



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 01:02 pm BST

PDB ID : 5NE4
Title : Crystal Structure of Foot and Mouth Disease Virus O PanAsia
Authors : Kotecha, A.; Stuart, D.
Deposited on : 2017-03-09
Resolution : 2.30 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

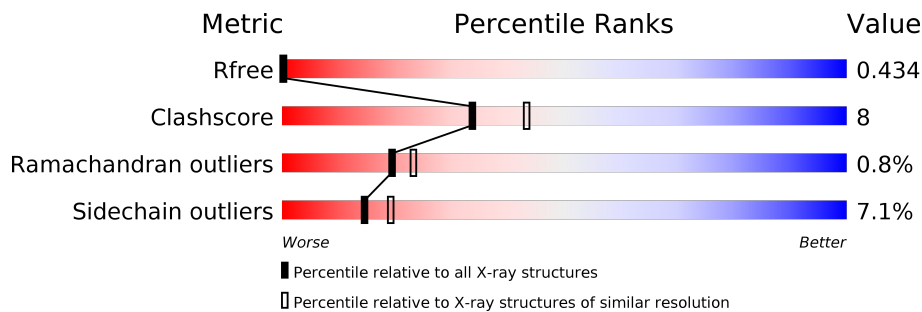
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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 on 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	1	211	69% 16% 13%
2	2	218	79% 15% 6%
3	3	220	81% 14%
4	4	85	46% 8% 46%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 5197 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 O PanAsia VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	1	184	1437	909	257	268	3	0	0	0

- Molecule 2 is a protein called O PanAsia VP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	2	206	1620	1031	278	304	7	0	0	0

- Molecule 3 is a protein called Polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	3	219	1677	1075	273	320	9	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	56	ARG	HIS	engineered mutation	UNP J3T9N5

- Molecule 4 is a protein called O PanAsia VP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	4	46	353	222	56	73	2	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	65	ASP	ASN	conflict	UNP E6Y5R5

- Molecule 5 is water.

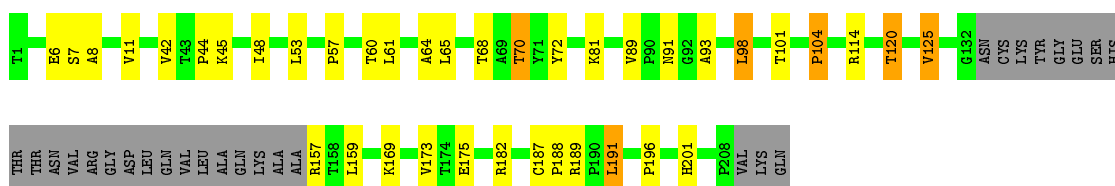
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	1	33	Total 33	O 33	0	0
5	2	25	Total 25	O 25	0	0
5	3	51	Total 51	O 51	0	0
5	4	1	Total 1	O 1	0	0

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA 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.

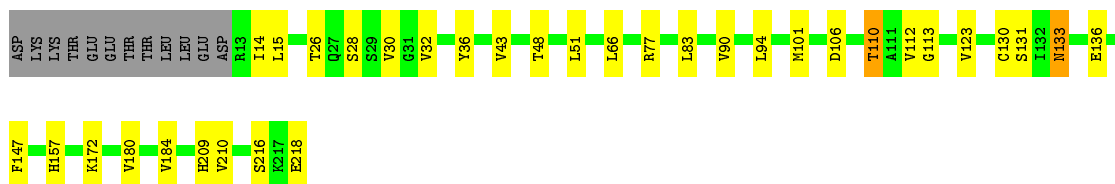
- Molecule 1: O PanAsia VP1

Chain 1: 




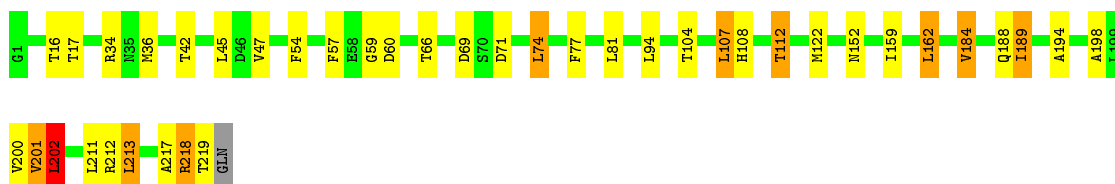
- Molecule 2: O PanAsia VP2

Chain 2: 



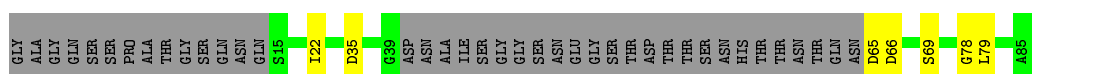
- Molecule 3: Polyprotein

Chain 3: 



- Molecule 4: O PanAsia VP4

Chain 4: 



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	345.01Å 345.01Å 345.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 48.79 – 2.32	Depositor EDS
% Data completeness (in resolution range)	76.9 (50.00-2.30) 79.4 (48.79-2.32)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.32Å)	Xtrriage
Refinement program	CNS v1.2	Depositor
R, R_{free}	0.210 , 0.220 0.436 , 0.434	Depositor DCC
R_{free} test set	11647 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	19.1	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 0.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.016 for -l,-k,-h	Xtrriage
F_o, F_c correlation	0.46	EDS
Total number of atoms	5197	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.40	0/1471	0.74	0/2012
2	2	0.45	0/1663	0.73	1/2271 (0.0%)
3	3	0.48	0/1726	0.76	1/2358 (0.0%)
4	4	0.49	0/359	0.66	0/481
All	All	0.45	0/5219	0.74	2/7122 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	202	LEU	CA-CB-CG	8.09	133.92	115.30
2	2	113	GLY	N-CA-C	-6.15	97.72	113.10

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	1	1437	0	1442	36	0
2	2	1620	0	1578	15	0
3	3	1677	0	1610	34	0
4	4	353	0	322	6	0
5	1	33	0	0	1	0
5	2	25	0	0	0	1
5	3	51	0	0	5	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	4	1	0	0	0	0
All	All	5197	0	4952	85	1

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 8.

All (85) 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)
3:3:66:THR:HB	3:3:188:GLN:HE22	1.33	0.94
3:3:34:ARG:HD3	5:3:302:HOH:O	1.74	0.88
3:3:107:LEU:HD22	3:3:159:ILE:HD11	1.60	0.82
2:2:26:THR:HG22	2:2:28:SER:H	1.45	0.81
1:1:91:ASN:HB3	1:1:120:THR:HG23	1.68	0.76
3:3:217:ALA:O	3:3:218:ARG:HB2	1.85	0.76
1:1:11:VAL:HB	5:1:333:HOH:O	1.86	0.75
2:2:216:SER:OG	2:2:218:GLU:HG2	1.88	0.74
3:3:66:THR:HB	3:3:188:GLN:NE2	2.02	0.73
1:1:70:THR:HG23	1:1:187:CYS:HB2	1.71	0.72
3:3:152:ASN:HA	5:3:303:HOH:O	1.88	0.72
1:1:104:PRO:HG3	3:3:17:THR:HG21	1.69	0.72
2:2:133:ASN:ND2	2:2:136:GLU:HG3	2.06	0.71
4:4:22:ILE:O	4:4:22:ILE:HD12	1.92	0.69
1:1:91:ASN:CB	1:1:120:THR:HG23	2.24	0.67
1:1:68:THR:HG21	1:1:191:LEU:HG	1.75	0.67
1:1:89:VAL:HG13	1:1:93:ALA:HB3	1.76	0.67
1:1:7:SER:O	1:1:8:ALA:HB3	1.95	0.67
2:2:101:MET:HG2	2:2:210:VAL:HG12	1.77	0.66
3:3:66:THR:CB	3:3:188:GLN:HE22	2.07	0.66
1:1:91:ASN:H	1:1:120:THR:HG21	1.60	0.66
2:2:43:VAL:HG11	2:2:209:HIS:CD2	2.32	0.65
4:4:65:ASP:HB2	4:4:69:SER:HB2	1.81	0.63
2:2:106:ASP:OD1	2:2:157:HIS:HE1	1.81	0.62
1:1:91:ASN:H	1:1:120:THR:CG2	2.12	0.62
2:2:133:ASN:HD22	2:2:136:GLU:HG3	1.66	0.60
1:1:196:PRO:HG3	1:1:201:HIS:HB2	1.83	0.60
2:2:30:VAL:O	2:2:30:VAL:HG12	2.01	0.59
3:3:218:ARG:O	3:3:219:THR:OG1	2.21	0.57
1:1:89:VAL:HG13	1:1:93:ALA:CB	2.34	0.57
1:1:89:VAL:CG1	1:1:93:ALA:HB3	2.34	0.57
3:3:122:MET:HB2	3:3:189:ILE:HD11	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:68:THR:CG2	1:1:191:LEU:HG	2.37	0.54
3:3:107:LEU:CD2	3:3:159:ILE:HD11	2.33	0.54
1:1:68:THR:O	1:1:188:PRO:HA	2.09	0.53
1:1:70:THR:HG23	1:1:187:CYS:O	2.08	0.53
3:3:104:THR:HB	5:3:333:HOH:O	2.08	0.53
1:1:157:ARG:HA	1:1:157:ARG:NE	2.24	0.52
1:1:81:LYS:HB2	1:1:175:GLU:HB2	1.92	0.52
3:3:57:PHE:HE2	3:3:201:VAL:HG13	1.75	0.51
4:4:78:GLY:C	4:4:79:LEU:HD12	2.31	0.51
3:3:107:LEU:HD22	3:3:159:ILE:CD1	2.36	0.51
4:4:22:ILE:C	4:4:22:ILE:HD12	2.30	0.51
3:3:77:PHE:CZ	3:3:184:VAL:HG21	2.46	0.51
3:3:42:THR:HG23	5:3:344:HOH:O	2.09	0.50
1:1:70:THR:HG22	1:1:189:ARG:CG	2.42	0.50
3:3:212:ARG:O	3:3:213:LEU:HB2	2.11	0.50
1:1:70:THR:CG2	1:1:187:CYS:O	2.60	0.50
2:2:112:VAL:O	2:2:112:VAL:HG23	2.12	0.50
3:3:112:THR:HB	3:3:198:ALA:O	2.11	0.50
1:1:91:ASN:CB	1:1:120:THR:CG2	2.89	0.49
1:1:7:SER:O	1:1:8:ALA:CB	2.59	0.49
1:1:182:ARG:NH2	4:4:35:ASP:OD2	2.46	0.49
2:2:48:THR:HA	3:3:162:LEU:HD12	1.95	0.48
2:2:14:ILE:N	2:2:14:ILE:HD12	2.28	0.48
1:1:91:ASN:HB2	1:1:120:THR:CG2	2.43	0.48
3:3:36:MET:HG3	3:3:36:MET:O	2.13	0.48
1:1:101:THR:HG23	3:3:16:THR:HG21	1.96	0.47
3:3:45:LEU:HD23	3:3:45:LEU:HA	1.74	0.47
3:3:57:PHE:CE2	3:3:201:VAL:HG13	2.50	0.47
1:1:98:LEU:HG	1:1:169:LYS:HB2	1.97	0.47
3:3:66:THR:OG1	3:3:194:ALA:O	2.32	0.46
3:3:69:ASP:OD2	3:3:71:ASP:HB3	2.15	0.46
3:3:59:GLY:O	3:3:60:ASP:HB2	2.16	0.46
3:3:54:PHE:CD1	3:3:202:LEU:HD13	2.52	0.45
3:3:42:THR:O	3:3:42:THR:HG22	2.17	0.45
1:1:48:ILE:N	1:1:48:ILE:HD12	2.32	0.45
2:2:30:VAL:O	2:2:30:VAL:CG1	2.64	0.44
2:2:43:VAL:HG11	2:2:209:HIS:NE2	2.32	0.44
3:3:74:LEU:HD12	3:3:74:LEU:HA	1.89	0.44
1:1:6:GLU:HA	2:2:147:PHE:HB2	1.98	0.44
1:1:45:LYS:O	1:1:173:VAL:HG22	2.18	0.44
1:1:61:LEU:HD23	1:1:61:LEU:C	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:70:THR:CG2	1:1:189:ARG:HH11	2.31	0.43
2:2:110:THR:HG23	2:2:112:VAL:HG13	2.01	0.42
3:3:104:THR:CB	5:3:333:HOH:O	2.65	0.42
1:1:64:ALA:O	1:1:68:THR:HG23	2.20	0.42
1:1:182:ARG:HH22	4:4:35:ASP:CG	2.22	0.42
3:3:108:HIS:O	3:3:201:VAL:HA	2.20	0.41
3:3:112:THR:O	3:3:112:THR:CG2	2.69	0.41
1:1:44:PRO:HB2	1:1:173:VAL:CG2	2.51	0.40
1:1:57:PRO:HB2	1:1:60:THR:HG23	2.02	0.40
3:3:122:MET:CB	3:3:189:ILE:HD11	2.52	0.40
3:3:218:ARG:HB3	3:3:219:THR:H	1.61	0.40
1:1:72:TYR:O	1:1:125:VAL:HG22	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:2:318:HOH:O	5:3:346:HOH:O[2_555]	1.38	0.82

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	Percentiles	
1	1	180/211 (85%)	175 (97%)	4 (2%)	1 (1%)	25	31
2	2	204/218 (94%)	195 (96%)	7 (3%)	2 (1%)	15	17
3	3	217/220 (99%)	209 (96%)	7 (3%)	1 (0%)	29	35
4	4	42/85 (49%)	39 (93%)	2 (5%)	1 (2%)	6	4
All	All	643/734 (88%)	618 (96%)	20 (3%)	5 (1%)	19	23

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	3	218	ARG
2	2	131	SER
4	4	66	ASP
2	2	36	TYR
1	1	104	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 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	Percentiles	
1	1	154/176 (88%)	144 (94%)	10 (6%)	17	23
2	2	180/192 (94%)	165 (92%)	15 (8%)	11	14
3	3	175/176 (99%)	161 (92%)	14 (8%)	12	15
4	4	37/67 (55%)	37 (100%)	0	100	100
All	All	546/611 (89%)	507 (93%)	39 (7%)	14	19

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	42	VAL
1	1	53	LEU
1	1	65	LEU
1	1	70	THR
1	1	98	LEU
1	1	114	ARG
1	1	120	THR
1	1	125	VAL
1	1	159	LEU
1	1	191	LEU
2	2	15	LEU
2	2	32	VAL
2	2	51	LEU
2	2	66	LEU
2	2	77	ARG
2	2	83	LEU
2	2	90	VAL

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Mol	Chain	Res	Type
2	2	94	LEU
2	2	110	THR
2	2	123	VAL
2	2	130	CYS
2	2	133	ASN
2	2	172	LYS
2	2	180	VAL
2	2	184	VAL
3	3	47	VAL
3	3	74	LEU
3	3	81	LEU
3	3	94	LEU
3	3	107	LEU
3	3	112	THR
3	3	162	LEU
3	3	184	VAL
3	3	189	ILE
3	3	200	VAL
3	3	201	VAL
3	3	202	LEU
3	3	211	LEU
3	3	213	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
2	2	65	HIS
2	2	157	HIS
3	3	152	ASN
3	3	181	GLN
3	3	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 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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

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

6.4 Ligands

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

6.5 Other polymers

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