

Oct 24, 2022 - 06:24 PM EDT

PDB ID	:	7NAN
EMDB ID	:	EMD-24275
Title	:	Human 20S proteasome core particle
Authors	:	Zhao, J.; Makhija, S.; Huang, B.; Cheng, Y.
Deposited on	:	2021-06-22
Resolution	:	2.80 Å(reported)

This is a Full wwPDB EM Validation 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 (1)) were used in the production of this report:

:	0.0.1. dev 43
:	4.02b-467
:	20191225.v01 (using entries in the PDB archive December 25th 2019)
:	1.9.9
:	Engh & Huber (2001)
:	Parkinson et al. (1996)
:	2.31.2
	::

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 2.80 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	Percentile Ranks	Value
Ramachandran outliers		0.0%
Sidechain outliers		0.2%
Worse		Better
Perce	ntile relative to all structures	
Perce	ntile relative to all EM structures	
Motric	Whole archive	EM structures
wietht	(#Entries)	(#Entries)

	(#Entries)	(#Diffices)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
		<u></u>

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain	
1	А	234	98%	·
1	Ο	234	98%	·
2	В	261	96%	•
2	Р	261	96%	•
3	С	248	95%	5%
3	Q	248	95%	5%
4	D	241	• 98%	·
4	R	241	98%	·
5	Е	263	90%	10%



Mol	Chain	Length	Quality of chain	
5	S	263	90%	10%
6	F	255	94%	6%
6	Т	255	94%	6%
7	G	246	99%	
7	U	246	98%	
8	Н	277	80%	20%
8	V	277	80%	20%
9	Ι	205	99%	
9	W	205	100%	
10	J	201	98%	
10	Х	201	97%	
11	K	263	76%	24%
11	Y	263	76%	24%
12	L	241	88%	12%
12	Z	241	88%	12%
13	М	264	81%	• 19%
13	a	264	81%	19%
14	N	239	85%	15%
14	b	239	85%	15%

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2 Entry composition (i)

There are 14 unique types of molecules in this entry. The entry contains 46360 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 Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	А	229	Total	C 1083	N 288	0	S 6	0	0
1	0	229	Total	1003 C	200 N	200 0	S C	0	0
_			1694	1097	296	295	6		

• Molecule 2 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues		At	AltConf	Trace			
2	В	250	Total 1795	C 1146	N 322	0 317	S 10	0	0
2	Р	251	Total 1850	C 1177	N 329	0 334	S 10	0	0

• Molecule 3 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	С	025	Total	С	Ν	0	S	0	0
3	U	230	1694	1077	317	295	5	0	0
9	0	226	Total	С	Ν	0	S	0	0
3	Q	2 230	1719	1093	319	302	5	0	0

• Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues		At	AltConf	Trace			
4	П	235	Total	С	Ν	Ο	\mathbf{S}	0	Ο
	D	200	1699	1079	292	317	11		0
4 R	D	225	Total	С	Ν	Ο	\mathbf{S}	0	0
	n	230	1688	1073	292	312	11	0	0

• Molecule 5 is a protein called Proteasome subunit alpha type-1.



Mol	Chain	Residues		At	AltConf	Trace			
5	F	238	Total	С	Ν	0	\mathbf{S}	0	0
5 E	Ľ	230	1794	1134	330	319	11	0	0
5	q	227	Total	С	Ν	0	S	0	0
5	3	231	1759	1120	329	299	11	0	0

• Molecule 6 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Б	240	Total	С	Ν	0	\mathbf{S}	0	0
ОГ	Г	240	1783	1145	315	313	10	0	0
6	5 Т	220	Total	С	Ν	0	S	0	0
0		1 239	1784	1144	315	315	10		

• Molecule 7 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues		At	oms			AltConf	Trace
7	G	243	Total 1781	C 1138	N 308	O 323	S 12	0	0
7	U	243	Total 1781	C 1139	N 307	0 323	S 12	0	0

• Molecule 8 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues		At	oms			AltConf	Trace
8	Н	222	Total 1604	C 1020	N 276	0 297	S 11	0	0
8	V	222	Total 1618	C 1027	N 275	O 306	S 10	0	0

• Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues		At	oms			AltConf	Trace
0	Т	204	Total	С	Ν	Ο	\mathbf{S}	0	0
9	1	204	1563	1001	264	279	19	0	0
0	W	204	Total	С	Ν	Ο	\mathbf{S}	0	0
9	vv	204	1559	1000	264	277	18	0	0

• Molecule 10 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues		At	oms			AltConf	Trace
10	J	197	Total 1541	C 996	N 265	0 271	S 9	0	0



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Mol	Chain	Residues		At	oms			AltConf	Trace
10	Х	196	Total 1531	C 988	N 264	0 271	S 8	0	0

• Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues		At	oms			AltConf	Trace
11	K	200	Total	С	Ν	0	S	0	0
	Γ	200	1525	968	273	275	9	0	0
11	v	200	Total	С	Ν	0	S	0	0
	1	200	1522	966	272	275	9	0	0

• Molecule 12 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues		At	oms			AltConf	Trace
19	т	012	Total	С	Ν	0	\mathbf{S}	0	0
		213	1604	1025	280	289	10	0	0
19	7	012	Total	С	Ν	0	S	0	0
		213	1593	1022	281	280	10	0	0

• Molecule 13 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues		At	oms			AltConf	Trace
13	М	215	Total	С	Ν	Ο	\mathbf{S}	0	0
10	111	210	1635	1038	288	297	12	0	0
12	0	214	Total	С	Ν	Ο	\mathbf{S}	0	0
10	a	214	1624	1033	288	291	12	0	0

• Molecule 14 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues		\mathbf{A}	toms			AltConf	Trace
14	N	202	Total	С	Ν	0	S	0	0
14 IN	202	1485	935	258	281	11	0	0	
14	h	202	Total	С	Ν	0	S	0	0
14	D	b 202	1470	929	257	272	12		0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Proteasome subunit alpha type-2





Chain Q:	95%	5%
MET 82 82 82 82 610 610 610 178 178 178 178 178 178 178 81A 81A 81A 855R		
• Molecule 4: Proteasome	e subunit alpha type-5	
Chain D:	98%	
MET PHE LLEU THR SRR SRR ARG C131 4128 A128 A128 A128 A128 A128 A128		
• Molecule 4: Proteasome	e subunit alpha type-5	
Chain R:	98%	
MET PHE LEU THR ARG SER A128 A128 A128		
• Molecule 5: Proteasome	e subunit alpha type-1	
Chain E:	90%	10%
MET MET R3 P240 P240 P240 P240 P240 P240 P240 P20 P20 P20 P20 P20 P20 P20 P20 P20 P2	dLU LIYS ASLA ASLA CLU CLU HIS HIS	
• Molecule 5: Proteasome	e subunit alpha type-1	
Chain S:	90%	10%
MET PHE ARG ARG CAN AR ARA PRO CLN PRO CLN ARA PRO CLN ARA ARA	PR0 CLU CLYS CLU CLYS ALA ALA ALA ALA CLU PR0 MET HIS CLU	
• Molecule 6: Proteasome	e subunit alpha type-3	
Chain F:	94%	6%
MET SER SER SER ILE ILE T5 GLV GLV GLV GLU ASP ASP ASP	MET	
• Molecule 6: Proteasome	e subunit alpha type-3	
Chain T:	94%	6%
MET SER SER SER TILE TILE GLY GLY GLY GLU GLU GLU GLU ASP ASP ASP ASP ASP	1 THE	
• Molecule 7: Proteasom	■ e subunit alpha type-6	



Chain G:	99%
MET SER R3 R3 R3 F3 F3 ASP	
• Molecule 7	: Proteasome subunit alpha type-6
Chain U:	98%
MET SER R3 M131 A131 ASP	
• Molecule 8	: Proteasome subunit beta type-7
Chain H:	80% 20%
MET ALA ALA VAL SER VAL TYR ALA ALA PRO	PR0 VAL GLY PFR0 GLY PFRE ASS ASS ASS ASS ASS ASS ASS ASS ASS AS
• Molecule 8	: Proteasome subunit beta type-7
Chain V:	80% 20%
MET ALA ALA VAL VAL VAL VAL TYR ALA PRO	PR0 VAL GLY PHE PHE ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP
• Molecule 9	: Proteasome subunit beta type-3
Chain I:	99%
MET S1 R98 D204	
• Molecule 9	: Proteasome subunit beta type-3
Chain W:	100%
MET S1 D204	
• Molecule 1	0: Proteasome subunit beta type-2
Chain J:	98% .
M1 P197 LYS GLN GLY SER	
• Molecule 1	0: Proteasome subunit beta type-2



Chain X:	97%	•
M1 K02 F196 F196 L178 CLN CLN SER SER		
• Molecule 11: Prote	asome subunit beta type-5	
Chain K:	76%	24%
MET ALA ALA LEU CLEU VAL CLEU CLEU PRO PRO PRO ASN SSI	ARG GLY PHE CLEU CLEU CLEU CLEU ALA ASP CLEU CLEU CLEU SER SER SER SER SER SER SER SER SER SER	PR0 GLY TRP GLY GLY GLY GLU GLY GLY HIS GLY HIS GLY FI
2000 SER THR PRO		
• Molecule 11: Prote	asome subunit beta type-5	
Chain Y:	76%	24%
MET ALA ALA LEU CEU VAL CLU CLU CLU PRO PRO PRO ASN ASN SSL	ALC CLY CLY CLY CLY CLY CLY CLY CLY CLY C	PRO GLY TRP GLY GLY GLU GLY GLY HIS GLY HIS GLY FI
M45 S200 GLY SER TTRR PR0		
• Molecule 12: Prote	asome subunit beta type-1	
Chain L:	88%	12%
MET LEU SER SER THR ALA MET ALA ARC GLY ARC GLY ARC CLY	GLY MET PRO ALA ALA ALA ALA ALA CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	
• Molecule 12: Prote	asome subunit beta type-1	
Chain Z:	88%	12%
MET LEU SER SER SER ALA ALA ALA ALA ALA ALA ARC ARC ARC	GLY GLY GLU GLU GLU ALA ALA GLN GLN CLEU CLEU CLEU CLEU CLEU	
• Molecule 13: Prote	asome subunit beta type-4	
Chain M:	81%	• 19%
MET MET ALIA ALIA ALIA CIUY CIUY SER SER SER SER CIUY ALIA ALIA ALIA	PRU ALA PRU GLY GLN PRU GLN TTYR TTYR PRO SER ASP PRO ASP ASP ASP ASP ASP ASP ASP ASP PRO ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	THR ARG T1 R100 R100 C1215 SER SER SER SER C17 C12 C12 C12 C12 C12 C12 C12 C12 C12 C12
• Molecule 13: Prote	easome subunit beta type-4	
Chain a:	81%	19%



• Molecule 14: Proteasome subunit beta type-6





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	499629	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	30.094	Depositor
Minimum map value	-13.549	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4.0	Depositor
Map size (Å)	388.992, 388.992, 388.992	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2156, 1.2156, 1.2156	Depositor



5 Model quality (i)

5.1 Standard geometry (i)

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).

Mal	Chain	Bond lengths		Bond angles		
	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.47	0/1704	0.53	0/2322	
1	0	0.48	0/1733	0.53	0/2358	
2	В	0.42	0/1824	0.53	0/2482	
2	Р	0.43	0/1879	0.53	0/2550	
3	С	0.44	0/1719	0.56	0/2341	
3	Q	0.43	0/1745	0.58	0/2375	
4	D	0.42	0/1725	0.51	0/2342	
4	R	0.41	0/1714	0.51	0/2327	
5	Е	0.44	0/1829	0.58	0/2484	
5	S	0.43	0/1794	0.57	0/2436	
6	F	0.46	0/1818	0.55	0/2461	
6	Т	0.46	0/1819	0.55	0/2462	
7	G	0.46	0/1813	0.51	0/2464	
7	U	0.45	0/1813	0.51	0/2464	
8	Н	0.48	0/1631	0.59	0/2217	
8	V	0.48	0/1645	0.57	0/2235	
9	Ι	0.50	0/1592	0.56	0/2149	
9	W	0.50	0/1588	0.55	0/2144	
10	J	0.50	0/1574	0.56	0/2134	
10	Х	0.52	0/1563	0.57	0/2119	
11	Κ	0.53	0/1556	0.60	0/2104	
11	Y	0.51	0/1553	0.61	1/2102~(0.0%)	
12	L	0.49	0/1634	0.57	0/2206	
12	Ζ	0.48	0/1623	0.56	0/2192	
13	М	0.52	0/1668	0.62	1/2263~(0.0%)	
13	a	0.50	0/1657	0.60	0/2248	
14	Ν	0.50	0/1511	0.54	0/2049	
14	b	0.51	0/1496	0.54	0/2029	
All	All	0.47	0/47220	0.56	2/64059~(0.0%)	

There are no bond length outliers.

All (2) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
11	Y	45	MET	C-N-CA	6.95	139.06	121.70
13	М	171	ARG	NE-CZ-NH1	5.14	122.87	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	Perce	ntiles
1	А	227/234~(97%)	226 (100%)	1 (0%)	0	100	100
1	Ο	227/234~(97%)	227 (100%)	0	0	100	100
2	В	248/261~(95%)	245 (99%)	3~(1%)	0	100	100
2	Р	249/261~(95%)	246 (99%)	3 (1%)	0	100	100
3	С	233/248~(94%)	229 (98%)	4 (2%)	0	100	100
3	Q	234/248~(94%)	229~(98%)	5 (2%)	0	100	100
4	D	233/241~(97%)	227 (97%)	6 (3%)	0	100	100
4	R	233/241~(97%)	227~(97%)	6 (3%)	0	100	100
5	Е	236/263~(90%)	232 (98%)	4 (2%)	0	100	100
5	S	235/263~(89%)	228 (97%)	6 (3%)	1 (0%)	34	66
6	F	238/255~(93%)	236 (99%)	2(1%)	0	100	100
6	Т	237/255~(93%)	232~(98%)	5 (2%)	0	100	100
7	G	241/246~(98%)	235 (98%)	6 (2%)	0	100	100
7	U	241/246~(98%)	236 (98%)	5 (2%)	0	100	100
8	Н	220/277 (79%)	213 (97%)	7 (3%)	0	100	100



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
8	V	220/277~(79%)	215~(98%)	5 (2%)	0	100	100
9	Ι	202/205~(98%)	193 (96%)	9 (4%)	0	100	100
9	W	202/205~(98%)	197 (98%)	5 (2%)	0	100	100
10	J	195/201~(97%)	192 (98%)	3 (2%)	0	100	100
10	Х	194/201~(96%)	190 (98%)	4 (2%)	0	100	100
11	К	198/263~(75%)	193 (98%)	5 (2%)	0	100	100
11	Y	198/263~(75%)	196 (99%)	2 (1%)	0	100	100
12	L	211/241 (88%)	206 (98%)	5 (2%)	0	100	100
12	Z	211/241 (88%)	209 (99%)	2 (1%)	0	100	100
13	М	213/264~(81%)	207 (97%)	6 (3%)	0	100	100
13	a	212/264~(80%)	205 (97%)	7 (3%)	0	100	100
14	Ν	200/239~(84%)	197 (98%)	3 (2%)	0	100	100
14	b	200/239~(84%)	199 (100%)	1 (0%)	0	100	100
All	All	6188/6876 (90%)	6067 (98%)	120 (2%)	1 (0%)	100	100

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All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	S	61	LYS

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Perce	entiles
1	А	151/191~(79%)	151 (100%)	0	100	100
1	Ο	158/191~(83%)	158 (100%)	0	100	100
2	В	159/221~(72%)	159 (100%)	0	100	100
2	Р	173/221~(78%)	173 (100%)	0	100	100
3	С	149/211~(71%)	149 (100%)	0	100	100



Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
3	\mathbf{Q}	156/211~(74%)	156 (100%)	0	100	100
4	D	167/203~(82%)	167 (100%)	0	100	100
4	R	162/203~(80%)	162 (100%)	0	100	100
5	Ε	179/224~(80%)	179 (100%)	0	100	100
5	S	169/224~(75%)	169 (100%)	0	100	100
6	F	166/212~(78%)	165 (99%)	1 (1%)	86	96
6	Т	168/212~(79%)	168 (100%)	0	100	100
7	G	174/210~(83%)	174 (100%)	0	100	100
7	U	171/210~(81%)	170 (99%)	1 (1%)	86	96
8	Н	164/228~(72%)	164 (100%)	0	100	100
8	V	167/228~(73%)	167 (100%)	0	100	100
9	Ι	164/174~(94%)	163 (99%)	1 (1%)	86	96
9	W	162/174~(93%)	162 (100%)	0	100	100
10	J	156/171~(91%)	156 (100%)	0	100	100
10	Х	155/171~(91%)	154 (99%)	1 (1%)	86	96
11	Κ	146/202~(72%)	146 (100%)	0	100	100
11	Υ	144/202~(71%)	144 (100%)	0	100	100
12	L	163/199~(82%)	162~(99%)	1 (1%)	86	96
12	Z	160/199~(80%)	160 (100%)	0	100	100
13	М	164/215~(76%)	163~(99%)	1 (1%)	86	96
13	a	161/215~(75%)	160 (99%)	1 (1%)	86	96
14	Ν	148/181~(82%)	148 (100%)	0	100	100
14	b	143/181~(79%)	143 (100%)	0	100	100
All	All	4499/5684~(79%)	4492 (100%)	7 (0%)	93	98

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All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	181	MET
9	Ι	98	ARG
12	L	100	ARG
13	М	100	ARG
7	U	131	MET
10	Х	62	LYS



 $Continued \ from \ previous \ page...$

Mol	Chain	Res	Type
13	a	100	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
2	В	20	GLN
5	Ε	21	GLN
12	L	58	HIS
14	Ν	110	GLN
4	R	204	GLN
13	a	2	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-24275. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map



The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map



X Index: 160

Y Index: 160



Z Index: 160

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 180

Y Index: 179

Z Index: 197

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.



6.5 Mask visualisation (i)

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



7 Map analysis (i)

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

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



7.2 Volume estimate (i)



The volume at the recommended contour level is 408 nm^3 ; this corresponds to an approximate mass of 369 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.



7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.357 \AA^{-1}



8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.357 \AA^{-1}



8.2 Resolution estimates (i)

$\begin{bmatrix} Bosolution ostimato (Å) \end{bmatrix}$	Estim	Estimation criterion (FSC cut-off)			
Resolution estimate (A)	0.143	0.5	Half-bit		
Reported by author	2.80	-	-		
Author-provided FSC curve	2.80	3.12	2.84		
Unmasked-calculated*	-	-	-		

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-24275 and PDB model 7NAN. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.



9.2 Q-score mapped to coordinate model (i)



The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (4.0).



9.4 Atom inclusion (i)



At the recommended contour level, 99% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.



1.0

0.0 <0.0

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (4.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9415	0.5310
А	0.9546	0.5270
В	0.9431	0.5210
С	0.9484	0.5120
D	0.9168	0.5180
Е	0.9389	0.5190
F	0.9449	0.5180
G	0.9417	0.5200
Н	0.9424	0.5380
Ι	0.9329	0.5430
J	0.9382	0.5430
К	0.9525	0.5500
L	0.9395	0.5410
М	0.9465	0.5420
Ν	0.9394	0.5490
0	0.9511	0.5290
Р	0.9283	0.5160
Q	0.9426	0.5140
R	0.9169	0.5160
S	0.9499	0.5240
Т	0.9438	0.5200
U	0.9452	0.5200
V	0.9379	0.5350
W	0.9405	0.5490
Х	0.9385	0.5510
Y	0.9511	0.5420
Ζ	0.9365	0.5430
a	0.9512	0.5520
b	0.9534	0.5500

