



# wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 03:55 PM GMT

PDB ID : 4KD9

Title : 70S Ribosome translocation intermediate FA-3.6A CONTAINING ELONGATION FACTOR EFG/FUSIDIC ACID/GDP, MRNA, AND TRNA BOUND IN THE  $pe^*/E$  STATE. THIS ENTRY CONTAINS THE 50S RIBOSOMAL SUBUNIT A. THE 30S SUBUNIT A CAN BE FOUND IN 4KD8. MOLECULE B IN THE SAME ASYMMETRIC UNIT IS DEPOSITED AS 4KDA (30S) AND 4KDB (50S).

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Deposited on : 2013-04-24

Resolution : 3.50 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

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

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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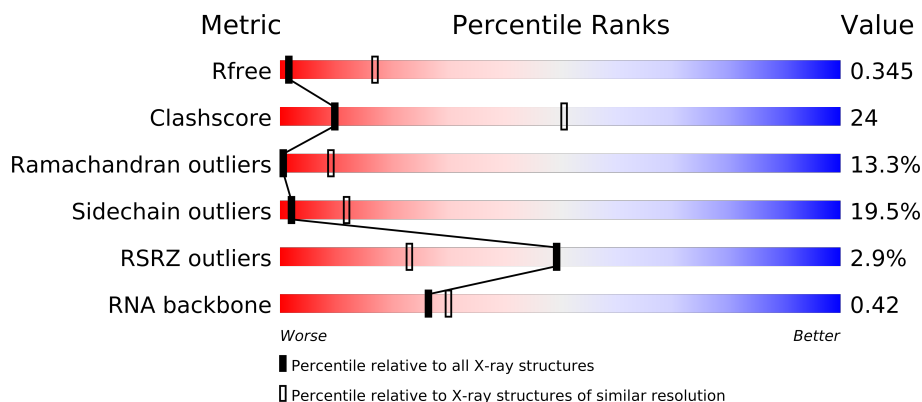
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	<b>FAILED</b>
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1243 (3.70-3.30)
Clashscore	79885	1039 (3.66-3.34)
Ramachandran outliers	78287	1000 (3.66-3.34)
Sidechain outliers	78261	1000 (3.66-3.34)
RSRZ outliers	66119	1243 (3.70-3.30)
RNA backbone	1838	1007 (4.22-2.76)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	C	228	
2	D	275	
3	E	205	
4	F	208	
5	G	181	
6	H	167	
7	J	170	
8	K	140	
9	N	138	
10	O	122	
11	P	146	
12	Q	141	

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Mol	Chain	Length	Quality of chain
13	R	117	
14	S	99	
15	T	138	
16	U	117	
17	V	101	
18	W	113	
19	X	93	
20	Y	107	
21	Z	185	
22	0	84	
23	2	71	
24	3	60	
25	5	59	
26	6	50	
27	7	49	
28	8	64	
29	9	37	
30	e	102	
31	f	31	
31	g	31	
32	h	30	
33	1	93	
34	4	35	
35	A	2879	
36	B	119	

## 2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 95124 atoms, of which 0 are hydrogen and 0 are deuterium.

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 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	228	Total	C	N	O	S	0	0	0
			1742	1101	319	319	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	20	VAL	ILE	CONFLICT	UNP Q72GV9
C	28	ARG	HIS	CONFLICT	UNP Q72GV9

- Molecule 2 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	275	Total	C	N	O	S	0	0	0
			2145	1353	428	361	3			

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	205	Total	C	N	O	S	0	0	0
			1569	991	300	272	6			

- Molecule 4 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	208	Total	C	N	O	S	0	0	0
			1628	1037	304	284	3			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	2	LYS	-	INSERTION	UNP Q72I05
F	3	GLU	-	INSERTION	UNP Q72I05

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Chain	Residue	Modelled	Actual	Comment	Reference
F	4	VAL	-	INSERTION	UNP Q72I05
F	5	ALA	-	INSERTION	UNP Q72I05
F	6	VAL	-	INSERTION	UNP Q72I05

- Molecule 5 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	181	Total	C	N	O	S	0	0	0
			1474	942	268	260	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	5	VAL	LEU	CONFLICT	UNP Q72I16

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	167	Total	C	N	O	S	0	0	0
			1274	806	238	229	1			

- Molecule 7 is a protein called 50S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	J	170	Total	C	N	O	S	0	0	0
			851	510	170	171				

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	K	140	Total	C	N	O	S	0	0	0
			1035	659	183	188	5			

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	N	138	Total	C	N	O	S	0	0	0
			1104	712	206	182	4			

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	O	122	Total	C	N	O	S	0	0	0
			933	588	171	170	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	69	ILE	VAL	CONFLICT	UNP Q72I14

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	P	146	Total	C	N	O	S	0	0	0
			1114	692	227	193	2			

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	Q	141	Total	C	N	O	S	0	0	0
			1122	715	212	188	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	32	TYR	PHE	CONFLICT	UNP Q72I11

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	R	117	Total	C	N	O		0	0	0
			960	599	202	159				

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	S	99	Total	C	N	O		0	0	0
			775	488	155	132				

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	T	138	Total	C	N	O	S	0	0	0
			1147	713	235	198	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	123	GLN	LYS	CONFLICT	UNP Q72JU9
T	135	ALA	VAL	CONFLICT	UNP Q72JU9

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	U	117	Total	C	N	O	S	0	0	0
			964	610	202	151	1			

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	V	101	Total	C	N	O	S	0	0	0
			779	501	142	135	1			

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	W	113	Total	C	N	O	S	0	0	0
			900	566	177	155	2			

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	X	93	Total	C	N	O	S	0	0	0
			734	477	132	125				

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	Y	107	Total	C	N	O	S	0	0	0
			818	524	155	134	5			

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	Z	185	Total	C	N	O	S	0	0	0
			1473	939	262	270	2			

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	0	84	Total	C	N	O	S	0	0	0
			662	410	140	111	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	11	ARG	LYS	CONFLICT	UNP Q72HR3

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	2	71	Total	C	N	O	S	0	0	0
			598	370	121	106	1			

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	3	60	Total	C	N	O	S	0	0	0
			477	303	91	82	1			

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	5	59	Total	C	N	O	S	0	0	0
			459	288	90	76	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	29	THR	ILE	CONFLICT	UNP P62652

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
26	6	50	Total	C	N	O	S	0	0	0
			433	270	88	71	4			

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
27	7	49	Total	C	N	O	S	0	0	0
			430	263	108	57	2			



- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
28	8	64	Total	C	N	O	S	0	0	0
			517	331	102	82	2			

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
29	9	37	Total	C	N	O	S	0	0	0
			307	188	68	47	4			

- Molecule 30 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
30	e	102	Total	C	N	O		0	0	0
			686	430	119	137				

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L7/L12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
31	f	31	Total	C	N	O		0	0	0
			156	93	31	32				
31	g	31	Total	C	N	O		0	0	0
			156	93	31	32				

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L7/L12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
32	h	30	Total	C	N	O		0	0	0
			151	90	30	31				

- Molecule 33 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
33	1	93	Total	C	N	O	S	0	0	0
			732	460	145	126	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	81	LYS	ARG	CONFLICT	UNP Q72G84

- Molecule 34 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
34	4	35	Total	C	N	O	S	0	0	0
			271	174	44	50	3			

- Molecule 35 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
35	A	2879	Total	C	N	O	P	0	0	0
			61997	27594	11582	19943	2878			

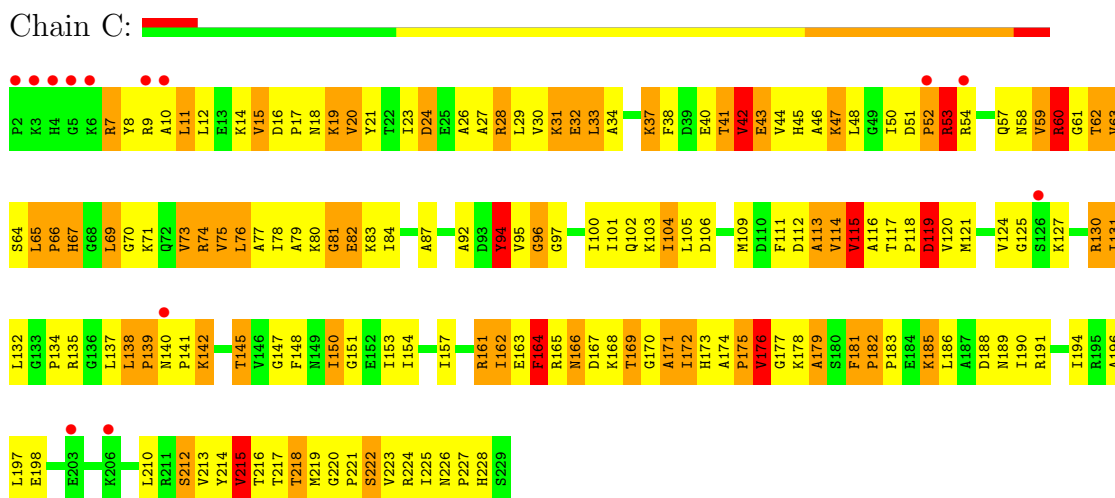
- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
36	B	119	Total	C	N	O	P	0	0	0
			2551	1136	471	826	118			

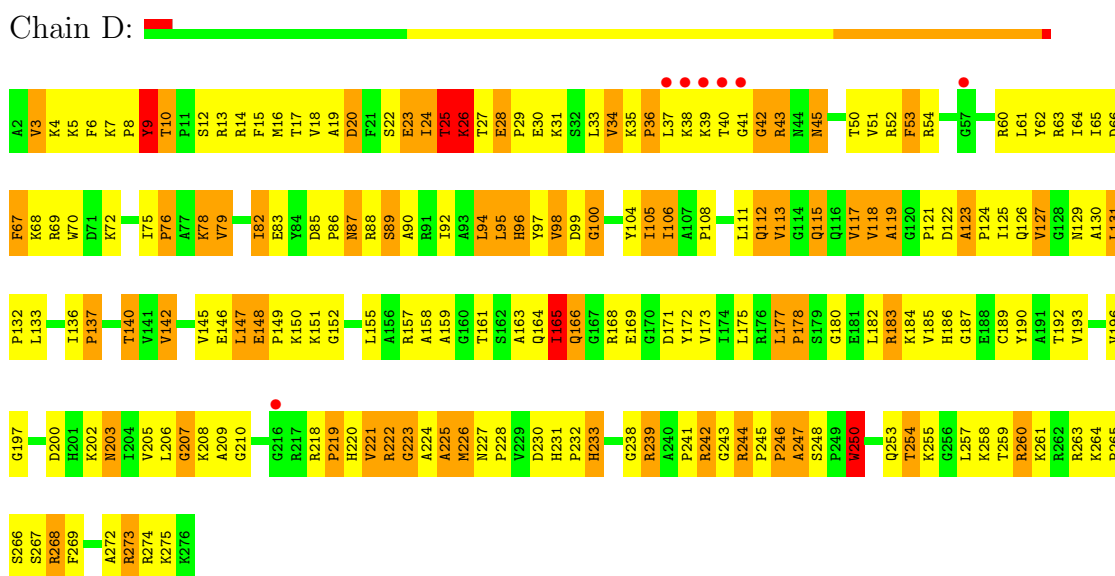
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). 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: 50S ribosomal protein L1

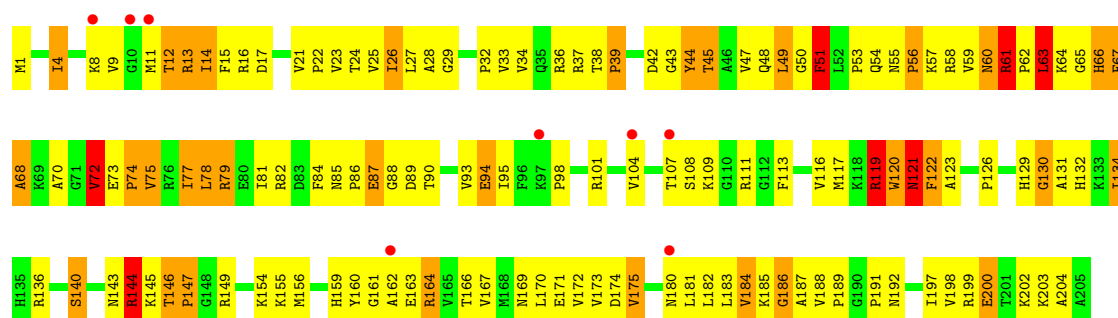


- Molecule 2: 50S ribosomal protein L2



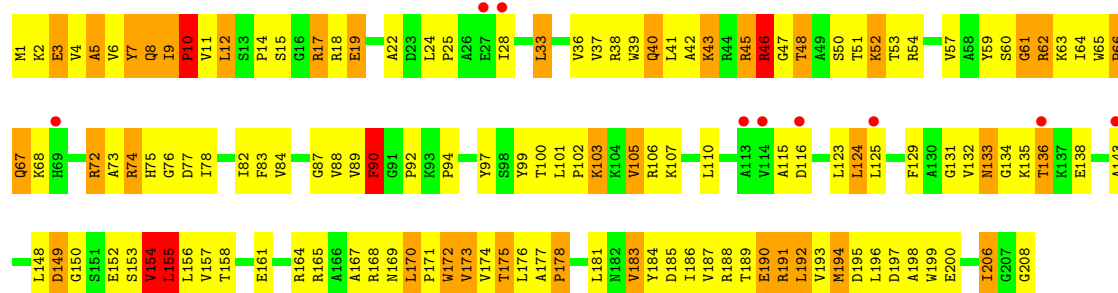
- Molecule 3: 50S ribosomal protein L3





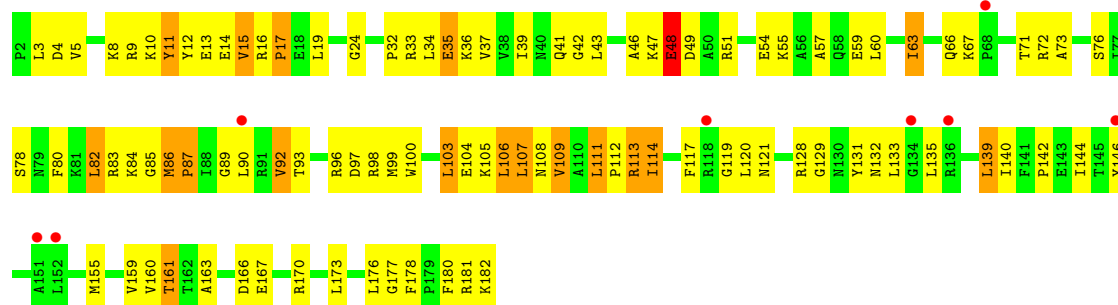
• Molecule 4: 50S ribosomal protein L4

Chain F:



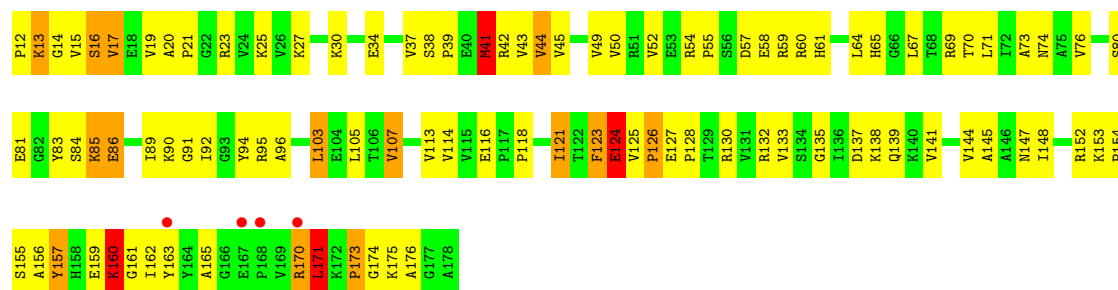
• Molecule 5: 50S ribosomal protein L5

Chain G:



• Molecule 6: 50S ribosomal protein L6

Chain H:

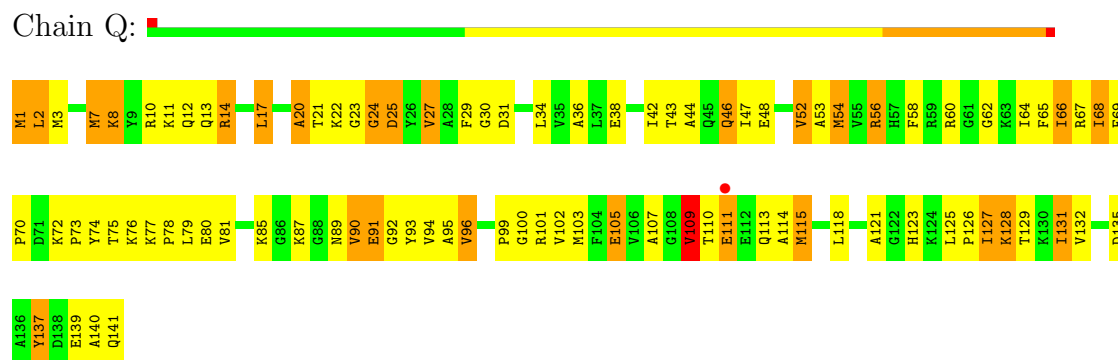


• Molecule 7: 50S RIBOSOMAL PROTEIN L10

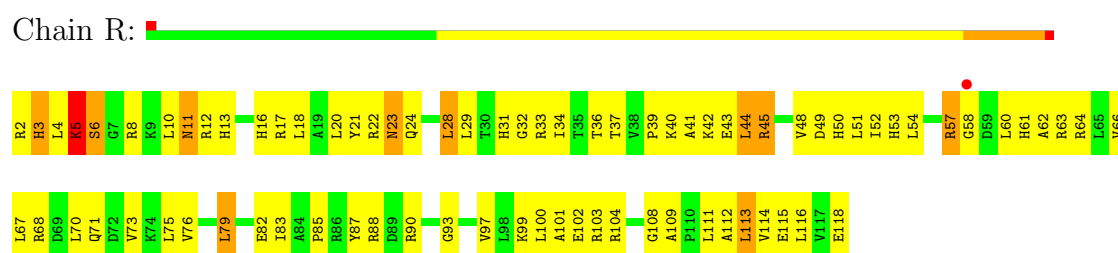
Chain J:



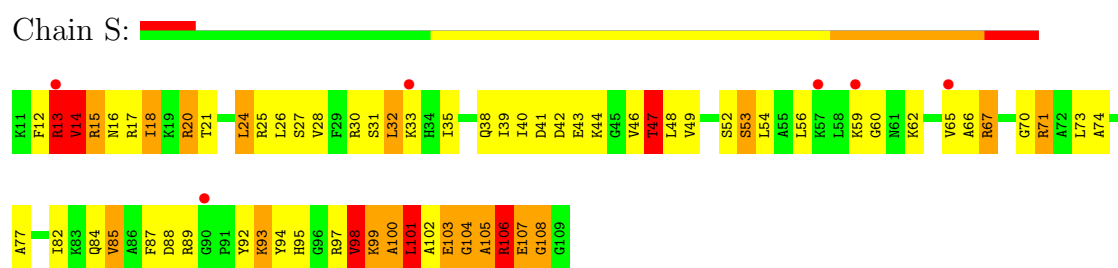
- Molecule 12: 50S ribosomal protein L16



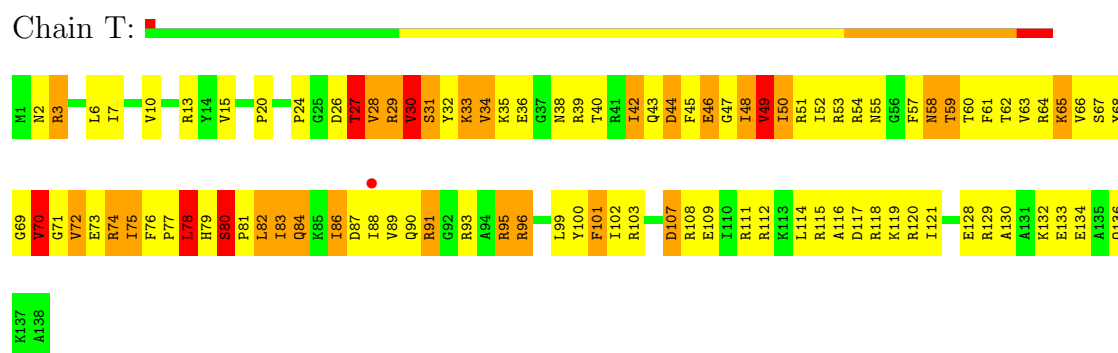
- Molecule 13: 50S ribosomal protein L17



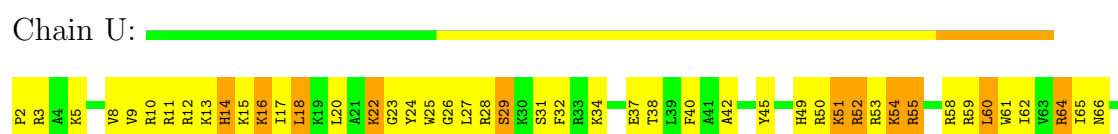
- Molecule 14: 50S ribosomal protein L18

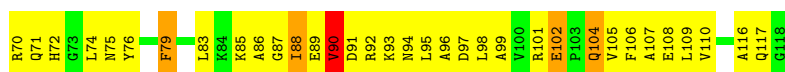


- Molecule 15: 50S ribosomal protein L19



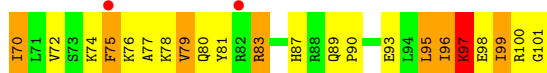
- Molecule 16: 50S ribosomal protein L20





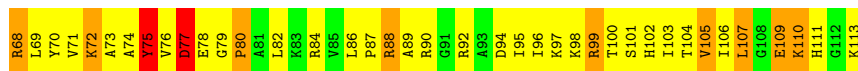
• Molecule 17: 50S ribosomal protein L21

Chain V:



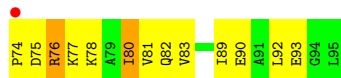
• Molecule 18: 50S ribosomal protein L22

Chain W:



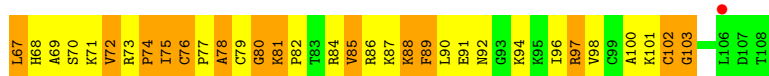
• Molecule 19: 50S ribosomal protein L23

Chain X:



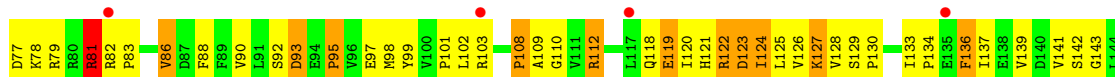
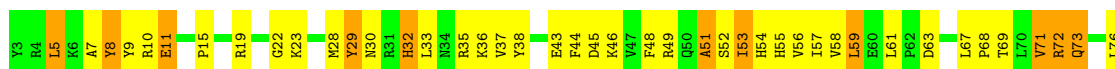
• Molecule 20: 50S ribosomal protein L24

Chain Y:



• Molecule 21: 50S ribosomal protein L25

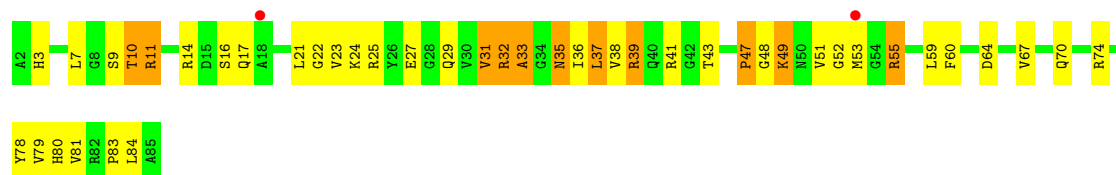
Chain Z:





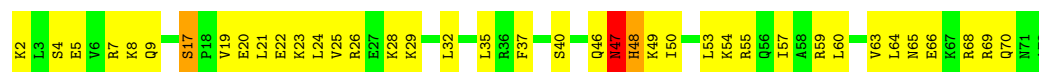
• Molecule 22: 50S ribosomal protein L27

Chain 0:



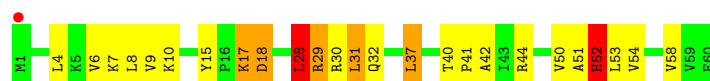
• Molecule 23: 50S ribosomal protein L29

Chain 2:



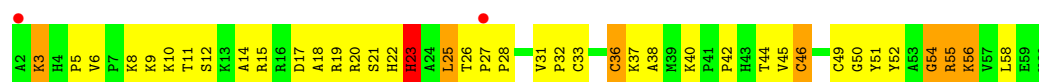
• Molecule 24: 50S ribosomal protein L30

Chain 3:



• Molecule 25: 50S ribosomal protein L32

Chain 5:



• Molecule 26: 50S ribosomal protein L33

Chain 6:



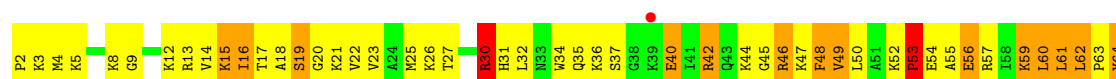
• Molecule 27: 50S ribosomal protein L34

Chain 7:



• Molecule 28: 50S ribosomal protein L35

Chain 8:

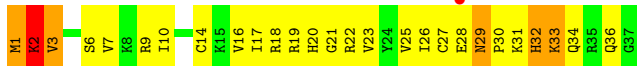




E65

- Molecule 29: 50S ribosomal protein L36

Chain 9:



- Molecule 30: 50S ribosomal protein L7/L12

Chain e:



- Molecule 31: 50S RIBOSOMAL PROTEIN L7/L12

Chain f:

There are no outlier residues recorded for this chain.

- Molecule 31: 50S RIBOSOMAL PROTEIN L7/L12

Chain g:

There are no outlier residues recorded for this chain.

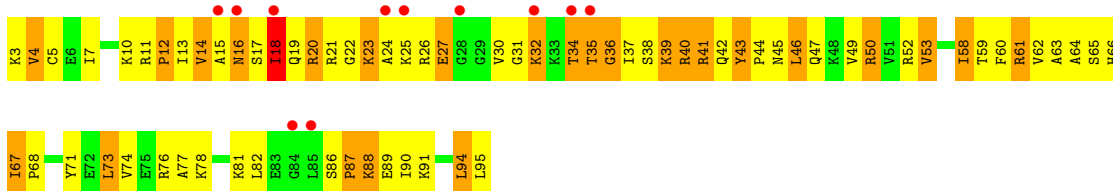
- Molecule 32: 50S RIBOSOMAL PROTEIN L7/L12

Chain h:

There are no outlier residues recorded for this chain.

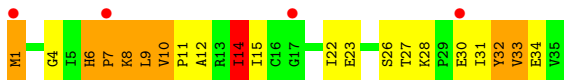
- Molecule 33: 50S ribosomal protein L28

Chain 1:



- Molecule 34: 50S ribosomal protein L31

Chain 4:

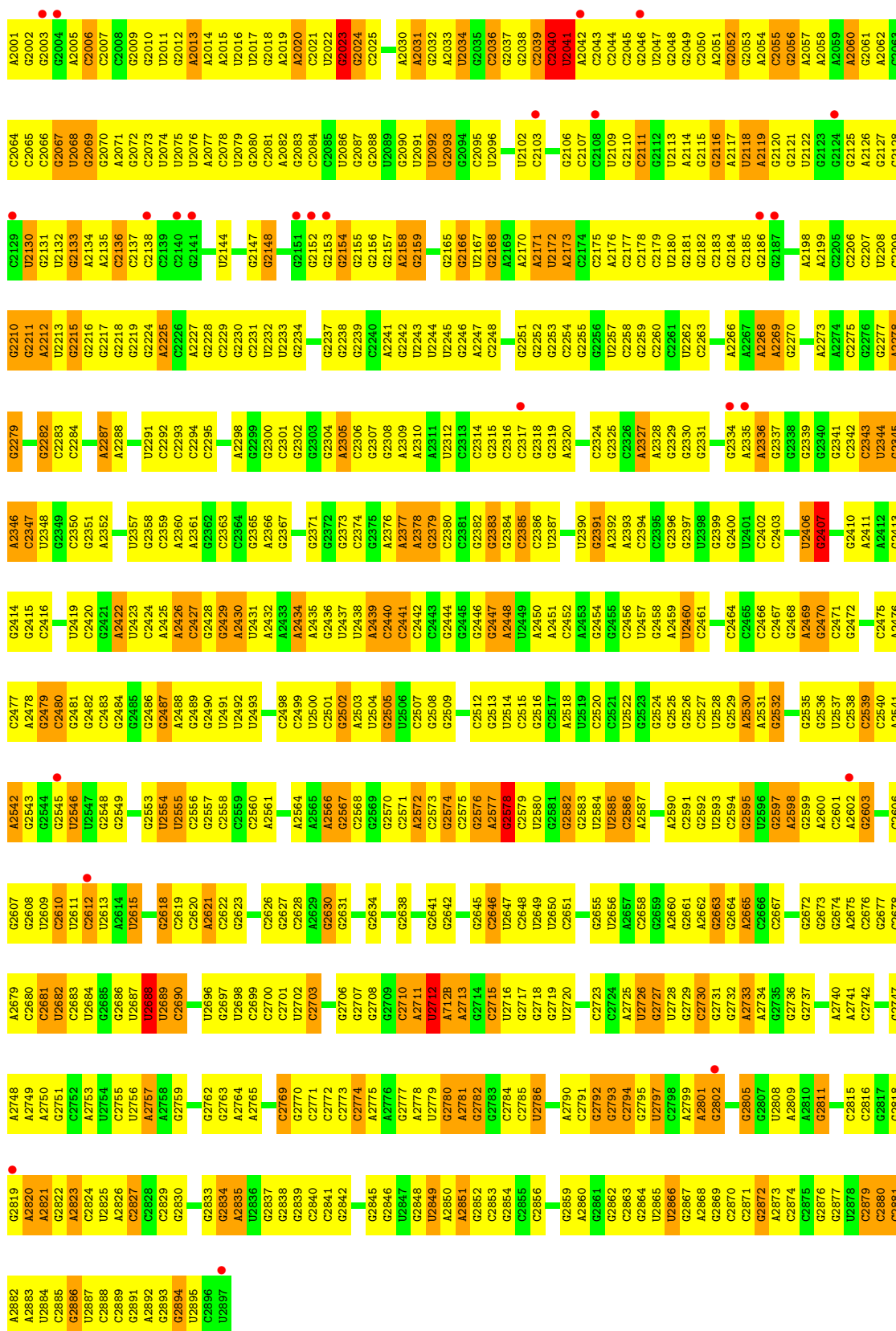


- Molecule 35: 23S ribosomal RNA

Chain A:

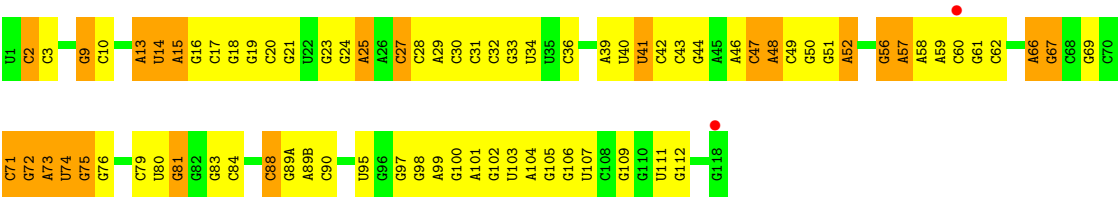
U943	G944	A945	G946	G947	G948	G949	G950	G951	G954	G955	G956	A957	G958	A959	A960	G961	G962	G963	G964	G965	A966	A967	G968	G969	A970	G971	G972	G973	A974	G975	G976	G977	G978	G979	A980	A981	G982	A983	A984	G985	G986	G987	A988	G989	A990	G991	G992	G993	G994	A995	G996	G997	G998	G999	A1000	A1001	G1002																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
C678	C679	G680	G681	G682	G683	G684	G685	G686	G687	G688	G689	G690	G691	G692	G693	G694	G695	G696	G697	G698	G704	A705	A706	G707	G708	G709	G710	G711	G712	G717	A718	G719	G720	G721	A722	G723	G724	A727	G728	G729	C730	C731	C732	G733	G734	A735	G736	A737	G738	G739	A740	G741	G742	G743	G744	G745																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
A746	U747	G748	A749	A750	A751	A752	C753	C754	U757	G758	G759	G760	A761	U762	G763	A764	G765	G766	U767	G768	G769	G770	G771	C772	U773	A774	G775	G776	A777	G778	U779	G780	G781	A782	A783	G784	A785	G786	U787	A788	A789	U790	G791	G792	A793	G794	U795	U796	G797	G798	U799	A800	G801	A802	U803	A804	A805																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
U807	G808	G809	U810	U811	G812	U813	G814	G815	G816	G817	G818	A819	A820	A821	U822	G823	A824	G825	U826	U827	U828	A829	G830	G831	G834	A835	G836	G837	G838	G839	U839	G840	A841	G842	G843	C844	G845	G846	U847	G848	A849	G850	U851	G852	G853	G854	U857	U858	G859	U860	A861	G862	A863	G864	G865	A866	G867	U868	U869	G870	G871	G872	G873	G874	G875	G876	G877	G878	G879	G880	G881	G882	G883	G884	G885	G886	G887	G888	G889	G890	G891	G892	G893	G894	G895	G896	G897	G898	G899	G900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	A941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	A1000	A1001	G1002																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
C141B	G142	C143	G144	G145	A73	A74	G75	C76	C77	A78	G83	A84	G85	C86	C87	G88	G89	U90	G95	G96	G97	A98	G99	A100	G101	G102	U103	C104	U105	C106	G109	G110	A111	U114	A117	C118	A119	U120	G121	G124	G125	A126	A127	C128	C210	A211	G131	G132	G136	C137A	U63	A138	G139	C65	C66	A141																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
A222	A223	G224	A225	G226	A227	A228	U229	C230	C231	G232	A233	C234	G235	A236	C237	A241	G242	G245	G246	G247	G248	C249	A251	G252	C253	G254	A255	A256	G259	G260	C263	C264	A265	C266	A270A	G270B	G270C	C270G	A310	A311	G312	A320	G321	A322	U270H	G323	A324	G325	G326	G329	C329A	A330	A331	G332	A340	G341	G342	A343	A344	A345	A346	A347	A348	A349	A350	A351	A352	A353	A354	A355	A356	A357	A358	A359	A360	A361	A362	A363	A364	A365	A366	A367	A368	A369	A370	A371	A372	A373	A374	A375	A376	A377	A378	A379	A380	A381	A382	A383	A384	A385	A386	A387	A388	A389	A390	A391	A392	A393	A394	A395	A396	A397	A398	A399	A400	A401	A402	A403	A404	A405	A406	A407	A408	A409	A410	A411	A412	A413	A414	A415	A416	A417	A420	A421	A422	A423	A424	A429	A432	A433	U434	C435	A436	A437	A438	A439	A440	U441	A442	A443	A444	A445	A446	A447	U448	A449	A450	A451	A452	A453	A454	A455	A456	A457	A458	U459	A460	A463	U464	A465	A466	A467	A468	A469	A470	A471	A472	A473	A474	A475	A476	A477	A478	A479	A480	A481	A482	A483	A484	A485	A486	A487	A488	A489	A490	A491	A492	A493	A494	A495	A496	A497	A498	A499	A500	A501	A502	A503	A504	A505	G508	C509	C510	U511	A512	A513	A514	A515	C516	C517	G521	U525	A526	A527	A528	A529	G530	C531	A532	A533	A534	C535	U536	U537	A538	A539	A540	A541	A542	A543	A544	A545	A546	A547	A548	A549	A550	A551	A552	A553	A554	A555	A556	A557	A558	A559	A560	A561	A562	A563	A564	A565	A566	A567	A568	A569	A570	A571	A572	A573	A574	A575	A576	A577	A578	A579	A580	A581	A582	A583	A584	A585	A586	A587	A588	A589	A590	A591	A592	A593	A594	A595	A596	A597	A598	A599	A600	A601	A602	A603	A604	A605	A606	A607	A608	A609	A610	A611	A612	A613	A614	A615	A616	A617	A618	A619	A620	A621	A622	A623	A624	A625	A626	A627	A628	A629	A630	A631	A632	A633	A634	A635	A636	A637	A638	A639	A640	A641	A642	A643	A644	A645	A646	A647	A648	A649	A650	A651	A652	A653	A654	A655	A656	A657	A658	A659	A660	A661	A662	A663	A664	A665	A666	A667	A668	A669	A670	A671	A672	A673	A674	A675	A676	A677	A678	A679	A680	A681	A682	A683	A684	A685	A686	A687	A688	A689	A690	A691	A692	A693	A694	A695	A696	A697	A698	A699	A700	A701	A702	A703	A704	A705	A706	A707	A708	A709	A710	A711	A712	A713	A714	A715	A716	A717	A718	A719	A720	A721	A722	A723	A724	A725	A726	A727	A728	A729	A730	A731	A732	A733	A734	A735	A736	A737	A738	A739	A740	A741	A742	A743	A744	A745	A746	A747	A748	A749	A750	A751	A752	A753	A754	A755	A756	A757	A758	A759	A760	A761	A762	A763	A764	A765	A766	A767	A768	A769	A770	A771	A772	A773	A774	A775	A776	A777	A778	A779	A780	A781	A782	A783	A784	A785	A786	A787	A788	A789	A790	A791	A792	A793	A794	A795	A796	A797	A798	A799	A800	A801	A802	A803	A804	A805	A806	A807	A808	A809	A810	A811	A812	A813	A814	A815	A816	A817	A818	A819	A820	A821	A822	A823	A824	A825	A826	A827	A828	A829	A830	A831	A832	A833	A834	A835	A836	A837	A838	A839	A840	A841	A842	A843	A844	A845	A846	A847	A848	A849	A850	A851	A852	A853	A854	A855	A856	A857	A858	A859	A860	A861	A862	A863	A864	A865	A866	A867	A868	A869	A870	A871	A872	A873	A874	A875	A876	A877	A878	A879	A880	A881	A882	A883	A884	A885	A886	A887	A888	A889	A890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928	A929	A930	A931	A932	A933	A934	A935	A936	A937	A938	A939	A940	A941	A942	A943	A944	A945	A946	A947	A948	A949	A950	A951	A952	A953	A954	A955	A956	A957	A958	A959	A960	A961	A962	A963	A964	A965	A966	A967	A968	A969	A970	A971	A972	A973	A974	A975	A976	A977	A978	A979	A980	A981	A982	A983	A984	A985	A986	A987	A988	A989	A990	A991	A992	A993	A994	A995	A996	A997	A998	A999	A1000	A1001	G1002
G68	C69	G70	A73	A74	G75	C76	C77	A78	G83	A84	G85	C86	C87	G88	G89	U90	G95	G96	G97	A98	G99	A100	G101	G102	U103	C104	U105	C106	G109	G110	A111	U114	A117	C118	A119	U120	G121	G124	G125	A126	A127	C128	C210	A211	G131	G132	G136	C137A	U63	A138	G139	C65	C66	A141																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
C141B	G142	C143	G144	G145	A73	A74	G75	C76	C77	A78	G83	A84	G85	C86	C87	G88	G89	U90	G95	G96	G97	A98	G99	A100	G101	G102	U103	C104	U105	C106	G109	G110	A111	U114	A117	C118	A119	U120	G121	G124	G125	A126	A127	C128	C210	A211	G131	G132	G136	C137A	U63	A138	G139	C65	C66	A141																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
A222	A223	G224	A225	G226	A227	A228	U229	C230	C231	G232	A233	C234	G235	A236	C237	A241	G242	G245	G246	G247	G248	C249	A251	G252	C253	G254	A255	A256	G259	G260	C263	C264	A265	C266	A270A	G270B	G270C	C270G	A310	A311	G312	A320	G321	A322	U270H	G323	A324	G325	G326	G329	C329A	A330	A331	G332	A340	G341	G342	A343	A344	A345	A346	A347	A348	A349	A350	A351	A352	A353	A354	A355	A356	A357	A358	A359	A360	A361	A362	A363	A364	A365	A366	A367	A368	A369	A370	A371																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					





● Molecule 36: 5S ribosomal RNA

Chain B:



## 4 Data and refinement statistics

Xtriage (Phenix) failed to run properly - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	308.96Å 670.66Å 347.77Å 90.00° 92.52° 90.00°	Depositor
Resolution (Å)	40.00 – 3.50 140.20 – 3.57	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.50) 74.7 (140.20-3.57)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.284 , 0.328 0.343 , 0.345	Depositor DCC
$R_{free}$ test set	33479 reflections (4.99%)	DCC
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.20 , 76.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.54	EDS
Total number of atoms	95124	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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	C	0.41	0/1774	0.74	1/2391 (0.0%)
2	D	0.33	0/2195	0.65	1/2955 (0.0%)
3	E	0.32	0/1602	0.66	0/2160
4	F	0.35	0/1663	0.73	2/2249 (0.1%)
5	G	0.40	1/1499 (0.1%)	0.59	0/2016
6	H	0.30	0/1298	0.60	0/1751
8	K	0.27	0/1054	0.51	0/1427
9	N	0.45	0/1131	0.77	0/1525
10	O	0.30	0/943	0.57	0/1269
11	P	0.30	0/1131	0.62	0/1504
12	Q	0.35	0/1143	0.63	0/1527
13	R	0.30	0/974	0.60	0/1302
14	S	0.34	0/783	0.69	0/1041
15	T	0.34	0/1161	0.67	0/1549
16	U	0.36	0/982	0.57	0/1306
17	V	0.38	0/790	0.70	1/1057 (0.1%)
18	W	0.31	0/911	0.59	0/1220
19	X	0.30	0/748	0.55	0/1004
20	Y	0.32	0/831	0.62	0/1108
21	Z	0.29	0/1505	0.58	0/2042
22	0	0.28	0/671	0.49	0/892
23	2	0.31	0/600	0.55	0/793
24	3	0.27	0/482	0.53	0/646
25	5	0.33	0/473	0.59	0/639
26	6	0.29	0/440	0.70	1/586 (0.2%)
27	7	0.33	0/438	0.64	0/575
28	8	0.34	0/525	0.68	0/691
29	9	0.30	0/310	0.55	0/407
30	e	0.28	0/538	0.50	0/715
33	1	0.46	0/739	0.82	0/981
34	4	0.32	0/276	0.58	0/372
35	A	0.40	0/69437	1.04	158/108401 (0.1%)
36	B	0.37	0/2853	1.08	11/4451 (0.2%)
All	All	0.38	1/101900 (0.0%)	0.95	175/152552 (0.1%)

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	C	0	1
2	D	0	1
4	F	0	2
5	G	0	2
7	J	0	1
14	S	0	3
18	W	0	1
33	1	0	2
All	All	0	13

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	114	ILE	N-CA	-7.50	1.31	1.46

The worst 5 of 175 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	A	1006	C	C6-N1-C2	-12.54	115.28	120.30
35	A	1139	G	O5'-P-OP1	-11.12	95.69	105.70
35	A	1007	C	C6-N1-C1'	-9.64	109.23	120.80
35	A	2040	C	C5-C6-N1	9.26	125.63	121.00
35	A	1249	U	C2-N1-C1'	8.87	128.35	117.70

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	171	ALA	Peptide
2	D	164	GLN	Peptide
4	F	154	VAL	Peptide
4	F	173	VAL	Peptide
5	G	111	LEU	Mainchain



## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1742	0	1798	166	0
2	D	2145	0	2234	202	0
3	E	1569	0	1634	124	0
4	F	1628	0	1680	132	0
5	G	1474	0	1535	72	0
6	H	1274	0	1342	57	0
7	J	851	0	197	31	0
8	K	1035	0	1082	58	0
9	N	1104	0	1180	84	0
10	O	933	0	996	60	0
11	P	1114	0	1187	87	0
12	Q	1122	0	1179	74	0
13	R	960	0	1021	70	0
14	S	775	0	835	68	0
15	T	1147	0	1207	99	0
16	U	964	0	1022	84	0
17	V	779	0	852	66	0
18	W	900	0	964	69	0
19	X	734	0	789	44	0
20	Y	818	0	908	58	0
21	Z	1473	0	1497	80	0
22	0	662	0	688	33	0
23	2	598	0	653	28	0
24	3	477	0	529	23	0
25	5	459	0	477	46	0
26	6	433	0	461	26	0
27	7	430	0	480	38	0
28	8	517	0	582	52	0
29	9	307	0	338	22	0
30	e	686	0	615	0	0
31	f	156	0	40	0	0
31	g	156	0	41	0	0
32	h	151	0	39	0	0
33	1	732	0	808	72	0
34	4	271	0	284	19	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	A	61997	0	31250	2031	0
36	B	2551	0	1295	85	0
All	All	95124	0	63719	3790	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 24.

The worst 5 of 3790 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
35:A:2681:C:C5	35:A:2725:A:N6	2.09	1.20
35:A:2681:C:N4	35:A:2725:A:H62	1.41	1.19
35:A:1311:G:N2	35:A:1603:A:H62	1.50	1.08
35:A:2023:G:N1	35:A:2040:C:O2	1.85	1.07
35:A:1802:A:C8	35:A:1815:A:N6	2.23	1.05

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	226/228 (99%)	110 (49%)	66 (29%)	50 (22%)	0	1
2	D	273/275 (99%)	174 (64%)	47 (17%)	52 (19%)	0	3
3	E	203/205 (99%)	128 (63%)	40 (20%)	35 (17%)	0	4
4	F	206/208 (99%)	130 (63%)	46 (22%)	30 (15%)	0	7
5	G	179/181 (99%)	122 (68%)	48 (27%)	9 (5%)	3	37
6	H	165/167 (99%)	118 (72%)	27 (16%)	20 (12%)	1	11
8	K	138/140 (99%)	96 (70%)	30 (22%)	12 (9%)	1	19
9	N	136/138 (99%)	86 (63%)	28 (21%)	22 (16%)	0	5
10	O	120/122 (98%)	86 (72%)	24 (20%)	10 (8%)	1	20
11	P	144/146 (99%)	85 (59%)	39 (27%)	20 (14%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	Q	139/141 (99%)	96 (69%)	27 (19%)	16 (12%)	1	12
13	R	115/117 (98%)	80 (70%)	27 (24%)	8 (7%)	2	26
14	S	97/99 (98%)	56 (58%)	21 (22%)	20 (21%)	0	2
15	T	136/138 (99%)	80 (59%)	31 (23%)	25 (18%)	0	3
16	U	115/117 (98%)	84 (73%)	25 (22%)	6 (5%)	3	35
17	V	99/101 (98%)	66 (67%)	16 (16%)	17 (17%)	0	4
18	W	111/113 (98%)	85 (77%)	11 (10%)	15 (14%)	0	8
19	X	91/93 (98%)	72 (79%)	15 (16%)	4 (4%)	4	41
20	Y	105/107 (98%)	51 (49%)	30 (29%)	24 (23%)	0	1
21	Z	183/185 (99%)	132 (72%)	33 (18%)	18 (10%)	1	16
22	0	82/84 (98%)	59 (72%)	16 (20%)	7 (8%)	1	20
23	2	69/71 (97%)	51 (74%)	14 (20%)	4 (6%)	3	32
24	3	58/60 (97%)	48 (83%)	6 (10%)	4 (7%)	2	27
25	5	57/59 (97%)	43 (75%)	11 (19%)	3 (5%)	3	35
26	6	48/50 (96%)	28 (58%)	13 (27%)	7 (15%)	0	7
27	7	47/49 (96%)	35 (74%)	8 (17%)	4 (8%)	1	20
28	8	62/64 (97%)	35 (56%)	17 (27%)	10 (16%)	0	5
29	9	35/37 (95%)	18 (51%)	12 (34%)	5 (14%)	0	7
30	e	70/102 (69%)	38 (54%)	24 (34%)	8 (11%)	1	12
33	1	91/93 (98%)	60 (66%)	19 (21%)	12 (13%)	0	9
34	4	33/35 (94%)	15 (46%)	13 (39%)	5 (15%)	0	6
All	All	3633/3725 (98%)	2367 (65%)	784 (22%)	482 (13%)	0	9

5 of 482 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	17	PRO
1	C	42	VAL
1	C	52	PRO
1	C	66	PRO
1	C	96	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	
1	C	180/180 (100%)	140 (78%)	40 (22%)	1	8
2	D	217/217 (100%)	169 (78%)	48 (22%)	1	8
3	E	165/165 (100%)	134 (81%)	31 (19%)	2	13
4	F	165/165 (100%)	133 (81%)	32 (19%)	2	12
5	G	155/155 (100%)	130 (84%)	25 (16%)	3	22
6	H	136/136 (100%)	116 (85%)	20 (15%)	4	26
8	K	105/105 (100%)	90 (86%)	15 (14%)	5	28
9	N	117/117 (100%)	95 (81%)	22 (19%)	2	13
10	O	100/100 (100%)	80 (80%)	20 (20%)	2	11
11	P	112/112 (100%)	87 (78%)	25 (22%)	1	8
12	Q	111/111 (100%)	82 (74%)	29 (26%)	1	5
13	R	100/100 (100%)	87 (87%)	13 (13%)	6	33
14	S	77/77 (100%)	62 (80%)	15 (20%)	2	12
15	T	120/120 (100%)	94 (78%)	26 (22%)	1	9
16	U	93/93 (100%)	72 (77%)	21 (23%)	1	8
17	V	82/82 (100%)	60 (73%)	22 (27%)	1	5
18	W	92/92 (100%)	68 (74%)	24 (26%)	1	5
19	X	75/75 (100%)	64 (85%)	11 (15%)	4	26
20	Y	88/88 (100%)	69 (78%)	19 (22%)	1	9
21	Z	162/162 (100%)	133 (82%)	29 (18%)	2	15
22	0	66/66 (100%)	54 (82%)	12 (18%)	2	14
23	2	66/66 (100%)	62 (94%)	4 (6%)	26	73
24	3	52/52 (100%)	45 (86%)	7 (14%)	6	30
25	5	51/51 (100%)	44 (86%)	7 (14%)	5	29
26	6	49/49 (100%)	38 (78%)	11 (22%)	1	8
27	7	42/42 (100%)	35 (83%)	7 (17%)	3	19
28	8	54/54 (100%)	39 (72%)	15 (28%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
29	9	34/34 (100%)	28 (82%)	6 (18%)	3 16
30	e	54/54 (100%)	47 (87%)	7 (13%)	6 33
33	1	78/78 (100%)	59 (76%)	19 (24%)	1 6
34	4	31/31 (100%)	23 (74%)	8 (26%)	1 5
All	All	3029/3029 (100%)	2439 (80%)	590 (20%)	2 12

5 of 590 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	P	68	GLN
14	S	99	LYS
28	8	53	PRO
11	P	115	LEU
12	Q	93	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
9	N	69	GLN
10	O	82	ASN
15	T	58	ASN
8	K	30	HIS
15	T	84	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	A	2878/2879 (99%)	665 (23%)	27 (0%)
36	B	118/119 (99%)	21 (17%)	1 (0%)
All	All	2996/2998 (99%)	686 (22%)	28 (0%)

5 of 686 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	A	12	U
35	A	15	G
35	A	17	G
35	A	34	C
35	A	35	G

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	A	1558	A
35	A	1913	A
35	A	2781	A
35	A	1786	A
35	A	1912	A

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	C	228/228 (100%)	0.31	13 (5%) 23 10	45, 128, 217, 259	0
2	D	275/275 (100%)	0.03	7 (2%) 54 25	4, 26, 103, 166	0
3	E	205/205 (100%)	0.17	8 (3%) 37 16	1, 31, 135, 229	0
4	F	208/208 (100%)	0.39	9 (4%) 34 14	6, 49, 162, 216	0
5	G	181/181 (100%)	0.19	8 (4%) 33 14	11, 91, 152, 197	0
6	H	167/167 (100%)	-0.13	4 (2%) 56 26	3, 47, 130, 224	0
7	J	0/170	-	-	-	-
8	K	140/140 (100%)	0.19	7 (5%) 28 12	17, 104, 194, 230	0
9	N	138/138 (100%)	0.21	13 (9%) 9 5	59, 83, 108, 111	0
10	O	122/122 (100%)	-0.02	1 (0%) 83 53	5, 33, 94, 148	0
11	P	146/146 (100%)	0.04	3 (2%) 60 29	7, 55, 131, 173	0
12	Q	141/141 (100%)	-0.20	1 (0%) 84 56	20, 43, 113, 170	0
13	R	117/117 (100%)	-0.04	1 (0%) 81 51	7, 38, 125, 156	0
14	S	99/99 (100%)	0.18	6 (6%) 21 9	27, 104, 191, 225	0
15	T	138/138 (100%)	-0.03	1 (0%) 84 56	6, 53, 139, 225	0
16	U	117/117 (100%)	-0.09	0 100 100	11, 22, 80, 175	0
17	V	101/101 (100%)	-0.21	2 (1%) 62 30	0, 32, 104, 143	0
18	W	113/113 (100%)	0.02	1 (0%) 81 51	8, 32, 103, 140	0
19	X	93/93 (100%)	-0.00	2 (2%) 59 28	5, 51, 118, 172	0
20	Y	107/107 (100%)	-0.03	3 (2%) 50 23	12, 69, 151, 213	0
21	Z	185/185 (100%)	0.04	5 (2%) 52 24	13, 52, 123, 175	0
22	0	84/84 (100%)	0.00	2 (2%) 56 26	6, 53, 127, 163	0
23	2	71/71 (100%)	-0.41	0 100 100	12, 61, 137, 175	0
24	3	60/60 (100%)	-0.12	1 (1%) 67 34	8, 31, 96, 111	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	5	59/59 (100%)	0.05	2 (3%) 43 19	8, 37, 148, 208	0
26	6	50/50 (100%)	-0.16	1 (2%) 62 30	12, 92, 147, 163	0
27	7	49/49 (100%)	0.56	3 (6%) 21 9	9, 16, 135, 218	0
28	8	64/64 (100%)	0.20	1 (1%) 68 35	5, 46, 98, 130	0
29	9	37/37 (100%)	-0.11	1 (2%) 52 24	10, 26, 148, 246	0
30	e	72/102 (70%)	0.20	4 (5%) 24 10	24, 113, 183, 201	0
31	f	0/31	-	-	-	-
31	g	0/31	-	-	-	-
32	h	0/30	-	-	-	-
33	1	93/93 (100%)	0.51	11 (11%) 5 4	1, 79, 187, 243	0
34	4	35/35 (100%)	0.68	4 (11%) 6 4	74, 144, 233, 266	0
35	A	2879/2879 (100%)	0.06	68 (2%) 56 26	3, 43, 145, 276	0
36	B	119/119 (100%)	0.17	2 (1%) 67 34	21, 108, 175, 210	0
All	All	6693/6985 (95%)	0.07	195 (2%) 49 23	0, 50, 156, 276	0

The worst 5 of 195 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	4	HIS	6.9
4	F	27	GLU	6.9
1	C	5	GLY	6.8
35	A	1384	A	6.6
6	H	167	GLU	6.5

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.



## 6.5 Other polymers ⓘ

There are no such residues in this entry.