



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:56 AM GMT

PDB ID : 2JEB
Title : STRUCTURE OF A 9-SUBUNIT ARCHAEAL EXOSOME BOUND TO MN
IONS
Authors : Lorentzen, E.; Conti, E.
Deposited on : 2007-01-16
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

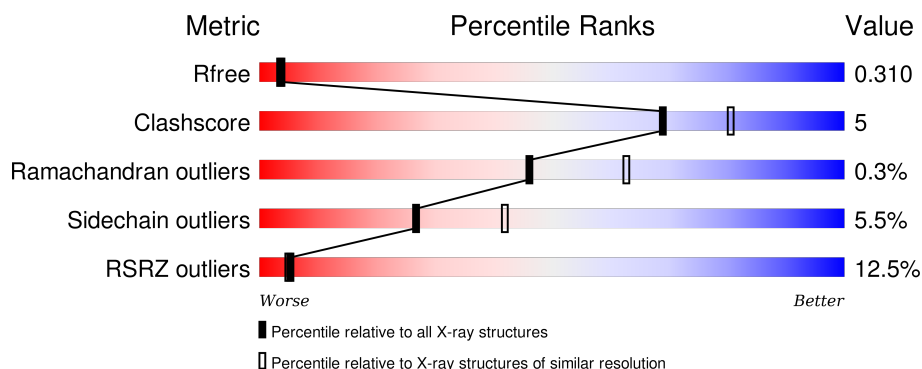
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	277	<div> <div>3%</div> <div>87%</div> <div>10% ..</div> </div>
2	B	250	<div> <div>2%</div> <div>76%</div> <div>15% • 7%</div> </div>
3	I	251	<div> <div>31%</div> <div>69%</div> <div>7% • 22%</div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5434 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called EXOSOME COMPLEX EXONUCLEASE 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	1	0
			2058	1313	335	405	5			

- Molecule 2 is a protein called EXOSOME COMPLEX EXONUCLEASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	233	Total	C	N	O	S	0	1	0
			1773	1123	307	333	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	182	ALA	ASP	ENGINEERED MUTATION	UNP Q9UXC2

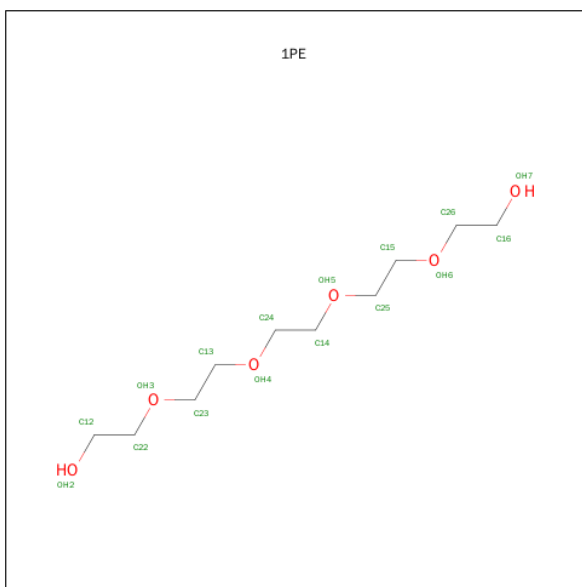
- Molecule 3 is a protein called EXOSOME COMPLEX RNA-BINDING PROTEIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	197	Total	C	N	O	S	0	0	0
			1416	924	229	261	2			

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	1	Total	Mn	0	0
			1	1		
4	A	1	Total	Mn	0	0
			1	1		

- Molecule 5 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	C O	0	0
			16	10 6		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Cl	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	97	Total	O	0	0
			97	97		
7	B	55	Total	O	0	0
			55	55		
7	I	16	Total	O	0	0
			16	16		

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Chain A:

Chain B:

Sequence logo for Chain B. The y-axis represents information content in bits (0.00 to 0.10). The x-axis lists amino acids. A color scale at the top indicates conservation levels: 2% (red), 76% (green), 15% (yellow), and 7% (grey).

Position	Amino Acid	Information Content (bits)
1	GLY	0.00
2	HIS	0.00
3	NET	0.00
4	ARG	0.00
5	GLU	0.00
6	NET	0.00
7	LEU	0.00
8	GLN	0.00
9	VAL	0.00
10	GLU	0.00
11	R9	0.00
12	D15	0.00
13	R19	0.00
14	M49	0.00
15	M64	0.00
16	H68	0.00
17	R74	0.00
18	A75	0.00
19	V76	0.00
20	V79	0.00
21	R80	0.00
22	Y81	0.00
23	E90	0.00
24	P96	0.00
25	R99	0.00
26	E100	0.00
27	L103	0.00
28	R108	0.00
29	F109	0.00
30	A110	0.00
31	P121	0.00
32	R122	0.00
33	D126	0.00
34	F127	0.00
35	T129	0.00
36	E130	0.00
37	I131	0.00
38	D135	0.00
39	A136	0.00
40	G137	0.00
41	S138	0.00
42	S142	0.00
43	R158	0.00
44	V164	0.00
45	A165	0.00
46	L177	0.00
47	E181	0.00
48	M189	0.00
49	P190	0.00
50	M193	0.00
51	M194	0.00
52	P195	0.00
53	M198	0.00
54	T201	0.00
55	L205	0.00
56	N206	0.00
57	G207	0.00
58	S208	0.00
59	R215	0.00
60	F218	0.00
61	I225	0.00
62	I228	0.00
63	L236	0.00
64	V241	0.00
65	GLU	0.00
66	PHE	0.00
67	LYS	0.00
68	GLU	0.00
69	GLU	0.00
70	GLY	0.00
71	VAL	0.00

Chain I:

31% 69% 7% 22%

GLY HIS MET MET ASN MET MET SER GLN SER SER SER K3 I9 V10 L11 P13 V17 E21 L22 L23 G26 E27 F28 Q29 Y35 H40 S41 V53 T56 Q57 F58 P62 S66 M73 V76 V83 E84 I85 Y86 G87 V90 D91 I92 K97 A98 Y99 L100 P101 A102 S103 N104 L105 L106 G107 R108 S109 I110 N111 V112 G113 E114 D115 L116 R117 R118 Y119 L120 V126 I130 E131 M132 F133 D134 ARG SER ILE D138 P139 V140 L141 S142 V143 K144 G145 L148 G149 R150 V151 S152 N153 G154 I157 V162 K163 V164 P165 K170 M171 A172 SER M173 Y175 E176 T177 T178 T179 S180 R181 SER SER GLY CYS SER ILE F187 M191 I194 W195 A196 THR CYS PRO SER ARG ARG PHE SER SER GLU GLU T206 L207 L208 E209 A210 I214 L220 K221 GLY LEU THR ASP ARG ILE LYS GLN PHE ILE GLU GLU LYS LEU GLY GLU ARG ASN ALA SER SER GLY

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	133.64Å 133.64Å 133.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.54 – 2.40 42.26 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.54-2.40) 100.0 (42.26-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.198 , 0.258 0.254 , 0.310	Depositor DCC
R_{free} test set	1567 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	44.4	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.0	EDS
Estimated twinning fraction	0.034 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 31364 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5434	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, MN, 1PE

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.46	0/2093	0.64	2/2851 (0.1%)
2	B	0.50	0/1803	0.70	2/2440 (0.1%)
3	I	0.39	0/1441	0.56	0/1972
All	All	0.46	0/5337	0.64	4/7263 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	215	ARG	NE-CZ-NH1	6.68	123.64	120.30
2	B	215	ARG	NE-CZ-NH2	-6.60	117.00	120.30
1	A	112	ARG	NE-CZ-NH1	5.47	123.03	120.30
1	A	112	ARG	NE-CZ-NH2	-5.07	117.77	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2058	0	2074	15	0
2	B	1773	0	1805	24	0
3	I	1416	0	1340	10	0
4	A	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	1	0	0	0	0
5	A	16	0	22	0	0
6	B	1	0	0	0	0
7	A	97	0	0	4	0
7	B	55	0	0	2	0
7	I	16	0	0	0	0
All	All	5434	0	5241	48	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 5.

The worst 5 of 48 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)
2:B:129:THR:HG21	2:B:142:SER:OG	1.75	0.87
3:I:92:ILE:O	3:I:191:ASN:ND2	2.18	0.76
2:B:110:ALA:HB1	2:B:201:THR:HG23	1.74	0.68
1:A:240:LYS:NZ	7:A:2087:HOH:O	2.19	0.60
1:A:218:GLU:OE2	7:A:2080:HOH:O	2.17	0.59

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 X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	270/277 (98%)	261 (97%)	9 (3%)	0	100	100
2	B	232/250 (93%)	225 (97%)	6 (3%)	1 (0%)	39	56
3	I	189/251 (75%)	178 (94%)	10 (5%)	1 (0%)	34	48
All	All	691/778 (89%)	664 (96%)	25 (4%)	2 (0%)	46	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	I	13	PRO
2	B	136	ALA

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	226/243 (93%)	219 (97%)	7 (3%)	47	69
2	B	186/208 (89%)	175 (94%)	11 (6%)	24	38
3	I	137/223 (61%)	124 (90%)	13 (10%)	11	15
All	All	549/674 (82%)	518 (94%)	31 (6%)	27	41

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	206[A]	ASN
2	B	236	LEU
3	I	174	MET
2	B	206[B]	ASN
3	I	17	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	198	ASN
3	I	191	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
5	1PE	A	401	-	15,15,15	0.51	0	14,14,14	0.24	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
5	1PE	A	401	-	-	0/13/13/13	0/0/0/0

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.

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.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	273/277 (98%)	0.44	7 (2%) 59 58	42, 47, 59, 65	1 (0%)
2	B	233/250 (93%)	0.36	4 (1%) 73 72	39, 47, 56, 66	0
3	I	197/251 (78%)	1.68	77 (39%) 0 0	41, 47, 51, 55	0
All	All	703/778 (90%)	0.76	88 (12%) 5 5	39, 47, 57, 66	1 (0%)

The worst 5 of 88 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	9	ILE	6.6
3	I	112	VAL	6.4
3	I	140	VAL	5.9
3	I	171	ASN	5.4
3	I	207	LEU	5.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	1PE	A	401	16/16	0.91	0.16	-0.01	49,51,59,60	0
6	CL	B	301	1/1	0.88	0.12	-4.34	52,52,52,52	0
4	MN	I	301	1/1	0.98	0.26	-	66,66,66,66	0
4	MN	A	301	1/1	0.84	0.12	-	76,76,76,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.