

wwPDB EM Validation Summary Report (i)

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PDB ID	:	6ZMW
EMDB ID	:	EMD-11302
Title	:	Structure of a human 48S translational initiation complex
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Deposited on	:	2020-07-04
Resolution	:	3.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org* A user guide is available at https://www.wwpdb.org/validation/2017/EMValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

EMDB validation analysis	:	0.0.1. dev 92
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 (i)

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

The reported resolution of this entry is 3.70 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 (i)

There are 59 unique types of molecules in this entry. The entry contains 118155 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 Eukaryotic translation initiation factor 3 subunit I.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
1	2	304	Total 1493	C 885	N 304	O 304	0	0

• Molecule 2 is a protein called Eukaryotic translation initiation factor 3 subunit B.

Mol	Chain	Residues		At	oms			AltConf	Trace
2	1	588	Total 3258	C 1986	N 633	O 634	${f S}{5}$	0	0

• Molecule 3 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues		At	oms			AltConf	Trace
3	6	350	Total 1917	C 1159	N 376	O 380	${ m S} { m 2}$	0	0

• Molecule 4 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
4	4	257	Total 1272	C 757	N 257	O 258	0	0

• Molecule 5 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues		At	oms			AltConf	Trace
5	u	706	Total 5383	C 3379	N 982	O 999	S 23	1	0

• Molecule 6 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues		At	oms			AltConf	Trace
6	V	384	Total 2635	C 1657	N 477	0 489	S 12	0	0



• Molecule 7 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues		Ate	AltConf	Trace			
7	S	230	Total 1862	C 1164	N 371	O 320	${f S}7$	0	0

• Molecule 8 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues		At	toms			AltConf	Trace
8	У	697	Total 5470	C 3437	N 980	O 1018	S 35	0	0

• Molecule 9 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues		Ato	ms		AltConf	Trace
9	8	317	Total 1571	C 936	N 317	O 318	0	0

• Molecule 10 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues		At	oms			AltConf	Trace
10	G	177	Total 1430	C 917	N 260	O 252	S 1	0	0

• Molecule 11 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues		At	oms			AltConf	Trace
11	Н	81	Total 631	C 397	N 116	0 111	${f S}{7}$	0	0

• Molecule 12 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues		At	\mathbf{oms}	AltConf	Trace		
12	K	81	Total 617	C 380	N 114	0 118	${ m S}{ m 5}$	0	0

• Molecule 13 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues		At	oms			AltConf	Trace
13	L	220	Total 1707	C 1104	N 292	O 301	S 10	0	0

• Molecule 14 is a protein called 40S ribosomal protein S3a.



Mol	Chain	Residues		At	oms			AltConf	Trace
14	0	211	Total 1715	C 1088	N 307	O 306	S 14	0	0

• Molecule 15 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues		Ate		AltConf	Trace		
15	Ν	207	Total 1633	C 1040	N 288	O 297	S 8	0	0

• Molecule 16 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues		At	oms	AltConf	Trace		
16	Q	99	Total 792	C 492	N 165	0 130	${ m S}{ m 5}$	0	0

• Molecule 17 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues		At	oms			AltConf	Trace
17	Р	133	Total 997	C 610	N 196	0 185	S 6	0	0

• Molecule 18 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues		At	oms			AltConf	Trace
18	Ι	150	Total 1208	С 773	N 229	O 205	S 1	0	0

• Molecule 19 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues		At	oms			AltConf	Trace
19	x	421	Total 2831	C 1746	N 521	O 555	S 9	0	0

• Molecule 20 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues		Ato	ms	AltConf	Trace	
20	3	213	Total 1057	C 631	N 213	O 213	0	0

• Molecule 21 is a protein called Eukaryotic translation initiation factor 3 subunit L.



Mol	Chain	Residues		Ato	ms	AltConf	Trace	
21	5	319	Total 1581	C 943	N 319	O 319	0	0

• Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues		Ator	ns	AltConf	Trace	
22	7	28	Total 336	C 140	0 168	Р 28	0	0

• Molecule 23 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues		Ato	\mathbf{ms}	AltConf	Trace		
23	9	24	Total 230	C 139	N 62	O 26	${ m S} { m 3}$	0	0

• Molecule 24 is a RNA chain called 18S rRNA.

Mol	Chain	Residues		1	Atoms			AltConf	Trace
24	А	1719	Total 36670	C 16380	N 6574	0 11998	Р 1718	0	0

• Molecule 25 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues		At	Atoms						
25	В	142	Total 1166	C 743	N 218	O 199	S 6	0	0		

• Molecule 26 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues		Ate	AltConf	Trace			
26	С	256	Total 2035	C 1302	N 378	0 347	S 8	0	0

• Molecule 27 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues		At	oms			AltConf	Trace
27	D	177	Total 1477	C 941	N 295	O 239	${ m S} { m 2}$	0	0

• Molecule 28 is a protein called 40S ribosomal protein S23.



Mol	Chain	Residues		At	oms			AltConf	Trace
28	E	140	Total 1087	C 687	N 215	O 182	${ m S} { m 3}$	0	0

• Molecule 29 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
29	F	47	Total 378	C 231	N 85	O 61	S 1	0	0

• Molecule 30 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues		At	AltConf	Trace			
30	r	275	Total 2215	C 1398	N 387	0 418	S 12	0	0

• Molecule 31 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues		At	oms	AltConf	Trace		
31	J	129	Total 1034	C 659	N 193	0 176	S 6	0	0

• Molecule 32 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues		At	AltConf	Trace			
32	R	198	Total 1627	C 1021	N 322	0 279	$\frac{S}{5}$	0	0

• Molecule 33 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues		At	oms	AltConf	Trace		
33	Т	125	Total 1015	C 642	N 199	O 169	${ m S}{ m 5}$	0	0

• Molecule 34 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues		At	oms			AltConf	Trace
34	V	184	Total 1461	C 914	N 276	0 264	${f S}{7}$	0	0

• Molecule 35 is a protein called 40S ribosomal protein S16.



Mol	Chain	Residues		At	oms	AltConf	Trace		
35	Y	141	Total 1124	C 715	N 212	0 194	${ m S} { m 3}$	0	0

• Molecule 36 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues		Ate	AltConf	Trace			
36	Z	227	Total 1765	C 1125	N 317	0 315	S 8	0	0

• Molecule 37 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues		At	oms			AltConf	Trace
37	a	99	Total 834	С 544	N 149	0 135	S 6	0	0

• Molecule 38 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues		At	oms	AltConf	Trace		
38	b	110	Total 913	C 580	N 168	0 158	${ m S} 7$	0	0

• Molecule 39 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues		At	oms			AltConf	Trace
39	С	313	Total 2436	$\begin{array}{c} \mathrm{C} \\ 1535 \end{array}$	N 424	0 465	S 12	0	0

• Molecule 40 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues		At	oms			AltConf	Trace
40	d	142	Total 1105	C 692	N 213	O 197	${ m S} { m 3}$	0	0

• Molecule 41 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
41	е	66	Total 523	C 338	N 93	0 91	S 1	0	0

• Molecule 42 is a protein called 40S ribosomal protein S18.



Mol	Chain	Residues		At	oms			AltConf	Trace
42	f	142	Total 1176	C 737	N 239	O 199	S 1	0	0

• Molecule 43 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
43	i	50	Total 419	C 262	N 85	O 67	${ m S}{ m 5}$	0	0

• Molecule 44 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues		Atc	\mathbf{ms}	AltConf	Trace		
44	k	53	Total 435	C 276	N 82	O 70	${f S}{7}$	0	0

• Molecule 45 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues		At	oms			AltConf	Trace
45	m	122	Total 950	C 596	N 168	0 177	S 9	0	0

• Molecule 46 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues		Ate	oms			AltConf	Trace
46	n	63	Total 498	C 302	N 101	O 93	${S \over 2}$	0	0

• Molecule 47 is a protein called Eukaryotic translation initiation factor 3 subunit G.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	О	77	Total 616	C 389	N 111	O 116	0	0

• Molecule 48 is a protein called Eukaryotic translation initiation factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	р	85	Total 691	C 438	N 125	0 126	$\begin{array}{c} \mathrm{S} \\ \mathrm{2} \end{array}$	0	0

• Molecule 49 is a protein called Eukaryotic translation initiation factor 1A, X-chromosomal.



Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	88	Total 714	C 451	N 129	O 130	$\frac{S}{4}$	0	0

• Molecule 50 is a protein called Eukaryotic translation initiation factor 3 subunit J.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	Z	160	Total 795	C 475	N 160	O 160	0	0

• Molecule 51 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	М	131	Total 1064	C 668	N 198	0 194	$\frac{S}{4}$	0	0

• Molecule 52 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	h	103	Total 817	C 511	N 155	0 147	${f S}$ 4	0	0

• Molecule 53 is a protein called Eukaryotic translation initiation factor 2 subunit 2.

Mol	Chain	Residues		Atoms					Trace
53	s	138	Total 1123	C 709	N 206	0 199	S 9	0	0

• Molecule 54 is a RNA chain called Initiator Met-tRNA-i.

Mol	Chain	Residues		Atoms					Trace
54	W	75	Total	C 717	N 208	0 515	P 74	0	0
			1004	111	290	510	14		

• Molecule 55 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	t	356	Total 1750	C 1038	N 356	O 356	0	0

• Molecule 56 is a protein called Eukaryotic initiation factor 4A-I.



Mol	Chain	Residues		Atoms					Trace
56	j	384	Total 3073	C 1940	N 533	O 581	S 19	0	0

• Molecule 57 is a protein called Eukaryotic translation initiation factor 4 gamma 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	g	224	Total 1848	C 1168	N 324	0 341	S 15	0	0

• Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
58	Q	1	Total Zn 1 1	0
58	k	1	Total Zn 1 1	0

• Molecule 59 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
59	А	87	TotalMg8787	0
59	d	1	Total Mg 1 1	0
59	f	1	Total Mg 1 1	0

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



3 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37870	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	107	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor



4 Model quality (i)

4.1 Standard geometry (i)

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

4.2 Too-close contacts (i)

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

4.3 Torsion angles (i)

4.3.1 Protein backbone (i)

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

4.3.2 Protein sidechains (i)

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

4.3.3 RNA (i)

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

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

28 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).

Mal	Turne	Chain	Dec	Tink	Bond lengths			Bond angles		
MOI	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
24	OMG	А	509	59,24	18,26,27	1.09	3 (16%)	19,38,41	0.78	0
24	PSU	А	823	24	18,21,22	1.05	1 (5%)	22,30,33	0.68	0
24	OMC	А	517	24	19,22,23	0.46	0	26,31,34	0.41	0



Mal	Tune	Chain	Dec	Tink	Bond lengths			Bond angles		
WIOI	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	OMG	А	644	24	$18,\!26,\!27$	1.08	3 (16%)	19,38,41	0.74	1 (5%)
24	OMC	А	174	59,24	19,22,23	0.43	0	26,31,34	0.44	0
24	5MU	А	814	24	19,22,23	0.45	0	28,32,35	0.50	0
24	JMH	А	1219	59,24	18,22,23	0.64	0	21,32,35	0.65	0
24	MA6	А	1850	24	18,26,27	0.84	1(5%)	19,38,41	0.52	0
24	5MC	А	1374	24	18,22,23	0.44	0	26,32,35	0.61	0
24	OMU	А	116	24	19,22,23	0.39	0	26,31,34	0.51	0
24	A2M	А	1031	24	18,25,26	0.61	0	18,36,39	0.91	1(5%)
24	MA6	А	1851	24	18,26,27	0.81	1 (5%)	19,38,41	0.64	0
24	PSU	А	822	24	18,21,22	1.04	2 (11%)	22,30,33	0.84	1 (4%)
24	PSU	А	119	24	18,21,22	0.97	1(5%)	22,30,33	0.69	0
24	OMU	А	121	24	19,22,23	0.44	0	26,31,34	0.51	0
24	OMG	А	683	24	18,26,27	1.06	3 (16%)	19,38,41	0.92	1 (5%)
24	PSU	А	1243	24	18,21,22	1.00	1 (5%)	22,30,33	0.70	0
24	UR3	А	1830	24	19,22,23	0.41	0	26,32,35	1.00	2(7%)
24	A2M	А	1678	24	18,25,26	0.61	0	18,36,39	0.76	0
24	6MZ	А	1832	59,24	$18,\!25,\!26$	0.79	0	16,36,39	0.74	1 (6%)
24	A2M	А	166	24	18,25,26	0.59	0	18,36,39	0.96	1 (5%)
24	OMC	А	1703	24	19,22,23	0.44	0	26,31,34	0.49	0
24	A2M	А	484	24	$18,\!25,\!26$	0.65	1(5%)	18,36,39	0.76	1(5%)
24	A2M	А	27	59,24	18,25,26	0.63	0	18,36,39	0.77	1(5%)
24	A2M	А	668	59,24	18,25,26	0.66	0	18,36,39	0.83	1 (5%)
24	PSU	А	612	24	18,21,22	1.10	2 (11%)	22,30,33	0.75	1 (4%)
24	A2M	A	159	24	18,25,26	0.64	1 (5%)	18,36,39	0.76	1 (5%)
24	PSU	А	1081	24	18,21,22	1.04	2 (11%)	22,30,33	0.82	0

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
24	OMG	А	509	59,24	-	0/5/27/28	0/3/3/3
24	PSU	А	823	24	-	0/7/25/26	0/2/2/2
24	OMC	А	517	24	-	0/9/27/28	0/2/2/2
24	OMG	А	644	24	-	1/5/27/28	0/3/3/3
24	OMC	А	174	59,24	-	0/9/27/28	0/2/2/2
24	5MU	А	814	24	-	0/7/25/26	0/2/2/2
24	JMH	А	1219	59,24	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	MA6	А	1850	24	-	3/7/29/30	0/3/3/3
24	5MC	А	1374	24	-	0/7/25/26	0/2/2/2
24	OMU	А	116	24	-	0/9/27/28	0/2/2/2
24	A2M	А	1031	24	-	0/5/27/28	0/3/3/3
24	MA6	А	1851	24	-	5/7/29/30	0/3/3/3
24	PSU	А	822	24	-	0/7/25/26	0/2/2/2
24	PSU	А	119	24	-	0/7/25/26	0/2/2/2
24	OMU	А	121	24	-	0/9/27/28	0/2/2/2
24	OMG	А	683	24	-	0/5/27/28	0/3/3/3
24	PSU	А	1243	24	-	0/7/25/26	0/2/2/2
24	UR3	А	1830	24	-	2/7/25/26	0/2/2/2
24	A2M	А	1678	24	-	0/5/27/28	0/3/3/3
24	6MZ	А	1832	59,24	-	2/5/27/28	0/3/3/3
24	A2M	А	166	24	-	0/5/27/28	0/3/3/3
24	OMC	А	1703	24	-	0/9/27/28	0/2/2/2
24	A2M	А	484	24	-	0/5/27/28	0/3/3/3
24	A2M	А	27	59,24	-	0/5/27/28	0/3/3/3
24	A2M	А	668	59,24	-	2/5/27/28	0/3/3/3
24	PSU	А	612	24	-	0/7/25/26	0/2/2/2
24	A2M	А	159	24	-	2/5/27/28	0/3/3/3
24	PSU	A	1081	24	-	1/7/25/26	0/2/2/2

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The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	А	1243	PSU	C6-C5	3.37	1.39	1.35
24	А	823	PSU	C6-C5	3.35	1.39	1.35
24	А	119	PSU	C6-C5	3.23	1.39	1.35
24	А	612	PSU	C6-C5	3.22	1.39	1.35
24	А	1081	PSU	C6-C5	3.20	1.39	1.35

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
24	А	1832	6MZ	C2-N1-C6	2.44	118.68	116.59
24	А	668	A2M	C5-C6-N6	2.32	123.88	120.35
24	А	1031	A2M	C5-C6-N6	2.31	123.86	120.35
24	А	822	PSU	O4'-C1'-C2'	2.28	108.36	105.14
24	А	1830	UR3	C6-N1-C2	-2.25	119.77	121.79

There are no chirality outliers.



Mol	Chain	\mathbf{Res}	Type	Atoms
24	А	1832	6MZ	N1-C6-N6-C9
24	А	1850	MA6	C5-C6-N6-C10
24	А	1850	MA6	N1-C6-N6-C10
24	А	1851	MA6	O4'-C4'-C5'-O5'
24	А	1851	MA6	C5-C6-N6-C10

5 of 18 torsion outliers are listed below:

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 (i)

Of 91 ligands modelled in this entry, 91 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 (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



5 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-11302. 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 (i)

This section was not generated.

5.2 Central slices (i)

This section was not generated.

5.3 Largest variance slices (i)

This section was not generated.

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

This section was not generated.

5.5 Orthogonal surface views (i)

This section was not generated.

5.6 Mask visualisation (i)

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



6 Map analysis (i)

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

6.1 Map-value distribution (i)

This section was not generated.

6.2 Volume estimate versus contour level (i)

This section was not generated.

6.3 Rotationally averaged power spectrum (i)

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



7 Fourier-Shell correlation (i)

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



8 Map-model fit (i)

This section was not generated.

