

Dec 5, 2023 – 06:13 PM JST

PDB ID	:	8HM0
EMDB ID	:	EMD-34887
Title	:	F8-A22-E4 complex of MPXV in trimeric form
Authors	:	Li, Y.N.; Shen, Y.P.; Hu, Z.W.; Yan, R.H.
Deposited on	:	2022-12-02
Resolution	:	3.10 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:

EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
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 3.10 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f EM} {f structures} \ (\#{f Entries})$
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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				
			29%				
1	С	426	63%	12%	24%	)	_
			11%				
2	А	1006	64%		27%	·	7%
			<b>_</b>				
3	В	218	60%		36%		••



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 11331 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 DNA polymerase processivity factor component A20.

Mol	Chain	Residues	Atoms			AltConf	Trace		
1	С	323	Total 1996	C 1243	N 361	O 389	${ m S} { m 3}$	0	0

• Molecule 2 is a protein called DNA polymerase.

Mol	Chain	Residues	Atoms				AltConf	Trace	
9	Λ	025	Total	С	Ν	Ο	$\mathbf{S}$	0	0
	A	900	7592	4845	1270	1425	52	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	108	PHE	LEU	$\operatorname{conflict}$	UNP A0A2L0AR76

• Molecule 3 is a protein called E4R.

Mol	Chain	Residues	Atoms			AltConf	Trace		
3	В	216	Total 1743	C 1131	N 284	O 323	${ m S}{ m 5}$	0	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.











# 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	854700	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	50	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.125	Depositor
Minimum map value	-0.075	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	274.432, 274.432, 274.432	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.072, 1.072, 1.072	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).

Mol Chain		Bond	lengths	Bond	angles
	Ullalli	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	С	0.25	0/2016	0.44	0/2768
2	А	0.33	0/7745	0.47	0/10451
3	В	0.29	0/1792	0.46	0/2439
All	All	0.31	0/11553	0.46	0/15658

There are no bond length outliers.

There are no bond angle outliers.

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	С	1996	0	1428	30	0
2	А	7592	0	7560	183	0
3	В	1743	0	1721	53	0
All	All	11331	0	10709	263	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 12.

All (263) 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:A:439:ASP:OD1	2:A:439:ASP:N	2.16	0.76



	h i c	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
2:A:573:VAL:HG21	2:A:608:LEU:HD13	1.70	0.74	
2:A:23:ARG:NH1	2:A:29:THR:OG1	2.22	0.72	
2:A:8:TRP:HB2	2:A:489:PRO:HB3	1.69	0.72	
2:A:439:ASP:HB2	2:A:442:GLN:HB3	1.72	0.72	
2:A:738:PRO:HB2	2:A:741:TYR:HE1	1.56	0.70	
3:B:8:HIS:HB3	3:B:38:LEU:HD11	1.74	0.70	
2:A:187:SER:HG	2:A:459:CYS:HG	1.38	0.70	
2:A:205:GLU:OE2	2:A:223:ARG:NH1	2.24	0.69	
1:C:9:ASN:HB2	1:C:34:LEU:HD11	1.73	0.69	
2:A:187:SER:OG	2:A:459:CYS:SG	2.51	0.69	
2:A:81:ARG:HH21	2:A:568:LEU:HB3	1.58	0.68	
2:A:115:ILE:HD12	2:A:508:LYS:HG3	1.76	0.67	
1:C:225:VAL:HA	1:C:235:PRO:HA	1.77	0.66	
2:A:773:GLU:OE2	2:A:776:ARG:NH2	2.27	0.66	
2:A:68:ILE:HD13	2:A:517:LEU:HB3	1.78	0.66	
2:A:835:VAL:HG12	2:A:836:SER:H	1.61	0.66	
2:A:808:THR:O	2:A:826:LYS:NZ	2.27	0.65	
2:A:356:CYS:SG	2:A:357:MET:N	2.69	0.65	
2:A:709:ASN:HB3	2:A:739:ILE:HA	1.77	0.65	
2:A:863:GLN:O	2:A:867:ASP:HB2	1.97	0.65	
3:B:60:LYS:HD3	3:B:117:ILE:HB	1.78	0.64	
2:A:838:PHE:HB2	2:A:958:PHE:HE2	1.62	0.64	
2:A:718:LEU:HG	2:A:782:VAL:HG23	1.80	0.64	
2:A:604:ARG:HG3	2:A:605:LEU:HG	1.80	0.64	
1:C:239:THR:N	1:C:243:LYS:O	2.27	0.63	
2:A:23:ARG:NH2	2:A:257:ASP:OD2	2.31	0.63	
2:A:634:ARG:HE	2:A:661:LYS:HB2	1.63	0.63	
3:B:105:TYR:HB3	3:B:216:PHE:HD2	1.64	0.63	
2:A:305:SER:HB3	2:A:308:LYS:HE3	1.81	0.62	
2:A:800:MET:H	2:A:982:LEU:HD21	1.64	0.62	
2:A:842:MET:O	2:A:846:TYR:N	2.32	0.62	
2:A:989:CYS:SG	2:A:990:ILE:N	2.73	0.61	
1:C:378:LYS:HB3	1:C:386:ASN:HB3	1.82	0.61	
3:B:62:VAL:HB	3:B:116:VAL:HG23	1.82	0.61	
1:C:238:ILE:HA	1:C:238:ILE:HA 1:C:244:LYS:HA		0.60	
3:B:6:ILE:HG22	3:B:27:VAL:HG13	1.83	0.60	
2:A:775:GLU:HA	2:A:778:ILE:HG12	1.84	0.60	
1:C:361:LEU:HD11	1:C:406:ASN:HB3	1.83	0.59	
2:A:810:LYS:HB2	2:A:823:ARG:HG3	1.83	0.59	
3:B:87:LYS:HE3	3:B:183:ALA:HA	1.83	0.59	
2:A:836:SER:O	2:A:890:PHE:HB2	2.02	0.59	



	ht o	Interatomic	Clash	
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)	
2:A:768:ILE:HD13	2:A:791:PHE:HZ	1.67	0.59	
2:A:111:SER:O	2:A:115:ILE:HG12	2.03	0.58	
1:C:407:PHE:HA	1:C:410:PHE:HB3	1.84	0.58	
2:A:185:HIS:HD2	2:A:203:ILE:HG12	1.69	0.58	
2:A:52:PRO:O	2:A:97:ARG:NH2	2.30	0.58	
2:A:565:PRO:HB3	2:A:680:SER:HB3	1.86	0.58	
2:A:523:LYS:O	2:A:674:ARG:NH2	2.32	0.57	
3:B:78:PRO:HB2	3:B:118:PRO:HB2	1.85	0.57	
3:B:20:GLU:HG2	3:B:21:PRO:HD3	1.84	0.57	
2:A:971:TYR:HB3	2:A:974:ARG:HH21	1.69	0.57	
2:A:563:LEU:HD13	2:A:686:SER:HB3	1.87	0.57	
2:A:840:LYS:HZ2	2:A:974:ARG:HH12	1.53	0.57	
2:A:266:ASN:OD1	2:A:270:ARG:NH2	2.30	0.56	
3:B:163:PHE:HA	3:B:166:ILE:HD11	1.87	0.56	
2:A:114:TYR:CD2	2:A:487:VAL:HG12	2.40	0.56	
2:A:960:LEU:HD13	2:A:966:ILE:HD12	1.87	0.56	
3:B:50:PHE:HB3	3:B:53:LEU:HG	1.86	0.56	
2:A:397:VAL:HG12	2:A:398:ASP:H	1.70	0.56	
2:A:836:SER:OG	2:A:837:LYS:N	2.39	0.56	
2:A:720:ASN:HB2	2:A:727:ARG:HH12	1.71	0.55	
1:C:375:MET:HG2	1:C:389:ILE:HA	1.87	0.55	
2:A:373:ASP:OD1	2:A:375:THR:N	2.37	0.55	
1:C:344:VAL:O	1:C:348:ILE:HG12	2.06	0.55	
2:A:209:THR:HG22	2:A:211:GLN:H	1.71	0.55	
2:A:843:ILE:O	2:A:847:LYS:N	2.37	0.55	
1:C:379:ILE:HD12	2:A:582:ILE:HG12	1.89	0.55	
2:A:76:LEU:HD11	2:A:587:LEU:HG	1.89	0.55	
2:A:227:LEU:HD13	2:A:246:ARG:HB3	1.88	0.55	
2:A:841:ASN:ND2	2:A:888:GLU:HB2	2.22	0.54	
2:A:216:ALA:HB2	2:A:449:LEU:HD11	1.88	0.54	
2:A:809:MET:HG3	2:A:810:LYS:H	1.73	0.54	
3:B:167:ARG:NH1	3:B:176:THR:OG1	2.32	0.54	
2:A:362:ASN:N	2:A:362:ASN:OD1	2.39	0.54	
2:A:699:GLU:HG2	2:A:748:VAL:HG22	1.88	0.54	
3:B:142:LYS:HG2	3:B:169:LYS:HB2	1.90	0.54	
2:A:883:ARG:HD3	2:A:964:GLN:HE21	1.72	0.54	
1:C:417:VAL:HA	1:C:417:VAL:HA 1:C:420:VAL:HG12		0.54	
2:A:39:TYR:CE1	2:A:92:GLU:HG2	2.43	0.54	
2:A:973:LYS:O	2:A:977:SER:OG	2.22	0.53	
1:C:13:LEU:HD22	1:C:34:LEU:HB3	1.89	0.53	
2:A:446:ASP:N	2:A:446:ASP:OD1	2.40	0.53	



		Interatomic	Clash		
Atom-1	Atom-2	distance (Å)	overlap (Å)		
3:B:4:VAL:HG11	3:B:27:VAL:HG21	1.90	0.53		
2:A:545:VAL:HA	2:A:759:ILE:HG22	1.91	0.53		
3:B:177:ILE:HD12	3:B:177:ILE:H	1.74	0.52		
3:B:22:VAL:HG21	3:B:147:HIS:HB2	1.91	0.52		
3:B:41:GLU:O	3:B:126:LYS:NZ	2.31	0.52		
3:B:154:VAL:HG11	3:B:198:ILE:HG23	1.90	0.52		
1:C:369:ILE:HA	1:C:372:VAL:HG12	1.92	0.52		
3:B:6:ILE:HD11	3:B:10:PRO:HD2	1.91	0.52		
3:B:178:VAL:HG22	3:B:179:GLY:H	1.74	0.52		
1:C:369:ILE:HB	2:A:576:ASN:ND2	2.25	0.52		
2:A:936:ALA:HB2	2:A:966:ILE:HA	1.92	0.52		
1:C:28:ILE:HA	1:C:31:TYR:HB3	1.92	0.51		
2:A:577:ARG:HG3	2:A:578:LEU:N	2.25	0.51		
2:A:786:ASN:OD1	2:A:786:ASN:N	2.42	0.51		
3:B:196:GLU:O	3:B:200:VAL:HG23	2.10	0.51		
2:A:782:VAL:HG13	2:A:783:LEU:HD22	1.93	0.51		
2:A:70:GLU:OE2	2:A:604:ARG:NH2	2.26	0.51		
2:A:843:ILE:HA	2:A:846:TYR:HB3	1.91	0.51		
2:A:974:ARG:HD2	2:A:978:GLU:OE2	2.10	0.51		
2:A:717:THR:OG1	2:A:719:SER:OG	2.24	0.51		
2:A:811:TYR:HE1	2:A:826:LYS:HD3	1.76	0.51		
3:B:55:GLN:NE2	3:B:111:ASN:OD1	2.43	0.51		
2:A:857:GLY:H	2:A:860:ASN:HB2	1.75	0.51		
1:C:5:ALA:O	1:C:8:THR:OG1	2.21	0.51		
2:A:620:GLU:OE1	2:A:628:ARG:NH1	2.44	0.51		
3:B:185:ARG:H	3:B:185:ARG:HD2	1.76	0.50		
3:B:113:ILE:HB	3:B:116:VAL:HG12	1.93	0.50		
2:A:673:PHE:HD2	2:A:676:SER:HB2	1.76	0.50		
2:A:735:THR:OG1	2:A:736:SER:N	2.44	0.50		
2:A:717:THR:HA	2:A:731:PRO:HG3	1.93	0.49		
2:A:714:PHE:CZ	2:A:778:ILE:HG22	2.48	0.49		
2:A:104:MET:HG3	2:A:516:ILE:HG23	1.94	0.49		
2:A:604:ARG:N	2:A:611:GLU:OE1	2.45	0.49		
2:A:850:LEU:HA	2:A:853:MET:HG2	1.94	0.49		
2:A:24:CYS:HB2	2:A:28:GLU:HG2	1.95	0.49		
1:C:216:SER:O	1:C:265:LYS:HA	2.12	0.49		
3:B:16:HIS:CE1	3:B:56:PRO:HB3	2.47	0.49		
2:A:403:CYS:HB2	2:A:419:LEU:HG	1.95	0.49		
1:C:130:VAL:CB	1:C:137:ILE:O	2.60	0.49		
1:C:409:GLN:O	1:C:413:ILE:HG22	2.13	0.48		
2:A:497:ARG:H	2:A:497:ARG:HE	1.61	0.48		



	hi a	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
2:A:838:PHE:HZ	2:A:883:ARG:HE	1.59	0.48	
2:A:373:ASP:OD1	2:A:375:THR:OG1	2.28	0.48	
2:A:573:VAL:HG23	2:A:611:GLU:H	1.79	0.48	
3:B:167:ARG:HH22	3:B:173:PRO:HA	1.78	0.48	
2:A:733:VAL:HG12	2:A:734:LYS:H	1.78	0.48	
2:A:741:TYR:HE2	2:A:766:LYS:HD2	1.79	0.48	
1:C:332:ASP:OD1	1:C:332:ASP:N	2.47	0.48	
2:A:880:PHE:HA	2:A:964:GLN:HB2	1.96	0.48	
2:A:853:MET:SD	2:A:864:VAL:HG23	2.53	0.48	
2:A:721:PRO:HD2	2:A:784:PHE:CZ	2.49	0.48	
3:B:146:GLN:HG2	3:B:170:LEU:HD23	1.96	0.48	
2:A:856:GLU:H	2:A:860:ASN:HD22	1.61	0.48	
2:A:284:ILE:HB	2:A:297:LEU:HB2	1.95	0.47	
3:B:42:THR:OG1	3:B:43:SER:N	2.46	0.47	
2:A:682:ALA:O	2:A:686:SER:HB2	2.14	0.47	
2:A:2:ASP:OD1	2:A:2:ASP:N	2.46	0.47	
2:A:124:CYS:SG	2:A:155:ARG:HA	2.54	0.47	
3:B:7:SER:OG	3:B:8:HIS:N	2.47	0.47	
1:C:325:ILE:HG13	1:C:326:ASN:N	C:326:ASN:N 2.30		
2:A:549:ASP:OD1	2:A:790:GLU:HB2	2.14	0.47	
2:A:555:PRO:HA	2:A:627:LEU:HD13	1.96	0.47	
3:B:61:ARG:HH21	3:B:210:ILE:HD13	1.79	0.47	
2:A:577:ARG:HG3	2:A:578:LEU:H	1.80	0.47	
3:B:56:PRO:HG2	3:B:59:ASN:HD21	1.78	0.47	
2:A:45:GLU:HG2	2:A:46:ILE:N	2.30	0.47	
2:A:290:ASP:N	2:A:290:ASP:OD1	2.38	0.47	
2:A:11:SER:HB2	2:A:19:TYR:HE2	1.79	0.47	
2:A:767:SER:HA	2:A:770:ILE:HG22	1.96	0.47	
1:C:319:LEU:HD22	1:C:413:ILE:HD11	1.96	0.47	
2:A:6:ILE:HD11	2:A:23:ARG:HB2	1.96	0.47	
2:A:384:THR:O	2:A:388:VAL:HG23	2.15	0.47	
3:B:42:THR:HG21	3:B:49:PHE:HZ	1.80	0.47	
2:A:299:ILE:CG2	2:A:318:PHE:HB3	2.45	0.46	
2:A:143:ASP:OD1	2:A:143:ASP:N	2.36	0.46	
2:A:371:ILE:HD12	2:A:416:LYS:HB2	1.96	0.46	
2:A:563:LEU:HD12	2:A:687:CYS:HB3	1.98	0.46	
2:A:866:ILE:HG21	2:A:870:ARG:HH21	1.80	0.46	
2:A:486:TYR:HE1	2:A:663:VAL:HB	1.80	0.46	
2:A:705:ALA:HA	2:A:744:ARG:HA	1.98	0.46	
2:A:398:ASP:N	2:A:398:ASP:OD1	2.47	0.46	
2:A:72:ILE:HD12	2:A:604:ARG:HD2	1.97	0.46	



	to as pagem	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
3:B:123:LEU:HD11	3:B:144:LEU:HD12	1.98	0.46	
2:A:305:SER:OG	2:A:307:HIS:O	2.33	0.46	
2:A:78:ILE:H	2:A:78:ILE:HG12	1.57	0.45	
2:A:185:HIS:CD2	2:A:203:ILE:HG12	2.51	0.45	
1:C:16:LEU:HD13	1:C:31:TYR:HB2	1.97	0.45	
2:A:398:ASP:HA	2:A:430:LYS:HE3	1.97	0.45	
3:B:213:ALA:HA	3:B:216:PHE:CE1	2.52	0.45	
2:A:19:TYR:OH	2:A:290:ASP:OD2	2.26	0.45	
2:A:602:GLU:O	2:A:685:LYS:NZ 2.28		0.45	
2:A:825:ASN:OD1	2:A:827:GLY:N	2.45	0.45	
2:A:825:ASN:CG	2:A:827:GLY:H	2.20	0.45	
2:A:890:PHE:HE2	2:A:892:LEU:HD23	1.81	0.45	
3:B:55:GLN:HE22	3:B:111:ASN:HD21	1.65	0.45	
3:B:154:VAL:HG13	3:B:177:ILE:HD13	1.97	0.45	
2:A:960:LEU:HD11	2:A:968:TYR:OH	2.17	0.45	
2:A:627:LEU:O	2:A:631:LEU:HG	2.17	0.45	
3:B:203:GLU:OE1	3:B:209:PRO:HG3	2.17	0.45	
2:A:169:CYS:SG	2:A:183:ILE:HG22	2.57	0.45	
2:A:224:ILE:HG22	2:A:229:GLU:HB3	1.99	0.45	
2:A:317:THR:OG1	2:A:319:HIS:NE2	2.42	0.45	
3:B:63:CYS:SG	3:B:152:VAL:HG21 2.57		0.45	
2:A:23:ARG:HH22	2:A:257:ASP:CG	2.20	0.44	
3:B:119:TRP:HZ2	3:B:144:LEU:HB3	1.83	0.44	
2:A:709:ASN:OD1	2:A:735:THR:HG23	2.16	0.44	
2:A:853:MET:HA	2:A:863:GLN:NE2	2.32	0.44	
2:A:992:PHE:HA	2:A:995:ARG:HG2	1.98	0.44	
3:B:205:ASP:OD1	3:B:205:ASP:N	2.49	0.44	
2:A:4:ARG:NH1	2:A:156:PHE:O	2.45	0.44	
2:A:370:PHE:HE2	2:A:429:TYR:HB2	1.83	0.44	
2:A:20:LEU:O	2:A:31:PHE:HA	2.18	0.44	
2:A:545:VAL:HG12	2:A:758:GLU:HA	2.00	0.44	
2:A:973:LYS:HA	2:A:976:THR:HG22	2.00	0.44	
2:A:990:ILE:O	2:A:994:GLN:HG2	2.18	0.44	
3:B:104:ASP:OD1	3:B:104:ASP:N	2.32	0.44	
3:B:198:ILE:HD12 3:B:198:ILE:H		1.83	0.44	
3:B:216:PHE:HB2 3:B:218:TYR:CZ		2.53	0.44	
2:A:766:LYS:HA	2:A:766:LYS:HA 2:A:766:LYS:HD3		0.43	
3:B:81:SER:OG	3:B:89:ILE:HG21	2.19	0.43	
2:A:420:SER:O	2:A:420:SER:OG	2.25	0.43	
2:A:809:MET:HG3	2:A:810:LYS:N	2.33	0.43	
2:A:521:GLU:OE2	2:A:522:THR:N	2.46	0.43	



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
2:A:103:THR:OG1	2:A:104:MET:N	2.51	0.43	
2:A:810:LYS:HD3	2:A:810:LYS:HA	1.75	0.43	
2:A:423:THR:O	2:A:424:LEU:HD23	2.19	0.43	
2:A:573:VAL:HG22	2:A:608:LEU:HD22	2.00	0.43	
3:B:153:SER:O	3:B:154:VAL:HG23	2.18	0.43	
2:A:358:GLY:HA2	2:A:371:ILE:O	2.18	0.43	
1:C:4:SER:O	1:C:8:THR:HG23	2.18	0.43	
1:C:383:LYS:HB3	1:C:383:LYS:HE2	1.79	0.43	
2:A:106:GLU:H	2:A:106:GLU:HG2	1.66	0.43	
2:A:401:ILE:HG22	2:A:403:CYS:SG	2.59	0.43	
2:A:638:LYS:HD3	2:A:657:GLN:HG3	2.01	0.43	
3:B:167:ARG:NH2	3:B:173:PRO:HA	2.33	0.43	
2:A:642:LYS:HB2	2:A:642:LYS:HE3	1.80	0.42	
2:A:64:ARG:HE	2:A:515:THR:HG22	1.83	0.42	
2:A:108:PHE:CE2	2:A:500:THR:HG23	2.54	0.42	
2:A:575:THR:HA	2:A:608:LEU:HD23	2.01	0.42	
2:A:867:ASP:O	2:A:871:SER:OG	2.25	0.42	
2:A:64:ARG:NE	2:A:515:THR:HG22	2.35	0.42	
3:B:113:ILE:HG12	3:B:215:GLY:HA3	2.00	0.42	
1:C:314:ALA:HB3	1:C:409:GLN:HB3	2.00	0.42	
2:A:811:TYR:CE1	2:A:826:LYS:HD3	2.55	0.42	
2:A:844:LYS:HA	2:A:847:LYS:HE2	2.01	0.42	
2:A:685:LYS:HE3	2:A:685:LYS:HB3	1.84	0.42	
2:A:339:GLU:HG3	2:A:341:LEU:HD13	2.01	0.42	
2:A:862:ASN:HA	2:A:865:CYS:SG	2.60	0.42	
2:A:751:ASP:OD1	2:A:751:ASP:N	2.53	0.42	
3:B:165:ASN:OD1	3:B:165:ASN:N	2.53	0.42	
2:A:335:ILE:HG21	2:A:349:ILE:HD13	2.02	0.42	
2:A:828:THR:HG22	2:A:828:THR:O	2.20	0.42	
2:A:114:TYR:HD2	2:A:487:VAL:HG12	1.84	0.41	
2:A:840:LYS:NZ	2:A:974:ARG:HH12	2.16	0.41	
2:A:213:ILE:O	2:A:217:VAL:HG23	2.20	0.41	
3:B:140:ILE:H	3:B:140:ILE:HG12	1.45	0.41	
2:A:488:LEU:HD23	2:A:488:LEU:HA	1.94	0.41	
3:B:86:LYS:O	3:B:90:LYS:HE2	2.21	0.41	
1:C:19:SER:O	1:C:19:SER:OG	2.32	0.41	
1:C:3:SER:HA	3:B:192:ASP:HA	2.03	0.41	
1:C:155:ALA:O	1:C:159:GLY:N	2.54	0.41	
2:A:132:LEU:HB3	2:A:140:TYR:HB3	2.03	0.41	
2:A:607:ASN:OD1	2:A:607:ASN:N	2.52	0.41	
2:A:749:TYR:CE2	2:A:756:PHE:HB2	2.56	0.41	



Atom 1	Atom 2	Interatomic	Clash		
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)		
1:C:383:LYS:HE3 1:C:415:ASN:HB3		2.03	0.41		
2:A:131:TYR:HD2	2:A:148:CYS:HB2	1.85	0.41		
2:A:532:LYS:HA	2:A:532:LYS:HD2	1.84	0.41		
2:A:809:MET:HG3	2:A:823:ARG:HA	2.03	0.41		
3:B:178:VAL:HG22	3:B:179:GLY:N	2.35	0.41		
2:A:132:LEU:HD23	2:A:142:CYS:HB2	2.03	0.40		
2:A:283:LYS:HE3	2:A:283:LYS:HB2	1.79	0.40		
2:A:342:ASP:OD1	2:A:343:SER:N	2.53	0.40		
2:A:695:ILE:O	2:A:699:GLU:HG3	2.20	0.40		
2:A:249:LYS:O	2:A:253:GLU:HG3	2.21	0.40		
2:A:706:GLU:OE1	2:A:770:ILE:HD11	2.21	0.40		
2:A:778:ILE:O	2:A:783:LEU:HD23	2.22	0.40		
3:B:121:TYR:OH	3:B:169:LYS:HD3	2.22	0.40		
2:A:251:LEU:HD23	2:A:251:LEU:HA	1.95	0.40		
2:A:860:ASN:O	2:A:864:VAL:HG12	2.21	0.40		
3:B:196:GLU:HA	3:B:199:ASN:ND2	2.36	0.40		

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	Perce	ntiles
1	С	315/426~(74%)	290 (92%)	24 (8%)	1 (0%)	41	73
2	А	927/1006~(92%)	830 (90%)	97 (10%)	0	100	100
3	В	214/218~(98%)	192 (90%)	22 (10%)	0	100	100
All	All	1456/1650~(88%)	1312 (90%)	143 (10%)	1 (0%)	54	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	С	364	PRO



#### 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	С	118/396~(30%)	111 (94%)	7~(6%)	19 50
2	А	856/928~(92%)	790~(92%)	66 (8%)	13 41
3	В	195/200~(98%)	179 (92%)	16 (8%)	11 38
All	All	1169/1524~(77%)	1080 (92%)	89 (8%)	17 41

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	С	32	ASN
1	С	316	LEU
1	С	320	THR
1	С	332	ASP
1	С	363	TYR
1	С	372	VAL
1	С	419	ASP
2	А	2	ASP
2	А	42	VAL
2	А	65	THR
2	А	73	SER
2	А	77	ASP
2	А	78	ILE
2	А	83	CYS
2	А	84	SER
2	А	95	LYS
2	А	126	SER
2	А	136	ASN
2	А	152	GLU
2	А	157	ASP
2	А	161	SER
2	A	170	HIS
2	А	223	ARG
2	А	225	GLN
2	A	230	MET
2	А	280	THR



Mol	Chain	Res	Type
2	А	288	SER
2	А	290	ASP
2	А	322	ASN
2	А	338	SER
2	А	347	ASP
2	А	348	SER
2	А	355	SER
2	А	403	CYS
2	А	409	ASP
2	А	420	SER
2	А	430	LYS
2	А	433	PHE
2	А	436	ASP
2	А	439	ASP
2	А	443	MET
2	А	462	ASP
2	А	486	TYR
2	А	497	ARG
2	А	499	SER
2	А	547	ILE
2	А	566	GLU
2	А	578	LEU
2	А	589	GLN
2	А	599	VAL
2	А	605	LEU
2	А	657	GLN
2	А	658	TYR
2	А	686	SER
2	А	687	CYS
2	А	709	ASN
2	А	717	THR
2	A	735	THR
2	A	748	VAL
2	A	749	TYR
2	A	752	THR
2	A	757	THR
2	A	763	ASP
2	A	775	GLU
2	A	784	PHE
2	A	791	PHE
2	А	832	ARG
2	А	836	SER



Mol	Chain	Res	Type
2	А	870	ARG
2	А	887	LEU
2	А	972	PHE
2	А	977	SER
2	А	992	PHE
3	В	14	THR
3	В	38	LEU
3	В	68	ASP
3	В	84	PHE
3	В	85	THR
3	В	116	VAL
3	В	120	ASN
3	В	135	ILE
3	В	140	ILE
3	В	153	SER
3	В	158	LEU
3	В	160	LYS
3	В	165	ASN
3	В	180	TYR
3	В	185	ARG
3	В	208	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	С	321	ASN
2	А	185	HIS
2	А	322	ASN
2	А	336	GLN
2	А	442	GLN
2	А	562	ASN
2	А	860	ASN
2	А	863	GLN
3	В	25	GLN
3	В	55	GLN
3	В	59	ASN
3	В	111	ASN
3	В	146	GLN
3	В	188	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-34887. 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.

## 6.1 Orthogonal projections (i)

#### 6.1.1 Primary map



6.1.2 Raw map



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



### 6.2 Central slices (i)

#### 6.2.1 Primary map



X Index: 128



Y Index: 128



Z Index: 128

#### 6.2.2 Raw map



X Index: 128

Y Index: 128

Z Index: 128

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: 148



Y Index: 130



Z Index: 103

#### 6.3.2 Raw map



X Index: 125

Y Index: 130



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



## 6.4 Orthogonal standard-deviation projections (False-color) (i)

#### 6.4.1 Primary map



6.4.2 Raw map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



## 6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

#### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

#### 6.6 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 99  $\rm nm^3;$  this corresponds to an approximate mass of 89 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 0.323  $\mathrm{\AA^{-1}}$ 



## 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 0.323  $\mathrm{\AA^{-1}}$ 



## 8.2 Resolution estimates (i)

$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	Estimation criterion (FSC cut-off)		
Resolution estimate (A)	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.30	3.64	3.35

\*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-34887 and PDB model 8HM0. Per-residue inclusion information can be found in section 3 on page 4.

## 9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.012 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 (0.012).



### 9.4 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 80% 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 (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7950	0.4650
А	0.8320	0.5040
В	0.8710	0.4600
С	0.5910	0.3190

