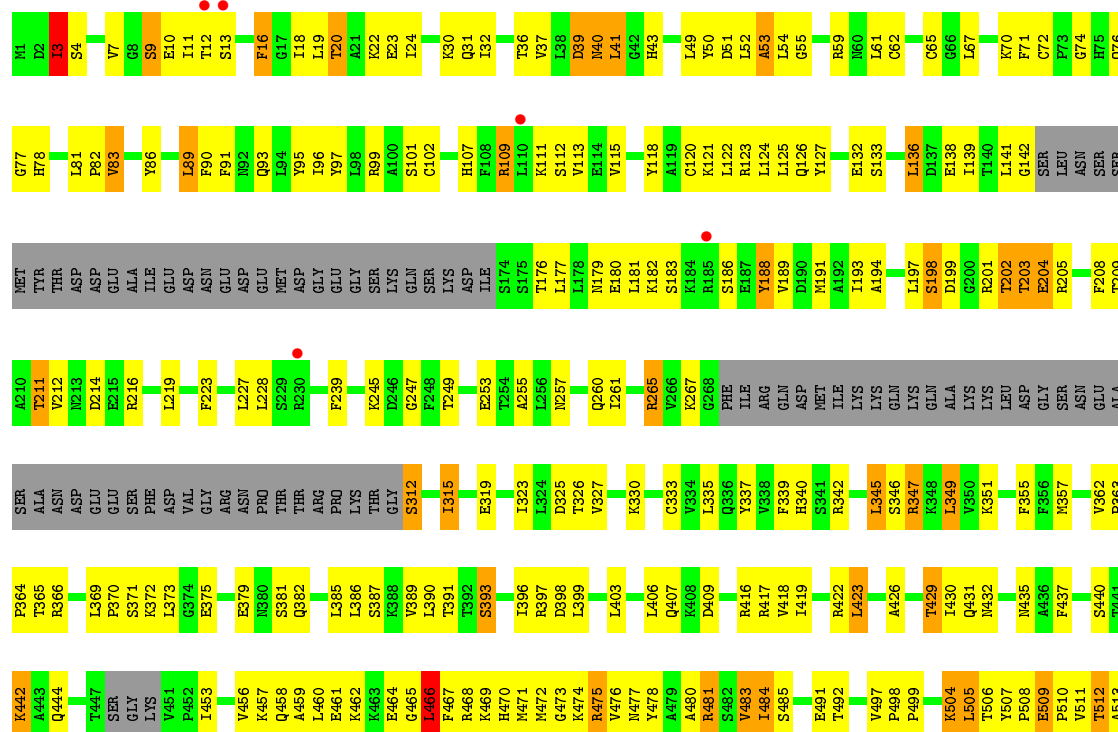
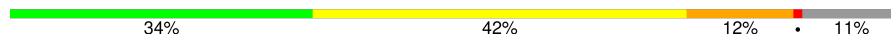


H162	H163	K164	K165	K166	R167	A168	L169	M170	Q171	L172	K173	L174	M175	R176	S177	L178	G182	V185	G186	I187	S189	S190	S191	S192	S193	S194	S195	S196	S197	S198	S199	S200	S201	S202	S203	S204	S205	S206	S207	S208	S209	S210	S211	S212	S213	S214	S215	S216	S217	S218	S219	S220	S221	S222	S223	S224	S225	S226	S227	S228	S229	S230	S231	S232	S233	S234	S235	S236	S237	S238	S239	S240	S241	S242	S243	S244	S245	S246	S247	S248	S249	S250	S251	S252	S253	S254	S255	S256	S257	S258	S259	S260	S261	S262	S263	S264	S265	S266	S267	S268	S269	S270	S271	S272	S273	S274	S275	S276	S277	S278	S279	S280	S281	S282	S283	S284	S285	S286	S287	S288	S289	S290	S291	S292	S293	S294	S295	S296	S297	S298	S299	S300	S301	S302	S303	S304	S305	S306	S307	S308	S309	S310	S311	S312	S313	S314	S315	S316	S317	S318	S319	S320	S321	S322	S323	S324	S325	S326	S327	S328	S329	S330	S331	S332	S333	S334	S335	S336	S337	S338	S339	S340	S341	S342	S343	S344	S345	S346	S347	S348	S349	S350	S351	S352	S353	S354	S355	S356	S357	S358	S359	S360	S361	S362	S363	S364	S365	S366	S367	S368	S369	S370	S371	S372	S373	S374	S375	S376	S377	S378	S379	S380	S381	S382	S383	S384	S385	S386	S387	S388	S389	S390	S391	S392	S393	S394	S395	S396	S397	S398	S399	S400	S401	S402	S403	S404	S405	S406	S407	S408	S409	S410	S411	S412	S413	S414	S415	S416	S417	S418	S419	S420	S421	S422	S423	S424	S425	S426	S427	S428	S429	S430	S431	S432	S433	S434	S435	S436	S437	S438	S439	S440	S441	S442	S443	S444	S445	S446	S447	S448	S449	S450	S451	S452	S453	S454	S455	S456	S457	S458	S459	S460	S461	S462	S463	S464	S465	S466	S467	S468	S469	S470	S471	S472	S473	S474	S475	S476	S477	S478	S479	S480	S481	S482	S483	S484	S485	S486	S487	S488	S489	S490	S491	S492	S493	S494	S495	S496	S497	S498	S499	S500	S501	S502	S503	S504	S505	S506	S507	S508	S509	S510	S511	S512	S513	S514	S515	S516	S517	S518	S519	S520	S521	S522	S523	S524	S525	S526	S527	S528	S529	S530	S531	S532	S533	S534	S535	S536	S537	S538	S539	S540	S541	S542	S543	S544	S545	S546	S547	S548	S549	S550	S551	S552	S553	S554	S555	S556	S557	S558	S559	S560	S561	S562	S563	S564	S565	S566	S567	S568	S569	S570	S571	S572	S573	S574	S575	S576	S577	S578	S579	S580	S581	S582	S583	S584	S585	S586	S587	S588	S589	S590	S591	S592	S593	S594	S595	S596	S597	S598	S599	S600	S601	S602	S603	S604	S605	S606	S607	S608	S609	S610	S611	S612	S613	S614	S615	S616	S617	S618	S619	S620	S621	S622	S623	S624	S625	S626	S627	S628	S629	S630	S631	S632	S633	S634	S635	S636	S637	S638	S639	S640	S641	S642	S643	S644	S645	S646	S647	S648	S649	S650	S651	S652	S653	S654	S655	S656	S657	S658	S659	S660	S661	S662	S663	S664	S665	S666	S667	S668	S669	S670	S671	S672	S673	S674	S675	S676	S677	S678	S679	S680	S681	S682	S683	S684	S685	S686	S687	S688	S689	S690	S691	S692	S693	S694	S695	S696	S697	S698	S699	S700	S701	S702	S703	S704	S705	S706	S707	S708	S709	S710	S711	S712	S713	S714	S715	S716	S717	S718	S719	S720	S721	S722	S723	S724	S725	S726	S727	S728	S729	S730	S731	S732	S733	S734	S735	S736	S737	S738	S739	S740	S741	S742	S743	S744	S745	S746	S747	S748	S749	S750	S751	S752	S753	S754	S755	S756	S757	S758	S759	S760	S761	S762	S763	S764	S765	S766	S767	S768	S769	S770	S771	S772	S773	S774	S775	S776	S777	S778	S779	S780	S781	S782	S783	S784	S785	S786	S787	S788	S789	S790	S791	S792	S793	S794	S795	S796	S797	S798	S799	S800	S801	S802	S803	S804	S805	S806	S807	S808	S809	S810	S811	S812	S813	S814	S815	S816	S817	S818	S819	S820	S821	S822	S823	S824	S825	S826	S827	S828	S829	S830	S831	S832	S833	S834	S835	S836	S837	S838	S839	S840	S841	S842	S843	S844	S845	S846	S847	S848	S849	S850	S851	S852	S853	S854	S855	S856	S857	S858	S859	S860	S861	S862	S863	S864	S865	S866	S867	S868	S869	S870	S871	S872	S873	S874	S875	S876	S877	S878	S879	S880	S881	S882	S883	S884	S885	S886	S887	S888	S889	S890	S891	S892	S893	S894	S895	S896	S897	S898	S899	S900	S901	S902	S903	S904	S905	S906	S907	S908	S909	S910	S911	S912	S913	S914	S915	S916	S917	S918	S919	S920	S921	S922	S923	S924	S925	S926	S927	S928	S929	S930	S931	S932	S933	S934	S935	S936	S937	S938	S939	S940	S941	S942	S943	S944	S945	S946	S947	S948	S949	S950	S951	S952	S953	S954	S955	S956	S957	S958	S959	S960	S961	S962	S963	S964	S965	S966	S967	S968	S969	S970	S971	S972	S973	S974	S975	S976	S977	S978	S979	S980	S981	S982	S983	S984	S985	S986	S987	S988	S989	S990	S991	S992	S993	S994	S995	S996	S997	S998	S999	S1000	S1001	S1002	S1003	S1004	S1005	S1006	S1007	S1008	S1009	S1010	S1011	S1012	S1013	S1014	S1015	S1016	S1017	S1018	S1019	S1020	S1021	S1022	S1023	S1024	S1025	S1026	S1027	S1028	S1029	S1030	S1031	S1032	S1033	S1034	S1035	S1036	S1037	S1038	S1039	S1040	S1041	S1042	S1043	S1044	S1045	S1046	S1047	S1048	S1049	S1050	S1051	S1052	S1053	S1054	S1055	S1056	S1057	S1058	S1059	S1060	S1061	S1062	S1063	S1064	S1065	S1066	S1067	S1068	S1069	S1070	S1071	S1072	S1073	S1074	S1075	S1076	S1077	S1078	S1079	S1080	S1081	S1082	S1083	S1084	S1085	S1086	S1087	S1088	S1089	S1090	S1091	S1092	S1093	S1094	S1095	S1096	S1097	S1098	S1099	S1100	S1101	S1102	S1103	S1104	S1105	S1106	S1107	S1108	S1109	S1110	S1111	S1112	S1113	S1114	S1115	S1116	S1117	S1118	S1119	S1120	S1121	S1122	S1123	S1124	S1125	S1126	S1127	S1128	S1129	S1130	S1131	S1132	S1133	S1134	S1135	S1136	S1137	S1138	S1139	S1140	S1141	S1142	S1143	S1144	S1145	S1146	S1147	S1148	S1149	S1150	S1151	S1152	S1153	S1154	S1155	S1156	S1157	S1158	S1159	S1160	S1161	S1162	S1163	S1164	S1165	S1166	S1167	S1168	S1169	S1170	S1171	S1172	S1173	S1174	S1175	S1176	S1177	S1178	S1179	S1180	S1181	S1182	S1183	S1184	S1185	S1186	S1187	S1188	S1189	S1190	S1191	S1192	S1193	S1194	S1195	S1196	S1197	S1198	S1199	S1200	S1201	S1202	S1203	S1204	S1205	S1206	S1207	S1208	S1209	S1210	S1211	S1212	S1213	S1214	S1215	S1216	S1217	S1218	S1219	S1220	S1221	S1222	S1223	S1224	S1225	S1226	S1227	S1228	S1229	S1230	S1231	S1232	S1233	S1234	S1235	S1236	S1237	S1238	S1239	S1240	S1241	S1242	S1243	S1244	S1245	S1246	S1247	S1248	S1249	S1250	S1251	S1252	S1253	S1254	S1255	S1256	S1257	S1258	S1259	S1260	S1261	S1262	S1263	S1264	S1265	S1266	S1267	S1268	S1269	S1270	S1271	S1272	S1273	S1274	S1275	S1276	S1277	S1278	S1279	S1280	S1281	S1282	S1283	S1284	S1285	S1286	S1287	S1288	S1289	S1290	S1291	S1292	S1293	S1294	S1295	S1296	S1297	S1298	S1299	S1300	S1301	S1302	S1303	S1304	S1305	S1306	S1307	S1308	S1309	S1310	S1311	S1312	S1313	S1314	S1315	S1316	S1317	S1318	S1319	S1320	S1321	S1322	S1323	S1324	S1325	S1326	S1327	S1328	S1329	S1330	S1331	S1332	S1333	S1334	S1335	S1336	S1337	S1338	S1339	S1340	S1341	S1342	S1343	S1344	S1345	S1346	S1347	S1348	S1349	S1350	S1351	S1352	S1353	S1354	S1355	S1356	S1357	S1358	S1359	S1360	S1361	S1362	S1363	S1364	S1365	S1366	S1367	S1368	S1369	S1370	S1371	S1372	S1373	S1374	S1375	S1376	S1377	S1378	S1379	S1380	S1381	S1382	S1383	S1384	S1385	S1386	S1387	S1388	S1389	S1390	S1391	S1392	S1393	S1394	S1395	S1396	S1397	S1398	S1399	S1400	S1401	S1402	S1403	S1404	S1405	S1406	S1407	S1408	S1409	S1410	S1411	S1412	S1413	S1414	S1415	S1416	S1417	S1418	S1419	S1420	S1421	S1422	S1423	S1424	S1425	S1426	S1427	S1428	S1429	S1430	S1431	S1432	S1433	S1434	S1435	S1436	S1437	S1438	S1439	S1440	S1441	S1442	S1443	S1444	S1445	S1446	S1447	S1448	S1449	S1450	S1451	S1452	S1453	S1454	S1455	S1456	S1457	S1458	S1459	S1460	S1461	S1462	S1463	S1464	S1465	S1466	S1467	S1468	S1469	S1470	S1471	S1472	S1473	S1474	S1475	S1476	S1477	S1478	S1479	S1480	S1481	S1482	S1483	S1484	S1485	S1486	S1487	S1488	S1489	S1490	S1491	S1492	S1493	S1494	S1495	S1496	S1497	S1498	S1499	S1500	S1501	S1502	S1503	S1504	S1505	S1506	S1507	S1508	S1509	S1510	S1511	S1512	S1513	S1514	S1515	S1516	S1517	S1518	S1519	S1520	S1521	S1522	S1523	S1524	S1525	S1526	S1527	S1528	S1529	S1530	S1531	S1532	S1533	S1534	S1535	S1536	S1537	S1538	S1539	S1540	S1541	S1542	S1543	S1544	S1545	S1546	S1547	S1548	S1549	S1550	S1551	S1552	S1553	S1554	S1555	S1556	S1557	S1558	S1559	S1560	S1561	S1562	S1563	S1564	S1565	S1566	S1567	S1568	S1569	S1570	S1571	S1572	S1573	S1574	S1575	S1576	S1577	S1578	S1579	S1580	S1581	S1582	S1583	S1584	S1585	S1586	S1587	S1588	S1589	S1590	S1591	S1592	S1593	S1594	S1595	S1596	S1597	S1598	S1599	S1600	S1601	S1602	S1603	S1604	S1605	S1606	S1607	S1608	S1609	S1610	S1611	S1612	S1613	S1614	S1615	S1616	S1617	S1618	S1619	S1620	S
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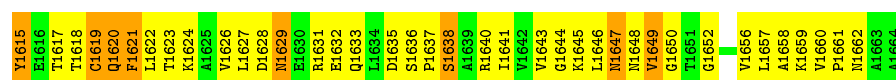


• Molecule 1: DNA-directed RNA polymerase I subunit RPA190

Chain CA:

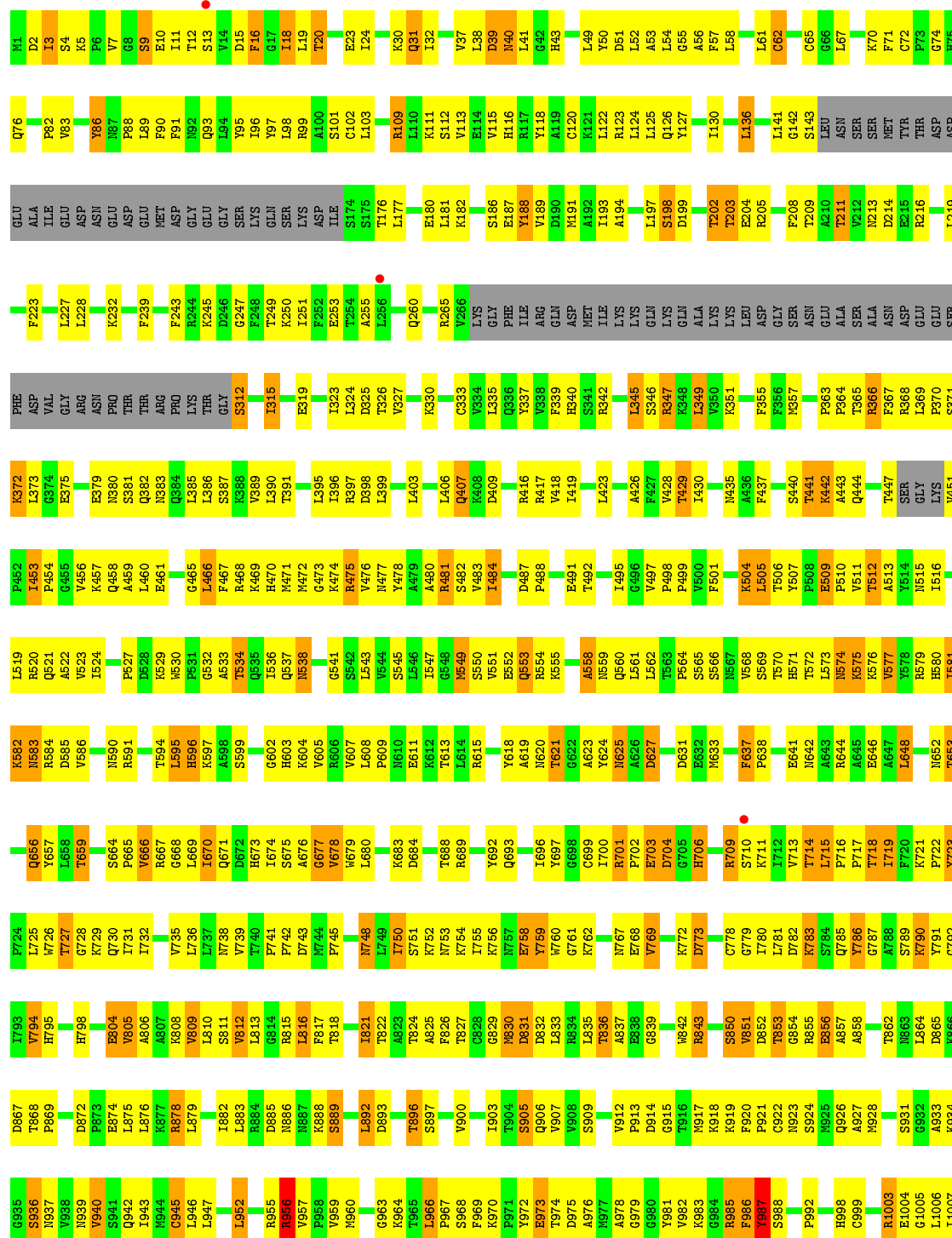


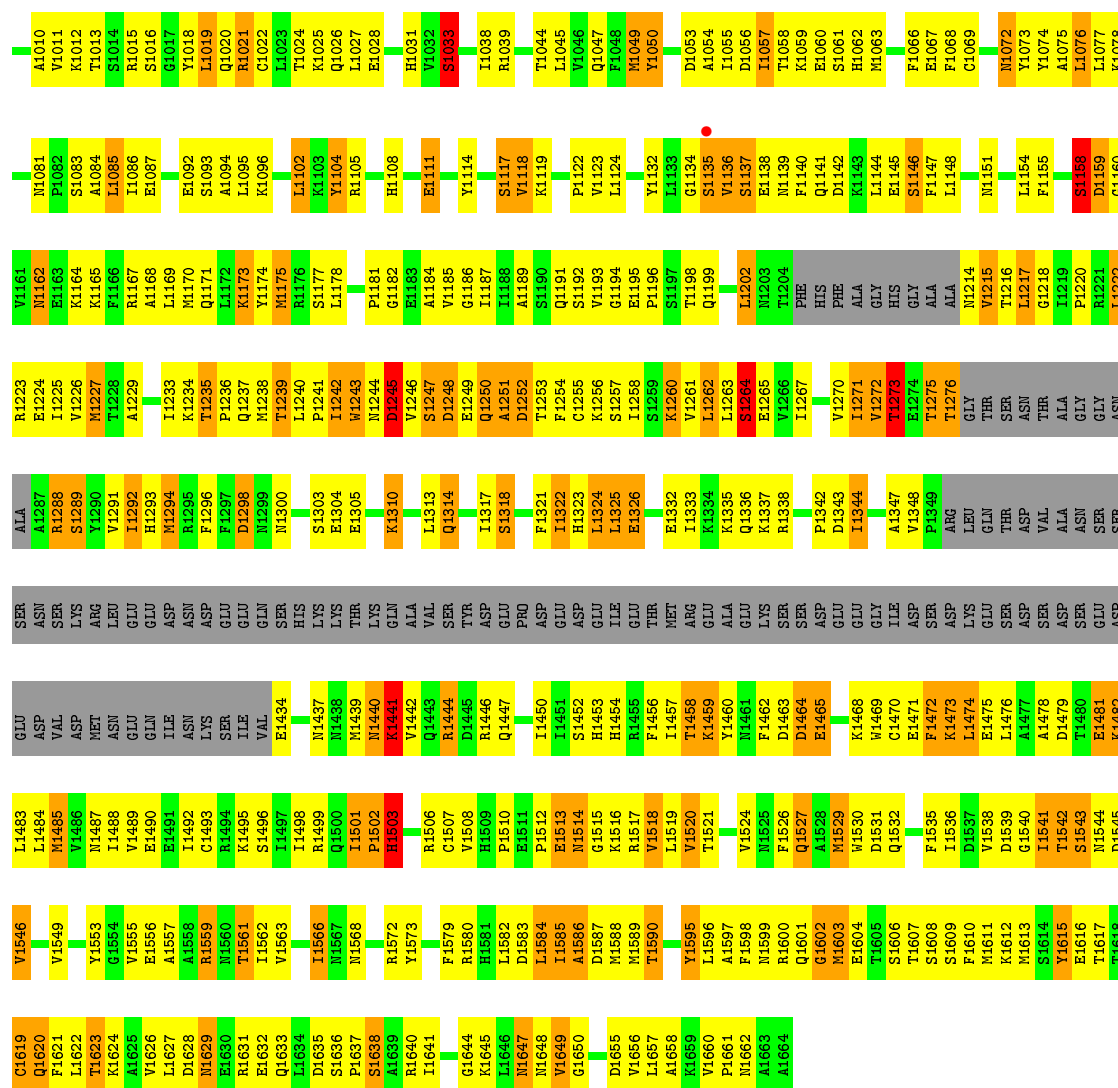




• Molecule 1: DNA-directed RNA polymerase I subunit RPA190

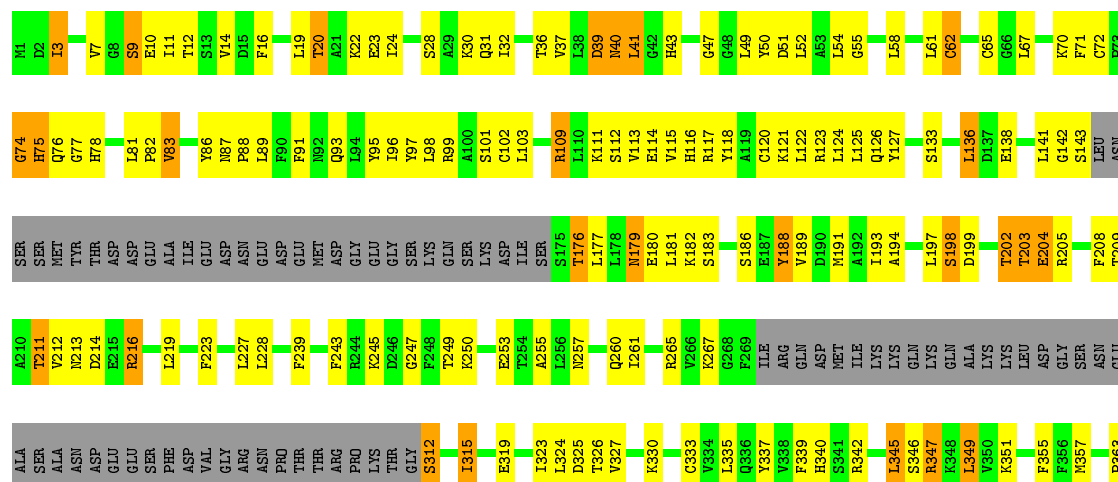
Chain DA: 34% 42% 12% 11%



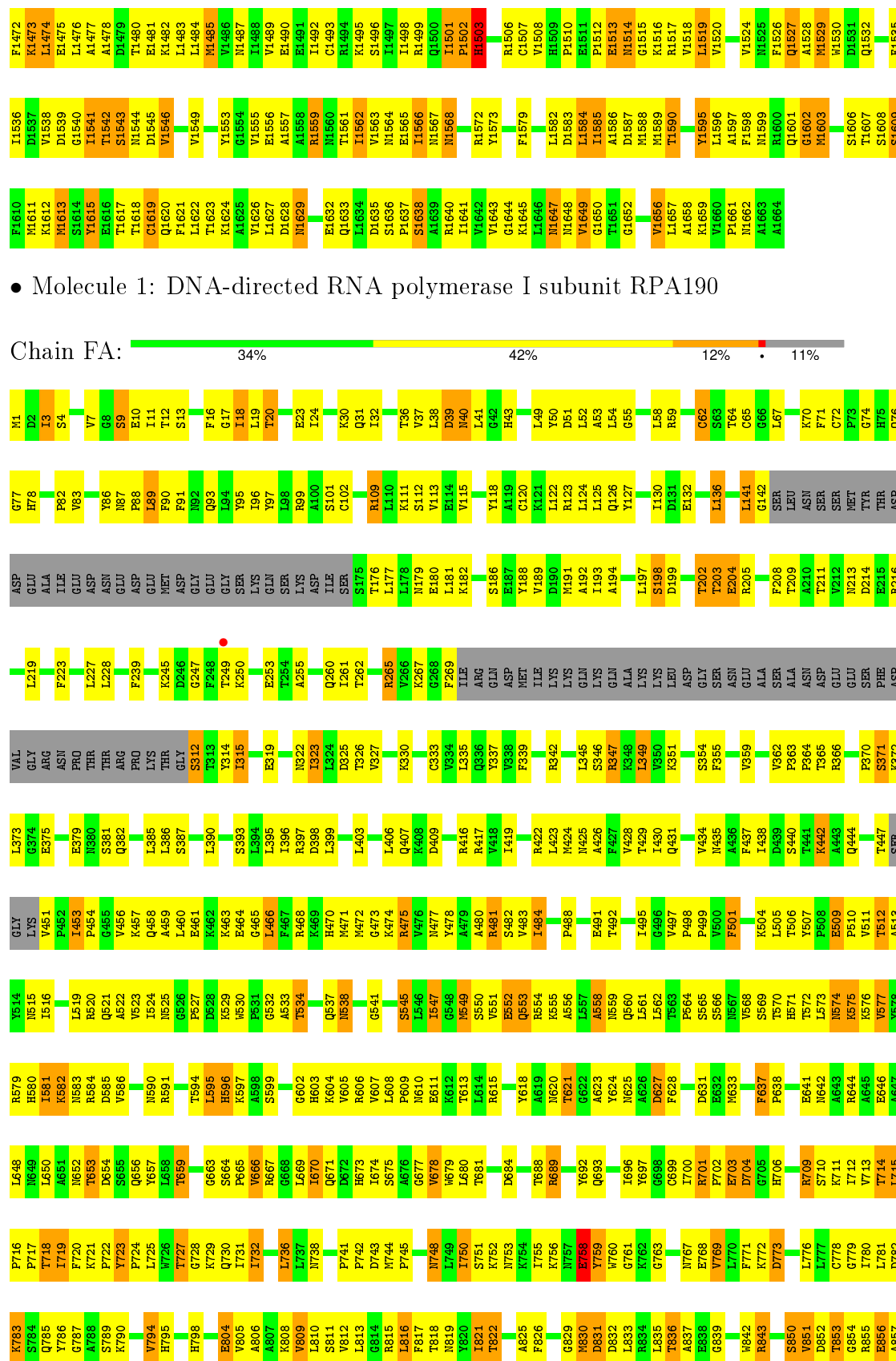


• Molecule 1: DNA-directed RNA polymerase I subunit RPA190

Chain EA: 34% 43% 12% 11%







- Molecule 2: DNA-directed RNA polymerase I subunit RPA135

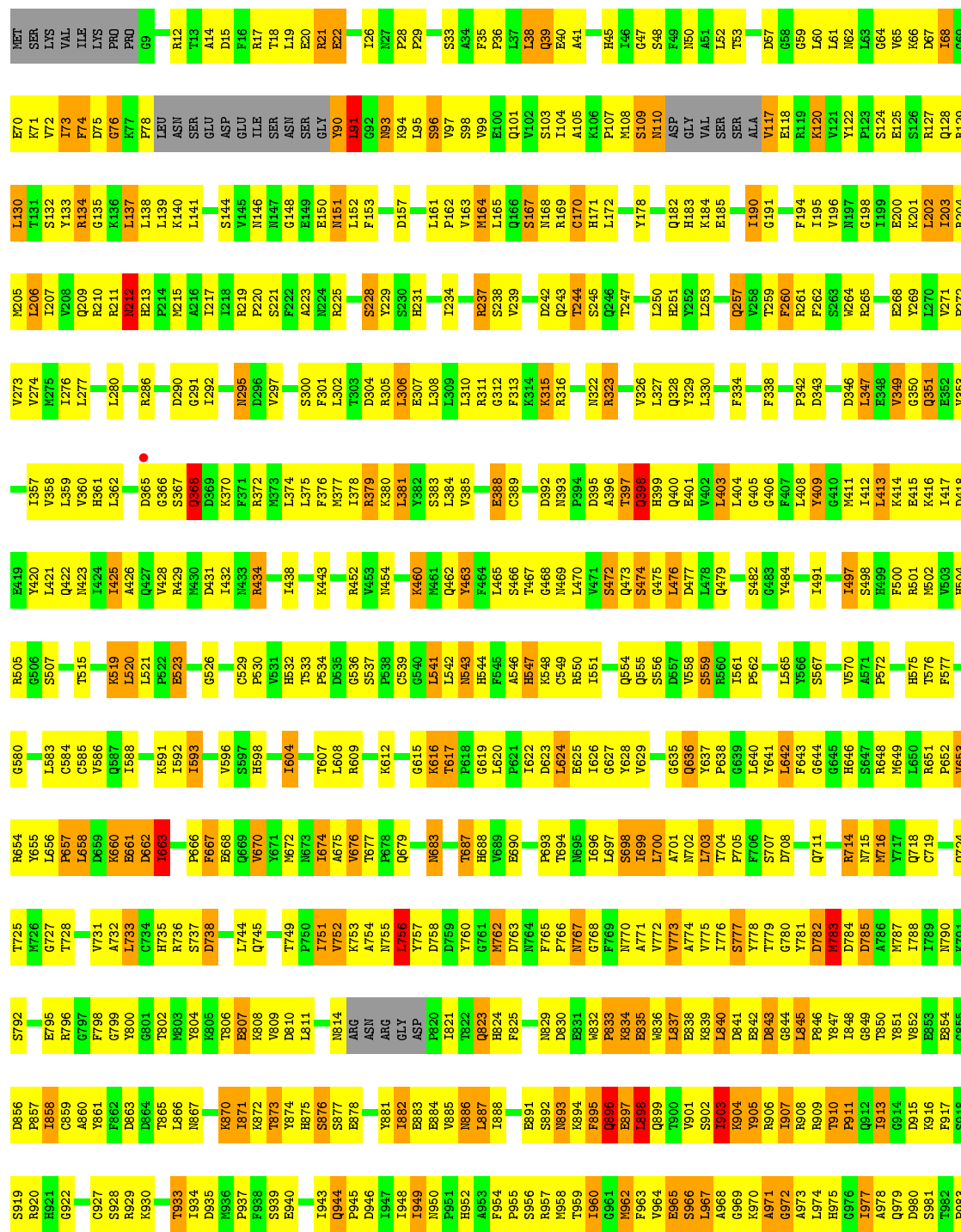
L130	L131	L132	L133	L134	L135	L136	L137	L138	L139	L140	L141	L142	L143	L144	L145	L146	L147	L148	L149	L150	L151	L152	L153	L154	L155	L156	L157	L158	L159	L160	L161	L162	L163	L164	L165	L166	L167	L168	L169	L170	L171	L172	L173	L174	L175	L176	L177	L178	L179	L180	L181	L182	L183	L184	L185	L186	L187	L188	L189	L190	L191	L192	L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316	L317	L318	L319	L320	L321	L322	L323	L324	L325	L326	L327	L328	L329	L330	L331	L332	L333	L334	L335	L336	L337	L338	L339	L340	L341	L342	L343	L344	L345	L346	L347	L348	L349	L350	L351	L352	L353	L354	L355	L356	L357	L358	L359	L360	L361	L362	L363	L364	L365	L366	L367	L368	L369	L370	L371	L372	L373	L374	L375	L376	L377	L378	L379	L380	L381	L382	L383	L384	L385	L386	L387	L388	L389	L390	L391	L392	L393	L394	L395	L396	L397	L398	L399	L400	L401	L402	L403	L404	L405	L406	L407	L408	L409	L410	L411	L412	L413	L414	L415	L416	L417	L418	L419	L420	L421	L422	L423	L424	L425	L426	L427	L428	L429	L430	L431	L432	L433	L434	L435	L436	L437	L438	L439	L440	L441	L442	L443	L444	L445	L446	L447	L448	L449	L450	L451	L452	L453	L454	L455	L456	L457	L458	L459	L460	L461	L462	L463	L464	L465	L466	L467	L468	L469	L470	L471	L472	L473	L474	L475	L476	L477	L478	L479	L480	L481	L482	L483	L484	L485	L486	L487	L488	L489	L490	L491	L492	L493	L494	L495	L496	L497	L498	L499	L500	L501	L502	L503	L504	L505	L506	L507	L508	L509	L510	L511	L512	L513	L514	L515	L516	L517	L518	L519	L520	L521	L522	L523	L524	L525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L
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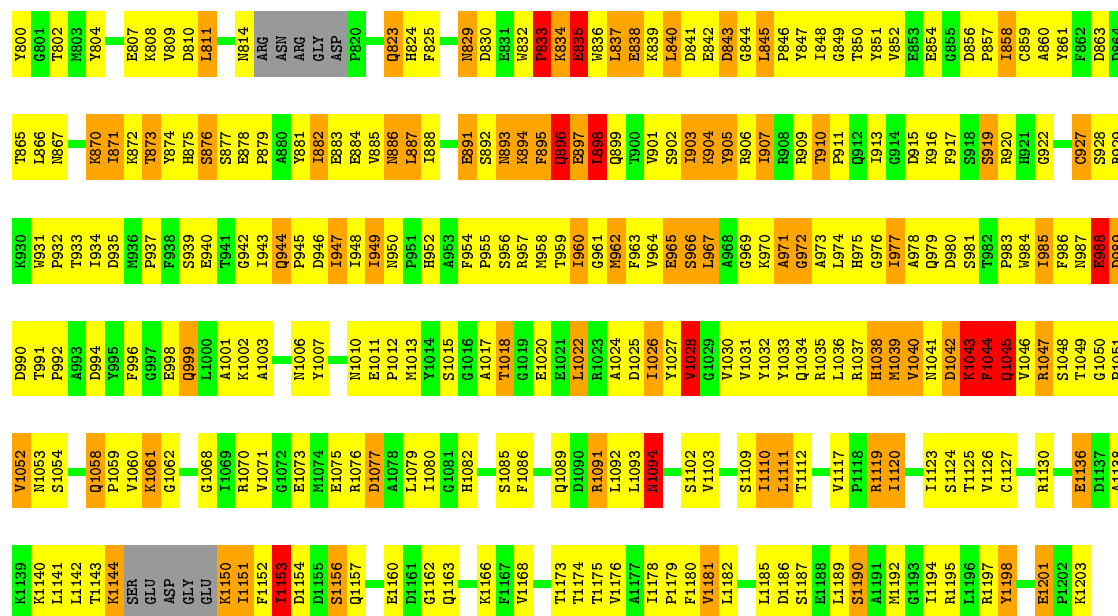


- Molecule 2: DNA-directed RNA polymerase I subunit RPA135

Response	Percentage
Yes	36%
No	45%
Don't know	14%
Other	2%

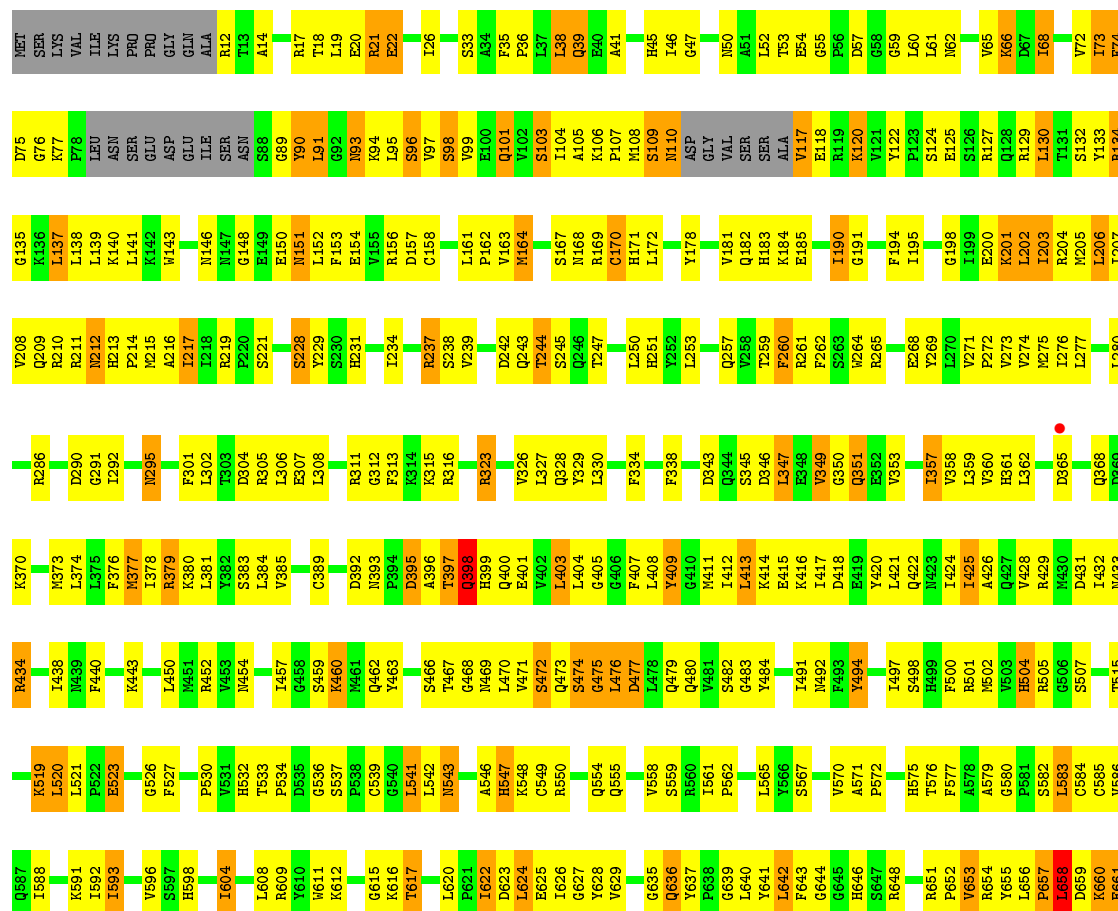


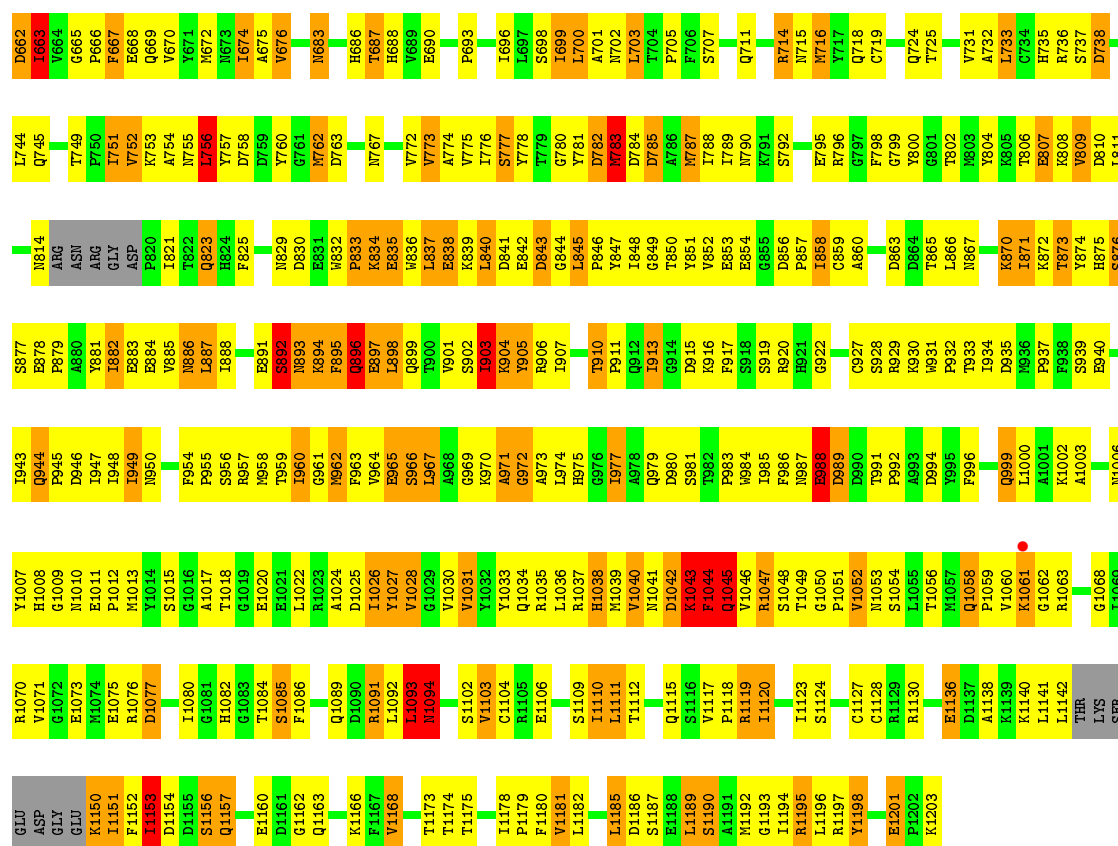




• Molecule 2: DNA-directed RNA polymerase I subunit RPA135

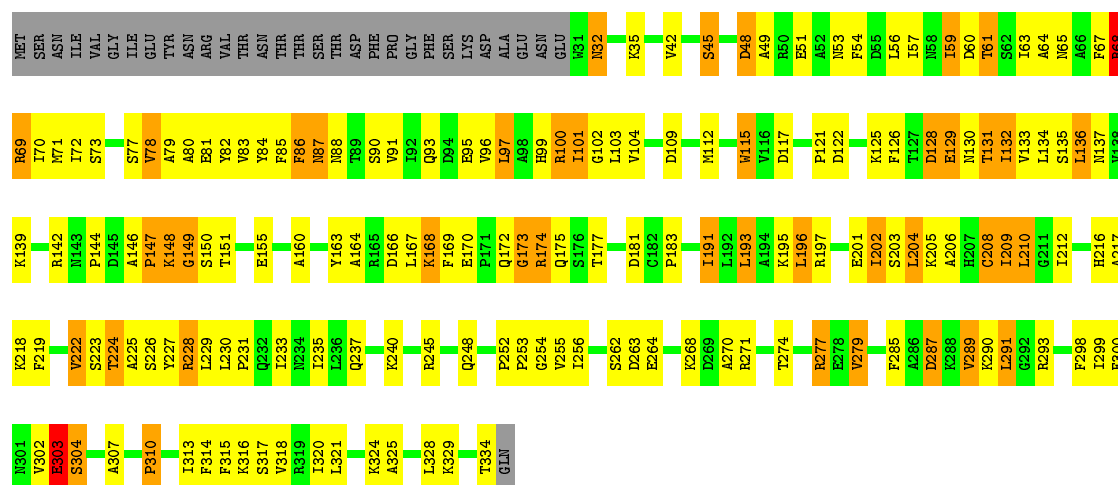
Chain FB: 36% 45% 14%





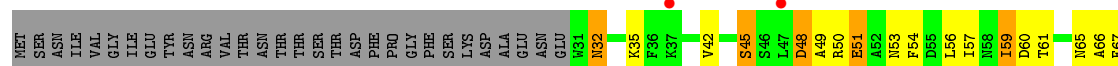
• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1

Chain AC: 41% 37% 13% 9%



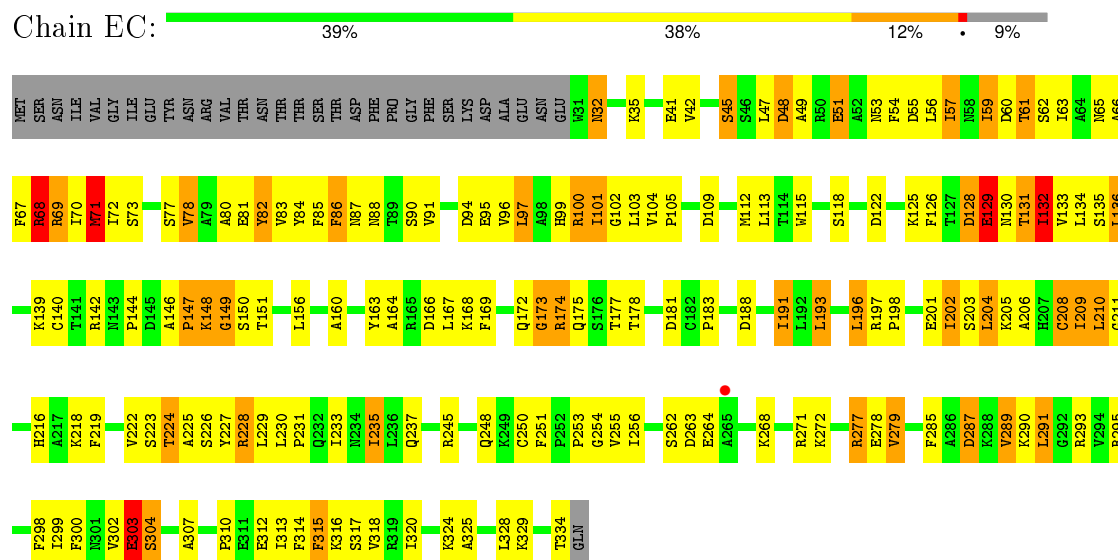
• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1

Chain BC: 2% 41% 38% 12% 9%

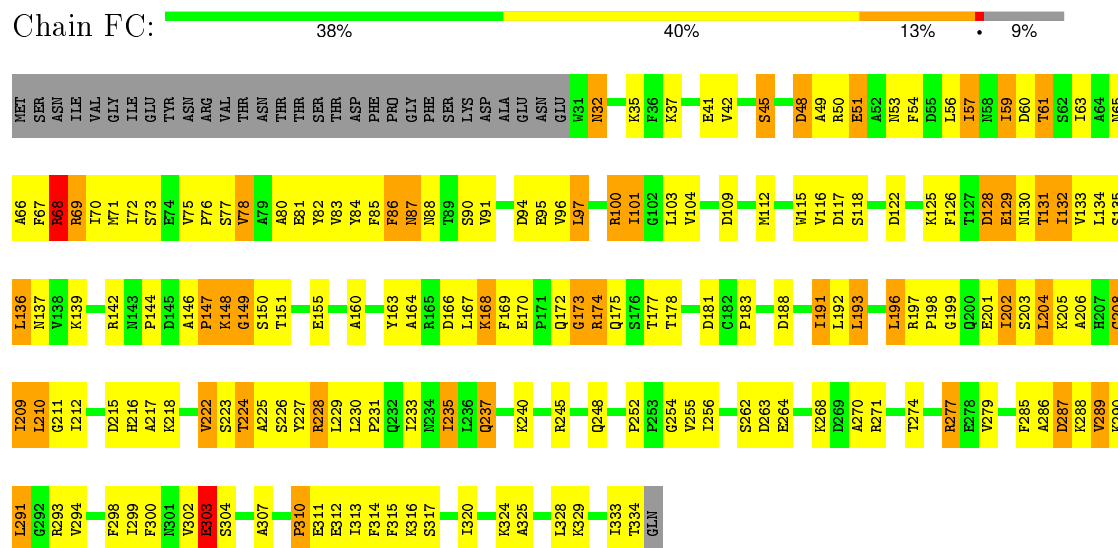




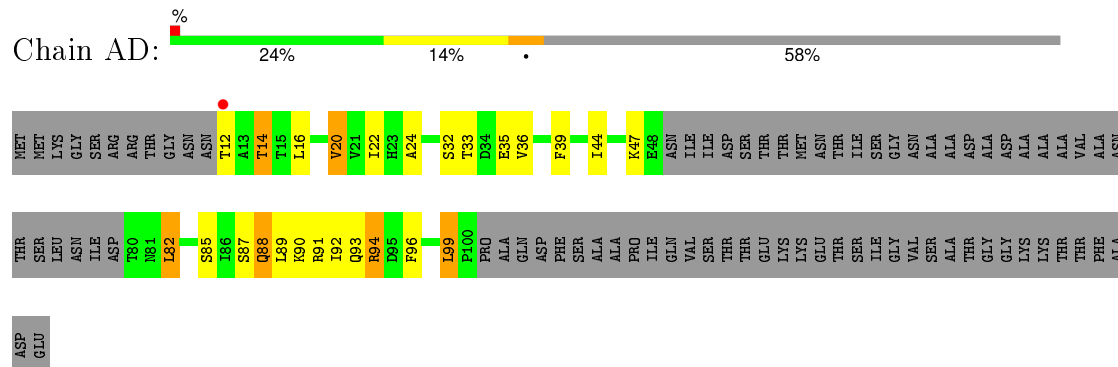
• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1



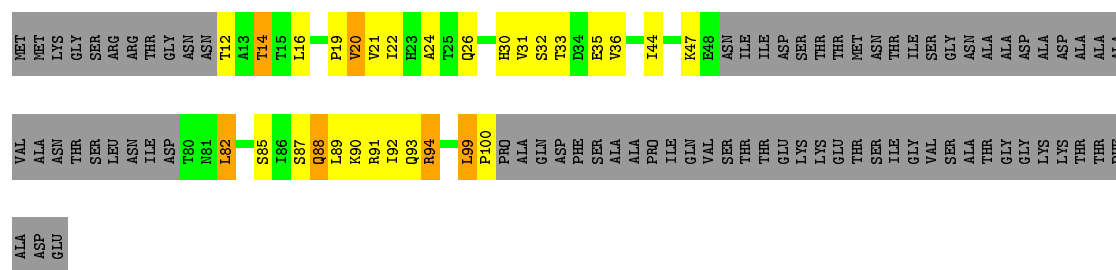
• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1



• Molecule 4: DNA-directed RNA polymerase I subunit RPA14

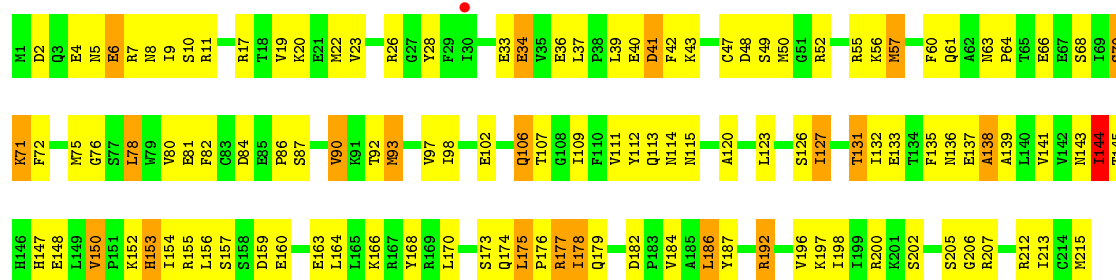


- Chain FD:  21% 17% . 58%



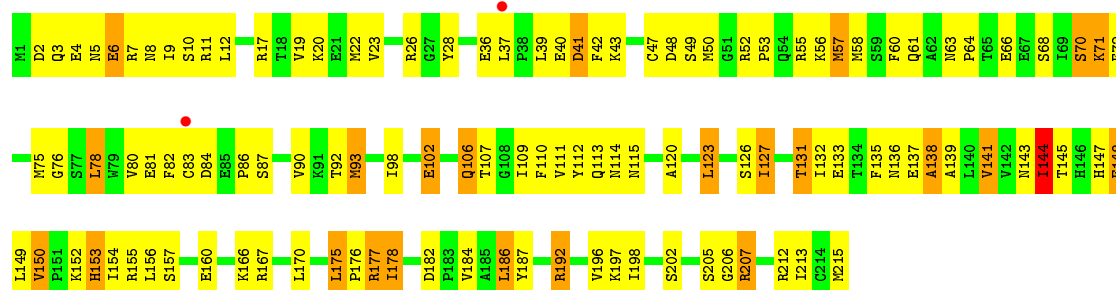
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain AE: 44% 46% 9%



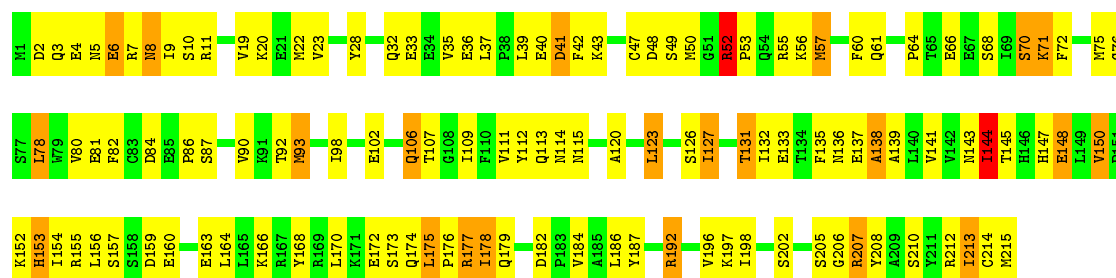
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain BE: 46% 43% 11%

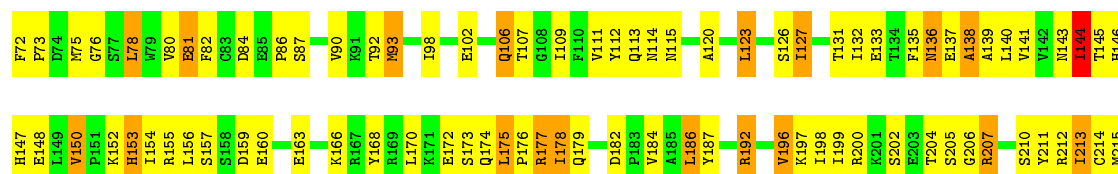
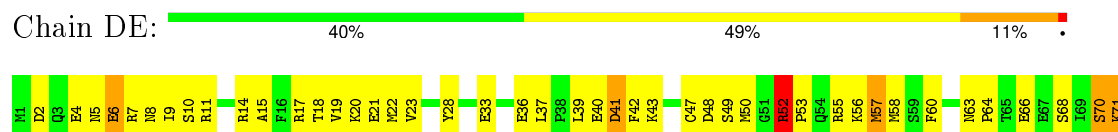


- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

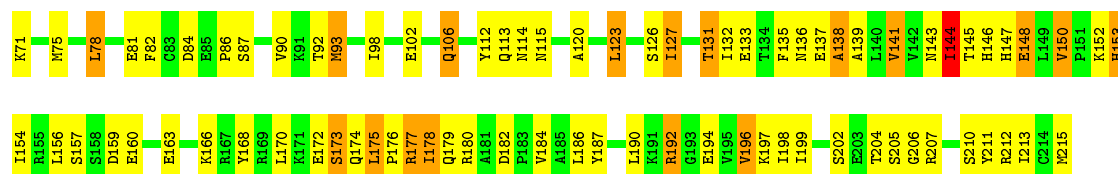
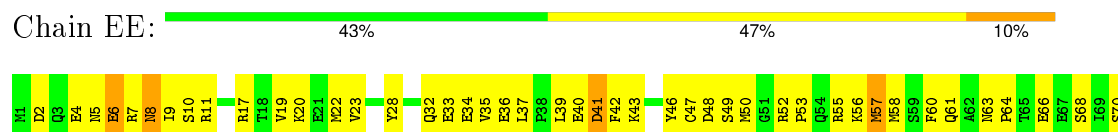
Chain CE: 43% 46% 10%



- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1



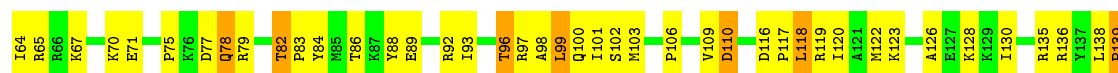
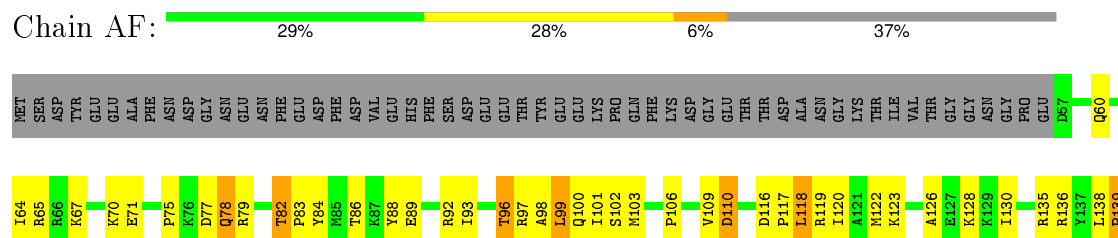
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1



- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1

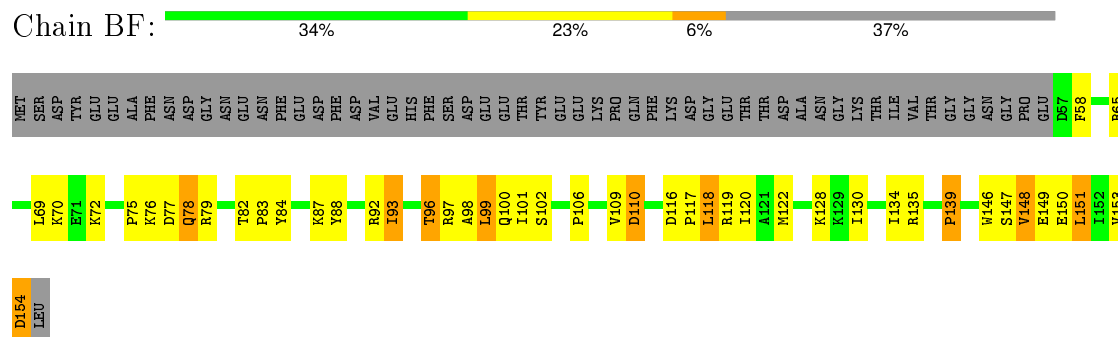


- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

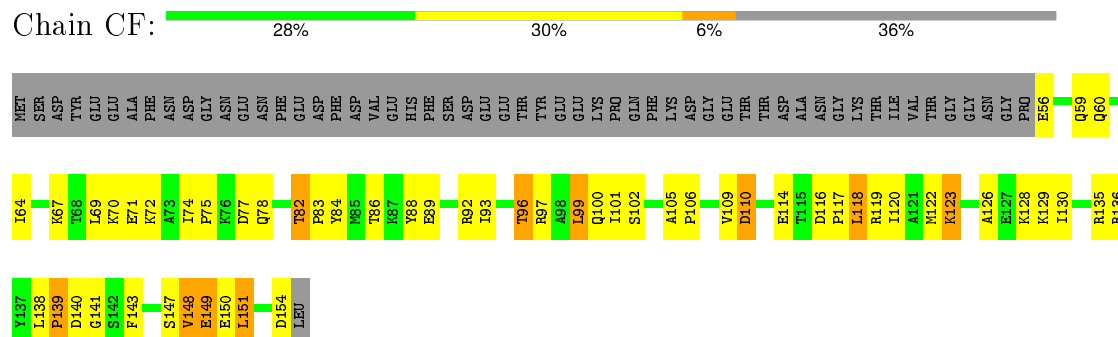




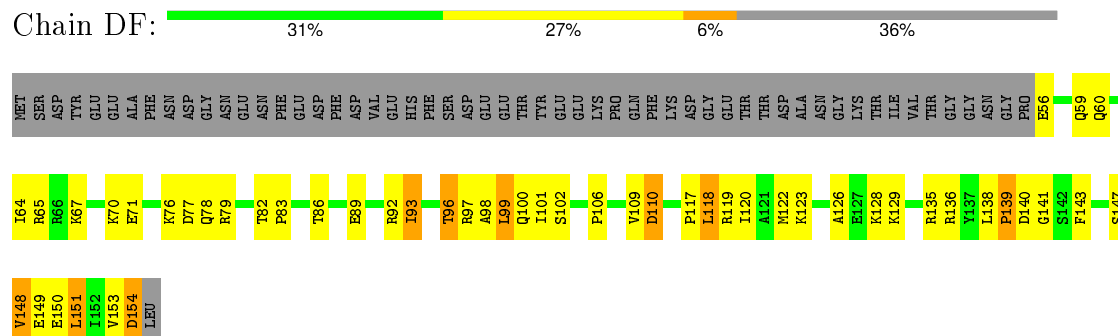
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2



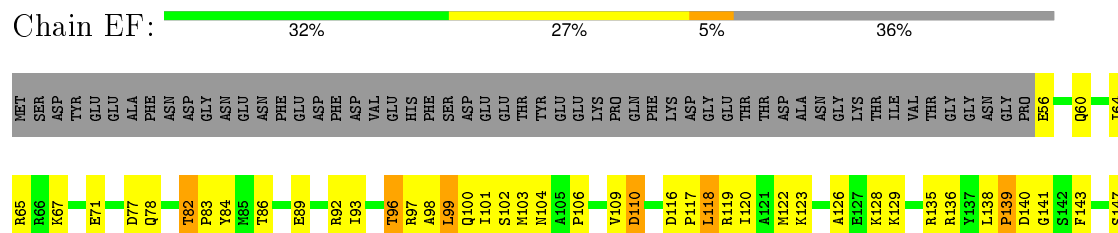
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

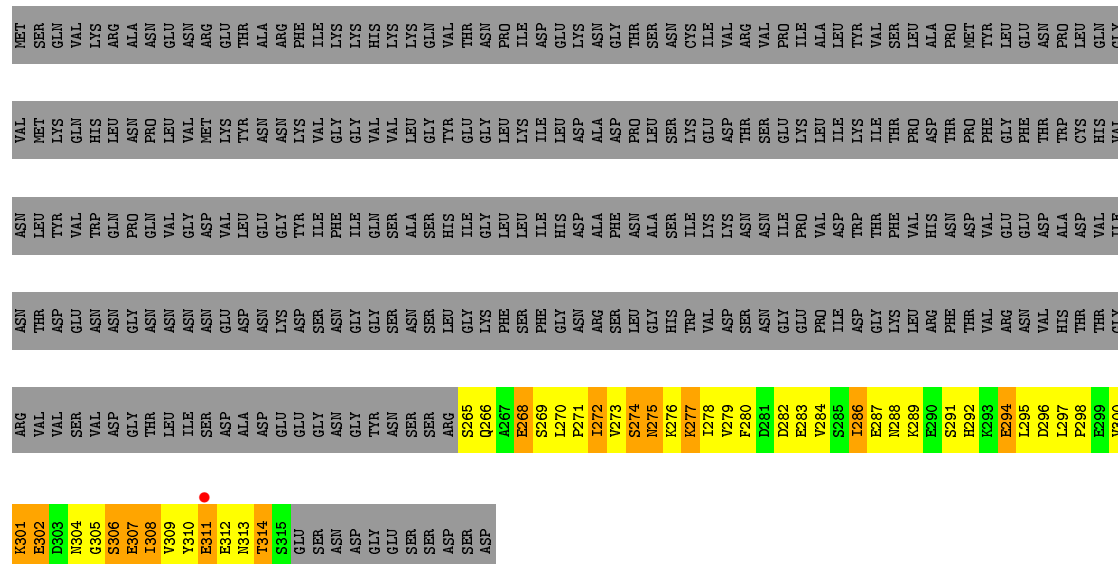
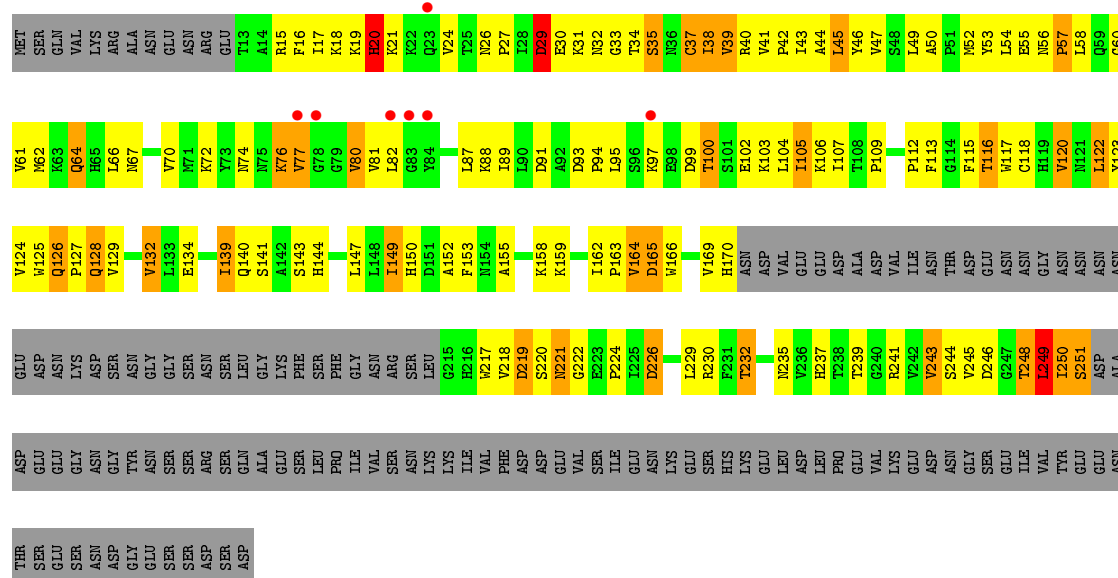
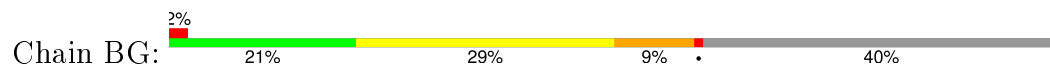
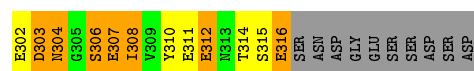


- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

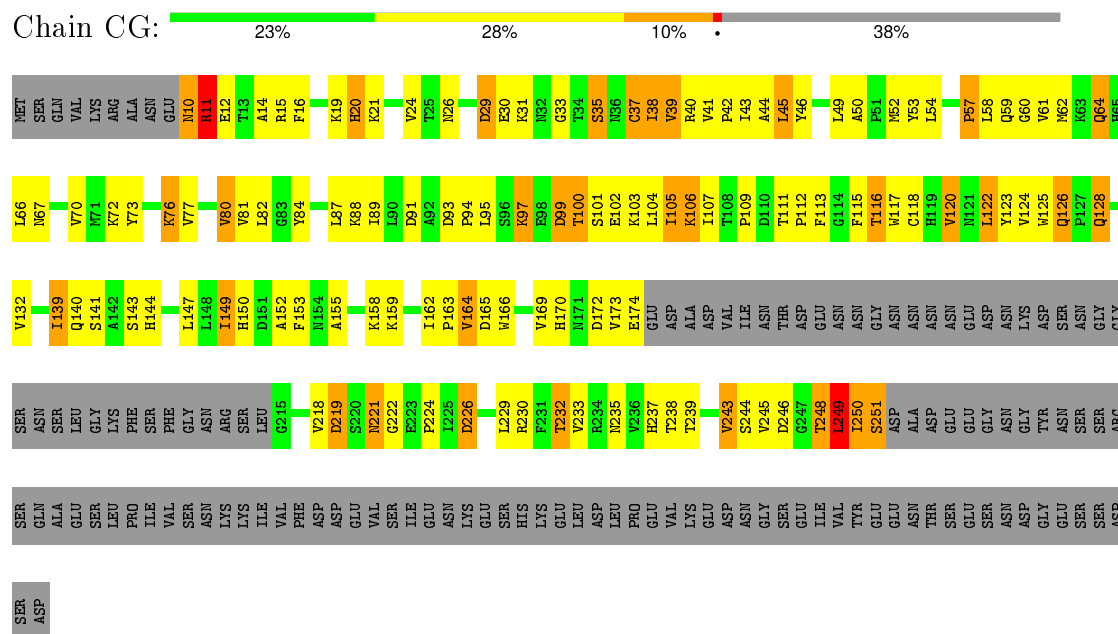


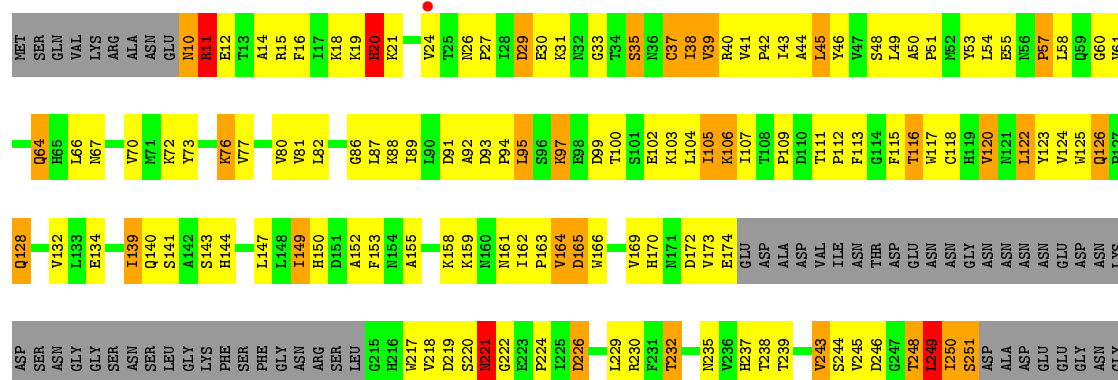
- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2





• Molecule 7: DNA-directed RNA polymerase I subunit RPA43



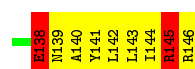
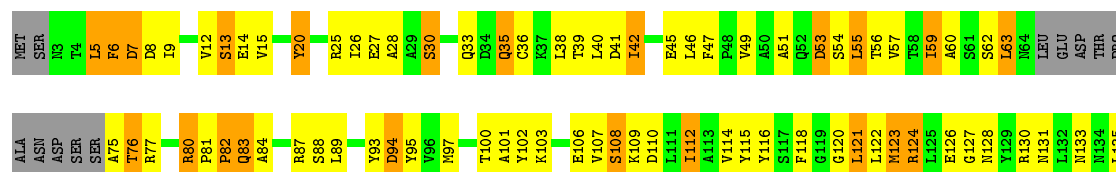






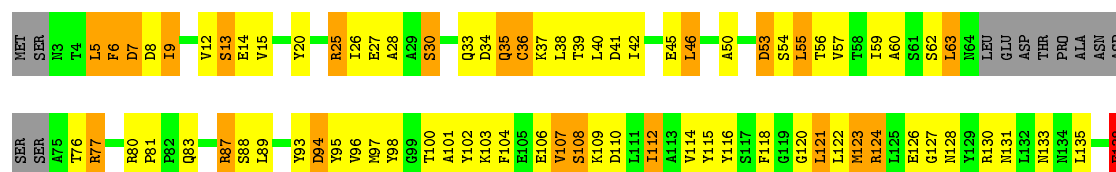
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain DH: 32% 43% 15% 8%



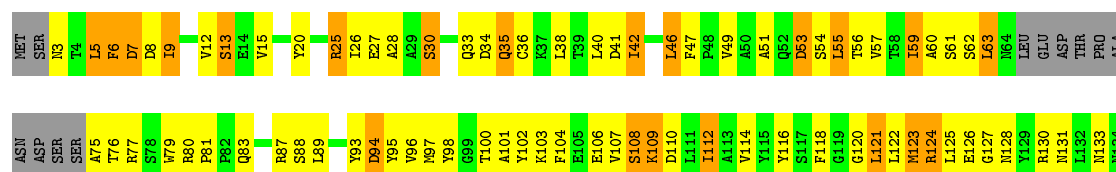
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain EH: 33% 43% 15% 8%



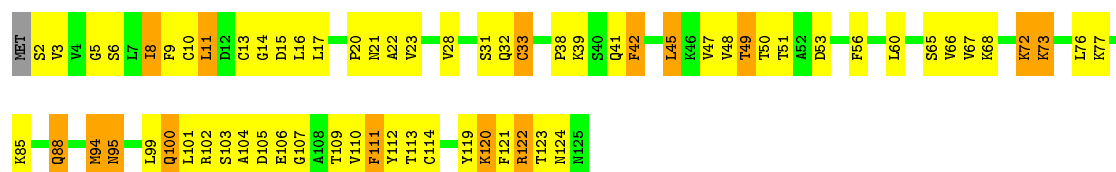
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain FH: 32% 45% 16% 8%

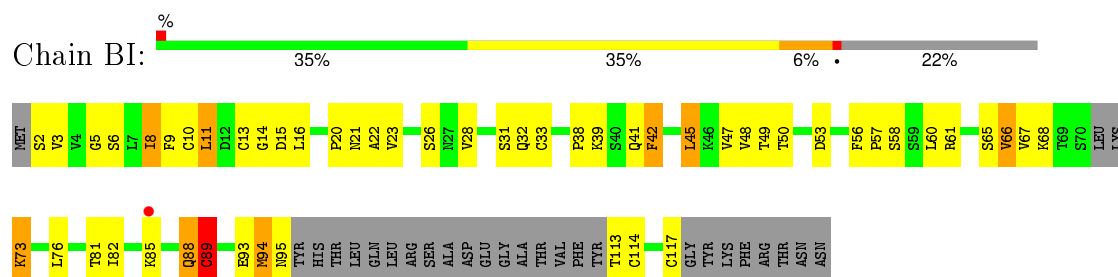


- Molecule 9: DNA-directed RNA polymerase I subunit RPA12

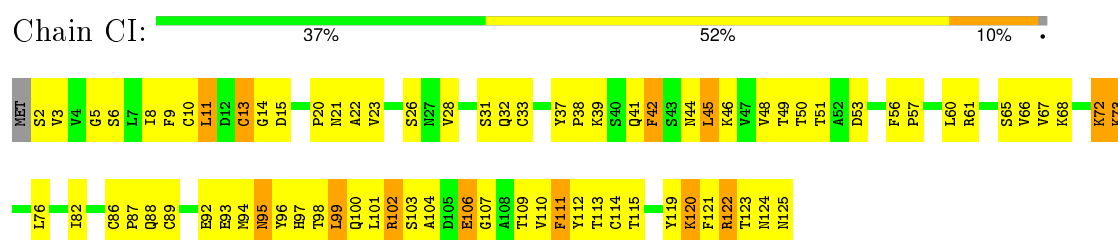
Chain AI: 46% 42% 12%



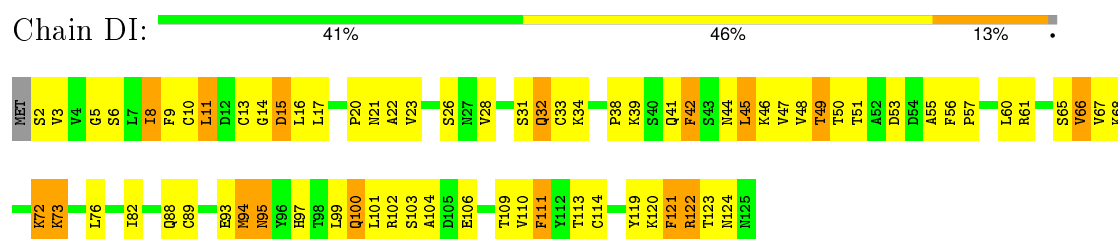
- Molecule 9: DNA-directed RNA polymerase I subunit RPA12



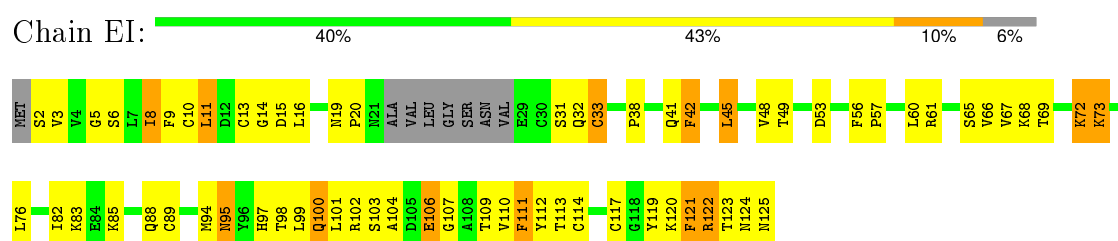
- Molecule 9: DNA-directed RNA polymerase I subunit RPA12



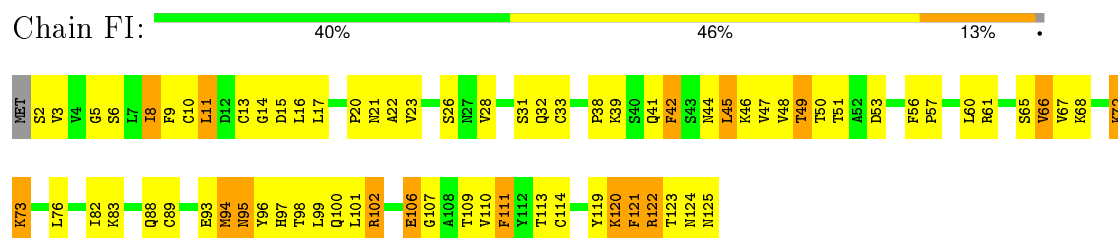
- Molecule 9: DNA-directed RNA polymerase I subunit RPA12



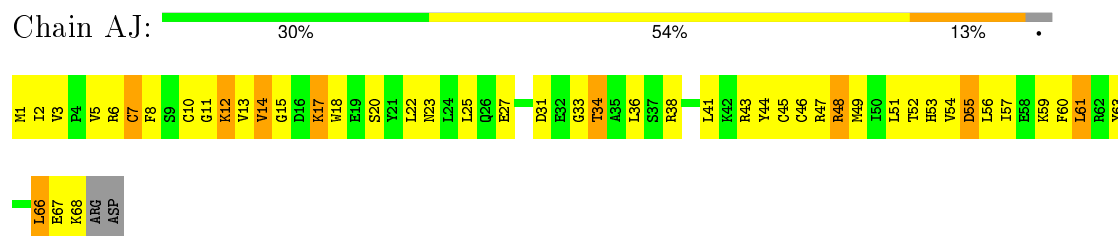
- Molecule 9: DNA-directed RNA polymerase I subunit RPA12



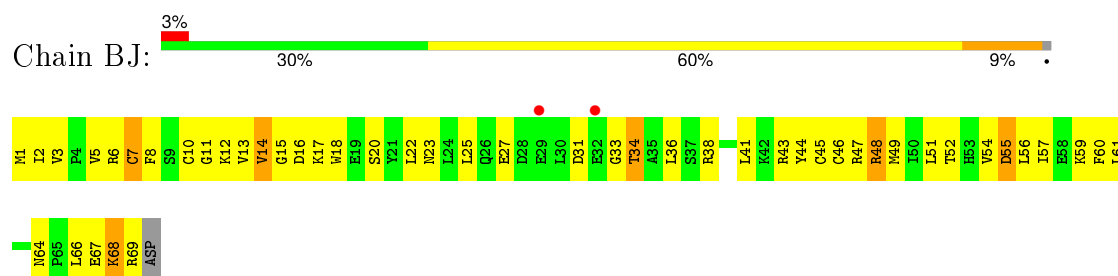
- Molecule 9: DNA-directed RNA polymerase I subunit RPA12



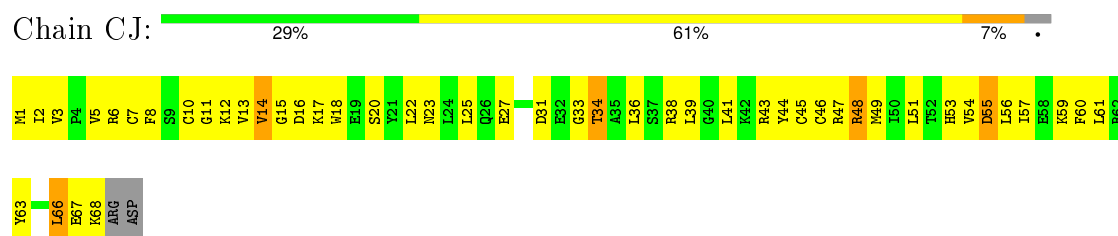
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



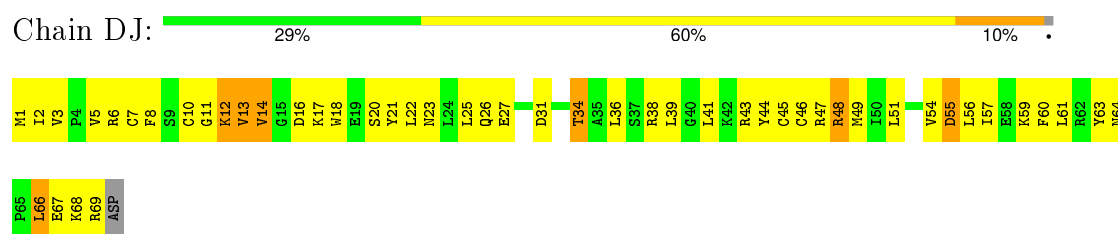
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



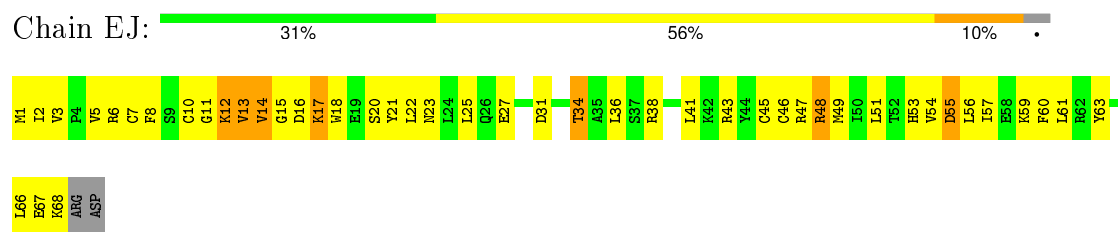
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5

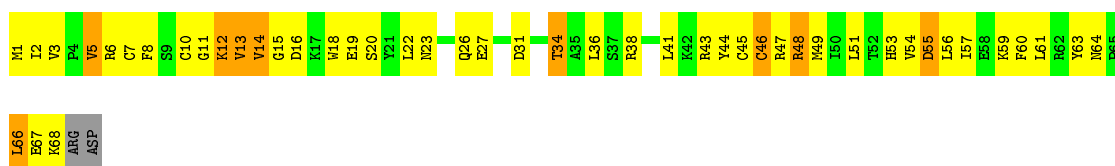


- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



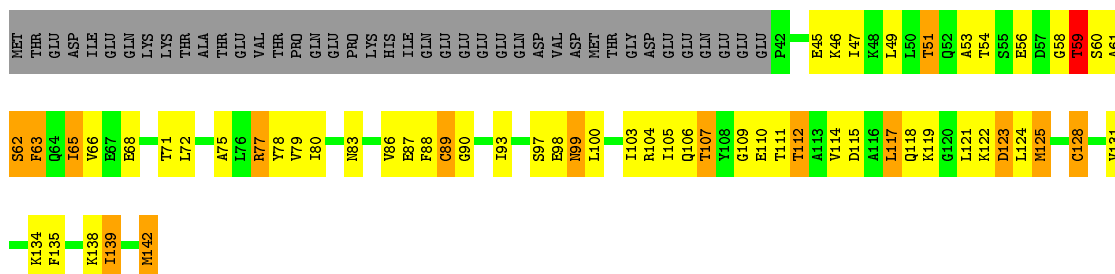
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5





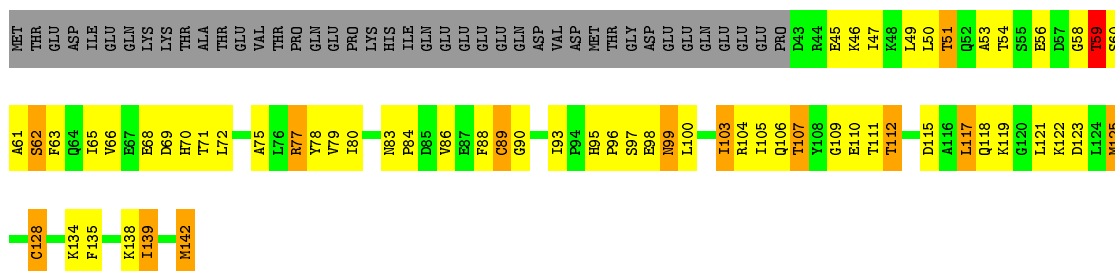
- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2

Chain AK: 28% 32% 11% 29%



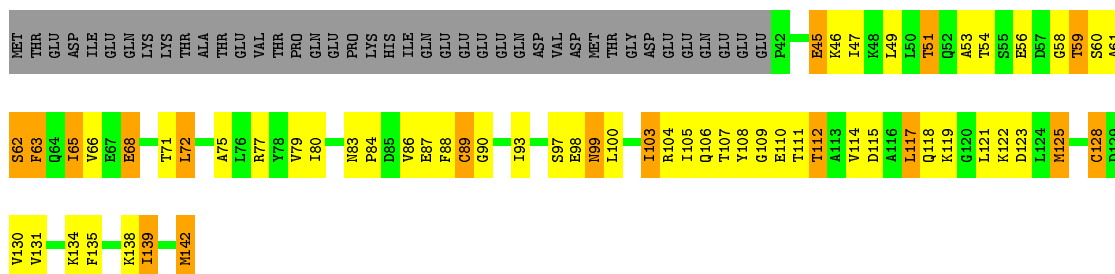
- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2

Chain BK: 26% 35% 9% 30%



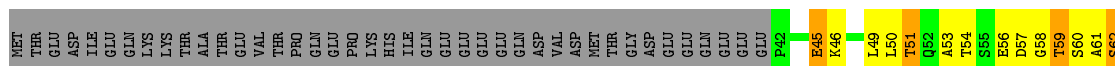
- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2

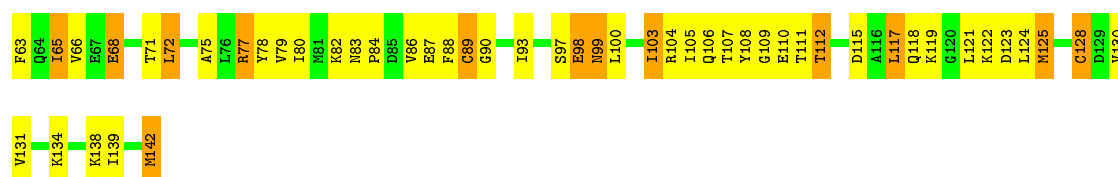
Chain CK: 27% 32% 12% 29%



- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2

Chain DK: 26% 33% 12% 29%





- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2

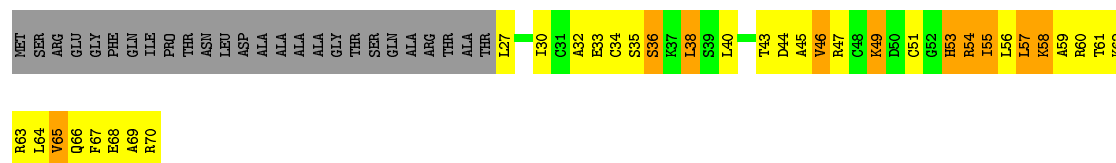
- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2

- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

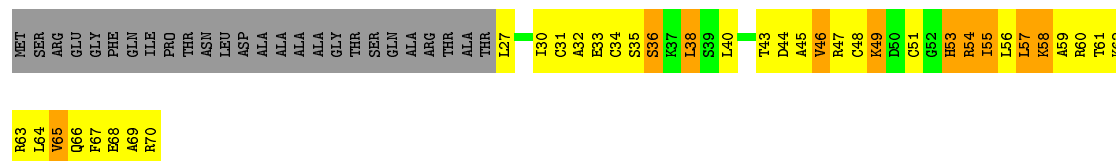
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

Chain CL: 14% 34% 14% 37%



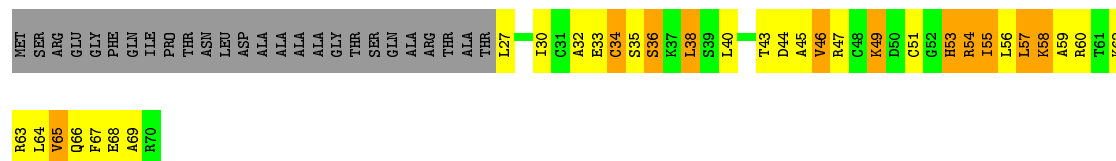
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

Chain DL: 11% 37% 14% 37%



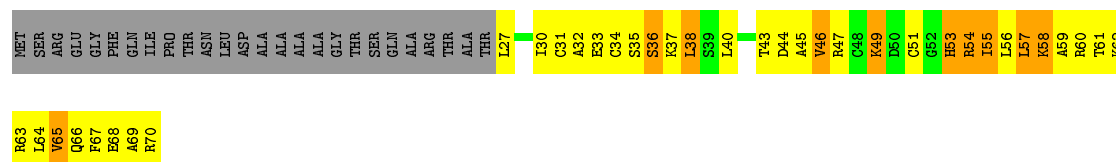
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

Chain EL: 17% 30% 16% 37%



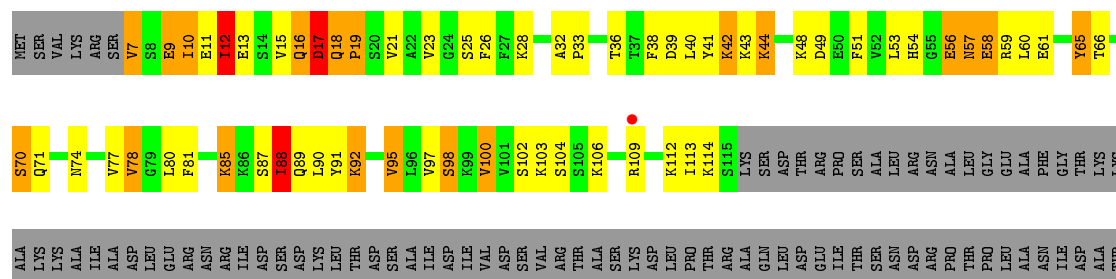
- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4

Chain FL: 11% 37% 14% 37%



- Molecule 13: DNA-directed RNA polymerase I subunit RPA49

Chain AM: 11% 10% 5% 74%



[illegible]

- Molecule 13: DNA-directed RNA polymerase I subunit RPA49

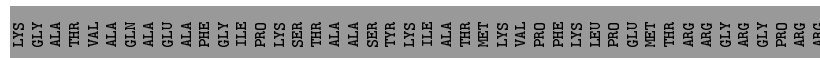
Chain BM:  10% 12% • 74%

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ALA	THR	ASP	GLN	VAL	THR	ASP	GLN	LEU	ILE	GLY	VAL	GLY	GLY	ASP	THR	ALA	LYS	LYS	S68
VAL	VAL	ARG	MET	ALA	THR	ASP	THR	VAL	THR	VAL	VAL	LYS	LYS	VAL	ALA	LYS	LYS	LYS	S69
ALA	ALA	SER	THR	ALA	SER	THR	THR	VAL	THR	THR	THR	LYS	LYS	VAL	ALA	LYS	LYS	LYS	S70
GLN	GLN	SER	THR	VAL	SER	THR	THR	VAL	THR	THR	THR	LYS	LYS	VAL	ALA	LYS	LYS	LYS	N74
ALA	ALA	PHE	LEU	GLY	PHE	LEU	GLN	LEU	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	Q75
GLY	GLY	ILE	GLN	ALA	ILE	GLY	GLN	LEU	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	Y76
ALA	ALA	ASP	LEU	ALA	ASP	LEU	LEU	LEU	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	Y77
PHE	PHE	PRO	ASP	PRO	PRO	PRO	LEU	LEU	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	Y78
GLY	GLY	GLN	THR	GLY	GLN	THR	THR	THR	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	Q79
ILE	ILE	ASN	THR	THR	THR	THR	THR	THR	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	L60
PRO	PRO	GLY	LEU	LEU	GLY	GLY	LEU	LEU	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	Q81
ASP	ASP	ASP	SER	SER	ASP	ASP	SER	SER	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	N82
LYS	LYS	LYS	LEU	LEU	ILE	ILE	LEU	LEU	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	P83
THR	THR	ILE	LEU	LEU	ILE	ILE	LEU	LEU	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	E84
ALA	ALA	CYS	GLY	GLY	GLY	GLY	GLY	GLY	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	K85
THR	THR	TYR	VAL	VAL	VAL	VAL	VAL	VAL	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	K86
SER	SER	ILE	TYR	TYR	ILE	ILE	GLY	GLY	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	S87
LYS	LYS	LEU	LEU	LEU	ILE	ILE	GLY	GLY	ILE	GLY	VAL	LYS	LYS	GLY	ILE	ALA	ALA	ALA	I88
ILE	ILE	ALA	ASN	ASN	ILE	ILE	ASN	ASN	PHE	ILE	GLY	VAL	VAL	VAL	THR	THR	THR	THR	Q89
ALA	ALA	ILE	ALA	ALA	ILE	ILE	ALA	ALA	ARG	ILE	GLY	VAL	VAL	VAL	ASP	ASP	ASP	ASP	L90
THR	THR	ILE	ALA	ALA	ILE	ILE	ALA	ALA	ARG	ILE	GLY	VAL	VAL	VAL	ASP	ASP	ASP	ASP	Y91
MET	MET	MET	VAL	VAL	MET	MET	VAL	VAL	ARG	ILE	GLY	VAL	VAL	VAL	ILE	ALA	ALA	ALA	K92
LYS	LYS	LYS	HIS	HIS	LYS	LYS	HIS	ASN	VAL	ILE	GLY	VAL	VAL	VAL	ILE	ALA	ALA	ALA	Y95
VAL	VAL	VAL	LEU	LEU	ASN	ASN	ASN	ASN	SER	ILE	GLY	VAL	VAL	VAL	ASP	ASP	ASP	ASP	L96
PRO	PRO	PRO	ASN	ASN	LYS	LYS	LYS	LYS	SER	ILE	GLY	VAL	VAL	VAL	ILE	ALA	ALA	ALA	Y97
PHE	PHE	PHE	ASN	ASN	THR	THR	THR	THR	THR	ILE	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	S98
LYS	LYS	PHE	ASN	ASN	LYS	LYS	LYS	LYS	THR	ILE	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	R99
LEU	LEU	ILE	LEU	LEU	VAL	VAL	VAL	VAL	VAL	ILE	GLY	VAL	VAL	VAL	ASP	ASP	ASP	ASP	Y100
PRO	PRO	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ILE	GLY	VAL	VAL	VAL	ASP	ASP	ASP	ASP	Y101
GLY	GLY	MET	MET	MET	GLY	GLY	GLY	GLY	GLY	ILE	GLY	VAL	VAL	VAL	ASP	ASP	ASP	ASP	Y102
GLY	GLY	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	Y103
GLY	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	S104
ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	K103
GLY	GLY	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	S104
GLY	GLY	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	R109
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																			LYS
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																			ALA
																			E63

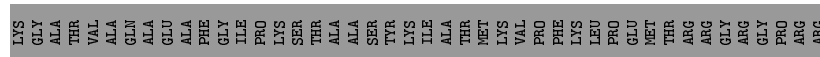
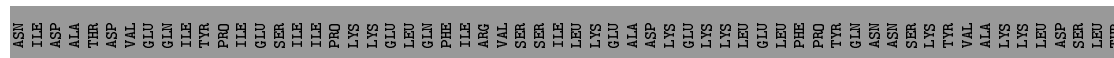
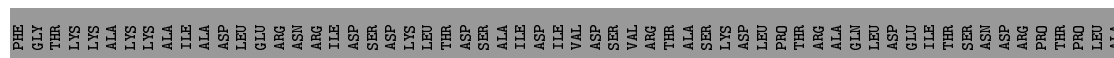
- Molecule 13: DNA-directed RNA polymerase I subunit RPA49

Chain CM: 11% 12% 2% 74%

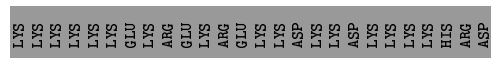
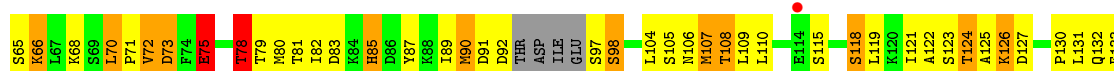
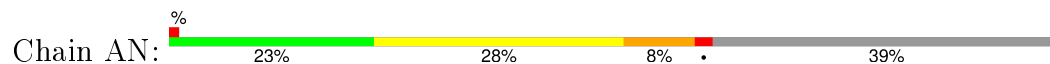
[illegible]



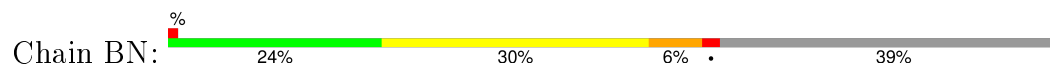
- Molecule 13: DNA-directed RNA polymerase I subunit RPA49

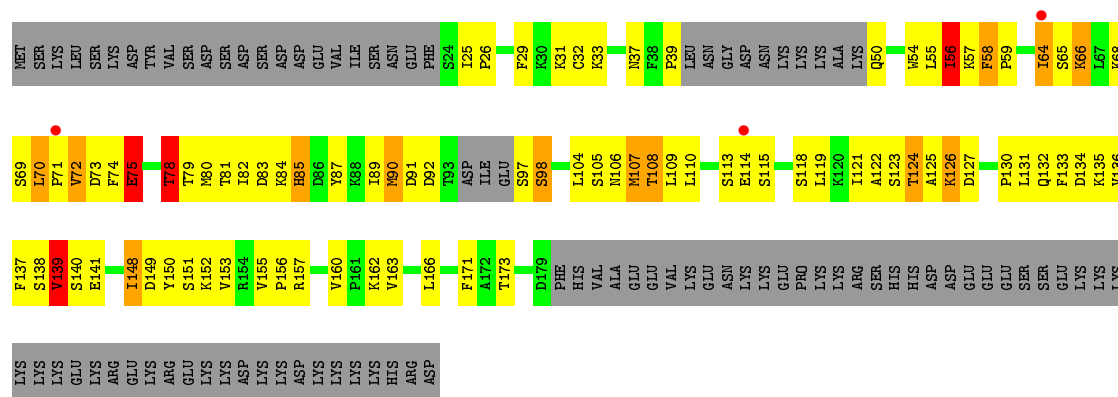


- Molecule 14: DNA-directed RNA polymerase I subunit RPA34

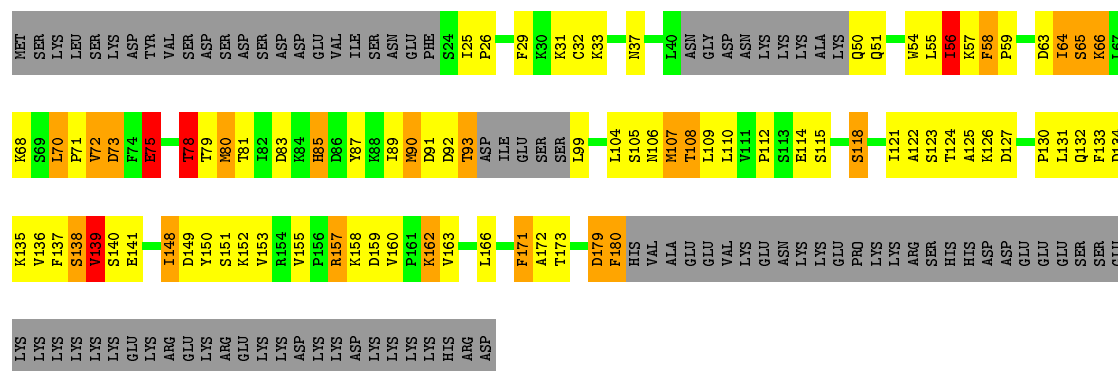
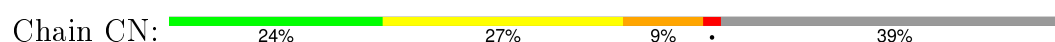


- Molecule 14: DNA-directed RNA polymerase I subunit RPA34

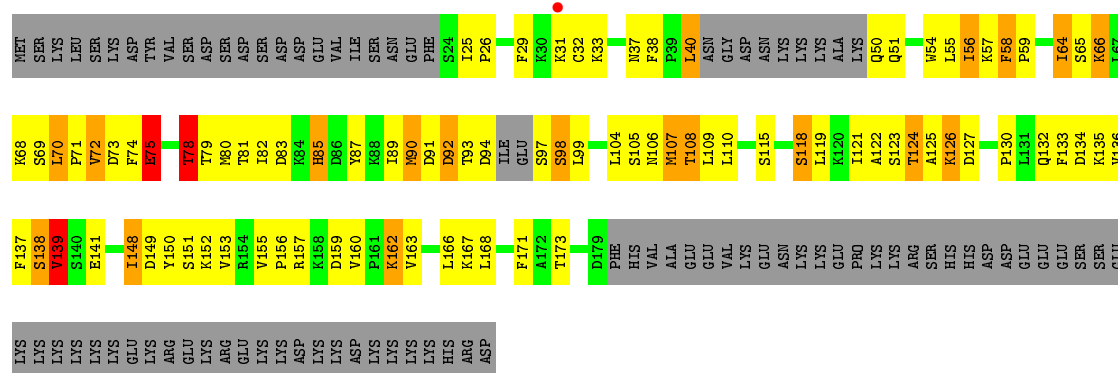
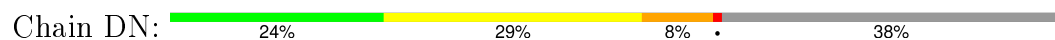




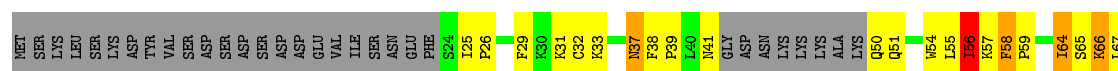
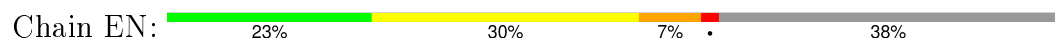
- Molecule 14: DNA-directed RNA polymerase I subunit RPA34

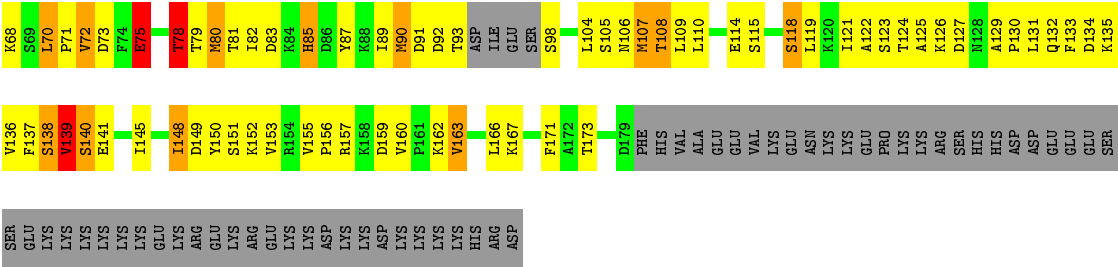


- Molecule 14: DNA-directed RNA polymerase I subunit RPA34

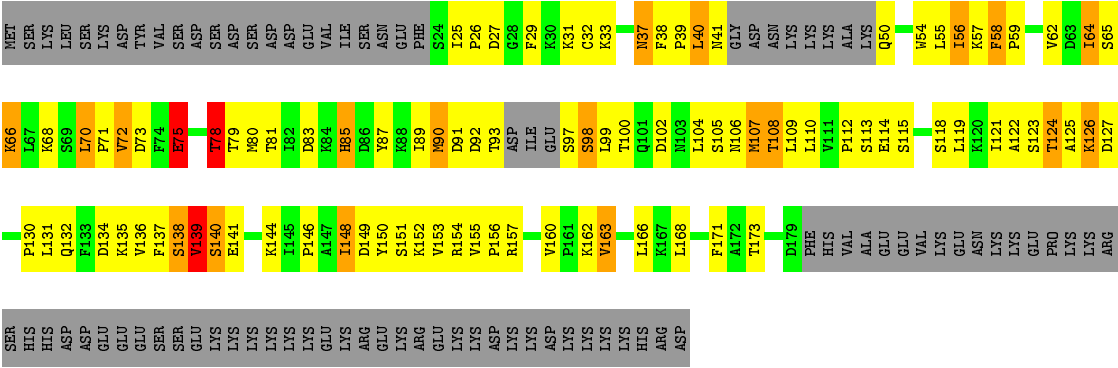


- Molecule 14: DNA-directed RNA polymerase I subunit RPA34





● Molecule 14: DNA-directed RNA polymerase I subunit RPA34



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	619.48Å 306.62Å 251.78Å 90.00° 97.50° 90.00°	Depositor
Resolution (Å)	49.69 – 5.50 49.69 – 5.50	Depositor EDS
% Data completeness (in resolution range)	99.1 (49.69-5.50) 99.1 (49.69-5.50)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 5.39Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.196 , 0.235 0.197 , 0.238	Depositor DCC
R_{free} test set	1989 reflections (1.33%)	DCC
Wilson B-factor (Å ²)	117.0	Xtriage
Anisotropy	0.698	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 214.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.34$, $\langle L^2 \rangle = 0.17$	Xtriage
Outliers	0 of 149611 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	204233	wwPDB-VP
Average B, all atoms (Å ²)	195.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% 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, 0.375 respectively for untwinned datasets, and 0.333, 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:
ZN

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	AA	0.61	0/11916	0.69	0/16097
1	BA	0.53	0/11752	0.66	0/15875
1	CA	0.66	2/11908 (0.0%)	0.72	0/16086
1	DA	0.67	2/11910 (0.0%)	0.72	0/16090
1	EA	0.68	3/11919 (0.0%)	0.74	2/16099 (0.0%)
1	FA	0.69	2/11923 (0.0%)	0.73	0/16106
2	AB	0.60	0/9389	0.70	0/12685
2	BB	0.57	1/9377 (0.0%)	0.69	0/12671
2	CB	0.70	7/9509 (0.1%)	0.75	1/12847 (0.0%)
2	DB	0.69	4/9474 (0.0%)	0.75	2/12802 (0.0%)
2	EB	0.70	2/9470 (0.0%)	0.75	1/12796 (0.0%)
2	FB	0.70	1/9475 (0.0%)	0.75	1/12802 (0.0%)
3	AC	0.61	0/2465	0.70	0/3342
3	BC	0.53	0/2465	0.66	0/3342
3	CC	0.68	0/2465	0.73	0/3342
3	DC	0.67	0/2465	0.72	0/3342
3	EC	0.73	0/2465	0.76	0/3342
3	FC	0.70	0/2465	0.73	0/3342
4	AD	0.58	0/465	0.69	0/630
4	BD	0.52	0/465	0.68	0/630
4	CD	0.69	0/465	0.76	0/630
4	DD	0.64	0/465	0.75	0/630
4	ED	0.67	0/465	0.74	0/630
4	FD	0.71	0/465	0.78	0/630
5	AE	0.54	0/1796	0.66	0/2416
5	BE	0.49	0/1796	0.64	0/2416
5	CE	0.60	0/1796	0.71	2/2416 (0.1%)
5	DE	0.60	0/1796	0.72	2/2416 (0.1%)
5	EE	0.59	0/1796	0.69	0/2416
5	FE	0.64	0/1796	0.71	0/2416
6	AF	0.56	0/821	0.64	0/1106
6	BF	0.50	0/821	0.59	0/1106

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	CF	0.66	0/830	0.68	0/1118
6	DF	0.64	0/830	0.68	0/1118
6	EF	0.66	0/830	0.68	0/1118
6	FF	0.65	0/830	0.68	0/1118
7	AG	0.59	0/1637	0.72	1/2226 (0.0%)
7	AO	0.83	0/417	0.78	0/562
7	BG	0.52	0/1577	0.67	0/2145
7	BO	0.84	0/408	0.78	0/550
7	CG	0.68	0/1637	0.76	1/2226 (0.0%)
7	CO	1.02	3/402 (0.7%)	0.93	0/542
7	DG	0.66	0/1637	0.77	1/2226 (0.0%)
7	DO	0.95	0/417	0.91	0/562
7	EG	0.65	0/1637	0.73	2/2226 (0.1%)
7	EO	0.94	0/417	0.86	0/562
7	FG	0.70	0/1637	0.79	2/2226 (0.1%)
7	FO	0.97	2/417 (0.5%)	0.90	0/562
8	AH	0.70	0/1081	0.72	0/1463
8	BH	0.52	0/1070	0.63	0/1449
8	CH	0.70	0/1070	0.72	0/1449
8	DH	0.71	0/1093	0.71	0/1480
8	EH	0.73	1/1093 (0.1%)	0.75	0/1480
8	FH	0.78	0/1093	0.78	0/1480
9	AI	0.69	0/956	0.73	0/1288
9	BI	0.61	1/721 (0.1%)	0.66	0/969
9	CI	0.72	2/956 (0.2%)	0.75	1/1288 (0.1%)
9	DI	0.71	0/956	0.73	0/1288
9	EI	0.83	1/910 (0.1%)	0.77	0/1223
9	FI	0.81	2/956 (0.2%)	0.75	0/1288
10	AJ	0.60	0/567	0.64	0/761
10	BJ	0.59	0/578	0.65	0/775
10	CJ	0.72	0/567	0.69	0/761
10	DJ	0.64	0/578	0.67	0/775
10	EJ	0.74	0/567	0.71	0/761
10	FJ	0.71	1/567 (0.2%)	0.70	0/761
11	AK	0.64	0/804	0.69	0/1083
11	BK	0.50	0/796	0.63	0/1072
11	CK	0.69	0/804	0.70	0/1083
11	DK	0.64	0/804	0.69	0/1083
11	EK	0.68	0/796	0.71	0/1072
11	FK	0.66	0/796	0.70	0/1072
12	AL	0.71	0/354	0.74	0/468
12	BL	0.64	1/354 (0.3%)	0.71	0/468
12	CL	0.77	0/354	0.79	0/468

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
12	DL	0.71	1/354 (0.3%)	0.77	0/468
12	EL	0.83	1/354 (0.3%)	0.85	0/468
12	FL	0.72	0/354	0.75	0/468
13	AM	0.68	0/879	0.73	0/1180
13	BM	0.66	0/879	0.73	0/1180
13	CM	0.77	0/879	0.76	0/1180
13	DM	0.75	0/879	0.75	0/1180
13	EM	0.78	2/885 (0.2%)	0.78	0/1188
13	FM	0.79	1/885 (0.1%)	0.79	0/1188
14	AN	0.68	0/1148	0.76	1/1546 (0.1%)
14	BN	0.64	0/1151	0.77	1/1552 (0.1%)
14	CN	0.76	0/1159	0.82	1/1563 (0.1%)
14	DN	0.73	0/1167	0.82	0/1574
14	EN	0.78	0/1161	0.82	1/1566 (0.1%)
14	FN	0.76	1/1167 (0.1%)	0.82	0/1574
All	All	0.66	44/208122 (0.0%)	0.72	23/281066 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	EA	0	1

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	FO	294	GLU	CB-CG	7.84	1.67	1.52
1	EA	65	CYS	CB-SG	-7.74	1.69	1.82
9	EI	33	CYS	CB-SG	-7.71	1.69	1.82
1	EA	75	HIS	CA-CB	-7.70	1.37	1.53
7	FO	294	GLU	CG-CD	6.88	1.62	1.51

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	FG	11	ARG	NE-CZ-NH1	9.99	125.30	120.30
7	DG	11	ARG	NE-CZ-NH1	9.12	124.86	120.30
1	EA	75	HIS	CG-ND1-CE1	9.08	120.91	108.20
7	CG	11	ARG	NE-CZ-NH1	8.63	124.62	120.30
7	AG	11	ARG	NE-CZ-NH1	8.54	124.57	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	EA	75	HIS	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	11703	0	11787	744	0
1	BA	11540	0	11624	709	0
1	CA	11695	0	11780	785	0
1	DA	11697	0	11775	791	0
1	EA	11706	0	11788	781	0
1	FA	11709	0	11790	792	0
2	AB	9187	0	9100	594	0
2	BB	9175	0	9074	571	0
2	CB	9304	0	9216	623	0
2	DB	9269	0	9175	644	0
2	EB	9265	0	9179	642	0
2	FB	9270	0	9180	644	0
3	AC	2413	0	2404	153	0
3	BC	2413	0	2404	145	0
3	CC	2413	0	2404	172	0
3	DC	2413	0	2404	170	0
3	EC	2413	0	2404	160	0
3	FC	2413	0	2404	161	0
4	AD	459	0	462	25	0
4	BD	459	0	462	32	0
4	CD	459	0	462	26	0
4	DD	459	0	462	26	0
4	ED	459	0	462	29	0
4	FD	459	0	462	32	0
5	AE	1760	0	1788	79	0
5	BE	1760	0	1788	84	0
5	CE	1760	0	1788	83	0
5	DE	1760	0	1788	98	0
5	EE	1760	0	1788	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	FE	1760	0	1788	101	0
6	AF	807	0	827	43	0
6	BF	807	0	827	43	0
6	CF	816	0	833	40	0
6	DF	816	0	833	37	0
6	EF	816	0	833	42	0
6	FF	816	0	833	39	0
7	AG	1599	0	1602	112	0
7	AO	413	0	389	47	0
7	BG	1539	0	1552	106	0
7	BO	404	0	383	47	0
7	CG	1599	0	1602	101	0
7	CO	398	0	378	42	0
7	DG	1599	0	1602	115	0
7	DO	413	0	389	34	0
7	EG	1599	0	1602	116	0
7	EO	413	0	389	47	0
7	FG	1599	0	1602	112	0
7	FO	413	0	389	38	0
8	AH	1063	0	1034	58	0
8	BH	1052	0	1021	59	0
8	CH	1052	0	1021	70	0
8	DH	1075	0	1046	72	0
8	EH	1075	0	1046	63	0
8	FH	1075	0	1046	63	0
9	AI	943	0	929	62	0
9	BI	716	0	709	37	0
9	CI	943	0	929	63	0
9	DI	943	0	929	64	0
9	EI	898	0	880	54	0
9	FI	943	0	929	65	0
10	AJ	558	0	572	42	0
10	BJ	569	0	585	37	0
10	CJ	558	0	572	43	0
10	DJ	569	0	585	39	0
10	EJ	558	0	572	35	0
10	FJ	558	0	572	39	0
11	AK	793	0	790	41	0
11	BK	786	0	782	42	0
11	CK	793	0	790	46	0
11	DK	793	0	790	50	0
11	EK	786	0	782	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	FK	786	0	782	45	0
12	AL	352	0	374	48	0
12	BL	352	0	374	25	0
12	CL	352	0	374	42	0
12	DL	352	0	374	42	0
12	EL	352	0	374	34	0
12	FL	352	0	374	45	0
13	AM	863	0	864	59	0
13	BM	863	0	864	77	0
13	CM	863	0	864	61	0
13	DM	863	0	864	58	0
13	EM	869	0	869	67	0
13	FM	869	0	869	71	0
14	AN	1127	0	1133	85	0
14	BN	1130	0	1138	79	0
14	CN	1137	0	1148	84	0
14	DN	1146	0	1153	78	0
14	EN	1140	0	1150	77	0
14	FN	1146	0	1155	78	0
15	AA	2	0	0	0	0
15	AB	1	0	0	0	0
15	AI	2	0	0	0	0
15	AJ	1	0	0	0	0
15	AL	1	0	0	0	0
15	BA	2	0	0	0	0
15	BB	1	0	0	0	0
15	BI	2	0	0	0	0
15	BJ	1	0	0	0	0
15	BL	1	0	0	0	0
15	CA	2	0	0	0	0
15	CB	1	0	0	0	0
15	CI	2	0	0	0	0
15	CJ	1	0	0	0	0
15	CL	1	0	0	0	0
15	DA	2	0	0	0	0
15	DB	1	0	0	0	0
15	DI	2	0	0	0	0
15	DJ	1	0	0	0	0
15	DL	1	0	0	0	0
15	EA	2	0	0	0	0
15	EB	1	0	0	0	0
15	EI	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	EJ	1	0	0	0	0
15	EL	1	0	0	0	0
15	FA	2	0	0	0	0
15	FB	1	0	0	0	0
15	FI	2	0	0	0	0
15	FJ	1	0	0	0	0
15	FL	1	0	0	0	0
All	All	204233	0	204265	11918	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 29.

The worst 5 of 11918 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)
7:FG:11:ARG:HG2	7:FG:11:ARG:HH11	1.10	1.15
7:DG:11:ARG:HH11	7:DG:11:ARG:HG3	1.13	1.11
7:EG:11:ARG:HH11	7:EG:11:ARG:HG2	1.13	1.10
7:AG:11:ARG:HG3	7:AG:11:ARG:HH11	1.14	1.10
7:CG:11:ARG:HG3	7:CG:11:ARG:HH11	1.11	1.08

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	AA	1470/1664 (88%)	1124 (76%)	276 (19%)	70 (5%)	3	31
1	BA	1448/1664 (87%)	1124 (78%)	259 (18%)	65 (4%)	3	33
1	CA	1469/1664 (88%)	1131 (77%)	268 (18%)	70 (5%)	3	31
1	DA	1469/1664 (88%)	1138 (78%)	263 (18%)	68 (5%)	3	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EA	1468/1664 (88%)	1127 (77%)	272 (18%)	69 (5%)	3	32
1	FA	1470/1664 (88%)	1127 (77%)	274 (19%)	69 (5%)	3	32
2	AB	1142/1203 (95%)	926 (81%)	158 (14%)	58 (5%)	2	29
2	BB	1141/1203 (95%)	923 (81%)	164 (14%)	54 (5%)	3	32
2	CB	1160/1203 (96%)	921 (79%)	171 (15%)	68 (6%)	2	26
2	DB	1155/1203 (96%)	923 (80%)	172 (15%)	60 (5%)	2	29
2	EB	1154/1203 (96%)	928 (80%)	165 (14%)	61 (5%)	2	29
2	FB	1155/1203 (96%)	925 (80%)	165 (14%)	65 (6%)	2	28
3	AC	302/335 (90%)	231 (76%)	53 (18%)	18 (6%)	2	26
3	BC	302/335 (90%)	232 (77%)	53 (18%)	17 (6%)	2	28
3	CC	302/335 (90%)	234 (78%)	52 (17%)	16 (5%)	2	29
3	DC	302/335 (90%)	233 (77%)	51 (17%)	18 (6%)	2	26
3	EC	302/335 (90%)	233 (77%)	52 (17%)	17 (6%)	2	28
3	FC	302/335 (90%)	233 (77%)	51 (17%)	18 (6%)	2	26
4	AD	54/137 (39%)	49 (91%)	5 (9%)	0	100	100
4	BD	54/137 (39%)	50 (93%)	4 (7%)	0	100	100
4	CD	54/137 (39%)	49 (91%)	5 (9%)	0	100	100
4	DD	54/137 (39%)	50 (93%)	4 (7%)	0	100	100
4	ED	54/137 (39%)	50 (93%)	3 (6%)	1 (2%)	10	52
4	FD	54/137 (39%)	49 (91%)	4 (7%)	1 (2%)	10	52
5	AE	213/215 (99%)	176 (83%)	31 (15%)	6 (3%)	6	44
5	BE	213/215 (99%)	174 (82%)	32 (15%)	7 (3%)	5	40
5	CE	213/215 (99%)	174 (82%)	33 (16%)	6 (3%)	6	44
5	DE	213/215 (99%)	176 (83%)	31 (15%)	6 (3%)	6	44
5	EE	213/215 (99%)	175 (82%)	32 (15%)	6 (3%)	6	44
5	FE	213/215 (99%)	174 (82%)	33 (16%)	6 (3%)	6	44
6	AF	96/155 (62%)	85 (88%)	10 (10%)	1 (1%)	19	64
6	BF	96/155 (62%)	87 (91%)	8 (8%)	1 (1%)	19	64
6	CF	97/155 (63%)	87 (90%)	9 (9%)	1 (1%)	19	64
6	DF	97/155 (63%)	85 (88%)	11 (11%)	1 (1%)	19	64
6	EF	97/155 (63%)	88 (91%)	8 (8%)	1 (1%)	19	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles		
6	FF	97/155 (63%)	88 (91%)	7 (7%)	2 (2%)	9	50	
7	AG	198/326 (61%)	143 (72%)	40 (20%)	15 (8%)	1	20	
7	AO	50/326 (15%)	31 (62%)	11 (22%)	8 (16%)	0	5	
7	BG	191/326 (59%)	139 (73%)	37 (19%)	15 (8%)	1	19	
7	BO	49/326 (15%)	33 (67%)	11 (22%)	5 (10%)	1	13	
7	CG	198/326 (61%)	145 (73%)	38 (19%)	15 (8%)	1	20	
7	CO	48/326 (15%)	32 (67%)	10 (21%)	6 (12%)	0	8	
7	DG	198/326 (61%)	142 (72%)	38 (19%)	18 (9%)	1	16	
7	DO	50/326 (15%)	31 (62%)	12 (24%)	7 (14%)	0	6	
7	EG	198/326 (61%)	144 (73%)	40 (20%)	14 (7%)	1	21	
7	EO	50/326 (15%)	30 (60%)	13 (26%)	7 (14%)	0	6	
7	FG	198/326 (61%)	141 (71%)	40 (20%)	17 (9%)	1	17	
7	FO	50/326 (15%)	34 (68%)	13 (26%)	3 (6%)	2	26	
8	AH	128/146 (88%)	106 (83%)	19 (15%)	3 (2%)	8	48	
8	BH	127/146 (87%)	105 (83%)	17 (13%)	5 (4%)	4	36	
8	CH	127/146 (87%)	106 (84%)	18 (14%)	3 (2%)	7	47	
8	DH	130/146 (89%)	104 (80%)	20 (15%)	6 (5%)	3	32	
8	EH	130/146 (89%)	106 (82%)	17 (13%)	7 (5%)	2	29	
8	FH	130/146 (89%)	106 (82%)	19 (15%)	5 (4%)	4	37	
9	AI	122/125 (98%)	91 (75%)	28 (23%)	3 (2%)	7	46	
9	BI	91/125 (73%)	70 (77%)	19 (21%)	2 (2%)	8	49	
9	CI	122/125 (98%)	93 (76%)	25 (20%)	4 (3%)	5	40	
9	DI	122/125 (98%)	93 (76%)	26 (21%)	3 (2%)	7	46	
9	EI	113/125 (90%)	85 (75%)	25 (22%)	3 (3%)	6	44	
9	FI	122/125 (98%)	92 (75%)	25 (20%)	5 (4%)	3	34	
10	AJ	66/70 (94%)	45 (68%)	16 (24%)	5 (8%)	1	20	
10	BJ	67/70 (96%)	45 (67%)	18 (27%)	4 (6%)	2	26	
10	CJ	66/70 (94%)	47 (71%)	15 (23%)	4 (6%)	2	25	
10	DJ	67/70 (96%)	47 (70%)	16 (24%)	4 (6%)	2	26	
10	EJ	66/70 (94%)	47 (71%)	15 (23%)	4 (6%)	2	25	
10	FJ	66/70 (94%)	47 (71%)	16 (24%)	3 (4%)	3	33	

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	AK	99/142 (70%)	79 (80%)	17 (17%)	3 (3%)	5	42
11	BK	98/142 (69%)	80 (82%)	15 (15%)	3 (3%)	5	42
11	CK	99/142 (70%)	85 (86%)	11 (11%)	3 (3%)	5	42
11	DK	99/142 (70%)	81 (82%)	14 (14%)	4 (4%)	4	35
11	EK	98/142 (69%)	80 (82%)	14 (14%)	4 (4%)	3	34
11	FK	98/142 (69%)	82 (84%)	13 (13%)	3 (3%)	5	42
12	AL	42/70 (60%)	34 (81%)	5 (12%)	3 (7%)	1	21
12	BL	42/70 (60%)	33 (79%)	6 (14%)	3 (7%)	1	21
12	CL	42/70 (60%)	33 (79%)	6 (14%)	3 (7%)	1	21
12	DL	42/70 (60%)	33 (79%)	6 (14%)	3 (7%)	1	21
12	EL	42/70 (60%)	33 (79%)	6 (14%)	3 (7%)	1	21
12	FL	42/70 (60%)	34 (81%)	5 (12%)	3 (7%)	1	21
13	AM	107/415 (26%)	81 (76%)	17 (16%)	9 (8%)	1	17
13	BM	107/415 (26%)	81 (76%)	17 (16%)	9 (8%)	1	17
13	CM	107/415 (26%)	79 (74%)	19 (18%)	9 (8%)	1	17
13	DM	107/415 (26%)	82 (77%)	15 (14%)	10 (9%)	1	16
13	EM	108/415 (26%)	80 (74%)	18 (17%)	10 (9%)	1	16
13	FM	108/415 (26%)	80 (74%)	18 (17%)	10 (9%)	1	16
14	AN	136/233 (58%)	106 (78%)	17 (12%)	13 (10%)	1	14
14	BN	137/233 (59%)	110 (80%)	16 (12%)	11 (8%)	1	19
14	CN	137/233 (59%)	109 (80%)	17 (12%)	11 (8%)	1	19
14	DN	139/233 (60%)	112 (81%)	16 (12%)	11 (8%)	1	19
14	EN	138/233 (59%)	111 (80%)	15 (11%)	12 (9%)	1	17
14	FN	139/233 (60%)	112 (81%)	15 (11%)	12 (9%)	1	17
All	All	25348/33372 (76%)	19889 (78%)	4164 (16%)	1295 (5%)	2	29

5 of 1295 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AA	39	ASP
1	AA	547	ILE
1	AA	551	VAL
1	AA	710	SER
1	AA	851	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	AA	1310/1465 (89%)	1024 (78%)	286 (22%)	1	9
1	BA	1290/1465 (88%)	1012 (78%)	278 (22%)	1	9
1	CA	1308/1465 (89%)	1020 (78%)	288 (22%)	1	9
1	DA	1309/1465 (89%)	1019 (78%)	290 (22%)	1	9
1	EA	1309/1465 (89%)	1025 (78%)	284 (22%)	1	9
1	FA	1309/1465 (89%)	1019 (78%)	290 (22%)	1	9
2	AB	1012/1053 (96%)	780 (77%)	232 (23%)	1	8
2	BB	1010/1053 (96%)	783 (78%)	227 (22%)	1	9
2	CB	1024/1053 (97%)	778 (76%)	246 (24%)	1	7
2	DB	1020/1053 (97%)	784 (77%)	236 (23%)	1	8
2	EB	1021/1053 (97%)	782 (77%)	239 (23%)	1	7
2	FB	1021/1053 (97%)	780 (76%)	241 (24%)	1	7
3	AC	268/296 (90%)	217 (81%)	51 (19%)	2	13
3	BC	268/296 (90%)	217 (81%)	51 (19%)	2	13
3	CC	268/296 (90%)	216 (81%)	52 (19%)	2	13
3	DC	268/296 (90%)	217 (81%)	51 (19%)	2	13
3	EC	268/296 (90%)	216 (81%)	52 (19%)	2	13
3	FC	268/296 (90%)	218 (81%)	50 (19%)	2	14
4	AD	55/116 (47%)	47 (86%)	8 (14%)	4	25
4	BD	55/116 (47%)	46 (84%)	9 (16%)	3	20
4	CD	55/116 (47%)	47 (86%)	8 (14%)	4	25
4	DD	55/116 (47%)	46 (84%)	9 (16%)	3	20
4	ED	55/116 (47%)	47 (86%)	8 (14%)	4	25
4	FD	55/116 (47%)	47 (86%)	8 (14%)	4	25
5	AE	197/197 (100%)	158 (80%)	39 (20%)	1	12
5	BE	197/197 (100%)	159 (81%)	38 (19%)	2	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	CE	197/197 (100%)	157 (80%)	40 (20%)	1	11
5	DE	197/197 (100%)	157 (80%)	40 (20%)	1	11
5	EE	197/197 (100%)	157 (80%)	40 (20%)	1	11
5	FE	197/197 (100%)	156 (79%)	41 (21%)	1	10
6	AF	88/137 (64%)	75 (85%)	13 (15%)	4	24
6	BF	88/137 (64%)	75 (85%)	13 (15%)	4	24
6	CF	89/137 (65%)	73 (82%)	16 (18%)	2	15
6	DF	89/137 (65%)	74 (83%)	15 (17%)	2	19
6	EF	89/137 (65%)	75 (84%)	14 (16%)	3	22
6	FF	89/137 (65%)	73 (82%)	16 (18%)	2	15
7	AG	180/291 (62%)	131 (73%)	49 (27%)	0	5
7	AO	50/291 (17%)	29 (58%)	21 (42%)	0	0
7	BG	173/291 (60%)	128 (74%)	45 (26%)	0	5
7	BO	49/291 (17%)	33 (67%)	16 (33%)	0	2
7	CG	180/291 (62%)	131 (73%)	49 (27%)	0	5
7	CO	48/291 (16%)	35 (73%)	13 (27%)	0	5
7	DG	180/291 (62%)	132 (73%)	48 (27%)	0	5
7	DO	50/291 (17%)	32 (64%)	18 (36%)	0	1
7	EG	180/291 (62%)	133 (74%)	47 (26%)	0	5
7	EO	50/291 (17%)	33 (66%)	17 (34%)	0	2
7	FG	180/291 (62%)	130 (72%)	50 (28%)	0	4
7	FO	50/291 (17%)	36 (72%)	14 (28%)	0	4
8	AH	116/128 (91%)	86 (74%)	30 (26%)	0	5
8	BH	115/128 (90%)	87 (76%)	28 (24%)	1	7
8	CH	115/128 (90%)	84 (73%)	31 (27%)	0	5
8	DH	117/128 (91%)	86 (74%)	31 (26%)	0	5
8	EH	117/128 (91%)	84 (72%)	33 (28%)	0	3
8	FH	117/128 (91%)	85 (73%)	32 (27%)	0	4
9	AI	109/110 (99%)	84 (77%)	25 (23%)	1	8
9	BI	86/110 (78%)	67 (78%)	19 (22%)	1	9
9	CI	109/110 (99%)	83 (76%)	26 (24%)	1	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	DI	109/110 (99%)	81 (74%)	28 (26%)	0	6
9	EI	104/110 (94%)	79 (76%)	25 (24%)	1	7
9	FI	109/110 (99%)	80 (73%)	29 (27%)	0	5
10	AJ	63/65 (97%)	47 (75%)	16 (25%)	1	6
10	BJ	64/65 (98%)	49 (77%)	15 (23%)	1	7
10	CJ	63/65 (97%)	49 (78%)	14 (22%)	1	9
10	DJ	64/65 (98%)	49 (77%)	15 (23%)	1	7
10	EJ	63/65 (97%)	50 (79%)	13 (21%)	1	10
10	FJ	63/65 (97%)	49 (78%)	14 (22%)	1	9
11	AK	91/130 (70%)	66 (72%)	25 (28%)	0	4
11	BK	90/130 (69%)	66 (73%)	24 (27%)	0	5
11	CK	91/130 (70%)	67 (74%)	24 (26%)	0	5
11	DK	91/130 (70%)	66 (72%)	25 (28%)	0	4
11	EK	90/130 (69%)	66 (73%)	24 (27%)	0	5
11	FK	90/130 (69%)	65 (72%)	25 (28%)	0	4
12	AL	39/57 (68%)	27 (69%)	12 (31%)	0	3
12	BL	39/57 (68%)	27 (69%)	12 (31%)	0	3
12	CL	39/57 (68%)	27 (69%)	12 (31%)	0	3
12	DL	39/57 (68%)	27 (69%)	12 (31%)	0	3
12	EL	39/57 (68%)	27 (69%)	12 (31%)	0	3
12	FL	39/57 (68%)	27 (69%)	12 (31%)	0	3
13	AM	99/371 (27%)	73 (74%)	26 (26%)	0	5
13	BM	99/371 (27%)	74 (75%)	25 (25%)	1	6
13	CM	99/371 (27%)	74 (75%)	25 (25%)	1	6
13	DM	99/371 (27%)	74 (75%)	25 (25%)	1	6
13	EM	100/371 (27%)	73 (73%)	27 (27%)	0	5
13	FM	100/371 (27%)	75 (75%)	25 (25%)	1	6
14	AN	132/220 (60%)	96 (73%)	36 (27%)	0	4
14	BN	133/220 (60%)	98 (74%)	35 (26%)	0	5
14	CN	133/220 (60%)	95 (71%)	38 (29%)	0	3
14	DN	135/220 (61%)	97 (72%)	38 (28%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	EN	134/220 (61%)	97 (72%)	37 (28%)	0	4
14	FN	135/220 (61%)	99 (73%)	36 (27%)	0	5
All	All	22843/29562 (77%)	17621 (77%)	5222 (23%)	1	8

5 of 5222 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	CG	37	CYS
2	DB	306	LEU
2	FB	1034	GLN
8	CH	133	ASN
1	DA	506	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 426 such sidechains are listed below:

Mol	Chain	Res	Type
9	CI	124	ASN
2	DB	893	ASN
2	FB	896	GLN
13	CM	57	ASN
1	DA	1299	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 42 ligands modelled in this entry, 42 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
1	EA	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	EA	1261:VAL	C	1262:LEU	N	2.28

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	AA	1484/1664 (89%)	-0.15	11 (0%) 89 85	174, 197, 249, 308	0
1	BA	1462/1664 (87%)	0.05	19 (1%) 79 73	242, 262, 287, 314	0
1	CA	1483/1664 (89%)	-0.24	7 (0%) 91 88	143, 164, 201, 253	0
1	DA	1483/1664 (89%)	-0.25	4 (0%) 94 92	147, 170, 215, 278	0
1	EA	1484/1664 (89%)	-0.24	4 (0%) 94 92	149, 171, 207, 250	0
1	FA	1484/1664 (89%)	-0.28	2 (0%) 95 95	142, 160, 203, 262	0
2	AB	1154/1203 (95%)	-0.16	5 (0%) 93 90	179, 212, 250, 276	0
2	BB	1153/1203 (95%)	-0.09	9 (0%) 87 84	233, 245, 265, 279	0
2	CB	1170/1203 (97%)	-0.27	3 (0%) 94 92	144, 169, 196, 227	0
2	DB	1165/1203 (96%)	-0.22	2 (0%) 95 94	148, 169, 191, 223	0
2	EB	1164/1203 (96%)	-0.33	0 100 100	148, 162, 188, 225	0
2	FB	1165/1203 (96%)	-0.26	2 (0%) 95 94	142, 164, 191, 213	0
3	AC	304/335 (90%)	-0.06	0 100 100	190, 209, 237, 253	0
3	BC	304/335 (90%)	0.21	7 (2%) 64 58	248, 278, 311, 332	0
3	CC	304/335 (90%)	-0.18	0 100 100	162, 175, 191, 207	0
3	DC	304/335 (90%)	-0.14	2 (0%) 89 85	167, 182, 197, 206	0
3	EC	304/335 (90%)	-0.23	1 (0%) 94 92	158, 173, 190, 203	0
3	FC	304/335 (90%)	-0.20	0 100 100	154, 170, 187, 198	0
4	AD	58/137 (42%)	-0.03	1 (1%) 73 67	207, 243, 266, 270	0
4	BD	58/137 (42%)	0.43	3 (5%) 31 29	262, 281, 301, 303	0
4	CD	58/137 (42%)	-0.25	1 (1%) 73 67	171, 184, 195, 200	0
4	DD	58/137 (42%)	-0.19	1 (1%) 73 67	177, 190, 204, 207	0
4	ED	58/137 (42%)	-0.28	1 (1%) 73 67	185, 202, 214, 215	0
4	FD	58/137 (42%)	-0.26	0 100 100	162, 186, 211, 212	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
5	AE	215/215 (100%)	-0.42	1 (0%) 91 88	186, 214, 234, 243	0
5	BE	215/215 (100%)	0.06	2 (0%) 85 81	255, 281, 296, 307	0
5	CE	215/215 (100%)	-0.52	0 100 100	152, 178, 194, 206	0
5	DE	215/215 (100%)	-0.37	0 100 100	156, 187, 209, 222	0
5	EE	215/215 (100%)	-0.38	0 100 100	158, 189, 211, 228	0
5	FE	215/215 (100%)	-0.43	0 100 100	149, 179, 199, 212	0
6	AF	98/155 (63%)	-0.37	0 100 100	181, 190, 240, 243	0
6	BF	98/155 (63%)	-0.10	0 100 100	251, 265, 299, 302	0
6	CF	99/155 (63%)	-0.37	0 100 100	148, 157, 185, 188	0
6	DF	99/155 (63%)	-0.36	0 100 100	152, 162, 201, 207	0
6	EF	99/155 (63%)	-0.44	0 100 100	154, 168, 211, 214	0
6	FF	99/155 (63%)	-0.33	0 100 100	144, 152, 209, 213	0
7	AG	202/326 (61%)	-0.02	2 (0%) 84 79	199, 249, 286, 305	0
7	AO	52/326 (15%)	0.15	1 (1%) 70 64	209, 235, 287, 294	0
7	BG	195/326 (59%)	0.42	7 (3%) 46 42	259, 290, 311, 319	0
7	BO	51/326 (15%)	-0.01	1 (1%) 68 62	244, 259, 301, 312	0
7	CG	202/326 (61%)	-0.29	0 100 100	171, 186, 215, 221	0
7	CO	50/326 (15%)	-0.04	1 (2%) 68 62	159, 187, 235, 247	0
7	DG	202/326 (61%)	0.00	1 (0%) 91 88	165, 205, 241, 251	0
7	DO	52/326 (15%)	0.03	1 (1%) 70 64	167, 197, 258, 276	0
7	EG	202/326 (61%)	-0.06	1 (0%) 91 88	181, 209, 227, 234	0
7	EO	52/326 (15%)	-0.24	0 100 100	168, 190, 233, 246	0
7	FG	202/326 (61%)	-0.01	0 100 100	158, 197, 226, 232	0
7	FO	52/326 (15%)	-0.24	0 100 100	163, 191, 241, 257	0
8	AH	132/146 (90%)	-0.27	0 100 100	180, 190, 197, 206	0
8	BH	131/146 (89%)	0.47	2 (1%) 76 70	282, 313, 328, 335	0
8	CH	131/146 (89%)	-0.15	1 (0%) 87 84	162, 175, 183, 187	0
8	DH	134/146 (91%)	-0.25	0 100 100	167, 182, 196, 231	0
8	EH	134/146 (91%)	-0.20	0 100 100	164, 185, 201, 209	0
8	FH	134/146 (91%)	-0.18	0 100 100	151, 162, 173, 203	0
9	AI	124/125 (99%)	0.09	0 100 100	189, 209, 254, 260	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
9	BI	97/125 (77%)	0.22	1 (1%) 84 79	254, 264, 300, 307	0
9	CI	124/125 (99%)	-0.09	0 100 100	162, 179, 201, 206	0
9	DI	124/125 (99%)	-0.02	0 100 100	166, 187, 207, 214	0
9	EI	117/125 (93%)	-0.17	0 100 100	160, 177, 203, 235	0
9	FI	124/125 (99%)	-0.19	0 100 100	159, 181, 203, 211	0
10	AJ	68/70 (97%)	-0.24	0 100 100	194, 209, 227, 240	0
10	BJ	69/70 (98%)	0.00	2 (2%) 55 49	245, 263, 275, 279	0
10	CJ	68/70 (97%)	-0.30	0 100 100	162, 172, 183, 195	0
10	DJ	69/70 (98%)	-0.34	0 100 100	164, 174, 184, 191	0
10	EJ	68/70 (97%)	-0.42	0 100 100	155, 165, 177, 180	0
10	FJ	68/70 (97%)	-0.38	0 100 100	155, 165, 179, 186	0
11	AK	101/142 (71%)	-0.10	0 100 100	186, 193, 213, 221	0
11	BK	100/142 (70%)	0.02	0 100 100	259, 288, 305, 311	0
11	CK	101/142 (71%)	-0.22	0 100 100	157, 168, 182, 190	0
11	DK	101/142 (71%)	-0.36	0 100 100	161, 175, 190, 197	0
11	EK	100/142 (70%)	-0.38	0 100 100	154, 168, 182, 190	0
11	FK	100/142 (70%)	-0.41	0 100 100	150, 159, 174, 180	0
12	AL	44/70 (62%)	-0.04	0 100 100	201, 238, 253, 256	0
12	BL	44/70 (62%)	-0.08	0 100 100	241, 248, 255, 256	0
12	CL	44/70 (62%)	-0.26	0 100 100	163, 184, 192, 193	0
12	DL	44/70 (62%)	-0.16	0 100 100	167, 184, 191, 195	0
12	EL	44/70 (62%)	-0.40	0 100 100	158, 176, 188, 191	0
12	FL	44/70 (62%)	-0.27	0 100 100	159, 183, 193, 196	0
13	AM	109/415 (26%)	0.16	1 (0%) 85 81	228, 248, 259, 263	0
13	BM	109/415 (26%)	0.26	2 (1%) 71 66	247, 257, 278, 284	0
13	CM	109/415 (26%)	-0.11	1 (0%) 85 81	181, 196, 202, 205	0
13	DM	109/415 (26%)	0.09	1 (0%) 85 81	181, 197, 211, 218	0
13	EM	110/415 (26%)	-0.08	0 100 100	173, 189, 198, 203	0
13	FM	110/415 (26%)	0.01	1 (0%) 85 81	177, 191, 198, 200	0
14	AN	142/233 (60%)	0.16	2 (1%) 78 72	194, 234, 266, 270	0
14	BN	143/233 (61%)	0.29	3 (2%) 67 61	254, 266, 283, 297	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
14	CN	143/233 (61%)	-0.24	0 100 100	166, 187, 208, 219	0
14	DN	145/233 (62%)	-0.21	1 (0%) 89 85	167, 197, 213, 220	0
14	EN	144/233 (61%)	-0.35	0 100 100	160, 184, 203, 214	0
14	FN	145/233 (62%)	-0.26	0 100 100	157, 184, 204, 214	0
All	All	25720/33372 (77%)	-0.18	121 (0%) 91 88	142, 184, 273, 335	0

The worst 5 of 121 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	BD	12	THR	6.6
1	BA	634	ASN	3.7
3	BC	184	VAL	3.6
2	BB	441	LYS	3.5
1	AA	249	THR	3.4

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
15	ZN	AJ	3001	1/1	0.93	0.25	-0.41	197,197,197,197	0
15	ZN	FB	3001	1/1	0.97	0.19	-0.89	163,163,163,163	0
15	ZN	BI	3002	1/1	0.91	0.30	-0.97	311,311,311,311	0
15	ZN	EA	3001	1/1	0.98	0.16	-1.11	171,171,171,171	0
15	ZN	CJ	3001	1/1	0.99	0.25	-1.12	164,164,164,164	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
15	ZN	AB	3001	1/1	0.97	0.12	-1.18	214,214,214,214	0
15	ZN	CI	3002	1/1	0.97	0.11	-1.22	195,195,195,195	0
15	ZN	BB	3001	1/1	0.98	0.17	-1.27	252,252,252,252	0
15	ZN	BJ	3001	1/1	0.88	0.15	-1.31	267,267,267,267	0
15	ZN	AA	3002	1/1	0.97	0.10	-1.43	262,262,262,262	0
15	ZN	EL	3001	1/1	0.98	0.09	-1.50	176,176,176,176	0
15	ZN	DA	3002	1/1	0.97	0.08	-1.54	211,211,211,211	0
15	ZN	CB	3001	1/1	0.99	0.13	-1.55	167,167,167,167	0
15	ZN	AI	3002	1/1	0.95	0.10	-1.59	213,213,213,213	0
15	ZN	DA	3001	1/1	0.98	0.12	-1.63	177,177,177,177	0
15	ZN	BI	3001	1/1	0.98	0.09	-1.63	257,257,257,257	0
15	ZN	EB	3001	1/1	0.97	0.15	-1.64	169,169,169,169	0
15	ZN	CA	3002	1/1	0.96	0.11	-1.64	205,205,205,205	0
15	ZN	BA	3002	1/1	0.91	0.15	-1.69	283,283,283,283	0
15	ZN	FA	3001	1/1	0.98	0.13	-1.70	178,178,178,178	0
15	ZN	DL	3001	1/1	0.99	0.07	-1.75	184,184,184,184	0
15	ZN	FL	3001	1/1	0.97	0.10	-1.78	184,184,184,184	0
15	ZN	EJ	3001	1/1	0.99	0.20	-1.79	159,159,159,159	0
15	ZN	AL	3001	1/1	0.98	0.05	-1.82	241,241,241,241	0
15	ZN	CA	3001	1/1	0.96	0.09	-1.88	168,168,168,168	0
15	ZN	CL	3001	1/1	0.98	0.07	-1.95	185,185,185,185	0
15	ZN	BL	3001	1/1	0.97	0.07	-1.97	245,245,245,245	0
15	ZN	BA	3001	1/1	0.94	0.11	-2.00	248,248,248,248	0
15	ZN	EI	3001	1/1	0.97	0.08	-2.00	187,187,187,187	0
15	ZN	FA	3002	1/1	0.93	0.12	-2.05	202,202,202,202	0
15	ZN	AA	3001	1/1	0.96	0.07	-2.07	222,222,222,222	0
15	ZN	AI	3001	1/1	0.92	0.05	-2.07	247,247,247,247	0
15	ZN	FJ	3001	1/1	0.99	0.15	-2.12	157,157,157,157	0
15	ZN	EI	3002	1/1	0.96	0.06	-2.18	198,198,198,198	0
15	ZN	CI	3001	1/1	0.97	0.07	-2.23	194,194,194,194	0
15	ZN	EA	3002	1/1	0.94	0.11	-2.30	215,215,215,215	0
15	ZN	DJ	3001	1/1	0.98	0.22	-2.36	167,167,167,167	0
15	ZN	DI	3002	1/1	0.86	0.10	-2.40	195,195,195,195	0
15	ZN	FI	3001	1/1	0.97	0.09	-2.50	189,189,189,189	0
15	ZN	DB	3001	1/1	0.97	0.18	-2.52	172,172,172,172	0
15	ZN	FI	3002	1/1	0.98	0.07	-2.59	190,190,190,190	0
15	ZN	DI	3001	1/1	1.00	0.10	-3.11	195,195,195,195	0

6.5 Other polymers ⓘ

There are no such residues in this entry.