wwPDB EM Validation Summary Report ⓘ

Apr 16, 2024 – 02:56 am BST

PDB ID	:	7NWW
EMDB ID	:	EMD-12636
Title	:	CspA-27 cotranslational folding intermediate 1
Authors	:	Agirrezabala, X.; Samatova, E.; Macher, M.; Liutkute, M.; Gil-Carton, D.; Novacek, J.; Valle, M.; Rodnina, M.V.
Deposited on	:	2021-03-17
Resolution	:	3.05 Å(reported)
Based on initial model	:	6ORE

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

EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.05 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 145149 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 RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2903	62336	27816	11470	20147	2903	0	0

- Molecule 2 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	1534	32929	14693	6041	10661	1534	0	0

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	3	120	2569	1144	468	837	120	0	0

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	4	6	126	56	20	44	6	0	0

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	C	271	2082	1288	423	364	7	0	0

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	F	177	1410	899	249	256	6	0	0

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	G	175	1313	826	241	244	2	0	0

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	J	123	946	593	181	166	6	0	0

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	K	144	1053	654	207	190	2	0	0

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	M	119	951	588	195	163	5	0	0

- Molecule 16 is a protein called 50S ribosomal protein L18.

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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	T	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	80	Total	C	N	O	S	0	0
			601	370	121	109	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

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

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	b	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	g	208	1636	1036	307	290	3	0	0

- Molecule 36 is a protein called 30S ribosomal protein S4.

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

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	i	156	1152	717	217	212	6	0	0

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	j	104	848	536	153	152	7	0	0

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	k	151	1181	735	227	215	4	0	0

- Molecule 40 is a protein called 30S ribosomal protein S8.

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

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	m	127	1022	634	206	179	3	0	0

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 46 is a protein called 30S ribosomal protein S14.

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

- Molecule 47 is a protein called 30S ribosomal protein S15.

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

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	t	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	u	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	v	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	x	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	y	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 54 is a RNA chain called tRNA-Ser.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	z	88	Total	C	N	O	P	0	0
			1891	841	341	621	88		

- Molecule 55 is a protein called 7.4 kDa cold shock protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B	27	Total	C	N	O	S	0	0
			205	132	32	39	2		

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
56	1	278	Total Mg 278 278	0
56	2	119	Total Mg 119 119	0
56	3	8	Total Mg 8 8	0
56	C	1	Total Mg 1 1	0
56	D	1	Total Mg 1 1	0
56	P	1	Total Mg 1 1	0
56	a	1	Total Mg 1 1	0
56	h	1	Total Mg 1 1	0
56	q	1	Total Mg 1 1	0
56	z	2	Total Mg 2 2	0

- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
57	Z	1	Total Zn 1 1	0
57	e	1	Total Zn 1 1	0

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	35573	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	2.2	Depositor
Minimum defocus (nm)	0.5	Depositor
Maximum defocus (nm)	2.2	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor

4 Model quality ⓘ

4.1 Standard geometry ⓘ

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts ⓘ

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles ⓘ

4.3.1 Protein backbone ⓘ

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains ⓘ

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA ⓘ

MolProbity failed to run properly - this section is therefore empty.

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

37 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	$\#\|Z\|>2$
2	2MG	2	1516	2	18,26,27	2.30	7 (38%)	16,38,41	1.35	4 (25%)
2	UR3	2	1498	2	19,22,23	2.58	6 (31%)	26,32,35	1.08	1 (3%)
54	OMG	z	17	54	22,27,27	3.58	7 (31%)	26,41,41	11.78	12 (46%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
1	6MZ	1	1618	1	18,25,26	1.76	4 (22%)	16,36,39	3.61	3 (18%)
1	PSU	1	2504	1	18,21,22	1.03	2 (11%)	22,30,33	1.81	4 (18%)
1	6MZ	1	2030	1	18,25,26	1.78	3 (16%)	16,36,39	3.51	4 (25%)
1	5MU	1	747	1	19,22,23	4.60	7 (36%)	28,32,35	3.68	9 (32%)
2	4OC	2	1402	2	20,23,24	2.91	8 (40%)	26,32,35	0.91	0
2	MA6	2	1519	2	18,26,27	1.18	1 (5%)	19,38,41	3.64	2 (10%)
1	3TD	1	1915	1	18,22,23	4.06	7 (38%)	22,32,35	1.56	2 (9%)
1	PSU	1	2605	1	18,21,22	0.98	2 (11%)	22,30,33	1.92	4 (18%)
2	PSU	2	516	2,56	18,21,22	0.94	2 (11%)	22,30,33	1.86	5 (22%)
1	PSU	1	2457	1	18,21,22	1.00	2 (11%)	22,30,33	2.02	5 (22%)
2	2MG	2	966	2	18,26,27	2.38	7 (38%)	16,38,41	1.41	4 (25%)
55	FME	B	1	55	8,9,10	0.96	0	7,9,11	0.69	0
2	2MG	2	1207	2	18,26,27	2.35	7 (38%)	16,38,41	1.24	3 (18%)
1	1MG	1	745	1	18,26,27	2.75	5 (27%)	19,39,42	1.25	2 (10%)
1	OMC	1	2498	1,56	19,22,23	2.68	7 (36%)	26,31,34	0.83	0
44	0TD	p	89	44	7,9,10	1.43	1 (14%)	6,11,13	1.86	2 (33%)
2	G7M	2	527	2	20,26,27	2.30	7 (35%)	17,39,42	1.02	1 (5%)
1	5MC	1	1962	1	18,22,23	3.31	7 (38%)	26,32,35	1.07	2 (7%)
1	2MA	1	2503	1,56	17,25,26	2.28	5 (29%)	17,37,40	1.36	3 (17%)
1	OMU	1	2552	1	19,22,23	2.86	8 (42%)	26,31,34	1.63	4 (15%)
1	PSU	1	955	1,56	18,21,22	1.00	1 (5%)	22,30,33	1.97	4 (18%)
2	MA6	2	1518	2	18,26,27	1.16	2 (11%)	19,38,41	3.44	2 (10%)
2	5MC	2	1407	2	18,22,23	3.25	7 (38%)	26,32,35	1.07	1 (3%)
1	5MU	1	1939	1,56	19,22,23	4.58	7 (36%)	28,32,35	3.66	9 (32%)
1	PSU	1	1911	1	18,21,22	0.99	1 (5%)	22,30,33	1.89	4 (18%)
54	5MU	z	66	54	19,22,23	4.72	7 (36%)	28,32,35	3.94	9 (32%)
1	OMG	1	2251	54,1	18,26,27	2.23	7 (38%)	19,38,41	1.38	4 (21%)
1	PSU	1	746	1,56	18,21,22	1.00	1 (5%)	22,30,33	1.70	3 (13%)
1	PSU	1	1917	1	18,21,22	1.02	2 (11%)	22,30,33	1.99	5 (22%)
2	5MC	2	967	2	18,22,23	3.41	7 (38%)	26,32,35	0.98	2 (7%)
1	G7M	1	2069	1	20,26,27	2.19	9 (45%)	17,39,42	1.28	2 (11%)
1	PSU	1	2580	1	18,21,22	1.02	1 (5%)	22,30,33	2.02	6 (27%)
1	2MG	1	1835	1	18,26,27	2.25	7 (38%)	16,38,41	1.27	3 (18%)
1	2MG	1	2445	1	18,26,27	2.21	7 (38%)	16,38,41	1.28	4 (25%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2MG	2	1516	2	-	0/5/27/28	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
54	OMG	z	17	54	-	4/8/28/28	0/3/3/3
1	6MZ	1	1618	1	-	4/5/27/28	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	4/5/27/28	0/3/3/3
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	MA6	2	1519	2	-	2/7/29/30	0/3/3/3
1	3TD	1	1915	1	-	2/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
2	PSU	2	516	2,56	-	2/7/25/26	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
2	2MG	2	966	2	-	2/5/27/28	0/3/3/3
55	FME	B	1	55	-	5/7/9/11	-
2	2MG	2	1207	2	-	0/5/27/28	0/3/3/3
1	1MG	1	745	1	-	0/3/25/26	0/3/3/3
1	OMC	1	2498	1,56	-	0/9/27/28	0/2/2/2
44	0TD	p	89	44	-	2/7/12/14	-
2	G7M	2	527	2	-	3/3/25/26	0/3/3/3
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
1	2MA	1	2503	1,56	-	2/3/25/26	0/3/3/3
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
1	PSU	1	955	1,56	-	0/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/7/29/30	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	5MU	1	1939	1,56	-	0/7/25/26	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
54	5MU	z	66	54	-	4/7/25/26	0/2/2/2
1	OMG	1	2251	54,1	-	0/5/27/28	0/3/3/3
1	PSU	1	746	1,56	-	1/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	1/3/25/26	0/3/3/3
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	2MG	1	1835	1	-	2/5/27/28	0/3/3/3
1	2MG	1	2445	1	-	2/5/27/28	0/3/3/3

The worst 5 of 178 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	11.81	1.49	1.35
54	z	66	5MU	C6-N1	10.76	1.56	1.38
1	1	747	5MU	C2-N1	10.70	1.55	1.38
1	1	1939	5MU	C2-N1	10.26	1.54	1.38
1	1	1939	5MU	C6-N1	9.96	1.55	1.38

The worst 5 of 134 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
54	z	17	OMG	O6-C6-N1	-48.97	62.83	120.65
54	z	17	OMG	O6-C6-C5	-31.10	63.64	124.37
2	2	1519	MA6	N1-C6-N6	-14.62	101.67	117.06
2	2	1518	MA6	N1-C6-N6	-13.81	102.53	117.06
1	1	747	5MU	C5-C4-N3	12.34	125.85	115.31

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	527	G7M	C3'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'
55	B	1	FME	O1-CN-N-CA

There are no ring outliers.

No monomer is involved in short contacts.

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry ⓘ

Of 415 ligands modelled in this entry, 415 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers ⓘ

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

5 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-12636. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections ⓘ

This section was not generated.

5.2 Central slices ⓘ

This section was not generated.

5.3 Largest variance slices ⓘ

This section was not generated.

5.4 Orthogonal standard-deviation projections (False-color) ⓘ

This section was not generated.

5.5 Orthogonal surface views ⓘ

This section was not generated.

5.6 Mask visualisation ⓘ

This section was not generated. No masks/segmentation were deposited.

6 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

6.1 Map-value distribution ⓘ

This section was not generated.

6.2 Volume estimate versus contour level ⓘ

This section was not generated.

6.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

7 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

8 Map-model fit (i)

This section was not generated.