



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:38 AM UTC

PDB ID : 1B5I / pdb_00001b5i
Title : OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KNK
Authors : Tame, J.R.H.; Wilkinson, A.J.
Deposited on : 1999-01-06
Resolution : 1.90 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
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

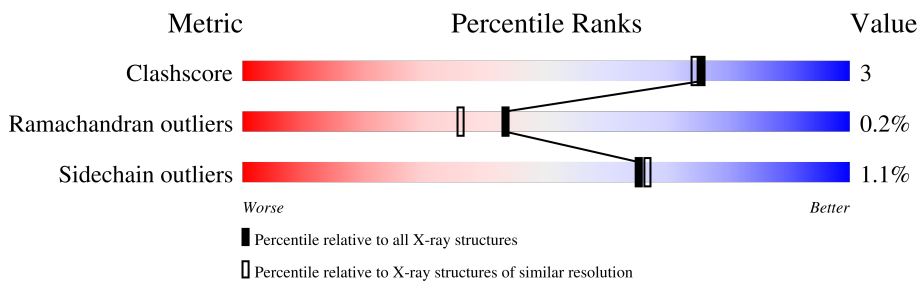
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)

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	
2	B	3	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4543 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 PROTEIN (OLIGO-PEPTIDE BINDING PROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	517	Total	C	N	O	S	28	4	0
			4177	2675	700	797	5			

- Molecule 2 is a protein called PROTEIN (LYS-ASN-LYS).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			27	16	6	5			

- 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.

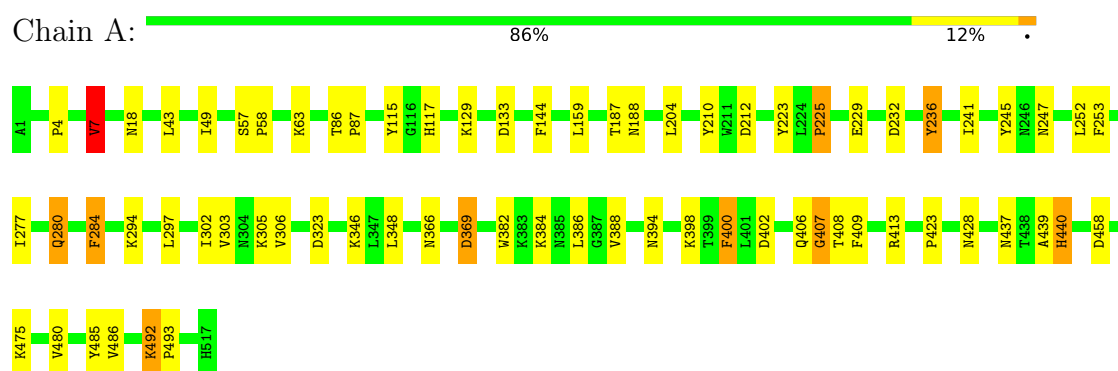
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	328	Total	O	0	0
			328	328		
4	B	3	Total	O	0	0
			3	3		

3 Residue-property plots

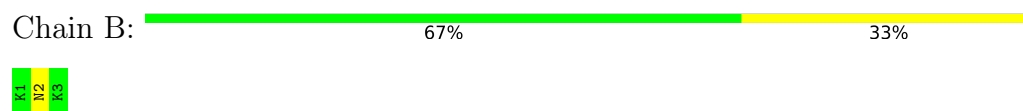
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: PROTEIN (OLIGO-PEPTIDE BINDING PROTEIN)



• Molecule 2: PROTEIN (LYS-ASN-LYS)



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	109.69Å 76.09Å 70.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.90	Depositor
% Data completeness (in resolution range)	95.7 (15.00-1.90)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.182 , 0.223	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4543	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.94	4/4306 (0.1%)	1.63	38/5872 (0.6%)
2	B	0.69	0/26	1.74	1/30 (3.3%)
All	All	0.94	4/4332 (0.1%)	1.63	39/5902 (0.7%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	407	GLY	C-N	27.40	1.72	1.33
1	A	408	THR	C-N	23.06	1.62	1.33
1	A	346	LYS	CE-NZ	17.89	2.03	1.49
1	A	398	LYS	CD-CE	-5.80	1.35	1.52

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	407	GLY	O-C-N	-43.89	82.63	122.57
1	A	408	THR	CA-C-N	-16.04	95.48	122.10
1	A	408	THR	C-N-CA	-16.04	95.48	122.10
1	A	408	THR	O-C-N	10.30	136.29	122.59
1	A	305	LYS	CB-CG-CD	8.59	131.06	111.30
1	A	280	GLN	CA-CB-CG	7.70	129.50	114.10
1	A	400	PHE	CA-CB-CG	7.59	121.39	113.80
1	A	369	ASP	CA-CB-CG	7.15	119.75	112.60
1	A	284	PHE	CA-CB-CG	-7.15	106.65	113.80
1	A	303	VAL	N-CA-C	6.36	116.51	110.53
1	A	252	LEU	N-CA-C	6.32	122.06	113.97
1	A	117	HIS	CA-CB-CG	-6.07	107.73	113.80
1	A	485	TYR	CA-CB-CG	5.97	124.65	113.90
1	A	247	ASN	CA-CB-CG	5.90	118.50	112.60
1	A	232	ASP	CA-CB-CG	5.85	118.45	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	475	LYS	CA-CB-CG	5.82	125.73	114.10
1	A	437	ASN	OD1-CG-ND2	-5.76	116.84	122.60
1	A	252	LEU	N-CA-CB	-5.72	102.71	110.67
2	B	2	ASN	CA-CB-CG	-5.62	106.97	112.60
1	A	384	LYS	CB-CG-CD	5.59	124.16	111.30
1	A	7	VAL	N-CA-CB	5.58	118.84	110.13
1	A	253	PHE	N-CA-C	5.49	117.70	111.11
1	A	245	TYR	N-CA-C	-5.44	103.72	110.41
1	A	188	ASN	CA-C-N	-5.44	116.89	122.27
1	A	188	ASN	C-N-CA	-5.44	116.89	122.27
1	A	18	ASN	CA-CB-CG	-5.38	107.22	112.60
1	A	439	ALA	N-CA-C	-5.25	106.37	112.89
1	A	458	ASP	CA-CB-CG	5.23	117.83	112.60
1	A	159	LEU	N-CA-C	5.20	119.37	113.19
1	A	486	VAL	N-CA-C	-5.19	101.15	109.20
1	A	144	PHE	CA-CB-CG	5.19	118.99	113.80
1	A	394	ASN	O-C-N	-5.14	117.19	123.10
1	A	386	LEU	N-CA-CB	-5.14	103.55	110.95
1	A	223	TYR	CA-C-O	-5.13	114.79	120.38
1	A	49	ILE	CA-C-O	-5.12	116.56	121.63
1	A	407	GLY	CA-C-O	5.05	126.09	120.03
1	A	236	TYR	N-CA-C	-5.03	105.70	111.14
1	A	492	LYS	CA-C-O	5.03	126.38	120.69
1	A	440	HIS	CA-CB-CG	-5.01	108.78	113.80

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	4177	0	4090	25	0
2	B	27	0	34	0	0
3	A	8	0	0	0	0
4	A	328	0	0	0	0
4	B	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4543	0	4124	25	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 3.

All (25) 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:4:PRO:O	1:A:7:VAL:HG13	2.06	0.54
1:A:115:TYR:CE1	1:A:428:ASN:HB3	2.42	0.54
1:A:43:LEU:HD21	1:A:204:LEU:HD22	1.91	0.53
1:A:280:GLN:HG3	1:A:440:HIS:HB3	1.90	0.53
1:A:382:TRP:HB3	1:A:388:VAL:CG2	2.39	0.52
1:A:402[A]:ASP:OD2	1:A:406:GLN:OE1	2.28	0.52
1:A:129:LYS:HD3	1:A:133:ASP:OD2	2.10	0.51
1:A:57[B]:SER:HB2	1:A:58:PRO:CD	2.42	0.50
1:A:407:GLY:O	1:A:409:PHE:N	2.44	0.50
1:A:297:LEU:HD21	1:A:302:ILE:HD12	1.93	0.50
1:A:57[B]:SER:HB2	1:A:58:PRO:HD2	1.93	0.49
1:A:57[A]:SER:HB3	1:A:58:PRO:CD	2.43	0.49
1:A:277:ILE:CG2	1:A:284:PHE:HB3	2.45	0.47
1:A:323:ASP:O	1:A:423:PRO:HD3	2.15	0.46
1:A:210:TYR:CE2	1:A:212:ASP:HB3	2.50	0.46
1:A:57[A]:SER:HB3	1:A:58:PRO:HD2	1.98	0.45
1:A:115:TYR:CD1	1:A:428:ASN:HB3	2.53	0.44
1:A:294:LYS:HA	1:A:480:VAL:HG13	1.99	0.44
1:A:43:LEU:O	1:A:187:THR:HB	2.20	0.42
1:A:229:GLU:OE1	1:A:369:ASP:HB2	2.20	0.42
1:A:236:TYR:HA	1:A:241:ILE:HB	2.02	0.41
1:A:348:LEU:HD23	1:A:348:LEU:HA	1.93	0.41
1:A:86:THR:HA	1:A:87:PRO:HD3	1.94	0.41
1:A:366:ASN:HB3	1:A:400:PHE:CD2	2.57	0.40
1:A:492:LYS:HA	1:A:493:PRO:HD3	1.94	0.40

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	519/517 (100%)	504 (97%)	14 (3%)	1 (0%)	43	36
2	B	1/3 (33%)	1 (100%)	0	0	100	100
All	All	520/520 (100%)	505 (97%)	14 (3%)	1 (0%)	43	36

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	459/455 (101%)	454 (99%)	5 (1%)	65	67
2	B	3/3 (100%)	3 (100%)	0	100	100
All	All	462/458 (101%)	457 (99%)	5 (1%)	65	67

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	63	LYS
1	A	225	PRO
1	A	306	VAL
1	A	413	ARG

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	55	HIS
1	A	199	ASN
1	A	304	ASN
1	A	391	ASN
1	A	395	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	407:GLY	C	408:THR	N	1.72
1	A	408:THR	C	409:PHE	N	1.62

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.