



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 01:04 PM GMT

PDB ID : 2GOL
Title : Xray Structure of Gag278
Authors : Kelly, B.N.
Deposited on : 2006-04-13
Resolution : 2.20 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

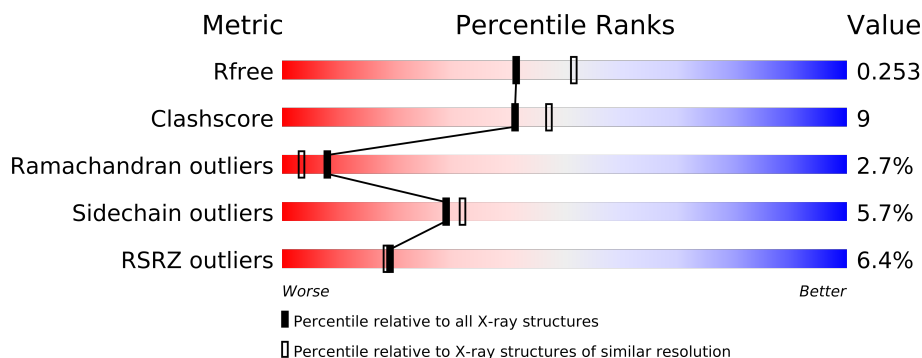
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.20 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}	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	133	
2	B	146	
2	D	146	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3219 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Matrix protein p17 (MA).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	102	Total	C	N	O	S	0	1	0
			825	519	146	158	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	CLONING ARTIFACT	UNP P12497
A	1	MET	-	CLONING ARTIFACT	UNP P12497

- Molecule 2 is a protein called Capsid protein p24 (CA).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	135	Total	C	N	O	S	0	0	0
			1051	665	185	194	7			
2	D	135	Total	C	N	O	S	0	2	0
			1059	670	186	195	8			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	63	Total	O	0	0
			63	63		
4	B	104	Total	O	0	0
			104	104		
4	D	107	Total	O	0	0
			107	107		

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	111.03Å 111.03Å 113.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	79.81 – 2.20 29.85 – 2.20	Depositor EDS
% Data completeness (in resolution range)	93.8 (79.81-2.20) 93.9 (29.85-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.203 , 0.258 0.198 , 0.253	Depositor DCC
R_{free} test set	1703 reflections (5.22%)	DCC
Wilson B-factor (Å ²)	40.0	Xtriage
Anisotropy	0.686	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.0	EDS
Estimated twinning fraction	0.017 for -h,l,k 0.010 for -l,-k,-h	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 34342 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3219	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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: SO4

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	A	1.19	1/841 (0.1%)	1.02	4/1130 (0.4%)
2	B	1.20	2/1078 (0.2%)	1.06	3/1468 (0.2%)
2	D	1.09	0/1094	1.01	5/1489 (0.3%)
All	All	1.16	3/3013 (0.1%)	1.03	12/4087 (0.3%)

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
2	B	0	2
2	D	0	1
All	All	0	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	186	THR	N-CA	6.15	1.58	1.46
1	A	77	SER	CB-OG	-5.84	1.34	1.42
2	B	244	GLN	CG-CD	5.27	1.63	1.51

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	204	THR	N-CA-C	9.78	137.41	111.00
1	A	14	ASP	CB-CG-OD2	7.96	125.47	118.30
1	A	76	ARG	NE-CZ-NH2	-7.66	116.47	120.30
2	D	213	ASP	CB-CG-OD2	6.39	124.05	118.30
2	B	232	ARG	NE-CZ-NH2	-6.27	117.16	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	225	PRO	N-CA-C	-6.18	96.04	112.10
2	D	226	GLY	N-CA-C	-6.09	97.87	113.10
1	A	70	THR	N-CA-C	-5.85	95.21	111.00
2	B	264	ARG	NE-CZ-NH2	-5.78	117.41	120.30
2	D	232	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	70	THR	C-N-CA	-5.13	111.53	122.30
2	D	235	ASP	CB-CG-OD2	5.08	122.88	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	203	GLU	Peptide
2	B	204	THR	Peptide
2	D	225	PRO	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	825	0	839	23	0
2	B	1051	0	1043	18	0
2	D	1059	0	1050	13	0
3	A	5	0	0	0	0
3	D	5	0	0	0	0
4	A	63	0	0	7	1
4	B	104	0	0	4	1
4	D	107	0	0	7	1
All	All	3219	0	2932	54	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (54) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:242:THR:HG22	2:B:245:GLU:H	1.10	1.09
1:A:55[A]:GLU:OE1	4:A:188:HOH:O	1.73	1.06
2:D:223:ILE:CD1	4:D:316:HOH:O	2.27	0.81
1:A:30:LYS:H	1:A:33:HIS:HD2	1.29	0.78
1:A:30:LYS:H	1:A:33:HIS:CD2	2.02	0.78
2:B:242:THR:CG2	2:B:245:GLU:H	1.94	0.77
1:A:102:ASP:O	1:A:105:GLU:HB2	1.84	0.77
2:B:242:THR:HG22	2:B:245:GLU:N	1.95	0.75
1:A:83:ALA:HB1	1:A:104:ILE:HD13	1.70	0.73
1:A:8:LEU:HD22	1:A:12:GLU:HB3	1.73	0.70
1:A:73:GLU:OE1	4:A:173:HOH:O	2.12	0.68
2:D:176:SER:OG	2:D:263:LYS:HE3	1.93	0.67
1:A:95:LYS:HD2	1:A:95:LYS:N	2.12	0.65
2:B:244:GLN:HG3	4:B:343:HOH:O	1.95	0.65
1:A:69:GLN:C	1:A:70:THR:O	2.29	0.64
2:D:186:THR:O	2:D:190:THR:HG23	1.99	0.62
1:A:32:LYS:HA	4:A:180:HOH:O	2.01	0.60
2:D:223:ILE:HD12	4:D:346:HOH:O	2.01	0.60
2:B:167:GLU:HB2	4:B:351:HOH:O	2.02	0.60
2:B:242:THR:HG23	2:B:244:GLN:HG3	1.83	0.59
1:A:40:GLU:OE1	1:A:43:ARG:NH1	2.37	0.58
2:B:162:LYS:HE3	2:B:167:GLU:OE1	2.04	0.57
2:D:223:ILE:HD11	4:D:316:HOH:O	2.00	0.57
2:B:195:GLN:HB2	4:B:310:HOH:O	2.05	0.56
1:A:6:SER:OG	1:A:7:VAL:N	2.38	0.56
2:D:160:GLU:HB3	4:D:385:HOH:O	2.05	0.55
2:D:147:ILE:O	2:D:147:ILE:CG2	2.54	0.54
1:A:32:LYS:CA	4:A:180:HOH:O	2.56	0.53
1:A:50:LEU:HB2	1:A:60:ILE:HD11	1.89	0.53
1:A:30:LYS:N	1:A:33:HIS:HD2	2.03	0.52
1:A:55[A]:GLU:CD	4:A:188:HOH:O	2.36	0.52
2:B:216:HIS:O	2:B:232:ARG:NH2	2.37	0.51
2:D:153[A]:ASN:ND2	4:D:353:HOH:O	2.45	0.50
2:B:227:GLN:HG3	2:B:227:GLN:O	2.09	0.50
1:A:76:ARG:HD3	4:A:173:HOH:O	2.11	0.50
1:A:30:LYS:HB2	1:A:32:LYS:HG2	1.94	0.49
1:A:36:TRP:CZ2	1:A:40:GLU:HG3	2.49	0.48
2:D:169:ILE:N	2:D:170:PRO:HD2	2.29	0.47
2:B:270:LEU:O	2:B:274:VAL:HG13	2.15	0.47
1:A:65:GLN:HB3	1:A:66:PRO:HD3	1.96	0.47
1:A:92:ILE:HG21	1:A:103:LYS:HG2	1.97	0.47
2:D:223:ILE:HD11	4:D:334:HOH:O	2.14	0.46
2:B:244:GLN:CG	4:B:343:HOH:O	2.58	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:32:LYS:CB	4:A:180:HOH:O	2.63	0.46
2:B:167:GLU:O	2:B:170:PRO:HD2	2.16	0.46
2:B:146:ALA:O	2:B:147:ILE:C	2.55	0.45
2:D:147:ILE:O	2:D:147:ILE:HG23	2.16	0.45
2:B:198:MET:O	2:B:202:LYS:HG3	2.18	0.43
1:A:20:ARG:O	1:A:96:ASP:HA	2.20	0.42
2:B:165:SER:O	2:B:168:VAL:HG12	2.19	0.41
2:B:201:LEU:HB2	2:B:273:ILE:HD11	2.03	0.41
2:B:253:ASN:HA	2:B:254:PRO:HA	1.70	0.40
2:D:270:LEU:O	2:D:274:VAL:HG13	2.22	0.40
2:D:252:HIS:HE1	4:D:310:HOH:O	2.04	0.40

All (2) 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	Distance(Å)	Clash(Å)
4:A:187:HOH:O	4:B:357:HOH:O[7_555]	1.96	0.24
4:D:363:HOH:O	4:D:363:HOH:O[7_555]	2.15	0.05

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	A	101/133 (76%)	96 (95%)	5 (5%)	0	100	100
2	B	133/146 (91%)	120 (90%)	6 (4%)	7 (5%)	3	1
2	D	135/146 (92%)	127 (94%)	5 (4%)	3 (2%)	10	5
All	All	369/425 (87%)	343 (93%)	16 (4%)	10 (3%)	8	3

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	204	THR
2	B	205	ILE
2	B	222	PRO

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Mol	Chain	Res	Type
2	B	225	PRO
2	D	163	ALA
2	D	146	ALA
2	D	147	ILE
2	B	221	GLY
2	B	227	GLN
2	B	228	MET

5.3.2 Protein sidechains ⓘ

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	A	91/113 (80%)	81 (89%)	10 (11%)	9	8
2	B	113/123 (92%)	108 (96%)	5 (4%)	39	45
2	D	115/123 (94%)	112 (97%)	3 (3%)	59	70
All	All	319/359 (89%)	301 (94%)	18 (6%)	29	33

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LEU
1	A	18	LYS
1	A	22	ARG
1	A	26	LYS
1	A	65	GLN
1	A	75	LEU
1	A	93	ASP
1	A	95	LYS
1	A	103	LYS
1	A	106	GLU
2	B	195	GLN
2	B	242	THR
2	B	268	LEU
2	B	274	VAL
2	B	275	ARG
2	D	147	ILE

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Mol	Chain	Res	Type
2	D	152	LEU
2	D	272	LYS

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

Mol	Chain	Res	Type
1	A	33	HIS

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	133	-	4,4,4	0.32	0	6,6,6	0.46	0
3	SO4	D	2	-	4,4,4	0.89	0	6,6,6	1.83	1 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical

component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	A	133	-	-	0/0/0/0	0/0/0/0
3	SO4	D	2	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	2	SO4	O2-S-O1	3.30	120.45	109.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	102/133 (76%)	-0.06	3 (2%) 49 50	32, 49, 68, 92	0
2	B	135/146 (92%)	0.50	15 (11%) 6 5	27, 42, 88, 101	0
2	D	135/146 (92%)	-0.02	6 (4%) 33 33	31, 45, 73, 86	0
All	All	372/425 (87%)	0.16	24 (6%) 19 18	27, 45, 78, 101	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	225	PRO	8.6
2	B	226	GLY	8.2
2	B	224	ALA	7.8
2	B	222	PRO	5.9
2	D	145	GLN	5.9
2	D	144	HIS	4.7
2	B	253	ASN	4.7
2	B	223	ILE	4.2
2	B	220	ALA	4.2
2	B	227	GLN	4.0
2	D	276	MET	3.9
2	B	221	GLY	3.7
2	D	277	TYR	3.3
2	B	254	PRO	3.3
1	A	105	GLU	3.1
2	D	278	SER	3.0
2	B	144	HIS	2.8
2	B	184	LEU	2.4
2	B	228	MET	2.4
2	D	195	GLN	2.4
1	A	14	ASP	2.3
2	B	252	HIS	2.3
1	A	106	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	244	GLN	2.3

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	SO4	D	2	5/5	0.09	-0.81	41,50,56,57	0
3	SO4	A	133	5/5	0.08	-1.05	57,57,65,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.