

#### Feb 13, 2024 – 08:37 AM EST

PDB ID	:	3J9D
EMDB ID	:	EMD-6239
Title	:	Atomic structure of a non-enveloped virus reveals pH sensors for a coordinated
		process of cell entry
Authors	:	Zhang, X.; Patel, A.; Celma, C.; Roy, P.; Zhou, Z.H.
Deposited on	:	2015-01-09
Resolution	:	3.30  Å(reported)
This is	a I	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 3.30 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				
1	А	961	36%	32%	9%	22%	



# 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6086 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 Outer capsid protein VP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	А	746	Total 6085	C 3891	N 1057	0 1105	S 32	0	0

• Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
2	А	1	Total Zn 1 1	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: Outer capsid protein VP2





# L633 1854 6778 8779 8779 K944 D866 Y780 Y711 L941 V860 T781 Y713 L942 V860 T781 Y713 F944 D866 Y780 Y713 F944 D866 Y780 Y713 F944 D866 Y780 Y713 F944 D866 Y780 Y713 F943 D865 T865 T719 F943 T865 T781 T719 D865 D876 T781 T719 D865 D875 T789 T719 D865 D876 T793 T719 D865 D888 T780 T724 D866 D888 T780 T724 D866 D888 T780 T743 D866 D888 T800 T743 D866 D888 T800 T744 D890 D866 T803 T744



# 4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	5008	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	20	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	24140	Depositor
Image detector	GATAN K2 $(4k \times 4k)$	Depositor
Maximum map value	5.239	Depositor
Minimum map value	-3.042	Depositor
Average map value	0.013	Depositor
Map value standard deviation	0.220	Depositor
Recommended contour level	0.9	Depositor
Map size (Å)	133.31999, 161.6, 147.45999	wwPDB
Map dimensions	160, 132, 146	wwPDB
Map angles $(^{\circ})$	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.01, 1.01, 1.01	Depositor



# 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: ZN

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	Bo	nd lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	1.35	9/6221~(0.1%)	0.92	12/8420~(0.1%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	А	0	6

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\operatorname{Ideal}(\operatorname{\AA})$
1	А	465	TYR	CD2-CE2	45.19	2.07	1.39
1	А	465	TYR	CD1-CE1	44.69	2.06	1.39
1	А	465	TYR	CE1-CZ	33.15	1.81	1.38
1	А	465	TYR	CE2-CZ	32.32	1.80	1.38
1	А	465	TYR	CG-CD2	24.61	1.71	1.39
1	А	465	TYR	CG-CD1	24.48	1.71	1.39
1	А	771	MET	SD-CE	21.19	2.96	1.77
1	А	156	GLU	CG-CD	8.55	1.64	1.51
1	А	156	GLU	CB-CG	8.30	1.68	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	771	MET	CG-SD-CE	18.30	129.48	100.20
1	А	723	LEU	CA-CB-CG	7.79	133.21	115.30
1	А	63	ASN	C-N-CD	-7.43	104.25	120.60
1	А	778	GLY	N-CA-C	-6.53	96.77	113.10



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	724	LEU	CA-CB-CG	6.24	129.65	115.30
1	А	727	LEU	CA-CB-CG	5.88	128.83	115.30
1	А	16	HIS	N-CA-C	-5.75	95.49	111.00
1	А	63	ASN	N-CA-C	5.69	126.36	111.00
1	А	47	ASN	C-N-CA	5.34	135.04	121.70
1	А	63	ASN	C-N-CA	5.34	144.42	122.00
1	А	862	LEU	CA-CB-CG	5.17	127.19	115.30
1	А	922	ILE	CG1-CB-CG2	-5.14	100.09	111.40

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	27	VAL	Peptide
1	А	34	VAL	Peptide
1	А	38	HIS	Peptide
1	А	49	TYR	Peptide
1	А	55	SER	Peptide
1	А	62	TYR	Peptide

# 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	А	6085	0	6087	282	0
2	А	1	0	0	0	0
All	All	6086	0	6087	282	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 23.

All (282) 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)
1:A:465:TYR:CZ	1:A:465:TYR:CE2	1.80	1.65



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Atom-1	Atom_2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:465:TYR:CZ	1:A:465:TYR:CE1	1.81	1.60
1:A:465:TYR:CE1	1:A:465:TYR:CD1	2.06	1.43
1:A:465:TYR:CE2	1:A:465:TYR:CD2	2.07	1.39
1:A:465:TYR:CE2	1:A:771:MET:SD	2.35	1.19
1:A:465:TYR:CD2	1:A:771:MET:SD	2.36	1.18
1:A:465:TYR:CZ	1:A:771:MET:SD	2.39	1.16
1:A:465:TYR:CD1	1:A:771:MET:SD	2.39	1.15
1:A:465:TYR:CE1	1:A:771:MET:SD	2.41	1.14
1:A:465:TYR:CZ	1:A:771:MET:CE	2.33	1.12
1:A:465:TYR:CE1	1:A:771:MET:CE	2.32	1.12
1:A:465:TYR:CG	1:A:771:MET:SD	2.44	1.11
1:A:465:TYR:CE2	1:A:771:MET:CE	2.35	1.10
1:A:465:TYR:CD1	1:A:771:MET:CE	2.38	1.07
1:A:465:TYR:CD2	1:A:771:MET:CE	2.39	1.05
1:A:465:TYR:CG	1:A:771:MET:CE	2.46	0.98
1:A:559:ILE:HG12	1:A:628:ARG:HE	1.29	0.96
1:A:465:TYR:CZ	1:A:771:MET:HE3	2.00	0.94
1:A:607:ARG:HE	1:A:627:GLU:HG3	1.33	0.92
1:A:47:ASN:O	1:A:47:ASN:ND2	2.03	0.91
1:A:465:TYR:CD2	1:A:771:MET:HE1	2.06	0.90
1:A:465:TYR:CD1	1:A:771:MET:HE2	2.08	0.88
1:A:47:ASN:HB2	1:A:119:LYS:HG2	1.57	0.86
1:A:435:THR:HA	1:A:654:PRO:HD2	1.55	0.85
1:A:544:ASP:HB3	1:A:577:ARG:HG3	1.62	0.82
1:A:714:ALA:HB2	1:A:721:GLY:HA3	1.62	0.81
1:A:803:PHE:O	1:A:805:LYS:N	2.13	0.81
1:A:74:ARG:NE	1:A:114:ASP:OD2	2.16	0.78
1:A:516:TYR:HE1	1:A:532:ILE:HD11	1.49	0.78
1:A:1:MET:HG2	1:A:948:VAL:HG13	1.68	0.75
1:A:465:TYR:CE1	1:A:771:MET:HE2	2.23	0.73
1:A:177:GLU:HA	1:A:180:HIS:CE1	2.23	0.72
1:A:734:GLN:HA	1:A:737:MET:HE3	1.71	0.72
1:A:465:TYR:CE2	1:A:771:MET:HE3	2.26	0.70
1:A:661:GLU:HB3	1:A:686:ARG:HD3	1.73	0.70
1:A:47:ASN:HA	1:A:48:ALA:CB	2.23	0.69
1:A:483:LYS:HB2	1:A:486:LYS:HD3	1.75	0.68
1:A:772:VAL:HG21	1:A:813:ILE:HG21	1.75	0.68
1:A:73:PRO:HD2	1:A:114:ASP:HB3	1.77	0.67
1:A:459:LYS:HB2	1:A:489:LYS:HD3	1.77	0.67
1:A:611:GLN:HB3	1:A:612:ILE:HB	1.76	0.67
1:A:6:ILE:HG21	1:A:23:PHE:HD2	1.60	0.67



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		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:506:THR:OG1	1:A:507:THR:N	2.25	0.67
1:A:617:CYS:SG	1:A:619:THR:OG1	2.50	0.67
1:A:169:MET:HE1	1:A:623:GLN:HG3	1.78	0.66
1:A:458:THR:HG22	1:A:493:ASN:HA	1.76	0.66
1:A:465:TYR:OH	1:A:771:MET:HA	1.96	0.65
1:A:641:VAL:HG21	1:A:681:ILE:HG23	1.77	0.65
1:A:458:THR:CG2	1:A:493:ASN:HA	2.27	0.65
1:A:146:ASP:N	1:A:146:ASP:OD1	2.25	0.65
1:A:83:TYR:HB2	1:A:961:VAL:HG21	1.78	0.64
1:A:559:ILE:HD11	1:A:628:ARG:HH11	1.61	0.64
1:A:607:ARG:HE	1:A:627:GLU:CG	2.07	0.64
1:A:140:ILE:HG13	1:A:148:MET:HE1	1.78	0.64
1:A:47:ASN:HA	1:A:48:ALA:HB2	1.79	0.64
1:A:687:ARG:HH11	1:A:687:ARG:HB2	1.63	0.64
1:A:425:VAL:HG21	1:A:499:PHE:CE1	2.33	0.63
1:A:923:VAL:HG13	1:A:944:PHE:CE1	2.34	0.63
1:A:559:ILE:HG12	1:A:628:ARG:NE	2.08	0.63
1:A:420:PRO:HD3	1:A:540:ARG:HB3	1.81	0.62
1:A:184:GLU:OE1	1:A:184:GLU:N	2.23	0.62
1:A:702:ARG:HA	1:A:709:ARG:HH12	1.65	0.61
1:A:465:TYR:CE1	1:A:771:MET:HG3	2.36	0.61
1:A:493:ASN:O	1:A:497:ILE:HG23	2.01	0.61
1:A:557:ASP:HB3	1:A:597:ARG:CZ	2.31	0.61
1:A:563:ARG:O	1:A:791:GLU:HG3	2.01	0.60
1:A:631:LEU:HD13	1:A:658:HIS:H	1.65	0.60
1:A:465:TYR:CE1	1:A:771:MET:CG	2.85	0.60
1:A:599:ASP:OD2	1:A:628:ARG:NH2	2.34	0.60
1:A:732:VAL:HA	1:A:805:LYS:HA	1.84	0.60
1:A:446:CYS:HB3	1:A:795:PHE:CD1	2.37	0.59
1:A:155:ILE:HG12	1:A:853:GLY:O	2.04	0.58
1:A:859:VAL:HB	1:A:875:GLU:HG2	1.85	0.58
1:A:63:ASN:HA	1:A:835:VAL:HG22	1.86	0.58
1:A:763:LEU:HD13	1:A:775:LEU:HD21	1.84	0.58
1:A:687:ARG:HB2	1:A:687:ARG:NH1	2.19	0.58
1:A:634:ILE:HD11	1:A:676:LEU:HD13	1.86	0.57
1:A:176:ILE:HD13	1:A:670:ILE:HG13	1.86	0.57
1:A:419:GLU:HG3	1:A:420:PRO:HD2	1.85	0.57
1:A:448:LEU:HD11	1:A:767:THR:HG21	1.86	0.57
1:A:116:GLN:HG3	1:A:118:LEU:HD21	1.86	0.57
1:A:863:PRO:HG3	1:A:955:LEU:HD23	1.85	0.57
1:A:86:ARG:HG2	1:A:100:THR:HA	1.86	0.56



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		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:663:PHE:O	1:A:687:ARG:HA	2.05	0.56
1:A:64:PRO:HG3	1:A:838:THR:HG21	1.86	0.56
1:A:657:ASP:HB3	1:A:660:LEU:HB2	1.88	0.56
1:A:606:ARG:HH11	1:A:606:ARG:HB3	1.71	0.56
1:A:548:LYS:HG3	1:A:553:PRO:HB2	1.88	0.56
1:A:23:PHE:CD1	1:A:140:ILE:HG12	2.41	0.55
1:A:885:ILE:HG13	1:A:886:ARG:N	2.21	0.55
1:A:49:TYR:CD2	1:A:841:LEU:HD13	2.41	0.55
1:A:757:ARG:O	1:A:758:GLN:HB2	2.07	0.55
1:A:74:ARG:O	1:A:78:ILE:HG12	2.05	0.55
1:A:516:TYR:CE1	1:A:532:ILE:HD11	2.37	0.55
1:A:444:ASN:N	1:A:445:PRO:HD3	2.22	0.55
1:A:477:TRP:CH2	1:A:774:PRO:HB3	2.42	0.55
1:A:415:ASP:HA	1:A:541:GLN:HE21	1.72	0.54
1:A:3:GLU:HB3	1:A:943:LYS:HA	1.89	0.54
1:A:9:TYR:HE1	1:A:24:ILE:HG23	1.73	0.54
1:A:681:ILE:HG22	1:A:682:PHE:CD2	2.42	0.54
1:A:771:MET:SD	1:A:771:MET:CE	2.96	0.53
1:A:27:VAL:HG12	1:A:136:CYS:HB3	1.91	0.53
1:A:73:PRO:HB3	1:A:893:ARG:NH1	2.23	0.53
1:A:172:HIS:HD1	1:A:750:ASP:HB3	1.73	0.53
1:A:841:LEU:O	1:A:845:THR:HG23	2.09	0.53
1:A:798:SER:H	1:A:801:ILE:HD12	1.74	0.53
1:A:446:CYS:HB3	1:A:795:PHE:CE1	2.43	0.53
1:A:598:GLN:O	1:A:599:ASP:HB3	2.09	0.53
1:A:102:ASP:O	1:A:106:GLN:HG2	2.09	0.53
1:A:184:GLU:HG3	1:A:426:HIS:ND1	2.24	0.53
1:A:23:PHE:HD1	1:A:140:ILE:HG12	1.73	0.53
1:A:740:ASN:O	1:A:743:PRO:HD2	2.09	0.53
1:A:62:TYR:CE2	1:A:64:PRO:HB3	2.44	0.52
1:A:527:ASN:HB2	1:A:795:PHE:HZ	1.74	0.52
1:A:683:GLU:HB3	1:A:685:ARG:HG3	1.91	0.52
1:A:737:MET:HG3	1:A:766:TYR:OH	2.09	0.52
1:A:57:ARG:H	1:A:57:ARG:HD2	1.73	0.52
1:A:78:ILE:HD12	1:A:108:MET:CG	2.40	0.52
1:A:520:TRP:HA	1:A:531:ARG:HB3	1.91	0.52
1:A:465:TYR:CG	1:A:771:MET:HE1	2.35	0.52
1:A:460:PHE:CE2	$1:A:525:ME\overline{T:HG2}$	2.45	0.52
1:A:938:ASP:N	1:A:938:ASP:OD1	2.42	0.52
1:A:490:SER:O	1:A:492:GLY:HA2	2.10	0.51
1:A:750:ASP:OD1	1:A:750:ASP:N	2.43	0.51



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		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:425:VAL:HG21	1:A:499:PHE:HE1	1.74	0.51
1:A:524:PRO:HD2	1:A:525:MET:HE2	1.91	0.51
1:A:559:ILE:CG1	1:A:628:ARG:HE	2.12	0.51
1:A:438:ILE:HG12	1:A:444:ASN:H	1.76	0.51
1:A:170:TRP:HZ3	1:A:847:LEU:HB2	1.75	0.50
1:A:23:PHE:CE2	1:A:860:TRP:HZ3	2.29	0.50
1:A:639:GLN:HG3	1:A:653:HIS:NE2	2.27	0.50
1:A:864:ILE:HB	1:A:870:CYS:O	2.11	0.50
1:A:133:LEU:HD23	1:A:134:HIS:N	2.27	0.49
1:A:606:ARG:HD3	1:A:627:GLU:OE1	2.12	0.49
1:A:607:ARG:NE	1:A:627:GLU:HG3	2.14	0.49
1:A:23:PHE:CE1	1:A:138:VAL:HG13	2.47	0.49
1:A:755:SER:HA	1:A:829:GLY:HA3	1.94	0.49
1:A:655:LYS:HG2	1:A:656:ALA:O	2.12	0.49
1:A:861:TYR:HB3	1:A:871:ILE:HG23	1.93	0.49
1:A:187:TYR:HB2	1:A:425:VAL:CG2	2.42	0.49
1:A:438:ILE:HG12	1:A:444:ASN:N	2.27	0.49
1:A:544:ASP:OD2	1:A:589:THR:HG23	2.13	0.49
1:A:907:ILE:HD12	1:A:907:ILE:H	1.78	0.49
1:A:78:ILE:HD12	1:A:108:MET:HG3	1.94	0.49
1:A:746:PHE:N	1:A:746:PHE:CD1	2.80	0.49
1:A:747:LEU:HD21	1:A:777:VAL:HG11	1.95	0.48
1:A:62:TYR:CG	1:A:63:ASN:N	2.80	0.48
1:A:572:ILE:HG12	1:A:783:ARG:HH12	1.79	0.48
1:A:941:LEU:HD13	1:A:941:LEU:HA	1.61	0.48
1:A:441:ALA:N	1:A:647:GLU:HB3	2.29	0.48
1:A:676:LEU:HG	1:A:688:VAL:HG22	1.96	0.48
1:A:923:VAL:HG12	1:A:924:SER:N	2.28	0.48
1:A:433:HIS:CE1	1:A:436:ARG:HD3	2.49	0.48
1:A:411:VAL:HG21	1:A:416:PHE:CD1	2.49	0.48
1:A:777:VAL:HG23	1:A:777:VAL:O	2.14	0.48
1:A:120:VAL:HG12	1:A:131:HIS:CE1	2.49	0.48
1:A:133:LEU:HD23	1:A:134:HIS:H	1.78	0.48
1:A:182:ALA:HB1	1:A:554:ILE:HD11	1.96	0.48
1:A:522:ILE:HG12	1:A:529:LYS:HG3	1.95	0.47
1:A:568:ARG:HD3	1:A:780:TYR:HB3	1.96	0.47
1:A:70:PHE:CD1	1:A:70:PHE:N	2.82	0.47
1:A:711:ASN:O	1:A:715:GLU:HB2	2.14	0.47
1:A:544:ASP:CG	1:A:544:ASP:O	2.53	0.47
1:A:596:LYS:HB2	1:A:596:LYS:HE3	1.42	0.47
1:A:7:PRO:HG2	$1:A:24:ILE:HG1\overline{2}$	1.96	0.47



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		Interatomic	Clash	
Atom-1	Atom-2	distance $(\text{\AA})$	overlap (Å)	
1:A:78:ILE:HG23	1:A:108:MET:HG2	1.96	0.47	
1:A:480:GLU:OE2	1:A:759:TRP:NE1	2.48	0.47	
1:A:754:TYR:CE2	1:A:784:CYS:HB2	2.50	0.47	
1:A:477:TRP:HH2	1:A:774:PRO:HB3	1.80	0.47	
1:A:25:ILE:HG21	1:A:909:ILE:HD11	1.97	0.46	
1:A:74:ARG:NH1	1:A:78:ILE:HD11	2.30	0.46	
1:A:181:ALA:HB3	1:A:545:PRO:HB2	1.98	0.46	
1:A:604:LEU:HD12	1:A:604:LEU:HA	1.63	0.46	
1:A:123:ASP:OD1	1:A:124:ASP:N	2.48	0.46	
1:A:743:PRO:HG3	1:A:821:TYR:OH	2.15	0.46	
1:A:172:HIS:NE2	1:A:669:ASP:HA	2.30	0.46	
1:A:498:ASP:O	1:A:502:ASP:HB2	2.16	0.46	
1:A:19:ARG:HD3	1:A:126:SER:HB2	1.98	0.46	
1:A:916:THR:O	1:A:916:THR:OG1	2.31	0.46	
1:A:757:ARG:HG2	1:A:782:ASP:OD2	2.16	0.46	
1:A:444:ASN:ND2	1:A:794:VAL:O	2.50	0.45	
1:A:58:THR:HG22	1:A:61:TRP:NE1	2.32	0.45	
1:A:414:PHE:HB2	1:A:573:ARG:HH11	1.81	0.45	
1:A:587:GLN:NE2	1:A:591:ASP:OD2	2.49	0.45	
1:A:416:PHE:HB3	1:A:549:ARG:NH2	2.31	0.45	
1:A:708:GLU:H	1:A:708:GLU:HG3	1.52	0.45	
1:A:587:GLN:NE2	1:A:618:PRO:HD3	2.32	0.45	
1:A:677:ALA:O	1:A:681:ILE:HB	2.15	0.45	
1:A:776:GLU:HG2	1:A:778:GLY:HA2	1.98	0.45	
1:A:429:TYR:CD1	1:A:429:TYR:C	2.90	0.45	
1:A:714:ALA:HB2	1:A:721:GLY:CA	2.41	0.45	
1:A:905:VAL:CG2	1:A:923:VAL:HG11	2.47	0.45	
1:A:514:PRO:O	1:A:516:TYR:N	2.47	0.45	
1:A:62:TYR:CD1	1:A:63:ASN:N	2.78	0.44	
1:A:422:ILE:O	1:A:422:ILE:HG13	2.17	0.44	
1:A:434:SER:HB2	1:A:563:ARG:HH12	1.82	0.44	
1:A:465:TYR:CZ	1:A:771:MET:CG	3.00	0.44	
1:A:33:SER:HB2	1:A:38:HIS:HB3	2.00	0.44	
1:A:35:GLY:HA2	1:A:36:GLY:HA2	1.66	0.44	
1:A:181:ALA:HB1	1:A:546:MET:HB3	1.99	0.44	
1:A:742:LEU:HA	1:A:742:LEU:HD23	1.65	0.44	
1:A:755:SER:HA	1:A:829:GLY:CA	2.47	0.44	
1:A:151:HIS:CG	1:A:151:HIS:O	2.70	0.44	
1:A:956:THR:O	1:A:960:ASN:HB2	2.17	0.44	
1:A:43:ILE:HA	1:A:46:MET:HG2	2.00	0.44	
1:A:44:PRO:HD3	1:A:581:LEU:CD1	2.48	0.44	



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	h i o	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:653:HIS:HB3	1:A:654:PRO:HD3	2.00	0.44
1:A:606:ARG:NH2	1:A:660:LEU:O	2.50	0.44
1:A:923:VAL:HG12	1:A:924:SER:H	1.83	0.44
1:A:26:ASP:C	1:A:28:GLY:HA3	2.38	0.44
1:A:959:LEU:C	1:A:961:VAL:H	2.21	0.44
1:A:488:LEU:HB2	1:A:493:ASN:HD22	1.83	0.43
1:A:701:ILE:HD13	1:A:713:ILE:HG12	2.00	0.43
1:A:607:ARG:NH1	1:A:623:GLN:HG2	2.33	0.43
1:A:757:ARG:H	1:A:757:ARG:HG3	1.47	0.43
1:A:862:LEU:HA	1:A:863:PRO:HD3	1.90	0.43
1:A:9:TYR:CD1	1:A:9:TYR:N	2.86	0.43
1:A:9:TYR:OH	1:A:26:ASP:HB2	2.19	0.43
1:A:59:ALA:O	1:A:62:TYR:HB3	2.18	0.43
1:A:140:ILE:HG21	1:A:145:ALA:HA	2.01	0.43
1:A:435:THR:O	1:A:435:THR:OG1	2.31	0.43
1:A:80:LEU:HA	1:A:80:LEU:HD23	1.56	0.43
1:A:448:LEU:HD23	1:A:448:LEU:HA	1.71	0.43
1:A:502:ASP:HB3	1:A:514:PRO:HG3	2.00	0.43
1:A:854:ILE:HG12	1:A:855:SER:N	2.34	0.43
1:A:505:LEU:HB2	1:A:506:THR:HA	1.99	0.43
1:A:508:ASN:HA	1:A:509:GLU:HA	1.74	0.43
1:A:527:ASN:HB2	1:A:795:PHE:CZ	2.53	0.43
1:A:799:LYS:HG2	1:A:803:PHE:CE1	2.53	0.43
1:A:432:ASN:HB3	1:A:527:ASN:OD1	2.19	0.43
1:A:890:ILE:HD13	1:A:890:ILE:HA	1.66	0.43
1:A:559:ILE:H	1:A:559:ILE:HG13	1.67	0.42
1:A:637:LEU:HD23	1:A:637:LEU:HA	1.70	0.42
1:A:642:VAL:HG13	1:A:734:GLN:OE1	2.19	0.42
1:A:155:ILE:HG22	1:A:156:GLU:O	2.19	0.42
1:A:607:ARG:HA	1:A:607:ARG:HD3	1.42	0.42
1:A:705:ARG:HD3	1:A:705:ARG:HA	1.87	0.42
1:A:479:GLN:HG3	1:A:480:GLU:N	2.35	0.42
1:A:574:PRO:HB2	1:A:576:LEU:HD22	2.01	0.42
1:A:841:LEU:HD23	1:A:841:LEU:HA	1.92	0.42
1:A:74:ARG:HH12	1:A:78:ILE:HD11	1.85	0.42
1:A:144:LYS:HD2	1:A:144:LYS:HA	1.68	0.42
1:A:18:LEU:HA	1:A:18:LEU:HD12	1.59	0.42
1:A:473:ILE:HG13	1:A:813:ILE:HD12	2.00	0.42
1:A:419:GLU:O	1:A:422:ILE:HG23	2.20	0.42
1:A:592:GLU:O	1:A:595:SER:HB3	2.20	0.42
1:A:116:GLN:HA	1:A:117:PRO:HD3	1.90	0.41



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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:679:ASP:O	1:A:683:GLU:HB2	2.20	0.41
1:A:917:VAL:HG12	1:A:918:TYR:N	2.35	0.41
1:A:138:VAL:HB	1:A:858:ILE:HD11	2.01	0.41
1:A:665:GLU:HG3	1:A:690:ASP:OD1	2.20	0.41
1:A:631:LEU:HD23	1:A:631:LEU:HA	1.69	0.41
1:A:736:ILE:HG12	1:A:814:ALA:CB	2.51	0.41
1:A:739:LEU:HD11	1:A:818:LEU:HB2	2.01	0.41
1:A:737:MET:HE2	1:A:737:MET:HB2	1.82	0.41
1:A:949:PHE:O	1:A:949:PHE:CD1	2.74	0.41
1:A:187:TYR:HB2	1:A:425:VAL:HG22	2.02	0.41
1:A:758:GLN:HA	1:A:776:GLU:CD	2.41	0.41
1:A:910:ASP:HB2	1:A:914:GLU:O	2.21	0.41
1:A:661:GLU:HB3	1:A:686:ARG:CD	2.47	0.41
1:A:674:ILE:HG12	1:A:744:LEU:HD22	2.02	0.41
1:A:70:PHE:CE2	1:A:117:PRO:HB3	2.56	0.41
1:A:78:ILE:HD12	1:A:108:MET:HG2	2.03	0.41
1:A:747:LEU:HD22	1:A:747:LEU:HA	1.85	0.41
1:A:760:SER:HB2	1:A:774:PRO:HB2	2.03	0.41
1:A:881:VAL:HG23	1:A:882:PRO:HD2	2.02	0.41
1:A:154:PRO:HB3	1:A:848:ALA:CA	2.51	0.41
1:A:154:PRO:HB3	1:A:848:ALA:HA	2.02	0.41
1:A:31:ILE:HA	1:A:31:ILE:HD12	1.60	0.40
1:A:574:PRO:HB2	1:A:576:LEU:CD2	2.51	0.40
1:A:802:ARG:O	1:A:802:ARG:HG2	2.19	0.40
1:A:952:ASP:N	1:A:952:ASP:OD1	2.52	0.40
1:A:169:MET:CE	1:A:623:GLN:HG3	2.50	0.40
1:A:701:ILE:HG12	1:A:712:VAL:HG23	2.03	0.40
1:A:872:VAL:HG13	1:A:903:GLY:O	2.21	0.40
1:A:6:ILE:HG22	1:A:23:PHE:HB3	2.04	0.40
1:A:860:TRP:CD1	1:A:860:TRP:C	2.94	0.40
1:A:6:ILE:H	1:A:6:ILE:HG12	1.80	0.40
1:A:632:PHE:CZ	1:A:636:ILE:HD11	2.57	0.40
1:A:766:TYR:CD1	1:A:797:PRO:HG3	2.57	0.40
1:A:176:ILE:HD13	1:A:670:ILE:CG1	2.51	0.40
1:A:517:PHE:O	1:A:517:PHE:CG	2.75	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	Percentiles
1	А	742/961~(77%)	665~(90%)	61 (8%)	16 (2%)	6 30

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	48	ALA
1	А	804	SER
1	А	15	GLU
1	А	540	ARG
1	А	897	SER
1	А	516	TYR
1	А	729	SER
1	А	668	VAL
1	А	960	ASN
1	А	117	PRO
1	А	442	GLN
1	А	781	ASN
1	А	806	LEU
1	А	129	VAL
1	А	511	VAL
1	А	770	VAL

#### 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 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.



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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	666/863~(77%)	516~(78%)	150 (22%)	1 3

All (150) residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	А	3	GLU
1	А	6	ILE
1	А	8	VAL
1	А	15	GLU
1	А	16	HIS
1	А	17	LEU
1	А	18	LEU
1	А	29	THR
1	А	30	LYS
1	А	31	ILE
1	А	33	SER
1	А	37	ARG
1	А	38	HIS
1	А	47	ASN
1	А	50	ASP
1	А	56	ILE
1	А	57	ARG
1	А	58	THR
1	А	61	TRP
1	А	65	ILE
1	А	77	ASP
1	А	87	ARG
1	А	89	VAL
1	А	94	ARG
1	А	103	GLN
1	А	105	VAL
1	А	116	GLN
1	А	118	LEU
1	А	119	LYS
1	А	122	LEU
1	А	126	SER
1	А	132	SER
1	А	140	ILE
1	А	146	ASP
1	А	168	MET



Mol	Chain	Res	Type
1	А	177	GLU
1	А	178	THR
1	А	183	GLN
1	А	188	THR
1	А	190	LYS
1	А	407	ILE
1	А	413	LEU
1	А	422	ILE
1	А	426	HIS
1	А	429	TYR
1	А	433	HIS
1	А	439	THR
1	А	452	ASP
1	A	453	ASP
1	A	458	THR
1	А	469	ILE
1	А	473	ILE
1	А	481	GLN
1	А	490	SER
1	А	494	VAL
1	А	504	LYS
1	А	505	LEU
1	А	506	THR
1	А	513	MET
1	А	525	MET
1	А	530	LEU
1	А	532	ILE
1	А	537	ILE
1	А	548	LYS
1	А	550	THR
1	А	561	LEU
1	А	572	ILE
1	A	576	LEU
1	A	577	ARG
1	A	588	SER
1	A	589	THR
1	А	594	ILE
1	A	603	ILE
1	А	604	LEU
1	A	606	ARG
1	А	612	ILE
1	А	617	CYS



Mol	Chain	Res	Type
1	А	625	THR
1	А	627	GLU
1	А	642	VAL
1	А	643	ARG
1	А	650	VAL
1	А	658	HIS
1	А	669	ASP
1	А	670	ILE
1	А	675	ILE
1	А	676	LEU
1	А	679	ASP
1	А	698	ILE
1	А	704	MET
1	А	710	LEU
1	А	712	VAL
1	А	719	THR
1	А	723	LEU
1	А	724	LEU
1	А	727	LEU
1	А	733	VAL
1	А	739	LEU
1	А	747	LEU
1	А	750	ASP
1	A	755	SER
1	A	757	ARG
1	A	760	SER
1	A	763	LEU
1	A	764	LEU
1	A	765	LEU
1	A	784	CYS
1	A	787	ILE
1	A	789	TYR
1	A	794	VAL
1	A	818	LEU
1	A	819	LYS
1	A	823	ASN
1	A	831	VAL
1	A	836	VAL
1	A	838	THR
1	A	839	LYS
1	A	842	LEU
1	A	845	THR



Mol	Chain	Res	Type
1	А	849	SER
1	А	851	CYS
1	А	856	ASP
1	А	858	ILE
1	А	860	TRP
1	А	862	LEU
1	А	865	THR
1	А	875	GLU
1	А	880	ARG
1	А	881	VAL
1	А	885	ILE
1	А	886	ARG
1	А	889	ARG
1	А	896	LEU
1	А	899	ARG
1	А	914	GLU
1	А	916	THR
1	А	917	VAL
1	А	923	VAL
1	А	926	ARG
1	А	929	LYS
1	А	932	LEU
1	А	934	LYS
1	А	938	ASP
1	А	941	LEU
1	А	945	SER
1	А	955	LEU
1	А	956	THR
1	А	957	LYS
1	А	959	LEU
1	А	961	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	131	HIS
1	А	180	HIS
1	А	587	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)

Of 1 ligands modelled in this entry, 1 is 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.

# 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-6239. 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: 66



Y Index: 80



Z Index: 73



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: 55

Y Index: 92

Z Index: 51

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



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 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

# 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  $31 \text{ nm}^3$ ; this corresponds to an approximate mass of 28 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)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.



# 8 Fourier-Shell correlation (i)

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



# 9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-6239 and PDB model 3J9D. 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 0.9 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 (0.9).



# 9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 81% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8060	0.5380
А	0.8060	0.5380

