



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:15 AM UTC

PDB ID : 1B6H / pdb_00001b6h
Title : OLIGO-PEPTIDE BINDING PROTEIN COMPLEXED WITH LYSYL-NO
RVALYL-LYSINE
Authors : Davies, T.G.; Tame, J.R.H.
Deposited on : 1998-11-13
Resolution : 1.80 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 ⓘ 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

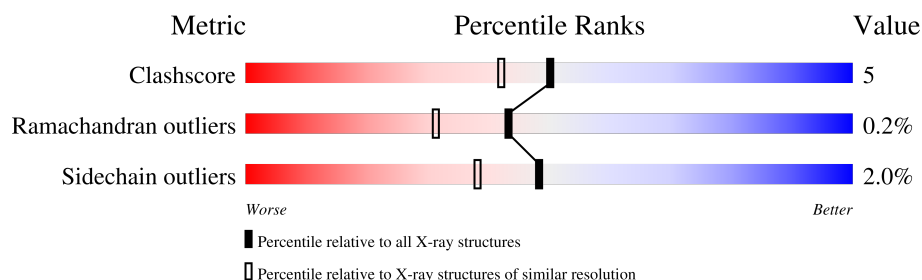
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

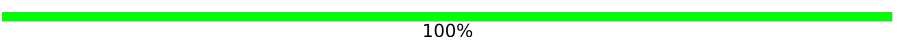
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	517	 82% 17% .
2	B	3	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	U1	A	519	-	-	X	-
3	U1	A	523	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4776 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 Periplasmic oligopeptide-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	517	Total	C	N	O	S	35	10	0
			4193	2688	701	799	5			

- Molecule 2 is a protein called LYS-NVA-LYS PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			26	17	5	4			

- Molecule 3 is URANIUM ATOM (CCD ID: U1) (formula: U).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	8	Total	U	0	0
			8	8		

- Molecule 4 is water.

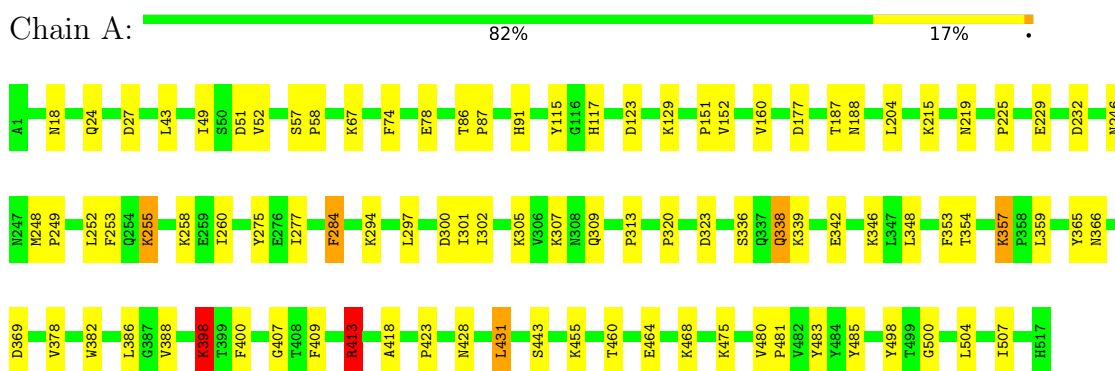
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	546	Total	O	0	0
			546	546		
4	B	3	Total	O	0	0
			3	3		

3 Residue-property plots

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.

Note EDS was not executed.

- Molecule 1: Periplasmic oligopeptide-binding protein



- Molecule 2: LYS-NVA-LYS PEPTIDE



There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	109.68Å 75.77Å 70.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.80	Depositor
% Data completeness (in resolution range)	90.0 (15.00-1.80)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.180 , 0.220	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4776	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

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: NVA, U1

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	0.87	8/4348 (0.2%)	1.50	41/5929 (0.7%)
2	B	0.62	0/17	1.08	0/16
All	All	0.87	8/4365 (0.2%)	1.50	41/5945 (0.7%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	255	LYS	CG-CD	25.21	2.28	1.52
1	A	300	ASP	CG-OD2	-14.80	0.97	1.25
1	A	475	LYS	CG-CD	11.68	1.87	1.52
1	A	300	ASP	CG-OD1	9.95	1.44	1.25
1	A	455	LYS	CG-CD	7.66	1.75	1.52
1	A	67	LYS	CG-CD	-5.67	1.35	1.52
1	A	346	LYS	CE-NZ	5.18	1.64	1.49
1	A	398	LYS	CE-NZ	5.14	1.64	1.49

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	255	LYS	CB-CG-CD	-13.53	80.19	111.30
1	A	468	LYS	CG-CD-CE	11.63	138.04	111.30
1	A	300	ASP	CB-CG-OD1	-10.11	95.14	118.40
1	A	475	LYS	CB-CG-CD	-8.02	92.86	111.30
1	A	353	PHE	CA-CB-CG	-6.83	106.97	113.80
1	A	284	PHE	CA-CB-CG	-6.80	107.00	113.80
1	A	455	LYS	CB-CG-CD	-6.60	96.13	111.30
1	A	443	SER	CA-C-O	6.56	126.25	119.49
1	A	407	GLY	N-CA-C	-6.53	103.66	114.76
1	A	468	LYS	CD-CE-NZ	6.48	132.65	111.90
1	A	188	ASN	CA-C-N	-6.36	115.97	122.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	188	ASN	C-N-CA	-6.36	115.97	122.27
1	A	260	ILE	CA-C-N	6.21	126.40	119.32
1	A	260	ILE	C-N-CA	6.21	126.40	119.32
1	A	18	ASN	CA-CB-CG	-6.18	106.42	112.60
1	A	67	LYS	CB-CG-CD	6.13	125.40	111.30
1	A	485	TYR	CA-CB-CG	5.87	124.47	113.90
1	A	219	ASN	CA-CB-CG	-5.83	106.77	112.60
1	A	313	PRO	N-CA-CB	5.81	108.36	103.25
1	A	481	PRO	N-CA-CB	5.66	108.37	103.27
1	A	117	HIS	CA-CB-CG	-5.61	108.19	113.80
1	A	336	SER	CA-C-O	-5.59	115.13	121.72
1	A	51	ASP	CA-CB-CG	5.57	118.17	112.60
1	A	78	GLU	CA-CB-CG	-5.54	103.02	114.10
1	A	413	ARG	CG-CD-NE	5.45	123.99	112.00
1	A	252	LEU	N-CA-C	5.42	120.91	113.97
1	A	300	ASP	CB-CG-OD2	5.34	130.69	118.40
1	A	151	PRO	N-CA-CB	5.28	108.02	103.27
1	A	275	TYR	CA-CB-CG	-5.22	104.50	113.90
1	A	74	PHE	CA-CB-CG	-5.16	108.64	113.80
1	A	91	HIS	CA-CB-CG	-5.11	108.69	113.80
1	A	500	GLY	N-CA-C	-5.11	108.57	115.36
1	A	320	PRO	N-CA-CB	5.09	108.57	103.48
1	A	152	VAL	CA-C-N	5.05	124.83	119.28
1	A	152	VAL	C-N-CA	5.05	124.83	119.28
1	A	232	ASP	CA-CB-CG	5.04	117.64	112.60
1	A	246	ASN	CA-C-N	5.04	129.87	122.77
1	A	246	ASN	C-N-CA	5.04	129.87	122.77
1	A	409	PHE	N-CA-C	5.01	115.92	108.60
1	A	27	ASP	CA-C-N	5.01	125.28	119.47
1	A	27	ASP	C-N-CA	5.01	125.28	119.47

There are no chirality outliers.

There are no planarity outliers.

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	A	4193	0	4117	41	0
2	B	26	0	37	0	0
3	A	8	0	0	3	2
4	A	546	0	0	9	8
4	B	3	0	0	0	0
All	All	4776	0	4154	44	8

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 5.

All (44) 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:A:519:U1:U	4:A:527:HOH:O	1.19	1.21
3:A:523:U1:U	4:A:580:HOH:O	1.24	1.17
1:A:49:ILE:HA	1:A:160[B]:VAL:HG13	1.63	0.79
3:A:519:U1:U	4:A:556:HOH:O	1.65	0.77
1:A:52[B]:VAL:HG22	4:A:723:HOH:O	2.00	0.61
1:A:354:THR:OG1	1:A:357:LYS:HG2	2.02	0.59
1:A:297:LEU:HD21	1:A:302:ILE:HD12	1.86	0.56
1:A:115:TYR:CE1	1:A:428:ASN:HB3	2.41	0.56
1:A:43:LEU:HD21	1:A:204:LEU:HD22	1.89	0.55
1:A:365:TYR:HB2	1:A:413:ARG:HG2	1.87	0.55
1:A:369:ASP:HB2	4:A:992:HOH:O	2.05	0.55
1:A:382:TRP:HB3	1:A:388[B]:VAL:CG2	2.38	0.54
1:A:428:ASN:HA	1:A:431:LEU:HD22	1.89	0.54
1:A:365:TYR:CB	1:A:413:ARG:HG2	2.40	0.51
1:A:57[A]:SER:HB2	1:A:58:PRO:CD	2.42	0.50
1:A:498:TYR:HE2	1:A:507[A]:ILE:HD11	1.77	0.50
1:A:342:GLU:OE1	4:A:526:HOH:O	2.19	0.49
1:A:302:ILE:HD11	1:A:378:VAL:HG22	1.95	0.49
1:A:215:LYS:HD2	4:A:763:HOH:O	2.14	0.48
1:A:57[B]:SER:HB3	1:A:58:PRO:CD	2.44	0.47
1:A:294:LYS:HA	1:A:480:VAL:HG13	1.95	0.47
1:A:301:ILE:O	1:A:305:LYS:HB2	2.14	0.47
1:A:43:LEU:O	1:A:187:THR:HB	2.15	0.47
1:A:57[A]:SER:HB2	1:A:58:PRO:HD2	1.96	0.46
1:A:366:ASN:HB3	1:A:400:PHE:CD2	2.50	0.46
1:A:160[B]:VAL:HG11	4:A:681:HOH:O	2.15	0.46
1:A:160[B]:VAL:CG1	4:A:681:HOH:O	2.65	0.44
1:A:359:LEU:HB3	1:A:388[B]:VAL:HG12	1.99	0.44
1:A:248:MET:HA	1:A:248:MET:HE2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:ASP:O	1:A:423:PRO:HD3	2.18	0.43
1:A:418:ALA:HB3	1:A:504:LEU:HD22	2.00	0.43
1:A:386:LEU:HG	1:A:388[A]:VAL:HG23	2.01	0.43
1:A:460:THR:O	1:A:464:GLU:HG3	2.19	0.42
1:A:498:TYR:CE2	1:A:507[A]:ILE:HD11	2.54	0.42
1:A:115:TYR:CD1	1:A:428:ASN:HB3	2.54	0.42
1:A:338:GLN:HG3	1:A:339:LYS:N	2.34	0.42
1:A:24:GLN:HA	1:A:398:LYS:HD3	2.02	0.42
1:A:57[B]:SER:HB3	1:A:58:PRO:HD2	2.01	0.42
1:A:277:ILE:CG2	1:A:284:PHE:HB3	2.49	0.42
1:A:86:THR:HA	1:A:87:PRO:HD3	1.86	0.41
1:A:253:PHE:CD2	1:A:309:GLN:HG2	2.56	0.41
1:A:307:LYS:HE3	1:A:483:TYR:OH	2.21	0.41
1:A:229:GLU:HB3	1:A:249:PRO:HD3	2.03	0.40
1:A:123:ASP:OD2	1:A:129:LYS:NZ	2.48	0.40

All (8) 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)
3:A:525:U1:U	4:A:526:HOH:O[1_554]	1.36	0.84
3:A:523:U1:U	4:A:590:HOH:O[4_455]	1.81	0.39
4:A:535:HOH:O	4:A:562:HOH:O[3_545]	1.97	0.23
4:A:722:HOH:O	4:A:806:HOH:O[3_555]	2.10	0.10
4:A:530:HOH:O	4:A:590:HOH:O[4_455]	2.11	0.09
4:A:580:HOH:O	4:A:590:HOH:O[4_455]	2.14	0.06
4:A:624:HOH:O	4:A:806:HOH:O[3_555]	2.18	0.02
4:A:578:HOH:O	4:A:806:HOH:O[3_555]	2.19	0.01

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	525/517 (102%)	508 (97%)	16 (3%)	1 (0%)	43 31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	PRO

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	465/455 (102%)	456 (98%)	9 (2%)	50 41
2	B	2/2 (100%)	2 (100%)	0	100 100
All	All	467/457 (102%)	458 (98%)	9 (2%)	48 41

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	177	ASP
1	A	255	LYS
1	A	258	LYS
1	A	338	GLN
1	A	348	LEU
1	A	357	LYS
1	A	398	LYS
1	A	413	ARG
1	A	431	LEU

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

Mol	Chain	Res	Type
1	A	8	GLN
1	A	195	ASN
1	A	199	ASN
1	A	209	GLN

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Mol	Chain	Res	Type
1	A	461	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
2	NVA	B	2	2	5,6,7	0.73	0	2,6,8	1.13	0

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
2	NVA	B	2	2	-	0/4/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.