



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:59 PM BST

PDB ID : 4V4N
EMDB ID: : EMD-5691
Title : Structure of the Methanococcus jannaschii ribosome-SecYEBeta channel complex
Authors : Menetret, J.F.; Park, E.; Gumbart, J.C.; Ludtke, S.J.; Li, W.; Whynot, A.; Rapoport, T.A.; Akey, C.W.
Deposited on : 2013-06-17
Resolution : 9.00 Å(reported)
Based on PDB ID : 3J2L, 3J21, 3J20, 1RHZ

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

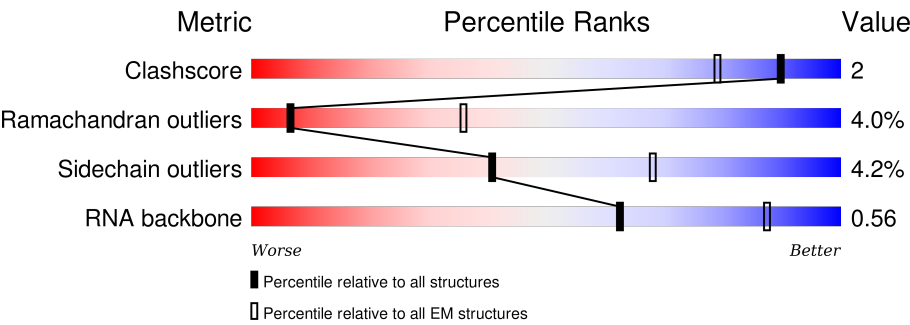
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 Å.

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













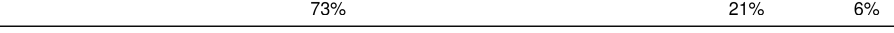
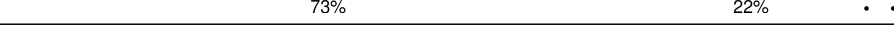
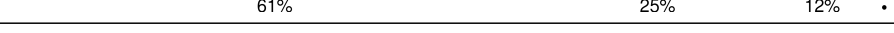


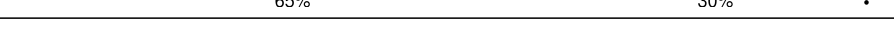









Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A7	67	<div><div>70%</div><div>24%</div><div>.</div><div>.</div></div>
2	A8	52	<div><div>54%</div><div>6%</div><div>.</div><div>38%</div></div>
3	Af	51	<div><div>59%</div><div>39%</div><div>.</div></div>
4	AQ	150	<div><div>71%</div><div>25%</div><div>.</div></div>
5	AS	150	<div><div>73%</div><div>22%</div><div>5%</div><div>.</div></div>
6	AT	84	<div><div>67%</div><div>32%</div><div>.</div></div>
7	AU	121	<div><div>71%</div><div>26%</div><div>.</div><div>.</div></div>
8	AW	72	<div><div>78%</div><div>11%</div><div>.</div><div>8%</div></div>


























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Mol	Chain	Length	Quality of chain
9	AX	436	 71% 25% ..
10	B1	77	 32% 51% 17%
11	B2	1495	 38% 46% 16%
12	AG	123	 81% 15% ..
12	B3	123	 80% 19% .
13	BA	190	 63% 29% 8%
14	BB	202	 68% 30% .
15	BC	186	 75% 22% .
16	BD	172	 74% 20% 6% .
17	BE	241	 68% 27% 5%
18	BF	217	 73% 21% 6%
19	BG	125	 73% 22% ..
20	BH	215	 61% 25% 12% .
21	BI	129	 77% 20% ..
22	BJ	127	 65% 30% 5%
23	BK	135	 65% 30% .
24	BL	102	 61% 29% 9% .
25	BM	133	 71% 26% .
26	BN	145	 70% 26% ..
27	BO	148	 72% 21% 7%
28	BP	56	 61% 27% 11% .
29	BQ	158	 70% 22% 6% .
30	BR	113	 70% 24% 6%
31	BS	67	 75% 21% ..
32	BT	111	 68% 25% 5% .








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Mol	Chain	Length	Quality of chain
33	BU	144	
34	BV	99	
35	BW	63	
36	BX	71	
37	BY	50	
38	A1	3049	
39	A3	126	
40	A5	81	
40	AK	81	
41	AA	216	
42	Aa	92	
43	AB	239	
44	Ab	127	
45	AC	365	
46	AD	255	
47	Ad	89	
48	AE	186	
49	Ae	62	
50	AF	184	
51	Ag	45	
52	AH	134	
53	Ah	24	
54	AI	142	
55	Ai	78	
56	AJ	132	

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Mol	Chain	Length	Quality of chain
57	Aj	94	 60% 33% 7%
58	Ak	212	 79% 17% .
59	AL	147	 67% 21% 10% .
60	AM	194	 68% 27% 5%
61	AN	168	 66% 28% . .
62	AO	197	 68% 28% . .
63	AP	120	 72% 23% . .
64	AR	95	 69% 25% . .
65	AV	66	 65% 29% 6%
66	AY	155	 76% 21% .
67	AZ	99	 73% 21% . .

2 Entry composition [i](#)

There are 67 unique types of molecules in this entry. The entry contains 171094 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Preprotein translocase subunit SecE.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A7	65	Total	C	N	O	S	0	0
			525	348	85	91	1		

- Molecule 2 is a protein called Preprotein translocase subunit SecG.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	A8	32	Total	C	N	O	0	0
			258	172	42	44		

- Molecule 3 is a protein called 50S ribosomal protein L39E.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Af	51	Total	C	N	O	S	0	0
			445	284	98	62	1		

- Molecule 4 is a protein called 50S ribosomal protein L19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AQ	150	Total	C	N	O	S	0	0
			1256	794	255	202	5		

- Molecule 5 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AS	150	Total	C	N	O	S	0	0
			1200	764	230	202	4		

- Molecule 6 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	AT	84	Total	C	N	O	0	0
			680	440	118	122		

- Molecule 7 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AU	121	Total	C	N	O	S	0	0
			1008	637	195	172	4		

- Molecule 8 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AW	66	Total	C	N	O	S	0	0
			546	338	105	99	4		

- Molecule 9 is a protein called Protein translocase subunit SecY.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AX	432	Total	C	N	O	S	0	0
			3309	2210	521	559	19		

- Molecule 10 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B1	77	Total	C	N	O	P	0	0
			1646	734	303	533	76		

- Molecule 11 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B2	1495	Total	C	N	O	P	0	0
			32132	14297	5954	10387	1494		

- Molecule 12 is a protein called 30S ribosomal protein L7AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	B3	123	Total	C	N	O	S	0	0
			939	599	155	181	4		
12	AG	123	Total	C	N	O	S	0	0
			939	599	155	181	4		

- Molecule 13 is a protein called 30S ribosomal protein S3AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BA	190	Total	C	N	O	S	0	0
			1559	1007	273	274	5		

- Molecule 14 is a protein called 30S ribosomal protein S2P.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BB	202	Total	C	N	O	S	0	0
			1623	1046	282	290	5		

- Molecule 15 is a protein called 30S ribosomal protein S3P.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BC	186	Total	C	N	O	S	0	0
			1460	933	271	252	4		

- Molecule 16 is a protein called 30S ribosomal protein S4P.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BD	172	Total	C	N	O	S	0	0
			1434	902	273	255	4		

- Molecule 17 is a protein called 30S ribosomal protein S4E.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BE	241	Total	C	N	O	S	0	0
			1976	1277	355	339	5		

- Molecule 18 is a protein called 30S ribosomal protein S5P.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BF	217	Total	C	N	O	S	0	0
			1717	1084	319	306	8		

- Molecule 19 is a protein called 30S ribosomal protein S6E.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BG	125	Total	C	N	O	S	0	0
			984	623	180	179	2		

- Molecule 20 is a protein called 30S ribosomal protein S7P.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BH	215	Total	C	N	O	S	0	0
			1736	1100	326	302	8		

- Molecule 21 is a protein called 30S ribosomal protein S8P.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BI	129	Total	C	N	O	S	0	0
			1028	668	178	180	2		

- Molecule 22 is a protein called 30S ribosomal protein S8E.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BJ	127	Total	C	N	O	S	0	0
			1004	622	207	174	1		

- Molecule 23 is a protein called 30S ribosomal protein S9P.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BK	135	Total	C	N	O	S	0	0
			1072	671	205	190	6		

- Molecule 24 is a protein called 30S ribosomal protein S10P.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BL	102	Total	C	N	O	S	0	0
			822	507	159	152	4		

- Molecule 25 is a protein called 30S ribosomal protein S11P.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BM	133	Total	C	N	O	S	0	0
			1004	623	200	179	2		

- Molecule 26 is a protein called 30S ribosomal protein S12P.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BN	145	Total	C	N	O	S	0	0
			1141	722	223	193	3		

- Molecule 27 is a protein called 30S ribosomal protein S13P.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BO	148	Total	C	N	O	S	0	0
			1189	746	237	200	6		

- Molecule 28 is a protein called 30S ribosomal protein S14P.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BP	56	Total	C	N	O	S	0	0
			462	292	95	69	6		

- Molecule 29 is a protein called 30S ribosomal protein S15P/S13E.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BQ	158	Total	C	N	O	S	0	0
			1310	834	250	221	5		

- Molecule 30 is a protein called 30S ribosomal protein S17P.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BR	113	Total	C	N	O	S	0	0
			934	592	177	160	5		

- Molecule 31 is a protein called 30S ribosomal protein S17E.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BS	67	Total	C	N	O	S	0	0
			556	353	105	95	3		

- Molecule 32 is a protein called 30S ribosomal protein S19P.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BT	111	Total	C	N	O	S	0	0
			924	594	173	151	6		

- Molecule 33 is a protein called 30S ribosomal protein S19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BU	144	Total	C	N	O	S	0	0
			1176	758	212	205	1		

- Molecule 34 is a protein called 30S ribosomal protein S24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BV	99	Total	C	N	O	S	0	0
			823	532	134	154	3		

- Molecule 35 is a protein called 30S ribosomal protein S27E.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BW	63	Total	C	N	O	S	0	0
			478	306	85	81	6		

- Molecule 36 is a protein called 30S ribosomal protein S28E.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BX	71	Total	C	N	O	S	0	0
			568	345	115	107	1		

- Molecule 37 is a protein called 30S ribosomal protein S27AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BY	50	Total	C	N	O	S	0	0
			409	262	75	66	6		

- Molecule 38 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	2969	Total	C	N	O	P	0	0
			63885	28427	11905	20589	2964		

- Molecule 39 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A3	126	Total	C	N	O	P	0	0
			2691	1199	492	875	125		

- Molecule 40 is a protein called 50S ribosomal protein L14E.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A5	81	Total	C	N	O	S	0	0
			614	386	119	108	1		
40	AK	81	Total	C	N	O	S	0	0
			614	386	119	108	1		

- Molecule 41 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AA	216	Total	C	N	O	S	0	0
			1677	1068	300	304	5		

- Molecule 42 is a protein called 50S ribosomal protein L31E.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	Aa	82	Total	C	N	O		
			677	444	126	107	0	0

- Molecule 43 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AB	239	Total	C	N	O	S		
			1838	1169	347	317	5	0	0

- Molecule 44 is a protein called 50S ribosomal protein L32E.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ab	127	Total	C	N	O	S		
			1075	689	217	168	1	0	0

- Molecule 45 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AC	342	Total	C	N	O	S		
			2717	1741	495	467	14	0	0

- Molecule 46 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AD	255	Total	C	N	O	S		
			2026	1288	391	342	5	0	0

- Molecule 47 is a protein called 50S ribosomal protein L34E.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ad	89	Total	C	N	O	S		
			740	463	158	108	11	0	0

- Molecule 48 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AE	186	Total	C	N	O	S		
			1489	937	278	265	9	0	0

- Molecule 49 is a protein called 50S ribosomal protein L37E.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ae	62	Total	C	N	O	S	0	0
			506	312	111	78	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AF	184	Total	C	N	O	S	0	0
			1476	956	252	266	2		

- Molecule 51 is a protein called 50S ribosomal protein L40E.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ag	45	Total	C	N	O	S	0	0
			372	236	76	56	4		

- Molecule 52 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AH	134	Total	C	N	O	S	0	0
			989	635	164	184	6		

- Molecule 53 is a protein called 50S ribosomal protein L41E.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ah	24	Total	C	N	O	S	0	0
			230	147	54	28	1		

- Molecule 54 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AI	142	Total	C	N	O	S	0	0
			1150	737	215	195	3		

- Molecule 55 is a protein called 50S ribosomal protein L37AE.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Ai	78	Total	C	N	O	S	0	0
			590	368	122	95	5		

- Molecule 56 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AJ	132	Total	C	N	O	S	0	0
			1014	631	204	176	3		

- Molecule 57 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Aj	94	Total	C	N	O	S	0	0
			788	499	162	122	5		

- Molecule 58 is a protein called 50S ribosomal protein P0/L10E.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ak	212	Total	C	N	O	S	0	0
			1633	1051	272	304	6		

- Molecule 59 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AL	147	Total	C	N	O	S	0	0
			1154	727	227	195	5		

- Molecule 60 is a protein called 50S ribosomal protein L15E.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AM	194	Total	C	N	O	S	0	0
			1595	1020	316	253	6		

- Molecule 61 is a protein called 50S ribosomal protein L10E/L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AN	168	Total	C	N	O	S	0	0
			1379	872	268	233	6		

- Molecule 62 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AO	197	Total	C	N	O	S	0	0
			1598	1021	299	275	3		

- Molecule 63 is a protein called 50S ribosomal protein L18E.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AP	120	Total	C	N	O	S	0	0
			966	606	186	171	3		

- Molecule 64 is a protein called 50S ribosomal protein L21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	AR	95	Total	C	N	O	S	0	0
			787	501	160	125	1		

- Molecule 65 is a protein called 50S ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AV	66	Total	C	N	O	S	0	0
			555	351	106	91	7		

- Molecule 66 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AY	155	Total	C	N	O	S	0	0
			1243	788	235	213	7		

- Molecule 67 is a protein called 50S ribosomal protein L30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	AZ	99	Total	C	N	O	S	0	0
			754	489	121	142	2		

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. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

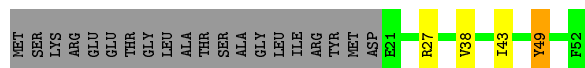
- Molecule 1: Preprotein translocase subunit SecE

Chain A7: 



- Molecule 2: Preprotein translocase subunit SecG

Chain A8: 



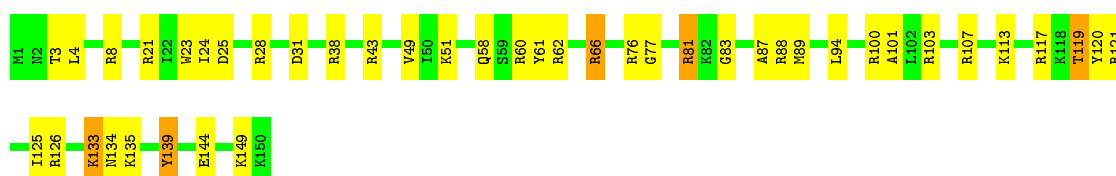
- Molecule 3: 50S ribosomal protein L39E

Chain Af: 



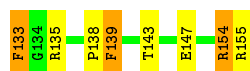
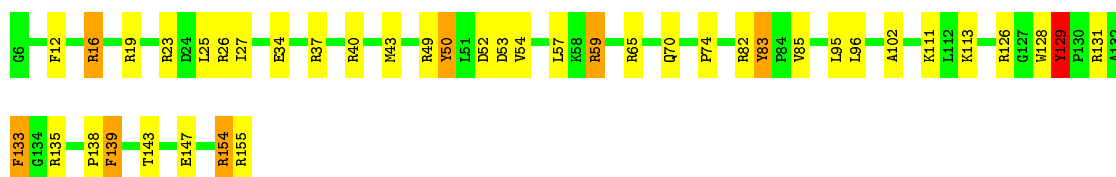
- Molecule 4: 50S ribosomal protein L19E

Chain AQ: 

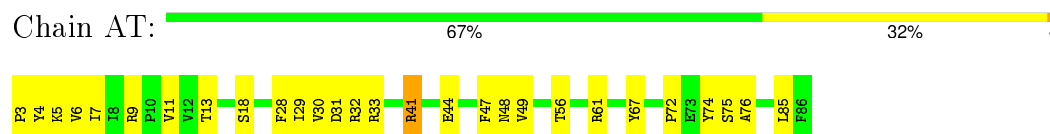


- Molecule 5: 50S ribosomal protein L22P

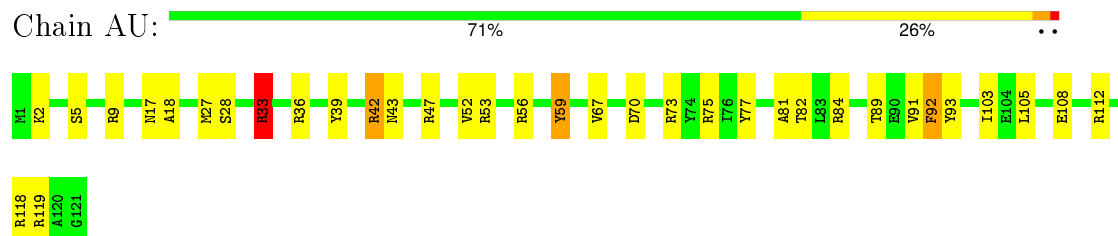
Chain AS: 



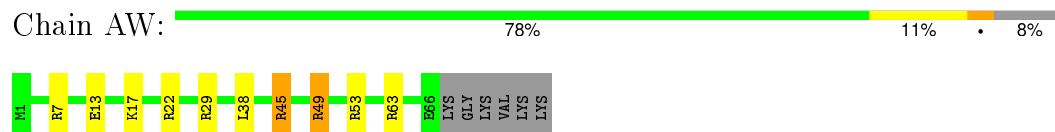
- Molecule 6: 50S ribosomal protein L23P



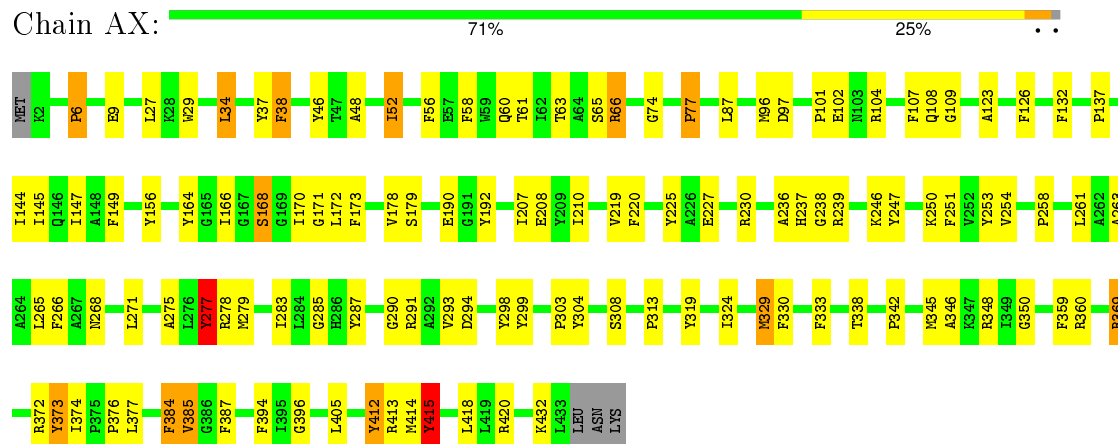
- Molecule 7: 50S ribosomal protein L24P



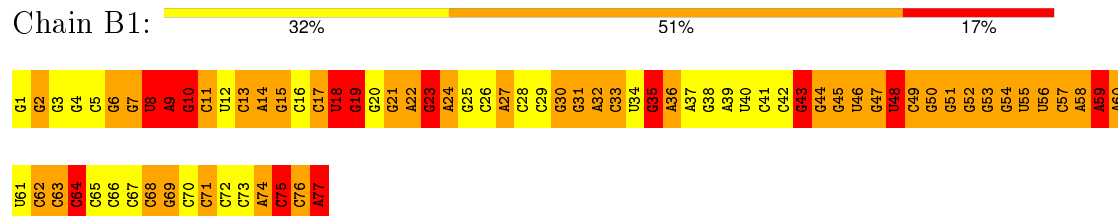
- Molecule 8: 50S ribosomal protein L29P



- Molecule 9: Protein translocase subunit SecY



- Molecule 10: E-tRNA



- Molecule 11: 16S ribosomal RNA

Chain B2:

38%


46%

16%

G901	C941	U781	A721	G661	G601	G541	C481	U421	A361	G301	U241	G181	A81	A1
U902	U942	A782	G722	G662	G602	G542	G482	U422	C362	A302	A242	G182	G82	U2
G903	G943	G783	G723	G663	G603	C543	G483	U423	C363	G303	G243	A183	G83	U3
G904	G944	G784	G724	G664	G604	C544	G484	U424	C364	C304	G244	G184	G84	C4
A905	G945	G785	G725	G665	G605	C545	A485	U425	C365	C305	U245	G185	G85	C5
G906	G946	G786	G726	G666	U606	C546	A486	U426	C366	C306	U246	U186	G86	G6
C907	A947	U787	G727	G667	U607	U547	U487	U427	G367	G307	U247	C187	C87	G7
G908	G948	C788	G728	G668	G608	A548	A488	G428	C368	G308	U248	A188	G88	U8
U909	U949	G789	G729	A669	G609	A549	A489	A429	A369	A309	U249	A189	G89	U9
G910	A850	G790	G730	G670	G610	G550	G490	G430	A370	G310	G250	C190	C70	G10
C911	C851	G791	A731	C671	A611	U551	C491	U431	U371	A311	G251	A191	C71	A11
G912	G852	C792	G732	G672	G612	C552	G492	G432	G372	U312	U252	G192	C72	U12
G913	G853	G793	G733	C673	C613	C553	C493	U433	C373	G313	G253	G193	U73	C13
U914	C854	A794	G734	C674	G614	C554	G494	A434	G374	G314	G254	C194	U74	C14
U915	C855	G795	A735	U675	G615	U555	G495	A435	G375	A315	G255	C195	U75	U15
U916	G856	C796	A736	G676	G616	G556	G496	A436	G376	C316	G256	A196	U76	G16
A917	U857	U797	G737	U677	G617	G557	C497	A437	A377	A317	U257	A197	G77	C17
A918	A858	U798	C738	G678	G618	C558	C498	A438	A378	C318	U258	A198	G78	C18
U919	A859	G799	G739	G679	A619	G559	C499	G439	A379	U319	A259	A199	G79	G19
U920	G860	G800	G740	G680	G620	A560	A500	C440	C380	G320	C260	A200	A80	G20
G921	G861	A801	A741	G681	G621	U561	G501	U441	C381	A321	G261	G201	C81	A21
G922	C862	G802	U742	A682	C622	U562	U502	C442	G382	G322	G262	G202	G82	G22
A923	U863	C803	U743	A683	C623	A563	G503	C443	C383	A323	C263	G203	C83	G23
U924	G864	U804	A744	G684	G624	C564	G504	G444	G384	C324	C264	G204	C84	C24
U925	A865	C805	G745	G685	G625	C565	U505	G445	A385	A325	C265	G205	A85	C25
C926	A866	G806	A746	C686	G626	C566	G506	G446	C386	C326	A266	C206	C86	A26
A927	A867	C807	U747	G687	G627	U567	G507	A447	G387	G327	C267	G207	C87	C27
A928	C868	G808	A748	C688	G628	C568	G508	A448	C388	G328	C268	U208	G88	U28
C929	U869	C809	C749	G689	U629	A569	C509	U449	G389	G329	A269	A209	G89	G29
G930	U870	G810	C750	G690	A630	G570	A510	A450	C390	U330	A270	A210	C90	C30
C931	A871	G811	C751	G691	C631	U571	C511	A451	C391	C331	G271	G211	G91	U31
C932	A872	U812	G752	G692	C632	U572	U512	G452	C392	C332	C272	G212	G92	A32
G933	A873	G813	G753	C693	C633	C573	A513	G453	C393	A333	C273	C213	A93	U32
G934	G874	C814	U754	A694	G634	A574	U514	G454	C394	G334	G274	C214	G94	C34
G935	G875	C815	U755	G695	C635	A575	U515	C455	C395	G335	A275	C215	G95	G35
A936	A876	G816	A756	G696	G636	C576	A516	U456	C396	C336	G276	G216	G96	G36
A937	A877	U817	G757	A697	G637	C577	U517	G457	C397	C337	A277	C217	C97	C37
C938	U878	A818	U758	A698	G638	G578	U518	G458	C398	C338	A278	C218	U98	C38
C939	U879	G819	C759	G699	G639	U579	G519	G459	A399	U339	U279	C219	C99	U39
U940	G880	G820	C760	G700	U640	G580	G520	C460	G400	A340	C280	G220	A100	C40
C941	G881	G821	U761	G701	A641	G581	G521	A461	U401	C341	G281	A221	G101	C41
A942	C882	A822	G762	G702	G642	G582	C522	A462	A402	G342	G282	G222	U102	C42
C943	G883	G823	G763	U703	G643	G583	C523	G463	C403	G343	U283	G223	A103	A43
C944	G884	G824	C764	C704	G644	G584	U524	G464	C404	G344	A284	A224	A104	C44
G945	G885	C825	U765	C705	G645	U585	A525	C465	U405	C345	G285	U225	C105	U45
G946	G886	G826	G766	G706	U646	C586	A526	G466	U406	C346	G286	G226	A106	A46
G947	G887	U827	U767	A707	G647	G587	A527	G467	G407	G347	C287	C227	C107	A47
G948	A888	U828	A768	C708	A648	G588	G528	G468	C408	C348	G288	G228	G108	C48
G949	G889	U829	A769	G709	A649	U589	C529	U469	C409	A349	C289	G229	U109	C49
C950	C890	A830	U770	G710	A650	G590	G530	G470	U410	G350	C290	C230	C110	C50
G951	A891	G831	G771	U711	U651	G591	G531	C471	C411	C351	G291	G231	G111	A51
A952	C892	G832	G772	G712	C652	G592	C532	C472	U412	A352	U292	G232	G112	U52
C953	U893	C833	A773	A713	C653	G593	C533	G473	G413	G353	U293	C233	U113	G53
G954	A894	G834	U774	G714	U654	A594	G534	G474	G414	A294	G294	G234	G114	C54
G955	C895	C835	G775	C715	A655	U595	U535	C475	C415	G355	G295	G235	G115	G55
C956	A896	G836	C776	G716	U656	A596	A536	C476	A416	G356	A296	C236	C116	A56
A957	A897	C837	G777	C717	A657	G597	G537	G477	C417	C357	G297	C237	C117	G57
G958	G898	G838	G778	U718	A658	U598	C538	C478	G418	A358	C298	G238	U118	U58
G959	G899	G779	G779	G719	U659	G599	C539	C479	G419	A359	G299	A239	U119	C59
A960	G900	C840	C780	A720	C660	C600	G540	G480	C420	A360	G300	U240	C120	A60


U961	C1021	C1081	G1141	G1201	U1261	U1321	G1381	G1441
G962	U1022	A1082	G1142	G1202	U1262	C1322	G1382	G1442
A963	C1023	G1083	G1143	G1203	U1263	A1323	A1383	G1443
A964	G1024	U1084	G1144	C1204	G1264	U1324	G1384	G1444
G965	U1025	C1085	C1145	G1205	G1265	G1325	U1385	G1445
G966	A1026	C1086	G1146	G1206	A1266	G1326	G1386	G1446
C967	C1027	C1087	G1147	G1207	U1267	C1327	G1387	A1447
C968	C1028	U1088	G1148	A1208	C1268	G1328	G1388	A1448
A969	G1029	C1089	C1149	G1209	G1269	G1329	G1389	G1449
G970	U1030	C1090	G1150	A1210	C1270	G1330	U1390	U1450
G971	G1031	C1091	A1151	A1211	G1271	G1331	G1391	U1451
C972	A1032	G1092	C1152	U1212	G1272	C1332	G1392	G1452
U973	G1033	C1093	G1153	G1213	G1273	G1333	A1393	G1453
G974	G1034	U1094	G1154	G1214	C1274	A1334	G1394	A1454
A975	C1035	C1095	U1155	G1215	U1275	A1335	G1395	A1455
A976	G1036	G1096	A1156	A1216	G1276	U1336	G1396	C1456
G977	U1037	G1097	G1157	C1217	G1277	A1337	G1397	A1457
G978	C1038	G1098	G1158	G1218	A1278	C1338	U1398	A1458
U979	G1039	A1099	U1159	C1219	A1279	G1339	G1399	G1459
C980	A1040	G1100	C1160	G1220	C1280	U1340	A1400	G1460
U981	C1041	G1101	A1161	A1221	U1281	C1341	U1401	U1461
U982	U1042	A1102	G1162	C1222	C1282	C1342	C1402	A1462
G983	U1043	G1103	U1163	C1223	G1283	C1343	U1403	A1463
C984	A1044	G1104	A1164	U1224	C1284	U1344	C1404	C1464
C985	A1045	C1105	U1165	C1225	C1285	G1345	C1405	C1465
G986	G1046	A1106	G1166	G1226	C1286	C1346	U1406	G1466
G987	U1047	C1107	C1167	A1227	G1287	U1347	U1407	U1467
A988	G1048	U1108	C1168	C1228	C1288	C1348	A1408	A1468
C989	U1049	C1109	G1169	A1229	G1289	U1349	G1409	G1469
G990	G1050	U1110	C1170	G1230	U1290	U1350	G1410	G1470
C991	U1051	G1111	G1171	G1231	G1291	U1351	G1411	G1471
G992	U1052	G1112	A1172	G1232	A1292	C1352	A1412	G1472
C993	A1053	G1113	A1173	G1233	A1293	G1353	G1413	G1473
C994	A1054	G1114	A1174	A1234	G1294	A1354	G1414	A1474
G995	C1055	G1115	C1175	A1235	C1295	C1355	U1415	C1475
A996	G1056	G1116	C1176	G1236	U1296	A1356	C1416	C1476
G997	A1057	G1117	C1177	G1237	G1297	C1357	A1417	U1477
A998	G1058	C1118	C1178	G1238	G1298	A1358	G1418	A1478
G999	C1059	U1119	C1179	A1239	A1299	C1359	G1419	C1479
G1000	G1060	G1120	G1180	A1240	A1300	C1360	U1420	G1480
A1001	A1061	C1121	C1181	U1241	U1301	G1361	G1421	G1481
G1002	G1062	C1122	G1182	C1242	C1302	C1362	G1422	C1482
G1003	A1063	G1123	C1183	C1243	C1303	C1363	G1423	U1483
U1004	C1064	G1124	U1184	C1244	C1304	C1364	G1424	C1484
G1005	C1065	C1125	A1185	C1245	U1305	G1365	C1425	G1485
C1006	G1066	G1126	C1186	U1246	A1306	U1366	C1426	A1486
A1007	G1067	A1127	A1187	A1247	G1307	C1367	G1427	U1487
U1008	C1068	U1128	C1188	A1248	A1308	A1368	G1428	C1488
G1009	G1069	A1129	G1189	A1249	A1309	C1369	G1429	A1489
G1010	C1070	U1130	C1190	C1250	C1310	U1370	G1430	C1490
C1011	C1071	G1131	G1191	C1251	C1311	C1371	A1431	C1491
G1012	C1072	C1132	C1192	C1252	C1312	C1372	U1432	U1492
G1013	C1073	G1133	G1193	G1253	C1313	A1373	C1433	C1493
C1014	C1074	C1134	C1194	C1254	C1314	C1374	G1434	C1494
C1015	A1075	G1135	U1195	C1255	C1315	C1375	G1435	U1495
G1016	G1076	A1136	A1196	C1256	U1316	C1376	U1436	G1496
U1017	U1077	G1137	C1197	U1257	G1317	G1377	G1437	G1497
C1018	U1078	G1138	A1198	C1258	U1318	A1378	A1438	C1498
A1019	G1079	A1139	A1199	A1259	C1319	G1379	G1439	G1499
G1020	C1080	U1140	U1200	G1260	A1320	C1380	G1440	

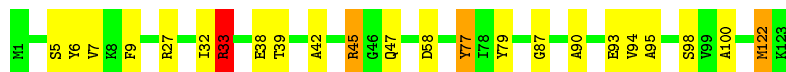
• Molecule 12: 30S ribosomal protein L7AE

Chain B3:  80% 19%



• Molecule 12: 30S ribosomal protein L7AE

Chain AG:  81% 15%



• Molecule 13: 30S ribosomal protein S3AE

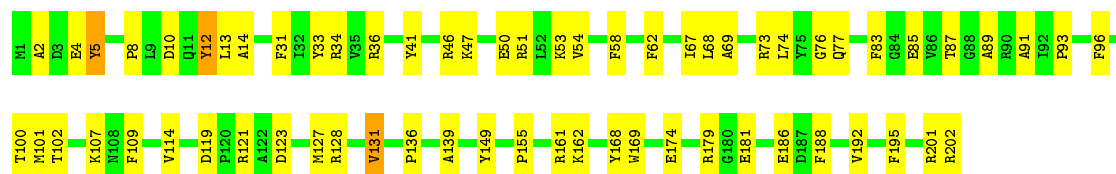
Chain BA:  63% 29% 8%





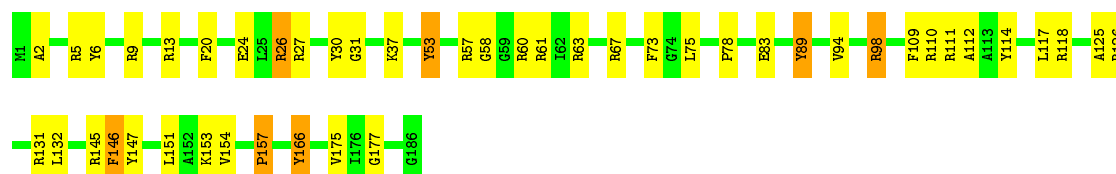
• Molecule 14: 30S ribosomal protein S2P

Chain BB: 68% 30%



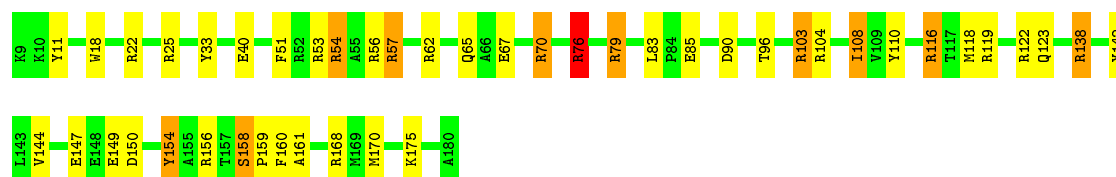
• Molecule 15: 30S ribosomal protein S3P

Chain BC: 75% 22%



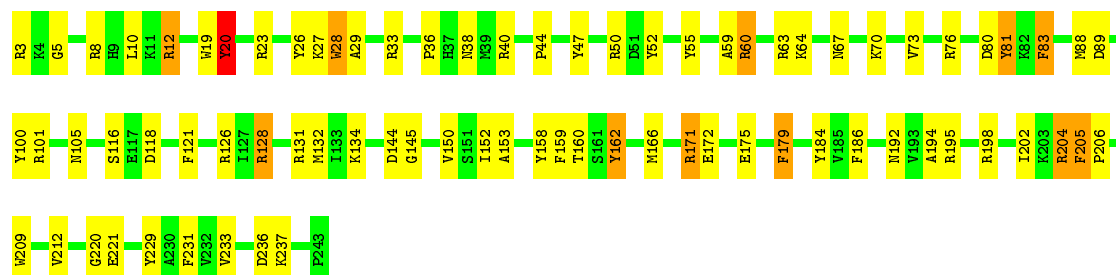
• Molecule 16: 30S ribosomal protein S4P

Chain BD: 74% 20% 6%



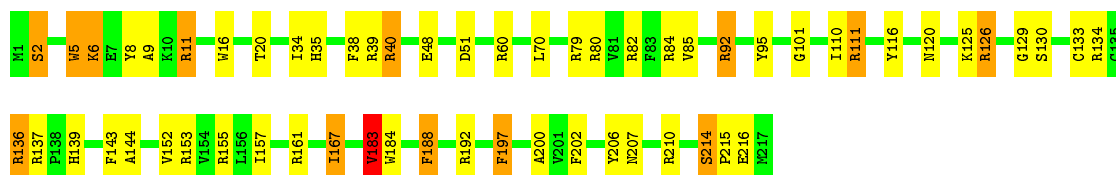
• Molecule 17: 30S ribosomal protein S4E

Chain BE: 68% 27% 5%



• Molecule 18: 30S ribosomal protein S5P

Chain BF: 73% 21% 6%



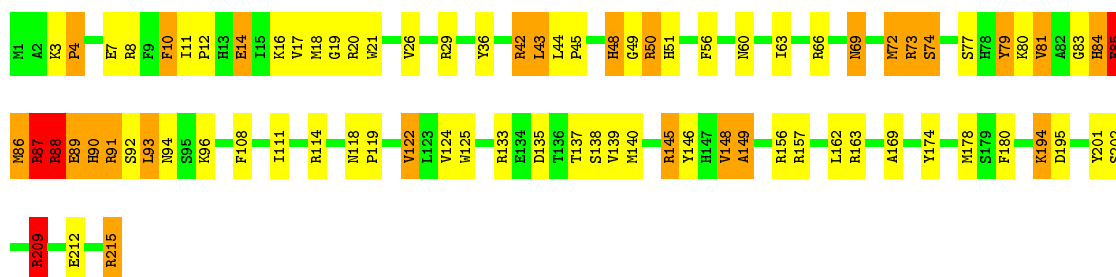
- Molecule 19: 30S ribosomal protein S6E

Chain BG:



- Molecule 20: 30S ribosomal protein S7P

Chain BH:



- Molecule 21: 30S ribosomal protein S8P

Chain BI:



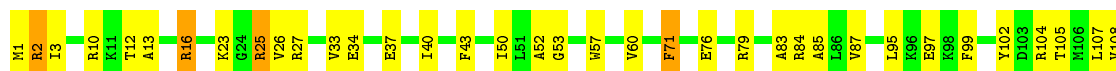
- Molecule 22: 30S ribosomal protein S8E

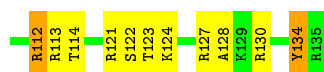
Chain BJ:



- Molecule 23: 30S ribosomal protein S9P

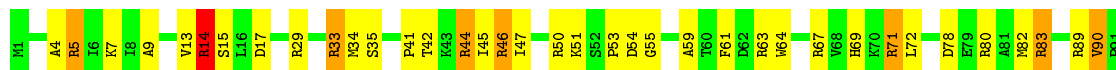
Chain BK:





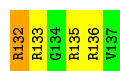
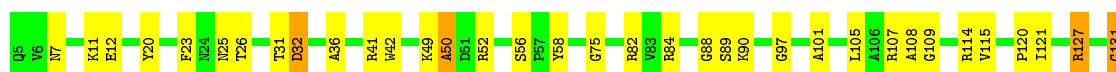
- Molecule 24: 30S ribosomal protein S10P

Chain BL: 61% 29% 9% .



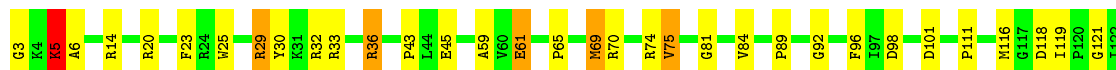
- Molecule 25: 30S ribosomal protein S11P

Chain BM: 71% 26% .



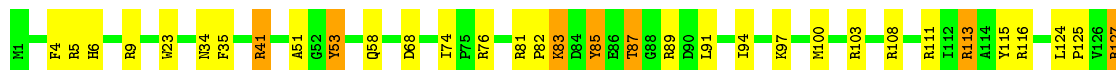
- Molecule 26: 30S ribosomal protein S12P

Chain BN: 70% 26% . .



- Molecule 27: 30S ribosomal protein S13P

Chain BO: 72% 21% 7%



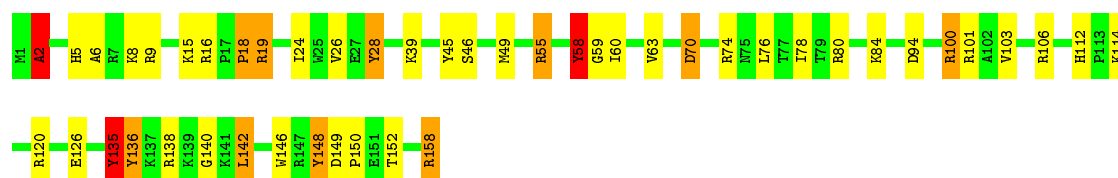
- Molecule 28: 30S ribosomal protein S14P

Chain BP: 61% 27% 11% .



- Molecule 29: 30S ribosomal protein S15P/S13E

Chain BQ: 



- Molecule 30: 30S ribosomal protein S17P

Chain BR: 



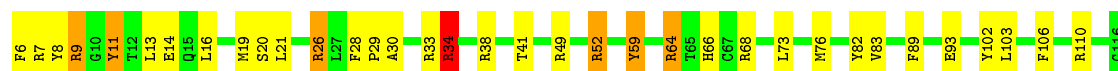
- Molecule 31: 30S ribosomal protein S17E

Chain BS:  75% 21% ..



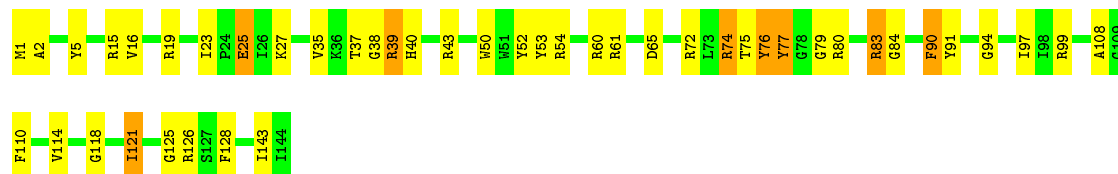
- Molecule 32: 30S ribosomal protein S19P

Chain BT:  68% 25% 5%



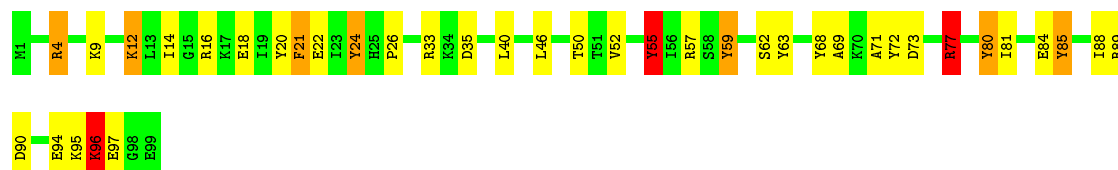
- Molecule 33: 30S ribosomal protein S19E

Chain BU:  69% 26% 6%



- Molecule 34: 30S ribosomal protein S24E

Chain BV: 



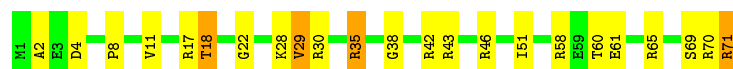
- Molecule 35: 30S ribosomal protein S27E

Chain BW: 



- Molecule 36: 30S ribosomal protein S28E

Chain BX: 



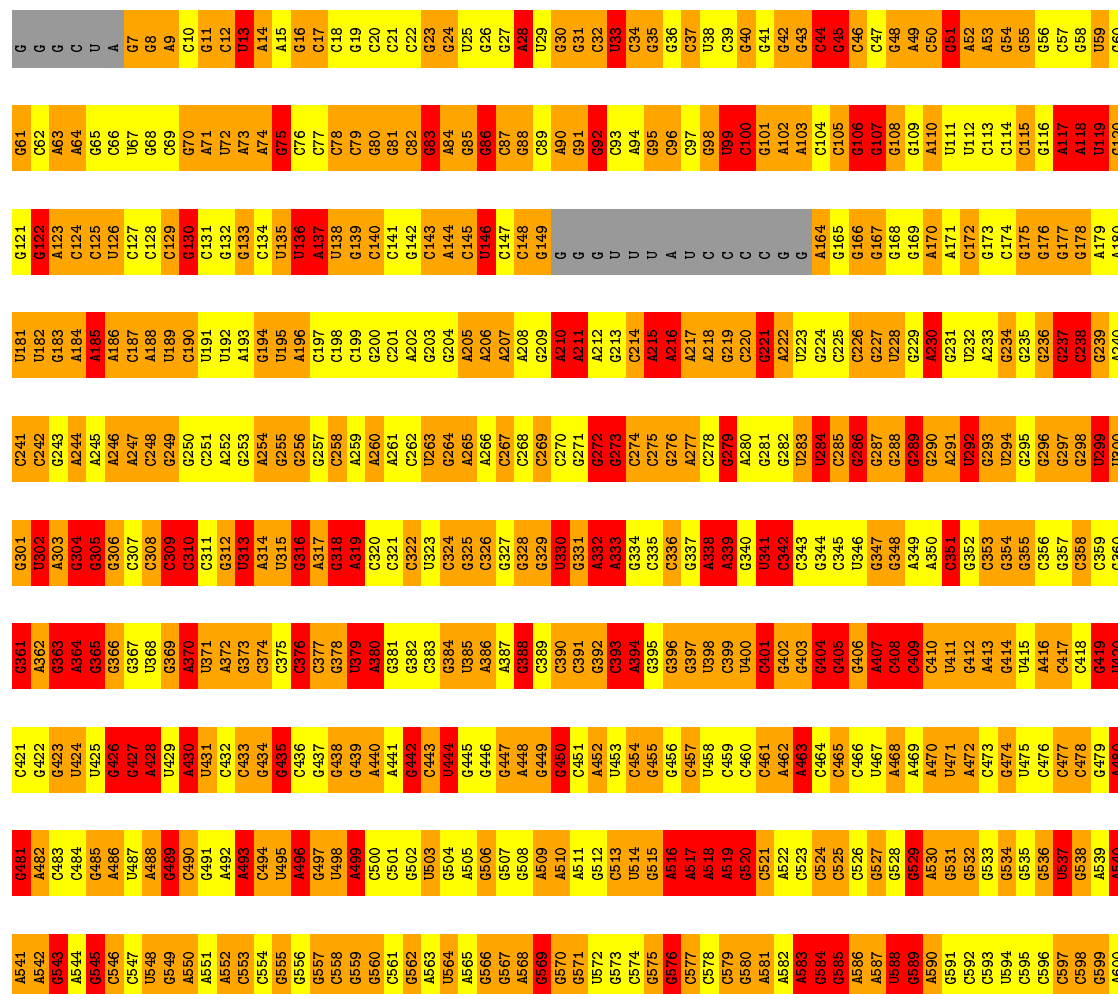
- Molecule 37: 30S ribosomal protein S27AE

Chain BY: 



- Molecule 38: 23S ribosomal RNA

Chain A1: 



G1501	G1441	C1381	C	G1261	G1201	C1141	U1081	G1021	G961	C901	U841	G781	G721	G661	A601
G1502	G1442	C1382	G1322	C1262	G1202	A1142	A1082	G1022	G962	C902	C842	G782	G722	A662	G602
G1503	G1443	C1383	U1323	G1263	C1203	A1143	G1083	C1023	G963	C903	C843	G783	G723	A663	G603
G1504	G1444	C1384	G1324	G1264	C1204	A1144	G1084	G1024	G964	G904	C844	G784	G724	A664	A604
G1505	G1445	C1385	U1325	A1265	U1205	G1145	G1085	A1025	G965	G905	U845	G785	G725	C665	A605
G1506	G1446	C1386	G1326	A1266	A1206	U1146	U1086	A1026	G966	G906	C846	G786	G726	C666	A606
G1507	G1447	C1387	C1327	A1267	G1207	G1147	G1087	A1027	G967	C907	A847	G787	A727	C667	G607
G1508	G1448	U1388	G1328	A1268	A1208	C1148	G1088	G1028	A968	U908	A848	A788	A728	G668	G608
G1509	G1449	G1389	G1329	U1269	A1209	C1149	C1089	C1029	U969	A909	C849	G789	A729	G669	G609
G1510	U1510	U1390	G1330	G1270	G1210	G1150	G1090	C1030	G970	G910	C850	G790	C730	G670	G610
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G1515	U1455	G1335	G1335	G1275	G1215	A1155	A1095	G1035	C975	G915	G855	G795	A735	G675	A615
G1516	U1456	A1396	G1336	G1276	A1216	G1156	A1096	C1036	C976	A916	A856	G796	U736	G676	C616
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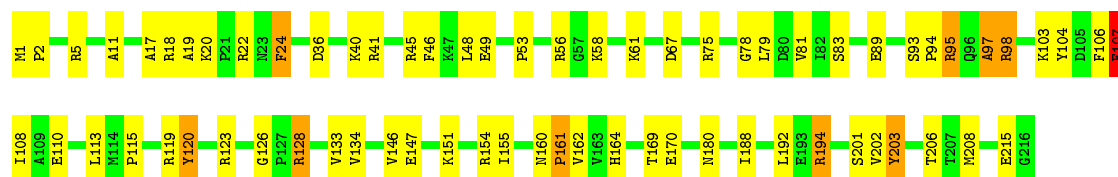
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A2508	A2448	U2388	G2328	C2268	U2148	G2088	C2028	A1968	C1908	A1848	G1788	C1728	G1668	G1608
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Chain AK: 



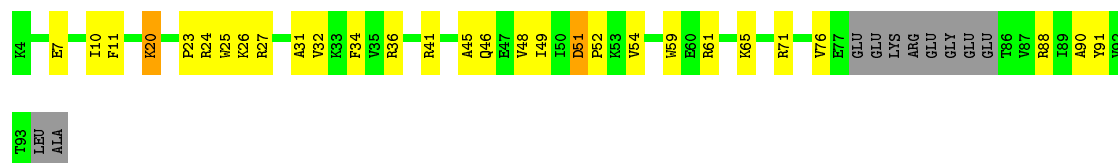
- Molecule 41: 50S ribosomal protein L1P

Chain AA: 



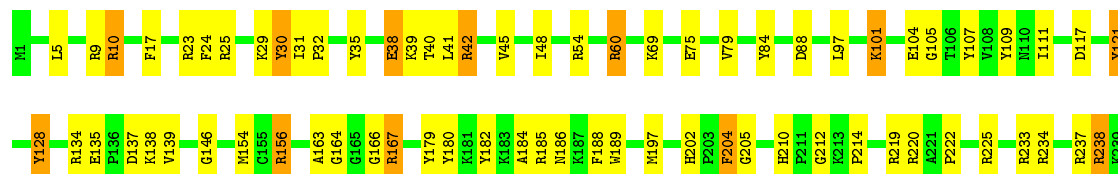
- Molecule 42: 50S ribosomal protein L31E

Chain Aa: 



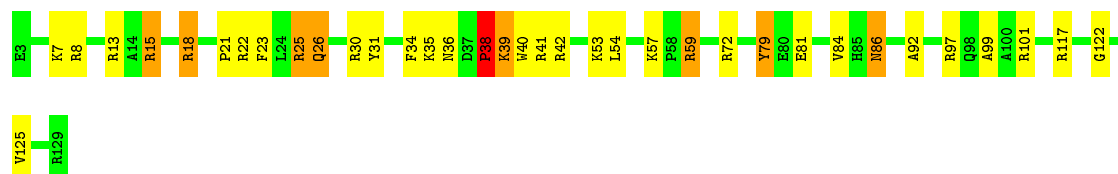
- Molecule 43: 50S ribosomal protein L2

Chain AB: 



- Molecule 44: 50S ribosomal protein L32E

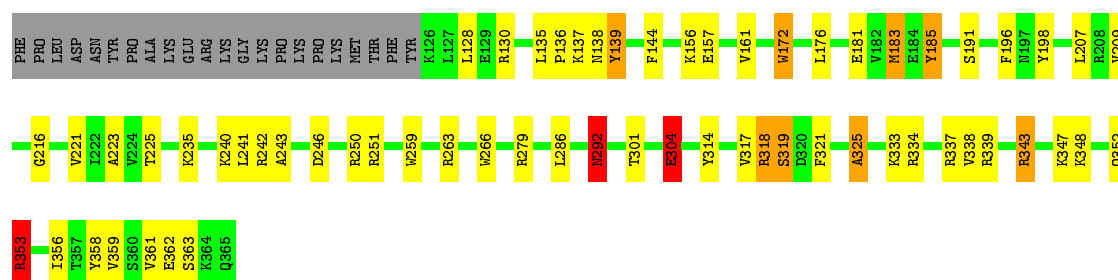
Chain Ab: 



- Molecule 45: 50S ribosomal protein L3P

Chain AC: 





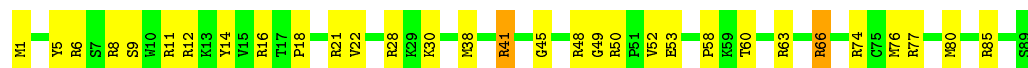
- Molecule 46: 50S ribosomal protein L4P

Chain AD: 67% 27% 5% .



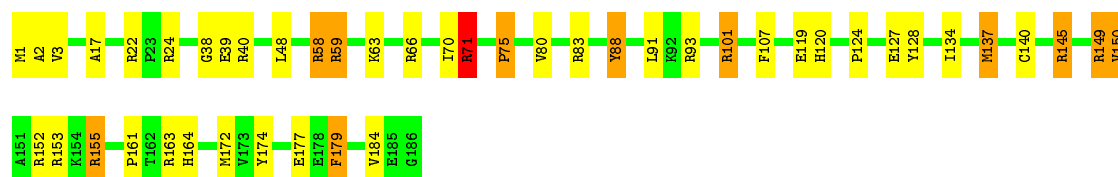
- Molecule 47: 50S ribosomal protein L34E

Chain Ad: 65% 33% .



- Molecule 48: 50S ribosomal protein L5P

Chain AE: 75% 18% 6% .



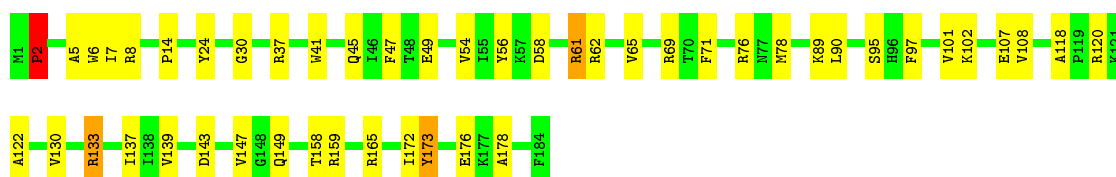
- Molecule 49: 50S ribosomal protein L37E

Chain Ae: 60% 32% 8%



- Molecule 50: 50S ribosomal protein L6P

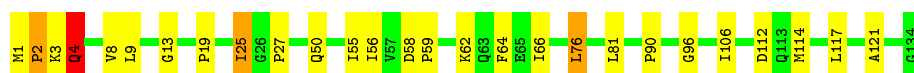
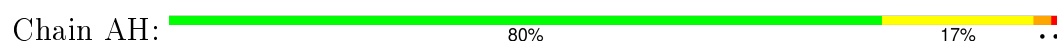
Chain AF: 74% 24% ..



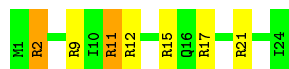
- Molecule 51: 50S ribosomal protein L40E



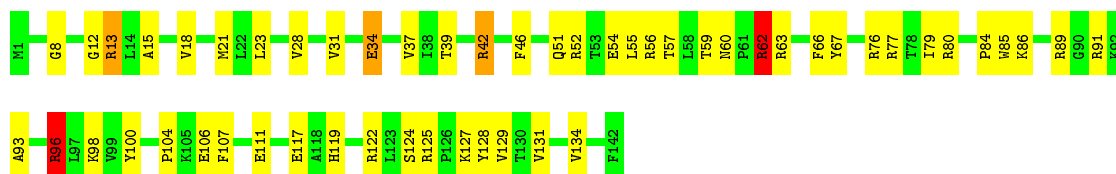
- Molecule 52: 50S ribosomal protein L11P



- Molecule 53: 50S ribosomal protein L41E



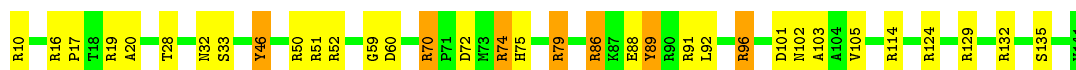
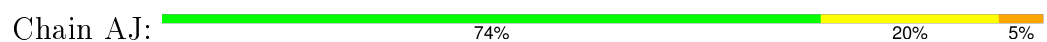
- Molecule 54: 50S ribosomal protein L13P



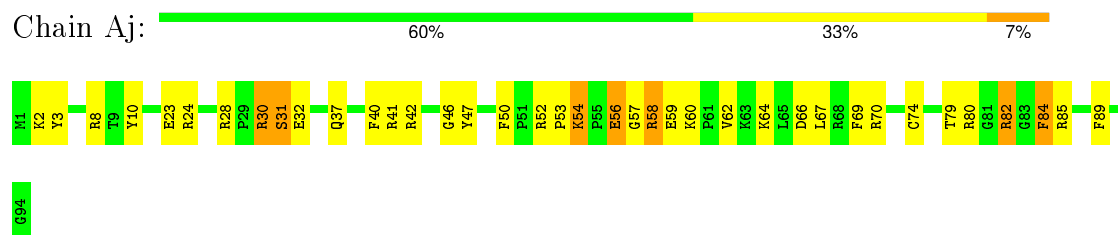
- Molecule 55: 50S ribosomal protein L37AE



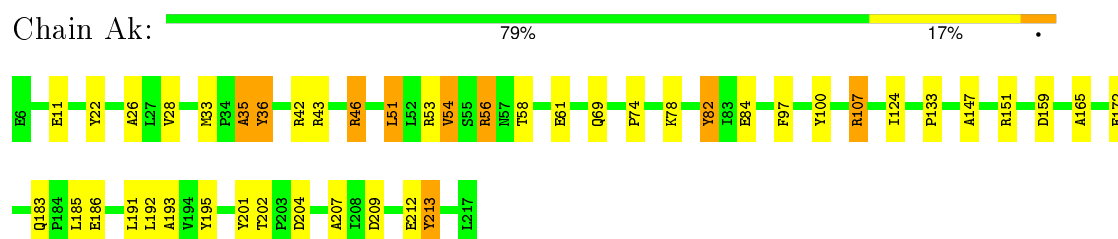
- Molecule 56: 50S ribosomal protein L14P



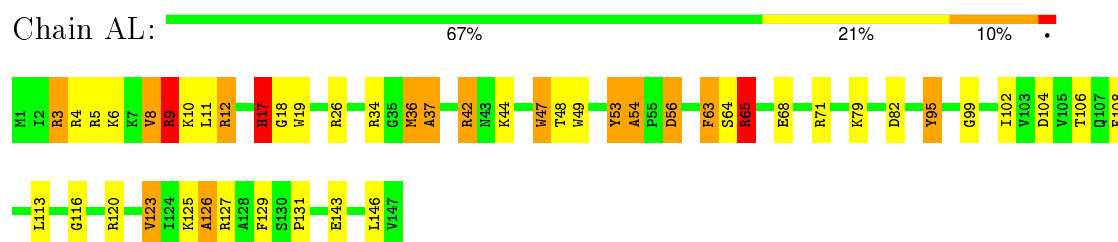
- Molecule 57: 50S ribosomal protein L44E



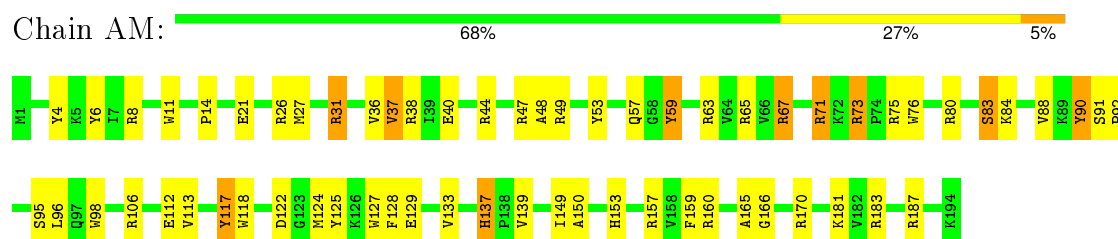
- Molecule 58: 50S ribosomal protein P0/L10E



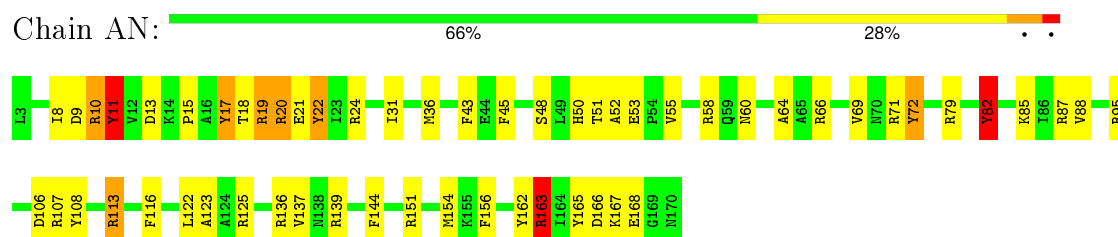
- Molecule 59: 50S ribosomal protein L15P



- Molecule 60: 50S ribosomal protein L15E



- Molecule 61: 50S ribosomal protein L10E/L16



- Molecule 62: 50S ribosomal protein L18P

M1	D2	R3	V17	R25	T29	I34	I35	I36	V37	M40	A41	P42	D48	Y51	Y52	D57	F63	B64	G65	T66	G71	T72	L73	L74	G75	G76	F77	F78	V79	A84	I85	V86	R99
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4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	37000	Depositor
Resolution determination method	FSC at 0.5 cut-off using a comparison between experimental map and a map of the docked ribosomal models calculated at 7 Angstrom resolution with EMAN	Depositor
CTF correction method	per micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	50000	Depositor
Image detector	Not provided	Depositor

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A7	1.64	2/534 (0.4%)	1.97	14/719 (1.9%)
10	B1	3.41	257/1840 (14.0%)	3.87	460/2869 (16.0%)
11	B2	3.43	4996/35963 (13.9%)	3.79	8330/56134 (14.8%)
12	AG	1.71	4/951 (0.4%)	1.82	14/1281 (1.1%)
12	B3	1.62	3/951 (0.3%)	1.78	13/1281 (1.0%)
13	BA	1.74	21/1585 (1.3%)	2.02	45/2124 (2.1%)
14	BB	1.72	15/1654 (0.9%)	1.96	43/2233 (1.9%)
15	BC	1.82	18/1481 (1.2%)	2.03	41/1985 (2.1%)
16	BD	1.77	14/1457 (1.0%)	2.13	51/1953 (2.6%)
17	BE	1.76	25/2025 (1.2%)	2.01	58/2732 (2.1%)
18	BF	1.81	29/1746 (1.7%)	2.04	51/2350 (2.2%)
19	BG	1.72	9/999 (0.9%)	1.94	22/1337 (1.6%)
2	A8	1.75	1/263 (0.4%)	1.81	4/354 (1.1%)
20	BH	1.79	22/1773 (1.2%)	2.00	62/2381 (2.6%)
21	BI	1.77	13/1049 (1.2%)	2.04	27/1408 (1.9%)
22	BJ	1.83	14/1013 (1.4%)	2.02	22/1349 (1.6%)
23	BK	1.76	10/1088 (0.9%)	1.96	31/1455 (2.1%)
24	BL	1.76	10/830 (1.2%)	2.00	26/1113 (2.3%)
25	BM	1.83	16/1022 (1.6%)	1.90	24/1375 (1.7%)
26	BN	1.74	8/1157 (0.7%)	2.06	37/1536 (2.4%)
27	BO	1.78	13/1208 (1.1%)	2.02	32/1619 (2.0%)
28	BP	1.94	12/471 (2.5%)	2.31	20/620 (3.2%)
29	BQ	1.75	14/1338 (1.0%)	1.95	34/1797 (1.9%)
3	Af	1.83	4/453 (0.9%)	2.10	15/603 (2.5%)
30	BR	1.75	12/956 (1.3%)	2.06	24/1287 (1.9%)
31	BS	1.70	4/562 (0.7%)	1.95	10/744 (1.3%)
32	BT	1.78	11/943 (1.2%)	2.23	35/1257 (2.8%)
33	BU	1.80	13/1204 (1.1%)	2.01	30/1621 (1.9%)
34	BV	1.80	13/839 (1.5%)	2.13	29/1122 (2.6%)
35	BW	1.68	2/485 (0.4%)	1.93	11/651 (1.7%)
36	BX	1.84	7/570 (1.2%)	1.93	9/760 (1.2%)
37	BY	1.66	4/421 (1.0%)	2.22	16/558 (2.9%)
38	A1	3.42	9848/71524 (13.8%)	3.76	16432/111652 (14.7%)
39	A3	3.37	408/3007 (13.6%)	3.87	667/4689 (14.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
4	AQ	1.80	16/1272 (1.3%)	2.05	35/1676 (2.1%)
40	A5	1.85	11/618 (1.8%)	1.97	14/829 (1.7%)
40	AK	1.64	4/618 (0.6%)	1.97	16/829 (1.9%)
41	AA	1.71	17/1702 (1.0%)	2.12	52/2293 (2.3%)
42	Aa	1.72	11/690 (1.6%)	2.12	23/926 (2.5%)
43	AB	1.80	20/1883 (1.1%)	1.99	66/2540 (2.6%)
44	Ab	1.81	13/1100 (1.2%)	1.99	30/1466 (2.0%)
45	AC	1.73	29/2774 (1.0%)	1.98	77/3727 (2.1%)
46	AD	1.74	29/2068 (1.4%)	2.04	58/2787 (2.1%)
47	Ad	1.84	13/758 (1.7%)	2.12	28/1007 (2.8%)
48	AE	1.75	14/1513 (0.9%)	1.98	30/2026 (1.5%)
49	Ae	1.87	6/517 (1.2%)	2.04	15/681 (2.2%)
5	AS	1.80	17/1226 (1.4%)	2.14	41/1649 (2.5%)
50	AF	1.71	18/1507 (1.2%)	1.89	24/2033 (1.2%)
51	Ag	1.89	5/381 (1.3%)	2.19	15/504 (3.0%)
52	AH	1.59	2/1002 (0.2%)	1.82	15/1351 (1.1%)
53	Ah	1.81	3/233 (1.3%)	2.32	10/301 (3.3%)
54	AI	1.81	11/1168 (0.9%)	1.94	31/1561 (2.0%)
55	Ai	1.86	10/599 (1.7%)	1.97	14/798 (1.8%)
56	AJ	1.86	13/1027 (1.3%)	1.92	17/1385 (1.2%)
57	Aj	1.85	12/806 (1.5%)	2.18	30/1065 (2.8%)
58	Ak	1.74	16/1660 (1.0%)	1.92	34/2253 (1.5%)
59	AL	1.82	14/1175 (1.2%)	2.03	34/1563 (2.2%)
6	AT	1.69	6/689 (0.9%)	2.00	19/924 (2.1%)
60	AM	1.85	27/1634 (1.7%)	2.11	53/2179 (2.4%)
61	AN	1.85	24/1410 (1.7%)	2.05	43/1890 (2.3%)
62	AO	1.73	17/1636 (1.0%)	2.11	47/2196 (2.1%)
63	AP	1.82	12/980 (1.2%)	2.03	26/1313 (2.0%)
64	AR	1.74	10/808 (1.2%)	1.97	23/1080 (2.1%)
65	AV	1.91	9/570 (1.6%)	2.18	23/758 (3.0%)
66	AY	1.69	8/1262 (0.6%)	1.98	33/1687 (2.0%)
67	AZ	1.68	2/764 (0.3%)	1.94	21/1028 (2.0%)
7	AU	1.81	15/1024 (1.5%)	2.04	30/1365 (2.2%)
8	AW	1.76	5/547 (0.9%)	1.95	12/725 (1.7%)
9	AX	1.71	31/3383 (0.9%)	1.98	79/4593 (1.7%)
All	All	2.89	16322/184366 (8.9%)	3.26	27857/271937 (10.2%)

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
10	B1	0	35
11	B2	0	725
12	AG	0	2
13	BA	0	11
14	BB	0	2
15	BC	0	8
16	BD	0	7
17	BE	0	9
18	BF	0	3
19	BG	1	4
2	A8	0	1
20	BH	4	13
21	BI	0	3
22	BJ	0	6
23	BK	0	7
24	BL	0	8
25	BM	0	2
26	BN	0	4
27	BO	0	5
28	BP	0	1
29	BQ	0	7
3	Af	0	6
30	BR	0	3
31	BS	0	2
32	BT	0	5
33	BU	0	4
34	BV	0	12
35	BW	0	1
36	BX	0	3
37	BY	0	3
38	A1	2	1412
39	A3	0	55
4	AQ	0	5
40	A5	0	2
40	AK	0	2
41	AA	0	4
42	Aa	0	2
43	AB	0	8
44	Ab	0	9
45	AC	0	7
46	AD	0	9
47	Ad	0	1
48	AE	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
49	Ae	1	9
5	AS	0	5
50	AF	0	3
51	Ag	1	5
52	AH	1	2
53	Ah	0	2
54	AI	0	7
55	Ai	0	2
56	AJ	0	4
57	Aj	0	7
58	Ak	0	4
59	AL	2	10
6	AT	0	2
60	AM	0	4
61	AN	0	7
62	AO	0	10
63	AP	0	4
64	AR	0	1
65	AV	0	5
66	AY	0	2
67	AZ	0	1
7	AU	0	4
9	AX	0	9
All	All	12	2533

The worst 5 of 16322 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	B2	770	A	N7-C5	-18.72	1.28	1.39
11	B2	470	G	N9-C8	18.32	1.50	1.37
38	A1	2257	A	N7-C5	-18.29	1.28	1.39
38	A1	910	G	N7-C5	-17.89	1.28	1.39
38	A1	2164	G	N7-C5	-17.73	1.28	1.39

The worst 5 of 27857 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	B2	1445	A	N1-C6-N6	27.58	135.15	118.60
38	A1	277	A	N1-C6-N6	27.04	134.82	118.60
38	A1	2347	G	N1-C6-O6	26.94	136.06	119.90
38	A1	1281	A	N1-C6-N6	26.62	134.57	118.60
38	A1	2540	A	N1-C6-N6	26.19	134.31	118.60

5 of 12 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
19	BG	53	LYS	CA
20	BH	85	PHE	CA
20	BH	86	MET	CA
20	BH	87	ARG	CA
20	BH	96	LYS	CA

5 of 2533 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A8	49	TYR	Sidechain
3	Af	2	ALA	Peptide
3	Af	33	ARG	Peptide
3	Af	34	ARG	Sidechain
3	Af	37	THR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A7	525	0	567	3	0
2	A8	258	0	272	0	0
3	Af	445	0	510	0	0
4	AQ	1256	0	1390	2	0
5	AS	1200	0	1255	1	0
6	AT	680	0	739	4	0
7	AU	1008	0	1077	3	0
8	AW	546	0	601	1	0
9	AX	3309	0	3523	5	0
10	B1	1646	0	835	73	0
11	B2	32132	0	16199	106	0
12	AG	939	0	994	3	0
12	B3	939	0	994	3	0
13	BA	1559	0	1648	4	0
14	BB	1623	0	1685	6	0
15	BC	1460	0	1549	1	0
16	BD	1434	0	1498	3	0
17	BE	1976	0	2046	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	BF	1717	0	1770	4	0
19	BG	984	0	1044	5	0
20	BH	1736	0	1787	15	0
21	BI	1028	0	1065	3	0
22	BJ	1004	0	1088	4	0
23	BK	1072	0	1128	8	0
24	BL	822	0	870	6	0
25	BM	1004	0	1041	1	0
26	BN	1141	0	1240	2	0
27	BO	1189	0	1248	7	0
28	BP	462	0	492	6	0
29	BQ	1310	0	1392	12	0
30	BR	934	0	960	2	0
31	BS	556	0	604	4	0
32	BT	924	0	986	4	0
33	BU	1176	0	1216	5	0
34	BV	823	0	847	5	0
35	BW	478	0	524	5	0
36	BX	568	0	600	0	0
37	BY	409	0	410	3	0
38	A1	63885	0	32208	253	0
39	A3	2691	0	1371	13	0
40	A5	614	0	670	5	0
40	AK	614	0	670	1	0
41	AA	1677	0	1796	13	0
42	Aa	677	0	749	0	0
43	AB	1838	0	1914	4	0
44	Ab	1075	0	1168	0	0
45	AC	2717	0	2875	8	0
46	AD	2026	0	2137	11	0
47	Ad	740	0	809	0	0
48	AE	1489	0	1550	4	0
49	Ae	506	0	529	0	0
50	AF	1476	0	1518	6	0
51	Ag	372	0	395	0	0
52	AH	989	0	1077	4	0
53	Ah	230	0	270	0	0
54	AI	1150	0	1240	8	0
55	Ai	590	0	631	0	0
56	AJ	1014	0	1072	5	0
57	Aj	788	0	842	0	0
58	Ak	1633	0	1726	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	AL	1154	0	1219	8	0
60	AM	1595	0	1695	1	0
61	AN	1379	0	1405	3	0
62	AO	1598	0	1639	4	0
63	AP	966	0	1019	3	0
64	AR	787	0	827	4	0
65	AV	555	0	548	1	0
66	AY	1243	0	1326	4	0
67	AZ	754	0	804	12	0
All	All	171094	0	125393	554	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 2.

The worst 5 of 554 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:B1:77:A:H5''	38:A1:2513:C:C2'	1.48	1.40
29:BQ:158:ARG:OXT	67:AZ:73:LEU:CD2	1.69	1.40
10:B1:57:C:H5'	38:A1:2291:G:C8	1.29	1.31
10:B1:57:C:C5'	38:A1:2291:G:C8	1.99	1.29
10:B1:77:A:N1	38:A1:2538:G:H2'	1.47	1.28

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A7	63/67 (94%)	43 (68%)	16 (25%)	4 (6%)	2	25
2	A8	30/52 (58%)	22 (73%)	7 (23%)	1 (3%)	5	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Af	49/51 (96%)	40 (82%)	6 (12%)	3 (6%)	2	26
4	AQ	148/150 (99%)	139 (94%)	5 (3%)	4 (3%)	6	45
5	AS	148/150 (99%)	135 (91%)	10 (7%)	3 (2%)	9	51
6	AT	82/84 (98%)	75 (92%)	4 (5%)	3 (4%)	4	38
7	AU	119/121 (98%)	113 (95%)	5 (4%)	1 (1%)	24	69
8	AW	64/72 (89%)	64 (100%)	0	0	100	100
9	AX	430/436 (99%)	322 (75%)	77 (18%)	31 (7%)	1	22
12	AG	121/123 (98%)	114 (94%)	4 (3%)	3 (2%)	7	46
12	B3	121/123 (98%)	100 (83%)	14 (12%)	7 (6%)	2	27
13	BA	188/190 (99%)	164 (87%)	12 (6%)	12 (6%)	2	25
14	BB	200/202 (99%)	182 (91%)	12 (6%)	6 (3%)	5	42
15	BC	184/186 (99%)	171 (93%)	9 (5%)	4 (2%)	8	49
16	BD	170/172 (99%)	148 (87%)	20 (12%)	2 (1%)	16	61
17	BE	239/241 (99%)	207 (87%)	20 (8%)	12 (5%)	3	31
18	BF	215/217 (99%)	188 (87%)	16 (7%)	11 (5%)	2	30
19	BG	123/125 (98%)	103 (84%)	13 (11%)	7 (6%)	2	28
20	BH	213/215 (99%)	186 (87%)	14 (7%)	13 (6%)	2	26
21	BI	127/129 (98%)	118 (93%)	8 (6%)	1 (1%)	24	69
22	BJ	125/127 (98%)	107 (86%)	15 (12%)	3 (2%)	7	47
23	BK	133/135 (98%)	116 (87%)	10 (8%)	7 (5%)	2	29
24	BL	100/102 (98%)	90 (90%)	7 (7%)	3 (3%)	5	42
25	BM	131/133 (98%)	112 (86%)	9 (7%)	10 (8%)	1	20
26	BN	143/145 (99%)	128 (90%)	7 (5%)	8 (6%)	2	28
27	BO	146/148 (99%)	122 (84%)	16 (11%)	8 (6%)	2	29
28	BP	54/56 (96%)	44 (82%)	8 (15%)	2 (4%)	4	38
29	BQ	156/158 (99%)	137 (88%)	9 (6%)	10 (6%)	2	25
30	BR	111/113 (98%)	105 (95%)	5 (4%)	1 (1%)	21	67
31	BS	65/67 (97%)	60 (92%)	5 (8%)	0	100	100
32	BT	109/111 (98%)	102 (94%)	5 (5%)	2 (2%)	11	53
33	BU	142/144 (99%)	123 (87%)	11 (8%)	8 (6%)	2	28
34	BV	97/99 (98%)	88 (91%)	5 (5%)	4 (4%)	3	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	BW	61/63 (97%)	52 (85%)	6 (10%)	3 (5%)	3	31
36	BX	69/71 (97%)	62 (90%)	6 (9%)	1 (1%)	14	58
37	BY	48/50 (96%)	41 (85%)	5 (10%)	2 (4%)	3	34
40	A5	79/81 (98%)	67 (85%)	9 (11%)	3 (4%)	4	37
40	AK	79/81 (98%)	70 (89%)	4 (5%)	5 (6%)	2	25
41	AA	214/216 (99%)	186 (87%)	19 (9%)	9 (4%)	3	34
42	Aa	78/92 (85%)	69 (88%)	9 (12%)	0	100	100
43	AB	237/239 (99%)	209 (88%)	23 (10%)	5 (2%)	9	50
44	Ab	125/127 (98%)	108 (86%)	11 (9%)	6 (5%)	3	32
45	AC	338/365 (93%)	303 (90%)	21 (6%)	14 (4%)	3	35
46	AD	253/255 (99%)	220 (87%)	23 (9%)	10 (4%)	4	35
47	Ad	87/89 (98%)	78 (90%)	6 (7%)	3 (3%)	5	40
48	AE	184/186 (99%)	161 (88%)	15 (8%)	8 (4%)	3	34
49	Ae	60/62 (97%)	43 (72%)	13 (22%)	4 (7%)	1	24
50	AF	182/184 (99%)	165 (91%)	14 (8%)	3 (2%)	12	56
51	Ag	43/45 (96%)	30 (70%)	8 (19%)	5 (12%)	0	9
52	AH	132/134 (98%)	114 (86%)	11 (8%)	7 (5%)	2	29
53	Ah	22/24 (92%)	21 (96%)	1 (4%)	0	100	100
54	AI	140/142 (99%)	121 (86%)	13 (9%)	6 (4%)	3	34
55	Ai	76/78 (97%)	69 (91%)	4 (5%)	3 (4%)	4	36
56	AJ	130/132 (98%)	121 (93%)	6 (5%)	3 (2%)	8	48
57	Aj	92/94 (98%)	69 (75%)	18 (20%)	5 (5%)	2	29
58	Ak	210/212 (99%)	192 (91%)	11 (5%)	7 (3%)	5	40
59	AL	145/147 (99%)	129 (89%)	11 (8%)	5 (3%)	5	40
60	AM	192/194 (99%)	175 (91%)	11 (6%)	6 (3%)	5	42
61	AN	166/168 (99%)	141 (85%)	19 (11%)	6 (4%)	4	38
62	AO	195/197 (99%)	166 (85%)	20 (10%)	9 (5%)	3	33
63	AP	118/120 (98%)	107 (91%)	5 (4%)	6 (5%)	2	30
64	AR	93/95 (98%)	85 (91%)	3 (3%)	5 (5%)	2	29
65	AV	64/66 (97%)	61 (95%)	3 (5%)	0	100	100
66	AY	153/155 (99%)	137 (90%)	12 (8%)	4 (3%)	7	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	AZ	97/99 (98%)	84 (87%)	9 (9%)	4 (4%)	3	35
All	All	8708/8907 (98%)	7624 (88%)	733 (8%)	351 (4%)	6	35

5 of 351 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A7	30	LYS
4	AQ	134	ASN
9	AX	239	ARG
9	AX	277	TYR
9	AX	346	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A7	57/59 (97%)	55 (96%)	2 (4%)	43	74
2	A8	28/44 (64%)	28 (100%)	0	100	100
3	Af	47/47 (100%)	46 (98%)	1 (2%)	61	84
4	AQ	130/130 (100%)	125 (96%)	5 (4%)	40	73
5	AS	126/126 (100%)	119 (94%)	7 (6%)	26	62
6	AT	75/75 (100%)	73 (97%)	2 (3%)	52	79
7	AU	110/110 (100%)	105 (96%)	5 (4%)	34	69
8	AW	61/66 (92%)	60 (98%)	1 (2%)	70	88
9	AX	351/355 (99%)	341 (97%)	10 (3%)	51	78
12	AG	99/99 (100%)	95 (96%)	4 (4%)	38	71
12	B3	99/99 (100%)	94 (95%)	5 (5%)	29	66
13	BA	166/166 (100%)	152 (92%)	14 (8%)	14	48
14	BB	173/173 (100%)	168 (97%)	5 (3%)	50	78
15	BC	145/145 (100%)	141 (97%)	4 (3%)	51	78
16	BD	153/153 (100%)	148 (97%)	5 (3%)	45	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	BE	212/212 (100%)	201 (95%)	11 (5%)	29	65
18	BF	181/181 (100%)	173 (96%)	8 (4%)	35	69
19	BG	108/108 (100%)	108 (100%)	0	100	100
20	BH	184/184 (100%)	165 (90%)	19 (10%)	9	37
21	BI	107/107 (100%)	105 (98%)	2 (2%)	65	86
22	BJ	103/103 (100%)	95 (92%)	8 (8%)	16	51
23	BK	111/111 (100%)	108 (97%)	3 (3%)	52	79
24	BL	91/91 (100%)	87 (96%)	4 (4%)	35	69
25	BM	100/100 (100%)	96 (96%)	4 (4%)	38	71
26	BN	119/119 (100%)	114 (96%)	5 (4%)	36	70
27	BO	122/122 (100%)	120 (98%)	2 (2%)	70	88
28	BP	46/46 (100%)	43 (94%)	3 (6%)	21	58
29	BQ	143/143 (100%)	135 (94%)	8 (6%)	26	62
30	BR	102/102 (100%)	92 (90%)	10 (10%)	10	39
31	BS	61/61 (100%)	58 (95%)	3 (5%)	31	67
32	BT	99/99 (100%)	95 (96%)	4 (4%)	38	71
33	BU	121/121 (100%)	118 (98%)	3 (2%)	55	81
34	BV	89/89 (100%)	87 (98%)	2 (2%)	60	83
35	BW	54/54 (100%)	51 (94%)	3 (6%)	26	62
36	BX	60/60 (100%)	53 (88%)	7 (12%)	7	32
37	BY	41/41 (100%)	40 (98%)	1 (2%)	57	82
40	A5	64/64 (100%)	62 (97%)	2 (3%)	47	77
40	AK	64/64 (100%)	59 (92%)	5 (8%)	16	51
41	AA	182/182 (100%)	173 (95%)	9 (5%)	31	67
42	Aa	73/81 (90%)	68 (93%)	5 (7%)	20	57
43	AB	189/189 (100%)	183 (97%)	6 (3%)	46	76
44	Ab	114/114 (100%)	108 (95%)	6 (5%)	28	64
45	AC	291/312 (93%)	278 (96%)	13 (4%)	34	69
46	AD	213/213 (100%)	207 (97%)	6 (3%)	51	78
47	Ad	81/81 (100%)	81 (100%)	0	100	100
48	AE	158/158 (100%)	153 (97%)	5 (3%)	46	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	Ae	51/51 (100%)	49 (96%)	2 (4%)	39	72
50	AF	156/156 (100%)	150 (96%)	6 (4%)	40	73
51	Ag	37/37 (100%)	36 (97%)	1 (3%)	52	79
52	AH	110/110 (100%)	108 (98%)	2 (2%)	66	87
53	Ah	23/23 (100%)	23 (100%)	0	100	100
54	AI	122/122 (100%)	118 (97%)	4 (3%)	45	76
55	Ai	57/57 (100%)	55 (96%)	2 (4%)	43	74
56	AJ	104/104 (100%)	98 (94%)	6 (6%)	25	61
57	Aj	83/83 (100%)	80 (96%)	3 (4%)	42	74
58	Ak	179/179 (100%)	173 (97%)	6 (3%)	44	75
59	AL	117/117 (100%)	112 (96%)	5 (4%)	35	70
60	AM	162/162 (100%)	155 (96%)	7 (4%)	35	70
61	AN	140/140 (100%)	134 (96%)	6 (4%)	35	70
62	AO	166/166 (100%)	159 (96%)	7 (4%)	36	70
63	AP	101/101 (100%)	99 (98%)	2 (2%)	63	85
64	AR	85/85 (100%)	79 (93%)	6 (7%)	18	55
65	AV	56/56 (100%)	56 (100%)	0	100	100
66	AY	133/133 (100%)	130 (98%)	3 (2%)	58	83
67	AZ	80/80 (100%)	73 (91%)	7 (9%)	12	45
All	All	7465/7521 (99%)	7153 (96%)	312 (4%)	41	70

5 of 312 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	BQ	76	LEU
36	BX	71	ARG
62	AO	37	VAL
30	BR	41	ASP
32	BT	64	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
29	BQ	57	GLN

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Mol	Chain	Res	Type
42	Aa	42	HIS
64	AR	42	HIS
30	BR	24	HIS
34	BV	25	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B1	76/77 (98%)	20 (26%)	4 (5%)
11	B2	1494/1495 (99%)	264 (17%)	103 (6%)
38	A1	2964/3049 (97%)	600 (20%)	158 (5%)
39	A3	125/126 (99%)	36 (28%)	11 (8%)
All	All	4659/4747 (98%)	920 (19%)	276 (5%)

5 of 920 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	B1	8	U
10	B1	9	A
10	B1	10	G
10	B1	18	U
10	B1	19	G

5 of 276 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A1	371	U
38	A1	994	G
38	A1	2891	A
38	A1	427	G
38	A1	588	U

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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.