



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:05 PM UTC

PDB ID : 4V5O / pdb_00004v5o
Title : CRYSTAL STRUCTURE OF THE EUKARYOTIC 40S RIBOSOMAL SUB-UNIT IN COMPLEX WITH INITIATION FACTOR 1.
Authors : Rabl, J.; Leibundgut, M.; Ataide, S.F.; Haag, A.; Ban, N.
Deposited on : 2010-11-26
Resolution : 3.93 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

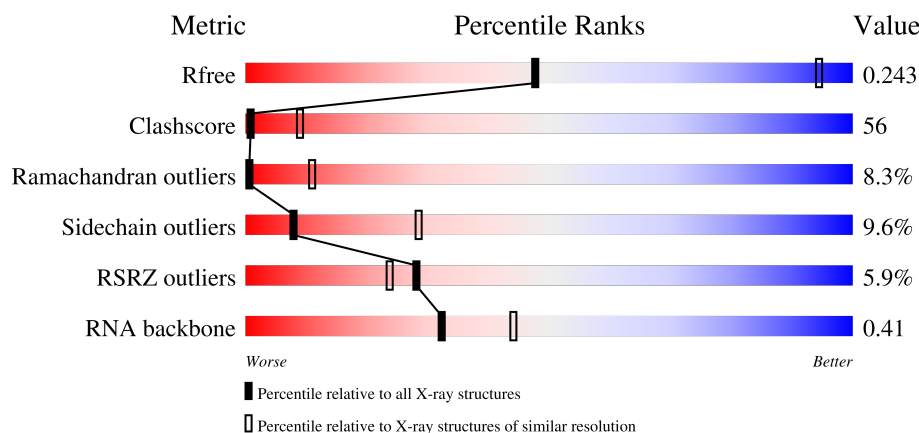
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.93 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1022 (4.12-3.76)
Clashscore	190562	1000 (4.10-3.78)
Ramachandran outliers	187476	1009 (4.12-3.76)
Sidechain outliers	187428	1002 (4.12-3.76)
RSRZ outliers	180081	1022 (4.12-3.76)
RNA backbone	3983	1015 (4.76-3.10)

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

Mol	Chain	Length	Quality of chain
1	A1	68	6% 28% 53% 18%
1	B1	68	3% 25% 59% 15%
2	A2	208	7% 20% 62% 17%
2	B2	208	5% 19% 62% 18%

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Mol	Chain	Length	Quality of chain
3	A3	197	
3	B3	197	
4	A4	265	
4	B4	265	
5	A5	119	
5	B5	119	
6	A6	81	
6	B6	81	
7	A7	162	
7	B7	162	
8	A8	143	
8	B8	143	
9	A9	189	
9	B9	189	
10	AA	1753	
10	BA	1753	
11	AB	241	
11	BB	241	
12	AC	243	
12	BC	243	
13	AD	181	
13	BD	181	
14	AE	296	
14	BE	296	
15	AF	101	

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Mol	Chain	Length	Quality of chain
15	BF	101	
16	AG	200	
16	BG	200	
17	AH	130	
17	BH	130	
18	AI	145	
18	BI	145	
19	AJ	120	
19	BJ	120	
20	AK	151	
20	BK	151	
21	AL	142	
21	BL	142	
22	AM	155	
22	BM	155	
23	AN	55	
23	BN	55	
24	AO	153	
24	BO	153	
25	AP	149	
25	BP	149	
26	AQ	157	
26	BQ	157	
27	AR	343	
27	BR	343	

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Mol	Chain	Length	Quality of chain
28	AS	144	
28	BS	144	
29	AT	155	
29	BT	155	
30	AU	126	
30	BU	126	
31	AV	130	
31	BV	130	
32	AW	260	
32	BW	260	
33	AX	80	
33	BX	80	
34	AY	293	
34	BY	293	
35	AZ	97	
35	BZ	97	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
36	MG	BA	1855	-	-	-	X

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 157632 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 RIBOSOMAL PROTEIN S28E CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A1	67	Total	C	N	O	S	0	0	0
			519	312	105	98	4			
1	B1	67	Total	C	N	O	S	0	0	0
			519	312	105	98	4			

- Molecule 2 is a protein called 40S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A2	207	Total	C	N	O	S	0	0	0
			1693	1057	336	296	4			
2	B2	207	Total	C	N	O	S	0	0	0
			1693	1057	336	296	4			

- Molecule 3 is a protein called RPS7E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A3	196	Total	C	N	O	S	0	0	0
			1629	1048	286	294	1			
3	B3	196	Total	C	N	O	S	0	0	0
			1629	1048	286	294	1			

- Molecule 4 is a protein called 40S RIBOSOMAL PROTEIN S3A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A4	215	Total	C	N	O	S	0	0	0
			1724	1090	314	316	4			
4	B4	215	Total	C	N	O	S	0	0	0
			1724	1090	314	316	4			

- Molecule 5 is a protein called RIBOSOMAL PROTEIN S26E CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	A5	98	Total	C	N	O	S	0	0	0
			797	485	170	136	6			
5	B5	98	Total	C	N	O	S	0	0	0
			797	485	170	136	6			

- Molecule 6 is a protein called RPS27E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	A6	80	Total	C	N	O	S	0	0	0
			632	398	110	116	8			
6	B6	80	Total	C	N	O	S	0	0	0
			632	398	110	116	8			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B6	54	CYS	-	expression tag	UNP Q22CK0
B6	55	GLU	-	expression tag	UNP Q22CK0
B6	56	LYS	-	expression tag	UNP Q22CK0
B6	57	CYS	-	expression tag	UNP Q22CK0
B6	58	SER	-	expression tag	UNP Q22CK0
B6	59	ALA	-	expression tag	UNP Q22CK0
B6	60	ILE	-	expression tag	UNP Q22CK0
B6	61	LEU	-	expression tag	UNP Q22CK0
B6	62	CYS	-	expression tag	UNP Q22CK0
B6	63	LYS	-	expression tag	UNP Q22CK0
B6	64	PRO	-	expression tag	UNP Q22CK0
B6	65	THR	-	expression tag	UNP Q22CK0
B6	66	GLY	-	expression tag	UNP Q22CK0
B6	67	GLY	-	expression tag	UNP Q22CK0
B6	68	LYS	-	expression tag	UNP Q22CK0
B6	69	VAL	-	expression tag	UNP Q22CK0
B6	70	GLN	-	expression tag	UNP Q22CK0
B6	71	ILE	-	expression tag	UNP Q22CK0
B6	72	GLN	-	expression tag	UNP Q22CK0
B6	73	ALA	-	expression tag	UNP Q22CK0
B6	74	GLY	-	expression tag	UNP Q22CK0
B6	75	CYS	-	expression tag	UNP Q22CK0
B6	76	ALA	-	expression tag	UNP Q22CK0
B6	77	PHE	-	expression tag	UNP Q22CK0
B6	78	LYS	-	expression tag	UNP Q22CK0
B6	79	ILE	-	expression tag	UNP Q22CK0
B6	80	LYS	-	expression tag	UNP Q22CK0

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Chain	Residue	Modelled	Actual	Comment	Reference
B6	81	ASN	-	expression tag	UNP Q22CK0

- Molecule 7 is a protein called PLECTIN/S10 DOMAIN CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	A7	104	Total	C	N	O	S	0	0	0
			859	560	142	155	2			
7	B7	104	Total	C	N	O	S	0	0	0
			859	560	142	155	2			

- Molecule 8 is a protein called RPS25E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	A8	93	Total	C	N	O	S	0	0	0
			725	460	135	128	2			
8	B8	93	Total	C	N	O	S	0	0	0
			725	460	135	128	2			

- Molecule 9 is a protein called RPS31E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	A9	98	Total	C	N	O	S	0	0	0
			742	479	139	119	5			
9	B9	98	Total	C	N	O	S	0	0	0
			742	479	139	119	5			

- Molecule 10 is a RNA chain called 18S RRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	AA	1745	Total	C	N	O	P	0	0	0
			37231	16654	6651	12181	1745			
10	BA	1745	Total	C	N	O	P	0	0	0
			37231	16654	6651	12181	1745			

- Molecule 11 is a protein called RPS0E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	AB	204	Total	C	N	O	S	0	0	0
			1642	1039	288	304	11			
11	BB	204	Total	C	N	O	S	0	0	0
			1642	1039	288	304	11			

- Molecule 12 is a protein called KH DOMAIN CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	AC	229	Total	C	N	O	S	0	0	0
			1820	1173	320	319	8			
12	BC	229	Total	C	N	O	S	0	0	0
			1820	1173	320	319	8			

- Molecule 13 is a protein called RIBOSOMAL PROTEIN S4 CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	AD	179	Total	C	N	O	S	0	0	0
			1475	931	286	252	6			
13	BD	179	Total	C	N	O	S	0	0	0
			1475	931	286	252	6			

- Molecule 14 is a protein called RIBOSOMAL PROTEIN S5 CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	AE	230	Total	C	N	O	S	0	0	0
			1827	1176	323	325	3			
14	BE	230	Total	C	N	O	S	0	0	0
			1827	1176	323	325	3			

- Molecule 15 is a protein called EIF1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	AF	89	Total	C	N	O	S	0	0	0
			736	465	131	137	3			
15	BF	89	Total	C	N	O	S	0	0	0
			736	465	131	137	3			

- Molecule 16 is a protein called RIBOSOMAL PROTEIN S7 CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	AG	192	Total	C	N	O	S	0	0	0
			1520	961	281	270	8			
16	BG	192	Total	C	N	O	S	0	0	0
			1520	961	281	270	8			

- Molecule 17 is a protein called RIBOSOMAL PROTEIN S8 CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	AH	129	Total	C	N	O	S	0	0	0
			1040	671	184	180	5			
17	BH	129	Total	C	N	O	S	0	0	0
			1040	671	184	180	5			

- Molecule 18 is a protein called RPS16E, 40S RIBOSOMAL PROTEIN RPS16E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	AI	143	Total	C	N	O	S	0	0	0
			1135	715	217	198	5			
18	BI	143	Total	C	N	O	S	0	0	0
			1135	715	217	198	5			

- Molecule 19 is a protein called RIBOSOMAL PROTEIN S10 CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	AJ	105	Total	C	N	O	S	0	0	0
			833	525	150	152	6			
19	BJ	105	Total	C	N	O	S	0	0	0
			833	525	150	152	6			

- Molecule 20 is a protein called RPS14E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	AK	140	Total	C	N	O	S	0	0	0
			1063	654	206	197	6			
20	BK	140	Total	C	N	O	S	0	0	0
			1063	654	206	197	6			

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	AL	141	Total	C	N	O	S	0	0	0
			1097	691	221	180	5			
21	BL	141	Total	C	N	O	S	0	0	0
			1097	691	221	180	5			

- Molecule 22 is a protein called RPS18E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	AM	154	Total	C	N	O	S	0	0	0
			1239	780	237	216	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	BM	154	Total	C	N	O	S	0	0	0
			1239	780	237	216	6			

- Molecule 23 is a protein called RPS29E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	AN	53	Total	C	N	O	S	0	0	0
			447	278	91	72	6			
23	BN	53	Total	C	N	O	S	0	0	0
			447	278	91	72	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BN	54	TYR	-	expression tag	UNP Q22MB0
BN	55	ARG	-	expression tag	UNP Q22MB0

- Molecule 24 is a protein called RPS13E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	AO	150	Total	C	N	O	S	0	0	0
			1214	782	228	200	4			
24	BO	150	Total	C	N	O	S	0	0	0
			1214	782	228	200	4			

- Molecule 25 is a protein called RPS24E.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
25	AP	148	Total	C	N	O	0	0	0
			1197	763	221	213			
25	BP	148	Total	C	N	O	0	0	0
			1197	763	221	213			

- Molecule 26 is a protein called RIBOSOMAL PROTEIN S17 CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	AQ	157	Total	C	N	O	S	0	0	0
			1275	818	235	217	5			
26	BQ	157	Total	C	N	O	S	0	0	0
			1275	818	235	217	5			

- Molecule 27 is a protein called RACK1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	AR	338	Total	C	N	O	S	0	0	0
			2682	1711	462	501	8			
27	BR	338	Total	C	N	O	S	0	0	0
			2682	1711	462	501	8			

- Molecule 28 is a protein called RPS15E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	AS	125	Total	C	N	O	S	0	0	0
			985	632	173	176	4			
28	BS	125	Total	C	N	O	S	0	0	0
			985	632	173	176	4			

- Molecule 29 is a protein called RPS19E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	AT	150	Total	C	N	O	S	0	0	0
			1211	769	227	213	2			
29	BT	150	Total	C	N	O	S	0	0	0
			1211	769	227	213	2			

- Molecule 30 is a protein called RIBOSOMAL PROTEIN L7AE CONTAINING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	AU	124	Total	C	N	O	S	0	0	0
			952	599	166	182	5			
30	BU	124	Total	C	N	O	S	0	0	0
			952	599	166	182	5			

- Molecule 31 is a protein called RPS17E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	AV	121	Total	C	N	O	S	0	0	0
			979	619	182	176	2			
31	BV	121	Total	C	N	O	S	0	0	0
			979	619	182	176	2			

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	AW	259	Total	C	N	O	S	0	0	0
			2079	1322	383	370	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	BW	259	Total	C	N	O	S	0	0	0
			2079	1322	383	370	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BW	1	MET	-	expression tag	UNP P0C233
BW	70	GLN	GLY	conflict	UNP P0C233
BW	236	SER	LEU	conflict	UNP P0C233
BW	237	TRP	TYR	conflict	UNP P0C233

- Molecule 33 is a protein called RPS30E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	AX	68	Total	C	N	O	S	0	0	0
			554	350	113	90	1			
33	BX	68	Total	C	N	O	S	0	0	0
			554	350	113	90	1			

- Molecule 34 is a protein called RPS6E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	AY	235	Total	C	N	O	S	0	0	0
			1868	1184	347	326	11			
34	BY	235	Total	C	N	O	S	0	0	0
			1868	1184	347	326	11			

- Molecule 35 is a protein called RPS21E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	AZ	97	Total	C	N	O	S	0	0	0
			747	458	139	146	4			
35	BZ	97	Total	C	N	O	S	0	0	0
			747	458	139	146	4			

- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	A4	1	Total	Mg	0	0
			1	1		
36	AA	90	Total	Mg	0	0
			90	90		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	AL	1	Total 1	Mg 1	0	0
36	B4	1	Total 1	Mg 1	0	0
36	BA	89	Total 89	Mg 89	0	0
36	BD	1	Total 1	Mg 1	0	0
36	BW	1	Total 1	Mg 1	0	0

- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
37	A5	1	Total 1	Zn 1	0	0
37	A6	1	Total 1	Zn 1	0	0
37	A9	1	Total 1	Zn 1	0	0
37	AN	1	Total 1	Zn 1	0	0
37	B5	1	Total 1	Zn 1	0	0
37	B6	1	Total 1	Zn 1	0	0
37	B9	1	Total 1	Zn 1	0	0
37	BN	1	Total 1	Zn 1	0	0

- Molecule 38 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	A2	2	Total 2	O 2	0	0
38	A4	2	Total 2	O 2	0	0
38	A5	1	Total 1	O 1	0	0
38	AA	516	Total 516	O 516	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	AC	1	Total 1	O 1	0	0
38	AD	4	Total 4	O 4	0	0
38	AE	3	Total 3	O 3	0	0
38	AL	3	Total 3	O 3	0	0
38	AM	4	Total 4	O 4	0	0
38	AO	1	Total 1	O 1	0	0
38	AP	1	Total 1	O 1	0	0
38	AQ	2	Total 2	O 2	0	0
38	AT	4	Total 4	O 4	0	0
38	AW	4	Total 4	O 4	0	0
38	AY	4	Total 4	O 4	0	0
38	B2	2	Total 2	O 2	0	0
38	B4	2	Total 2	O 2	0	0
38	B5	1	Total 1	O 1	0	0
38	BA	512	Total 512	O 512	0	0
38	BC	2	Total 2	O 2	0	0
38	BD	2	Total 2	O 2	0	0
38	BE	5	Total 5	O 5	0	0
38	BK	1	Total 1	O 1	0	0
38	BL	2	Total 2	O 2	0	0
38	BM	6	Total 6	O 6	0	0

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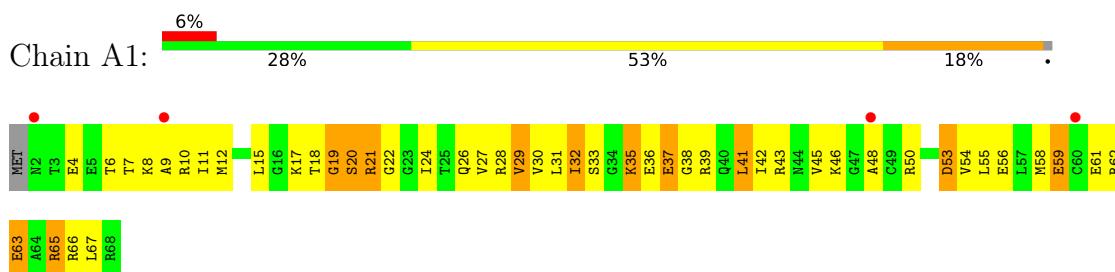
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
38	BO	1	Total 1	O 1	0	0
38	BP	1	Total 1	O 1	0	0
38	BQ	1	Total 1	O 1	0	0
38	BT	6	Total 6	O 6	0	0
38	BW	5	Total 5	O 5	0	0
38	BY	3	Total 3	O 3	0	0

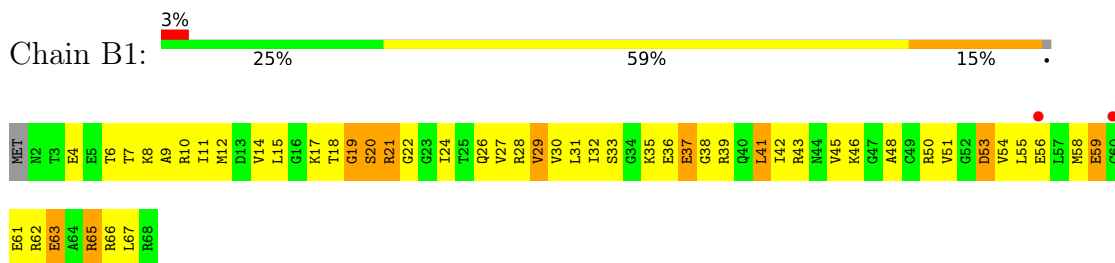
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

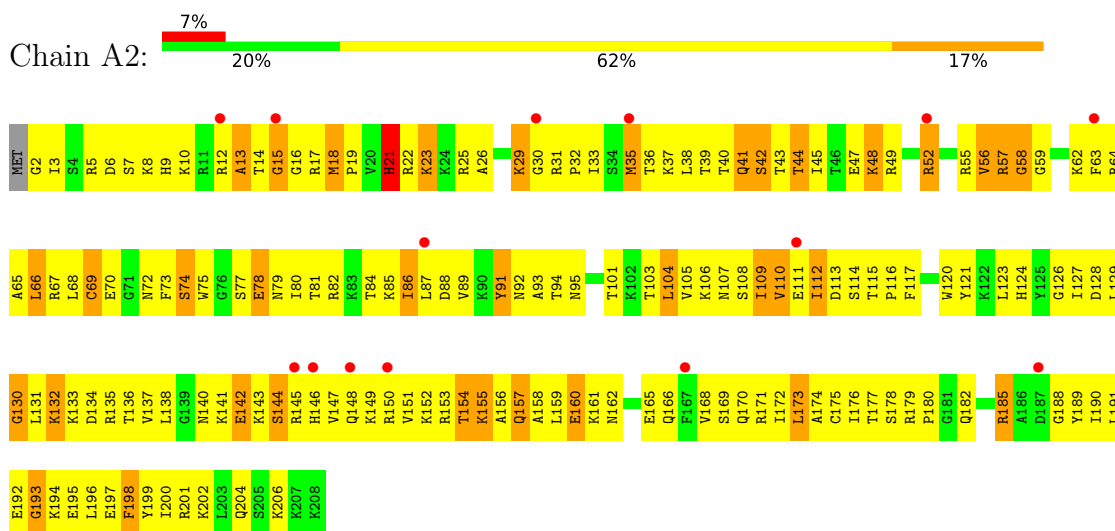
• Molecule 1: RIBOSOMAL PROTEIN S28E CONTAINING PROTEIN



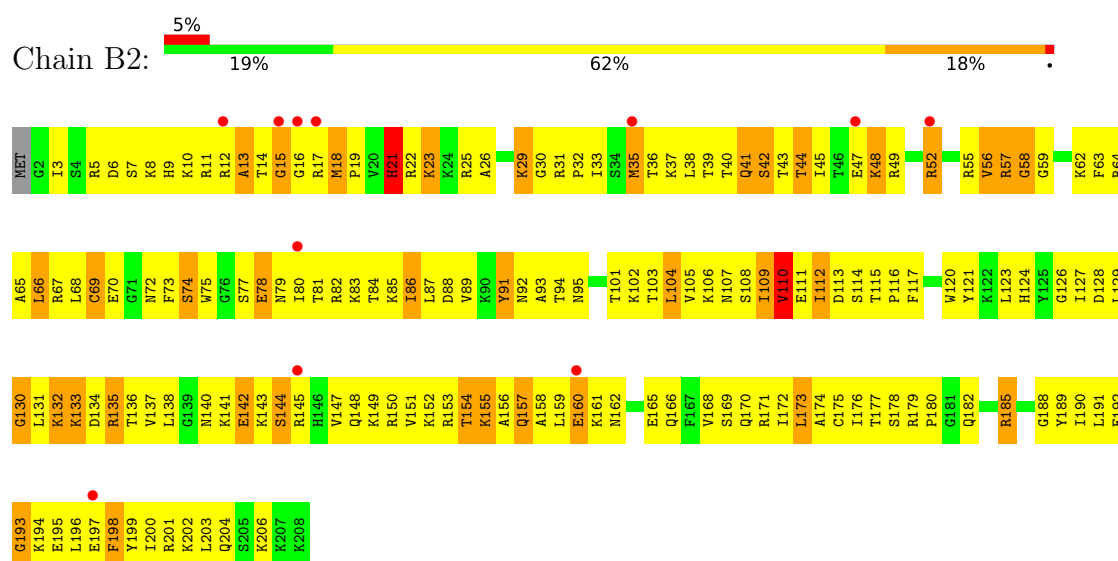
• Molecule 1: RIBOSOMAL PROTEIN S28E CONTAINING PROTEIN



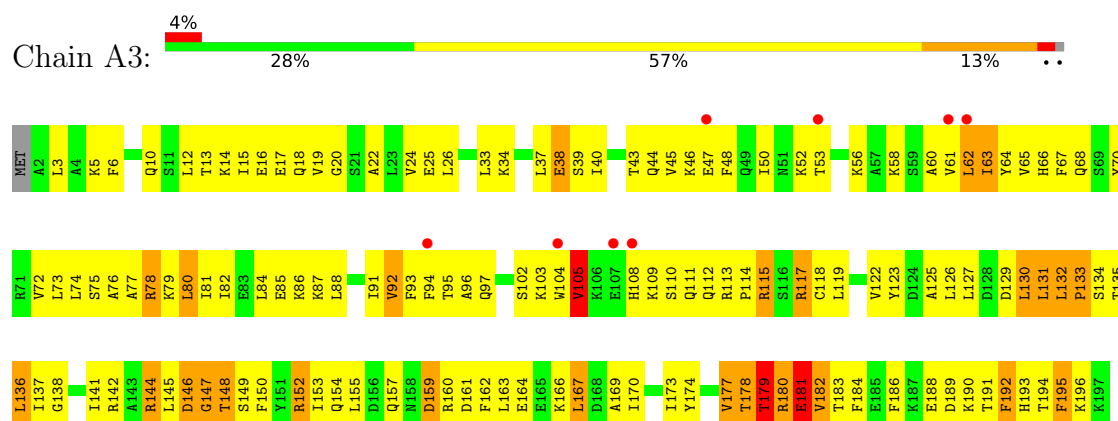
• Molecule 2: 40S RIBOSOMAL PROTEIN S8

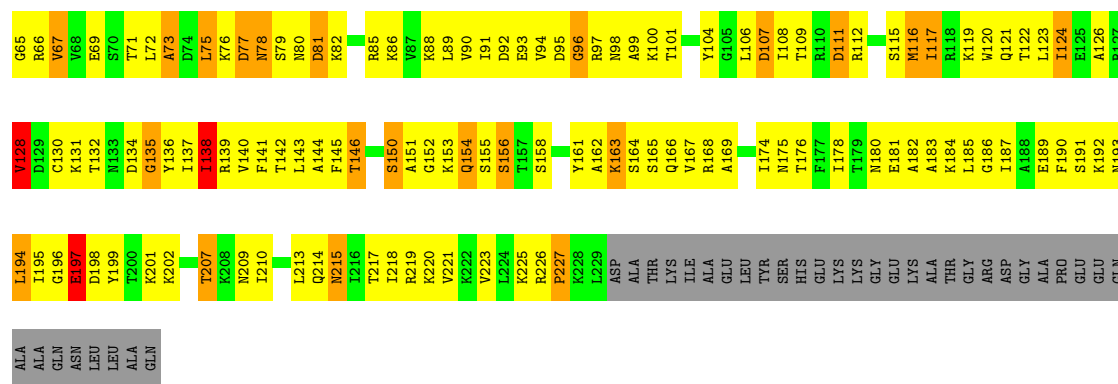


• Molecule 2: 40S RIBOSOMAL PROTEIN S8

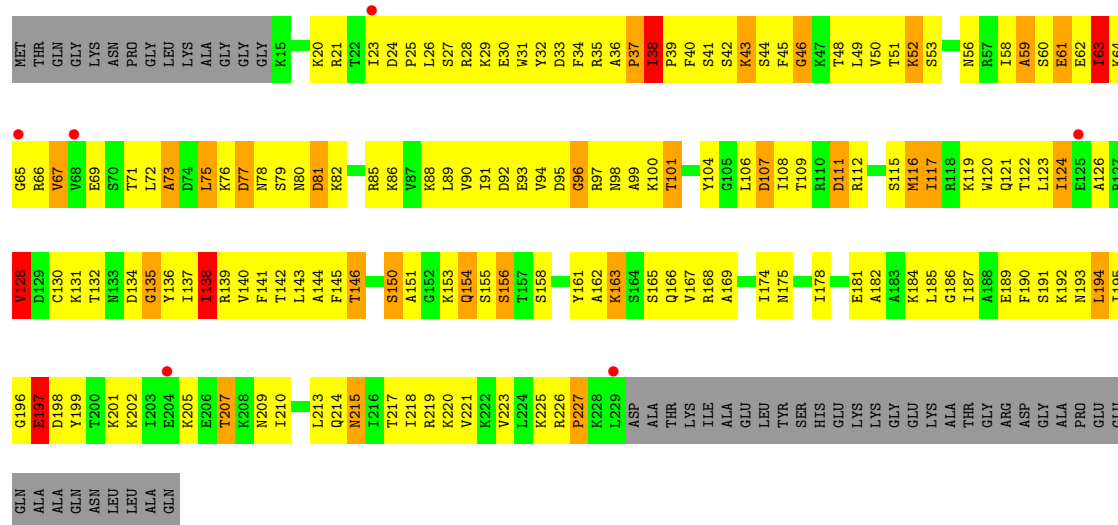
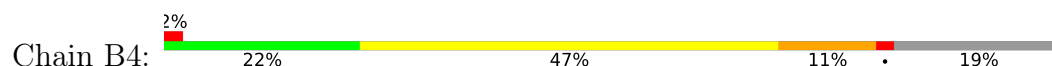


• Molecule 3: RPS7E

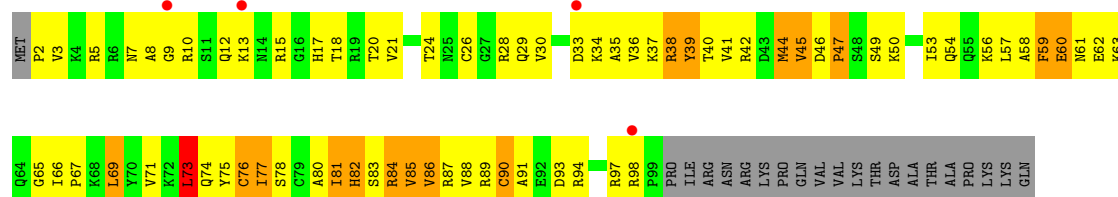
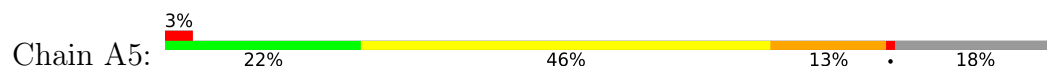




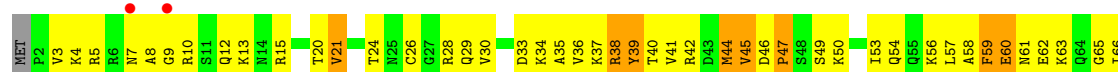
• Molecule 4: 40S RIBOSOMAL PROTEIN S3A



• Molecule 5: RIBOSOMAL PROTEIN S26E CONTAINING PROTEIN

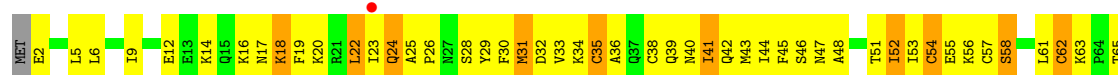


• Molecule 5: RIBOSOMAL PROTEIN S26E CONTAINING PROTEIN

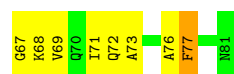
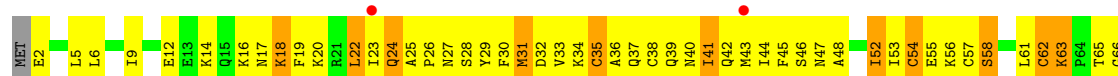




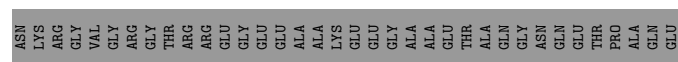
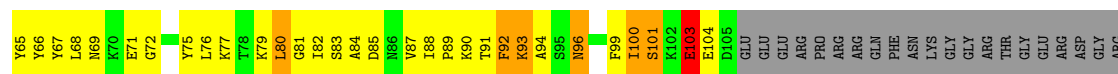
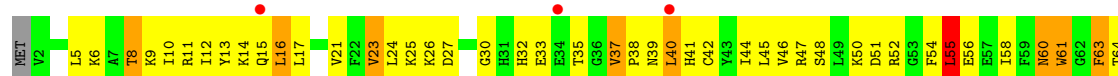
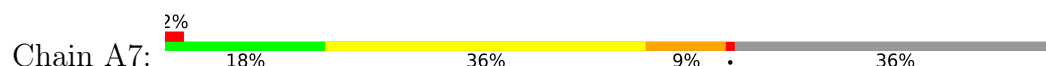
• Molecule 6: RPS27E



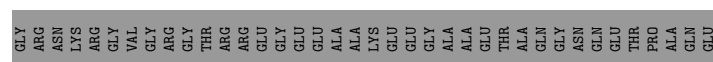
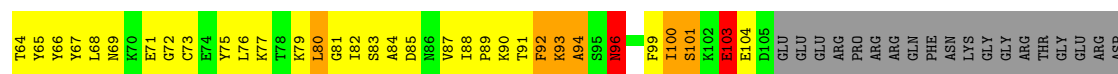
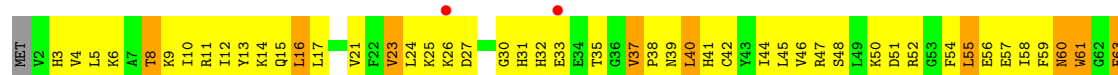
• Molecule 6: RPS27E



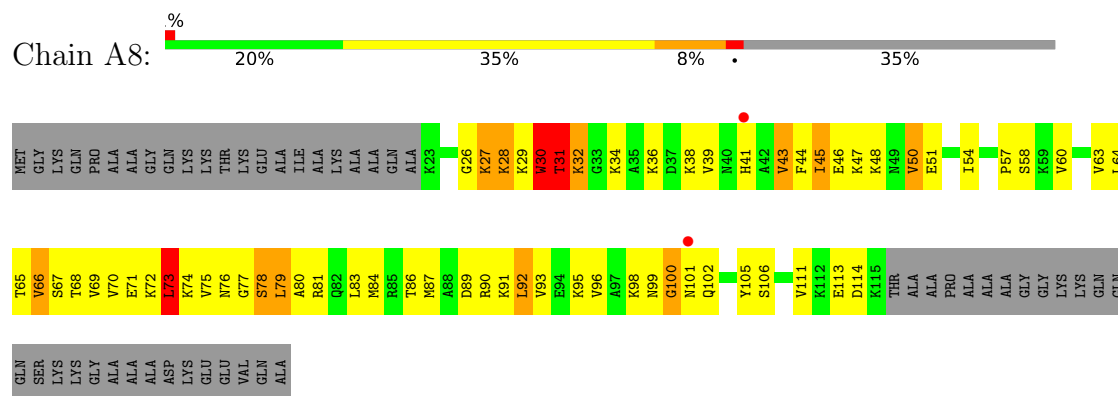
• Molecule 7: PLECTIN/S10 DOMAIN CONTAINING PROTEIN



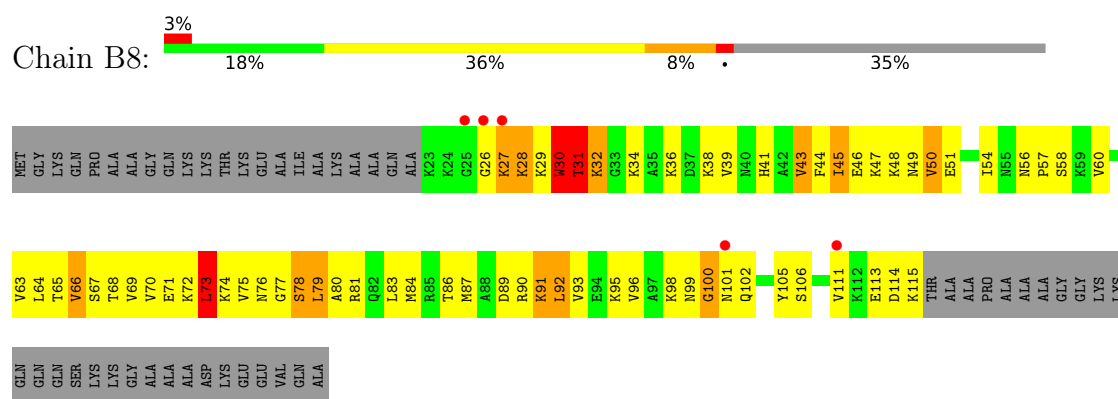
• Molecule 7: PLECTIN/S10 DOMAIN CONTAINING PROTEIN



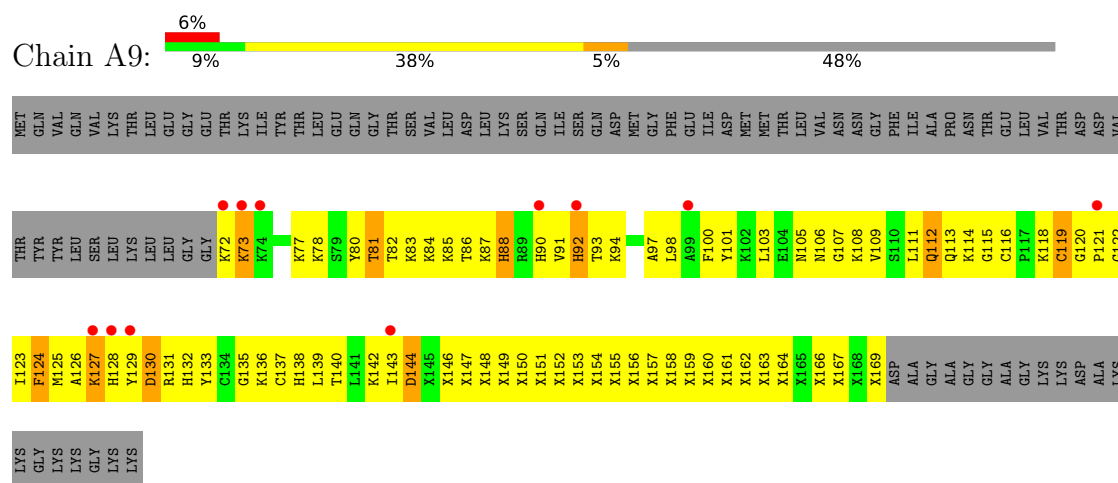
• Molecule 8: RPS25E



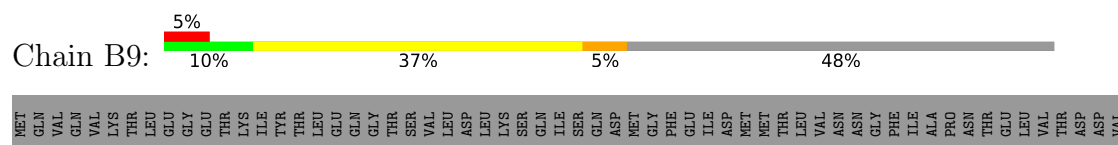
• Molecule 8: RPS25E

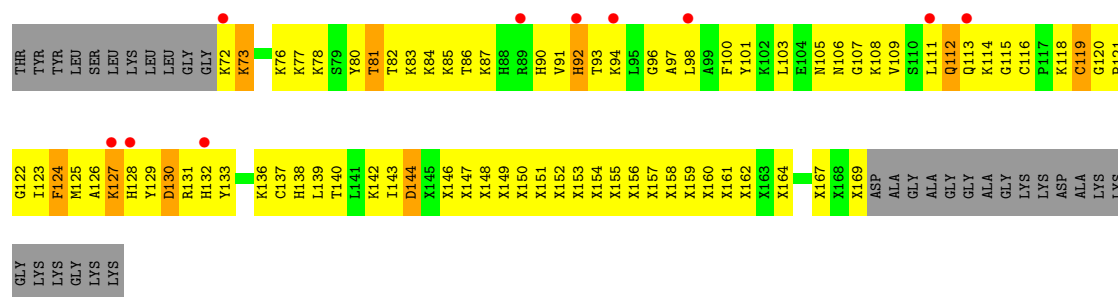


• Molecule 9: RPS31E

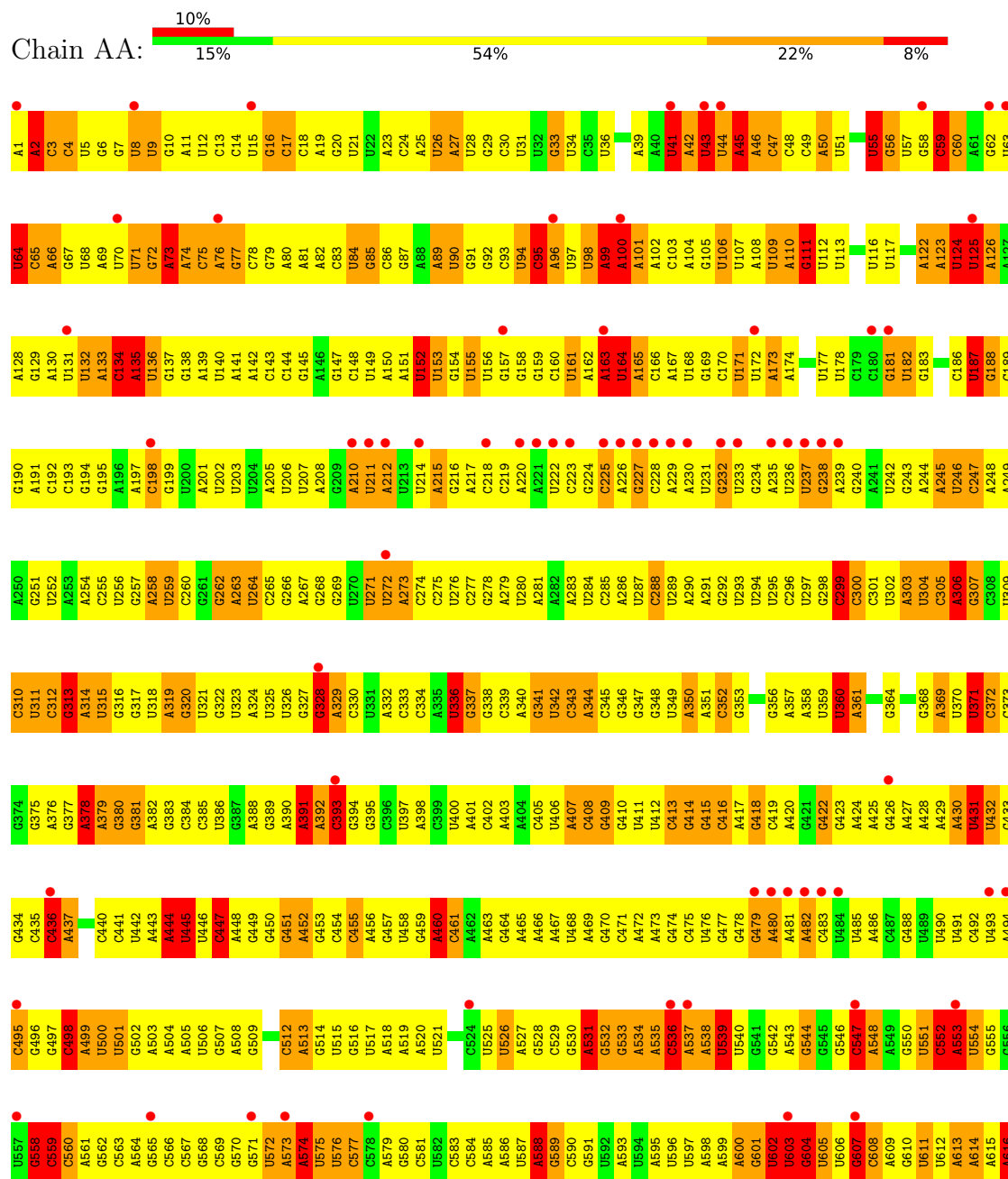


• Molecule 9: RPS31E

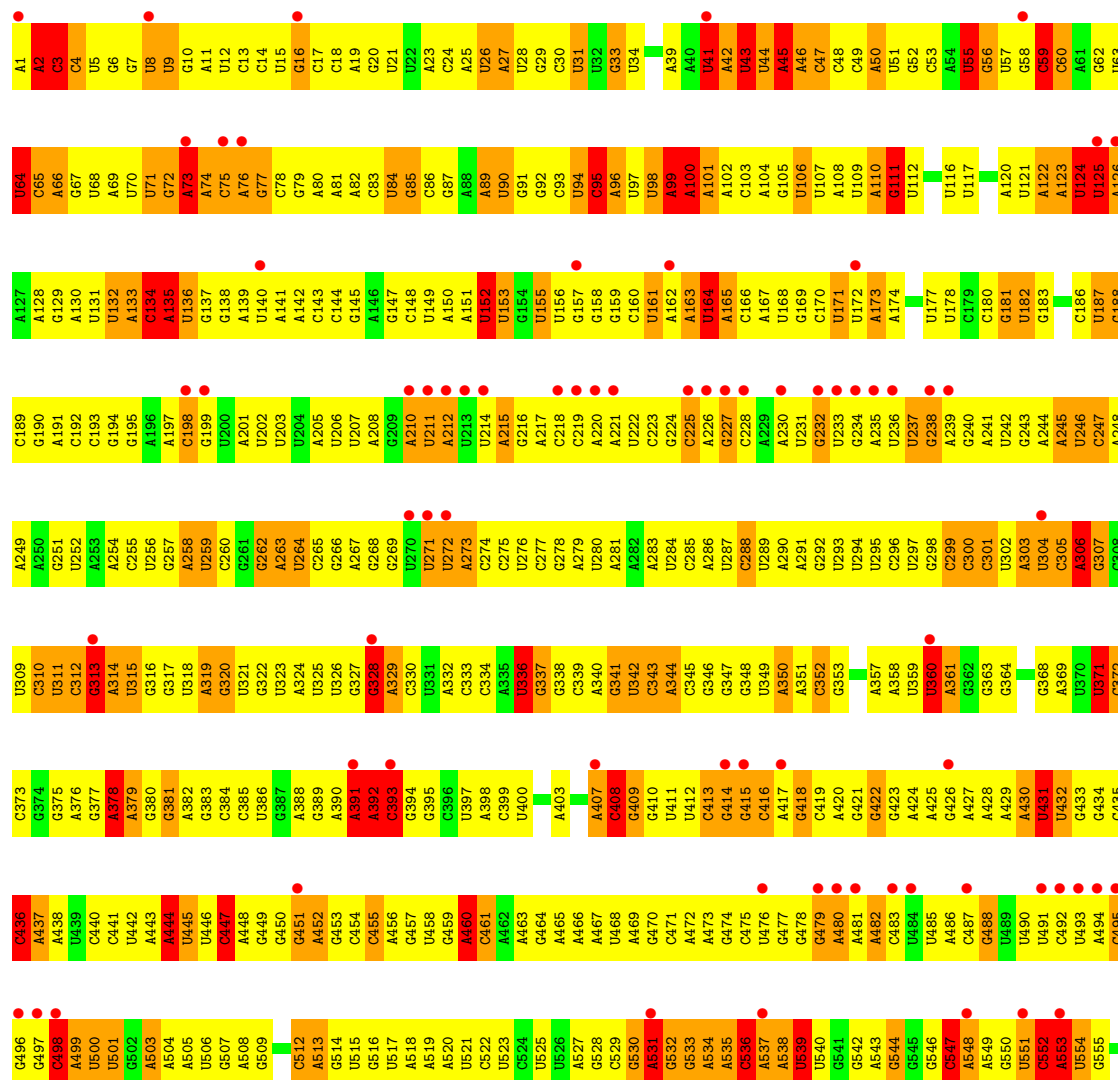


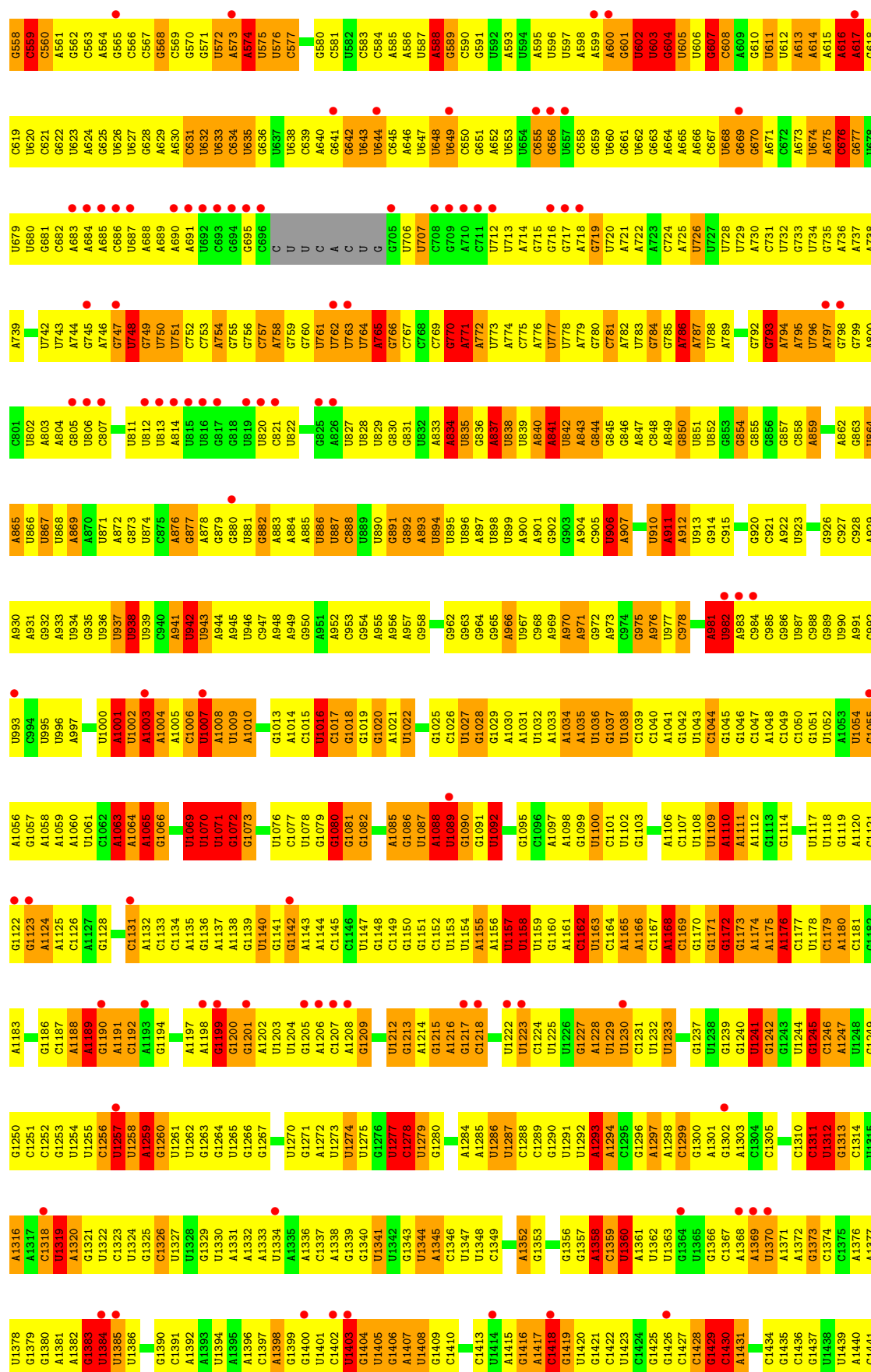


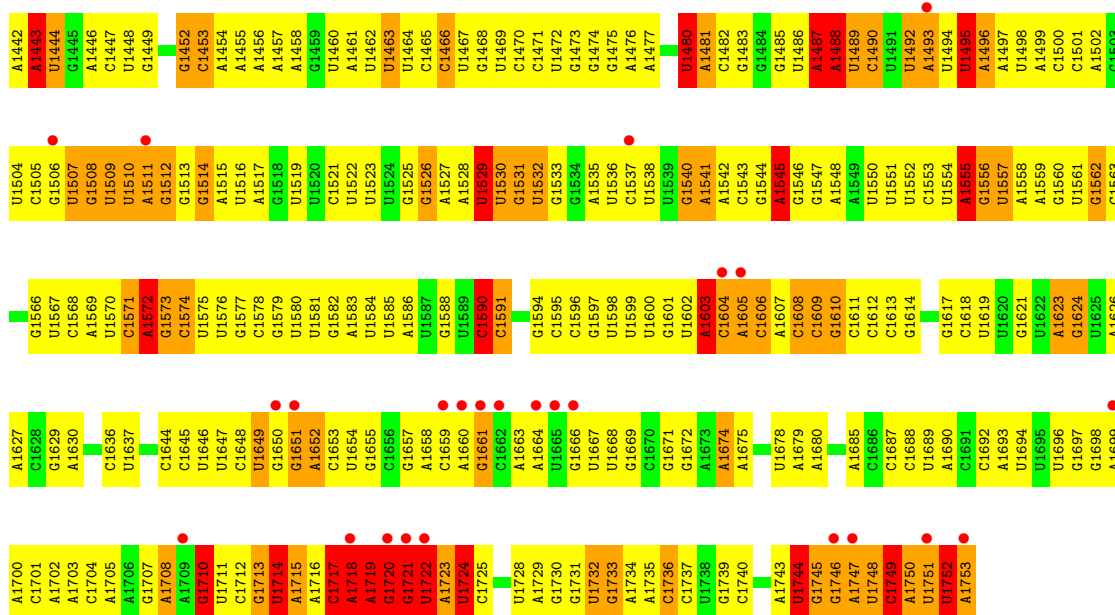
• Molecule 10: 18S RRNA



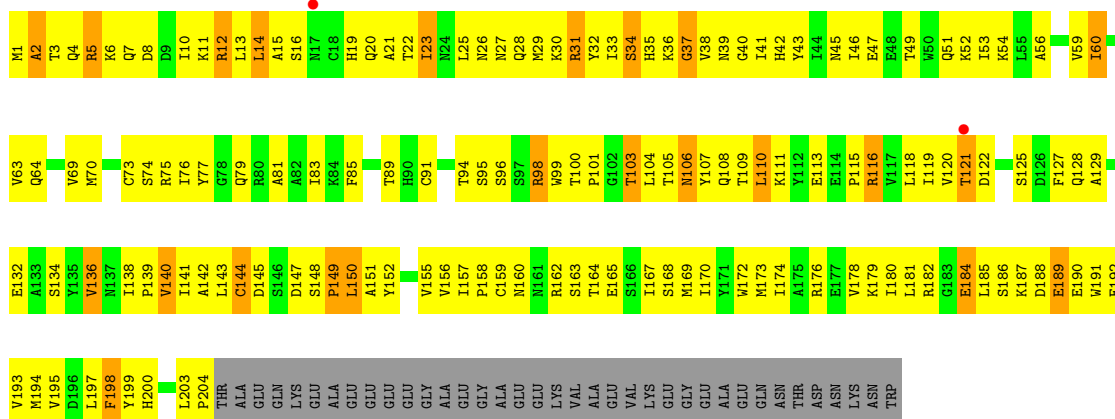






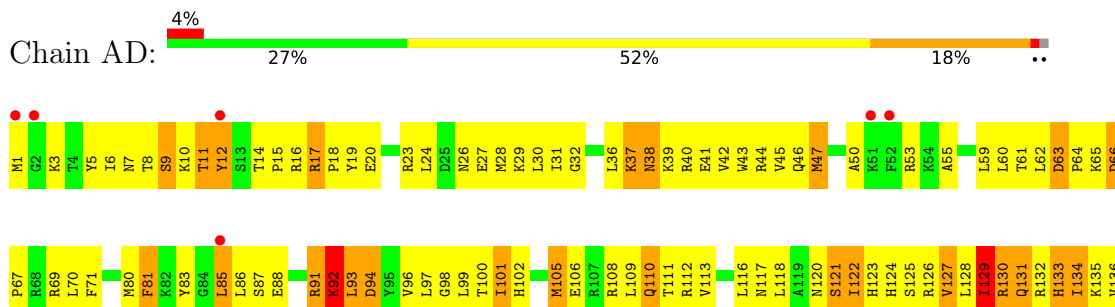


• Molecule 11: RPSOE



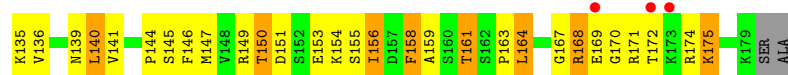
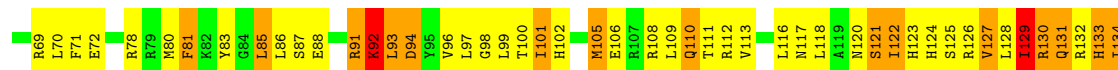
• Molecule 11: RPSOE



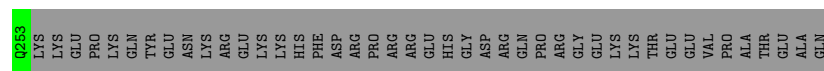
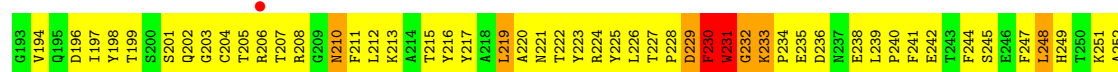
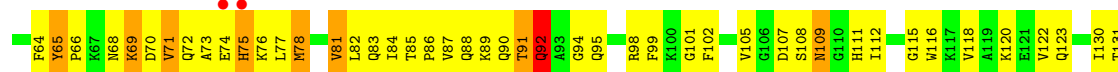
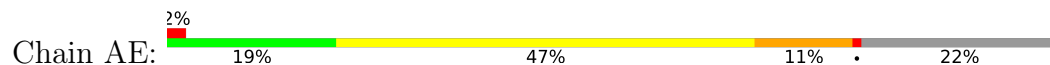




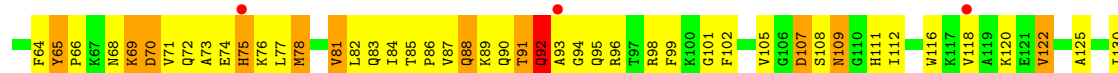
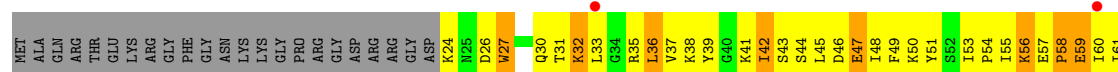
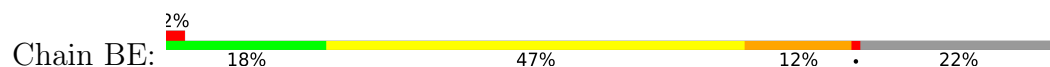
• Molecule 13: RIBOSOMAL PROTEIN S4 CONTAINING PROTEIN

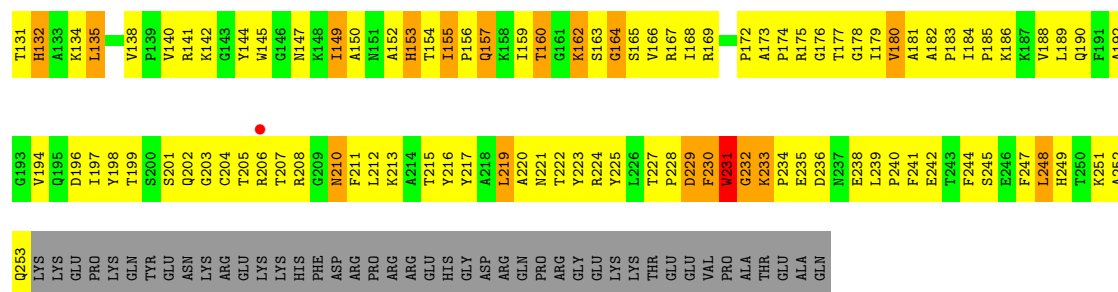


• Molecule 14: RIBOSOMAL PROTEIN S5 CONTAINING PROTEIN

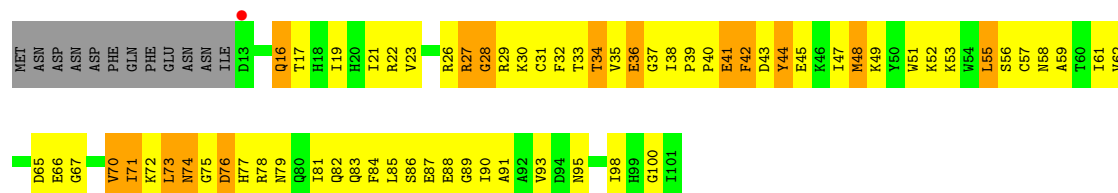


• Molecule 14: RIBOSOMAL PROTEIN S5 CONTAINING PROTEIN

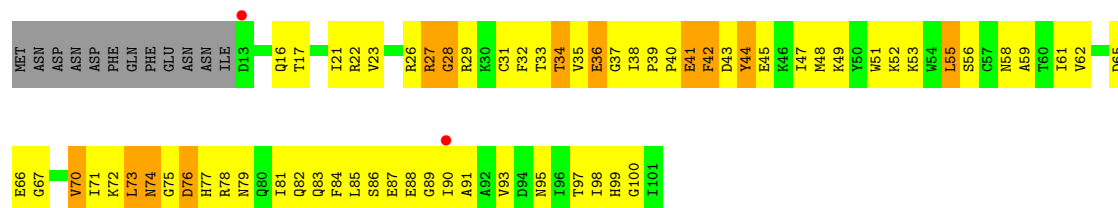




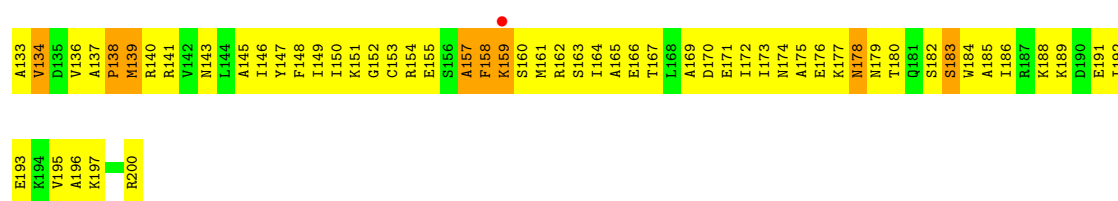
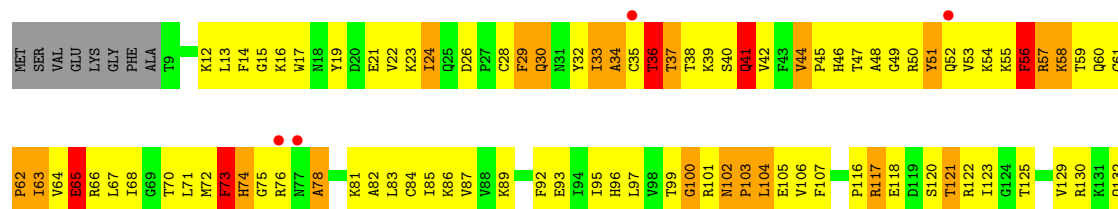
• Molecule 15: EIF1



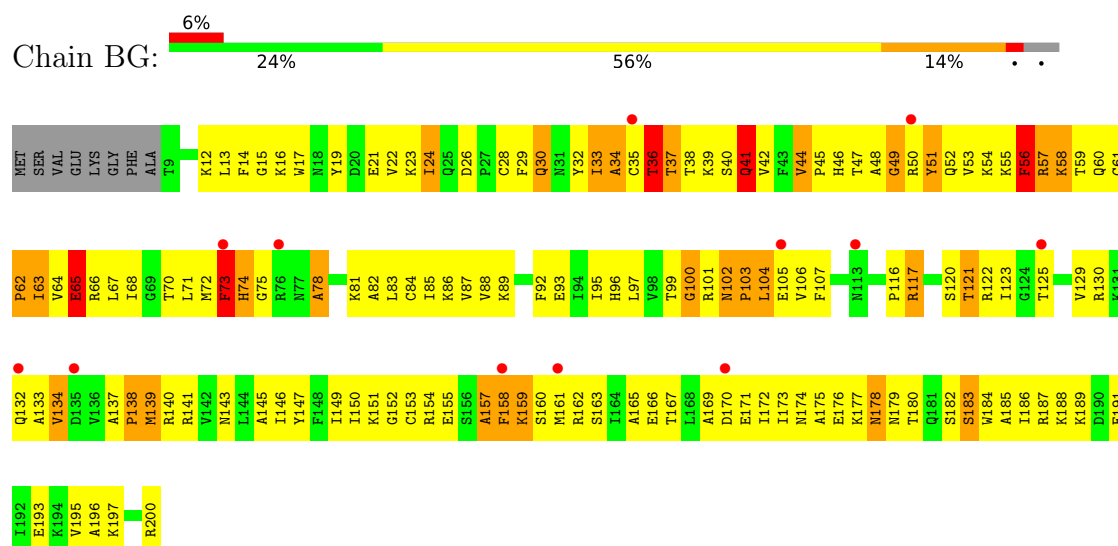
• Molecule 15: EIF1



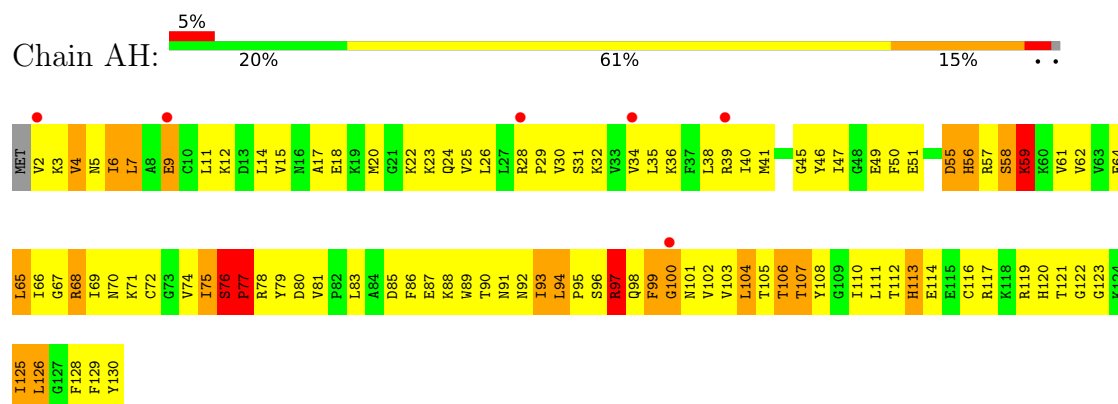
• Molecule 16: RIBOSOMAL PROTEIN S7 CONTAINING PROTEIN



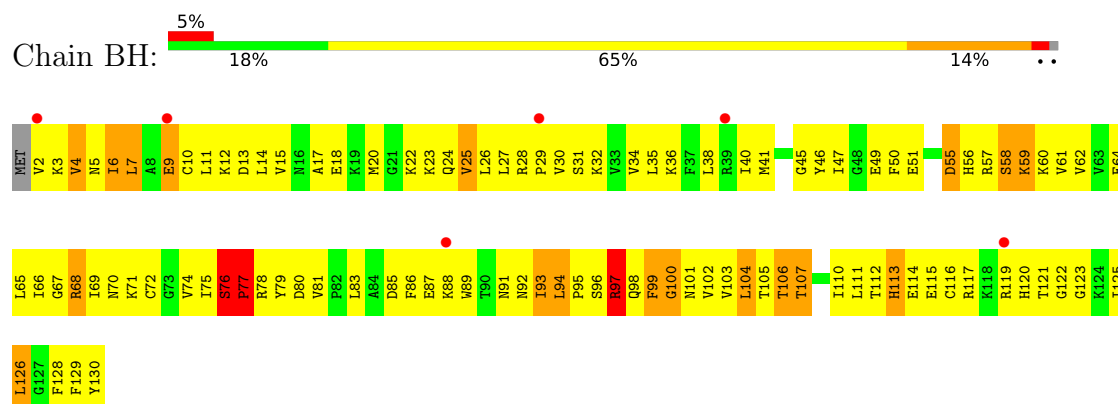
• Molecule 16: RIBOSOMAL PROTEIN S7 CONTAINING PROTEIN



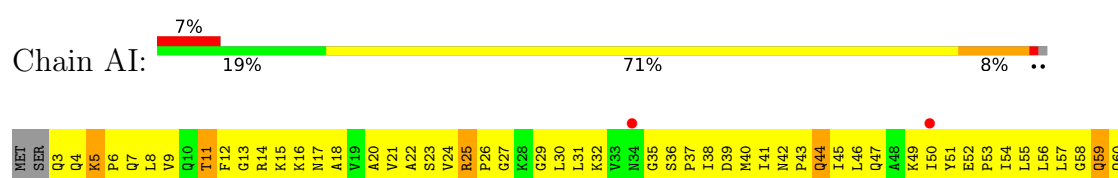
• Molecule 17: RIBOSOMAL PROTEIN S8 CONTAINING PROTEIN

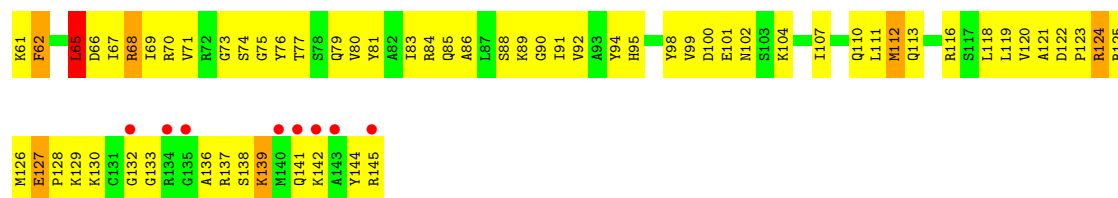


• Molecule 17: RIBOSOMAL PROTEIN S8 CONTAINING PROTEIN

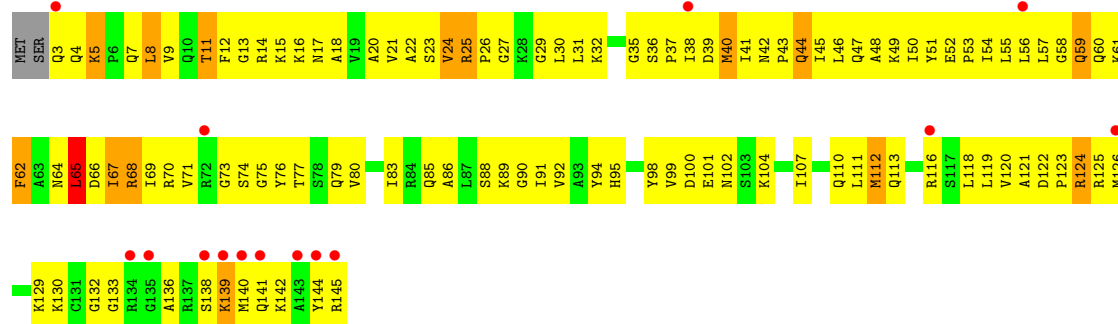


• Molecule 18: RPS16E, 40S RIBOSOMAL PROTEIN RPS16E

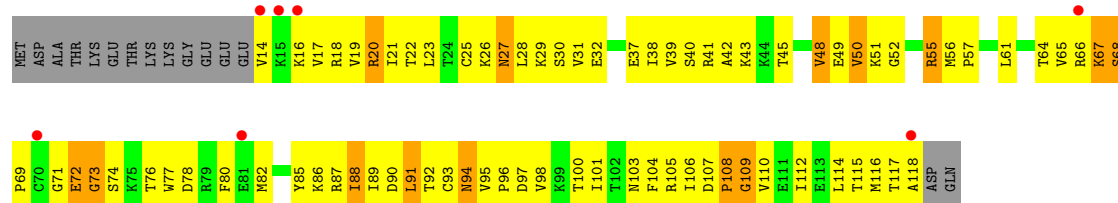




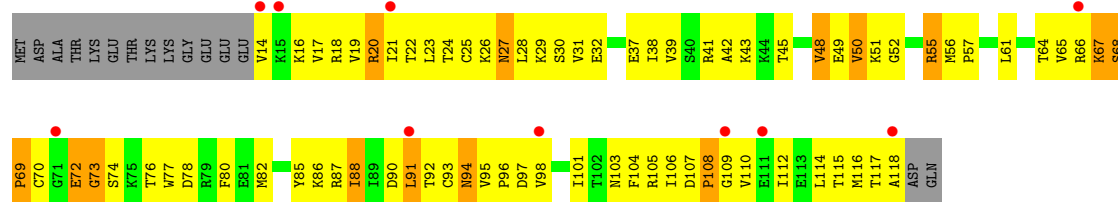
• Molecule 18: RPS16E, 40S RIBOSOMAL PROTEIN RPS16E



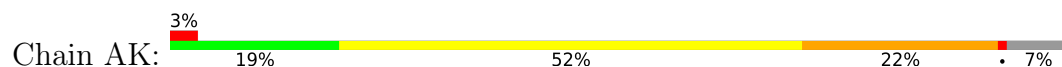
• Molecule 19: RIBOSOMAL PROTEIN S10 CONTAINING PROTEIN

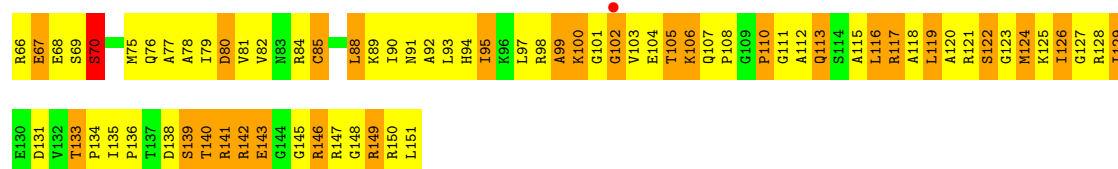


• Molecule 19: RIBOSOMAL PROTEIN S10 CONTAINING PROTEIN

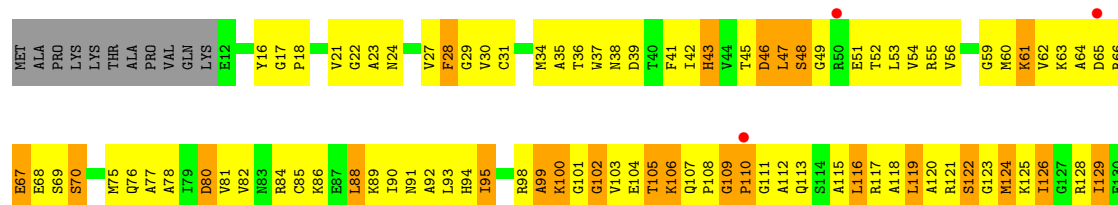
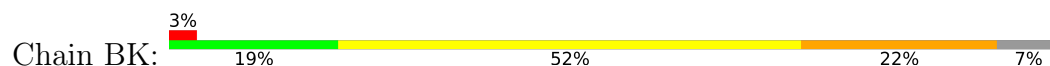


• Molecule 20: RPS14E

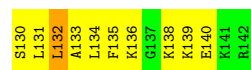
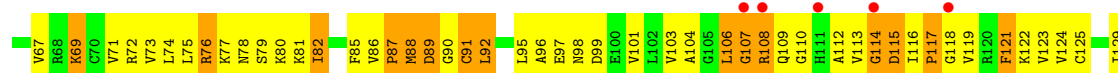
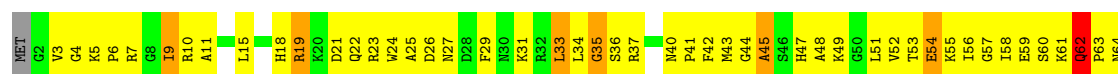




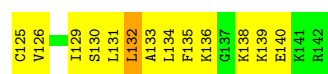
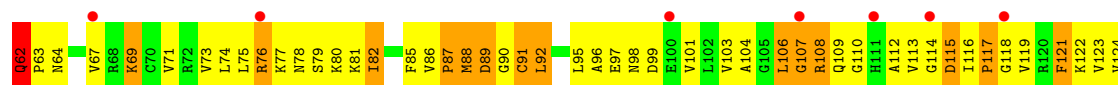
• Molecule 20: RPS14E



• Molecule 21: 40S RIBOSOMAL PROTEIN S12

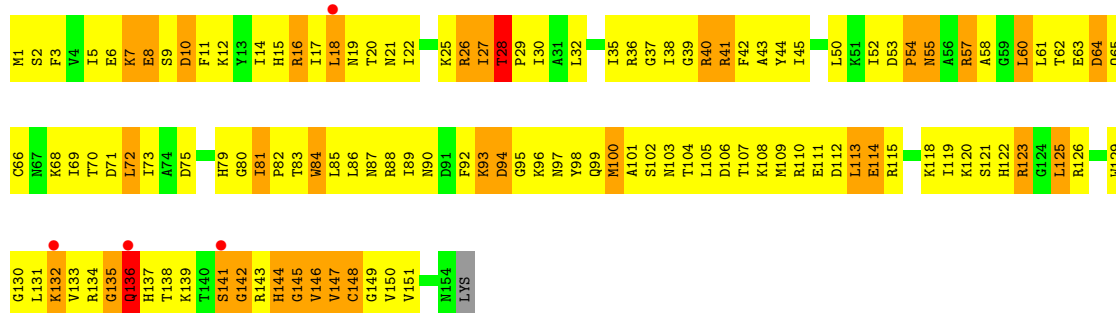


• Molecule 21: 40S RIBOSOMAL PROTEIN S12

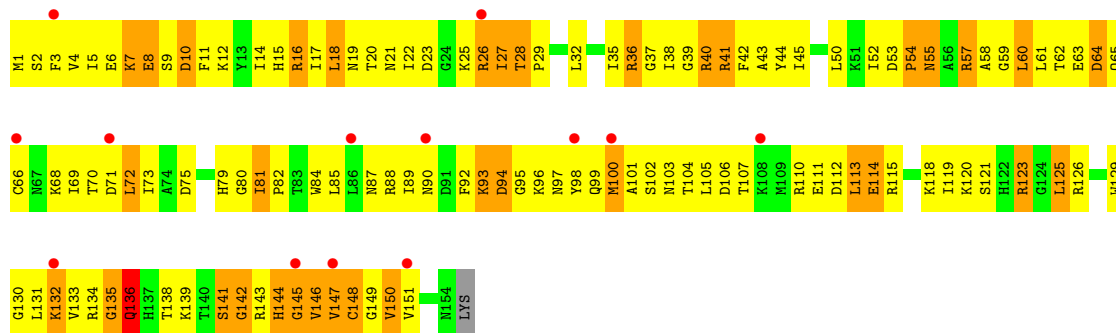


• Molecule 22: RPS18E

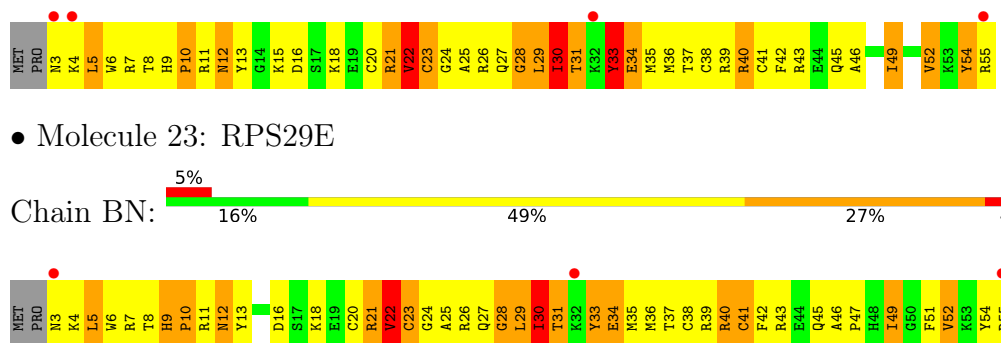
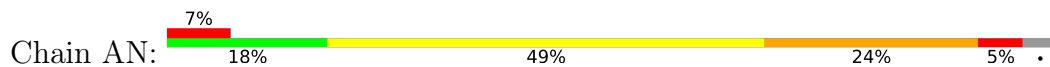




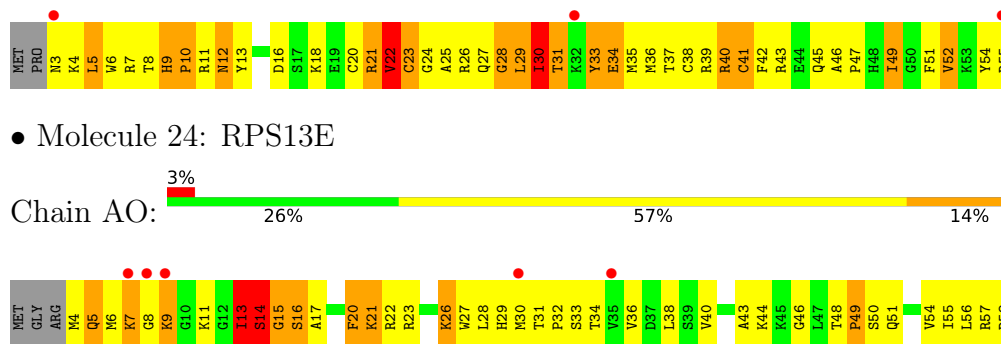
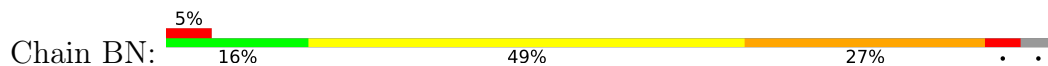
● Molecule 22: RPS18E



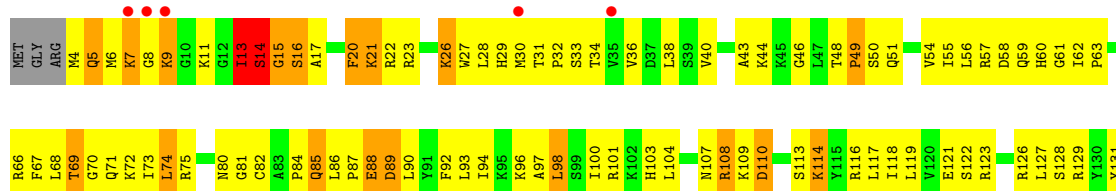
● Molecule 23: RPS29E

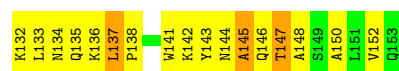


● Molecule 23: RPS29E

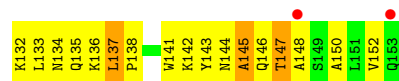
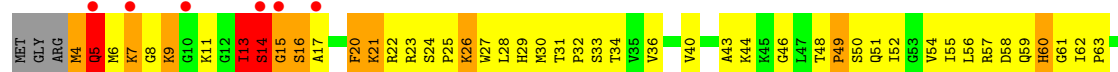


● Molecule 24: RPS13E

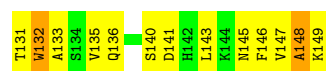
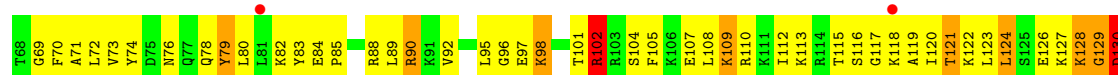
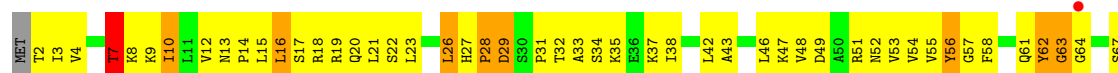




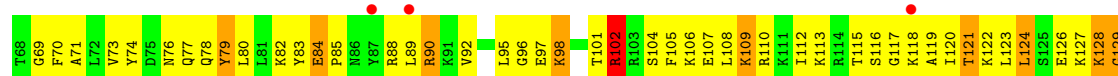
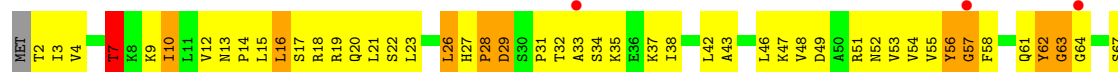
• Molecule 24: RPS13E



• Molecule 25: RPS24E

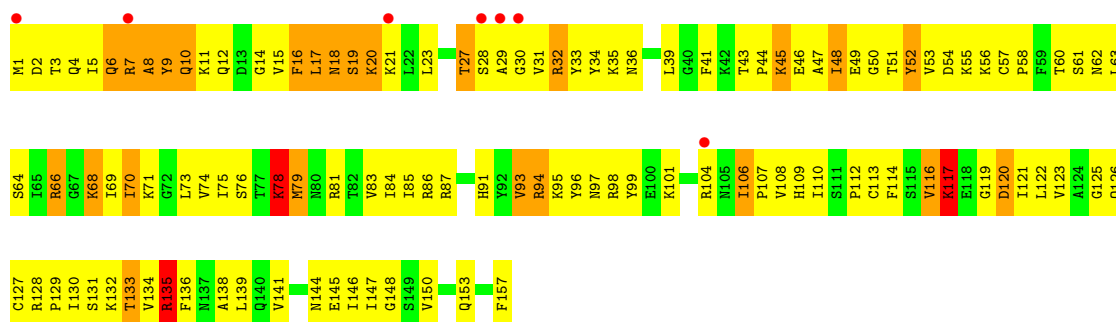


• Molecule 25: RPS24E

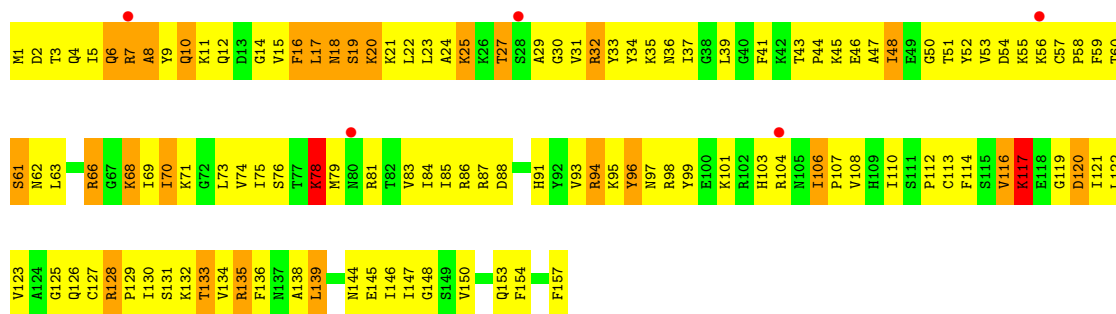


• Molecule 26: RIBOSOMAL PROTEIN S17 CONTAINING PROTEIN

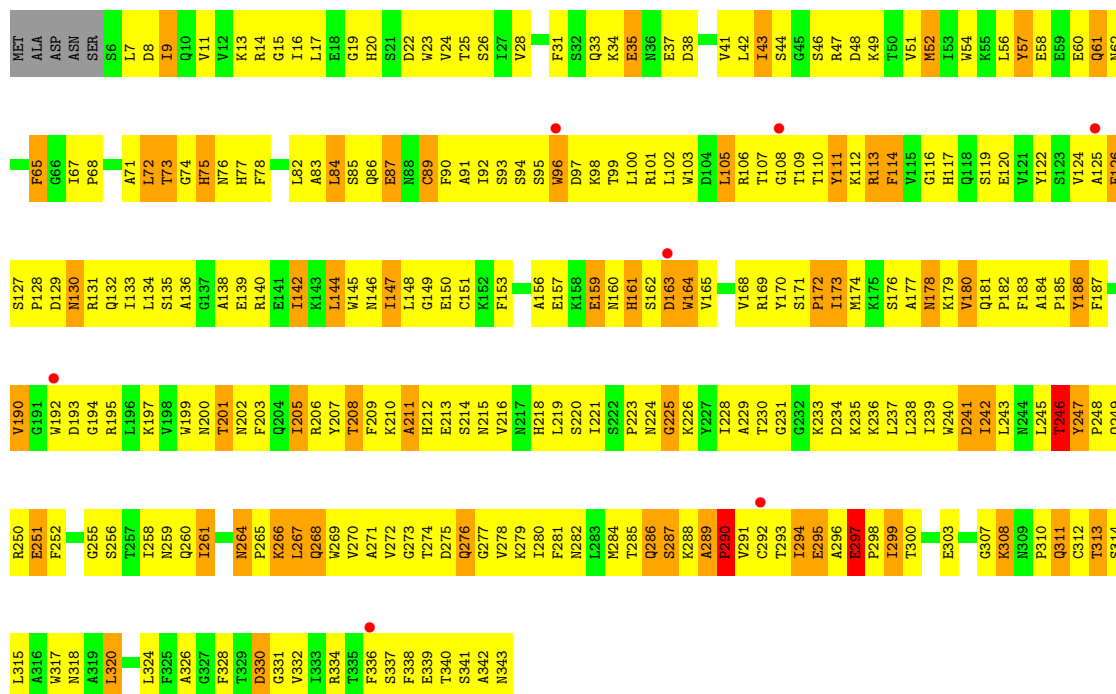




• Molecule 26: RIBOSOMAL PROTEIN S17 CONTAINING PROTEIN

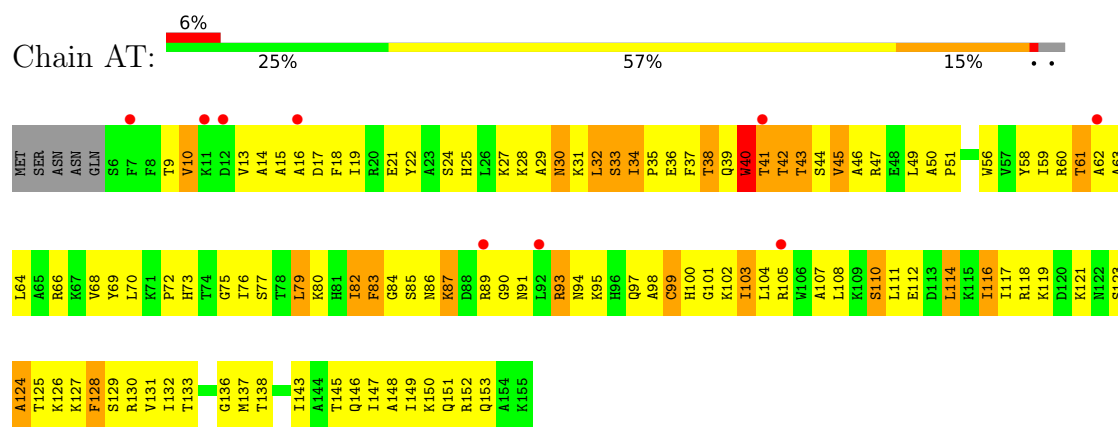


• Molecule 27: RACK1

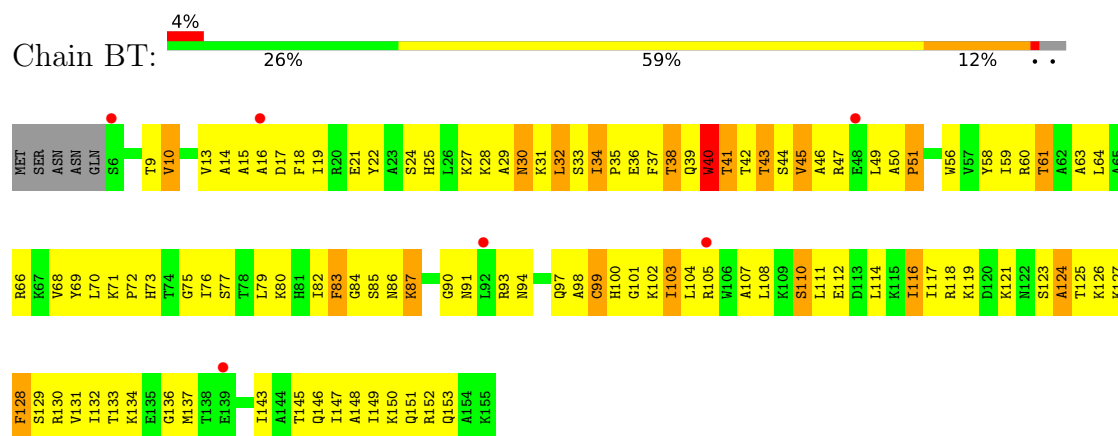


• Molecule 27: RACK1

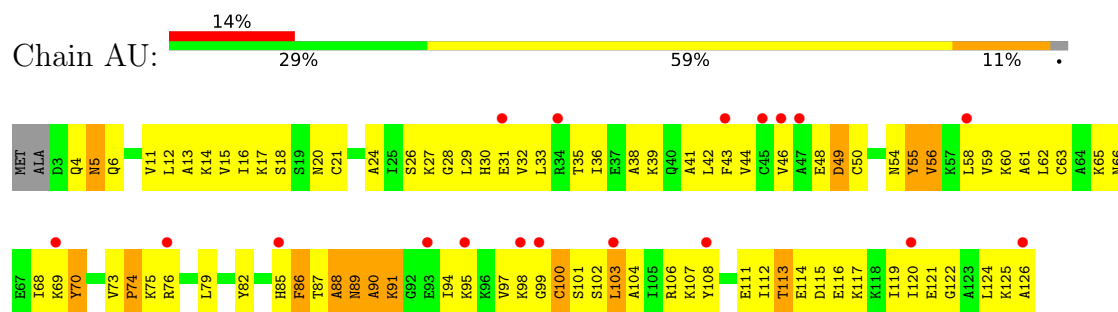




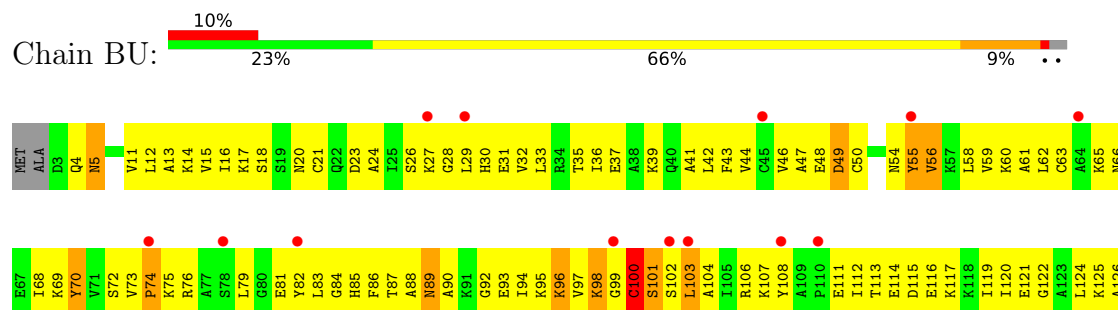
• Molecule 29: RPS19E



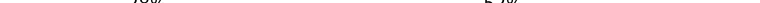
• Molecule 30: RIBOSOMAL PROTEIN L7AE CONTAINING PROTEIN

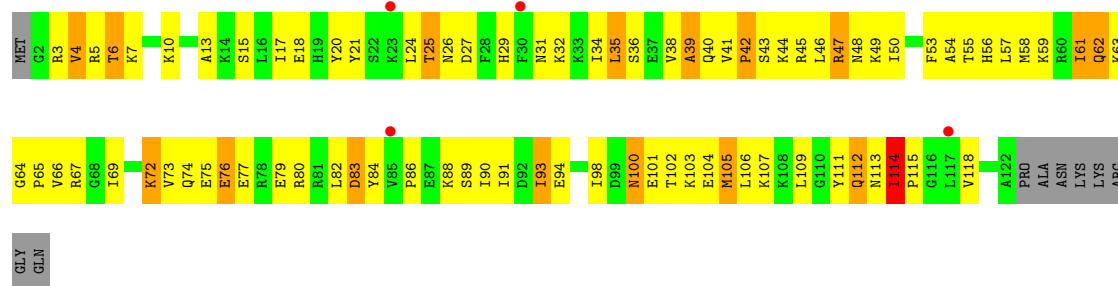


• Molecule 30: RIBOSOMAL PROTEIN L7AE CONTAINING PROTEIN

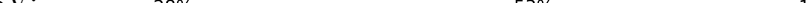


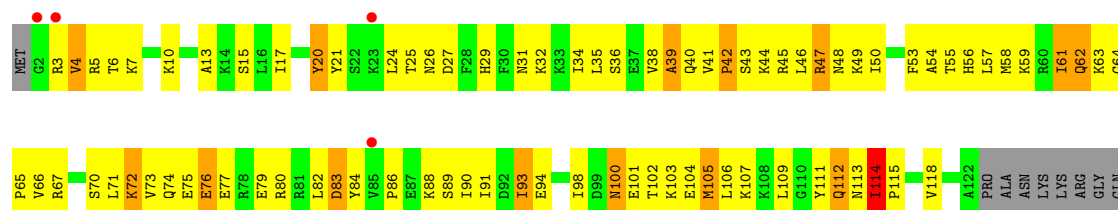
• Molecule 31: RPS17E

Chain AV: 

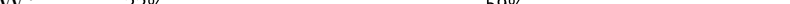


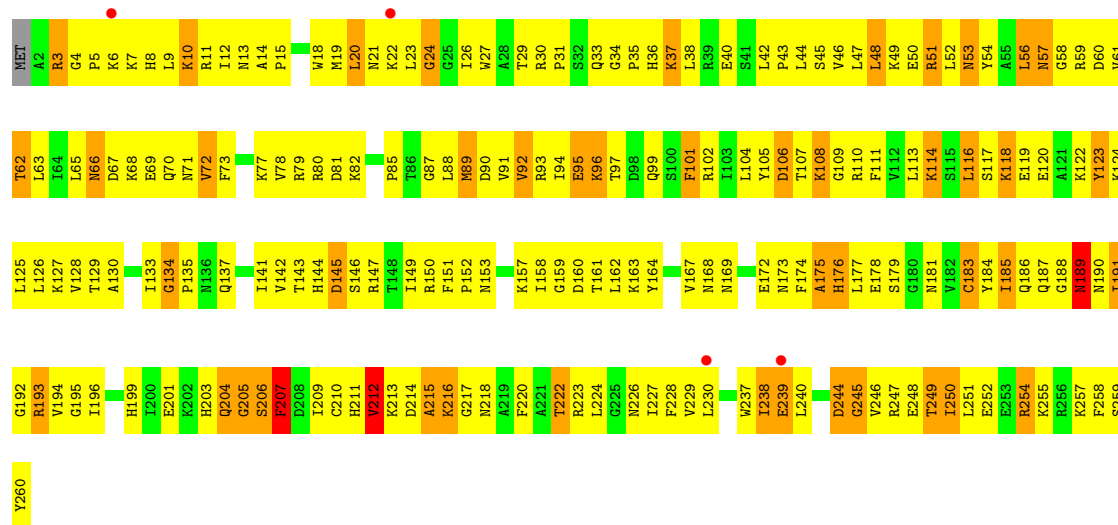
- Molecule 31: RPS17E

Chain BV: 

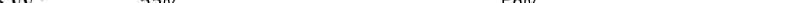


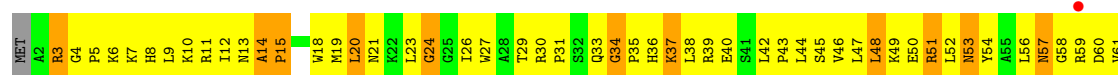
• Molecule 32: 40S RIBOSOMAL PROTEIN S4

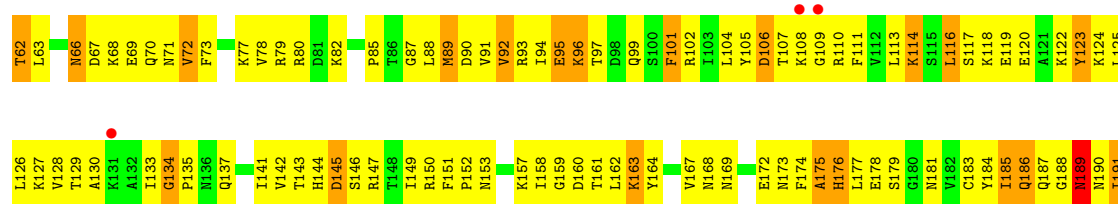
Chain AW: 



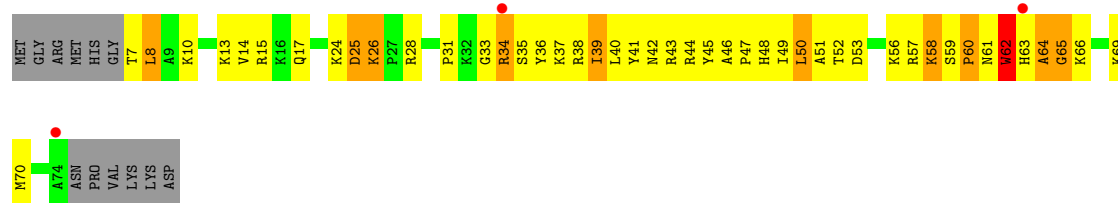
● Molecule 32: 40S RIBOSOMAL PROTEIN S4

Chain BW: 

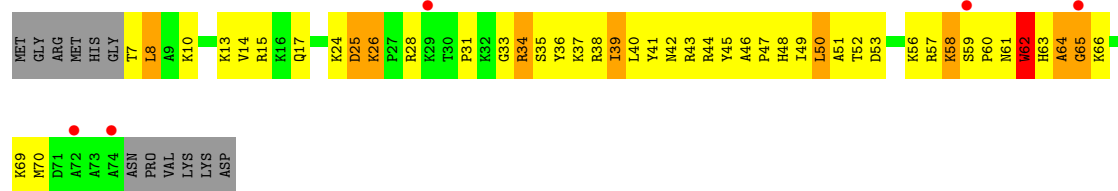




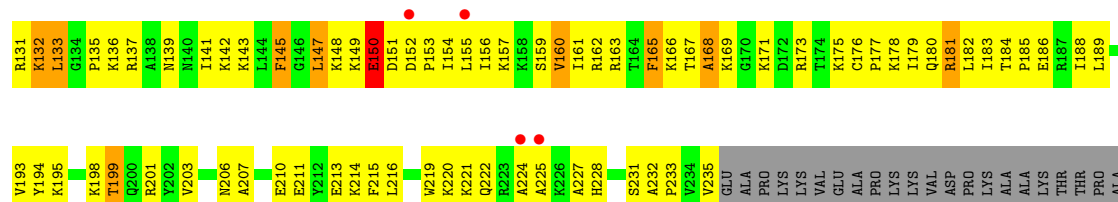
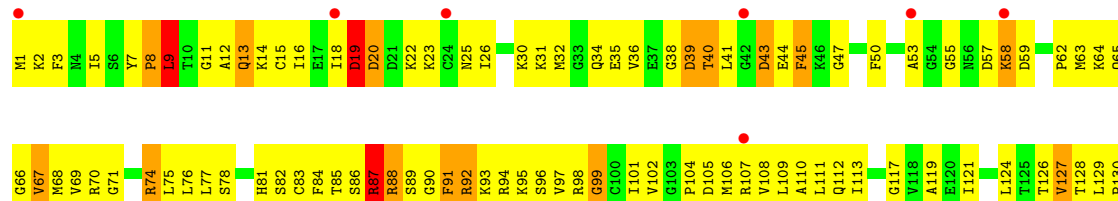
• Molecule 33: RPS30E



• Molecule 33: RPS30E



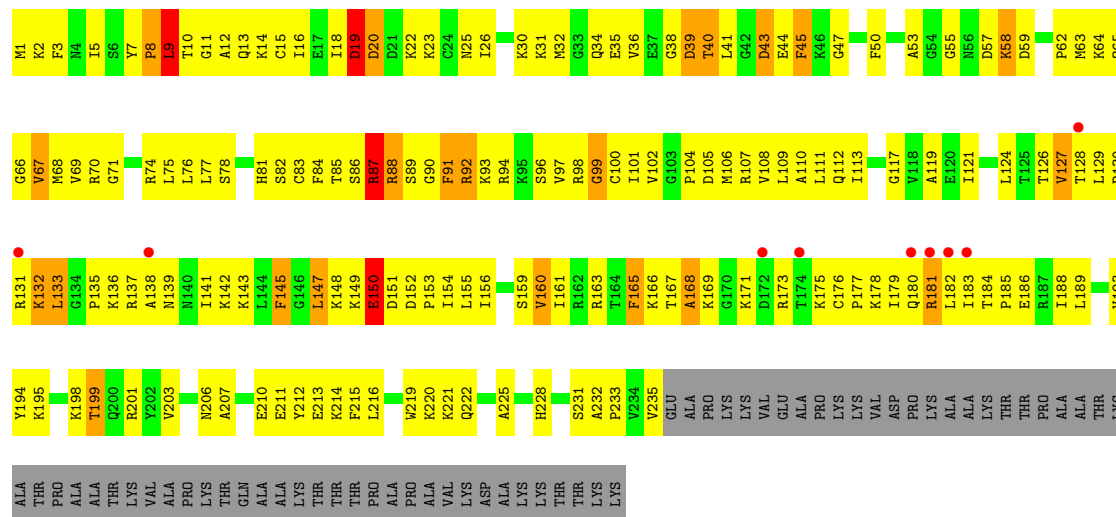
• Molecule 34: RPS6E



ALA THR LYS LYS ALA THR PRO PRO ALA ALA THR THR VAL VAL ALA PRO LYS THR GLN ALA ALA LYS THR THR THR PRO PRO ALA PRO ALA VAL LYS LYS ASP ALA LYS LYS THR THR LYS LYS

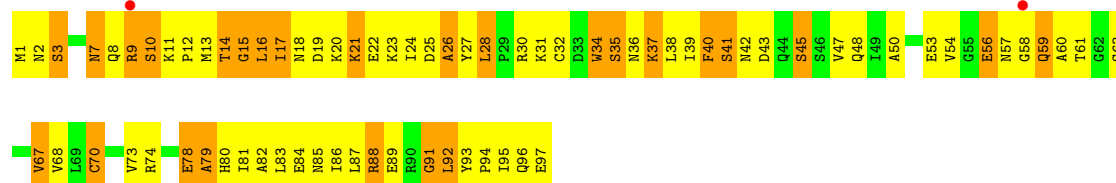
● Molecule 34: RPS6E

Chain BY: 3% 23% 49% 8% 20%



● Molecule 35: RPS21E

Chain AZ: 2% 23% 51% 27%



● Molecule 35: RPS21E

Chain BZ: % 24% 49% 27%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	320.52Å 362.21Å 412.11Å 90.00° 109.61° 90.00°	Depositor
Resolution (Å)	25.00 – 3.93 25.00 – 3.93	Depositor EDS
% Data completeness (in resolution range)	85.1 (25.00-3.93) 84.8 (25.00-3.93)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 3.89Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.206 , 0.243 0.209 , 0.243	Depositor DCC
R_{free} test set	7292 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	126.5	Xtriage
Anisotropy	0.335	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 101.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	157632	wwPDB-VP
Average B, all atoms (Å ²)	148.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.78% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	A1	0.47	0/518	1.06	2/688 (0.3%)
1	B1	0.46	0/518	1.06	2/688 (0.3%)
2	A2	0.49	0/1717	1.05	10/2288 (0.4%)
2	B2	0.49	0/1717	1.07	11/2288 (0.5%)
3	A3	0.46	0/1656	1.06	8/2223 (0.4%)
3	B3	0.51	0/1656	1.07	8/2223 (0.4%)
4	A4	0.49	0/1748	1.05	15/2340 (0.6%)
4	B4	0.50	0/1748	1.06	16/2340 (0.7%)
5	A5	0.50	0/807	1.09	5/1077 (0.5%)
5	B5	0.53	0/807	1.10	7/1077 (0.6%)
6	A6	0.54	0/640	1.07	3/855 (0.4%)
6	B6	0.59	0/640	1.09	6/855 (0.7%)
7	A7	0.49	0/879	1.12	9/1183 (0.8%)
7	B7	0.44	0/879	1.12	8/1183 (0.7%)
8	A8	0.46	0/732	0.99	2/974 (0.2%)
8	B8	0.46	0/732	0.99	2/974 (0.2%)
9	A9	0.47	0/605	1.01	3/799 (0.4%)
9	B9	0.48	0/605	1.00	4/799 (0.5%)
10	AA	0.46	2/41668 (0.0%)	0.87	140/64931 (0.2%)
10	BA	0.45	2/41668 (0.0%)	0.87	148/64931 (0.2%)
11	AB	0.51	0/1676	1.05	8/2273 (0.4%)
11	BB	0.51	0/1676	1.05	9/2273 (0.4%)
12	AC	0.56	0/1855	1.07	7/2490 (0.3%)
12	BC	0.52	0/1855	1.09	6/2490 (0.2%)
13	AD	0.56	0/1498	1.04	9/1998 (0.5%)
13	BD	0.50	0/1498	1.03	7/1998 (0.4%)
14	AE	0.59	0/1873	1.10	13/2533 (0.5%)
14	BE	0.55	0/1873	1.10	17/2533 (0.7%)
15	AF	0.53	0/751	1.03	2/1010 (0.2%)
15	BF	0.51	0/751	1.03	3/1010 (0.3%)
16	AG	0.54	0/1546	1.15	12/2079 (0.6%)
16	BG	0.56	0/1546	1.14	12/2079 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AH	0.63	0/1058	1.30	12/1421 (0.8%)
17	BH	0.63	0/1058	1.31	11/1421 (0.8%)
18	AI	0.54	0/1151	1.02	5/1540 (0.3%)
18	BI	0.54	0/1151	1.02	6/1540 (0.4%)
19	AJ	0.47	0/842	1.15	8/1133 (0.7%)
19	BJ	0.49	0/842	1.13	8/1133 (0.7%)
20	AK	0.53	0/1078	1.09	9/1452 (0.6%)
20	BK	0.52	0/1078	1.08	7/1452 (0.5%)
21	AL	0.53	0/1114	1.06	3/1485 (0.2%)
21	BL	0.55	0/1114	1.06	3/1485 (0.2%)
22	AM	0.49	0/1260	1.07	12/1690 (0.7%)
22	BM	0.48	0/1260	1.07	11/1690 (0.7%)
23	AN	0.52	0/457	1.09	5/608 (0.8%)
23	BN	0.51	0/457	1.10	4/608 (0.7%)
24	AO	0.56	0/1238	1.13	7/1658 (0.4%)
24	BO	0.57	0/1238	1.14	8/1658 (0.5%)
25	AP	0.50	0/1215	1.08	8/1626 (0.5%)
25	BP	0.47	0/1215	1.07	10/1626 (0.6%)
26	AQ	0.57	1/1298 (0.1%)	1.13	14/1741 (0.8%)
26	BQ	0.53	0/1298	1.14	11/1741 (0.6%)
27	AR	0.43	0/2750	1.05	20/3726 (0.5%)
27	BR	0.44	0/2750	1.05	20/3726 (0.5%)
28	AS	0.45	0/1003	1.03	6/1342 (0.4%)
28	BS	0.44	0/1003	1.05	7/1342 (0.5%)
29	AT	0.52	0/1233	1.02	3/1656 (0.2%)
29	BT	0.52	0/1233	1.03	2/1656 (0.1%)
30	AU	0.46	0/961	0.97	2/1288 (0.2%)
30	BU	0.42	0/961	0.97	0/1288
31	AV	0.52	0/992	1.10	4/1326 (0.3%)
31	BV	0.55	0/992	1.09	3/1326 (0.2%)
32	AW	0.52	0/2119	1.15	22/2849 (0.8%)
32	BW	0.50	0/2119	1.14	21/2849 (0.7%)
33	AX	0.46	0/566	1.18	5/753 (0.7%)
33	BX	0.43	0/566	1.19	5/753 (0.7%)
34	AY	0.46	0/1895	1.07	9/2523 (0.4%)
34	BY	0.45	0/1895	1.08	9/2523 (0.4%)
35	AZ	0.55	0/755	1.20	10/1013 (1.0%)
35	BZ	0.52	0/755	1.23	12/1013 (1.2%)
All	All	0.48	5/166308 (0.0%)	0.98	836/241142 (0.3%)

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

sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	A5	0	1
5	B5	0	1
10	AA	1	70
10	BA	1	74
26	BQ	0	1
27	AR	0	1
27	BR	0	1
All	All	2	149

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	AA	1109	U	O3'-P	5.95	1.70	1.61
10	BA	1109	U	O3'-P	-5.50	1.52	1.61
10	BA	1722	U	O5'-C5'	5.20	1.50	1.42
10	AA	1721	G	O3'-P	5.12	1.68	1.61
26	AQ	79	MET	SD-CE	-5.00	1.67	1.79

The worst 5 of 836 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	BH	107	THR	N-CA-C	-12.91	97.61	113.50
17	AH	107	THR	N-CA-C	-12.81	97.74	113.50
24	AO	70	GLY	N-CA-C	-11.79	97.92	115.72
34	BY	40	THR	N-CA-C	-11.67	100.60	112.97
34	AY	40	THR	N-CA-C	-11.65	100.62	112.97

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
10	AA	1718	A	C1'
10	BA	1718	A	C1'

5 of 149 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	A5	39	TYR	Sidechain
10	AA	43	U	Sidechain
10	AA	55	U	Sidechain
10	AA	59	C	Sidechain
10	AA	64	U	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	A1	519	0	550	78	0
1	B1	519	0	550	78	0
2	A2	1693	0	1795	270	0
2	B2	1693	0	1795	274	0
3	A3	1629	0	1708	189	0
3	B3	1629	0	1708	181	0
4	A4	1724	0	1822	204	0
4	B4	1724	0	1822	196	0
5	A5	797	0	836	124	0
5	B5	797	0	837	111	0
6	A6	632	0	646	89	0
6	B6	632	0	646	95	0
7	A7	859	0	860	126	0
7	B7	859	0	860	134	0
8	A8	725	0	795	141	0
8	B8	725	0	795	132	0
9	A9	742	0	785	153	0
9	B9	742	0	787	137	0
10	AA	37231	0	18715	3090	0
10	BA	37231	0	18715	3026	0
11	AB	1642	0	1653	215	0
11	BB	1642	0	1653	226	0
12	AC	1820	0	1920	257	0
12	BC	1820	0	1920	242	0
13	AD	1475	0	1571	223	0
13	BD	1475	0	1571	222	0
14	AE	1827	0	1861	297	0
14	BE	1827	0	1861	293	0
15	AF	736	0	722	87	0
15	BF	736	0	722	94	0
16	AG	1520	0	1572	236	0
16	BG	1520	0	1572	236	0
17	AH	1040	0	1096	171	0
17	BH	1040	0	1096	179	0
18	AI	1135	0	1204	162	0
18	BI	1135	0	1204	152	0
19	AJ	833	0	903	88	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	BJ	833	0	903	84	0
20	AK	1063	0	1088	195	0
20	BK	1063	0	1088	185	0
21	AL	1097	0	1169	141	0
21	BL	1097	0	1169	139	0
22	AM	1239	0	1288	204	0
22	BM	1239	0	1288	204	0
23	AN	447	0	446	81	0
23	BN	447	0	446	89	0
24	AO	1214	0	1322	134	0
24	BO	1214	0	1322	131	0
25	AP	1197	0	1285	158	0
25	BP	1197	0	1285	150	0
26	AQ	1275	0	1354	222	0
26	BQ	1275	0	1354	205	0
27	AR	2682	0	2629	365	0
27	BR	2682	0	2629	340	0
28	AS	985	0	1026	122	0
28	BS	985	0	1026	132	0
29	AT	1211	0	1265	163	0
29	BT	1211	0	1265	167	0
30	AU	952	0	993	110	0
30	BU	952	0	993	129	0
31	AV	979	0	1041	139	0
31	BV	979	0	1041	146	0
32	AW	2079	0	2151	295	0
32	BW	2079	0	2151	304	0
33	AX	554	0	604	66	0
33	BX	554	0	604	77	0
34	AY	1868	0	1999	264	0
34	BY	1868	0	1999	248	0
35	AZ	747	0	758	108	0
35	BZ	747	0	758	111	0
36	A4	1	0	0	0	0
36	AA	90	0	0	0	0
36	AL	1	0	0	0	0
36	B4	1	0	0	0	0
36	BA	89	0	0	0	0
36	BD	1	0	0	0	0
36	BW	1	0	0	0	0
37	A5	1	0	0	0	0
37	A6	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	A9	1	0	0	0	0
37	AN	1	0	0	0	0
37	B5	1	0	0	0	0
37	B6	1	0	0	0	0
37	B9	1	0	0	0	0
37	BN	1	0	0	0	0
38	A2	2	0	0	0	0
38	A4	2	0	0	0	0
38	A5	1	0	0	0	0
38	AA	516	0	0	14	0
38	AC	1	0	0	0	0
38	AD	4	0	0	0	0
38	AE	3	0	0	0	0
38	AL	3	0	0	0	0
38	AM	4	0	0	1	0
38	AO	1	0	0	0	0
38	AP	1	0	0	0	0
38	AQ	2	0	0	0	0
38	AT	4	0	0	0	0
38	AW	4	0	0	0	0
38	AY	4	0	0	0	0
38	B2	2	0	0	0	0
38	B4	2	0	0	0	0
38	B5	1	0	0	0	0
38	BA	512	0	0	5	0
38	BC	2	0	0	0	0
38	BD	2	0	0	0	0
38	BE	5	0	0	0	0
38	BK	1	0	0	0	0
38	BL	2	0	0	0	0
38	BM	6	0	0	0	0
38	BO	1	0	0	0	0
38	BP	1	0	0	0	0
38	BQ	1	0	0	0	0
38	BT	6	0	0	0	0
38	BW	5	0	0	0	0
38	BY	3	0	0	0	0
All	All	157632	0	122867	15711	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 56.

The worst 5 of 15711 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)
10:AA:604:G:H1	10:AA:1080:G:N2	1.23	1.36
4:A4:207:THR:HG21	4:A4:213:LEU:HG	1.21	1.21
10:BA:604:G:H1	10:BA:1080:G:N2	1.40	1.19
21:AL:9:ILE:H	21:AL:9:ILE:HD12	1.02	1.18
10:AA:534:A:H3'	10:AA:535:A:H5'	1.18	1.18

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 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	A1	65/68 (96%)	45 (69%)	11 (17%)	9 (14%)	0	3
1	B1	65/68 (96%)	44 (68%)	12 (18%)	9 (14%)	0	3
2	A2	205/208 (99%)	147 (72%)	38 (18%)	20 (10%)	0	8
2	B2	205/208 (99%)	146 (71%)	39 (19%)	20 (10%)	0	8
3	A3	194/197 (98%)	159 (82%)	25 (13%)	10 (5%)	1	18
3	B3	194/197 (98%)	159 (82%)	24 (12%)	11 (6%)	1	17
4	A4	213/265 (80%)	161 (76%)	33 (16%)	19 (9%)	0	10
4	B4	213/265 (80%)	161 (76%)	34 (16%)	18 (8%)	0	10
5	A5	96/119 (81%)	66 (69%)	20 (21%)	10 (10%)	0	7
5	B5	96/119 (81%)	65 (68%)	21 (22%)	10 (10%)	0	7
6	A6	78/81 (96%)	57 (73%)	15 (19%)	6 (8%)	1	12
6	B6	78/81 (96%)	57 (73%)	15 (19%)	6 (8%)	1	12
7	A7	102/162 (63%)	78 (76%)	17 (17%)	7 (7%)	1	14
7	B7	102/162 (63%)	78 (76%)	17 (17%)	7 (7%)	1	14
8	A8	91/143 (64%)	71 (78%)	13 (14%)	7 (8%)	1	12
8	B8	91/143 (64%)	71 (78%)	13 (14%)	7 (8%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	A9	72/189 (38%)	50 (69%)	17 (24%)	5 (7%)	1	14
9	B9	72/189 (38%)	50 (69%)	17 (24%)	5 (7%)	1	14
11	AB	202/241 (84%)	168 (83%)	28 (14%)	6 (3%)	3	26
11	BB	202/241 (84%)	167 (83%)	28 (14%)	7 (4%)	3	23
12	AC	227/243 (93%)	177 (78%)	31 (14%)	19 (8%)	0	10
12	BC	227/243 (93%)	176 (78%)	32 (14%)	19 (8%)	0	10
13	AD	177/181 (98%)	132 (75%)	36 (20%)	9 (5%)	1	18
13	BD	177/181 (98%)	130 (73%)	38 (22%)	9 (5%)	1	18
14	AE	228/296 (77%)	170 (75%)	40 (18%)	18 (8%)	1	12
14	BE	228/296 (77%)	172 (75%)	39 (17%)	17 (8%)	1	13
15	AF	87/101 (86%)	70 (80%)	12 (14%)	5 (6%)	1	17
15	BF	87/101 (86%)	70 (80%)	12 (14%)	5 (6%)	1	17
16	AG	190/200 (95%)	141 (74%)	33 (17%)	16 (8%)	0	10
16	BG	190/200 (95%)	142 (75%)	31 (16%)	17 (9%)	0	10
17	AH	127/130 (98%)	98 (77%)	24 (19%)	5 (4%)	2	22
17	BH	127/130 (98%)	98 (77%)	26 (20%)	3 (2%)	4	30
18	AI	141/145 (97%)	111 (79%)	25 (18%)	5 (4%)	3	23
18	BI	141/145 (97%)	110 (78%)	26 (18%)	5 (4%)	3	23
19	AJ	103/120 (86%)	89 (86%)	6 (6%)	8 (8%)	1	12
19	BJ	103/120 (86%)	89 (86%)	6 (6%)	8 (8%)	1	12
20	AK	138/151 (91%)	96 (70%)	28 (20%)	14 (10%)	0	8
20	BK	138/151 (91%)	95 (69%)	27 (20%)	16 (12%)	0	5
21	AL	139/142 (98%)	106 (76%)	17 (12%)	16 (12%)	0	5
21	BL	139/142 (98%)	106 (76%)	18 (13%)	15 (11%)	0	6
22	AM	152/155 (98%)	109 (72%)	22 (14%)	21 (14%)	0	3
22	BM	152/155 (98%)	110 (72%)	21 (14%)	21 (14%)	0	3
23	AN	51/55 (93%)	30 (59%)	11 (22%)	10 (20%)	0	1
23	BN	51/55 (93%)	31 (61%)	11 (22%)	9 (18%)	0	2
24	AO	148/153 (97%)	112 (76%)	20 (14%)	16 (11%)	0	6
24	BO	148/153 (97%)	113 (76%)	19 (13%)	16 (11%)	0	6
25	AP	146/149 (98%)	115 (79%)	20 (14%)	11 (8%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	BP	146/149 (98%)	115 (79%)	20 (14%)	11 (8%)	1	13
26	AQ	155/157 (99%)	115 (74%)	26 (17%)	14 (9%)	0	10
26	BQ	155/157 (99%)	112 (72%)	27 (17%)	16 (10%)	0	7
27	AR	336/343 (98%)	255 (76%)	48 (14%)	33 (10%)	0	8
27	BR	336/343 (98%)	256 (76%)	48 (14%)	32 (10%)	0	9
28	AS	123/144 (85%)	91 (74%)	25 (20%)	7 (6%)	1	17
28	BS	123/144 (85%)	90 (73%)	25 (20%)	8 (6%)	1	15
29	AT	148/155 (96%)	114 (77%)	17 (12%)	17 (12%)	0	5
29	BT	148/155 (96%)	113 (76%)	20 (14%)	15 (10%)	0	8
30	AU	122/126 (97%)	91 (75%)	20 (16%)	11 (9%)	0	10
30	BU	122/126 (97%)	89 (73%)	22 (18%)	11 (9%)	0	10
31	AV	119/130 (92%)	94 (79%)	16 (13%)	9 (8%)	1	13
31	BV	119/130 (92%)	96 (81%)	14 (12%)	9 (8%)	1	13
32	AW	257/260 (99%)	193 (75%)	40 (16%)	24 (9%)	0	10
32	BW	257/260 (99%)	195 (76%)	38 (15%)	24 (9%)	0	10
33	AX	66/80 (82%)	48 (73%)	12 (18%)	6 (9%)	0	10
33	BX	66/80 (82%)	48 (73%)	12 (18%)	6 (9%)	0	10
34	AY	233/293 (80%)	188 (81%)	31 (13%)	14 (6%)	1	16
34	BY	233/293 (80%)	187 (80%)	32 (14%)	14 (6%)	1	16
35	AZ	95/97 (98%)	70 (74%)	13 (14%)	12 (13%)	0	4
35	BZ	95/97 (98%)	69 (73%)	14 (15%)	12 (13%)	0	4
All	All	10052/11358 (88%)	7627 (76%)	1588 (16%)	837 (8%)	0	11

5 of 837 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A1	20	SER
1	A1	35	LYS
1	A1	37	GLU
1	A1	59	GLU
1	A1	63	GLU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A1	56/57 (98%)	54 (96%)	2 (4%)	31	54
1	B1	56/57 (98%)	54 (96%)	2 (4%)	31	54
2	A2	184/185 (100%)	168 (91%)	16 (9%)	9	33
2	B2	184/185 (100%)	169 (92%)	15 (8%)	10	34
3	A3	182/183 (100%)	164 (90%)	18 (10%)	7	27
3	B3	182/183 (100%)	163 (90%)	19 (10%)	7	25
4	A4	191/225 (85%)	171 (90%)	20 (10%)	6	24
4	B4	191/225 (85%)	171 (90%)	20 (10%)	6	24
5	A5	88/107 (82%)	77 (88%)	11 (12%)	4	20
5	B5	88/107 (82%)	77 (88%)	11 (12%)	4	20
6	A6	71/72 (99%)	66 (93%)	5 (7%)	14	40
6	B6	71/72 (99%)	66 (93%)	5 (7%)	14	40
7	A7	94/136 (69%)	83 (88%)	11 (12%)	5	21
7	B7	94/136 (69%)	83 (88%)	11 (12%)	5	21
8	A8	80/109 (73%)	67 (84%)	13 (16%)	2	14
8	B8	80/109 (73%)	67 (84%)	13 (16%)	2	14
9	A9	64/138 (46%)	56 (88%)	8 (12%)	4	20
9	B9	64/138 (46%)	57 (89%)	7 (11%)	6	24
11	AB	183/211 (87%)	166 (91%)	17 (9%)	8	29
11	BB	183/211 (87%)	166 (91%)	17 (9%)	8	29
12	AC	197/210 (94%)	177 (90%)	20 (10%)	7	26
12	BC	197/210 (94%)	177 (90%)	20 (10%)	7	26
13	AD	161/162 (99%)	139 (86%)	22 (14%)	3	17
13	BD	161/162 (99%)	138 (86%)	23 (14%)	3	17
14	AE	194/250 (78%)	170 (88%)	24 (12%)	4	20
14	BE	194/250 (78%)	171 (88%)	23 (12%)	5	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	AF	80/92 (87%)	70 (88%)	10 (12%)	4	20
15	BF	80/92 (87%)	71 (89%)	9 (11%)	5	22
16	AG	163/169 (96%)	146 (90%)	17 (10%)	7	25
16	BG	163/169 (96%)	146 (90%)	17 (10%)	7	25
17	AH	116/117 (99%)	101 (87%)	15 (13%)	4	19
17	BH	116/117 (99%)	102 (88%)	14 (12%)	5	21
18	AI	120/122 (98%)	113 (94%)	7 (6%)	18	44
18	BI	120/122 (98%)	112 (93%)	8 (7%)	15	41
19	AJ	98/111 (88%)	93 (95%)	5 (5%)	21	46
19	BJ	98/111 (88%)	93 (95%)	5 (5%)	21	46
20	AK	112/121 (93%)	96 (86%)	16 (14%)	3	17
20	BK	112/121 (93%)	97 (87%)	15 (13%)	4	18
21	AL	113/114 (99%)	103 (91%)	10 (9%)	9	33
21	BL	113/114 (99%)	104 (92%)	9 (8%)	11	35
22	AM	134/135 (99%)	118 (88%)	16 (12%)	5	21
22	BM	134/135 (99%)	118 (88%)	16 (12%)	5	21
23	AN	47/49 (96%)	40 (85%)	7 (15%)	3	16
23	BN	47/49 (96%)	40 (85%)	7 (15%)	3	16
24	AO	134/136 (98%)	125 (93%)	9 (7%)	15	41
24	BO	134/136 (98%)	124 (92%)	10 (8%)	12	37
25	AP	133/134 (99%)	124 (93%)	9 (7%)	14	40
25	BP	133/134 (99%)	124 (93%)	9 (7%)	14	40
26	AQ	141/141 (100%)	128 (91%)	13 (9%)	8	30
26	BQ	141/141 (100%)	127 (90%)	14 (10%)	7	27
27	AR	291/295 (99%)	260 (89%)	31 (11%)	6	24
27	BR	291/295 (99%)	258 (89%)	33 (11%)	5	22
28	AS	105/117 (90%)	101 (96%)	4 (4%)	29	52
28	BS	105/117 (90%)	101 (96%)	4 (4%)	29	52
29	AT	129/134 (96%)	118 (92%)	11 (8%)	10	33
29	BT	129/134 (96%)	119 (92%)	10 (8%)	11	36
30	AU	103/104 (99%)	98 (95%)	5 (5%)	22	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	BU	103/104 (99%)	100 (97%)	3 (3%)	37	58
31	AV	108/115 (94%)	98 (91%)	10 (9%)	8	29
31	BV	108/115 (94%)	99 (92%)	9 (8%)	10	34
32	AW	226/227 (100%)	199 (88%)	27 (12%)	5	21
32	BW	226/227 (100%)	200 (88%)	26 (12%)	5	22
33	AX	57/67 (85%)	55 (96%)	2 (4%)	32	55
33	BX	57/67 (85%)	55 (96%)	2 (4%)	32	55
34	AY	201/244 (82%)	187 (93%)	14 (7%)	14	40
34	BY	201/244 (82%)	189 (94%)	12 (6%)	17	43
35	AZ	82/82 (100%)	75 (92%)	7 (8%)	10	33
35	BZ	82/82 (100%)	76 (93%)	6 (7%)	13	38
All	All	8876/9742 (91%)	8020 (90%)	856 (10%)	8	28

5 of 856 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B3	177	VAL
13	BD	17	ARG
30	BU	100	CYS
4	B4	116	MET
3	B3	159	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 327 such sidechains are listed below:

Mol	Chain	Res	Type
15	BF	18	HIS
27	BR	77	HIS
16	BG	102	ASN
21	BL	78	ASN
29	BT	91	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	AA	1743/1753 (99%)	454 (26%)	194 (11%)
10	BA	1743/1753 (99%)	455 (26%)	194 (11%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	3486/3506 (99%)	909 (26%)	388 (11%)

5 of 909 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	AA	2	A
10	AA	3	C
10	AA	4	C
10	AA	9	U
10	AA	17	C

5 of 388 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	BA	336	U
10	BA	771	A
10	BA	380	G
10	BA	558	G
10	BA	911	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 192 ligands modelled in this entry, 192 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](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A1	67/68 (98%)	0.57	4 (5%) 27 23	99, 157, 220, 262	0
1	B1	67/68 (98%)	0.46	2 (2%) 52 37	99, 157, 220, 262	0
2	A2	207/208 (99%)	0.53	14 (6%) 23 21	96, 144, 194, 231	0
2	B2	207/208 (99%)	0.58	11 (5%) 32 26	98, 145, 194, 231	0
3	A3	196/197 (99%)	0.47	8 (4%) 41 31	82, 138, 187, 267	0
3	B3	196/197 (99%)	0.37	7 (3%) 46 33	75, 138, 186, 266	0
4	A4	215/265 (81%)	0.28	0 100 100	80, 146, 201, 228	0
4	B4	215/265 (81%)	0.52	6 (2%) 55 39	77, 145, 202, 229	0
5	A5	98/119 (82%)	0.43	4 (4%) 41 31	71, 124, 201, 246	0
5	B5	98/119 (82%)	0.53	4 (4%) 41 31	68, 124, 201, 246	0
6	A6	80/81 (98%)	0.25	3 (3%) 44 32	86, 130, 172, 187	0
6	B6	80/81 (98%)	0.35	2 (2%) 58 41	86, 128, 172, 186	0
7	A7	104/162 (64%)	0.68	3 (2%) 53 38	100, 150, 201, 249	0
7	B7	104/162 (64%)	0.56	2 (1%) 66 47	104, 151, 199, 249	0
8	A8	93/143 (65%)	0.55	2 (2%) 62 44	112, 159, 219, 255	0
8	B8	93/143 (65%)	0.68	5 (5%) 31 25	110, 159, 218, 256	0
9	A9	73/189 (38%)	0.96	11 (15%) 5 8	146, 185, 238, 253	0
9	B9	73/189 (38%)	1.10	10 (13%) 6 10	148, 186, 238, 254	0
10	AA	1745/1753 (99%)	0.86	184 (10%) 11 13	80, 134, 291, 454	0
10	BA	1745/1753 (99%)	0.91	193 (11%) 10 13	80, 134, 291, 454	0
11	AB	204/241 (84%)	0.44	2 (0%) 79 59	82, 136, 177, 225	0
11	BB	204/241 (84%)	0.44	3 (1%) 72 51	78, 136, 177, 224	0
12	AC	229/243 (94%)	0.50	7 (3%) 51 36	89, 131, 194, 244	0
12	BC	229/243 (94%)	0.41	10 (4%) 39 29	87, 132, 194, 246	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
13	AD	179/181 (98%)	0.55	7 (3%)	43	31	77, 122, 182, 214	0
13	BD	179/181 (98%)	0.42	6 (3%)	48	34	82, 125, 184, 215	0
14	AE	230/296 (77%)	0.35	5 (2%)	62	44	62, 114, 194, 243	0
14	BE	230/296 (77%)	0.29	6 (2%)	57	40	65, 116, 194, 244	0
15	AF	89/101 (88%)	0.39	1 (1%)	78	58	87, 136, 190, 230	0
15	BF	89/101 (88%)	0.38	2 (2%)	62	44	86, 137, 190, 229	0
16	AG	192/200 (96%)	0.37	5 (2%)	57	40	86, 140, 191, 286	0
16	BG	192/200 (96%)	0.56	12 (6%)	26	22	86, 140, 191, 287	0
17	AH	129/130 (99%)	0.45	6 (4%)	36	28	65, 105, 154, 194	0
17	BH	129/130 (99%)	0.48	6 (4%)	36	28	62, 106, 154, 193	0
18	AI	143/145 (98%)	0.60	10 (6%)	22	20	87, 135, 188, 222	0
18	BI	143/145 (98%)	0.62	15 (10%)	11	13	87, 135, 189, 221	0
19	AJ	105/120 (87%)	0.67	7 (6%)	24	21	84, 132, 199, 218	0
19	BJ	105/120 (87%)	0.66	10 (9%)	14	15	86, 133, 198, 218	0
20	AK	140/151 (92%)	0.60	4 (2%)	53	38	93, 144, 191, 223	0
20	BK	140/151 (92%)	0.53	4 (2%)	53	38	90, 144, 192, 224	0
21	AL	141/142 (99%)	0.41	5 (3%)	47	33	71, 126, 169, 213	0
21	BL	141/142 (99%)	0.56	9 (6%)	25	22	74, 128, 169, 212	0
22	AM	154/155 (99%)	0.47	4 (2%)	57	40	94, 154, 204, 233	0
22	BM	154/155 (99%)	0.64	13 (8%)	17	17	95, 155, 205, 233	0
23	AN	53/55 (96%)	0.43	4 (7%)	20	19	83, 124, 156, 193	0
23	BN	53/55 (96%)	0.46	3 (5%)	29	24	83, 126, 157, 192	0
24	AO	150/153 (98%)	0.50	5 (3%)	49	35	73, 124, 223, 287	0
24	BO	150/153 (98%)	0.48	8 (5%)	32	26	71, 124, 222, 288	0
25	AP	148/149 (99%)	0.42	3 (2%)	65	46	92, 141, 168, 200	0
25	BP	148/149 (99%)	0.47	7 (4%)	36	28	94, 141, 170, 200	0
26	AQ	157/157 (100%)	0.40	7 (4%)	38	29	69, 129, 214, 227	0
26	BQ	157/157 (100%)	0.45	5 (3%)	50	36	65, 128, 208, 258	0
27	AR	338/343 (98%)	0.42	7 (2%)	63	45	93, 146, 218, 268	0
27	BR	338/343 (98%)	0.47	14 (4%)	41	31	94, 145, 209, 244	0
28	AS	125/144 (86%)	0.63	8 (6%)	25	22	117, 164, 222, 245	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
28	BS	125/144 (86%)	0.58	3 (2%) 59 43	119, 165, 222, 245	0
29	AT	150/155 (96%)	0.60	9 (6%) 27 23	80, 152, 191, 230	0
29	BT	150/155 (96%)	0.47	6 (4%) 42 31	79, 151, 192, 229	0
30	AU	124/126 (98%)	0.99	18 (14%) 6 9	117, 177, 213, 227	0
30	BU	124/126 (98%)	0.94	13 (10%) 11 13	136, 185, 221, 250	0
31	AV	121/130 (93%)	0.40	4 (3%) 49 35	78, 143, 206, 254	0
31	BV	121/130 (93%)	0.46	4 (3%) 49 35	76, 142, 206, 253	0
32	AW	259/260 (99%)	0.37	4 (1%) 72 51	84, 125, 166, 200	0
32	BW	259/260 (99%)	0.39	7 (2%) 56 39	87, 126, 167, 199	0
33	AX	68/80 (85%)	0.55	3 (4%) 39 29	106, 155, 242, 271	0
33	BX	68/80 (85%)	0.64	5 (7%) 20 19	107, 158, 243, 271	0
34	AY	235/293 (80%)	0.59	11 (4%) 36 28	108, 159, 237, 316	0
34	BY	235/293 (80%)	0.66	9 (3%) 44 32	110, 159, 237, 315	0
35	AZ	97/97 (100%)	0.25	2 (2%) 63 45	74, 129, 185, 209	0
35	BZ	97/97 (100%)	0.12	1 (1%) 79 59	77, 129, 184, 210	0
All	All	13676/14864 (92%)	0.59	804 (5%) 28 24	62, 139, 215, 454	0

The worst 5 of 804 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
10	BA	211	U	17.5
10	AA	211	U	9.0
10	BA	213	U	7.6
10	AA	683	A	7.4
10	AA	684	A	6.6

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
36	MG	BA	1855	1/1	0.56	0.67	275,275,275,275	0
36	MG	BA	1830	1/1	0.61	0.21	204,204,204,204	0
36	MG	AA	1855	1/1	0.66	0.28	214,214,214,214	0
36	MG	BA	1875	1/1	0.67	0.18	193,193,193,193	0
36	MG	BA	1837	1/1	0.72	0.22	178,178,178,178	0
36	MG	AA	1883	1/1	0.73	0.14	209,209,209,209	0
36	MG	AA	1859	1/1	0.75	0.23	193,193,193,193	0
36	MG	AA	1888	1/1	0.75	0.30	205,205,205,205	0
36	MG	AA	1882	1/1	0.75	0.18	181,181,181,181	0
36	MG	BA	1889	1/1	0.75	0.20	209,209,209,209	0
36	MG	AA	1832	1/1	0.76	0.10	189,189,189,189	0
36	MG	BA	1887	1/1	0.76	0.34	206,206,206,206	0
36	MG	AA	1872	1/1	0.76	0.11	196,196,196,196	0
36	MG	BA	1848	1/1	0.77	0.28	206,206,206,206	0
36	MG	BA	1807	1/1	0.78	0.21	210,210,210,210	0
36	MG	BA	1853	1/1	0.78	0.11	194,194,194,194	0
36	MG	BD	201	1/1	0.78	0.30	233,233,233,233	0
36	MG	AA	1862	1/1	0.79	0.10	191,191,191,191	0
36	MG	AA	1809	1/1	0.79	0.17	193,193,193,193	0
36	MG	BA	1842	1/1	0.79	0.18	210,210,210,210	0
36	MG	BA	1883	1/1	0.79	0.25	187,187,187,187	0
36	MG	BA	1845	1/1	0.79	0.11	225,225,225,225	0
36	MG	AA	1861	1/1	0.79	0.16	204,204,204,204	0
36	MG	BA	1849	1/1	0.79	0.15	198,198,198,198	0
36	MG	BA	1866	1/1	0.80	0.34	186,186,186,186	0
36	MG	BA	1872	1/1	0.80	0.58	200,200,200,200	0
36	MG	BA	1847	1/1	0.80	0.14	204,204,204,204	0
36	MG	AA	1879	1/1	0.80	0.14	193,193,193,193	0
36	MG	BA	1838	1/1	0.80	0.20	172,172,172,172	0
36	MG	AA	1871	1/1	0.80	0.15	201,201,201,201	0
36	MG	AA	1813	1/1	0.80	0.15	191,191,191,191	0
36	MG	BA	1827	1/1	0.81	0.11	199,199,199,199	0
36	MG	BA	1835	1/1	0.81	0.15	187,187,187,187	0
36	MG	AA	1866	1/1	0.82	0.24	197,197,197,197	0
36	MG	BA	1843	1/1	0.82	0.10	196,196,196,196	0
36	MG	AA	1890	1/1	0.82	0.13	218,218,218,218	0
36	MG	BA	1884	1/1	0.83	0.14	219,219,219,219	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
36	MG	BA	1886	1/1	0.83	0.26	214,214,214,214	0
36	MG	BA	1854	1/1	0.83	0.18	189,189,189,189	0
36	MG	BA	1878	1/1	0.83	0.11	177,177,177,177	0
36	MG	BA	1850	1/1	0.83	0.23	221,221,221,221	0
36	MG	BA	1860	1/1	0.84	0.14	177,177,177,177	0
36	MG	AA	1802	1/1	0.84	0.16	175,175,175,175	0
36	MG	AA	1868	1/1	0.84	0.15	197,197,197,197	0
36	MG	BA	1873	1/1	0.84	0.33	218,218,218,218	0
36	MG	AA	1874	1/1	0.84	0.11	194,194,194,194	0
36	MG	BA	1859	1/1	0.84	0.15	194,194,194,194	0
36	MG	AA	1845	1/1	0.85	0.10	193,193,193,193	0
36	MG	BA	1869	1/1	0.85	0.16	188,188,188,188	0
36	MG	BA	1879	1/1	0.85	0.13	221,221,221,221	0
36	MG	AA	1848	1/1	0.86	0.12	183,183,183,183	0
36	MG	AA	1870	1/1	0.86	0.09	195,195,195,195	0
36	MG	BA	1851	1/1	0.86	0.11	169,169,169,169	0
36	MG	AA	1886	1/1	0.86	0.19	148,148,148,148	0
36	MG	AA	1856	1/1	0.86	0.11	182,182,182,182	0
36	MG	BA	1882	1/1	0.86	0.10	196,196,196,196	0
36	MG	AA	1876	1/1	0.87	0.15	180,180,180,180	0
36	MG	AL	201	1/1	0.87	0.17	182,182,182,182	0
36	MG	AA	1851	1/1	0.87	0.10	187,187,187,187	0
36	MG	BA	1814	1/1	0.87	0.15	214,214,214,214	0
36	MG	AA	1852	1/1	0.87	0.13	173,173,173,173	0
36	MG	AA	1814	1/1	0.87	0.17	197,197,197,197	0
36	MG	AA	1863	1/1	0.87	0.14	183,183,183,183	0
36	MG	BA	1870	1/1	0.87	0.10	205,205,205,205	0
36	MG	BA	1888	1/1	0.87	0.86	227,227,227,227	0
36	MG	BA	1836	1/1	0.87	0.18	175,175,175,175	0
36	MG	AA	1843	1/1	0.87	0.09	182,182,182,182	0
36	MG	BA	1881	1/1	0.88	0.09	149,149,149,149	0
36	MG	BA	1867	1/1	0.88	0.09	180,180,180,180	0
36	MG	BA	1824	1/1	0.88	0.19	172,172,172,172	0
36	MG	AA	1806	1/1	0.88	0.12	151,151,151,151	0
36	MG	AA	1884	1/1	0.88	0.14	190,190,190,190	0
36	MG	BA	1806	1/1	0.88	0.10	168,168,168,168	0
36	MG	AA	1858	1/1	0.88	0.14	162,162,162,162	0
36	MG	BA	1810	1/1	0.88	0.23	188,188,188,188	0
36	MG	AA	1839	1/1	0.88	0.10	143,143,143,143	0
36	MG	BW	301	1/1	0.88	0.09	166,166,166,166	0
36	MG	BA	1868	1/1	0.89	0.08	208,208,208,208	0
36	MG	BA	1852	1/1	0.89	0.10	170,170,170,170	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
36	MG	AA	1836	1/1	0.89	0.14	166,166,166,166	0
36	MG	AA	1873	1/1	0.89	0.32	196,196,196,196	0
36	MG	AA	1830	1/1	0.89	0.13	183,183,183,183	0
36	MG	AA	1812	1/1	0.89	0.22	173,173,173,173	0
36	MG	BA	1820	1/1	0.89	0.09	170,170,170,170	0
36	MG	B4	301	1/1	0.89	0.10	165,165,165,165	0
36	MG	BA	1825	1/1	0.89	0.28	153,153,153,153	0
36	MG	BA	1826	1/1	0.90	0.09	185,185,185,185	0
36	MG	BA	1803	1/1	0.90	0.25	169,169,169,169	0
36	MG	AA	1807	1/1	0.90	0.09	194,194,194,194	0
36	MG	BA	1833	1/1	0.90	0.14	172,172,172,172	0
36	MG	BA	1811	1/1	0.90	0.09	170,170,170,170	0
36	MG	BA	1812	1/1	0.90	0.19	166,166,166,166	0
36	MG	BA	1876	1/1	0.91	0.12	184,184,184,184	0
36	MG	BA	1801	1/1	0.91	0.17	186,186,186,186	0
36	MG	AA	1885	1/1	0.91	0.11	223,223,223,223	0
36	MG	AA	1841	1/1	0.91	0.11	170,170,170,170	0
36	MG	BA	1861	1/1	0.91	0.09	181,181,181,181	0
36	MG	AA	1887	1/1	0.91	0.16	198,198,198,198	0
36	MG	BA	1809	1/1	0.91	0.12	172,172,172,172	0
36	MG	BA	1832	1/1	0.91	0.10	194,194,194,194	0
36	MG	AA	1880	1/1	0.91	0.11	193,193,193,193	0
36	MG	AA	1889	1/1	0.91	0.30	200,200,200,200	0
36	MG	AA	1869	1/1	0.91	0.13	209,209,209,209	0
36	MG	AA	1850	1/1	0.91	0.09	185,185,185,185	0
36	MG	AA	1842	1/1	0.91	0.10	175,175,175,175	0
36	MG	BA	1816	1/1	0.92	0.08	127,127,127,127	0
36	MG	AA	1826	1/1	0.92	0.12	155,155,155,155	0
36	MG	BA	1822	1/1	0.92	0.07	151,151,151,151	0
36	MG	AA	1878	1/1	0.92	0.16	160,160,160,160	0
36	MG	BA	1871	1/1	0.92	0.08	209,209,209,209	0
36	MG	BA	1864	1/1	0.92	0.11	182,182,182,182	0
36	MG	AA	1820	1/1	0.92	0.07	157,157,157,157	0
36	MG	BA	1858	1/1	0.93	0.09	163,163,163,163	0
36	MG	AA	1864	1/1	0.93	0.17	176,176,176,176	0
36	MG	BA	1877	1/1	0.93	0.10	177,177,177,177	0
36	MG	BA	1828	1/1	0.93	0.07	145,145,145,145	0
36	MG	AA	1865	1/1	0.93	0.10	184,184,184,184	0
36	MG	BA	1880	1/1	0.93	0.21	193,193,193,193	0
36	MG	BA	1815	1/1	0.93	0.14	155,155,155,155	0
36	MG	BA	1865	1/1	0.93	0.19	183,183,183,183	0
36	MG	AA	1804	1/1	0.93	0.10	150,150,150,150	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
36	MG	BA	1834	1/1	0.93	0.26	138,138,138,138	0
36	MG	AA	1837	1/1	0.93	0.08	149,149,149,149	0
36	MG	AA	1860	1/1	0.93	0.09	176,176,176,176	0
36	MG	AA	1854	1/1	0.93	0.13	158,158,158,158	0
36	MG	AA	1849	1/1	0.93	0.07	159,159,159,159	0
36	MG	AA	1805	1/1	0.93	0.09	175,175,175,175	0
36	MG	BA	1856	1/1	0.93	0.05	173,173,173,173	0
36	MG	AA	1844	1/1	0.94	0.16	166,166,166,166	0
36	MG	BA	1840	1/1	0.94	0.07	128,128,128,128	0
36	MG	AA	1815	1/1	0.94	0.08	144,144,144,144	0
36	MG	BA	1808	1/1	0.94	0.14	140,140,140,140	0
36	MG	BA	1817	1/1	0.94	0.07	134,134,134,134	0
36	MG	BA	1857	1/1	0.94	0.08	130,130,130,130	0
36	MG	AA	1875	1/1	0.94	0.17	152,152,152,152	0
36	MG	BA	1802	1/1	0.94	0.12	169,169,169,169	0
36	MG	AA	1827	1/1	0.94	0.05	178,178,178,178	0
36	MG	BA	1874	1/1	0.94	0.11	164,164,164,164	0
36	MG	BA	1804	1/1	0.94	0.10	191,191,191,191	0
36	MG	BA	1862	1/1	0.94	0.07	177,177,177,177	0
36	MG	BA	1813	1/1	0.94	0.10	187,187,187,187	0
36	MG	AA	1847	1/1	0.95	0.09	186,186,186,186	0
36	MG	AA	1877	1/1	0.95	0.07	170,170,170,170	0
36	MG	AA	1838	1/1	0.95	0.08	144,144,144,144	0
36	MG	AA	1810	1/1	0.95	0.11	175,175,175,175	0
36	MG	BA	1823	1/1	0.95	0.09	123,123,123,123	0
36	MG	AA	1833	1/1	0.95	0.14	135,135,135,135	0
36	MG	AA	1834	1/1	0.95	0.11	182,182,182,182	0
36	MG	AA	1835	1/1	0.95	0.08	159,159,159,159	0
36	MG	BA	1885	1/1	0.95	0.08	161,161,161,161	0
36	MG	BA	1841	1/1	0.95	0.08	129,129,129,129	0
36	MG	AA	1853	1/1	0.95	0.05	177,177,177,177	0
36	MG	AA	1808	1/1	0.95	0.20	136,136,136,136	0
36	MG	AA	1822	1/1	0.95	0.06	139,139,139,139	0
36	MG	BA	1846	1/1	0.95	0.08	147,147,147,147	0
36	MG	BA	1831	1/1	0.95	0.09	115,115,115,115	0
36	MG	AA	1881	1/1	0.96	0.21	198,198,198,198	0
36	MG	AA	1811	1/1	0.96	0.10	154,154,154,154	0
36	MG	AA	1818	1/1	0.96	0.08	121,121,121,121	0
36	MG	BA	1829	1/1	0.96	0.07	163,163,163,163	0
36	MG	AA	1831	1/1	0.96	0.06	111,111,111,111	0
36	MG	BA	1844	1/1	0.96	0.05	157,157,157,157	0
36	MG	A4	301	1/1	0.96	0.07	174,174,174,174	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
36	MG	AA	1821	1/1	0.96	0.05	144,144,144,144	0
36	MG	AA	1803	1/1	0.96	0.08	147,147,147,147	0
36	MG	AA	1823	1/1	0.96	0.07	130,130,130,130	0
36	MG	AA	1846	1/1	0.96	0.06	161,161,161,161	0
36	MG	AA	1824	1/1	0.96	0.06	148,148,148,148	0
36	MG	AA	1801	1/1	0.96	0.04	160,160,160,160	0
37	ZN	B9	500	1/1	0.96	0.05	247,247,247,247	0
36	MG	AA	1828	1/1	0.97	0.06	133,133,133,133	0
36	MG	BA	1839	1/1	0.97	0.06	140,140,140,140	0
36	MG	BA	1819	1/1	0.97	0.07	122,122,122,122	0
36	MG	AA	1867	1/1	0.97	0.05	193,193,193,193	0
36	MG	BA	1821	1/1	0.97	0.05	160,160,160,160	0
36	MG	AA	1857	1/1	0.97	0.09	140,140,140,140	0
36	MG	BA	1863	1/1	0.98	0.06	166,166,166,166	0
36	MG	AA	1840	1/1	0.98	0.06	124,124,124,124	0
36	MG	AA	1817	1/1	0.98	0.06	126,126,126,126	0
36	MG	AA	1829	1/1	0.98	0.04	160,160,160,160	0
36	MG	BA	1805	1/1	0.98	0.04	150,150,150,150	0
36	MG	AA	1825	1/1	0.99	0.11	115,115,115,115	0
36	MG	BA	1818	1/1	0.99	0.03	111,111,111,111	0
36	MG	AA	1819	1/1	0.99	0.03	136,136,136,136	0
37	ZN	A5	500	1/1	0.99	0.05	95,95,95,95	0
37	ZN	A6	500	1/1	0.99	0.03	118,118,118,118	0
37	ZN	A9	500	1/1	0.99	0.03	169,169,169,169	0
37	ZN	B5	500	1/1	0.99	0.09	87,87,87,87	0
36	MG	AA	1816	1/1	0.99	0.03	96,96,96,96	0
37	ZN	BN	500	1/1	0.99	0.03	113,113,113,113	0
37	ZN	AN	500	1/1	1.00	0.05	105,105,105,105	0
37	ZN	B6	500	1/1	1.00	0.04	108,108,108,108	0

6.5 Other polymers ⓘ

There are no such residues in this entry.