

Full wwPDB X-ray Structure Validation Report (i)

Sep 12, 2023 – 08:41 AM EDT

PDB ID	:	4N43
Title	:	Human enterovirus 71 uncoating intermediate captured at atomic resolution
Authors	:	Chen, R.; Lyu, K.
Deposited on	:	2013-10-08
Resolution	:	3.80 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp 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:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 3.80 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	1212 (4.00-3.60)
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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%

Mol	Chain	Length	Quality of chain			
1	А	297	62%	13%	•	24%
2	В	254	74%		16%	10%
3	С	242	67%		24%	• 8%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5259 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

• Molecule 1 is a protein called Capsid protein VP1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	225	Total 1780	C 1139	N 300	O 330	S 11	0	0	0

• Molecule 2 is a protein called Capsid protein VP2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
2	В	229	Total 1777	C 1143	N 292	0 334	S 8	0	0	0

• Molecule 3 is a protein called Capsid protein VP3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
3	С	223	Total 1702	C 1097	N 278	O 316	S 11	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	227	GLN	LYS	conflict	UNP Q9WPJ0



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. 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: Capsid protein VP1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 42 3 2	Depositor
Cell constants	352.42Å 352.42Å 352.42Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Bosolution(A)	49.84 - 3.80	Depositor
Resolution (A)	49.84 - 3.80	EDS
% Data completeness	68.0 (49.84-3.80)	Depositor
(in resolution range)	59.4(49.84-3.80)	EDS
R_{merge}	0.38	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.68 (at 3.77 \text{\AA})$	Xtriage
Refinement program	PHENIX	Depositor
P. P.	0.245 , 0.274	Depositor
n, n_{free}	0.277 , 0.280	DCC
R_{free} test set	2000 reflections $(3.99%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	53.3	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.27, 33.8	EDS
L-test for twinning ²	$ < L >=0.46, < L^2>=0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.73	EDS
Total number of atoms	5259	wwPDB-VP
Average B, all atoms $(Å^2)$	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.01% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

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		
	Ullaili	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.22	0/1835	0.40	0/2501	
2	В	0.22	0/1830	0.41	0/2509	
3	С	0.22	0/1748	0.42	0/2393	
All	All	0.22	0/5413	0.41	0/7403	

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	А	1780	0	1724	31	0
2	В	1777	0	1712	39	0
3	С	1702	0	1692	41	0
All	All	5259	0	5128	92	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 9.

All (92) 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:149:GLN:HG2	1:A:247:LEU:HD11	1.64	0.79



			Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:271:TYR:H	3:C:235:ILE:HG12	1.49	0.78	
2:B:151:THR:HG22	2:B:152:GLN:HG3	1.74	0.70	
2:B:122:LEU:HB2	2:B:183:ILE:HB	1.74	0.68	
2:B:186:ARG:NH1	3:C:124:SER:O	2.27	0.67	
1:A:268:ASN:HB2	2:B:171:PRO:HD3	1.79	0.65	
2:B:134:THR:HG23	2:B:146:PRO:HG3	1.78	0.64	
3:C:85:VAL:HB	3:C:194:VAL:HG13	1.80	0.64	
3:C:59:PRO:HD2	3:C:68:ARG:HD3	1.80	0.63	
3:C:142:LEU:HD12	3:C:143:PRO:HD2	1.81	0.62	
1:A:262:ILE:HG21	2:B:128:PRO:HG2	1.83	0.61	
3:C:146:ARG:NH1	3:C:199:GLN:OE1	2.34	0.61	
1:A:181:VAL:HG11	1:A:188:ALA:HB2	1.83	0.61	
3:C:115:LEU:HB2	3:C:169:ILE:HD11	1.83	0.60	
2:B:85:VAL:HG23	2:B:86:LEU:HG	1.85	0.59	
2:B:80:TRP:HB3	2:B:85:VAL:HG11	1.85	0.59	
1:A:265:PRO:HB3	2:B:174:GLN:HB2	1.85	0.59	
2:B:177:VAL:HG11	3:C:100:LEU:HD22	1.85	0.58	
2:B:71:TRP:HD1	2:B:232:ILE:HB	1.68	0.58	
1:A:287:THR:HG21	3:C:94:GLY:H	1.68	0.58	
1:A:291:ARG:HH11	1:A:291:ARG:H	1.51	0.58	
2:B:23:ILE:HG21	2:B:237:THR:HG21	1.87	0.57	
2:B:71:TRP:NE1	2:B:222:LEU:HB2	2.20	0.56	
1:A:155:PHE:HB3	1:A:177:PRO:HG2	1.87	0.56	
2:B:87:THR:O	2:B:97:GLN:NE2	2.36	0.56	
1:A:127:THR:HG22	1:A:264:ARG:HE	1.70	0.56	
2:B:186:ARG:NH2	3:C:159:PHE:O	2.39	0.56	
1:A:93:ILE:HD11	1:A:109:TRP:HB2	1.88	0.56	
1:A:278:ASN:OD1	2:B:134:THR:N	2.38	0.55	
2:B:71:TRP:CD1	2:B:232:ILE:HB	2.41	0.54	
1:A:210:THR:O	2:B:208:ASN:ND2	2.40	0.54	
2:B:184:ASN:O	2:B:188:ASN:N	2.41	0.54	
3:C:57:ASN:HA	3:C:68:ARG:HD2	1.89	0.53	
2:B:71:TRP:CZ3	2:B:218:PRO:HB3	2.43	0.53	
3:C:59:PRO:HG2	3:C:67:GLU:HB2	1.92	0.52	
1:A:276:ASN:OD1	1:A:278:ASN:ND2	2.43	0.51	
1:A:106:TYR:OH	1:A:164:ASP:O	2.23	0.51	
2:B:174:GLN:HE22	3:C:103:GLN:HG3	1.74	0.51	
1:A:128:TYR:HB2	1:A:261:TRP:HB2	1.93	0.51	
1:A:156:VAL:HB	1:A:232:THR:HG23	1.94	0.50	
2:B:97:GLN:HA	2:B:207:LEU:HD11	1.92	0.50	
3:C:130:LYS:HB2	3:C:200:THR:HB	1.93	0.50	

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	A h C	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:131:PHE:HB3	1:A:258:VAL:HG12	1.94	0.49
3:C:121:PHE:HA	3:C:214:ILE:HG22	1.95	0.49
2:B:32:ILE:HD11	2:B:193:ILE:HG12	1.95	0.49
3:C:109:THR:OG1	3:C:228:LEU:HB3	2.13	0.48
1:A:116:TYR:HD2	1:A:119:MET:HB2	1.79	0.48
2:B:177:VAL:HG12	3:C:49:VAL:HG21	1.96	0.48
2:B:186:ARG:HG3	3:C:125:PHE:HA	1.96	0.48
1:A:166:ARG:NH2	1:A:237:THR:O	2.46	0.48
3:C:135:TYR:HB2	3:C:167:LEU:HD21	1.95	0.48
1:A:192:VAL:HG22	3:C:24:ILE:HG21	1.96	0.47
3:C:72:PRO:HB3	3:C:213:TYR:CE1	2.49	0.47
3:C:235:ILE:HA	3:C:236:LEU:HA	1.55	0.47
2:B:126:VAL:HG13	2:B:212:PHE:CD1	2.50	0.46
2:B:97:GLN:HG2	2:B:207:LEU:HD21	1.99	0.45
1:A:126:PHE:CG	1:A:260:ALA:HB1	2.52	0.45
1:A:164:ASP:OD1	1:A:164:ASP:N	2.47	0.45
1:A:284:ILE:HG22	1:A:285:LYS:H	1.81	0.45
1:A:191:SER:OG	3:C:21:SER:OG	2.35	0.44
3:C:46:LEU:O	3:C:49:VAL:HG22	2.17	0.44
2:B:71:TRP:CH2	2:B:218:PRO:HB3	2.53	0.44
3:C:78:GLY:O	3:C:79:LYS:HG2	2.18	0.44
1:A:211:PHE:HA	2:B:208:ASN:ND2	2.33	0.44
2:B:136:ALA:HB2	2:B:143:ASP:HB3	1.98	0.44
2:B:122:LEU:HD22	2:B:216:VAL:HG12	2.00	0.43
2:B:186:ARG:HE	3:C:162:GLN:HG3	1.82	0.43
3:C:91:GLY:HA3	3:C:111:TRP:CH2	2.53	0.43
1:A:261:TRP:HA	3:C:39:GLU:HA	2.00	0.43
2:B:89:THR:HG21	2:B:155:ALA:HB2	2.00	0.43
2:B:95:ASN:O	2:B:99:HIS:ND1	2.41	0.43
3:C:115:LEU:HG	3:C:172:ILE:HD13	1.99	0.43
1:A:268:ASN:HB2	2:B:171:PRO:CD	2.48	0.43
3:C:96:TRP:O	3:C:102:GLY:HA3	2.19	0.43
2:B:71:TRP:HB3	2:B:232:ILE:O	2.19	0.42
3:C:134:ALA:HA	3:C:154:HIS:HA	2.01	0.42
3:C:109:THR:HG22	3:C:230:LYS:HE3	2.00	0.42
3:C:29:HIS:HA	3:C:30:PRO:HD2	1.93	0.42
1:A:282:ASN:O	1:A:282:ASN:ND2	2.52	0.42
3:C:128:THR:OG1	3:C:129:GLY:N	2.53	0.42
1:A:196:SER:HB2	1:A:201:TYR:CE1	2.55	0.42
3:C:132:LEU:HB2	3:C:199:GLN:HB2	2.02	0.41
3:C:133:ILE:HG12	3:C:196:ILE:HG23	2.02	0.41

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Atom-1	Atom-2	${f Interatomic} \ {f distance} \ ({ m \AA})$	Clash overlap (Å)
2:B:81:LYS:HE2	2:B:130:TYR:HB3	2.01	0.41
2:B:249:ARG:H	2:B:249:ARG:HD2	1.84	0.41
3:C:113:GLY:HA3	3:C:224:PHE:HA	2.02	0.41
3:C:104:LEU:HD13	3:C:104:LEU:HA	1.92	0.41
3:C:132:LEU:HD23	3:C:156:ILE:HD13	2.02	0.41
3:C:50:GLU:HA	3:C:219:ALA:HB2	2.03	0.41
1:A:291:ARG:H	1:A:291:ARG:HD2	1.86	0.40
2:B:81:LYS:O	2:B:85:VAL:HG13	2.20	0.40
3:C:58:VAL:HB	3:C:59:PRO:HD3	2.03	0.40

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There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	А	223/297~(75%)	202 (91%)	21 (9%)	0	100	100
2	В	225/254 (89%)	209~(93%)	16 (7%)	0	100	100
3	С	219/242 (90%)	201 (92%)	16 (7%)	2(1%)	17	54
All	All	667/793~(84%)	612 (92%)	53 (8%)	2 (0%)	41	74

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	С	82	LEU
3	С	58	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 X-ray entries followed by that with respect to entries of similar



resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
1	А	193/251~(77%)	189~(98%)	4 (2%)	53	74
2	В	195/214~(91%)	194 (100%)	1 (0%)	88	94
3	С	187/202~(93%)	184 (98%)	3(2%)	62	79
All	All	575/667~(86%)	567~(99%)	8 (1%)	67	81

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	205	TYR
1	А	284	ILE
1	А	285	LYS
1	А	291	ARG
2	В	100	TYR
3	С	86	PHE
3	С	200	THR
3	С	236	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

