



## wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Feb 3, 2020 – 02:12 PM EST

PDB ID : 6TBM  
EMDB ID: : EMD-10446  
Title : Structure of SAGA bound to TBP, including Spt8 and DUB  
Authors : Papai, G.; Frechard, A.; Kolesnikova, O.; Crucifix, C.; Schultz, P.; Ben-Shem, A.  
Deposited on : 2019-11-01  
Resolution : 20.00 Å(reported)

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report  
for a publicly released PDB/EMDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

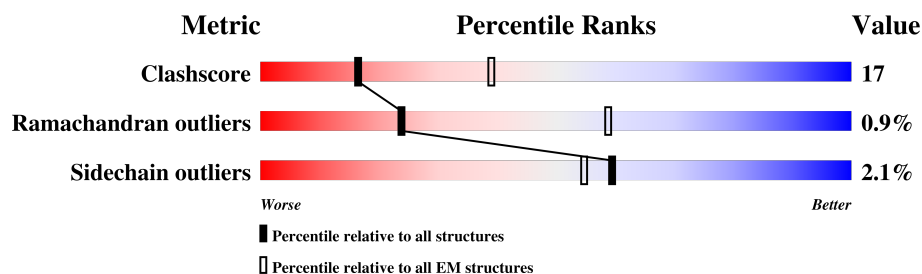
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 20.00 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)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	M	240	
2	A	448	
3	C	698	
4	F	517	
5	D	341	
6	E	1191	
7	J	217	
8	K	609	
9	G	722	

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Mol	Chain	Length	Quality of chain
10	H	485	
11	I	153	
12	L	3825	
13	B	722	
14	N	400	
15	R	76	
16	Q	502	
17	O	123	
18	P	96	

## 2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 48800 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 TATA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	M	180	Total	C	N	O	S	0	0
			1415	921	242	246	6		

- Molecule 2 is a protein called Transcriptional coactivator HFI1/ADA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	173	Total	C	N	O	S	0	0
			1300	816	228	250	6		

- Molecule 3 is a protein called Subunit of SAGA histone acetyltransferase complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	95	Total	C	N	O	S	0	0
			761	480	142	133	6		

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	645	LEU	-	expression tag	UNP C4QZ39
C	646	GLU	-	expression tag	UNP C4QZ39
C	647	GLY	-	expression tag	UNP C4QZ39
C	648	GLY	-	expression tag	UNP C4QZ39
C	649	GLY	-	expression tag	UNP C4QZ39
C	650	GLY	-	expression tag	UNP C4QZ39
C	651	SER	-	expression tag	UNP C4QZ39
C	652	MET	-	expression tag	UNP C4QZ39
C	653	ASP	-	expression tag	UNP C4QZ39
C	654	GLU	-	expression tag	UNP C4QZ39
C	655	LYS	-	expression tag	UNP C4QZ39
C	656	THR	-	expression tag	UNP C4QZ39
C	657	THR	-	expression tag	UNP C4QZ39
C	658	GLY	-	expression tag	UNP C4QZ39
C	659	TRP	-	expression tag	UNP C4QZ39

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Chain	Residue	Modelled	Actual	Comment	Reference
C	660	ARG	-	expression tag	UNP C4QZ39
C	661	GLY	-	expression tag	UNP C4QZ39
C	662	GLY	-	expression tag	UNP C4QZ39
C	663	HIS	-	expression tag	UNP C4QZ39
C	664	VAL	-	expression tag	UNP C4QZ39
C	665	VAL	-	expression tag	UNP C4QZ39
C	666	GLU	-	expression tag	UNP C4QZ39
C	667	GLY	-	expression tag	UNP C4QZ39
C	668	LEU	-	expression tag	UNP C4QZ39
C	669	ALA	-	expression tag	UNP C4QZ39
C	670	GLY	-	expression tag	UNP C4QZ39
C	671	GLU	-	expression tag	UNP C4QZ39
C	672	LEU	-	expression tag	UNP C4QZ39
C	673	GLU	-	expression tag	UNP C4QZ39
C	674	GLN	-	expression tag	UNP C4QZ39
C	675	LEU	-	expression tag	UNP C4QZ39
C	676	ARG	-	expression tag	UNP C4QZ39
C	677	ALA	-	expression tag	UNP C4QZ39
C	678	ARG	-	expression tag	UNP C4QZ39
C	679	LEU	-	expression tag	UNP C4QZ39
C	680	GLU	-	expression tag	UNP C4QZ39
C	681	HIS	-	expression tag	UNP C4QZ39
C	682	HIS	-	expression tag	UNP C4QZ39
C	683	PRO	-	expression tag	UNP C4QZ39
C	684	GLN	-	expression tag	UNP C4QZ39
C	685	GLY	-	expression tag	UNP C4QZ39
C	686	GLN	-	expression tag	UNP C4QZ39
C	687	ARG	-	expression tag	UNP C4QZ39
C	688	GLU	-	expression tag	UNP C4QZ39
C	689	PRO	-	expression tag	UNP C4QZ39
C	690	GLY	-	expression tag	UNP C4QZ39
C	691	GLY	-	expression tag	UNP C4QZ39
C	692	SER	-	expression tag	UNP C4QZ39
C	693	HIS	-	expression tag	UNP C4QZ39
C	694	HIS	-	expression tag	UNP C4QZ39
C	695	HIS	-	expression tag	UNP C4QZ39
C	696	HIS	-	expression tag	UNP C4QZ39
C	697	HIS	-	expression tag	UNP C4QZ39
C	698	HIS	-	expression tag	UNP C4QZ39

- Molecule 4 is a protein called Spt20.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	210	Total	C	N	O	S	0	0
			1682	1071	292	315	4		

- Molecule 5 is a protein called Subunit of the SAGA and SAGA-like transcriptional regulatory complexes, interacts with Spt15p to act.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	209	Total	C	N	O	S	0	0
			1616	1016	298	295	7		

- Molecule 6 is a protein called Subunit of the SAGA transcriptional regulatory complex, involved in proper assembly of the complex.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	154	Total	C	N	O	S	0	0
			1232	784	208	233	7		

- Molecule 7 is a protein called Transcription initiation factor TFIID subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	96	Total	C	N	O	S	0	0
			768	489	120	156	3		

- Molecule 8 is a protein called Subunit (61/68 kDa) of TFIID and SAGA complexes.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	154	Total	C	N	O	S	0	0
			1192	747	216	226	3		

- Molecule 9 is a protein called Subunit (90 kDa) of TFIID and SAGA complexes.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	522	Total	C	N	O	S	0	0
			4075	2581	719	756	19		

- Molecule 10 is a protein called Subunit (60 kDa) of TFIID and SAGA complexes.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	421	Total	C	N	O	S	0	0
			3263	2084	556	617	6		

- Molecule 11 is a protein called Subunit (17 kDa) of TFIID and SAGA complexes, involved

in RNA polymerase II transcription initiation.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	123	Total	C	N	O	S	0	0
			981	632	169	178	2		

- Molecule 12 is a protein called Transcription-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	2968	Total	C	N	O	S	0	0
			22318	14296	3864	4071	87		

- Molecule 13 is a protein called Transcriptional regulator involved in glucose repression of Gal4p-regulated genes.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	B	76	Total	C	N	O	0	0
			373	221	76	76		

- Molecule 14 is a protein called Spt8.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	335	Total	C	N	O	0	0
			1648	978	335	335		

- Molecule 15 is a protein called Polyubiquitin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	76	Total	C	N	O	S	2	0
			611	384	105	121	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	76	GLZ	-	expression tag	UNP J3QS39

- Molecule 16 is a protein called Ubiquitin carboxyl-terminal hydrolase.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	482	Total	C	N	O	S	0	0
			3817	2410	657	719	31		

- Molecule 17 is a protein called SAGA-associated factor 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	117	Total	C	N	O	S	0	0
			922	563	169	184	6		

- Molecule 18 is a protein called Transcription and mRNA export factor SUS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	90	Total	C	N	O	S	0	0
			735	470	122	142	1		

- Molecule 19 is water.

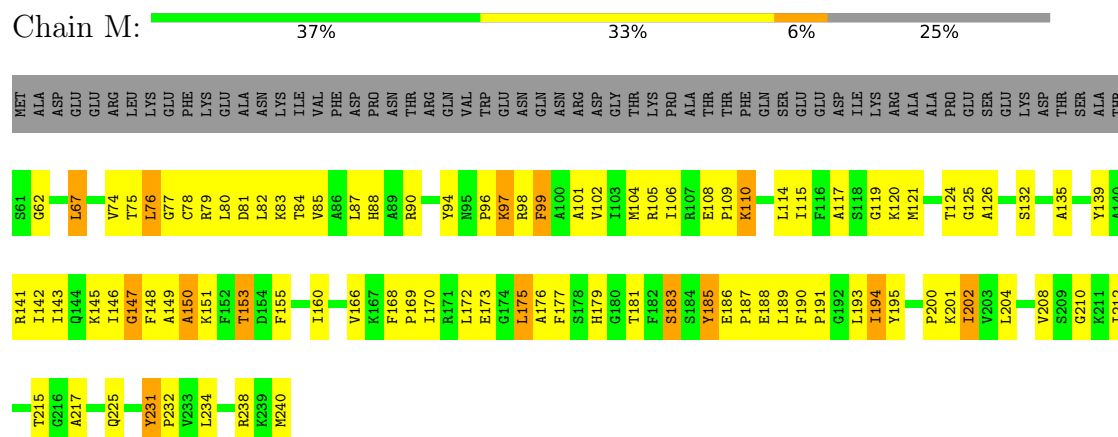
Mol	Chain	Residues	Atoms		AltConf
19	R	83	Total	O	0
			83	83	
19	Q	8	Total	O	0
			8	8	



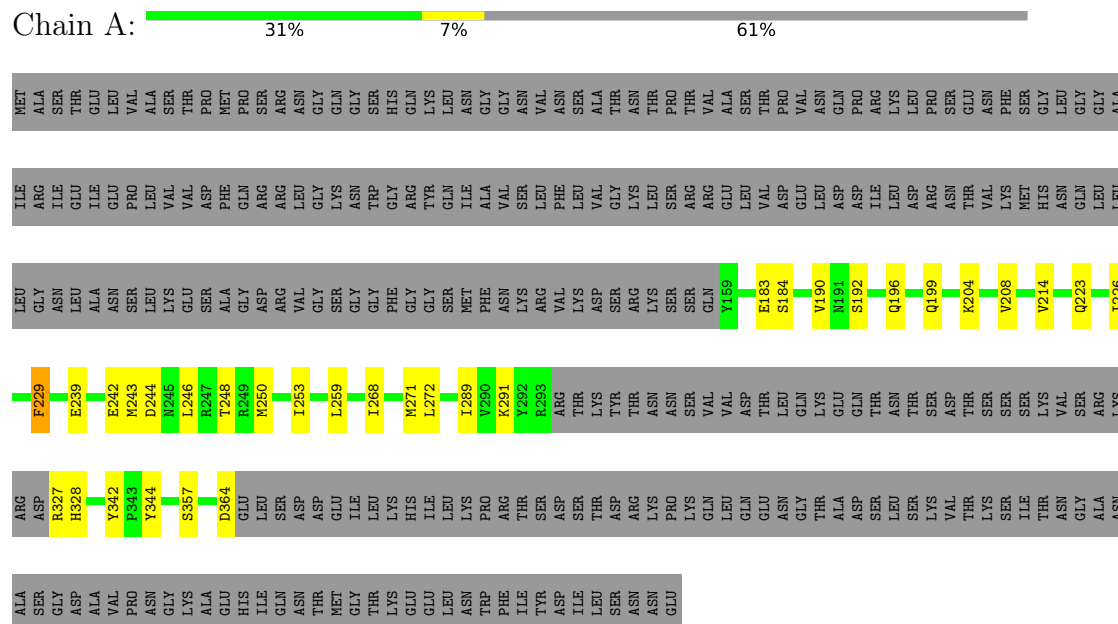
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: TATA-binding protein



- Molecule 2: Transcriptional coactivator HFI1/ADA1



- Molecule 3: Subunit of SAGA histone acetyltransferase complex



[illegible]

- Molecule 4: Spt20

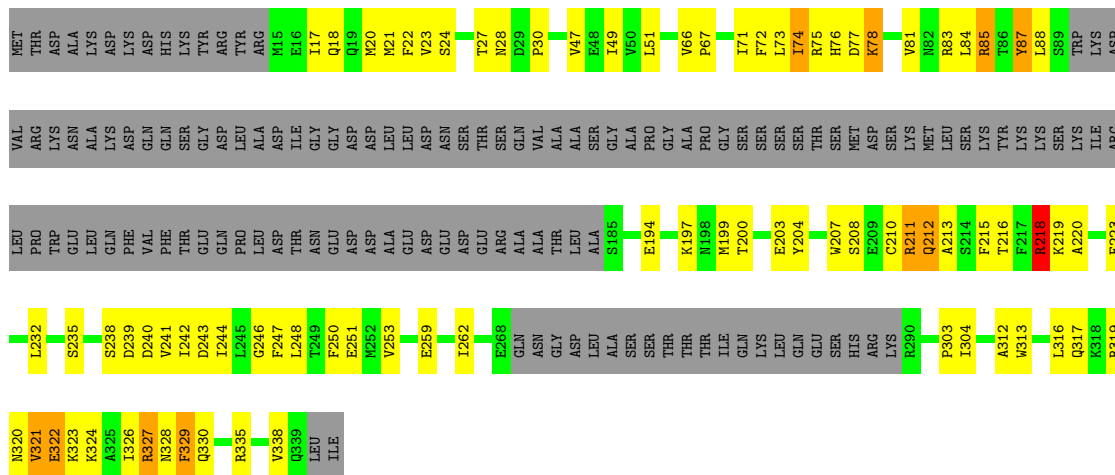
Chain F:  33% 7% 59%

GLN	ASN	ASP	THR	THR	LVS	MET
HIS	LEU	ASP	ASN	ASN	LVS	SER
ASN	THR	SER	ASN	GLU	TVR	GLN
GLN	PRO	GLN	THR	LVS	K64	ILE
HIS	GLN	GLN	THR	LVS	P80	GLN
GLN	LVS	GLY	GLU	PRO	L83	SER
ASN	ALA	SER	PRO	SER	T84	GLN
GLN	ALA	SER	SER	LVS	F85	VAL
ASP	ILE	VAL	THR	THR	E89	GLY
GLU	GLN	SER	PRO	ALA	F111	ALA
LEU	ARG	SER	K184	VAL	V115	LYS
ASN	SER	GLN	I189	R93	F94	ASN
LEU	MET	F324	L190	G95	T95	MET
SER	ILE	M325	R191	F111	E118	THR
ASP	GLN	R326	L195	V115	E119	ALA
ASP	GLY	R396	D201	E118	P122	GLN
LVS	ARG	GLU	L201	E119	K129	PRO
LVS	ALA	GLU	L202	P122	V133	PRO
ILE	PRO	ARG	L203	K129	Q134	ALA
LVS	GLN	LEU	T205	F212	E137	GLN
PRO	GLN	GLN	T212	L218	L142	GLN
GLN	GLN	GLU	T222	N219	R143	ARG
ALA	GLN	SER	E223	L218	R148	ILE
LVS	PRO	GLY	N277	N219	HIS	ASN
GLN	ASP	GLY	A278	D279	LEU	ASN
GLN	GLN	GLN	D279	T282	VAL	PRO
GLN	GLN	GLY	T282	TVR	ALA	GLN
GLN	PRO	ILE	ARG	ARG	HIS	ASN
GLN	ALA	PRO	LYS	LYS	ILE	LEU
ASN	MET	GLY	LYS	THR	ASP	THR
VAL	MET	LEU	THR	ASP	ALA	GLN
ALA	SER	LEU	HIS	GLU	ASP	GLN
GLY	GLN	SER	ASP	MET	LYS	GLN
THR	ARG	PHE	MET	GLN	ASP	GLN
ILE	GLN	SER	SER	GLN	GLN	ARG
PRO	GLN	SER	ASN	HIS	VAL	LEU
ALA	LEU	THR	THR	GLY	S295	GLN
GLY	GLN	GLY	S295	GLY	SER	GLN
SER	ASN	ASN	ASN	ASN	SER	LYS
THR	LEU	MET	L304	L304	GLU	VAL
PRO	TYR	ASN	S305	S305	SER	LEU
PRO	GLN	THR	D306	D306	SER	HIS
THR	ARG	MET	R307	R307	ALA	GLN
ALA	GLN	LEU	PHE	ASP	ASN	LYS
THR	GLN	ASP	ASP	ASP	ASN	THR

ALA  
ASN  
LYS  
LYS  
ARG  
GLY  
THR  
TYR  
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LYS  
TYR  
ILE  
LEU  
ILE  
ILE  
ASN  
ASP

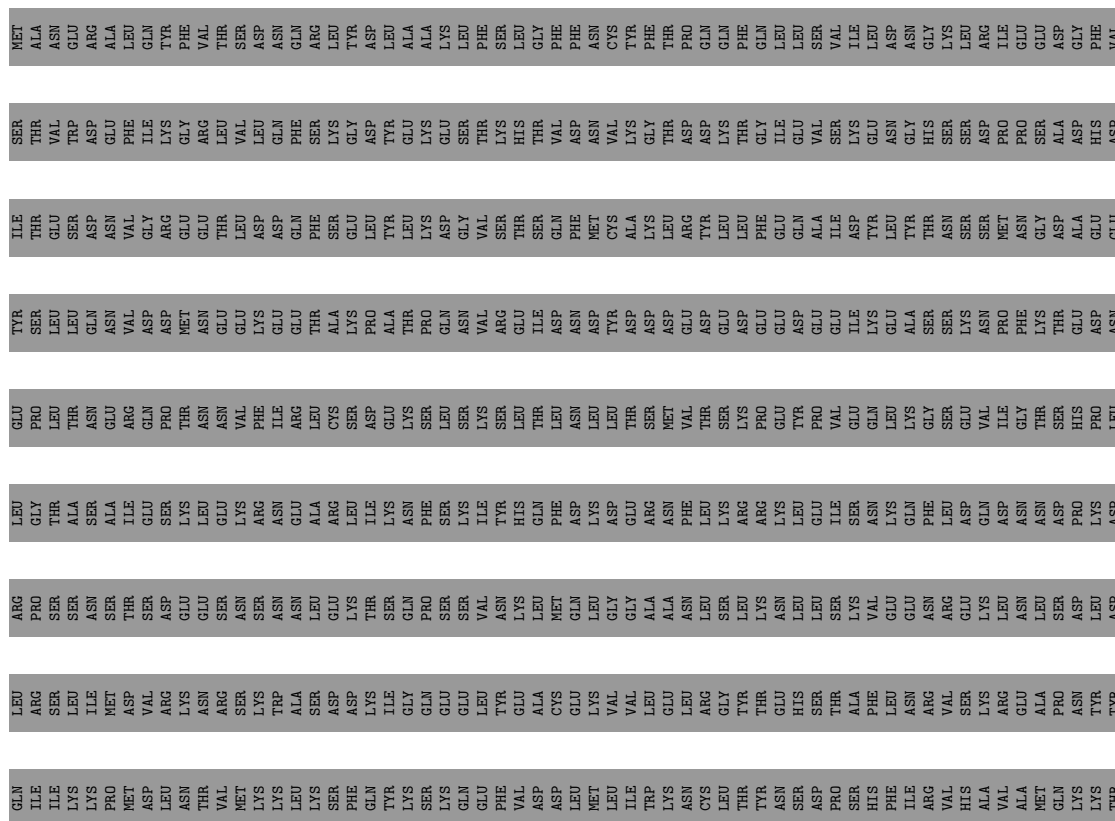
- Molecule 5: Subunit of the SAGA and SAGA-like transcriptional regulatory complexes, interacts with Spt15p to act

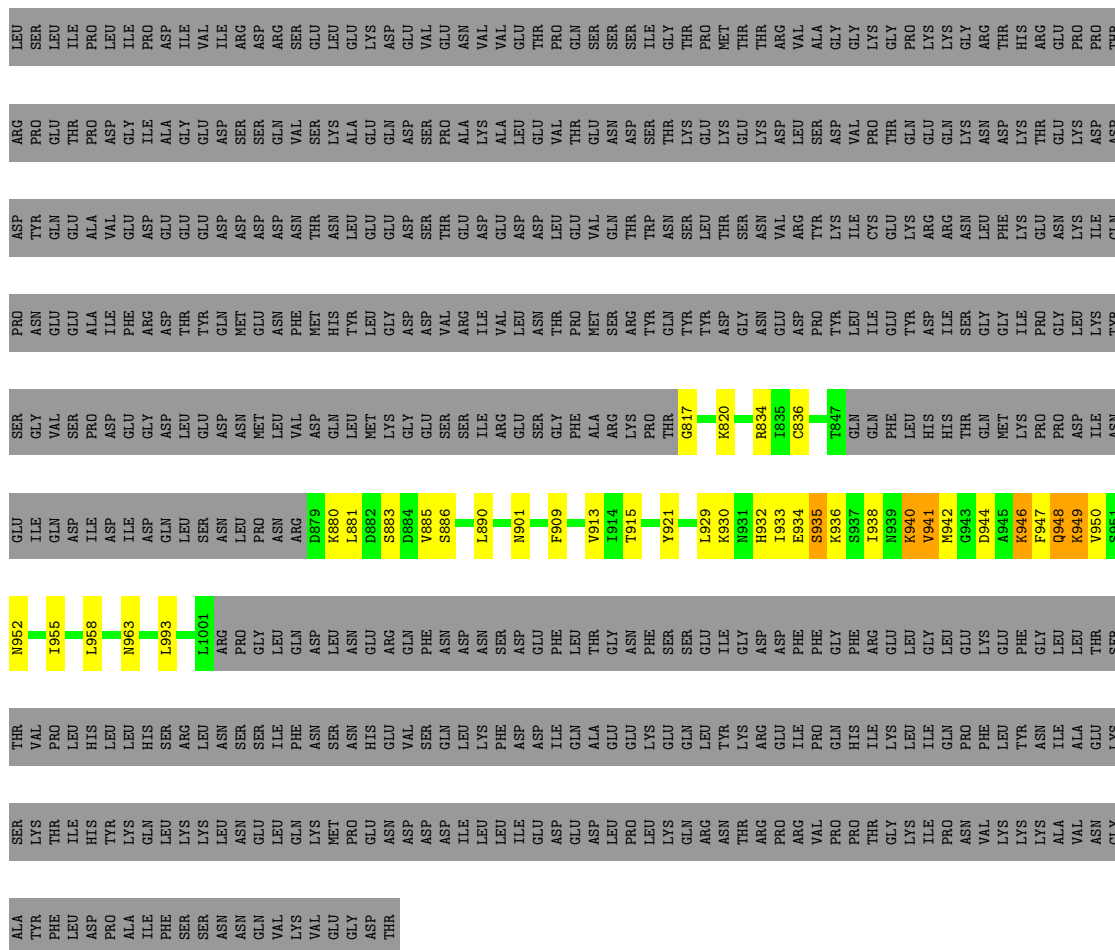
Chain D:  37% 21% . 39%



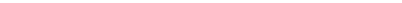
- Molecule 6: Subunit of the SAGA transcriptional regulatory complex, involved in proper assembly of the complex

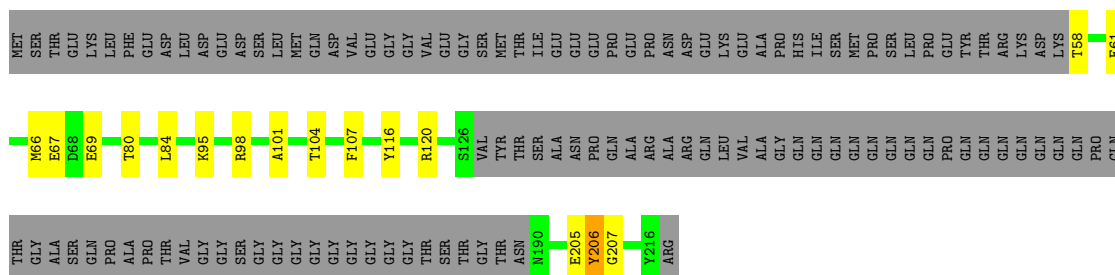
Chain E:  10% .. 87%





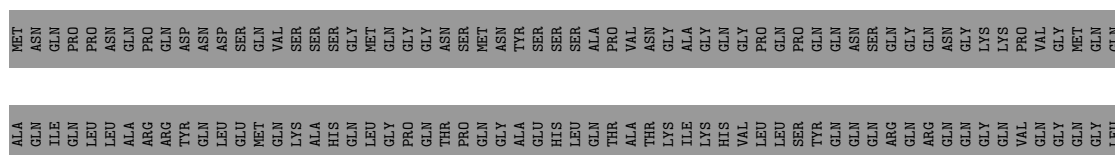
- Molecule 7: Transcription initiation factor TFIID subunit 10

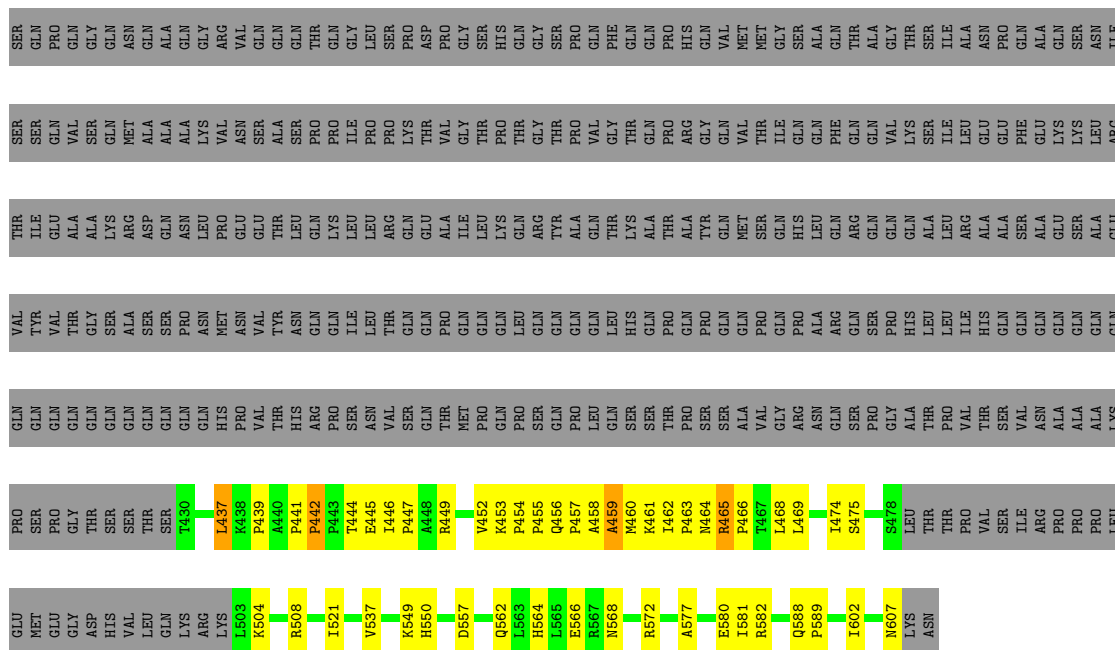
Chain J:  36% 7% 56%



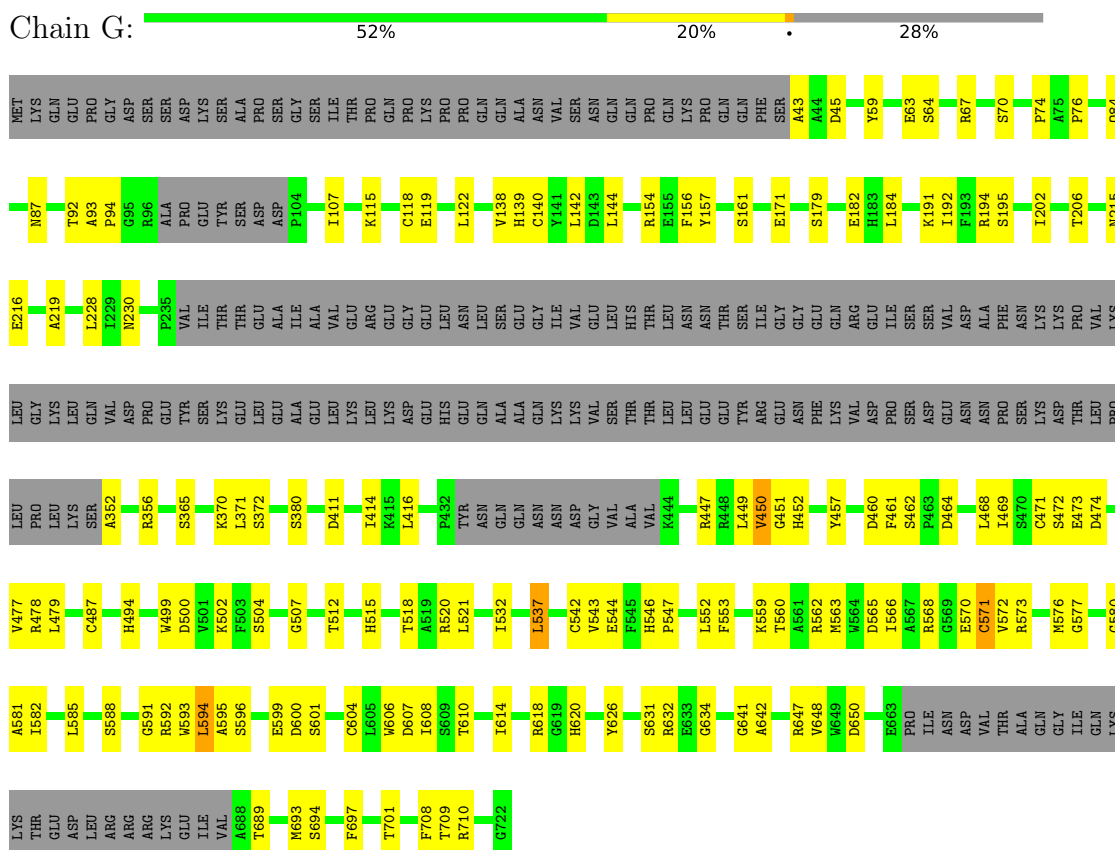
- Molecule 8: Subunit (61/68 kDa) of TFIID and SAGA complexes

Chain K:  17% 7% . 75%



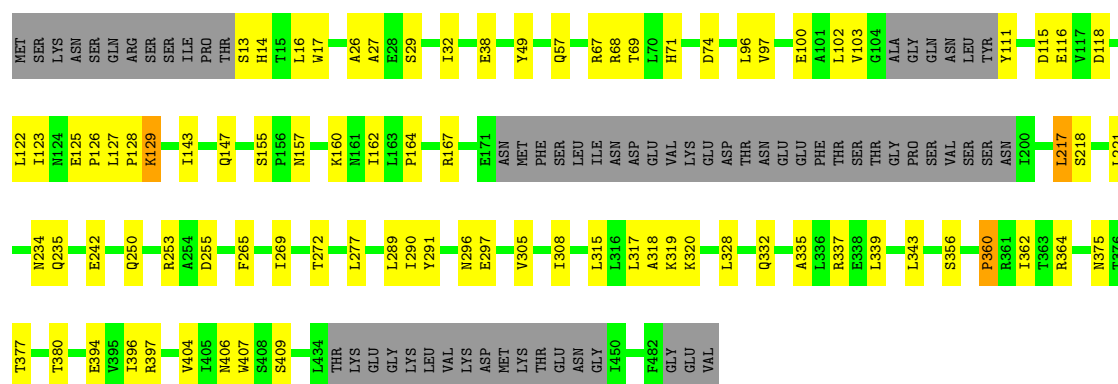


- Molecule 9: Subunit (90 kDa) of TFIID and SAGA complexes

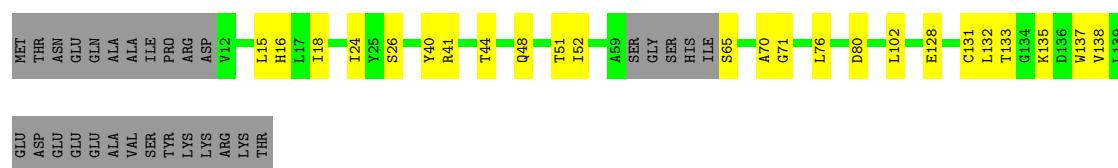


- Molecule 10: Subunit (60 kDa) of TFIID and SAGA complexes

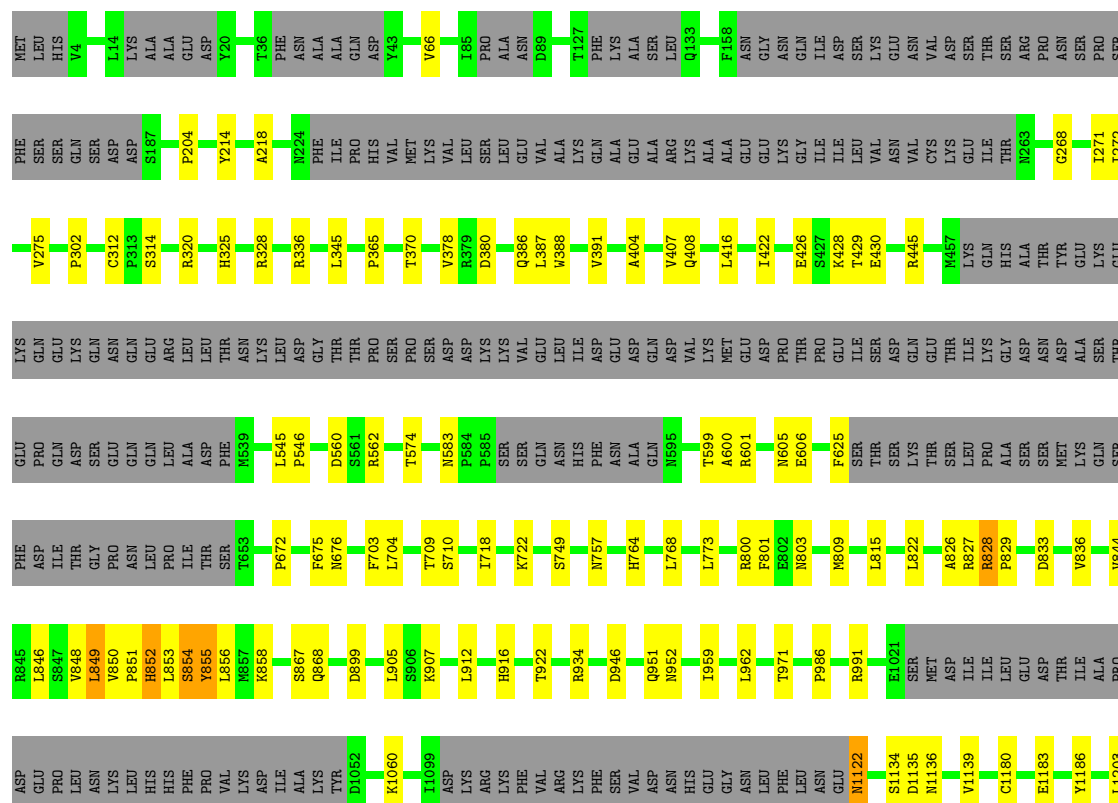




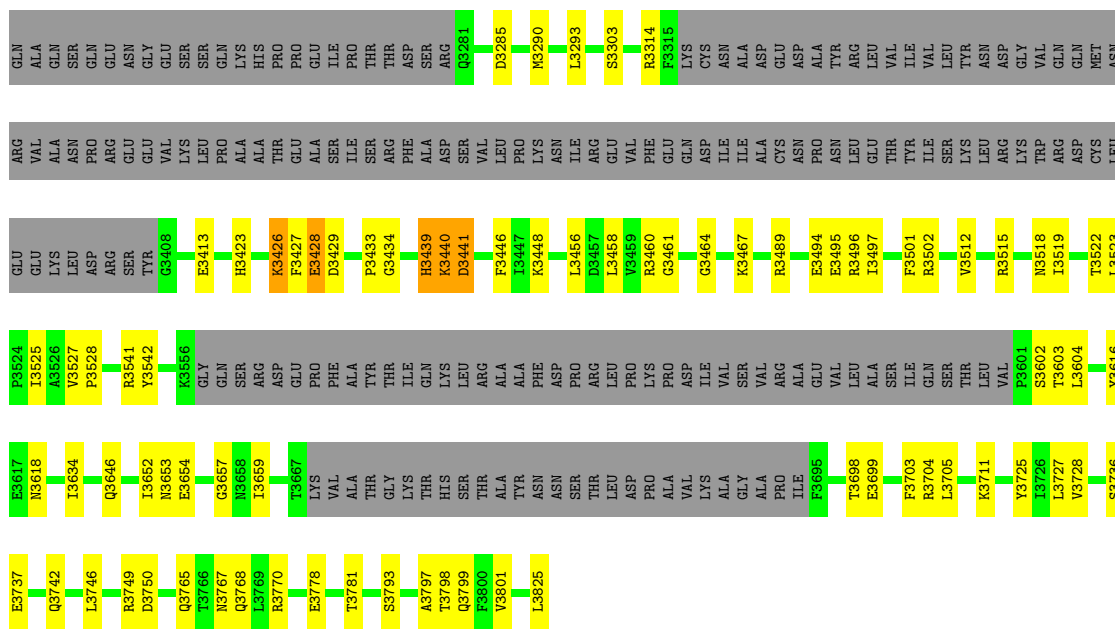
- Molecule 11: Subunit (17 kDa) of TFIID and SAGA complexes, involved in RNA polymerase II transcription initiation



- Molecule 12: Transcription-associated protein



SER	SER	K3101	GLN	D2896	Q2803	P2602	L2490	LYS	L2190	GLY	Y1964	A1811	K1685	K1495	ASP	D1204
ASN	ASN	L3102	GLU	I2897	G2804	N2603	S2491	THR	ARG	ASP	I1967	K1822	K1680	K1501	ALA	I1205
LYS	LYS	L3103	PHE	N2898	F2805	N2633	GLU	ASP	ASP	SER	R1978	A1823	L1680	K1506	GLU	P1206
ASP	GLN	S3111	LEU	I2899	S2806	N2633	GLU	PHE	ASN	ASP	R1978	T1824	L1680	L1507	SER	F1210
THR	LEU	H3126	LEU	N2900	Q2807	L2665	THR	PRO	Q2195	SER	V1994	L1827	R1684	A1508	LEU	R1219
ALA	ARG	HIS	ARG	V2904	D2810	E2666	LEU	THR	K2214	ASN	MET	L1837	S1690	W1509	VAL	A1220
ASP	GLU	GLY	GLU	T2905	T2811	M2669	SER	LEU	GLU	ILE	SER	D1837	P1691	A1510	SER	L1221
SER	GLN	GLU	GLN	W2906	L2812	F2677	PRO	PRO	THR	THR	ASN	R1840	Y1692	GLU	ALA	HIS
VAL	ALA	SER	ALA	R2907	L2812	F2677	GLN	GLY	GLY	SER	THR	R1840	Y1692	T1514	ARG	R1226
LYS	LYS	P3131	LYS	V2910	V2815	T2680	GLN	GLY	GLY	GLU	SER	A1848	F1694	Q1516	ILE	L1243
ASN	CYS	W3133	CYS	F2911	S2816	T2680	SER	PRO	GLU	ASP	Q1698	A1848	F1694	Q1517	SER	L1243
THR	HIS	H3136	HIS	F2911	R2817	Y2687	ILE	THR	E2221	TYR	E1701	P1855	E1701	D1522	GLU	T1257
ASN	GLN	G2912	GLN	G2912	L2818	Y2687	GLU	GLN	E2221	GLU	E1701	P1855	E1701	D1522	HIS	R1257
PRO	ASN	I3136	ASN	I2914	G2822	T2690	GLY	GLY	I2231	VAL	L1716	D1860	L1716	M1525	S1262	S1262
THR	PRO	V3139	PRO	N2915	G2822	T2690	LEU	VAL	V2235	SER	G1717	R1862	G1717	M1526	S1263	S1263
GLN	GLN	Q3141	SER	R2916	K2829	L2708	ALA	ALA	G2239	THR	H1718	D1864	H1718	Q1530	D1275	D1275
PRO	GLU	L3142	GLU	M2919	R2836	F2721	ARG	ARG	G2239	GLY	F1724	D1864	F1724	Q1530	C1394	C1394
THR	LEU	L3142	LEU	P2919	R2836	P2722	GLU	GLU	G2239	THR	K1727	D1864	K1727	H1540	R1413	R1413
ARG	ASN	K3149	THR	PHE	G2843	P2722	LYS	LYS	GLU	GLN	K1727	D1864	K1727	H1540	R1413	R1413
THR	GLY	E3150	GLY	VAL	L2844	Y2737	PRO	VAL	H2411	ARG	K1727	D1864	K1727	H1540	R1413	R1413
GLU	ASP	A3151	LEU	VAL	Q2849	E2740	GLU	VAL	H2411	SER	K1727	D1864	K1727	H1540	R1413	R1413
THR	VAL	V3154	VAL	VAL	Q2849	K2741	LYS	GLU	L2414	SER	P1734	Y1885	P1734	P1543	V1418	R1284
SER	ILE	L3158	ILE	GLN	L2854	K2741	ALA	LYS	T2415	GLU	F1735	Y1885	F1735	H1547	K1419	S1295
THR	SER	L3158	SER	GLN	L2854	W2745	PRO	THR	A2416	THR	W1736	Y1887	W1736	K1548	L1421	M1305
ALA	THR	I3161	ASN	ASN	S2858	T2758	GLN	GLN	M2418	SER	F1895	Y1887	L1737	V1422	I1306	I1306
GLU	ASN	A3162	THR	GLY	Q2858	T2758	ASN	ASN	V2248	SER	V1748	Y1887	L1737	M1563	V1423	S1307
SER	GLY	L3169	LEU	ASN	V2860	E2756	GLY	GLY	V2248	VAL	LYS	Y1887	L1737	M1563	V1423	S1307
LYS	VAL	S2862	VAL	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
THR	PHE	V2865	THR	GLY	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
THR	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
GLU	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
ASP	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
LYS	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563	V1423	S1307
PRO	ALA	V2865	THR	ASN	S2862	L2751	ASN	GLY	V2248	THR	THR	Y1887	L1737	M1563</		



- Molecule 13: Transcriptional regulator involved in glucose repression of Gal4p-regulated genes

Chain B:  10% . 89%

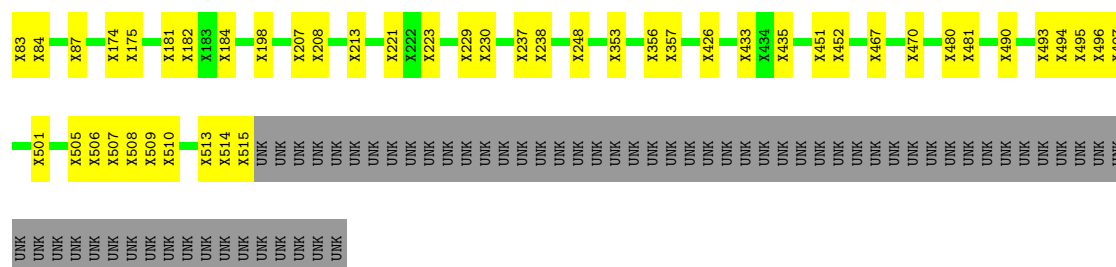




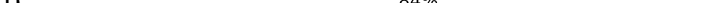
**A**: ASP LEU  
**B**: THR ARG  
**C**: TRP ARG  
**D**: ILE LEU  
**E**: GLY LYS  
**F**: ILE LEU  
**G**: GLY PRO  
**H**: PRO HIS  
**I**: MET LEU  
**J**: ARG MET  
**K**: ARG ARG  
**L**: PRO PRO  
**M**: SER SER  
**N**: VAL PHE  
**O**: LEU ASP  
**P**: VAL ASP  
**Q**: LEU ASP  
**R**: GLU LEU  
**S**: ASP ASP  
**T**: MET GLU  
**V**: LEU VAL  
**X**: ASP ASP  
**Z**: LEU ASP

- Molecule 14: Spt8

Chain N:  72% 12% 16%




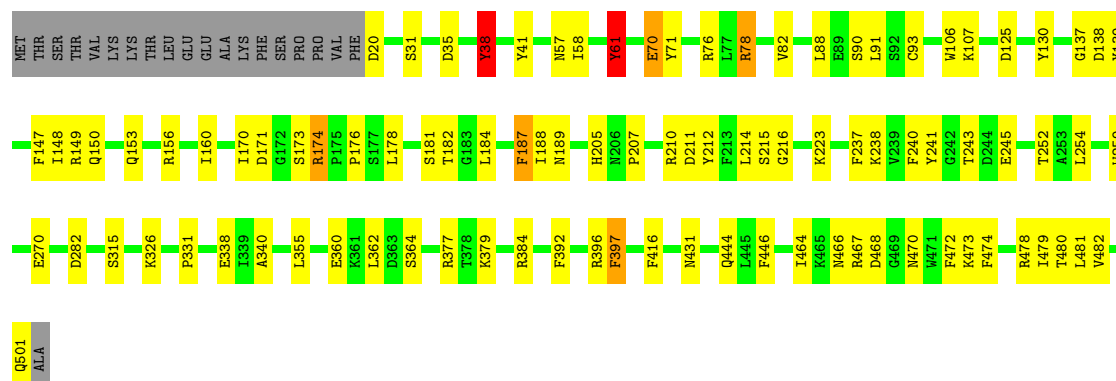
- Molecule 15: Polyubiquitin-B

Chain R:  84% 16%



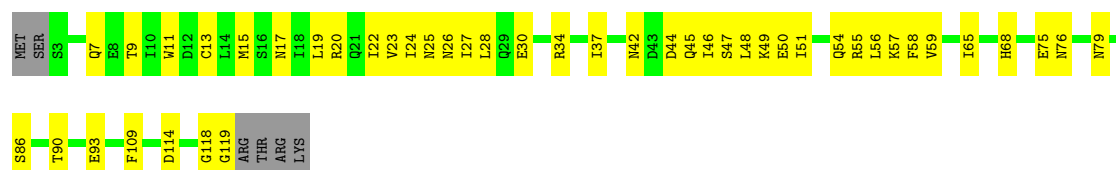
- Molecule 16: Ubiquitin carboxyl-terminal hydrolase

Chain Q:  77% 18% . .



- Molecule 17: SAGA-associated factor 11

Chain 0:  59% 37% 5%



- Molecule 18: Transcription and mRNA export factor SUS1

Chain P:  59% 34% 6%

MET	THR	ASN	SER	ASP	V6	K10	Q11	Q14	V18	E19	Y23	D24	S27	R31	Y35	D41	E42	I43	M44	R45	L46	T47	Q48	S49	T50	V51	T52	N53	P57	T58	F59	S60	N61	V62	I63	I66	E67	A70	V74	I82	L83	I86	P95	LYS
-----	-----	-----	-----	-----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	354104	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	52.8	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GLZ

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  >2	RMSZ	# Z  >2
1	M	0.88	2/1442 (0.1%)	0.78	2/1942 (0.1%)
10	H	0.38	0/3315	0.60	0/4500
11	I	0.44	0/1006	0.63	0/1374
12	L	0.33	0/22712	0.54	0/30825
13	B	0.64	0/370	0.70	1/509 (0.2%)
15	R	0.83	1/619 (0.2%)	0.75	0/833
16	Q	0.71	0/3897	1.09	15/5265 (0.3%)
17	O	0.79	0/931	1.13	2/1250 (0.2%)
18	P	0.75	0/747	1.01	0/1011
2	A	0.44	0/1319	0.60	0/1794
3	C	0.53	0/774	0.75	0/1039
4	F	0.34	0/1718	0.58	0/2335
5	D	0.51	0/1641	0.65	0/2213
6	E	0.45	0/1246	0.62	0/1667
7	J	0.47	0/779	0.60	0/1051
8	K	0.42	0/1213	0.66	0/1647
9	G	0.52	0/4177	0.60	0/5661
All	All	0.47	3/47906 (0.0%)	0.67	20/64916 (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	M	0	1
16	Q	2	5
All	All	2	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	194	ILE	C-N	27.38	1.97	1.34
1	M	183	SER	C-N	6.38	1.48	1.34
15	R	24	GLU	CB-CG	-5.25	1.42	1.52

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Q	61	TYR	CB-CG-CD1	9.83	126.90	121.00
16	Q	61	TYR	CB-CG-CD2	-9.38	115.37	121.00
1	M	62	GLY	N-CA-C	6.94	130.46	113.10
16	Q	78	ARG	NE-CZ-NH1	-6.80	116.90	120.30
13	B	527	PRO	N-CA-CB	6.57	111.18	103.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
16	Q	31	SER	CA
16	Q	222	THR	CA

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	M	183	SER	Mainchain
16	Q	149	ARG	Sidechain
16	Q	212	TYR	Sidechain
16	Q	38	TYR	Sidechain
16	Q	61	TYR	Sidechain

## 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	M	1415	0	1491	102	0
2	A	1300	0	1254	30	0
3	C	761	0	779	194	0
4	F	1682	0	1622	30	0
5	D	1616	0	1558	122	0
6	E	1232	0	1276	40	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	J	768	0	754	11	0
8	K	1192	0	1214	89	0
9	G	4075	0	3934	102	0
10	H	3263	0	3258	69	0
11	I	981	0	982	18	0
12	L	22318	0	20960	376	0
13	B	373	0	190	2	0
14	N	1648	0	382	61	0
15	R	611	0	636	20	0
16	Q	3817	0	3772	521	0
17	O	922	0	897	411	0
18	P	735	0	743	191	0
19	Q	8	0	0	10	0
19	R	83	0	0	7	0
All	All	48800	0	45702	1602	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 17.

The worst 5 of 1602 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)
16:Q:472:PHE:CZ	17:O:45:GLN:HB3	1.29	1.65
17:O:11:TRP:CD1	18:P:83:LEU:HD23	1.14	1.61
16:Q:479:ILE:HG23	17:O:47:SER:CA	1.19	1.61
16:Q:479:ILE:CG2	17:O:47:SER:HA	1.14	1.60
17:O:34:ARG:HH11	18:P:57:PRO:CB	1.11	1.58

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	M	178/240 (74%)	147 (83%)	24 (14%)	7 (4%)	3	30
2	A	169/448 (38%)	151 (89%)	18 (11%)	0	100	100
3	C	89/698 (13%)	83 (93%)	6 (7%)	0	100	100
4	F	202/517 (39%)	177 (88%)	24 (12%)	1 (0%)	31	74
5	D	203/341 (60%)	177 (87%)	19 (9%)	7 (3%)	4	33
6	E	150/1191 (13%)	135 (90%)	13 (9%)	2 (1%)	13	54
7	J	92/217 (42%)	82 (89%)	9 (10%)	1 (1%)	16	58
8	K	150/609 (25%)	125 (83%)	23 (15%)	2 (1%)	13	54
9	G	512/722 (71%)	448 (88%)	63 (12%)	1 (0%)	49	85
10	H	413/485 (85%)	365 (88%)	48 (12%)	0	100	100
11	I	119/153 (78%)	98 (82%)	21 (18%)	0	100	100
12	L	2874/3825 (75%)	2623 (91%)	233 (8%)	18 (1%)	27	70
13	B	70/722 (10%)	63 (90%)	7 (10%)	0	100	100
15	R	76/76 (100%)	75 (99%)	1 (1%)	0	100	100
16	Q	480/502 (96%)	444 (92%)	30 (6%)	6 (1%)	13	54
17	O	115/123 (94%)	103 (90%)	6 (5%)	6 (5%)	2	25
18	P	88/96 (92%)	85 (97%)	3 (3%)	0	100	100
All	All	5980/10965 (54%)	5381 (90%)	548 (9%)	51 (1%)	24	61

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	77	GLY
1	M	99	PHE
1	M	110	LYS
5	D	200	THR
5	D	327	ARG

### 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 PDB entries followed by that with respect to all EM entries.

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	M	152/205 (74%)	138 (91%)	14 (9%)	10	34
2	A	134/394 (34%)	132 (98%)	2 (2%)	67	85
3	C	85/627 (14%)	85 (100%)	0	100	100
4	F	179/471 (38%)	179 (100%)	0	100	100
5	D	166/306 (54%)	154 (93%)	12 (7%)	16	46
6	E	142/1101 (13%)	136 (96%)	6 (4%)	32	61
7	J	85/183 (46%)	84 (99%)	1 (1%)	74	87
8	K	133/524 (25%)	130 (98%)	3 (2%)	53	76
9	G	439/635 (69%)	430 (98%)	9 (2%)	56	78
10	H	352/438 (80%)	348 (99%)	4 (1%)	76	88
11	I	104/130 (80%)	103 (99%)	1 (1%)	78	89
12	L	2156/3450 (62%)	2114 (98%)	42 (2%)	60	80
15	R	70/68 (103%)	69 (99%)	1 (1%)	69	85
16	Q	431/449 (96%)	425 (99%)	6 (1%)	69	85
17	O	103/109 (94%)	102 (99%)	1 (1%)	78	89
18	P	85/91 (93%)	85 (100%)	0	100	100
All	All	4816/9181 (52%)	4714 (98%)	102 (2%)	59	78

5 of 102 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	G	594	LEU
12	L	1122	ASN
15	R	60	ASN
10	H	129	LYS
11	I	16	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
12	L	2698	GLN
15	R	25	ASN
17	O	76	ASN
15	R	2	GLN
15	R	60	ASN



### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
15	GLZ	R	76	15,16	3,3,3	0.68	0	1,2,2	1.36	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	GLZ	R	76	15,16	-	0/0/1/1	-

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.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
14	N	6
13	B	2
1	M	1

The worst 5 of 9 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	414:ASP	C	462:ALA	N	28.86
1	B	471:ASP	C	509:ASP	N	23.98
1	N	117:UNK	C	172:UNK	N	15.59
1	N	287:UNK	C	332:UNK	N	5.97
1	N	213:UNK	C	214:UNK	N	4.21