Full wwPDB X-ray Structure Validation Report (i)

Aug 2, 2023 – 08:30 AM EDT

PDB ID	:	1B58
Title	:	OLIGO-PEPTIDE BINDING PROTEIN (OPPA) COMPLEXED WITH KYK
Authors	:	Tame, J.R.H.; Wilkinson, A.J.
Deposited on	:	1999-01-12
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 (i) 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 (i)) were used in the production of this report:

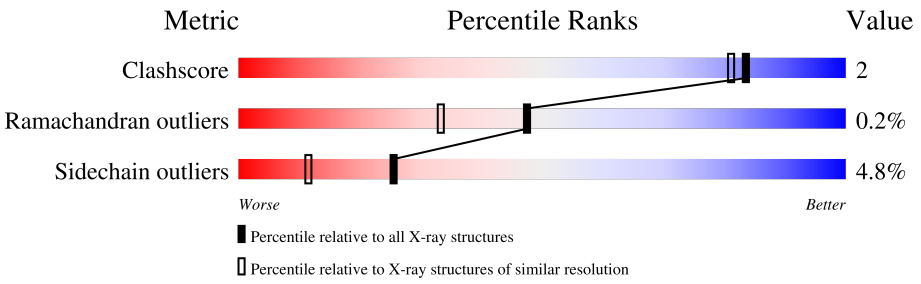
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.34

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 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	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	517	87% 12% •
2	B	3	100%

2 Entry composition (i)

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.

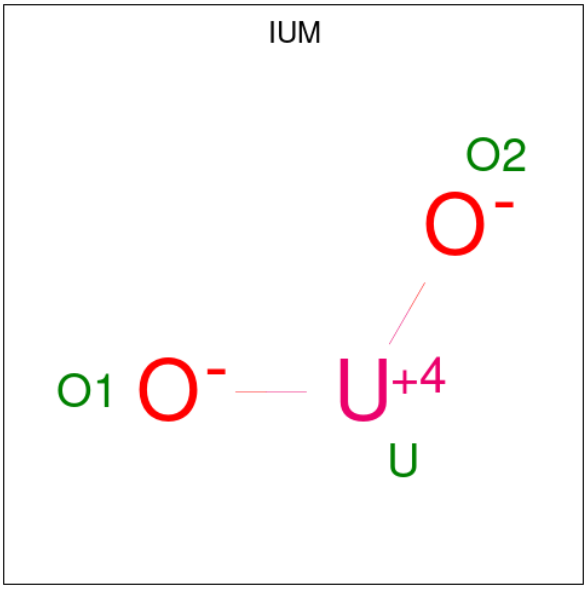
- Molecule 1 is a protein called PROTEIN (OLIGO-PEPTIDE BINDING PROTEIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	517	4165	2666	700	794	5	0	0	0

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	3	31	21	5	5	0	0	0

- Molecule 3 is URANYL (VI) ION (three-letter code: IUM) (formula: O_2U).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	U		
3	A	1	1	1	0	0
			Total	U		
3	A	1	1	1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total U 1 1	0	0
3	A	1	Total U 1 1	0	0
3	A	1	Total U 1 1	0	0
3	A	1	Total U 1 1	0	0
3	A	1	Total U 1 1	0	0
3	A	1	Total U 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	337	Total O 337 337	0	0
4	B	2	Total O 2 2	0	0

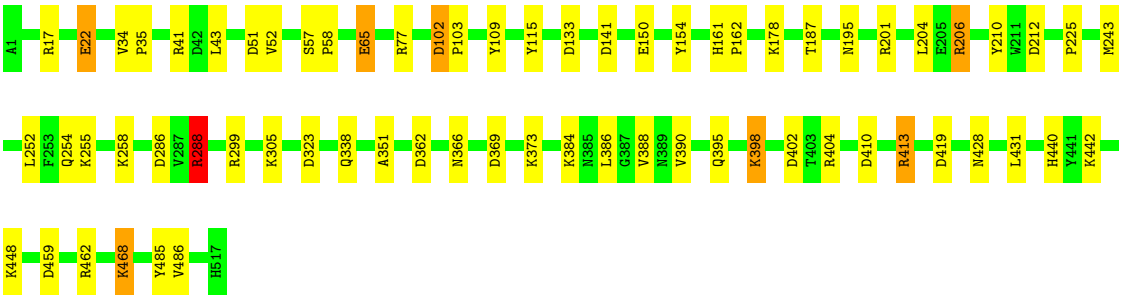
3 Residue-property plots (i)

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. 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.

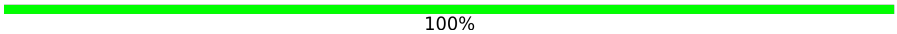
• Molecule 1: PROTEIN (OLIGO-PEPTIDE BINDING PROTEIN)

Chain A:



• Molecule 2: PROTEIN (LYS-TYR-LYS)

Chain B:



There are no outlier residues recorded for this chain.

4 Data and refinement statistics (i)

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	110.67Å 76.62Å 71.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.80	Depositor
% Data completeness (in resolution range)	94.6 (15.00-1.80)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.179 , 0.223	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4543	wwPDB-VP
Average B, all atoms (Å^2)	23.0	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: IUM

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	0.60	0/4276	1.36	32/5830 (0.5%)
2	B	0.89	0/31	1.47	0/37
All	All	0.61	0/4307	1.36	32/5867 (0.5%)

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	413	ARG	NE-CZ-NH2	-21.56	109.52	120.30
1	A	201	ARG	CD-NE-CZ	13.58	142.62	123.60
1	A	133	ASP	CB-CG-OD2	-12.81	106.77	118.30
1	A	206	ARG	NE-CZ-NH2	-12.70	113.95	120.30
1	A	77	ARG	CD-NE-CZ	9.83	137.37	123.60
1	A	459	ASP	CB-CG-OD2	-8.60	110.56	118.30
1	A	410	ASP	CB-CG-OD1	8.46	125.91	118.30
1	A	299	ARG	NE-CZ-NH1	-8.27	116.16	120.30
1	A	288	ARG	NE-CZ-NH2	8.25	124.42	120.30
1	A	402	ASP	CB-CG-OD2	-8.00	111.10	118.30
1	A	141	ASP	CB-CG-OD1	7.86	125.37	118.30
1	A	323	ASP	CB-CG-OD1	7.80	125.32	118.30
1	A	413	ARG	NH1-CZ-NH2	7.72	127.89	119.40
1	A	419	ASP	CB-CG-OD2	-7.26	111.77	118.30
1	A	17	ARG	NE-CZ-NH1	6.75	123.67	120.30
1	A	485	TYR	CA-CB-CG	6.72	126.17	113.40
1	A	201	ARG	NE-CZ-NH2	-6.71	116.94	120.30
1	A	369	ASP	CB-CG-OD1	-6.40	112.54	118.30
1	A	362	ASP	CB-CG-OD1	6.28	123.95	118.30
1	A	410	ASP	CB-CG-OD2	-6.27	112.65	118.30
1	A	41	ARG	NE-CZ-NH2	-6.26	117.17	120.30
1	A	65	GLU	CA-CB-CG	6.11	126.85	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	133	ASP	OD1-CG-OD2	5.95	134.60	123.30
1	A	462	ARG	NE-CZ-NH1	-5.91	117.35	120.30
1	A	102	ASP	CB-CG-OD1	5.78	123.50	118.30
1	A	51	ASP	CB-CG-OD1	5.75	123.48	118.30
1	A	323	ASP	CB-CG-OD2	-5.70	113.17	118.30
1	A	77	ARG	NE-CZ-NH1	5.69	123.15	120.30
1	A	243	MET	CA-CB-CG	5.49	122.63	113.30
1	A	486	VAL	N-CA-CB	5.46	123.51	111.50
1	A	206	ARG	CD-NE-CZ	5.32	131.05	123.60
1	A	22	GLU	OE1-CD-OE2	-5.14	117.14	123.30

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	4165	0	4076	20	0
2	B	31	0	37	0	0
3	A	8	0	0	0	0
4	A	337	0	0	2	0
4	B	2	0	0	0	0
All	All	4543	0	4113	20	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 2.

All (20) 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:252:LEU:O	1:A:255:LYS:HB3	1.99	0.62
1:A:22:GLU:O	1:A:398:LYS:HE2	2.00	0.61
1:A:57:SER:HB2	1:A:58:PRO:HD2	1.86	0.58
1:A:115:TYR:CE1	1:A:428:ASN:HB3	2.41	0.56
1:A:398:LYS:H	1:A:398:LYS:CE	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:468:LYS:HD2	1:A:468:LYS:N	2.25	0.51
1:A:43:LEU:O	1:A:187:THR:HB	2.11	0.51
1:A:398:LYS:H	1:A:398:LYS:HE3	1.79	0.48
1:A:404:ARG:O	1:A:440:HIS:HE1	1.98	0.46
1:A:43:LEU:HD21	1:A:204:LEU:HD22	1.98	0.45
1:A:34:VAL:HB	1:A:35:PRO:HD3	1.99	0.45
1:A:366:ASN:HA	1:A:395:GLN:O	2.17	0.44
1:A:288:ARG:NH1	1:A:351:ALA:HA	2.32	0.44
1:A:286:ASP:OD2	1:A:288:ARG:NH1	2.51	0.43
1:A:102:ASP:HA	1:A:103:PRO:HD3	1.93	0.42
1:A:210:TYR:CE2	1:A:212:ASP:HB3	2.54	0.42
1:A:34:VAL:N	1:A:35:PRO:CD	2.84	0.41
1:A:154:TYR:HB3	4:A:568:HOH:O	2.20	0.41
1:A:161:HIS:CD2	1:A:162:PRO:HD2	2.55	0.41
1:A:52:VAL:HG13	4:A:710:HOH:O	2.20	0.41

There are no symmetry-related clashes.

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	A	515/517 (100%)	499 (97%)	15 (3%)	1 (0%)	47	33
2	B	1/3 (33%)	1 (100%)	0	0	100	100
All	All	516/520 (99%)	500 (97%)	15 (3%)	1 (0%)	47	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	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	A	455/455 (100%)	433 (95%)	22 (5%)	25 11
2	B	3/3 (100%)	3 (100%)	0	100 100
All	All	458/458 (100%)	436 (95%)	22 (5%)	25 11

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	GLU
1	A	109	TYR
1	A	150	GLU
1	A	178	LYS
1	A	195	ASN
1	A	206	ARG
1	A	254	GLN
1	A	258	LYS
1	A	288	ARG
1	A	305	LYS
1	A	338	GLN
1	A	373	LYS
1	A	384	LYS
1	A	386	LEU
1	A	388	VAL
1	A	390	VAL
1	A	398	LYS
1	A	413	ARG
1	A	431	LEU
1	A	442	LYS
1	A	448	LYS
1	A	468	LYS

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	117	HIS
1	A	199	ASN
1	A	254	GLN
1	A	440	HIS
1	A	461	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 8 are modelled with single atom - 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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.