



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:48 PM BST

PDB ID : 3J9E
EMDB ID: : EMD-6240
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 : 2015-01-10
Resolution : 3.50 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

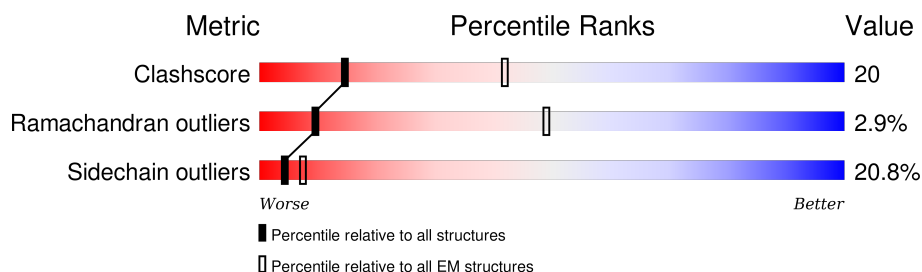
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	D	526	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4098 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.

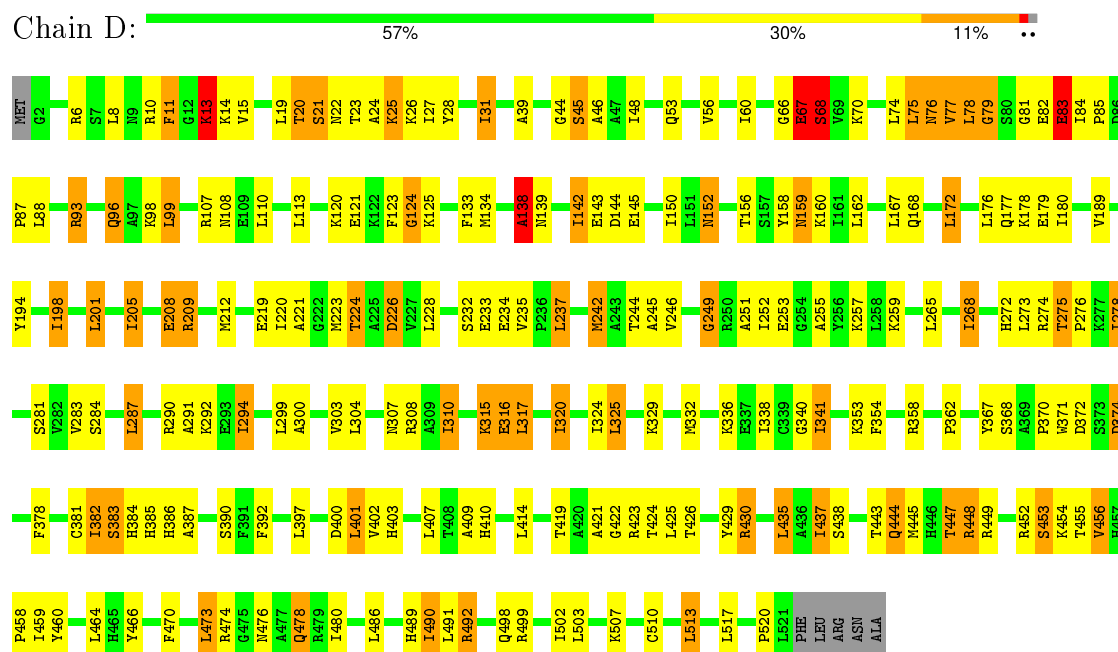
- Molecule 1 is a protein called VP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	D	520	4098	2584	722	777	15	0	0

3 Residue-property plots

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. 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. 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: VP5



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	5008	Depositor
Resolution determination method	FSC 0.143	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	14000	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	D	1.00	6/4164 (0.1%)	1.45	23/5605 (0.4%)

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	D	0	10

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	67	GLU	C-N	-25.77	0.74	1.34
1	D	13	LYS	C-N	-21.50	0.84	1.34
1	D	513	LEU	C-N	10.84	1.52	1.33
1	D	83	GLU	CB-CG	10.16	1.71	1.52
1	D	83	GLU	CG-CD	9.13	1.65	1.51
1	D	83	GLU	CD-OE2	6.16	1.32	1.25

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	138	ALA	O-C-N	-52.62	38.51	122.70
1	D	513	LEU	O-C-N	-47.36	42.70	123.20
1	D	13	LYS	O-C-N	-32.50	70.70	122.70
1	D	67	GLU	O-C-N	-19.20	91.99	122.70
1	D	13	LYS	C-N-CA	-16.14	81.35	121.70
1	D	13	LYS	CA-C-N	-14.44	85.42	117.20
1	D	138	ALA	CA-C-N	11.64	142.80	117.20
1	D	99	LEU	CA-CB-CG	-8.28	96.27	115.30
1	D	124	GLY	N-CA-C	7.87	132.78	113.10
1	D	513	LEU	CA-C-N	-7.16	101.88	116.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	67	GLU	CA-C-N	6.83	132.23	117.20
1	D	401	LEU	CA-CB-CG	6.53	130.32	115.30
1	D	45	SER	C-N-CA	5.54	135.56	121.70
1	D	414	LEU	CA-CB-CG	5.53	128.03	115.30
1	D	79	GLY	N-CA-C	-5.49	99.37	113.10
1	D	138	ALA	C-N-CA	-5.35	108.32	121.70
1	D	93	ARG	NE-CZ-NH1	-5.25	117.68	120.30
1	D	226	ASP	CB-CG-OD2	5.23	123.01	118.30
1	D	492	ARG	N-CA-C	5.15	124.92	111.00
1	D	45	SER	N-CA-C	5.14	124.88	111.00
1	D	287	LEU	CA-CB-CG	-5.06	103.67	115.30
1	D	473	LEU	CA-CB-CG	5.02	126.85	115.30
1	D	268	ILE	CB-CA-C	-5.00	101.59	111.60

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	123	PHE	Peptide
1	D	13	LYS	Mainchain
1	D	138	ALA	Mainchain,Peptide
1	D	249	GLY	Peptide
1	D	387	ALA	Peptide
1	D	513	LEU	Mainchain
1	D	67	GLU	Mainchain,Peptide
1	D	77	VAL	Peptide

5.2 Too-close contacts ⓘ

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	D	4098	0	4119	164	0
All	All	4098	0	4119	164	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 20.

All (164) 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:D:453:SER:C	1:D:455:THR:CG2	1.79	1.48
1:D:437:ILE:HD11	1:D:447:THR:CG2	1.48	1.42
1:D:143:GLU:O	1:D:145:GLU:N	1.63	1.31
1:D:453:SER:O	1:D:455:THR:CG2	1.77	1.28
1:D:453:SER:C	1:D:455:THR:HG21	1.09	1.18
1:D:453:SER:O	1:D:455:THR:HG21	1.35	1.18
1:D:453:SER:CA	1:D:455:THR:HG21	1.74	1.16
1:D:144:ASP:CA	1:D:145:GLU:HB2	1.80	1.10
1:D:437:ILE:CD1	1:D:447:THR:HG23	1.81	1.10
1:D:437:ILE:HD11	1:D:447:THR:HG23	1.16	1.07
1:D:437:ILE:HD11	1:D:447:THR:HG21	1.30	1.07
1:D:138:ALA:HB1	1:D:139:ASN:OD1	1.54	1.07
1:D:138:ALA:CB	1:D:139:ASN:OD1	2.04	1.06
1:D:139:ASN:O	1:D:142:ILE:HD12	1.55	1.04
1:D:453:SER:O	1:D:455:THR:HG23	1.54	1.04
1:D:144:ASP:HA	1:D:145:GLU:CB	1.91	1.01
1:D:144:ASP:HA	1:D:145:GLU:HB2	1.02	1.01
1:D:437:ILE:CD1	1:D:447:THR:CG2	2.38	0.93
1:D:142:ILE:HG22	1:D:143:GLU:N	1.84	0.90
1:D:142:ILE:HG22	1:D:143:GLU:H	1.37	0.88
1:D:224:THR:OG1	1:D:226:ASP:OD1	1.93	0.84
1:D:142:ILE:CG2	1:D:143:GLU:H	1.91	0.83
1:D:139:ASN:HA	1:D:142:ILE:HD11	1.62	0.82
1:D:45:SER:N	1:D:46:ALA:HB3	2.00	0.77
1:D:138:ALA:HB3	1:D:139:ASN:OD1	1.85	0.75
1:D:142:ILE:CG2	1:D:143:GLU:N	2.49	0.75
1:D:374:ASP:OD1	1:D:374:ASP:N	2.19	0.74
1:D:158:TYR:HE1	1:D:253:GLU:HG2	1.54	0.73
1:D:144:ASP:O	1:D:145:GLU:OE1	2.07	0.72
1:D:139:ASN:CA	1:D:142:ILE:HD11	2.21	0.71
1:D:249:GLY:O	1:D:253:GLU:HG3	1.90	0.71
1:D:139:ASN:O	1:D:142:ILE:CD1	2.38	0.70
1:D:383:SER:HB2	1:D:470:PHE:CG	2.28	0.69
1:D:139:ASN:C	1:D:142:ILE:HD12	2.14	0.68
1:D:24:ALA:HB2	1:D:60:ILE:HD11	1.76	0.68
1:D:144:ASP:CA	1:D:145:GLU:CB	2.62	0.67
1:D:143:GLU:C	1:D:145:GLU:N	2.48	0.65
1:D:430:ARG:CZ	1:D:430:ARG:HB2	2.24	0.65
1:D:139:ASN:C	1:D:142:ILE:CD1	2.65	0.65
1:D:144:ASP:C	1:D:145:GLU:OE1	2.34	0.65
1:D:340:GLY:HA2	1:D:341:ILE:HB	1.77	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:22:ASN:HB3	1:D:26:LYS:HE3	1.79	0.65
1:D:429:TYR:CE1	1:D:458:PRO:HD3	2.33	0.64
1:D:490:ILE:HD11	1:D:502:ILE:HA	1.79	0.64
1:D:437:ILE:CD1	1:D:447:THR:HG21	2.18	0.63
1:D:194:TYR:CE1	1:D:234:GLU:HG3	2.34	0.63
1:D:13:LYS:HB3	1:D:14:LYS:N	2.10	0.62
1:D:453:SER:HA	1:D:455:THR:HG21	1.72	0.62
1:D:144:ASP:C	1:D:145:GLU:HB2	2.21	0.61
1:D:10:ARG:O	1:D:11:PHE:HB2	2.01	0.61
1:D:13:LYS:CB	1:D:14:LYS:N	2.32	0.61
1:D:139:ASN:CA	1:D:142:ILE:CD1	2.79	0.60
1:D:168:GLN:HB3	1:D:235:VAL:HG11	1.83	0.60
1:D:159:ASN:HB2	1:D:317:LEU:HD12	1.82	0.59
1:D:307:ASN:HA	1:D:310:ILE:HG22	1.85	0.59
1:D:120:LYS:HA	1:D:124:GLY:HA2	1.84	0.58
1:D:316:GLU:HG2	1:D:386:HIS:HD2	1.68	0.58
1:D:67:GLU:C	1:D:68:SER:HB3	2.23	0.58
1:D:437:ILE:CG1	1:D:447:THR:HG23	2.32	0.58
1:D:74:LEU:HD23	1:D:510:CYS:HB2	1.86	0.58
1:D:370:PRO:HA	1:D:459:ILE:HD12	1.84	0.58
1:D:381:CYS:O	1:D:390:SER:HB2	2.05	0.57
1:D:8:LEU:HD21	1:D:402:VAL:HB	1.87	0.57
1:D:77:VAL:HG22	1:D:221:ALA:HB3	1.87	0.57
1:D:87:PRO:HB3	1:D:503:LEU:HD22	1.87	0.55
1:D:120:LYS:O	1:D:124:GLY:HA3	2.06	0.55
1:D:82:GLU:HG2	1:D:83:GLU:O	2.06	0.54
1:D:219:GLU:N	1:D:219:GLU:OE1	2.38	0.54
1:D:244:THR:HG22	1:D:245:ALA:H	1.72	0.54
1:D:208:GLU:HG2	1:D:221:ALA:HA	1.90	0.54
1:D:409:ALA:O	1:D:410:HIS:HB2	2.08	0.54
1:D:316:GLU:OE1	1:D:385:HIS:N	2.41	0.54
1:D:144:ASP:C	1:D:145:GLU:CB	2.77	0.54
1:D:66:GLY:O	1:D:68:SER:HB3	2.08	0.53
1:D:67:GLU:C	1:D:68:SER:CB	2.49	0.53
1:D:421:ALA:HB3	1:D:422:GLY:HA3	1.91	0.53
1:D:316:GLU:HG2	1:D:384:HIS:HB3	1.91	0.53
1:D:294:ILE:HD11	1:D:299:LEU:HD21	1.90	0.52
1:D:237:LEU:HD22	1:D:249:GLY:HA3	1.91	0.52
1:D:275:THR:HG22	1:D:276:PRO:HD2	1.93	0.51
1:D:74:LEU:O	1:D:76:ASN:N	2.43	0.51
1:D:172:LEU:HD23	1:D:303:VAL:HG11	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:172:LEU:HG	1:D:172:LEU:O	2.11	0.50
1:D:84:ILE:HG22	1:D:85:PRO:HD2	1.92	0.50
1:D:290:ARG:HH11	1:D:290:ARG:HG2	1.76	0.50
1:D:272:HIS:CG	1:D:362:PRO:HG2	2.47	0.49
1:D:426:THR:HA	1:D:429:TYR:CE2	2.47	0.49
1:D:249:GLY:HA2	1:D:252:ILE:HG13	1.93	0.49
1:D:152:ASN:O	1:D:156:THR:HG23	2.11	0.49
1:D:110:LEU:HA	1:D:113:LEU:HD12	1.95	0.48
1:D:367:TYR:CE2	1:D:460:TYR:HD1	2.31	0.48
1:D:371:TRP:HD1	1:D:372:ASP:H	1.56	0.48
1:D:476:ASN:O	1:D:480:ILE:HG12	2.13	0.48
1:D:315:LYS:HE3	1:D:315:LYS:HB2	1.60	0.48
1:D:299:LEU:HA	1:D:299:LEU:HD23	1.63	0.48
1:D:320:ILE:HD12	1:D:324:ILE:HD12	1.95	0.48
1:D:168:GLN:HG2	1:D:235:VAL:HG13	1.96	0.47
1:D:287:LEU:HA	1:D:287:LEU:HD23	1.44	0.47
1:D:304:LEU:HD23	1:D:304:LEU:HA	1.69	0.47
1:D:11:PHE:HZ	1:D:489:HIS:CD2	2.33	0.47
1:D:27:ILE:O	1:D:31:ILE:HB	2.15	0.47
1:D:489:HIS:O	1:D:492:ARG:HD3	2.14	0.47
1:D:176:LEU:HD23	1:D:176:LEU:HA	1.70	0.46
1:D:371:TRP:CD1	1:D:372:ASP:N	2.82	0.46
1:D:201:LEU:HD22	1:D:205:ILE:HD12	1.97	0.46
1:D:316:GLU:HA	1:D:386:HIS:HB3	1.97	0.46
1:D:329:LYS:HA	1:D:332:MET:HE2	1.97	0.46
1:D:139:ASN:HB3	1:D:142:ILE:HD12	1.98	0.45
1:D:362:PRO:HD3	1:D:385:HIS:NE2	2.32	0.45
1:D:198:ILE:HD12	1:D:198:ILE:HA	1.58	0.45
1:D:82:GLU:O	1:D:96:GLN:NE2	2.49	0.45
1:D:21:SER:C	1:D:23:THR:H	2.20	0.45
1:D:162:LEU:HD23	1:D:162:LEU:HA	1.61	0.45
1:D:362:PRO:HB3	1:D:383:SER:O	2.17	0.45
1:D:44:GLY:HA2	1:D:48:ILE:HB	1.98	0.45
1:D:44:GLY:CA	1:D:48:ILE:HB	2.47	0.44
1:D:142:ILE:C	1:D:144:ASP:H	2.21	0.44
1:D:237:LEU:CD2	1:D:249:GLY:HA3	2.48	0.44
1:D:194:TYR:HE1	1:D:234:GLU:HG3	1.79	0.44
1:D:88:LEU:HD22	1:D:499:ARG:HD3	2.00	0.44
1:D:99:LEU:HA	1:D:99:LEU:HD12	1.73	0.44
1:D:492:ARG:N	1:D:498:GLN:HG2	2.33	0.44
1:D:320:ILE:HA	1:D:320:ILE:HD12	1.84	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:362:PRO:HA	1:D:382:ILE:HB	2.00	0.43
1:D:25:LYS:HB2	1:D:25:LYS:NZ	2.32	0.43
1:D:78:LEU:HB3	1:D:79:GLY:HA2	1.99	0.43
1:D:278:ILE:HD12	1:D:278:ILE:H	1.82	0.43
1:D:28:TYR:CE1	1:D:56:VAL:HG21	2.52	0.43
1:D:158:TYR:CE1	1:D:253:GLU:HG2	2.44	0.43
1:D:139:ASN:HB3	1:D:142:ILE:CD1	2.48	0.43
1:D:316:GLU:HG3	1:D:384:HIS:CG	2.53	0.43
1:D:10:ARG:O	1:D:11:PHE:CB	2.67	0.43
1:D:142:ILE:O	1:D:144:ASP:N	2.44	0.43
1:D:325:LEU:HA	1:D:325:LEU:HD13	1.73	0.43
1:D:251:ALA:O	1:D:255:ALA:N	2.52	0.43
1:D:444:GLN:HG2	1:D:445:MET:HG3	2.01	0.43
1:D:478:GLN:HA	1:D:478:GLN:HE21	1.84	0.43
1:D:108:ASN:HB3	1:D:255:ALA:HA	2.01	0.42
1:D:265:LEU:HA	1:D:265:LEU:HD23	1.70	0.42
1:D:490:ILE:CD1	1:D:502:ILE:HA	2.48	0.42
1:D:307:ASN:HA	1:D:310:ILE:CG2	2.47	0.42
1:D:133:PHE:CD1	1:D:150:ILE:HD13	2.54	0.42
1:D:209:ARG:HA	1:D:212:MET:HE3	2.02	0.41
1:D:383:SER:HA	1:D:466:TYR:OH	2.20	0.41
1:D:378:PHE:CD1	1:D:392:PHE:CE2	3.08	0.41
1:D:316:GLU:HG2	1:D:386:HIS:CD2	2.53	0.41
1:D:294:ILE:HD11	1:D:299:LEU:CD2	2.50	0.41
1:D:392:PHE:HB2	1:D:407:LEU:HD11	2.02	0.41
1:D:226:ASP:N	1:D:226:ASP:OD1	2.53	0.41
1:D:503:LEU:HD12	1:D:503:LEU:HA	1.88	0.41
1:D:474:ARG:HH21	1:D:474:ARG:HG2	1.85	0.41
1:D:449:ARG:HH11	1:D:456:VAL:HG12	1.85	0.41
1:D:453:SER:HA	1:D:455:THR:CG2	2.46	0.41
1:D:242:MET:HE3	1:D:242:MET:O	2.21	0.41
1:D:435:LEU:HD22	1:D:435:LEU:HA	1.69	0.41
1:D:453:SER:CA	1:D:455:THR:CG2	2.65	0.41
1:D:445:MET:O	1:D:448:ARG:HB3	2.21	0.41
1:D:491:LEU:HA	1:D:491:LEU:HD23	1.91	0.41
1:D:252:ILE:HG13	1:D:252:ILE:H	1.64	0.41
1:D:220:ILE:HG21	1:D:283:VAL:HG11	2.03	0.41
1:D:176:LEU:HB3	1:D:300:ALA:HB2	2.02	0.40
1:D:78:LEU:HB3	1:D:79:GLY:CA	2.52	0.40
1:D:19:LEU:HB2	1:D:20:THR:HA	2.04	0.40
1:D:354:PHE:CD1	1:D:354:PHE:N	2.89	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	D	512/526 (97%)	447 (87%)	50 (10%)	15 (3%)	6	42

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	39	ALA
1	D	68	SER
1	D	142	ILE
1	D	180	ILE
1	D	400	ASP
1	D	11	PHE
1	D	81	GLY
1	D	21	SER
1	D	75	LEU
1	D	291	ALA
1	D	453	SER
1	D	15	VAL
1	D	83	GLU
1	D	341	ILE
1	D	520	PRO

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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	437/442 (99%)	346 (79%)	91 (21%)	1 8

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	6	ARG
1	D	20	THR
1	D	25	LYS
1	D	31	ILE
1	D	53	GLN
1	D	67	GLU
1	D	68	SER
1	D	70	LYS
1	D	75	LEU
1	D	76	ASN
1	D	78	LEU
1	D	93	ARG
1	D	96	GLN
1	D	98	LYS
1	D	107	ARG
1	D	121	GLU
1	D	125	LYS
1	D	134	MET
1	D	152	ASN
1	D	159	ASN
1	D	160	LYS
1	D	167	LEU
1	D	172	LEU
1	D	177	GLN
1	D	178	LYS
1	D	179	GLU
1	D	189	VAL
1	D	198	ILE
1	D	201	LEU
1	D	205	ILE
1	D	208	GLU
1	D	209	ARG
1	D	223	MET
1	D	224	THR
1	D	228	LEU
1	D	232	SER
1	D	233	GLU
1	D	237	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	242	MET
1	D	246	VAL
1	D	257	LYS
1	D	259	LYS
1	D	268	ILE
1	D	273	LEU
1	D	274	ARG
1	D	275	THR
1	D	278	ILE
1	D	281	SER
1	D	284	SER
1	D	292	LYS
1	D	294	ILE
1	D	308	ARG
1	D	310	ILE
1	D	315	LYS
1	D	316	GLU
1	D	317	LEU
1	D	320	ILE
1	D	325	LEU
1	D	336	LYS
1	D	338	ILE
1	D	353	LYS
1	D	358	ARG
1	D	368	SER
1	D	374	ASP
1	D	382	ILE
1	D	383	SER
1	D	397	LEU
1	D	401	LEU
1	D	403	HIS
1	D	419	THR
1	D	423	ARG
1	D	424	THR
1	D	425	LEU
1	D	430	ARG
1	D	435	LEU
1	D	437	ILE
1	D	438	SER
1	D	443	THR
1	D	444	GLN
1	D	447	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	448	ARG
1	D	452	ARG
1	D	454	LYS
1	D	456	VAL
1	D	464	LEU
1	D	473	LEU
1	D	478	GLN
1	D	486	LEU
1	D	490	ILE
1	D	507	LYS
1	D	517	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	489	HIS

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](#)

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 ⓘ

There are no chain breaks in this entry.