



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 17, 2024 – 10:45 PM EDT

PDB ID : 5YC0
Title : Crystal structure of LP-46/N44
Authors : Zhang, X.; Wang, X.; He, Y.
Deposited on : 2017-09-05
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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	:	2.37.1
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)	:	2.37.1

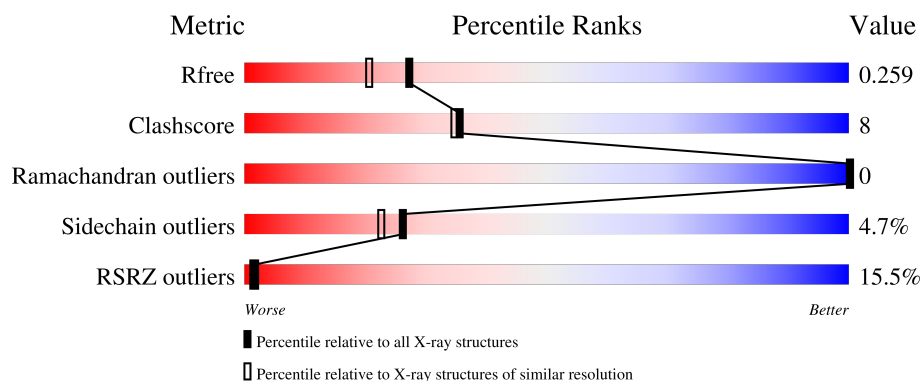
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	44	<div> <div>11%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>5%</div> </div> </div>
1	B	44	<div> <div>11%</div> <div> <div></div> <div>82%</div> <div>16%</div> <div>.</div> </div> </div>
1	C	44	<div> <div>5%</div> <div> <div></div> <div>80%</div> <div>18%</div> <div>.</div> </div> </div>
1	D	44	<div> <div>16%</div> <div> <div></div> <div>80%</div> <div>16%</div> <div>5%</div> </div> </div>
1	E	44	<div> <div>27%</div> <div> <div></div> <div>82%</div> <div>9%</div> <div>5%</div> <div>5%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	44	<div><div></div><div>18%</div><div>82%</div><div>16%</div><div></div></div>
2	G	31	<div><div></div><div>19%</div><div>77%</div><div>23%</div><div></div></div>
2	H	31	<div><div></div><div>6%</div><div>61%</div><div>26%</div><div></div><div></div><div>10%</div></div>
2	I	31	<div><div></div><div>3%</div><div>81%</div><div>6%</div><div>6%</div><div>6%</div></div>
2	P	31	<div><div></div><div>23%</div><div>77%</div><div>23%</div><div></div></div>
2	Q	31	<div><div></div><div>26%</div><div>74%</div><div>19%</div><div>6%</div></div>
2	W	31	<div><div></div><div>13%</div><div>81%</div><div>13%</div><div>6%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7582 atoms, of which 3736 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 Envelope glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	42	Total	C	H	N	O	0	0	0
			697	212	359	67	59			
1	B	44	Total	C	H	N	O	0	0	0
			725	221	374	69	61			
1	C	43	Total	C	H	N	O	0	0	0
			716	218	370	68	60			
1	D	42	Total	C	H	N	O	0	0	0
			697	212	359	67	59			
1	E	42	Total	C	H	N	O	0	0	0
			696	212	358	67	59			
1	F	43	Total	C	H	N	O	0	1	0
			730	223	377	70	60			

- Molecule 2 is a protein called LP-46.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Q	29	Total	C	H	N	O	0	0	0
			505	164	248	42	51			
2	W	29	Total	C	H	N	O	0	0	0
			505	164	248	42	51			
2	P	31	Total	C	H	N	O	0	0	0
			539	174	265	45	55			
2	H	28	Total	C	H	N	O	0	2	0
			509	166	250	40	53			
2	I	29	Total	C	H	N	O	0	0	0
			505	164	248	42	51			
2	G	31	Total	C	H	N	O	0	2	0
			564	181	280	46	57			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	19	Total 19	O 19	0	0
3	B	14	Total 14	O 14	0	0
3	C	15	Total 15	O 15	0	0
3	Q	14	Total 14	O 14	0	0
3	W	18	Total 18	O 18	0	0
3	P	16	Total 16	O 16	0	0
3	D	17	Total 17	O 17	0	0
3	E	11	Total 11	O 11	0	0
3	F	12	Total 12	O 12	0	0
3	H	15	Total 15	O 15	0	0
3	I	21	Total 21	O 21	0	0
3	G	22	Total 22	O 22	0	0

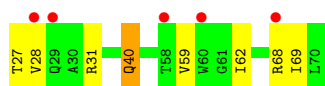
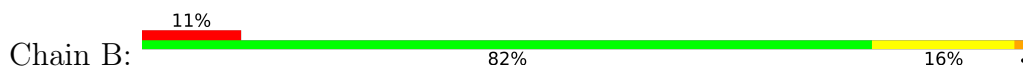
3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

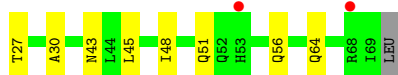
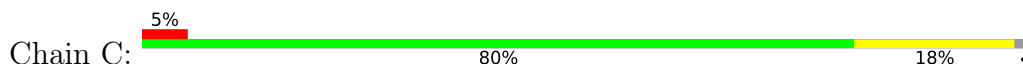
- Molecule 1: Envelope glycoprotein



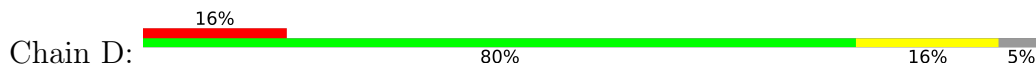
- Molecule 1: Envelope glycoprotein



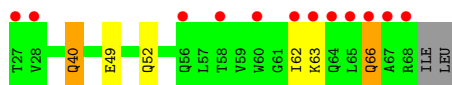
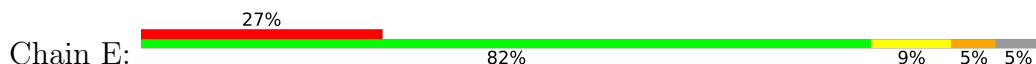
- Molecule 1: Envelope glycoprotein



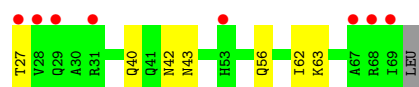
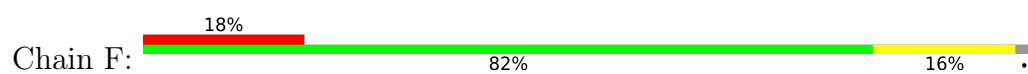
- Molecule 1: Envelope glycoprotein



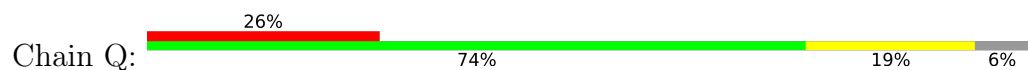
- Molecule 1: Envelope glycoprotein



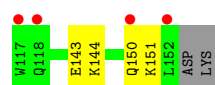
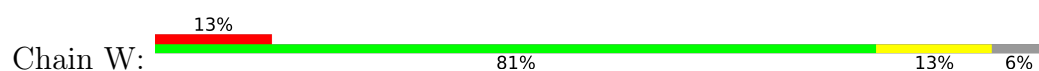
- Molecule 1: Envelope glycoprotein



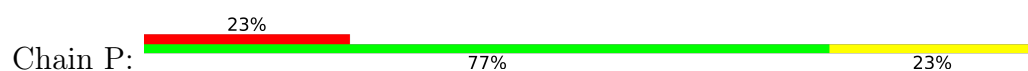
• Molecule 2: LP-46



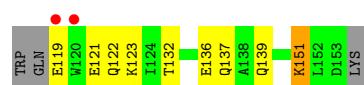
• Molecule 2: LP-46



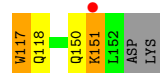
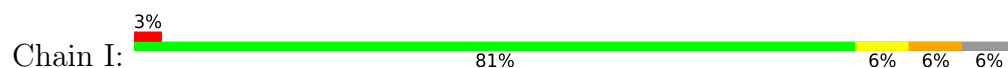
• Molecule 2: LP-46



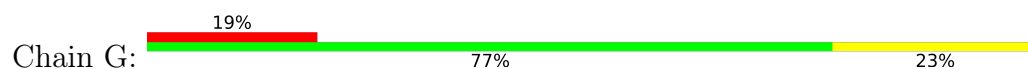
• Molecule 2: LP-46



• Molecule 2: LP-46



• Molecule 2: LP-46



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	34.09Å 53.26Å 59.34Å 94.42° 96.52° 90.02°	Depositor
Resolution (Å)	27.10 – 2.00 41.02 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.5 (27.10-2.00) 95.6 (41.02-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.220 , 0.256 0.222 , 0.259	Depositor DCC
R_{free} test set	1307 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	23.0	Xtriage
Anisotropy	0.411	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7582	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.87 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.4121e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	A	0.23	0/340	0.35	0/459
1	B	0.23	0/353	0.39	0/477
1	C	0.23	0/348	0.39	0/470
1	D	0.23	0/340	0.36	0/459
1	E	0.23	0/340	0.38	0/459
1	F	0.23	0/359	0.39	0/485
2	G	0.26	0/294	0.34	0/395
2	H	0.24	0/269	0.35	0/362
2	I	0.28	0/261	0.38	0/351
2	P	0.23	0/278	0.34	0/373
2	Q	0.25	0/261	0.37	0/351
2	W	0.24	0/261	0.32	0/351
All	All	0.24	0/3704	0.37	0/4992

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	A	338	359	359	8	0
1	B	351	374	372	7	0
1	C	346	370	370	4	0
1	D	338	359	359	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	338	358	359	6	0
1	F	353	377	377	5	0
2	G	284	280	280	7	0
2	H	259	250	250	8	0
2	I	257	248	248	5	0
2	P	274	265	265	7	0
2	Q	257	248	248	4	0
2	W	257	248	248	4	0
3	A	19	0	0	5	0
3	B	14	0	0	3	0
3	C	15	0	0	1	0
3	D	17	0	0	3	0
3	E	11	0	0	0	0
3	F	12	0	0	4	0
3	G	22	0	0	5	0
3	H	15	0	0	2	0
3	I	21	0	0	3	0
3	P	16	0	0	4	0
3	Q	14	0	0	2	0
3	W	18	0	0	4	0
All	All	3846	3736	3735	60	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 8.

The worst 5 of 60 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)
2:W:150:GLN:NE2	3:W:201:HOH:O	1.88	1.04
2:H:119:GLU:N	3:H:201:HOH:O	1.96	0.99
2:G:144:LYS:NZ	3:G:201:HOH:O	1.98	0.95
1:E:52:GLN:NE2	2:H:121[B]:GLU:OE1	2.01	0.93
1:B:27:THR:N	3:B:101:HOH:O	2.02	0.91

There are no symmetry-related clashes.

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	40/44 (91%)	40 (100%)	0	0	100	100
1	B	42/44 (96%)	42 (100%)	0	0	100	100
1	C	41/44 (93%)	41 (100%)	0	0	100	100
1	D	40/44 (91%)	40 (100%)	0	0	100	100
1	E	40/44 (91%)	39 (98%)	1 (2%)	0	100	100
1	F	42/44 (96%)	42 (100%)	0	0	100	100
2	G	31/31 (100%)	30 (97%)	1 (3%)	0	100	100
2	H	28/31 (90%)	28 (100%)	0	0	100	100
2	I	27/31 (87%)	27 (100%)	0	0	100	100
2	P	29/31 (94%)	29 (100%)	0	0	100	100
2	Q	27/31 (87%)	27 (100%)	0	0	100	100
2	W	27/31 (87%)	27 (100%)	0	0	100	100
All	All	414/450 (92%)	412 (100%)	2 (0%)	0	100	100

There are no Ramachandran outliers to report.

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	36/38 (95%)	34 (94%)	2 (6%)	21	17
1	B	37/38 (97%)	34 (92%)	3 (8%)	11	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	37/38 (97%)	35 (95%)	2 (5%)	22	18
1	D	36/38 (95%)	34 (94%)	2 (6%)	21	17
1	E	36/38 (95%)	34 (94%)	2 (6%)	21	17
1	F	38/38 (100%)	36 (95%)	2 (5%)	22	18
2	G	31/29 (107%)	31 (100%)	0	100	100
2	H	28/29 (97%)	27 (96%)	1 (4%)	35	34
2	I	27/29 (93%)	25 (93%)	2 (7%)	13	9
2	P	29/29 (100%)	29 (100%)	0	100	100
2	Q	27/29 (93%)	26 (96%)	1 (4%)	34	32
2	W	27/29 (93%)	26 (96%)	1 (4%)	34	32
All	All	389/402 (97%)	371 (95%)	18 (5%)	26	23

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	56	GLN
2	I	151	LYS
2	I	117	TRP
2	W	151	LYS
1	F	27	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	51	GLN
2	H	137	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 [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](#)

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	42/44 (95%)	0.82	5 (11%) 4 4	15, 27, 51, 59	0
1	B	44/44 (100%)	0.79	5 (11%) 5 4	15, 32, 46, 51	0
1	C	43/44 (97%)	0.41	2 (4%) 31 30	16, 28, 47, 56	0
1	D	42/44 (95%)	1.13	7 (16%) 1 1	13, 25, 59, 70	0
1	E	42/44 (95%)	1.26	12 (28%) 0 0	14, 30, 64, 72	0
1	F	43/44 (97%)	1.00	8 (18%) 1 1	15, 30, 59, 72	0
2	G	31/31 (100%)	1.28	6 (19%) 1 0	16, 28, 57, 67	0
2	H	28/31 (90%)	0.63	2 (7%) 16 15	15, 29, 41, 60	0
2	I	29/31 (93%)	0.34	1 (3%) 45 44	15, 22, 43, 44	0
2	P	31/31 (100%)	0.97	7 (22%) 0 0	16, 30, 58, 58	0
2	Q	29/31 (93%)	1.02	8 (27%) 0 0	15, 31, 51, 60	0
2	W	29/31 (93%)	0.49	4 (13%) 2 2	17, 26, 46, 48	0
All	All	433/450 (96%)	0.86	67 (15%) 2 1	13, 29, 57, 72	0

The worst 5 of 67 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	28	VAL	11.9
1	E	67	ALA	11.4
1	D	27	THR	9.3
1	E	66	GLN	9.0
2	Q	117	TRP	8.7

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 monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.