



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2018 – 03:09 pm GMT

PDB ID : 2QA4
Title : A more complete structure of the the L7/L12 stalk of the Haloarcula marismortui 50S large ribosomal subunit
Authors : Steitz, T.A.; Kavran, J.M.
Deposited on : 2007-06-14
Resolution : 3.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk31020
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk31020

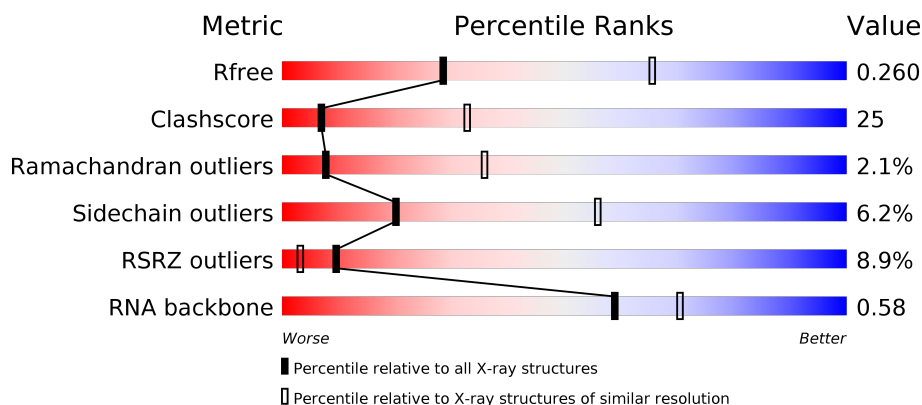
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	111664	1851 (3.00-3.00)
Clashscore	122126	2167 (3.00-3.00)
Ramachandran outliers	120053	2101 (3.00-3.00)
Sidechain outliers	120020	2104 (3.00-3.00)
RSRZ outliers	108989	1751 (3.00-3.00)
RNA backbone	2636	1017 (3.30-2.70)

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

Mol	Chain	Length	Quality of chain
1	0	2922	<div> <div>28%</div> <div>57%</div> <div>9%</div> <div>6%</div> </div>
2	9	122	<div> <div>17%</div> <div>69%</div> <div>13%</div> </div>
3	A	240	<div> <div>10%</div> <div>61%</div> <div>34%</div> </div>
4	B	338	<div> <div>4%</div> <div>59%</div> <div>36%</div> </div>

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Mol	Chain	Length	Quality of chain
5	C	246	
6	D	177	
7	E	178	
8	F	120	
9	G	348	
10	H	171	
11	I	162	
12	J	145	
13	K	132	
14	L	165	
15	M	196	
16	N	187	
17	O	116	
18	P	149	
19	Q	96	
20	R	155	
21	S	85	
22	T	120	
23	U	67	
24	V	71	
25	W	154	
26	X	92	
27	Y	241	
28	Z	92	
29	1	57	

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Mol	Chain	Length	Quality of chain
30	2	50	
31	3	92	

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
32	MG	0	2971	-	-	-	X
32	MG	0	2973	-	-	-	X
32	MG	0	2980	-	-	-	X
32	MG	0	2984	-	-	-	X
32	MG	0	2998	-	-	-	X
32	MG	0	3006	-	-	-	X
32	MG	0	3025	-	-	-	X
32	MG	0	3026	-	-	-	X
32	MG	0	3028	-	-	-	X
32	MG	0	3029	-	-	-	X
32	MG	3	93	-	-	-	X
32	MG	A	240	-	-	-	X
32	MG	B	338	-	-	-	X
32	MG	K	133	-	-	-	X
32	MG	Y	241	-	-	-	X
33	K	0	3031	-	-	-	X
33	K	M	196	-	-	-	X
34	NA	0	3033	-	-	-	X
34	NA	0	3034	-	-	-	X
34	NA	0	3039	-	-	-	X
34	NA	0	3044	-	-	-	X
34	NA	0	3050	-	-	-	X
34	NA	0	3052	-	-	-	X
34	NA	0	3057	-	-	-	X
34	NA	0	3059	-	-	-	X
34	NA	0	3075	-	-	-	X
34	NA	0	3077	-	-	-	X
34	NA	0	3082	-	-	-	X
34	NA	0	3084	-	-	-	X
34	NA	0	3094	-	-	-	X
34	NA	0	3098	-	-	-	X
34	NA	0	3099	-	-	-	X
34	NA	0	3100	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
34	NA	0	3103	-	-	-	X
34	NA	S	85	-	-	-	X
35	CL	0	3106	-	-	-	X
35	CL	0	3109	-	-	-	X
35	CL	0	3112	-	-	-	X
35	CL	3	95	-	-	X	X
35	CL	J	147	-	-	X	-
35	CL	J	149	-	-	X	-
35	CL	O	117	-	-	-	X
35	CL	Q	97	-	-	-	X
36	CD	O	116	-	-	-	X

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 92248 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 RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	0	2753	Total	C	N	O	P	0	0	0
			58979	26332	10869	19036	2742			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	560	C	U	CONFLICT	GB 3377779

- Molecule 2 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	9	122	Total	C	N	O	P	0	0	0
			2600	1160	472	847	121			

- Molecule 3 is a protein called 50S ribosomal protein L2P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	237	Total	C	N	O	S	0	0	0
			1753	1072	352	324	5			

- Molecule 4 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	337	Total	C	N	O	S	0	0	0
			2625	1616	493	511	5			

- Molecule 5 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	C	246	Total	C	N	O	S	0	0	0
			1859	1131	344	383	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	73	LEU	GLN	CONFLICT	UNP P12735

- Molecule 6 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	D	140	Total	C	N	O	S	0	0	0
			1094	685	195	210	4			

- Molecule 7 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	172	Total	C	N	O	S	0	0	0
			1357	840	224	289	4			

- Molecule 8 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	119	Total	C	N	O	S	0	0	0
			890	551	141	197	1			

- Molecule 9 is a protein called ACIDIC RIBOSOMAL PROTEIN P0 HOMO.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	G	125	Total	C	N	O	S	0	0	0
			959	592	162	203	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	248	ASP	ALA	CONFLICT	UNP P15825

- Molecule 10 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	H	160	Total	C	N	O	S	0	0	0
			1266	785	237	238	6			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	164	ASP	-	INSERTION	UNP P60617
H	165	SER	LYS	CONFLICT	UNP P60617
H	166	SER	VAL	CONFLICT	UNP P60617
H	167	PRO	GLU	CONFLICT	UNP P60617
H	168	ALA	ARG	CONFLICT	UNP P60617
H	?	-	GLU	DELETION	UNP P60617
H	?	-	GLU	DELETION	UNP P60617
H	?	-	LEU	DELETION	UNP P60617
H	?	-	LEU	DELETION	UNP P60617
H	170	ASN	ILE	CONFLICT	UNP P60617

- Molecule 11 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	I	118	Total	C	N	O	S	0	0	0
			876	548	135	192	1			

- Molecule 12 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	J	142	Total	C	N	O	S	0	0	0
			1120	696	199	222	3			

- Molecule 13 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	K	132	Total	C	N	O	S	0	0	0
			992	609	187	192	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	44	LEU	HIS	CONFLICT	UNP P22450

- Molecule 14 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	L	145	Total	C	N	O	0	0	0
			1118	670	222	226			

- Molecule 15 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	M	194	Total	C	N	O	S	0	0	0
			1559	943	332	283	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	13	GLU	LYS	CONFLICT	UNP P60618
M	194	ALA	GLY	CONFLICT	UNP P60618

- Molecule 16 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	N	186	Total	C	N	O	S	0	0	0
			1445	895	262	286	2			

- Molecule 17 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	O	115	Total	C	N	O	0	0	0
			865	529	161	175			

- Molecule 18 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	P	143	Total	C	N	O	0	0	0
			1136	683	229	224			

- Molecule 19 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
19	Q	95	Total	C	N	O	0	0	0
			735	450	141	144			

- Molecule 20 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	R	150	Total	C	N	O	S	0	0	0
			1149	713	209	223	4			

- Molecule 21 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	S	81	Total	C	N	O	S	0	0	0
			641	389	111	138	3			

- Molecule 22 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	T	119	Total	C	N	O		0	0	0
			950	568	180	202				

- Molecule 23 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	U	53	Total	C	N	O	S	0	0	0
			410	244	75	86	5			

- Molecule 24 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	V	65	Total	C	N	O	S	0	0	0
			499	304	94	100	1			

- Molecule 25 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	W	154	Total	C	N	O	S	0	0	0
			1196	737	209	244	6			

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L31E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	X	82	Total	C	N	O	S	0	0	0
			654	402	129	122	1			

- Molecule 27 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	Y	142	Total	C	N	O		0	0	0
			1130	686	228	216				

- Molecule 28 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	Z	73	Total	C	N	O	S	0	0	0
			578	346	116	111	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	10	ARG	SER	CONFLICT	UNP P60619

- Molecule 29 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	1	56	Total	C	N	O	S	0	0	0
			431	258	86	83	4			

- Molecule 30 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	2	46	Total	C	N	O	S	0	0	0
			396	239	89	67	1			

- Molecule 31 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	3	92	Total	C	N	O	S	0	0	0
			755	458	153	137	7			

- Molecule 32 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	0	108	Total	Mg	0	0
			108	108		
32	Y	1	Total	Mg	0	0
			1	1		
32	K	1	Total	Mg	0	0
			1	1		
32	B	1	Total	Mg	0	0
			1	1		
32	A	2	Total	Mg	0	0
			2	2		
32	T	1	Total	Mg	0	0
			1	1		
32	9	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
32	3	1	Total	Mg	0	0
			1	1		

- Molecule 33 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
33	0	1	Total	K	0	0
			1	1		
33	M	1	Total	K	0	0
			1	1		

- Molecule 34 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
34	0	73	Total	Na	0	0
			73	73		
34	J	1	Total	Na	0	0
			1	1		
34	Q	1	Total	Na	0	0
			1	1		
34	H	1	Total	Na	0	0
			1	1		
34	C	1	Total	Na	0	0
			1	1		
34	A	1	Total	Na	0	0
			1	1		
34	R	2	Total	Na	0	0
			2	2		
34	9	3	Total	Na	0	0
			3	3		
34	L	1	Total	Na	0	0
			1	1		
34	S	1	Total	Na	0	0
			1	1		
34	M	1	Total	Na	0	0
			1	1		

- Molecule 35 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	0	8	Total	Cl	0	0
			8	8		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
35	J	3	Total 3	Cl 3	0	0
35	Q	1	Total 1	Cl 1	0	0
35	K	1	Total 1	Cl 1	0	0
35	B	1	Total 1	Cl 1	0	0
35	A	1	Total 1	Cl 1	0	0
35	N	1	Total 1	Cl 1	0	0
35	O	1	Total 1	Cl 1	0	0
35	R	1	Total 1	Cl 1	0	0
35	Y	1	Total 1	Cl 1	0	0
35	L	1	Total 1	Cl 1	0	0
35	3	1	Total 1	Cl 1	0	0
35	M	1	Total 1	Cl 1	0	0

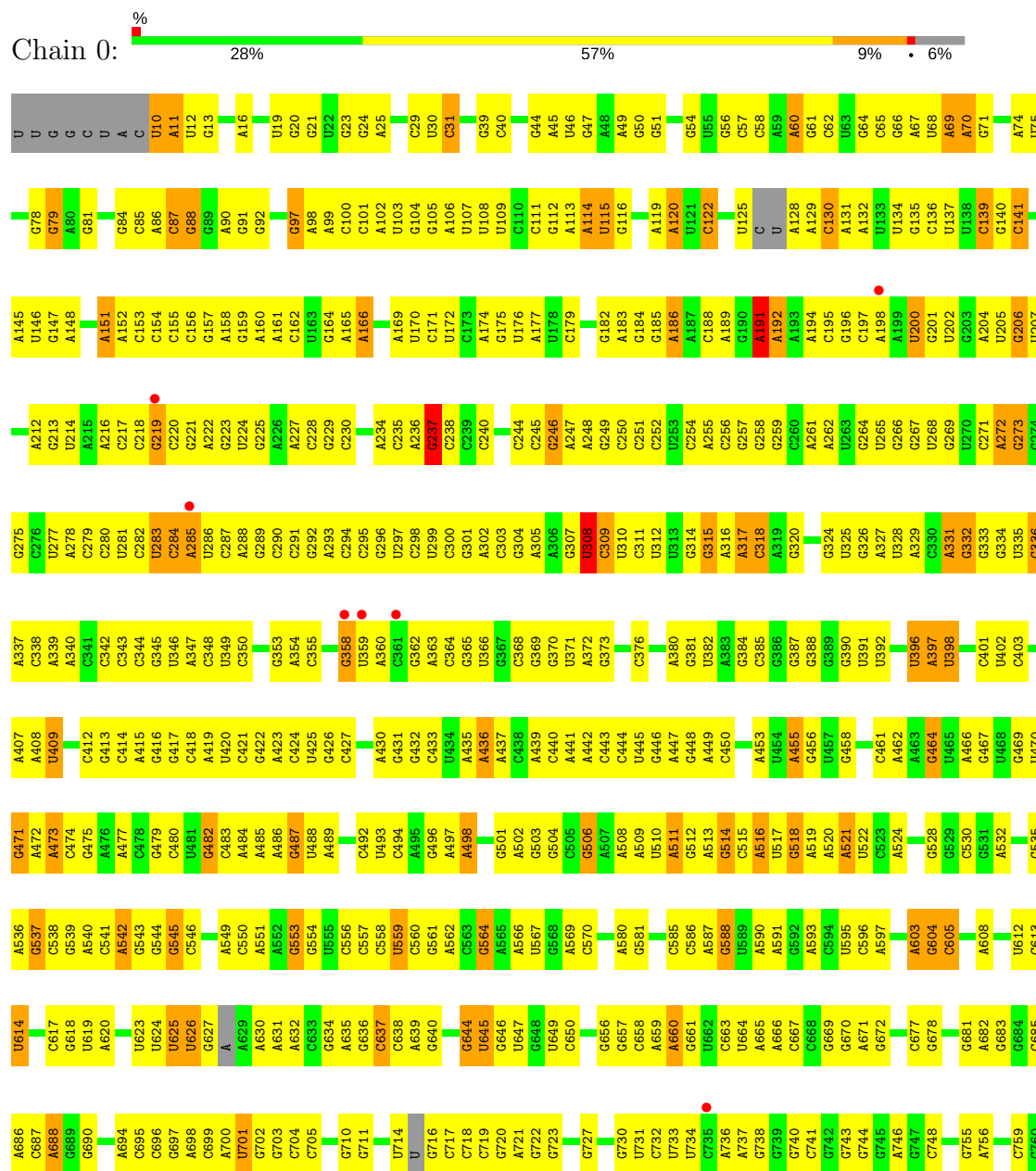
- Molecule 36 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
36	O	1	Total 1	Cd 1	0	0
36	Z	1	Total 1	Cd 1	0	0
36	1	1	Total 1	Cd 1	0	0
36	3	1	Total 1	Cd 1	0	0
36	U	1	Total 1	Cd 1	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

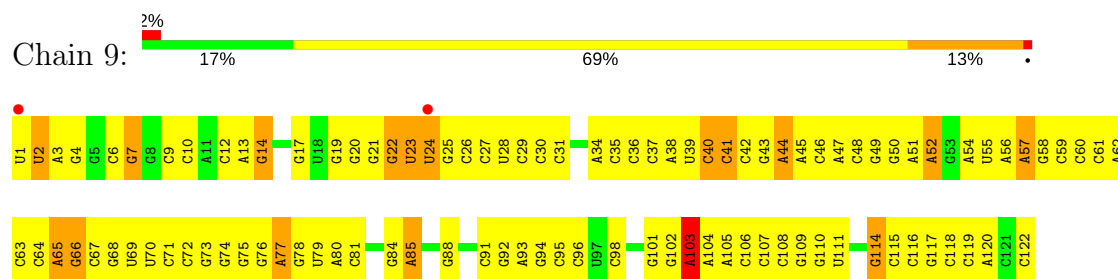
• Molecule 1: 23S RIBOSOMAL RNA



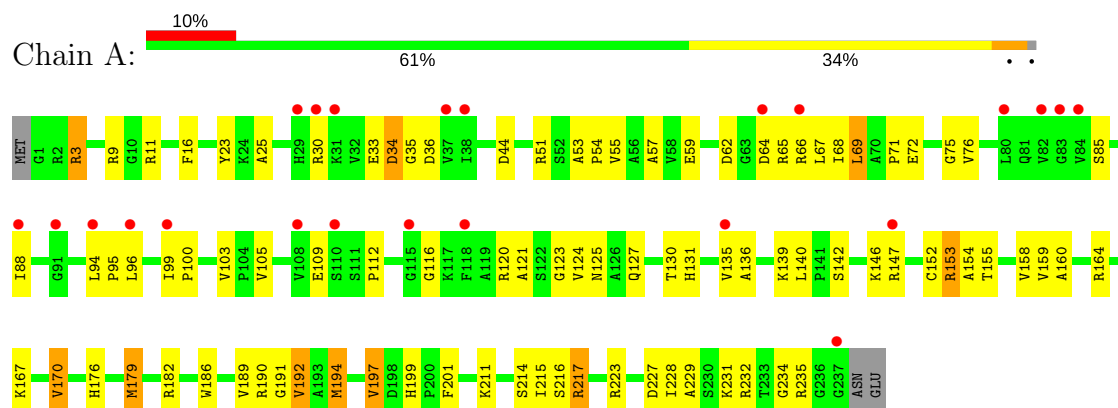


U2872	U2808	G2737	U2671	G2602	U2461	U2386	G2324	G2254	U2133	G2070	U2003	A1922	U1879
C2873	G2809	G2738	C2672	G2603	G2462	U2387	C2325	A2256	G2134	C2071	U2004	C1943	C1880
G2874	G2810	A2739	U2673	A2532	A2465	C2388	U2326	G2256	A2135	G2072	G2005	G1944	A1881
A2875	A2811	G2740	G2676	C2533	G2466	U2389	A2327	G2257	G2136	G2073	C2006	G1945	C1882
G2876	A2812	A2741	C2677	G2534	A2467	C2393	U2328	A2258	A	A2074	U2007	G1946	U1883
A2879	A2813	A2742	A2677	U2535	A2468	G2394	G2329	C2262	C	G2075	G2008	G1947	G1884
A2880	A2814	A2743	A2678	C2536	A2469	A2395	U2330	G2263	A	U2076	G2009	G1948	A1885
C2881	G2815	G2744	G2679	C2537	G2470	A2396	C2331	G2264	G	C2077	A2010	A1886	A1886
A2882	A2816	A2745	U2680	A2538	A2471	A2397	A2332	A2265	U	U2078	G2011	G1950	U1887
G2883	G2817	U2746	A2681	U2539	U2472	A2398	G2333	U2266	G	G2079	U2012	G1951	C1888
A2884	A2818	G2747	G2682	G2540	A2473	A2399	C2334	A2267	U	G2080	G2013	U	C1889
G2885	A2819	C2751	U2683	U2541	A2474	G2400	G2335	G2267	C	A2081	G2014	A	U1890
A2886	G2820	G2752	C2684	C2542	A2475	A2401	G2336	C2268	U	G2082		A	
C2887	A2821		G2685	G2543	C2476		G2337	C2269	C		C2020	C	C1894
G2888	G2822	U2756	C2686	G2544	C2477	C2406	G2338	G2270	A	A2085	C2021	U	A1895
A2889	G2823	A2757	U2687	U2545	U2478	U2407	A	G2271	A	C2086		A	G1896
G2890	C2824	U2758	U2688	U2546	A2479	G2407	C	G2272	C	C2087	G2025	U	U1897
A2891	G2825	C2759	A2689	C2547	G2480	A2408	A	C2273	A	G2088	G2026	G	G1898
C2892	A2826	U2760	U2690	C2548	G2481	C2409	G	A2274	U	A2089	U2027	A	C1899
G2893	G2827	U2761	U2691	C2549	G2482	G2410	A	G2275	U	G2090	U2028	C	A1900
A2894	A2828	A2762	A2692	U2550	A2483	C2411	G2344	U2276	G	C2091	C2029		G1901
C2895	G2829	G2763	G2696	C2551	U2484	G2412	A2345	U2277	A	G2092	A2030	C	U1902
G2896	C2830	C2764	G2697	C2552	G2489		C2346	U2278	A	G2093	C2031		U1903
A2897	G2831	U2765	A2697	U2553	A2490	G2415	C2347		A	G2094	U2032	C1965	A1904
C2898	C2832	G2766	G2698	U2554	G2491	A2416	C2348	G2281	U	A2095	G2033	U1966	U1905
A2899	G2833	C2767	A2699	U2555	U2492	C2417	G2349	U2282	A	A2096	U2034	U1967	C1906
G2900	C2834	A2768	G2700	U2563	C2493	G2418	G2350	G2283	C	C2097	C2035	A1968	U1907
C2901	G2835	G2769	U2701	G2564	U2494	U2419	C2351	G2284	U	C2098	C2036	G1908	G1908
A2902	U2836	G2770	A2702	C2565	A2497	G2420	G2352		A	G2099	C2037	G1970	A1909
C2903	G2837	U2771	G2703	A2566	G2498	G2421	A2353	G2289	C	A2100	A2038	G1971	A1910
A2906	A2838	A2775	C2704	U2567	U2499	U2422	A2354	U2290	C	A2101	A2039	U1972	
C2907	G2839	A2776	U2705	G2568	C2500		C2355	A2291	C	G2102	C2040	A1973	C1913
A2908	A2840	G2777	A2706	C2575	G2501	A2425	A2356	C2292	G	A2103	G2041	G1974	C1914
G2909	G2841	U2778	C2707	A2576	C2502		G2357	G2293	U	C2104	U2042	C1975	U1915
A2910	A2842	G2779	G2712	A2577	A2503	G2428	U2358	C2294	C	C2105	U2043	G1976	C1916
C2911	G2843	U2780	G2713	U2578	A2504		G2359	G2295	A	C2106	G2044	U1977	G1917
G2912	C2844	U2781	U2714	G2579	G2505	C2432	C2360	G2296	G	U2107	G2045	A1978	U1918
A2913	G2845	G2782	U2715	G2580	A2506	A2433	A2361	U2297	U		G2046	C1979	U1919
C2914	C2846	U2783	G2716	U2581	G2507	A2434	A2362	C2298	G	G2110	C2047	U1980	C1920
A2914	G2847	U2784	G2717	A2582	C2508	U2435	G2363	G2299	A	G2111	C2048	A1981	A1921
A	U2848	G2785	C2718	G2583	A2509	U2436	A2364	A2300	C	A2112	G2049	C1982	A1922
C	G2850	U2786	C2719	G2584	C2510	A2437	G2365	A2301	U	G2113	G2050	C1983	G1923
G	G2851	A2790	C2720	G2585	A2511	G2438	C2366	A2302	C	C2114	U2051	U1984	A1924
C	A2852	U2791	U2721	U2586	A2512	C2439	A2367		C	U2115	U2052	U1985	G1925
A	U2853	A2792	G2722	U2587	G2513	C2440	A2368	U2306	C	U2116	G2053	G1986	G1926
C	A2854	G2793	G2723	G2588	U2514	U2441	A2369	A2307	A	A2117	A2054	C1987	A1927
C	G2855	U2794	G2724	U2589	G2515	G2442	A2370	U2308	G	A2118	A2055	C1988	G1928
A	A2856	C2795	U2725	U2590	G2516	U2443	G2371	C2309	U	C2119	C2056	G1989	G1929
U		U2796	U2726	C2591	G2517	U2444		G2310	U	U2120		C1990	A1930
	G2859	U2797	A2727	G2592	C2518	U2445	A2374	C2311	A	G2121	U2059	A1991	A1931
		C2798	C2728	C2593	G2519	G2446	G2375	G2312	C	C2122	A2060	U1992	G1932
		A2799	U2729	U2594	A2521	G2449	U2377	C2313	C	A2123	C2061	U1993	G1933
	G2863	U2800	G2730	U2595	G2522	C2450	U2378	U2246	C	G2124	A2062	A1994	A1934
	A2864		U2731	U2596	U2523	G2451	G2379	C2247	G	G2125	U2063	G1995	C1935
	G2865		G2732	U2597	G2524	G2452	A2380	C2248	C	C2126	U2064	U1996	C1936
			U2733	U2598	G2525	G2453	C2381	U2249	C	U2127	C2065	U1937	U1937
	C2868		U2734	U2599	C2526	G2454	A2382	G2250	C	G2128	C2066	C1999	G1938
	G2869		U2735	A2600	U2527	G2459	U2376	G2251	U	U2129	A2067	G2000	U1939
	G2870		U2736	A2601		A2460	G2385	A2252	A		C2068	G2001	C1940
	G2871							G2253	G	C2132	U2069	C2002	A1941

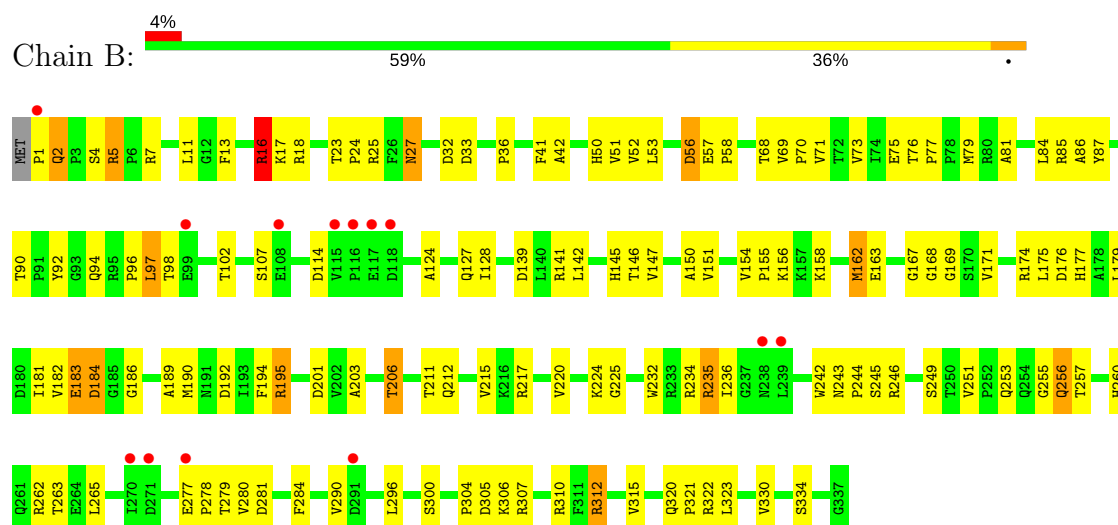
- Molecule 2: 5S RIBOSOMAL RNA



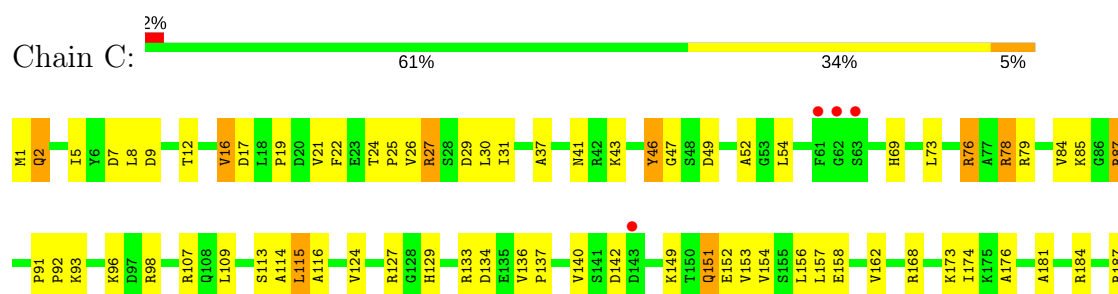
- Molecule 3: 50S ribosomal protein L2P



- Molecule 4: 50S ribosomal protein L3P

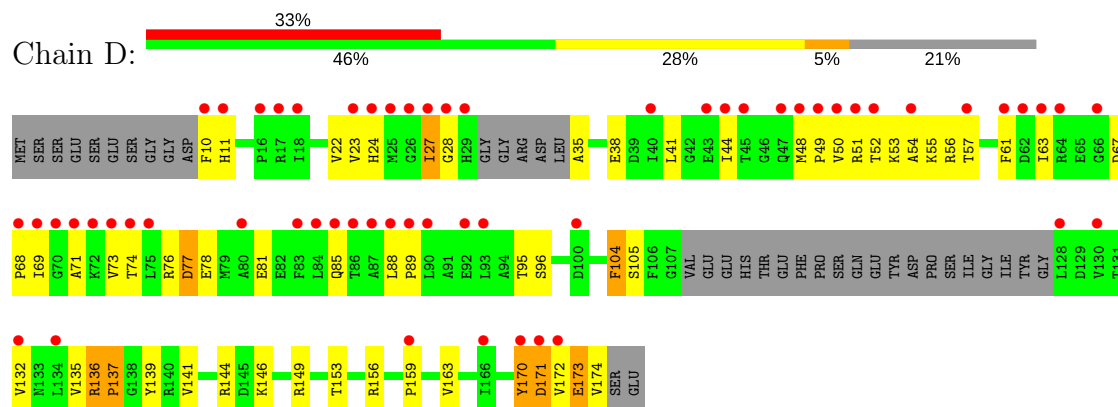


- Molecule 5: 50S ribosomal protein L4P

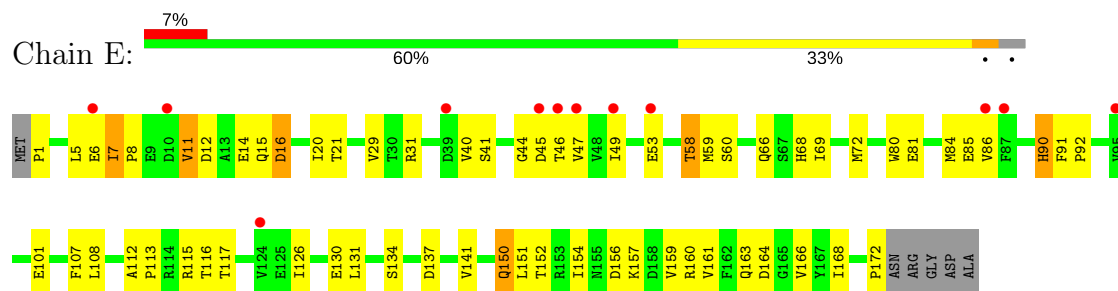




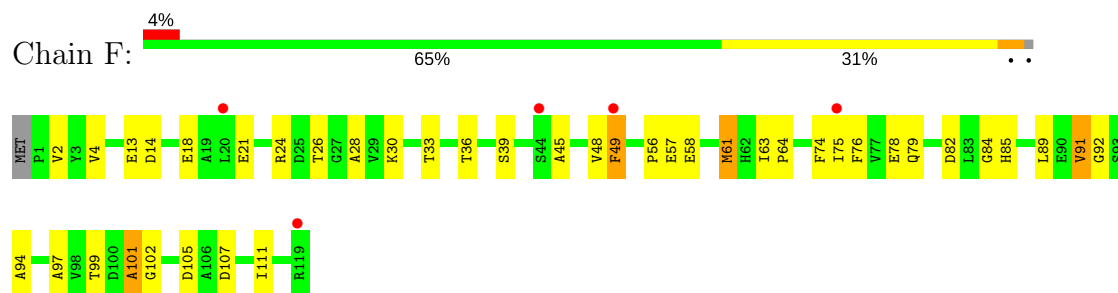
• Molecule 6: 50S ribosomal protein L5P



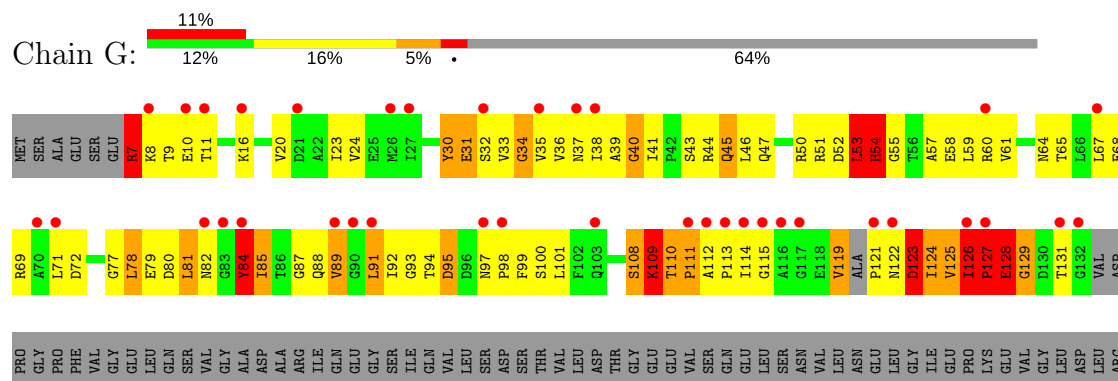
• Molecule 7: 50S ribosomal protein L6P

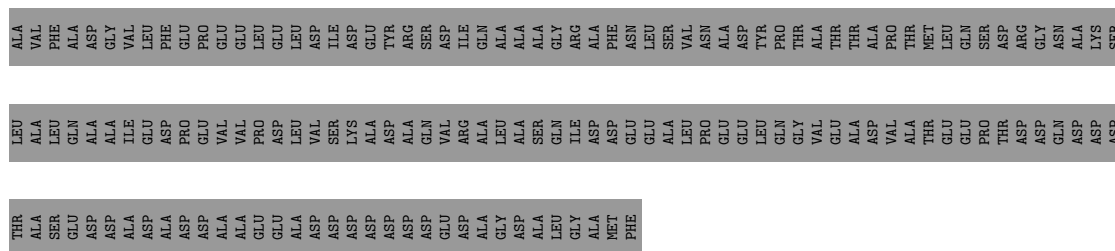


• Molecule 8: 50S ribosomal protein L7Ae

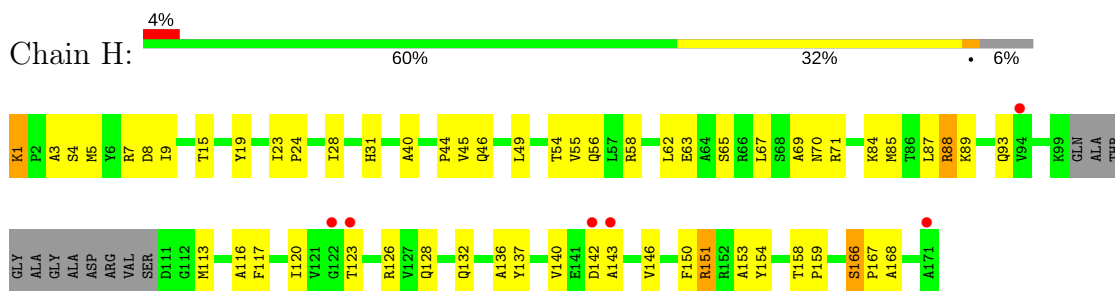


• Molecule 9: ACIDIC RIBOSOMAL PROTEIN P0 HOMO

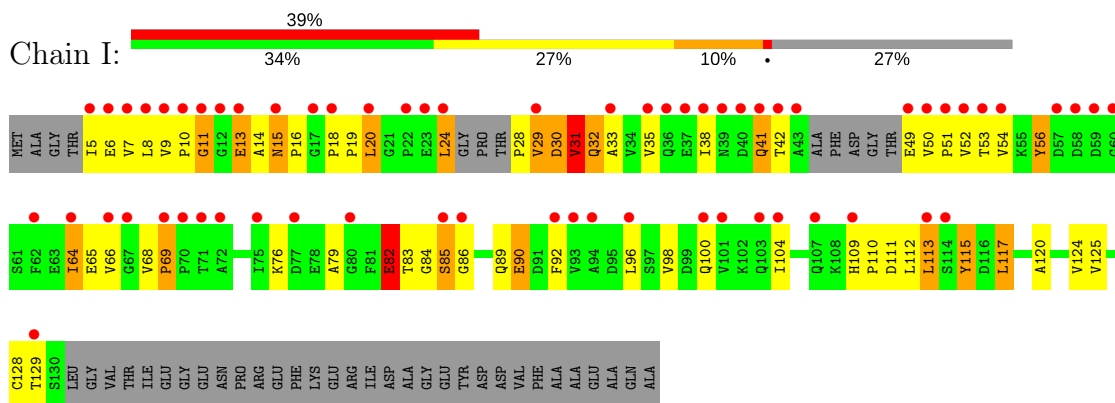




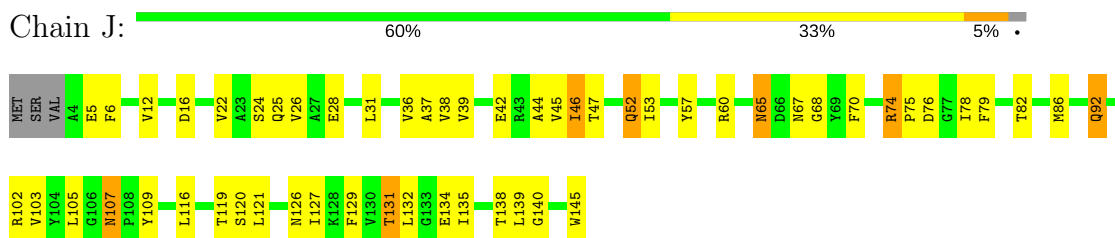
- Molecule 10: 50S ribosomal protein L10e



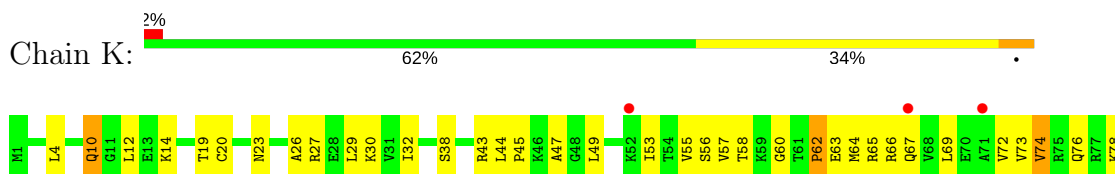
- Molecule 11: 50S ribosomal protein L11P



- Molecule 12: 50S ribosomal protein L13P

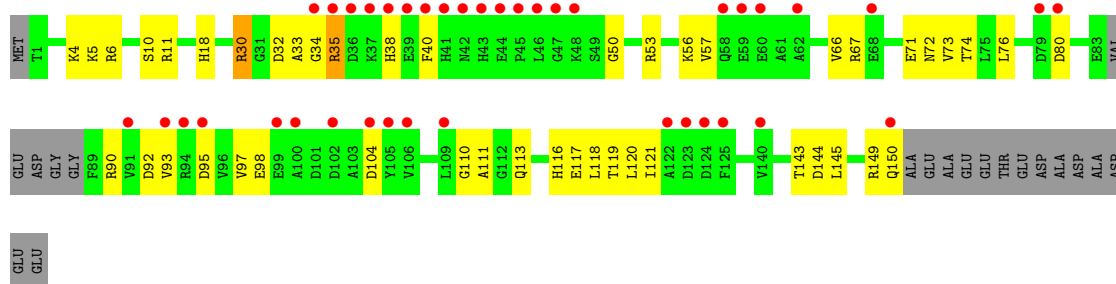


- Molecule 13: 50S ribosomal protein L14P

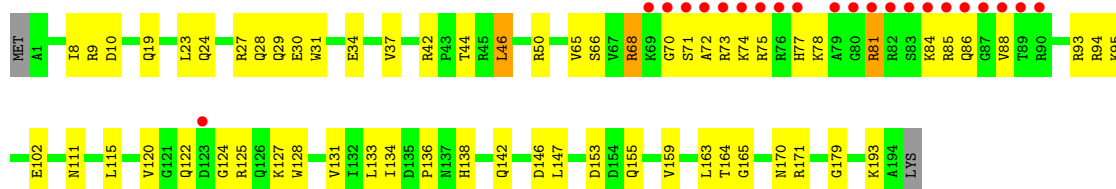




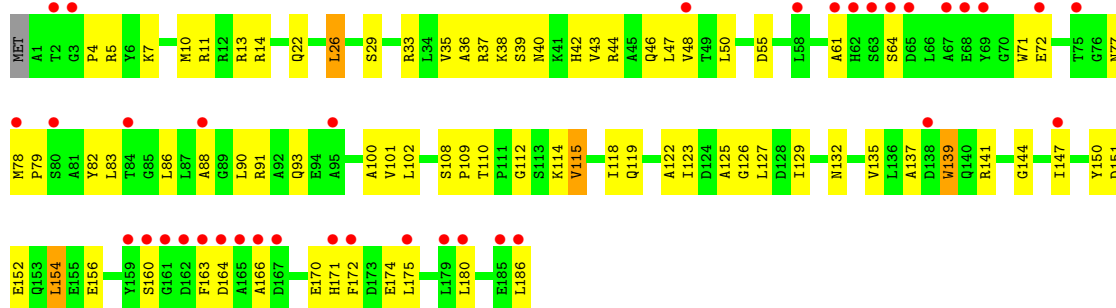
• Molecule 14: 50S ribosomal protein L15P



• Molecule 15: 50S ribosomal protein L15e



• Molecule 16: 50S ribosomal protein L18P

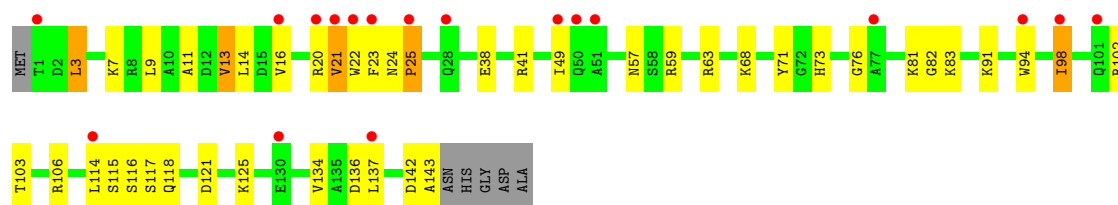


• Molecule 17: 50S ribosomal protein L18e

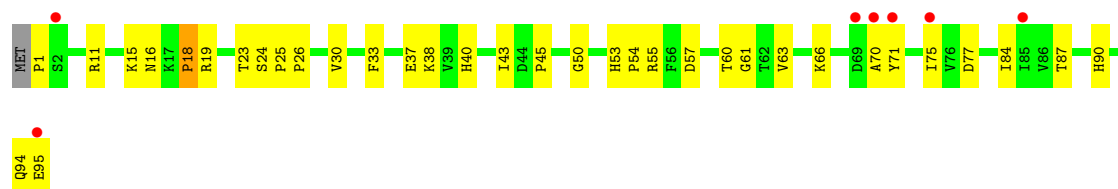


• Molecule 18: 50S ribosomal protein L19e

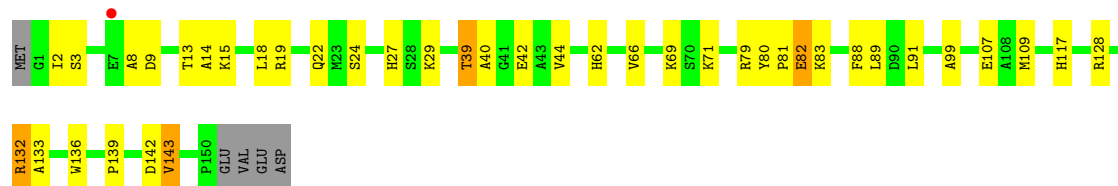




• Molecule 19: 50S ribosomal protein L21e



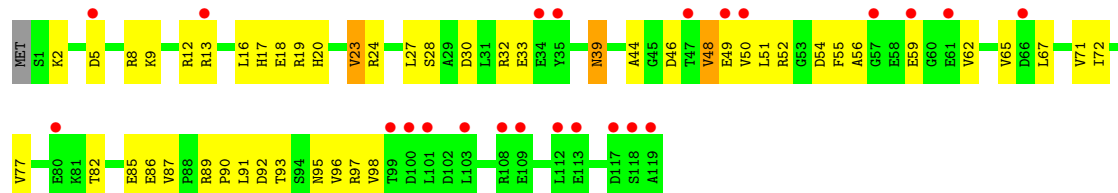
• Molecule 20: 50S ribosomal protein L22P



• Molecule 21: 50S ribosomal protein L23P

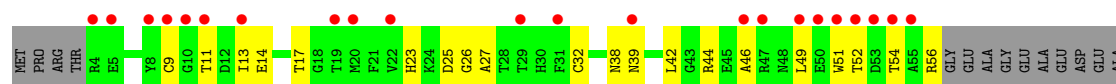


• Molecule 22: 50S ribosomal protein L24P

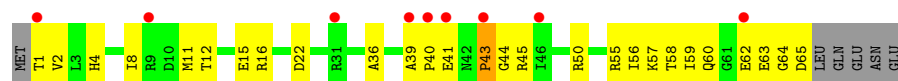


• Molecule 23: 50S ribosomal protein L24e

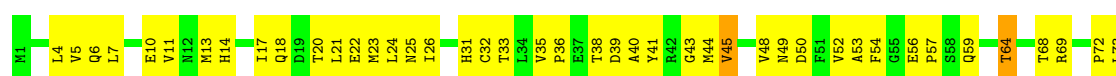




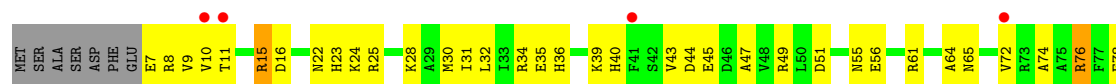
• Molecule 24: 50S ribosomal protein L29P



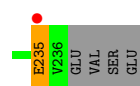
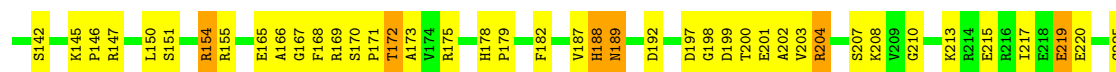
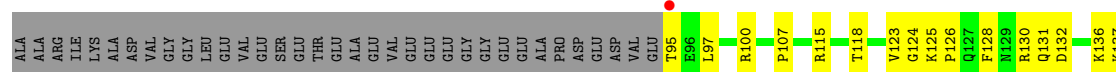
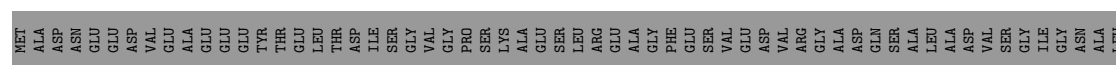
• Molecule 25: 50S ribosomal protein L30P



• Molecule 26: 50S RIBOSOMAL PROTEIN L31E

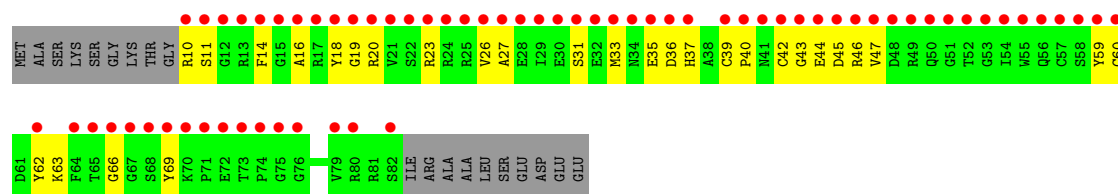


• Molecule 27: 50S ribosomal protein L32e



• Molecule 28: 50S ribosomal protein L37Ae





- Molecule 29: 50S ribosomal protein L37e

Chain 1: 54% 37% 7%



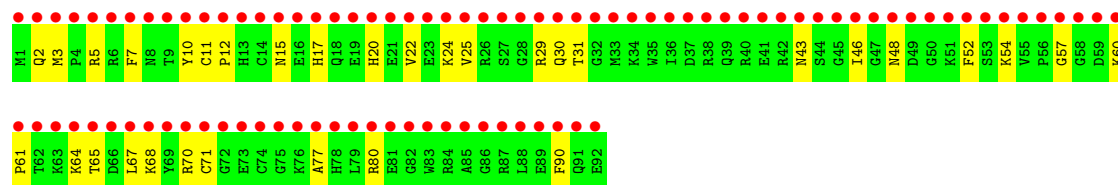
- Molecule 30: 50S ribosomal protein L39e

Chain 2: 26% 64% 28% 8%



- Molecule 31: 50S ribosomal protein L44E

Chain 3: 100% 64% 36%



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	214.49Å 302.43Å 578.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.00 49.83 – 3.01	Depositor EDS
% Data completeness (in resolution range)	98.2 (50.00-3.00) 96.9 (49.83-3.01)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 3.01Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.241 , 0.288 0.259 , 0.260	Depositor DCC
R_{free} test set	18014 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	69.6	Xtriage
Anisotropy	0.307	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 61.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	92248	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.71% 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, OMG, CL, NA, K, CD, OMU, UR3, PSU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.56	0/65932	0.75	36/102817 (0.0%)
2	9	0.42	0/2905	0.72	1/4528 (0.0%)
3	A	0.39	0/1786	0.69	0/2408
4	B	0.46	0/2690	0.76	0/3652
5	C	0.47	0/1884	0.76	1/2551 (0.0%)
6	D	0.36	0/1111	0.60	0/1498
7	E	0.45	0/1382	0.68	0/1880
8	F	0.34	0/901	0.58	0/1224
9	G	1.36	5/971 (0.5%)	1.67	22/1317 (1.7%)
10	H	0.41	0/1287	0.70	0/1725
11	I	4.03	6/890 (0.7%)	2.13	7/1216 (0.6%)
12	J	0.50	0/1136	0.70	0/1530
13	K	0.46	0/1001	0.77	0/1347
14	L	0.39	0/1130	0.68	0/1509
15	M	0.42	0/1583	0.68	0/2119
16	N	0.34	0/1474	0.66	0/1999
17	O	0.45	0/874	0.70	0/1181
18	P	0.42	0/1147	0.60	0/1528
19	Q	0.38	0/749	0.68	0/1005
20	R	0.50	0/1172	0.75	0/1578
21	S	0.42	0/648	0.64	0/875
22	T	0.42	0/958	0.71	0/1289
23	U	0.35	0/417	0.61	0/562
24	V	0.39	0/502	0.61	0/675
25	W	0.47	0/1219	0.77	0/1655
26	X	0.51	0/664	0.72	0/895
27	Y	0.48	0/1146	0.74	0/1536
28	Z	0.36	0/589	0.55	0/787
29	1	0.50	0/438	0.71	0/578
30	2	0.40	0/401	0.60	0/529
31	3	0.35	0/771	0.57	0/1024
All	All	0.66	11/99758 (0.0%)	0.77	67/149017 (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	0	6	93
2	9	0	1
9	G	0	8
11	I	2	4
All	All	8	106

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	I	24	LEU	CA-CB	82.97	3.44	1.53
11	I	24	LEU	CG-CD2	57.61	3.65	1.51
11	I	24	LEU	CG-CD1	50.48	3.38	1.51
11	I	24	LEU	CB-CG	34.68	2.53	1.52
9	G	54	HIS	CB-CG	28.65	2.01	1.50

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	I	24	LEU	CB-CA-C	-36.47	40.91	110.20
11	I	24	LEU	CD1-CG-CD2	-30.12	20.15	110.50
11	I	24	LEU	CB-CG-CD1	-29.18	61.40	111.00
11	I	24	LEU	CB-CG-CD2	-25.73	67.26	111.00
11	I	24	LEU	CA-CB-CG	-25.40	56.88	115.30

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	0	1161	A	C1'
1	0	1167	G	C3',C1'
1	0	1193	A	C4',C3',C1'
11	I	24	LEU	CA
11	I	30	ASP	CA

5 of 106 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	0	116	G	Sidechain
1	0	191	A	Sidechain

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Mol	Chain	Res	Type	Group
1	0	206	G	Sidechain
1	0	49	A	Sidechain
1	0	79	G	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	0	58979	0	29793	2515	0
2	9	2600	0	1326	157	0
3	A	1753	0	1766	73	0
4	B	2625	0	2533	110	0
5	C	1859	0	1816	84	0
6	D	1094	0	1085	50	0
7	E	1357	0	1266	46	0
8	F	890	0	843	31	0
9	G	959	0	928	154	0
10	H	1266	0	1268	49	0
11	I	876	0	835	60	0
12	J	1120	0	1098	49	0
13	K	992	0	1031	44	0
14	L	1118	0	1076	34	0
15	M	1559	0	1567	63	0
16	N	1445	0	1401	73	0
17	O	865	0	873	28	0
18	P	1136	0	1123	39	0
19	Q	735	0	728	27	0
20	R	1149	0	1122	44	0
21	S	641	0	605	13	0
22	T	950	0	924	50	0
23	U	410	0	367	15	0
24	V	499	0	511	21	0
25	W	1196	0	1137	72	0
26	X	654	0	653	42	0
27	Y	1130	0	1133	51	0
28	Z	578	0	543	36	0
29	1	431	0	427	24	0
30	2	396	0	413	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	3	755	0	732	34	0
32	0	108	0	0	0	0
32	3	1	0	0	0	0
32	9	1	0	0	0	0
32	A	2	0	0	0	0
32	B	1	0	0	0	0
32	K	1	0	0	0	0
32	T	1	0	0	0	0
32	Y	1	0	0	0	0
33	0	1	0	0	0	0
33	M	1	0	0	0	0
34	0	73	0	0	0	0
34	9	3	0	0	0	0
34	A	1	0	0	0	0
34	C	1	0	0	0	0
34	H	1	0	0	0	0
34	J	1	0	0	0	0
34	L	1	0	0	0	0
34	M	1	0	0	0	0
34	Q	1	0	0	0	0
34	R	2	0	0	0	0
34	S	1	0	0	0	0
35	0	8	0	0	1	0
35	3	1	0	0	5	0
35	A	1	0	0	0	0
35	B	1	0	0	0	0
35	J	3	0	0	4	0
35	K	1	0	0	0	0
35	L	1	0	0	0	0
35	M	1	0	0	1	0
35	N	1	0	0	0	0
35	O	1	0	0	1	0
35	Q	1	0	0	1	0
35	R	1	0	0	0	0
35	Y	1	0	0	0	0
36	1	1	0	0	1	0
36	3	1	0	0	0	0
36	O	1	0	0	0	0
36	U	1	0	0	0	0
36	Z	1	0	0	0	0
All	All	92248	0	60923	3719	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 25.

The worst 5 of 3719 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)
9:G:54:HIS:CB	9:G:54:HIS:CG	2.01	1.43
9:G:108:SER:O	9:G:109:LYS:HE3	1.32	1.30
1:O:1167:G:H5'	1:O:1168:C:OP2	1.34	1.28
9:G:33:VAL:C	9:G:123:ASP:OD2	1.72	1.27
9:G:35:VAL:HG21	9:G:122:ASN:OD1	1.37	1.25

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	
3	A	235/240 (98%)	206 (88%)	24 (10%)	5 (2%)	8	36
4	B	335/338 (99%)	287 (86%)	38 (11%)	10 (3%)	5	26
5	C	244/246 (99%)	209 (86%)	28 (12%)	7 (3%)	5	26
6	D	134/177 (76%)	95 (71%)	34 (25%)	5 (4%)	4	21
7	E	170/178 (96%)	156 (92%)	12 (7%)	2 (1%)	14	51
8	F	117/120 (98%)	101 (86%)	13 (11%)	3 (3%)	6	30
9	G	121/348 (35%)	79 (65%)	29 (24%)	13 (11%)	0	2
10	H	156/171 (91%)	141 (90%)	11 (7%)	4 (3%)	6	30
11	I	112/162 (69%)	76 (68%)	28 (25%)	8 (7%)	1	6
12	J	140/145 (97%)	129 (92%)	9 (6%)	2 (1%)	12	47
13	K	130/132 (98%)	117 (90%)	11 (8%)	2 (2%)	11	45
14	L	141/165 (86%)	127 (90%)	13 (9%)	1 (1%)	24	64
15	M	192/196 (98%)	161 (84%)	31 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	N	184/187 (98%)	162 (88%)	19 (10%)	3 (2%)	11	43
17	O	113/116 (97%)	103 (91%)	9 (8%)	1 (1%)	19	59
18	P	141/149 (95%)	129 (92%)	11 (8%)	1 (1%)	24	64
19	Q	93/96 (97%)	85 (91%)	5 (5%)	3 (3%)	4	24
20	R	148/155 (96%)	129 (87%)	18 (12%)	1 (1%)	24	64
21	S	79/85 (93%)	65 (82%)	14 (18%)	0	100	100
22	T	117/120 (98%)	105 (90%)	11 (9%)	1 (1%)	19	59
23	U	51/67 (76%)	48 (94%)	3 (6%)	0	100	100
24	V	63/71 (89%)	57 (90%)	5 (8%)	1 (2%)	11	43
25	W	152/154 (99%)	134 (88%)	17 (11%)	1 (1%)	24	64
26	X	80/92 (87%)	66 (82%)	13 (16%)	1 (1%)	13	49
27	Y	140/241 (58%)	130 (93%)	7 (5%)	3 (2%)	8	36
28	Z	71/92 (77%)	64 (90%)	7 (10%)	0	100	100
29	1	54/57 (95%)	45 (83%)	8 (15%)	1 (2%)	9	39
30	2	42/50 (84%)	41 (98%)	1 (2%)	0	100	100
31	3	90/92 (98%)	82 (91%)	7 (8%)	1 (1%)	16	53
All	All	3845/4442 (87%)	3329 (87%)	436 (11%)	80 (2%)	8	36

5 of 80 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	16	ARG
6	D	27	ILE
8	F	91	VAL
9	G	127	PRO
11	I	11	GLY

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	
3	A	179/182 (98%)	164 (92%)	15 (8%)	12	41
4	B	282/283 (100%)	264 (94%)	18 (6%)	19	55
5	C	193/193 (100%)	174 (90%)	19 (10%)	9	33
6	D	117/148 (79%)	109 (93%)	8 (7%)	17	52
7	E	152/156 (97%)	142 (93%)	10 (7%)	18	53
8	F	93/94 (99%)	92 (99%)	1 (1%)	76	92
9	G	106/283 (38%)	95 (90%)	11 (10%)	8	29
10	H	132/138 (96%)	124 (94%)	8 (6%)	20	57
11	I	99/130 (76%)	84 (85%)	15 (15%)	3	15
12	J	118/121 (98%)	107 (91%)	11 (9%)	10	36
13	K	106/106 (100%)	98 (92%)	8 (8%)	15	47
14	L	113/127 (89%)	108 (96%)	5 (4%)	31	69
15	M	158/160 (99%)	150 (95%)	8 (5%)	26	64
16	N	149/150 (99%)	144 (97%)	5 (3%)	40	76
17	O	93/94 (99%)	89 (96%)	4 (4%)	32	70
18	P	113/117 (97%)	107 (95%)	6 (5%)	25	62
19	Q	79/80 (99%)	76 (96%)	3 (4%)	36	73
20	R	117/122 (96%)	113 (97%)	4 (3%)	40	76
21	S	71/74 (96%)	66 (93%)	5 (7%)	16	50
22	T	105/106 (99%)	99 (94%)	6 (6%)	23	60
23	U	44/53 (83%)	44 (100%)	0	100	100
24	V	51/57 (90%)	49 (96%)	2 (4%)	35	73
25	W	130/130 (100%)	121 (93%)	9 (7%)	17	51
26	X	66/74 (89%)	62 (94%)	4 (6%)	20	57
27	Y	120/196 (61%)	111 (92%)	9 (8%)	15	47
28	Z	60/74 (81%)	60 (100%)	0	100	100
29	1	46/47 (98%)	43 (94%)	3 (6%)	19	54
30	2	42/46 (91%)	41 (98%)	1 (2%)	52	83
31	3	79/79 (100%)	78 (99%)	1 (1%)	71	91
All	All	3213/3620 (89%)	3014 (94%)	199 (6%)	20	56

5 of 199 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	I	9	VAL
12	J	79	PHE
26	X	76	ARG
11	I	15	ASN
11	I	90	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
15	M	24	GLN
16	N	107	ASN
27	Y	189	ASN
15	M	58	GLN
16	N	40	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2741/2922 (93%)	291 (10%)	35 (1%)
2	9	121/122 (99%)	16 (13%)	4 (3%)
All	All	2862/3044 (94%)	307 (10%)	39 (1%)

5 of 307 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	11	A
1	0	31	C
1	0	60	A
1	0	67	A
1	0	69	A

5 of 39 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	1352	A
1	0	1506	U
2	9	43	G
1	0	1377	C
1	0	1450	C

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

4 non-standard protein/DNA/RNA residues are 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
1	OMU	0	2587	1	14,22,23	0.96	1 (7%)	18,31,34	3.65	2 (11%)
1	OMG	0	2588	1	19,26,27	1.08	2 (10%)	22,38,41	2.46	4 (18%)
1	UR3	0	2619	1	13,22,23	0.90	1 (7%)	15,32,35	0.74	0
1	PSU	0	2621	1	16,21,22	1.70	3 (18%)	20,30,33	5.46	5 (25%)

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
1	OMU	0	2587	1	-	0/5/27/28	0/2/2/2
1	OMG	0	2588	1	-	0/5/27/28	0/3/3/3
1	UR3	0	2619	1	-	0/3/25/26	0/2/2/2
1	PSU	0	2621	1	-	0/7/25/26	0/2/2/2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2621	PSU	C5-C1'	-5.05	1.47	1.52
1	0	2619	UR3	C6-C5	-2.52	1.32	1.38
1	0	2588	OMG	C8-N7	-2.16	1.30	1.34
1	0	2587	OMU	C4-N3	2.46	1.37	1.33
1	0	2621	PSU	C4-N3	2.77	1.38	1.33

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	N1-C2-N3	-17.48	114.36	128.41
1	0	2588	OMG	C5-C6-N1	-8.27	111.71	123.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2621	PSU	C5-C4-N3	-8.15	114.86	125.36
1	0	2587	OMU	C5-C4-N3	-3.80	114.35	123.17
1	0	2588	OMG	C2-N3-C4	-2.85	111.83	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	0	2587	OMU	5	0
1	0	2588	OMG	3	0
1	0	2619	UR3	1	0
1	0	2621	PSU	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 231 ligands modelled in this entry, 231 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
9	G	2
1	0	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	0	1207:A	O3'	1208:C	P	2.51
1	G	53:LEU	C	54:HIS	N	1.63
1	G	54:HIS	C	55:GLY	N	0.99

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	0	2749/2922 (94%)	-0.18	16 (0%) 89 71	17, 56, 120, 184	0
2	9	122/122 (100%)	-0.01	2 (1%) 72 44	41, 89, 136, 181	0
3	A	237/240 (98%)	0.56	23 (9%) 8 2	34, 90, 133, 148	0
4	B	337/338 (99%)	0.15	13 (3%) 39 16	25, 60, 100, 112	0
5	C	246/246 (100%)	0.16	6 (2%) 59 30	29, 58, 91, 106	0
6	D	140/177 (79%)	1.95	58 (41%) 0 0	89, 146, 170, 178	0
7	E	172/178 (96%)	0.48	12 (6%) 16 5	46, 73, 100, 109	0
8	F	119/120 (99%)	0.37	5 (4%) 36 14	74, 110, 150, 166	0
9	G	125/348 (35%)	1.41	37 (29%) 0 0	100, 133, 165, 168	0
10	H	160/171 (93%)	0.34	6 (3%) 40 16	51, 76, 109, 120	0
11	I	118/162 (72%)	2.78	63 (53%) 0 0	20, 181, 199, 200	0
12	J	142/145 (97%)	-0.05	0 100 100	31, 54, 83, 99	0
13	K	132/132 (100%)	0.19	3 (2%) 60 31	33, 61, 98, 103	0
14	L	145/165 (87%)	1.49	39 (26%) 0 0	49, 111, 158, 162	0
15	M	194/196 (98%)	0.77	22 (11%) 5 1	2, 62, 161, 180	0
16	N	186/187 (99%)	1.18	37 (19%) 1 0	62, 106, 176, 189	0
17	O	115/116 (99%)	0.10	0 100 100	48, 70, 88, 91	0
18	P	143/149 (95%)	0.79	18 (12%) 3 1	44, 68, 103, 109	0
19	Q	95/96 (98%)	0.67	7 (7%) 14 4	52, 74, 87, 100	0
20	R	150/155 (96%)	0.04	1 (0%) 87 68	30, 48, 74, 81	0
21	S	81/85 (95%)	0.40	2 (2%) 57 29	56, 87, 108, 123	0
22	T	119/120 (99%)	0.99	23 (19%) 1 0	51, 74, 106, 139	0
23	U	53/67 (79%)	1.90	22 (41%) 0 0	96, 108, 126, 133	0
24	V	65/71 (91%)	0.84	9 (13%) 3 1	66, 105, 145, 148	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
25	W	154/154 (100%)	-0.02	0 100 100	38, 55, 81, 95	0
26	X	82/92 (89%)	0.57	7 (8%) 11 3	43, 63, 84, 95	0
27	Y	142/241 (58%)	0.26	2 (1%) 75 49	23, 51, 87, 106	0
28	Z	73/92 (79%)	6.73	67 (91%) 0 0	164, 174, 200, 200	0
29	1	56/57 (98%)	0.06	0 100 100	28, 43, 56, 65	0
30	2	46/50 (92%)	1.29	13 (28%) 0 0	48, 87, 150, 152	0
31	3	92/92 (100%)	11.33	92 (100%) 0 0	184, 198, 200, 200	0
All	All	6790/7486 (90%)	0.51	605 (8%) 9 3	2, 67, 162, 200	0

The worst 5 of 605 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
31	3	9	THR	24.4
31	3	33	MET	23.0
31	3	69	TYR	22.4
31	3	78	HIS	20.9
31	3	25	VAL	20.2

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
1	OMU	0	2587	21/22	0.94	0.18	33,36,42,43	0
1	OMG	0	2588	24/25	0.95	0.18	38,42,48,49	0
1	UR3	0	2619	21/22	0.96	0.18	34,42,44,47	0
1	PSU	0	2621	20/21	0.97	0.15	35,37,44,44	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
34	NA	0	3103	1/1	-0.15	0.88	198,198,198,198	0
34	NA	0	3050	1/1	-0.11	1.21	137,137,137,137	0
32	MG	0	3027	1/1	-0.00	0.96	110,110,110,110	0
32	MG	0	2946	1/1	0.09	0.34	200,200,200,200	0
32	MG	0	2971	1/1	0.18	0.41	200,200,200,200	0
34	NA	0	3100	1/1	0.30	1.21	56,56,56,56	0
35	CL	O	117	1/1	0.38	1.01	127,127,127,127	0
32	MG	0	3025	1/1	0.41	0.47	57,57,57,57	0
34	NA	0	3093	1/1	0.45	0.39	116,116,116,116	0
32	MG	0	2998	1/1	0.45	0.50	73,73,73,73	0
34	NA	0	3057	1/1	0.45	0.80	124,124,124,124	0
32	MG	0	3029	1/1	0.47	0.99	69,69,69,69	0
32	MG	3	93	1/1	0.49	0.51	69,69,69,69	0
34	NA	0	3054	1/1	0.50	0.34	63,63,63,63	0
35	CL	0	3109	1/1	0.53	0.61	135,135,135,135	0
34	NA	0	3047	1/1	0.55	0.36	53,53,53,53	0
35	CL	0	3106	1/1	0.56	1.27	120,120,120,120	0
34	NA	0	3082	1/1	0.56	0.48	43,43,43,43	0
36	CD	O	116	1/1	0.59	0.47	200,200,200,200	0
35	CL	0	3112	1/1	0.59	0.56	96,96,96,96	0
34	NA	S	85	1/1	0.59	0.67	64,64,64,64	0
34	NA	0	3052	1/1	0.60	0.52	72,72,72,72	0
35	CL	3	95	1/1	0.61	0.65	124,124,124,124	0
32	MG	0	2988	1/1	0.61	0.34	52,52,52,52	0
34	NA	0	3065	1/1	0.64	0.19	27,27,27,27	0
32	MG	0	3028	1/1	0.64	0.97	66,66,66,66	0
34	NA	0	3068	1/1	0.65	0.25	68,68,68,68	0
32	MG	Y	241	1/1	0.66	0.47	68,68,68,68	0
34	NA	0	3098	1/1	0.67	0.52	62,62,62,62	0
34	NA	0	3094	1/1	0.67	0.43	116,116,116,116	0
34	NA	0	3075	1/1	0.67	0.46	41,41,41,41	0
34	NA	0	3046	1/1	0.67	0.28	26,26,26,26	0
32	MG	B	338	1/1	0.68	0.59	43,43,43,43	0
32	MG	0	2964	1/1	0.69	0.34	50,50,50,50	0
34	NA	0	3038	1/1	0.69	0.32	67,67,67,67	0
34	NA	0	3059	1/1	0.69	0.42	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
32	MG	0	2980	1/1	0.71	0.47	48,48,48,48	0
35	CL	0	3111	1/1	0.72	0.25	54,54,54,54	0
32	MG	A	240	1/1	0.72	0.48	56,56,56,56	0
33	K	M	196	1/1	0.73	0.42	127,127,127,127	0
34	NA	0	3044	1/1	0.73	0.85	46,46,46,46	0
34	NA	C	247	1/1	0.73	0.34	41,41,41,41	0
34	NA	A	242	1/1	0.74	0.28	55,55,55,55	0
34	NA	0	3077	1/1	0.74	0.55	119,119,119,119	0
34	NA	0	3092	1/1	0.74	0.25	45,45,45,45	0
32	MG	0	2987	1/1	0.75	0.16	35,35,35,35	0
32	MG	0	2984	1/1	0.75	0.51	59,59,59,59	0
34	NA	9	125	1/1	0.75	0.35	78,78,78,78	0
32	MG	0	2973	1/1	0.75	0.42	51,51,51,51	0
34	NA	R	156	1/1	0.76	0.33	53,53,53,53	0
34	NA	0	3034	1/1	0.76	0.77	91,91,91,91	0
34	NA	0	3099	1/1	0.76	0.90	56,56,56,56	0
34	NA	0	3064	1/1	0.77	0.30	60,60,60,60	0
32	MG	0	2969	1/1	0.77	0.40	38,38,38,38	0
32	MG	0	3007	1/1	0.78	0.29	54,54,54,54	0
34	NA	0	3058	1/1	0.78	0.26	61,61,61,61	0
32	MG	0	2985	1/1	0.78	0.29	34,34,34,34	0
32	MG	0	3006	1/1	0.78	0.42	49,49,49,49	0
34	NA	0	3039	1/1	0.79	0.63	29,29,29,29	0
34	NA	0	3033	1/1	0.79	0.45	60,60,60,60	0
33	K	0	3031	1/1	0.79	0.47	153,153,153,153	0
35	CL	Q	97	1/1	0.79	0.57	93,93,93,93	0
32	MG	0	3026	1/1	0.79	1.06	79,79,79,79	0
34	NA	9	124	1/1	0.79	0.16	34,34,34,34	0
32	MG	0	2974	1/1	0.79	0.19	51,51,51,51	0
34	NA	0	3084	1/1	0.79	0.43	62,62,62,62	0
34	NA	0	3051	1/1	0.80	0.33	49,49,49,49	0
34	NA	J	146	1/1	0.80	0.24	41,41,41,41	0
32	MG	0	3014	1/1	0.80	0.32	87,87,87,87	0
32	MG	0	3013	1/1	0.80	0.38	41,41,41,41	0
32	MG	A	241	1/1	0.80	0.38	142,142,142,142	0
34	NA	0	3056	1/1	0.80	0.33	42,42,42,42	0
32	MG	K	133	1/1	0.80	0.45	35,35,35,35	0
34	NA	0	3060	1/1	0.80	0.15	101,101,101,101	0
35	CL	0	3108	1/1	0.81	0.36	72,72,72,72	0
32	MG	0	2989	1/1	0.81	0.67	56,56,56,56	0
32	MG	0	2944	1/1	0.81	0.18	25,25,25,25	0
32	MG	0	3011	1/1	0.81	0.86	71,71,71,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
34	NA	9	126	1/1	0.81	0.85	91,91,91,91	0
35	CL	R	157	1/1	0.81	0.24	55,55,55,55	0
32	MG	0	3030	1/1	0.82	0.18	46,46,46,46	0
34	NA	0	3061	1/1	0.82	0.12	39,39,39,39	0
34	NA	0	3043	1/1	0.82	0.38	115,115,115,115	0
32	MG	0	3018	1/1	0.82	0.35	78,78,78,78	0
35	CL	L	166	1/1	0.82	0.27	68,68,68,68	0
32	MG	0	3024	1/1	0.83	0.35	1,1,1,1	0
34	NA	0	3063	1/1	0.83	0.19	162,162,162,162	0
36	CD	Z	93	1/1	0.83	0.35	200,200,200,200	0
34	NA	0	3101	1/1	0.83	0.17	43,43,43,43	0
35	CL	A	243	1/1	0.83	0.40	90,90,90,90	0
32	MG	0	2962	1/1	0.84	0.48	60,60,60,60	0
34	NA	Q	96	1/1	0.84	0.24	64,64,64,64	0
34	NA	0	3067	1/1	0.85	0.30	47,47,47,47	0
32	MG	0	3004	1/1	0.85	0.53	27,27,27,27	0
32	MG	0	2949	1/1	0.85	0.35	45,45,45,45	0
32	MG	0	2993	1/1	0.85	0.44	78,78,78,78	0
35	CL	M	198	1/1	0.86	0.36	77,77,77,77	0
34	NA	0	3041	1/1	0.86	0.36	70,70,70,70	0
32	MG	0	3010	1/1	0.86	0.17	56,56,56,56	0
32	MG	0	2938	1/1	0.86	0.47	42,42,42,42	0
32	MG	0	2947	1/1	0.86	0.27	15,15,15,15	0
32	MG	0	3017	1/1	0.87	0.34	166,166,166,166	0
34	NA	0	3032	1/1	0.87	0.45	30,30,30,30	0
34	NA	0	3035	1/1	0.87	0.17	17,17,17,17	0
32	MG	0	2968	1/1	0.87	0.10	60,60,60,60	0
32	MG	0	3023	1/1	0.87	0.34	29,29,29,29	0
32	MG	0	2956	1/1	0.87	0.18	24,24,24,24	0
32	MG	0	3019	1/1	0.87	0.40	41,41,41,41	0
32	MG	0	2929	1/1	0.88	0.19	14,14,14,14	0
32	MG	0	3022	1/1	0.88	0.38	44,44,44,44	0
35	CL	N	187	1/1	0.88	0.29	64,64,64,64	0
32	MG	0	2981	1/1	0.88	0.50	44,44,44,44	0
32	MG	0	2950	1/1	0.88	0.23	17,17,17,17	0
34	NA	0	3088	1/1	0.88	0.26	33,33,33,33	0
34	NA	0	3089	1/1	0.88	0.14	51,51,51,51	0
35	CL	J	149	1/1	0.88	0.15	45,45,45,45	0
32	MG	0	2986	1/1	0.88	0.35	53,53,53,53	0
32	MG	0	2943	1/1	0.88	0.37	23,23,23,23	0
32	MG	0	2935	1/1	0.89	0.38	28,28,28,28	0
32	MG	0	3009	1/1	0.89	0.28	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
32	MG	0	3015	1/1	0.89	0.49	53,53,53,53	0
32	MG	0	2963	1/1	0.89	0.15	72,72,72,72	0
32	MG	0	2951	1/1	0.89	0.38	11,11,11,11	0
32	MG	0	2979	1/1	0.89	0.23	20,20,20,20	0
32	MG	0	2975	1/1	0.90	0.16	45,45,45,45	0
34	NA	0	3102	1/1	0.90	0.31	47,47,47,47	0
34	NA	0	3078	1/1	0.90	0.16	78,78,78,78	0
34	NA	0	3080	1/1	0.90	0.41	57,57,57,57	0
36	CD	3	94	1/1	0.90	1.15	200,200,200,200	0
32	MG	0	2936	1/1	0.90	0.13	17,17,17,17	0
32	MG	0	3020	1/1	0.90	0.18	84,84,84,84	0
34	NA	0	3072	1/1	0.90	0.24	65,65,65,65	0
34	NA	0	3073	1/1	0.90	0.27	25,25,25,25	0
32	MG	0	2999	1/1	0.90	0.19	25,25,25,25	0
35	CL	0	3105	1/1	0.91	0.17	59,59,59,59	0
34	NA	H	172	1/1	0.91	0.16	43,43,43,43	0
34	NA	0	3055	1/1	0.91	0.14	36,36,36,36	0
32	MG	0	2945	1/1	0.91	0.32	27,27,27,27	0
35	CL	0	3110	1/1	0.91	0.55	56,56,56,56	0
35	CL	K	134	1/1	0.91	0.34	55,55,55,55	0
32	MG	0	2992	1/1	0.91	0.26	52,52,52,52	0
32	MG	9	123	1/1	0.91	0.17	37,37,37,37	0
34	NA	0	3081	1/1	0.91	0.18	49,49,49,49	0
34	NA	0	3090	1/1	0.91	0.29	81,81,81,81	0
32	MG	0	1	1/1	0.91	0.20	26,26,26,26	0
34	NA	0	3069	1/1	0.91	0.28	58,58,58,58	0
32	MG	0	2960	1/1	0.91	0.29	11,11,11,11	0
32	MG	0	3016	1/1	0.91	0.20	43,43,43,43	0
32	MG	0	2959	1/1	0.92	0.18	39,39,39,39	0
32	MG	0	2924	1/1	0.92	0.23	35,35,35,35	0
32	MG	0	3005	1/1	0.92	0.16	47,47,47,47	0
35	CL	B	339	1/1	0.92	0.46	61,61,61,61	0
32	MG	0	3001	1/1	0.92	0.15	38,38,38,38	0
35	CL	J	148	1/1	0.92	0.07	49,49,49,49	0
34	NA	0	3071	1/1	0.92	0.13	27,27,27,27	0
34	NA	0	3074	1/1	0.92	0.47	66,66,66,66	0
34	NA	M	197	1/1	0.92	0.16	28,28,28,28	0
34	NA	0	3040	1/1	0.92	0.18	29,29,29,29	0
32	MG	0	2970	1/1	0.92	0.19	32,32,32,32	0
34	NA	0	3066	1/1	0.92	0.11	9,9,9,9	0
34	NA	0	3085	1/1	0.92	0.41	15,15,15,15	0
32	MG	0	2930	1/1	0.92	0.12	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
34	NA	0	3095	1/1	0.92	0.49	126,126,126,126	0
34	NA	R	155	1/1	0.93	0.21	31,31,31,31	0
34	NA	0	3083	1/1	0.93	0.17	27,27,27,27	0
35	CL	J	147	1/1	0.93	0.16	69,69,69,69	0
32	MG	0	2978	1/1	0.93	0.17	46,46,46,46	0
34	NA	0	3104	1/1	0.93	0.59	34,34,34,34	0
32	MG	0	2991	1/1	0.93	0.16	20,20,20,20	0
34	NA	0	3042	1/1	0.93	0.38	32,32,32,32	0
32	MG	0	3003	1/1	0.93	0.18	26,26,26,26	0
34	NA	0	3091	1/1	0.93	0.25	31,31,31,31	0
34	NA	0	3076	1/1	0.93	0.22	51,51,51,51	0
34	NA	0	3086	1/1	0.93	0.40	26,26,26,26	0
32	MG	0	2966	1/1	0.93	0.13	46,46,46,46	0
32	MG	0	2937	1/1	0.93	0.24	14,14,14,14	0
35	CL	Y	242	1/1	0.93	0.26	27,27,27,27	0
32	MG	0	2990	1/1	0.93	0.15	31,31,31,31	0
34	NA	0	3070	1/1	0.94	0.10	27,27,27,27	0
32	MG	0	2928	1/1	0.94	0.14	32,32,32,32	0
32	MG	0	3000	1/1	0.94	0.20	7,7,7,7	0
34	NA	0	3045	1/1	0.94	0.22	33,33,33,33	0
32	MG	0	3008	1/1	0.94	0.30	52,52,52,52	0
32	MG	0	2957	1/1	0.94	0.14	37,37,37,37	0
32	MG	0	2997	1/1	0.94	0.27	59,59,59,59	0
32	MG	0	3012	1/1	0.94	0.27	39,39,39,39	0
32	MG	0	2942	1/1	0.94	0.41	16,16,16,16	0
32	MG	0	2977	1/1	0.94	0.52	43,43,43,43	0
34	NA	0	3048	1/1	0.94	0.21	46,46,46,46	0
32	MG	0	2954	1/1	0.94	0.18	29,29,29,29	0
32	MG	0	2967	1/1	0.94	0.30	50,50,50,50	0
32	MG	0	2952	1/1	0.95	0.23	4,4,4,4	0
34	NA	0	3079	1/1	0.95	0.12	53,53,53,53	0
34	NA	0	3096	1/1	0.95	0.21	47,47,47,47	0
34	NA	0	3087	1/1	0.95	0.08	22,22,22,22	0
34	NA	0	3097	1/1	0.95	0.17	50,50,50,50	0
32	MG	0	2995	1/1	0.95	0.16	13,13,13,13	0
32	MG	0	2983	1/1	0.95	0.29	43,43,43,43	0
32	MG	0	2931	1/1	0.95	0.11	27,27,27,27	0
32	MG	0	2939	1/1	0.95	0.31	20,20,20,20	0
32	MG	0	2982	1/1	0.95	0.25	14,14,14,14	0
32	MG	0	2941	1/1	0.96	0.16	15,15,15,15	0
34	NA	L	165	1/1	0.96	0.07	42,42,42,42	0
36	CD	U	67	1/1	0.96	0.10	134,134,134,134	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
34	NA	0	3037	1/1	0.96	0.34	61,61,61,61	0
32	MG	0	2932	1/1	0.96	0.14	10,10,10,10	0
35	CL	0	3107	1/1	0.96	0.15	55,55,55,55	0
34	NA	0	3062	1/1	0.96	0.07	38,38,38,38	0
32	MG	0	2994	1/1	0.96	0.20	14,14,14,14	0
32	MG	0	2925	1/1	0.96	0.19	5,5,5,5	0
32	MG	0	3021	1/1	0.96	0.23	20,20,20,20	0
32	MG	0	2976	1/1	0.96	0.18	19,19,19,19	0
32	MG	0	2933	1/1	0.96	0.32	1,1,1,1	0
34	NA	0	3049	1/1	0.97	0.27	28,28,28,28	0
32	MG	0	2958	1/1	0.97	0.43	33,33,33,33	0
32	MG	T	120	1/1	0.97	0.25	38,38,38,38	0
34	NA	0	3053	1/1	0.97	0.07	19,19,19,19	0
32	MG	0	2955	1/1	0.97	0.30	11,11,11,11	0
32	MG	0	2953	1/1	0.97	0.11	8,8,8,8	0
34	NA	0	3036	1/1	0.97	0.36	49,49,49,49	0
32	MG	0	2972	1/1	0.97	0.20	109,109,109,109	0
32	MG	0	2940	1/1	0.97	0.33	24,24,24,24	0
32	MG	0	2965	1/1	0.98	0.22	47,47,47,47	0
32	MG	0	2926	1/1	0.98	0.15	17,17,17,17	0
32	MG	0	3002	1/1	0.98	0.06	20,20,20,20	0
32	MG	0	2961	1/1	0.98	0.19	41,41,41,41	0
32	MG	0	2996	1/1	0.98	0.24	21,21,21,21	0
32	MG	0	2934	1/1	0.98	0.34	22,22,22,22	0
32	MG	0	2927	1/1	0.99	0.19	18,18,18,18	0
36	CD	1	57	1/1	0.99	0.06	76,76,76,76	0
32	MG	0	2948	1/1	0.99	0.27	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.