



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:48 PM BST

PDB ID : 4V7A
EMDB ID: : EMD-1724
Title : E. coli 70S-fMetVal-tRNAVal post-translocation complex (post4)
Authors : Blau, C.; Bock, L.V.; Schroder, G.F.; Davydov, I.; Fischer, N.; Stark, H.;
Rodnina, M.V.; Vaiana, A.C.; Grubmuller, H.
Deposited on : 2013-10-14
Resolution : 9.00 Å(reported)
Based on PDB ID : 3I1O, 2HGP, 2WRI, 2K4C

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 : 1.7.1 (RC1), CSD as537be (2016)
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

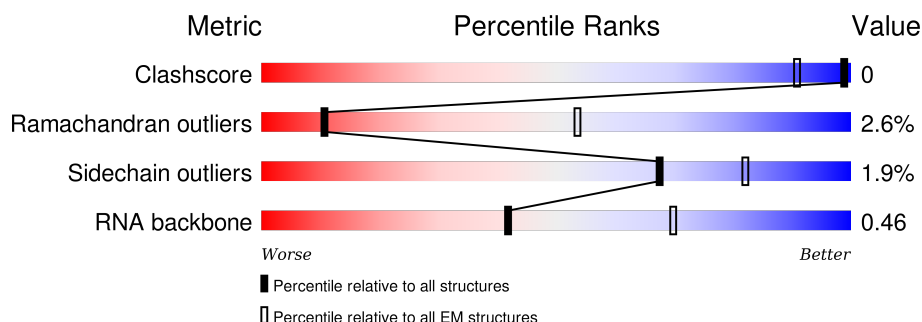
1 Overall quality at a glance

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.













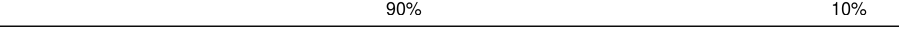
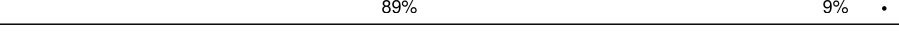
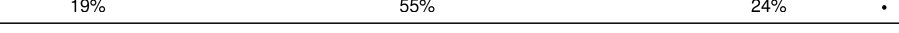
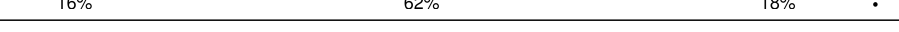
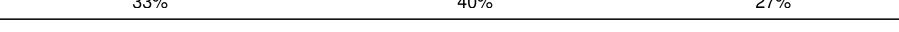
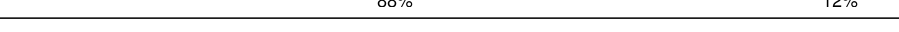









Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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	AB	220	94% 6%
2	AC	208	87% 13%
3	AD	206	91% 8%
4	AE	152	91% 8% .
5	AF	101	90% 10%
6	AG	152	89% 11%
7	AH	130	95% . ..
8	AI	128	86% 14%












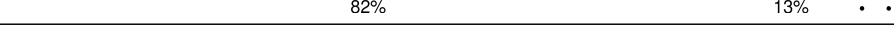







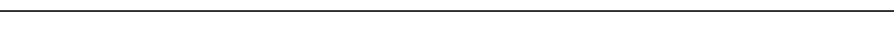

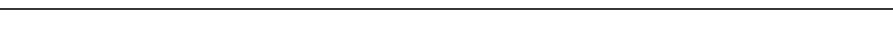
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Mol	Chain	Length	Quality of chain
9	AJ	100	 86% 13% .
10	AK	118	 92% 7% .
11	AL	124	 83% 16% .
12	AM	115	 87% 12% .
13	AN	101	 86% 11% ..
14	AO	89	 84% 15% .
15	AP	81	 91% 9%
16	AQ	82	 90% 9% .
17	AR	57	 89% 7% .
18	AS	81	 88% 11% .
19	AT	86	 90% 10%
20	AU	53	 89% 9% .
21	AA	1533	 19% 55% 24% .
22	A1	76	 16% 62% 18% .
23	A2	15	 33% 40% 27%
24	BC	273	 88% 12%
25	BD	209	 89% 11%
26	BE	201	 91% 8%
27	BF	179	 84% 15% ..
28	BG	177	 90% 8% ..
29	BH	149	 94% 6%
30	BI	142	 96% ..
31	BJ	142	 91% 8% .
32	BK	123	 85% 15% .
33	BL	144	 83% 15% ..

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Mol	Chain	Length	Quality of chain
34	BM	136	 89% 10% .
35	BN	121	 83% 16% .
36	BO	117	 91% 9% .
37	BP	115	 90% 9% ..
38	BQ	118	 87% 12% .
39	BR	103	 88% 12%
40	BS	110	 89% 11%
41	BT	94	 85% 15%
42	BU	104	 90% 8% ..
43	BV	94	 89% 11%
44	BW	80	 79% 20% .
45	BX	79	 82% 13% . .
46	BY	63	 90% 10%
47	BZ	59	 86% 8% . .
48	B0	57	 84% 14% .
49	B1	52	 87% 13%
50	B2	46	 78% 22%
51	B3	65	 85% 14% .
52	B4	38	 87% 11% .
53	BA	2903	 16% 55% 25% .
54	BB	118	 21% 53% 19% 5% .
55	B5	234	 89% 6% 5%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 146011 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 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AB	220	Total	C	N	O	S	0	1
			1708	1083	306	312	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AB	7	ACE	-	ACETYLATION	UNP P0A7V0
AB	226	NH2	-	AMIDATION	UNP P0A7V0

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AC	207	Total	C	N	O	S	0	1
			1625	1028	306	288	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AC	207	NH2	-	AMIDATION	UNP P0A7V3

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AD	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AE	152	Total	C	N	O	S	0	1
			1109	689	212	202	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	8	ACE	-	ACETYLATION	UNP P0A7W1
AE	159	NH2	-	AMIDATION	UNP P0A7W1

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AF	101	Total	C	N	O	S	0	1
			818	515	149	148	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AF	101	NH2	-	AMIDATION	UNP P02358

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AG	152	Total	C	N	O	S	0	1
			1178	732	227	215	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AG	1	ACE	-	ACETYLATION	UNP P02359
AG	152	NH2	-	AMIDATION	UNP P02359

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AH	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AI	128	Total	C	N	O	S	0	0
			1025	636	206	180	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	2	ACE	-	ACETYLATION	UNP P0A7X3

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AJ	100	Total	C	N	O	S	0	1
			790	495	151	143	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AJ	4	ACE	-	ACETYLATION	UNP P0A7R5
AJ	103	NH2	-	AMIDATION	UNP P0A7R5

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AK	118	Total	C	N	O	S	0	0
			880	542	174	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	11	ACE	-	ACETYLATION	UNP P0A7R9

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AM	114	Total	C	N	O	S	0	1
			877	541	178	155	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AM	114	NH2	-	AMIDATION	UNP P0A7S9

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AN	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AO	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AP	81	Total	C	N	O	S	0	1
			639	400	127	111	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AP	81	NH2	-	AMIDATION	UNP P0A7T3

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	82	Total	C	N	O	S	0	1
			652	413	122	114	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AQ	2	ACE	-	ACETYLATION	UNP P0AG63
AQ	83	NH2	-	AMIDATION	UNP P0AG63

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	AR	57	Total	C	N	O	0	1
			459	290	87	82		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	18	ACE	-	ACETYLATION	UNP P0A7T7

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Chain	Residue	Modelled	Actual	Comment	Reference
AR	74	NH2	-	AMIDATION	UNP P0A7T7

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS	81	Total	C	N	O	S	0	1
			641	410	121	108	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS	1	ACE	-	ACETYLATION	UNP P0A7U3
AS	81	NH2	-	AMIDATION	UNP P0A7U3

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AT	86	Total	C	N	O	S	0	0
			668	413	137	115	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AT	1	ACE	-	ACETYLATION	UNP P0A7U7

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AU	53	Total	C	N	O	S	0	1
			429	267	87	74	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AU	2	ACE	-	ACETYLATION	UNP P68679
AU	54	NH2	-	AMIDATION	UNP P68679

- Molecule 21 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AA	1530	Total	C	N	O	P	0	0
			32828	14642	6024	10633	1529		

- Molecule 22 is a RNA chain called fMet-Val-tRNA-Val.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	A1	76	Total	C	N	O	P	S	0	0
			1627	728	292	531	75	1		

- Molecule 23 is a RNA chain called 5'-R(*AP*CP*UP*AP*UP*GP*GP*UP*UP*UP*UP*UP*AP*UP*U)-3'.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A2	15	Total	C	N	O	P	0	0
			309	140	46	109	14		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BC	272	Total	C	N	O	S	0	1
			2083	1288	424	364	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BC	272	NH2	-	AMIDATION	UNP P60422

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BD	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BE	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BF	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BG	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BH	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BI	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 31 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BJ	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 32 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BK	123	Total	C	N	O	S	0	1
			939	587	181	165	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BK	123	NH2	-	AMIDATION	UNP P0ADY3

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BL	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 34 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BM	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 35 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BN	121	Total	C	N	O	S	0	1
			961	593	197	166	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BN	121	NH2	-	AMIDATION	UNP P0AG44

- Molecule 36 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BO	116	Total	C	N	O		0	0
			892	552	178	162			

- Molecule 37 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BP	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 38 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BQ	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 39 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BR	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 40 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BS	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 41 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BT	94	Total	C	N	O	S	0	1
			739	466	140	131	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BT	94	NH2	-	AMIDATION	UNP P0ADZ0

- Molecule 42 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	BU	103	Total	C	N	O	0	1
			780	492	147	141		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BU	103	NH2	-	AMIDATION	UNP P60624

- Molecule 43 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BV	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BW	80	Total	C	N	O	S	0	0
			599	369	120	109	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BW	5	ACE	-	ACETYLATION	UNP P0A7L8

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BX	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BX	-1	ACE	-	ACETYLATION	UNP P0A7M2

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BY	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 47 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BZ	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	B1	52	Total	C	N	O	0	1
			413	265	76	72		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B1	2	ACE	-	ACETYLATION	UNP P0A7N9
B1	53	NH2	-	AMIDATION	UNP P0A7N9

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BA	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

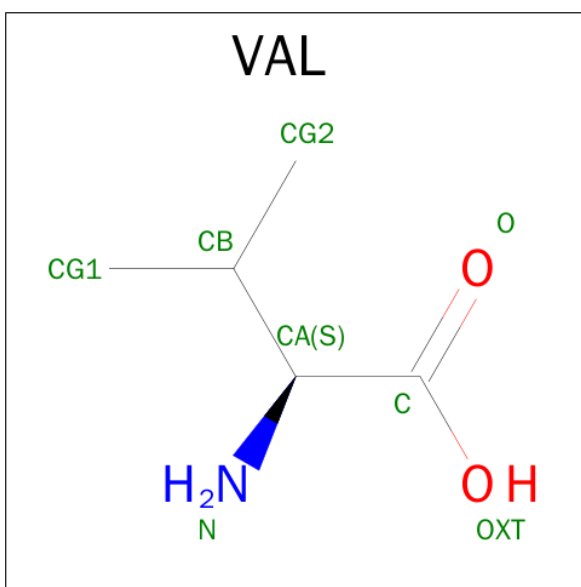
- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BB	117	Total	C	N	O	P	0	0
			2504	1116	459	813	116		

- Molecule 55 is a protein called 50S ribosomal protein L1.

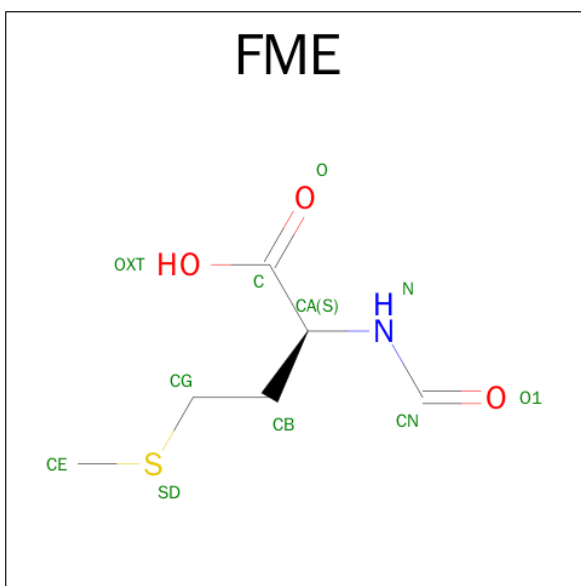
Mol	Chain	Residues	Atoms					AltConf	Trace
55	B5	223	Total	C	N	O	S	0	0
			1658	1038	302	312	6		

- Molecule 56 is VALINE (three-letter code: VAL) (formula: C₅H₁₁NO₂).



Mol	Chain	Residues	Atoms				AltConf
56	A1	1	Total	C	N	O	0
			7	5	1	1	

- Molecule 57 is N-FORMYLMETHIONINE (three-letter code: FME) (formula: $C_6H_{11}NO_3S$).



Mol	Chain	Residues	Atoms					AltConf
57	BA	1	Total	C	N	O	S	0
			10	6	1	2	1	



- Molecule 7: 30S ribosomal protein S8

Chain AH: 95%



- Molecule 8: 30S ribosomal protein S9

Chain AI: 86%



- Molecule 9: 30S ribosomal protein S10

Chain AJ: 86%



- Molecule 10: 30S ribosomal protein S11

Chain AK: 92%



- Molecule 11: 30S ribosomal protein S12

Chain AL: 83%



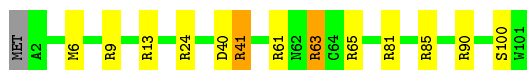
- Molecule 12: 30S ribosomal protein S13

Chain AM: 87%

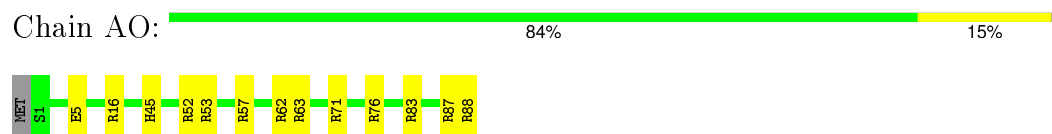


- Molecule 13: 30S ribosomal protein S14

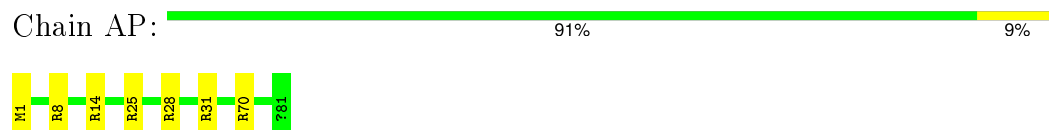
Chain AN: 86%



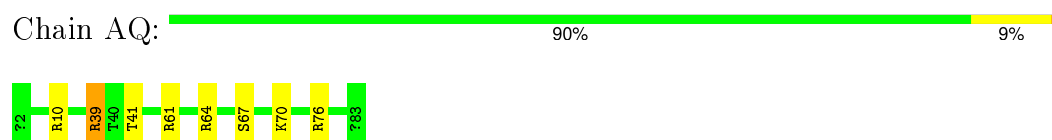
- Molecule 14: 30S ribosomal protein S15



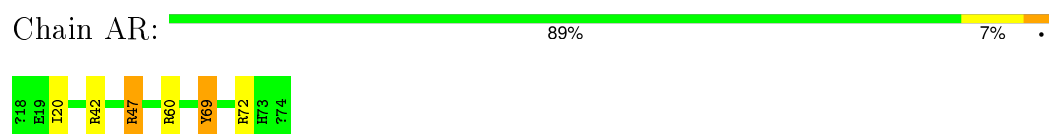
- Molecule 15: 30S ribosomal protein S16



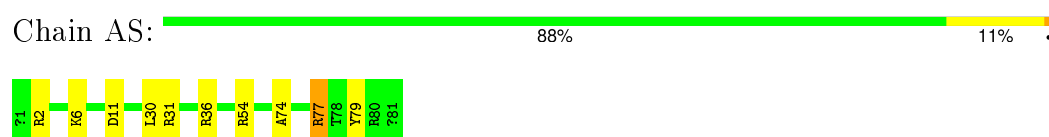
- Molecule 16: 30S ribosomal protein S17



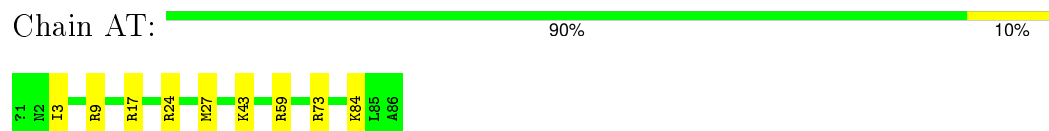
- Molecule 17: 30S ribosomal protein S18



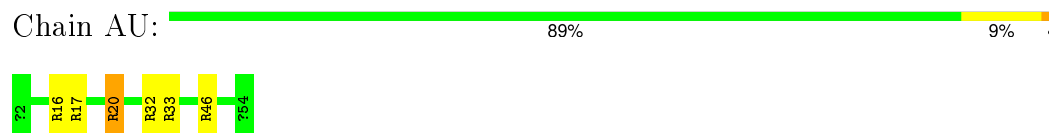
- Molecule 18: 30S ribosomal protein S19



- Molecule 19: 30S ribosomal protein S20



- Molecule 20: 30S ribosomal protein S21

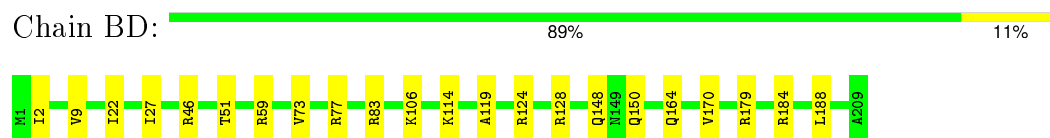


- Molecule 21: 16S ribosomal RNA

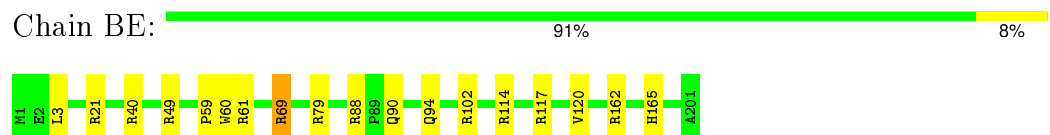


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G953	U956	U957	U958	A959	U960	G962	G963	A964	A965	U966	G966	G967	A968	A969	C970	G971	C972	G973	A974	C975	G976	A977	A978	C979	A980	A981	A982	A983	A984	C985	U986	G987	U988	U989	C990	U991	U992	G993	A994	C995	A996	U997	C998	U999	A1000	C1001	G1002	A1003	A1004	A1005	G1006	U1007	U1008	U1009	U1010	C1011	A1012	G1013					
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G829	G830	A831	C832	U835	U836	U837	C838	C839	C840	C841	U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	C853	U854	U855	C856	C857	U858	U859	U860	U861	U862	U863	U864	U865	G866	U867	G868	G869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888						
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C634	A635	U636	C637	U638	A639	A640	U641	A642	C643	G646	A647	A648	A649	G650	A651	U652	U653	A654	A655	G656	U657	C658	U659	A660	A661	A662	A663	A664	A665	G666	U667	G668	G669	G670	G671	U672	A673	A674	A675	A676	U677	U678	C679	C680	A681	U684	A687	G688	C689	G690	G691	U692	G693	A694	A695	A696							
G505	G506	C507	U508	A509	A510	C511	U512	C513	G514	U515	U516	U517	C518	C519	U520	A521	A522	A523	G524	C525	A526	G527	C528	A529	G530	U531	A532	A533	U534	A535	C536	G537	G538	A539	U543	G544	C545	A546	A547	G548	C549	G550	A553	A554	U555	C556	G557	G558	A559	A560	U561	U562	A563	C564	U565	G566							
A441	G442	C443	G444	U448	U449	A450	A451	A452	U453	G454	G455	A456	U459	A460	A461	G462	U463	U464	A465	A466	U467	U468	C469	U470	U471	U472	U473	A474	U475	U476	U477	U478	U479	U480	G481	A482	C483	U484	A487	C488	C489	U490	C492	A493	U494	A495	A496	U497	A498	A499	U500	C501	A502	C503	C504								
C381	A382	A383	G384	C385	C386	U387	G388	A389	U390	C391	A392	C393	G394	C395	A396	C397	C400	C401	A402	C403	G404	U405	G406	U407	U408	U409	U410	A411	A412	A413	A414	G415	G416	C417	C418	C419	U420	A421	C422	A423	G424	G425	U426	U427	G428	U429	A430	A431	A432	G433	U434	U435	A436	A437	C438	C439	C440						
G318	G319	A320	A321	C322	U323	G324	A325	C326	C327	C328	A329	C330	G331	U332	C333	A334	C335	A336	C337	C338	C339	C342	U343	A344	C345	G346	C347	G348	A349	C350	G351	A352	C353	C354	C355	A356	G360	G361	A362	A363	A364	U365	U367	U368	G369	C370	A371	C372	A373	C374	U375	U376	G377	C378	C379	G380							
C67	G68	G69	U70	A71	A72	C73	A74	C75	G76	A77	G78	A79	A80	A81	C82	C83	U84	U85	C86	C87	U88	G89	U90	U91	U92	U93	G94	C95	U96	G97	A98	C99	G100	A101	C102	U103	G104	G105	C106	G107	G108	C109	U110	A111	G112	U113	A114	U115	U116	U117	U118	A119	A120	U121	G122	A123	U124	G125	A126	U127	A128	C129	A130
A	A	U	U5	G6	A7	A8	G9	A10	G15	U16	U17	C18	A19	U20	G21	C22	C23	U24	C25	U26	G27	U28	C29	U30	U32	A32	A33	C34	G35	C36	U37	C38	G39	A101	C102	U103	G104	G105	C106	G107	G108	C109	U110	A111	G112	U113	A114	U115	U116	U117	U118	A119	A120	U121	G122	A123	U124	G125	A126	U127	A128	C129	A130

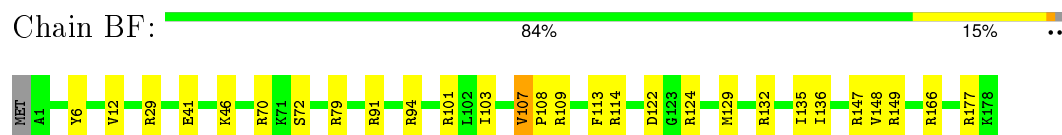
- Molecule 25: 50S ribosomal protein L3



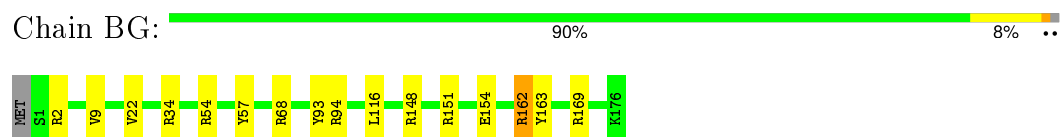
- Molecule 26: 50S ribosomal protein L4



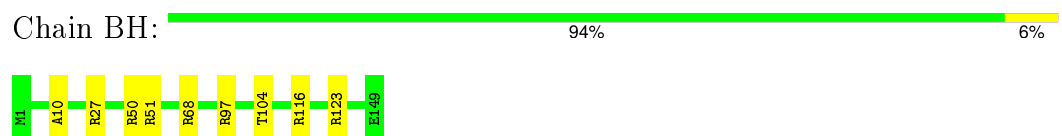
- Molecule 27: 50S ribosomal protein L5



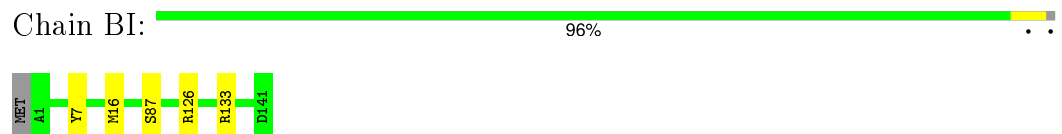
- Molecule 28: 50S ribosomal protein L6



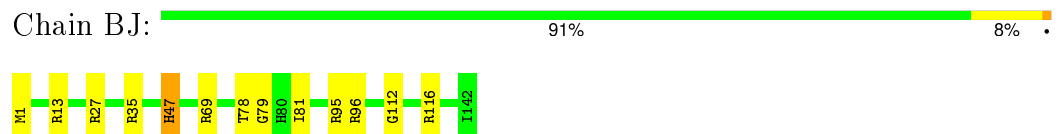
- Molecule 29: 50S ribosomal protein L9




- Molecule 30: 50S ribosomal protein L11



- Molecule 31: 50S ribosomal protein L13




- Molecule 32: 50S ribosomal protein L14

Chain BK:  85% 15%



- Molecule 33: 50S ribosomal protein L15

Chain BL:  83% 15%




- Molecule 34: 50S ribosomal protein L16

Chain BM:  89% 10%



- Molecule 35: 50S ribosomal protein L17

Chain BN:  83% 16%



- Molecule 36: 50S ribosomal protein L18

Chain BO:  91% 9%




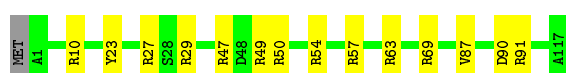
- Molecule 37: 50S ribosomal protein L19

Chain BP:  90% 9%



- Molecule 38: 50S ribosomal protein L20

Chain BQ:  87% 12%



- Molecule 39: 50S ribosomal protein L21

Chain BR:  88% 12%



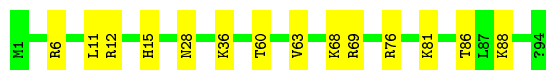
- Molecule 40: 50S ribosomal protein L22

Chain BS: 89% 11%



- Molecule 41: 50S ribosomal protein L23

Chain BT: 85% 15%



- Molecule 42: 50S ribosomal protein L24

Chain BU: 90% 8% ..



- Molecule 43: 50S ribosomal protein L25

Chain BV: 89% 11%



- Molecule 44: 50S ribosomal protein L27

Chain BW: 79% 20% .



- Molecule 45: 50S ribosomal protein L28

Chain BX: 82% 13% . .




- Molecule 46: 50S ribosomal protein L29

Chain BY: 90% 10%




- Molecule 47: 50S ribosomal protein L30

Chain BZ:  86% 8%




- Molecule 48: 50S ribosomal protein L32

Chain B0:  84% 14%




- Molecule 49: 50S ribosomal protein L33

Chain B1:  87% 13%




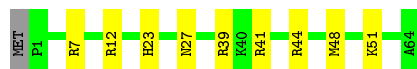
- Molecule 50: 50S ribosomal protein L34

Chain B2:  78% 22%




- Molecule 51: 50S ribosomal protein L35

Chain B3:  85% 14%



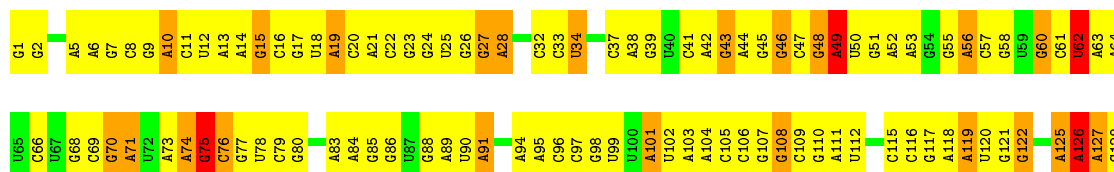
- Molecule 52: 50S ribosomal protein L36

Chain B4:  87% 11%



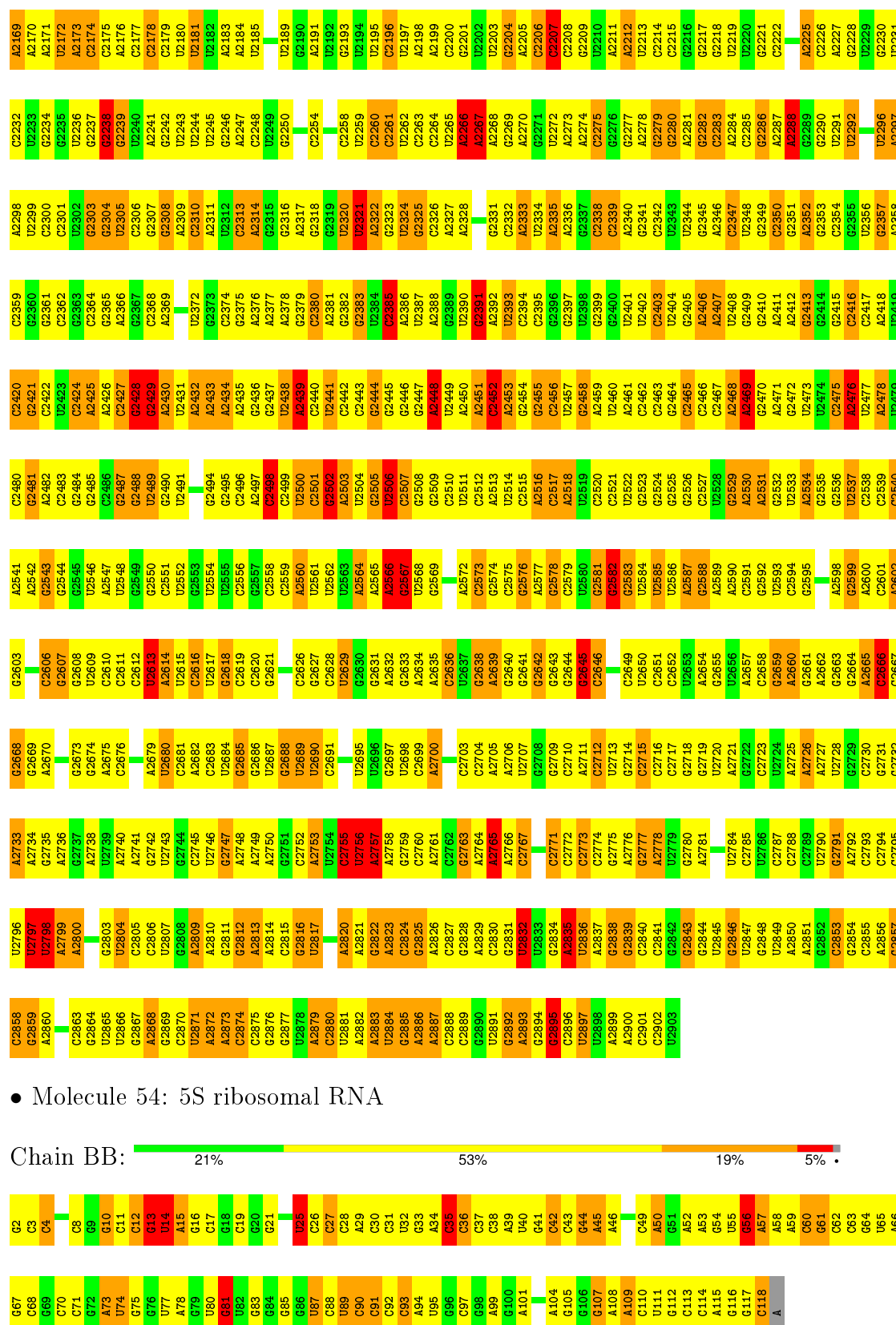
- Molecule 53: 23S ribosomal RNA


Chain BA:  16% 55% 25%



G1114	A1054	C991	U929	G869	G839	U744	U558	G498	U437	G376	C316	G254	G194	C129
G1115	G1055	C992	G930	U870	U810	U744	G859	U499	G438	G377	G317	A255	A195	C130
G1116	G1056	C993	U931	U871	U811	U747	G860	G500	A439	G378	G318	A256	A196	A131
G1117	G1057	G994	U932	U872	G812	G748	G561	A501	G440	G379	G319	C257	A197	G132
G1118	U1058	C995	A933	G873	U813	A749	U562	A502	U441	G380	G320	G258	C198	U133
	G1059	A996	G934	G874	G814	A750	A563	A503	G442	G381	U321		A199	
G1121	U1060	G997	G935	G875	G815	A751	C564	A504	A443	A382	A322	G261	U200	U137
G1122	U1061	C998	A936	C876	C816	A752	U565	A505	C444	A383	A323	A262	C201	U138
G1123	U1062	U999	C937	A877	C817	A753	U566	G506	G445	A384	A324	G263	U202	U139
G1124	G1063	A1000	G938	A878	G818		U567	A507	G446	G385	G325	G264	A203	C140
G1125	C1064	A1001	G939	A879	A819		U568	A508	A447	G386	G326	A265	A204	G141
A1126	U1065	G1002	G940	G880	A820	G757	U569	C509	U448	U387	G327	G266	G205	A142
A1127	U1066	G1003	G941	G881	A821	G758	G570	C510	A449	U388	U328	C267	U206	C143
G1128	A1067	G1004	G942	G882	G822	G759	U571	U511	G450	G389	G329	C268	A207	A144
A1129	G1068	C1005	A943	G883	C823	G760	A572	G512	U451	U390	A330	C269	C208	C145
	A1069	C1006	G944	U884	U824	A761	U573	A513	G452	A391	A331	A270	C209	A146
U1132	A1070	C1007	A945	C885	A825	U762	A574	A514	A453	U392	A332	G271	C210	C147
A1133	G1071	A1008	G946	A886	U826	G763	A575	A515	A454	C393	G333	A272	C211	U148
A1134	C1072	A1009	A947	U887	U827	A764	U576	C516	C455	C394	C334	G273	G212	A149
G1135	A1073	A1010	A948	U888	U828	G765	G577	C517	C456	U395	C335	C274	U150	
G1136	G1074	U1011	G949	C889	U829	U766	U579	U519	G458	U397	G337	U276	G215	C151
G1137	C1075	U1012	G950	G890	G830	U767	U580	U520	U459	U398	G338	G277	A216	A152
G1138	C1076	C1013	C951	G891	G831		U581		C460	U399	U339	A278	A217	A155
A1139	U1077	A1014	A892	C893	U832	G772	C582	U521	C461	G400	A340	A279	A218	A156
C1140	U1078	U1015	C894	C894	G834	G773	A581	A522	C462	G401	A341	U280	A219	C157
U1141	C1079	G1016	U895	G835	G835	G774	U582	C523	C463	A402	A342	C281	G220	U158
A1142	A1080		C957	U836	G836		G585	U525	U464	U403	C343	A282	A221	A159
A1143	U1081	A1020	U958	U837	G837	G775	U586	C531	A472	A404	G344	G283	A222	A160
A1144	U1082	A1021	A959	C838	G838	G776	U587	C532	A473	U405	A345	U284	A223	A161
C1145	U1083	G1022	A960	U839	U839	G777	U588	C533	G474	U406	A346	G285	U224	U162
C1146	A1084	U1023	A961	U840	G840	G778	U589	A529	C475	G407	A347	U286	C225	C163
A1147	A1085	G1024	G962	C841	C841	G779	U590	G530	A476	A415	A348	G287	A226	C164
U1148	A1086	G1025	U963	C901	G842	A781	U591	C531	A477	U416	U349	U288	A227	A165
U1149	G1087	A1026	C964	U843	U843	A782	A592		A478	G417	G350	G289	C228	U166
C1150	A1088	G1027	C965	G844	A844	G783	U593	G533	G479	C418	G351	U290	C229	A167
A1151	A1089	A1028	G966	U845	U845	G784	U594	U534	G474	C419	A352	G291	G230	G168
C1152	A1090	A1029	U967	A846	U846	G785	C595	G535	C475	C414	C353	U293	A231	
C1153	G1091	C1030	C968	U847	U847	G786	U596	G536	A476	A415	A354	A294	G232	A172
C1154	U1092	G1031	G969	U848	C848	G787	U597	G537	A477	U416	U355	G295	A233	A173
A1155	G1093	A1032	C970	C849	U849	A788	U598	A538	A478	C417	G356	U296	U234	U174
A1156	U1094	U1033	G971	A849	U849	A789	U599	G539	A479	C418	C357	G297	U235	G175
G1157	A1095	G1034	A972	U850	U850	G790	G600	C540	A480	U419	U358	G298	C236	A176
C1158	A1096	U1035	A973	C851	C851	G791	C601	A541	G481	C420	G359	A299	C237	G177
U1159	U1097	G1036	G974	U852	U852	A792	A602	C542	A482	C421	U360	A300	C238	G178
A1160	A1098	G1037	A975	C853	C853	A793	A603	G543	A483	A422	G361	G301	C239	C179
C1161	G1099	G1038	G976	G854	C854	A794	G606	C544	C484	A423	A362	C302	C240	G180
G1162	C1100	A1039	G977	G855	G855	C795	U607	U545	C485	G424	G363	G303	A241	A181
G1163	U1101	A1040	G978	G856	G856	C796	U608	U546	C486	G425	G364	U304	G242	A182
C1164	C1102		A979	G857	G857	G797	A609	A547	C487	U426	U365	C305	U243	C183
A1165	A1103	C1043	A980	G858	G858	G798	C609	G548	G488	U427	C366	U306	A244	C184
G1166	U1104	C1044	U981	G859	G859	G799	A609	G549	G489	A428	G367	G307	G245	G185
C1167	U1105	G1045	C982	U860	U860	A800	C610	G549	C490	A429	A368	G308	C246	G186
G1168	A1106	A1046	A983	A861	G861	G801	C611	C550	C491	A430	U369	A309	G247	G187
A1169	G1107	G1047	A984	G862	G862	A802	G612	G551	G491	A431	U370	A310	G248	G188
C1170	U1108	A1048	C985	A863	G863	G803	A613	U552	A492	U432	A371	A311	C249	G189
G1171	C1109	C986	G924	G864	G864	A804	A614	G553	G493	A433	G372	G312	G250	A190
C1172	G1110	A1050	A925	C865	C865	A805	U615	U554	G494	C434	U373	G313	A251	A191
A1173	A1111	G1051	G926	A866	A866	C806	A616	G555	G495	U435	A374	C314	G252	C192
U1174	G1112	C1052	G989	C867	C867	U807	G617	A556	G496	C436	G375	G315	C253	
A1175	U1113	C1053	A990	U868	U868	G808		C557	A497					

C2104	U2041	A1978	C1914	A1854	C1793	G1733	U1671	A1608	G1546	U1484	A1420	G1358	C1298	G1236	U1176
A2108	A2042	U1979	U1915	U1855	A1794	G1734	A1672	A1609	C1547	U1487	G1421	A1359	G1299	A1237	G1177
U2109	C2043	G1980	A1916	U1856	C1795	A1735	G1673	A1610	A1548	U1488	G1422	G1360	G1300	U1240	C1178
G2110	C2044	A1981	U1917	G1857	U1796	U1736	G1674	A1611	A1549	C1488	G1423	G1361	A1301	U1241	U1180
G2111	G2045	U1982	A1918	A1858	G1797	G1737	A1675	A1612	C1550	C1489	G1424	C1362	A1302	U1242	U1181
G2112	G2046	G1983	A1919	U1859	U1798	G1738	A1676	G1613	A1551	C1490	G1425	C1363	A1303	U1243	G1182
G2113	C2047	G1984	C1920	G1860	G1799	A1739	A1677	A1614	A1552	G1491	G1426	G1364	A1304	G1244	U1183
A2114	G2048	G1985	G1921	G1861	C1800	A1740	A1678	A1615	A1553	G1492	A1427	A1365	C1305	A1245	U1184
G2115	A2049	G1986	G1922	G1862	A1801	G1741	A1679	A1616	G1554	C1493	G1428	A1366	C1306	G1246	G1185
G2116	C2050	A1987	U1923	G1863	A1802	G1742	U1680	C1617	G1555	A1494	G1429	A1367	A1307	A1247	G1186
G2117	G2051	G1988	A1924	A1864	A1803	G1743	G1681	A1618	C1556	A1495	A1431	A1308	A1308	U1248	G1187
A2118	A2052	G1989	G1925	G1865	A1804	A1744	G1682	A1619	C1557	A1496	G1430	G1370	G1309	U1249	U1188
G2119	G2053	C1990	U1926	A1866	A1805	A1745	U1683	G1620	C1558	U1497	G1432	A1371	G1310	U1250	U1189
A2120	A2054	U1991	A1927	G1867	C1806	A1746	G1684	U1624	U1559	C1498	A1433	U1372	G1311	C1251	A1189
C2121	C2055	G1992	A1928	G1868	C1807	U1747	C1685	G1625	G1560	C1499	A1434	U1373	G1312	G1252	G1190
G2122	G2056	U1993	G1929	G1869	A1808	G1748	C1686	G1626	C1561	G1500	G1435	A1374	U1313	A1253	G1191
A2123	A2057	C1994	A1930	C1870	A1809	A1749	U1687	A1627	U1562	G1501	U1375	U1375	C1314	A1254	G1192
G2124	G2058	U1995	A1932	A1871	A1810	U1750	G1688	G1628	C1563	A1502	A1439	C1315	C1315	U1255	G1193
G2125	A2059	C1996	G1933	A1872	G1811	U1751	U1689	U1629	C1564	A1503	U1440	G1377	U1316	G1256	A1194
G2126	A2060	C1997	G1934	G1873	U1812	C1752	A1690	G1630	C1565	A1504	G1441	A1378	G1317	C1257	G1195
C2127	C2061	A1998	U1935	G1874	G1813	G1753	A1691	A1631	G1567	U1506	U1443	A1379	U1318	U1258	G1196
U2130	A2062	C1999	A1936	G1875	A1814	A1754	G1692	A1632	C1568	C1507	G1444	G1382	C1320	A1260	U1197
U2131	C2063	C2000	A1937	A1876	A1815	A1755	U1693	A1633	A1569	A1508	G1445	A1383	A1321	A1261	U1199
U2132	C2064	C2001	A1938	G1877	C1816	G1756	G1695	A1634	A1570	A1509	G1446	A1384	A1322	A1262	C1200
G2133	C2065	G2002	U1939	G1878	A1817	U1757	G1696	A1635	A1571	G1510	C1447	A1385	C1323	U1263	U1201
A2134	C2066	A2003	U1940	C1879	U1818	U1758	G1697	A1636	A1572	G1511	G1448	C1386	G1324	A1264	G1202
G2135	U2004	G2004	C1941	U1880	A1819	U1759	A1698	A1637	C1573	G1512	C1451	A1387	U1325	A1265	U1203
G2136	C2069	A2005	C1942	G1881	U1820	C1760	G1699	A1638	C1574	U1513	C1452	G1389	A1327	G1267	A1205
U2137	A2070	C2006	U1943	U1882	C1821	A1762	A1700	C1639	C1575	G1514	A1453	A1390	A1328	A1268	G1206
G2138	A2071	C2007	U1944	U1883	C1822	G1763	G1702	A1640	U1576	U1515	C1454	U1391	A1329	A1269	C1207
U2139	C2072	C2008	G1945	A1884	G1823	C1764	G1703	A1641	C1577	U1518	G1455	A1392	C1330	C1270	U1208
G2140	C2073	A2009	U1946	A1885	G1824	U1765	C1704	A1642	U1578	G1456	G1456	A1393	G1331	A1271	U1209
G2141	U2081	A2013	U1951	C1886	U1825	U1766	A1705	G1643	A1579	U1520	G1457	U1394	G1332	A1272	G1210
A2142	A2077	A2014	A1952	G1887	U1826	G1767	C1706	A1644	A1580	G1521	U1458	A1395	G1333	U1273	G1211
G2143	C2078	A2015	A1953	U1888	G1827	C1768	G1707	G1645	G1581	G1522	G1459	U1396	G1334	A1274	G1212
C2145	U2079	A2016	G1954	A1890	A1828	U1769	C1708	C1646	C1582	U1523	U1460	U1397	C1335	A1275	A1213
C2146	A2080	U2016	G1954	A1891	C1830	G1770	U1709	U1647	A1583	G1524	C1461	C1398	A1336	A1276	A1214
U2081	U2081	A2019	U1955	C1892	G1831	C1771	G1710	G1648	U1584	A1525	C1462	C1399	G1337	G1277	G1215
G2148	A2082	A2020	U1956	C1893	C1832	A1772	A1711	A1650	U1586	G1527	U1463	U1400	G1338	C1278	G1216
U2149	G2083	C2021	C1957	C1894	C1833	A1773	U1712	G1651	U1590	A1528	U1466	G1401	G1339	G1279	U1217
C2150	C2084	U2022	C1958	C1895	U1834	C1774	A1713	A1652	A1591	A1529	U1467	A1403	U1340	G1280	G1218
U2151	U2085	C2023	G1959	G1896	G1835	U1775	U1714	G1653	C1592	G1530	U1468	C1404	A1342	U1281	U1219
G2152	U2086	G2024	A1960	G1897	C1836	G1776	G1715	A1654	A1591	U1531	U1469	U1405	G1343	U1282	G1220
C2153	G2087	C2025	C1961	U1898	C1837	U1777	U1716	A1655	A1593	A1532	A1470	U1406	G1344	A1284	U1221
A2154	A2088	U2026	C1962	A1899	G1838	U1778	A1717	C1656	C1594	U1533	G1471	U1407	U1345	A1285	G1222
U2155	C2089	G2027	U1963	G1839	G1839	U1779	G1718	U1657	C1596	G1472	G1472	G1408	G1346	A1286	G1223
G2156	A2090	U2028	G1964	A1901	G1840	A1780	C1718	U1658	A1596	U1534	G1473	U1409	G1347	A1287	U1224
G2157	C2091	G2029	C1965	C1902	U1841	U1781	A1722	G1659	A1597	A1535	U1474	U1410	C1348	G1288	G1225
A2158	U2092	A2030	A1966	G1903	G1842	U1782	G1723	G1660	A1598	C1536	U1475	U1411	C1349	A1289	A1226
G2159	G2093	A2031	G1967	G1904	C1843	A1783	G1724	G1661	U1599	G1537	G1475	U1412	C1349	G1227	G1227
C2160	A2094	G2032	G1968	C1905	C1844	U1784	U1725	A1664	C1600	U1538	U1476	A1413	C1350	G1228	G1228
C2161	A2095	A2033	G1969	G1845	G1846	A1785	C1726	A1665	G1601	U1539	A1477	A1414	C1351	C1291	G1229
G2162	C2096	U2034	A1970	G1907	G1846	U1786	C1727	A1666	U1602	G1540	G1478	C1414	U1352	G1292	C1230
A2163	A2097	G2035	A1971	A1847	A1847	A1787	C1728	A1667	A1603	C1541	G1479	U1415	A1353	G1293	U1231
C2164	U2098	C2036	G1972	G1908	G1848	C1788	U1729	G1667	C1604	U1542	C1480	G1416	A1354	U1294	G1232
C2165	A2037	G1973	G1973	G1910	G1849	A1789	U1730	A1668	C1605	U1543	U1481	G1417	G1355	G1295	G1233
U2166	G2038	U1911	U1911	A1912	U1852	C1790	G1731	A1669	C1606	A1544	G1482	G1418	G1356	U1234	U1234
U2167	C2039	A1912	U1912	A1912	U1852	A1791	C1732	A1669	C1606	A1544	G1482	G1418	G1356	U1234	U1234
G2168	C2103	A1913	A1913	A1913	A1853	G1792	C1732	C1670	C1607	A1545	G1483	A1419	C1357	C1297	G1235



Chain B5:  89% 6% 5%

MET	A2	R7	E40	D51	A52	R53	R60	G91	M97	M109	R122	Q126	R134	N148	R162	Y163	R164	V207	V224	ASP	GLN	ALA	GLY	LEU	SER	ALA	SER	VAL	ASN
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4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	26429	Depositor
Resolution determination method	FSC at 0.5 cut-off	Depositor
CTF correction method	local	Depositor
Microscope	FEI/PHILIPS CM200FEG	Depositor
Voltage (kV)	160	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	161000	Depositor
Image detector	4k CCD camera (TVIPS)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, FME, ACE, CM0, 6MZ, NH2, 4SU, 7MG, PSU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 2$	RMSZ	$\# Z > 2$
1	AB	0.69	0/1736	1.15	8/2340 (0.3%)
10	AK	0.76	0/894	1.26	9/1207 (0.7%)
11	AL	0.77	0/969	1.37	17/1300 (1.3%)
12	AM	0.79	0/884	1.35	11/1181 (0.9%)
13	AN	0.82	0/817	1.41	11/1088 (1.0%)
14	AO	0.72	0/722	1.29	13/964 (1.3%)
15	AP	0.84	0/648	1.28	7/870 (0.8%)
16	AQ	0.73	0/658	1.19	5/883 (0.6%)
17	AR	0.80	0/463	1.21	5/623 (0.8%)
18	AS	0.76	0/653	1.27	4/879 (0.5%)
19	AT	0.71	0/672	1.12	5/890 (0.6%)
2	AC	0.77	0/1651	1.28	18/2225 (0.8%)
20	AU	0.85	0/431	1.31	6/572 (1.0%)
21	AA	1.75	365/36759 (1.0%)	2.28	2447/57346 (4.3%)
22	A1	1.75	20/1668 (1.2%)	2.26	110/2595 (4.2%)
23	A2	1.66	1/343 (0.3%)	2.18	17/531 (3.2%)
24	BC	0.81	0/2121	1.35	26/2852 (0.9%)
25	BD	0.71	0/1586	1.18	9/2134 (0.4%)
26	BE	0.72	0/1571	1.19	11/2113 (0.5%)
27	BF	0.77	0/1444	1.26	16/1937 (0.8%)
28	BG	0.71	0/1343	1.18	10/1816 (0.6%)
29	BH	0.68	0/1122	1.16	7/1515 (0.5%)
3	AD	0.80	0/1665	1.26	20/2227 (0.9%)
30	BI	0.68	0/1046	1.07	5/1410 (0.4%)
31	BJ	0.75	0/1152	1.23	9/1551 (0.6%)
32	BK	0.76	0/947	1.23	10/1268 (0.8%)
33	BL	0.79	0/1054	1.29	12/1403 (0.9%)
34	BM	0.80	0/1093	1.22	10/1460 (0.7%)
35	BN	0.83	0/973	1.44	18/1301 (1.4%)
36	BO	0.77	0/902	1.29	9/1209 (0.7%)
37	BP	0.78	0/929	1.25	9/1242 (0.7%)
38	BQ	0.81	0/960	1.36	14/1278 (1.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	BR	0.72	0/829	1.13	6/1107 (0.5%)
4	AE	0.72	0/1119	1.20	11/1506 (0.7%)
40	BS	0.70	0/864	1.28	10/1156 (0.9%)
41	BT	0.72	0/744	1.22	4/994 (0.4%)
42	BU	0.72	0/787	1.15	5/1051 (0.5%)
43	BV	0.74	0/766	1.27	8/1025 (0.8%)
44	BW	0.78	0/604	1.24	6/799 (0.8%)
45	BX	0.84	0/635	1.35	10/848 (1.2%)
46	BY	0.71	0/510	1.24	4/677 (0.6%)
47	BZ	0.73	0/453	1.31	6/605 (1.0%)
48	B0	0.80	0/450	1.26	8/599 (1.3%)
49	B1	0.73	0/417	1.14	3/556 (0.5%)
5	AF	0.76	0/835	1.23	7/1128 (0.6%)
50	B2	0.89	0/380	1.58	10/498 (2.0%)
51	B3	0.79	0/513	1.23	6/676 (0.9%)
52	B4	0.80	0/303	1.35	6/397 (1.5%)
53	BA	1.77	819/69796 (1.2%)	2.30	4869/108888 (4.5%)
54	BB	1.74	17/2800 (0.6%)	2.24	176/4367 (4.0%)
55	B5	0.69	0/1673	1.11	8/2255 (0.4%)
6	AG	0.76	0/1188	1.28	12/1593 (0.8%)
7	AH	0.71	0/989	1.11	5/1326 (0.4%)
8	AI	0.83	0/1035	1.37	14/1377 (1.0%)
9	AJ	0.78	0/797	1.33	11/1079 (1.0%)
All	All	1.54	1222/158363 (0.8%)	2.07	8093/236717 (3.4%)

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
18	AS	0	1
21	AA	0	328
22	A1	0	18
23	A2	0	2
53	BA	0	652
54	BB	0	27
All	All	0	1028

The worst 5 of 1222 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	BA	2078	C	C4-N4	-7.15	1.27	1.33
21	AA	1521	C	C4-N4	-7.01	1.27	1.33
53	BA	897	C	C4-N4	-6.68	1.27	1.33
21	AA	1214	C	C4-N4	-6.67	1.27	1.33
21	AA	637	C	C4-N4	-6.64	1.27	1.33

The worst 5 of 8093 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	BA	323	C	O4'-C1'-N1	14.98	120.18	108.20
53	BA	1932	A	N1-C6-N6	-13.12	110.73	118.60
53	BA	800	A	N1-C6-N6	-12.78	110.93	118.60
21	AA	1502	A	N1-C6-N6	-12.44	111.14	118.60
53	BA	219	A	N1-C6-N6	-12.42	111.15	118.60

There are no chirality outliers.

5 of 1028 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	AA	21	G	Sidechain
21	AA	35	G	Sidechain
21	AA	36	C	Sidechain
21	AA	6	G	Sidechain
18	AS	74	ALA	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AB	1708	0	1736	1	0
2	AC	1625	0	1699	2	0
3	AD	1643	0	1710	0	0
4	AE	1109	0	1152	0	0
5	AF	818	0	808	0	0
6	AG	1178	0	1234	0	0
7	AH	979	0	1034	0	0
8	AI	1025	0	1074	0	0
9	AJ	790	0	832	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	AK	880	0	891	0	0
11	AL	955	0	1019	0	0
12	AM	877	0	937	0	0
13	AN	805	0	844	0	0
14	AO	714	0	737	0	0
15	AP	639	0	656	0	0
16	AQ	652	0	695	1	0
17	AR	459	0	482	0	0
18	AS	641	0	669	0	0
19	AT	668	0	718	0	0
20	AU	429	0	453	0	0
21	AA	32828	0	16108	7	0
22	A1	1627	0	808	0	0
23	A2	309	0	158	0	0
24	BC	2083	0	2157	0	0
25	BD	1565	0	1616	0	0
26	BE	1552	0	1619	0	0
27	BF	1420	0	1460	1	0
28	BG	1323	0	1374	0	0
29	BH	1111	0	1148	0	0
30	BI	1032	0	1088	0	0
31	BJ	1129	0	1162	1	0
32	BK	939	0	1012	1	0
33	BL	1045	0	1117	2	0
34	BM	1074	0	1157	1	0
35	BN	961	0	1000	0	0
36	BO	892	0	923	0	0
37	BP	917	0	965	0	0
38	BQ	947	0	1022	0	0
39	BR	816	0	839	1	0
40	BS	857	0	922	0	0
41	BT	739	0	807	0	0
42	BU	780	0	834	0	0
43	BV	753	0	780	0	0
44	BW	599	0	614	0	0
45	BX	625	0	655	0	0
46	BY	509	0	543	0	0
47	BZ	449	0	491	1	0
48	B0	444	0	461	0	0
49	B1	413	0	444	1	0
50	B2	377	0	418	0	0
51	B3	504	0	574	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	B4	302	0	343	0	0
53	BA	62317	0	30428	10	0
54	BB	2504	0	1247	0	0
55	B5	1658	0	1751	0	0
56	A1	7	0	8	0	0
57	BA	10	0	10	1	0
All	All	146011	0	97443	27	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 0.

The worst 5 of 27 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)
53:BA:2644:G:H2'	53:BA:2645:G:C8	2.46	0.51
53:BA:1287:A:H2'	53:BA:1288:G:C2	2.47	0.50
49:B1:9:LYS:HE3	49:B1:19:PHE:CD2	2.49	0.48
21:AA:292:G:C5	21:AA:293:G:H1'	2.48	0.47
33:BL:54:GLN:HE21	53:BA:2428:G:N2	2.11	0.47

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	AB	218/220 (99%)	193 (88%)	24 (11%)	1 (0%)	34 77
2	AC	205/208 (99%)	186 (91%)	11 (5%)	8 (4%)	4 36
3	AD	203/206 (98%)	192 (95%)	9 (4%)	2 (1%)	19 65
4	AE	150/152 (99%)	141 (94%)	5 (3%)	4 (3%)	6 45
5	AF	99/101 (98%)	87 (88%)	11 (11%)	1 (1%)	19 65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AG	150/152 (99%)	138 (92%)	8 (5%)	4 (3%)	6	45
7	AH	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	24	69
8	AI	126/128 (98%)	115 (91%)	9 (7%)	2 (2%)	12	56
9	AJ	98/100 (98%)	87 (89%)	8 (8%)	3 (3%)	5	42
10	AK	116/118 (98%)	108 (93%)	6 (5%)	2 (2%)	11	55
11	AL	121/124 (98%)	111 (92%)	6 (5%)	4 (3%)	5	40
12	AM	112/115 (97%)	94 (84%)	15 (13%)	3 (3%)	6	45
13	AN	98/101 (97%)	89 (91%)	7 (7%)	2 (2%)	9	51
14	AO	86/89 (97%)	78 (91%)	8 (9%)	0	100	100
15	AP	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
16	AQ	80/82 (98%)	73 (91%)	6 (8%)	1 (1%)	15	60
17	AR	55/57 (96%)	51 (93%)	2 (4%)	2 (4%)	4	38
18	AS	79/81 (98%)	73 (92%)	3 (4%)	3 (4%)	4	37
19	AT	84/86 (98%)	74 (88%)	7 (8%)	3 (4%)	4	38
20	AU	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
24	BC	270/273 (99%)	245 (91%)	17 (6%)	8 (3%)	5	42
25	BD	207/209 (99%)	174 (84%)	21 (10%)	12 (6%)	2	27
26	BE	199/201 (99%)	182 (92%)	13 (6%)	4 (2%)	9	51
27	BF	176/179 (98%)	143 (81%)	26 (15%)	7 (4%)	4	35
28	BG	174/177 (98%)	152 (87%)	18 (10%)	4 (2%)	8	48
29	BH	147/149 (99%)	131 (89%)	15 (10%)	1 (1%)	26	71
30	BI	139/142 (98%)	128 (92%)	11 (8%)	0	100	100
31	BJ	140/142 (99%)	129 (92%)	6 (4%)	5 (4%)	4	38
32	BK	121/123 (98%)	105 (87%)	11 (9%)	5 (4%)	3	35
33	BL	141/144 (98%)	117 (83%)	14 (10%)	10 (7%)	1	22
34	BM	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	13	57
35	BN	119/121 (98%)	103 (87%)	13 (11%)	3 (2%)	7	46
36	BO	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
37	BP	112/115 (97%)	99 (88%)	10 (9%)	3 (3%)	6	45
38	BQ	115/118 (98%)	108 (94%)	5 (4%)	2 (2%)	11	55
39	BR	101/103 (98%)	91 (90%)	8 (8%)	2 (2%)	9	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	BS	108/110 (98%)	97 (90%)	10 (9%)	1 (1%)	21	67
41	BT	92/94 (98%)	73 (79%)	11 (12%)	8 (9%)	1	17
42	BU	101/104 (97%)	86 (85%)	10 (10%)	5 (5%)	3	31
43	BV	92/94 (98%)	82 (89%)	8 (9%)	2 (2%)	8	49
44	BW	78/80 (98%)	62 (80%)	8 (10%)	8 (10%)	1	12
45	BX	75/79 (95%)	64 (85%)	8 (11%)	3 (4%)	4	35
46	BY	61/63 (97%)	55 (90%)	4 (7%)	2 (3%)	5	40
47	BZ	56/59 (95%)	50 (89%)	5 (9%)	1 (2%)	11	53
48	B0	54/57 (95%)	50 (93%)	3 (6%)	1 (2%)	10	52
49	B1	50/52 (96%)	45 (90%)	4 (8%)	1 (2%)	9	51
50	B2	44/46 (96%)	41 (93%)	2 (4%)	1 (2%)	8	48
51	B3	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
52	B4	36/38 (95%)	32 (89%)	2 (6%)	2 (6%)	2	28
55	B5	221/234 (94%)	211 (96%)	8 (4%)	2 (1%)	21	67
All	All	5876/6008 (98%)	5278 (90%)	447 (8%)	151 (3%)	11	45

5 of 151 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AE	105	ILE
24	BC	206	LYS
25	BD	9	VAL
25	BD	150	GLN
25	BD	188	LEU

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	AB	180/180 (100%)	177 (98%)	3 (2%)	68	87
2	AC	170/171 (99%)	169 (99%)	1 (1%)	90	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AD	172/173 (99%)	171 (99%)	1 (1%)	90	95
4	AE	113/113 (100%)	112 (99%)	1 (1%)	84	93
5	AF	87/87 (100%)	85 (98%)	2 (2%)	58	83
6	AG	123/123 (100%)	122 (99%)	1 (1%)	86	94
7	AH	104/105 (99%)	103 (99%)	1 (1%)	82	92
8	AI	105/105 (100%)	102 (97%)	3 (3%)	50	78
9	AJ	86/86 (100%)	84 (98%)	2 (2%)	58	83
10	AK	90/90 (100%)	88 (98%)	2 (2%)	60	83
11	AL	103/104 (99%)	101 (98%)	2 (2%)	65	86
12	AM	91/92 (99%)	91 (100%)	0	100	100
13	AN	83/84 (99%)	80 (96%)	3 (4%)	42	74
14	AO	76/77 (99%)	74 (97%)	2 (3%)	54	80
15	AP	65/65 (100%)	64 (98%)	1 (2%)	72	88
16	AQ	74/74 (100%)	73 (99%)	1 (1%)	74	89
17	AR	48/48 (100%)	47 (98%)	1 (2%)	61	84
18	AS	70/70 (100%)	67 (96%)	3 (4%)	35	70
19	AT	65/65 (100%)	64 (98%)	1 (2%)	72	88
20	AU	44/44 (100%)	43 (98%)	1 (2%)	58	83
24	BC	216/217 (100%)	214 (99%)	2 (1%)	84	93
25	BD	164/164 (100%)	162 (99%)	2 (1%)	78	90
26	BE	165/165 (100%)	161 (98%)	4 (2%)	57	82
27	BF	149/150 (99%)	144 (97%)	5 (3%)	44	75
28	BG	137/138 (99%)	134 (98%)	3 (2%)	60	83
29	BH	114/114 (100%)	113 (99%)	1 (1%)	84	93
30	BI	109/110 (99%)	108 (99%)	1 (1%)	84	93
31	BJ	116/116 (100%)	115 (99%)	1 (1%)	84	93
32	BK	103/103 (100%)	98 (95%)	5 (5%)	31	67
33	BL	102/103 (99%)	100 (98%)	2 (2%)	63	85
34	BM	109/109 (100%)	106 (97%)	3 (3%)	51	78
35	BN	100/100 (100%)	98 (98%)	2 (2%)	63	85
36	BO	86/87 (99%)	85 (99%)	1 (1%)	78	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	BP	99/100 (99%)	98 (99%)	1 (1%)	82	92
38	BQ	89/90 (99%)	89 (100%)	0	100	100
39	BR	84/84 (100%)	82 (98%)	2 (2%)	57	82
40	BS	93/93 (100%)	91 (98%)	2 (2%)	60	83
41	BT	80/80 (100%)	78 (98%)	2 (2%)	55	81
42	BU	83/84 (99%)	83 (100%)	0	100	100
43	BV	78/78 (100%)	76 (97%)	2 (3%)	54	80
44	BW	59/59 (100%)	55 (93%)	4 (7%)	20	57
45	BX	67/68 (98%)	65 (97%)	2 (3%)	48	77
46	BY	55/55 (100%)	55 (100%)	0	100	100
47	BZ	48/49 (98%)	45 (94%)	3 (6%)	22	59
48	B0	47/48 (98%)	46 (98%)	1 (2%)	61	84
49	B1	45/45 (100%)	44 (98%)	1 (2%)	60	83
50	B2	38/38 (100%)	37 (97%)	1 (3%)	54	80
51	B3	51/52 (98%)	48 (94%)	3 (6%)	24	61
52	B4	34/34 (100%)	34 (100%)	0	100	100
55	B5	173/181 (96%)	167 (96%)	6 (4%)	43	74
All	All	4842/4870 (99%)	4748 (98%)	94 (2%)	67	86

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	BF	113	PHE
32	BK	29	HIS
51	B3	27	ASN
27	BF	122	ASP
28	BG	163	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
52	B4	37	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	AA	1530/1533 (99%)	195 (12%)	46 (3%)
22	A1	73/76 (96%)	7 (9%)	2 (2%)
23	A2	14/15 (93%)	4 (28%)	2 (14%)
53	BA	2902/2903 (99%)	455 (15%)	123 (4%)
54	BB	116/118 (98%)	19 (16%)	2 (1%)
All	All	4635/4645 (99%)	680 (14%)	175 (3%)

5 of 680 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	AA	6	G
21	AA	8	A
21	AA	9	G
21	AA	16	A
21	AA	32	A

5 of 175 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	BA	643	A
53	BA	962	G
53	BA	2581	G
53	BA	686	U
53	BA	811	U

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
22	CM0	A1	34	22,23	15,26,27	1.84	2 (13%)	18,37,40	3.22	2 (11%)
22	6MZ	A1	37	22	17,25,26	1.01	2 (11%)	15,36,39	1.30	1 (6%)
22	7MG	A1	46	22	20,26,27	2.40	3 (15%)	23,39,42	2.01	2 (8%)
22	5MU	A1	54	22	13,22,23	1.11	1 (7%)	16,32,35	4.62	3 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	PSU	A1	55	22	15,21,22	1.19	2 (13%)	16,30,33	3.26	3 (18%)
22	4SU	A1	7	22	12,21,22	1.07	1 (8%)	15,30,33	1.96	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	CM0	A1	34	22,23	-	0/6/30/31	0/2/2/2
22	6MZ	A1	37	22	-	0/5/27/28	0/3/3/3
22	7MG	A1	46	22	-	0/7/37/38	0/3/3/3
22	5MU	A1	54	22	-	0/3/25/26	0/2/2/2
22	PSU	A1	55	22	-	0/7/25/26	0/2/2/2
22	4SU	A1	7	22	-	0/3/25/26	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A1	46	7MG	C8-N9	-9.61	1.31	1.45
22	A1	34	CM0	O5-C5	-5.80	1.25	1.37
22	A1	46	7MG	C8-N7	-2.76	1.30	1.43
22	A1	37	6MZ	C8-N7	-2.30	1.30	1.34
22	A1	55	PSU	C2'-C1'	-2.21	1.51	1.53

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A1	54	5MU	C5-C4-N3	-12.80	114.61	125.35
22	A1	7	4SU	C5-C4-N3	-7.17	115.95	123.56
22	A1	46	7MG	C5-C6-N1	-6.63	113.52	123.39
22	A1	55	PSU	C5-C6-N1	-2.85	120.41	124.38
22	A1	34	CM0	O5-C7-C8	2.10	112.36	108.01

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
56	VAL	A1	101	57,22	5,6,7	0.49	0	5,7,9	1.81	1 (20%)
57	FME	BA	3001	56	8,9,10	0.61	0	5,9,11	1.27	1 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	VAL	A1	101	57,22	-	0/4/6/8	0/0/0/0
57	FME	BA	3001	56	-	1/6/9/11	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	A1	101	VAL	O-C-CA	-3.71	115.55	125.69
57	BA	3001	FME	O-C-CA	-2.11	119.92	125.69

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	BA	3001	FME	O1-CN-N-CA

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	BA	3001	FME	1	0

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.