Full wwPDB X-ray Structure Validation Report (i)

Jun 13, 2024 – 09:20 AM EDT

PDB ID	:	4D8O
Title	:	Crystal Structure of the ankyrin-B ZU5-ZU5-UPA-DD tandem
Authors	:	Wei, Z.; Wang, C.; Yu, C.; Zhang, M.
Deposited on	:	2012-01-11
Resolution	:	2.20 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 (1)) were used in the production of this report:

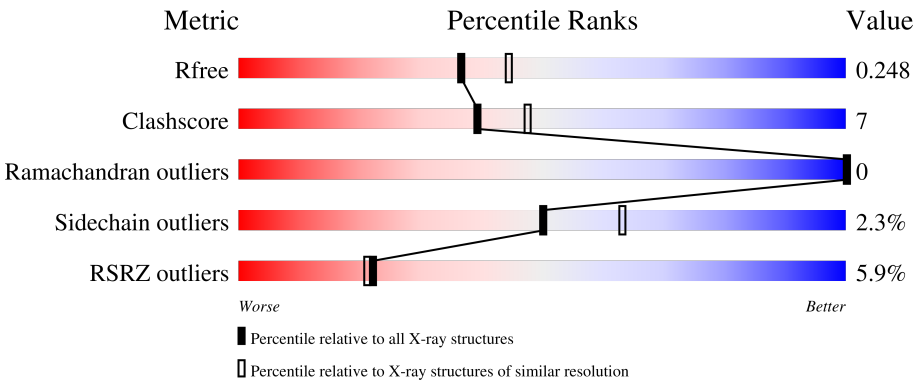
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

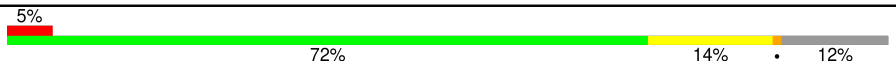
The reported resolution of this entry is 2.20 Å.

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}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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 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% 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	581	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4090 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 Ankyrin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	509	3989	2536	709	718	26	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	946	MET	-	expression tag	UNP Q01484
A	947	HIS	-	expression tag	UNP Q01484
A	948	HIS	-	expression tag	UNP Q01484
A	949	HIS	-	expression tag	UNP Q01484
A	950	HIS	-	expression tag	UNP Q01484
A	951	HIS	-	expression tag	UNP Q01484
A	952	HIS	-	expression tag	UNP Q01484
A	953	SER	-	expression tag	UNP Q01484
A	954	SER	-	expression tag	UNP Q01484
A	955	GLY	-	expression tag	UNP Q01484
A	956	LEU	-	expression tag	UNP Q01484
A	957	GLU	-	expression tag	UNP Q01484
A	958	VAL	-	expression tag	UNP Q01484
A	959	LEU	-	expression tag	UNP Q01484
A	960	PHE	-	expression tag	UNP Q01484
A	961	GLN	-	expression tag	UNP Q01484
A	962	GLY	-	expression tag	UNP Q01484
A	963	PRO	-	expression tag	UNP Q01484
A	964	GLU	-	expression tag	UNP Q01484
A	965	PHE	-	expression tag	UNP Q01484

- Molecule 2 is water.

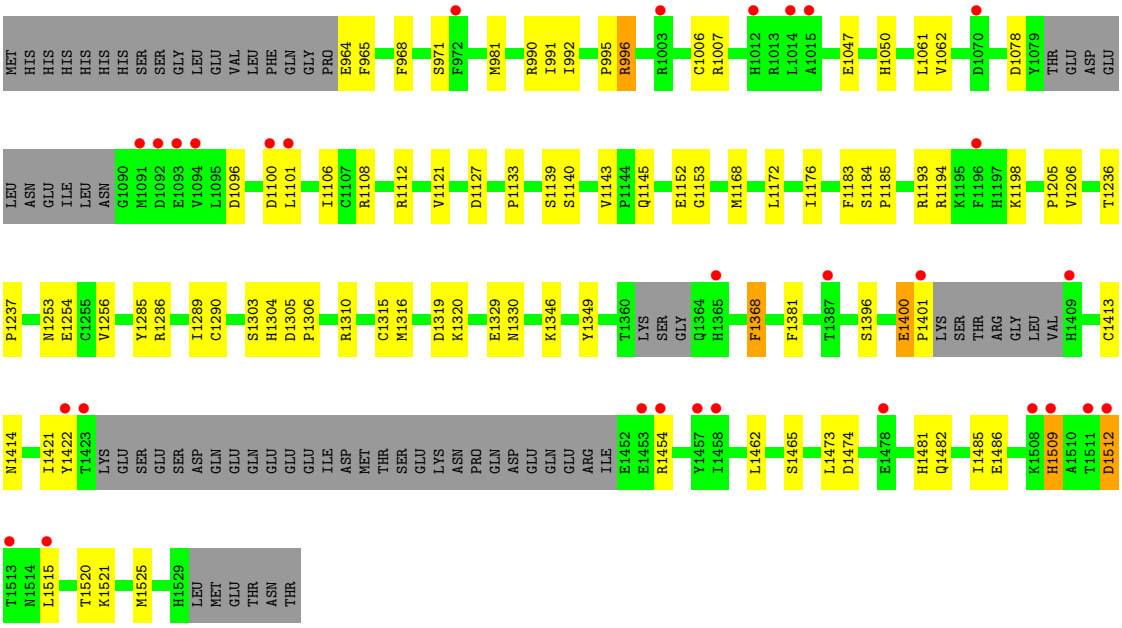
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	101	101	101	0	0

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: Ankyrin-2

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	75.67Å 80.06Å 94.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.89 – 2.20 36.89 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.3 (36.89-2.20) 99.1 (36.89-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.80 (at 2.20Å)	Xtriage
Refinement program	REFMAC, PHENIX 1.6.4_486	Depositor
R, R_{free}	0.208 , 0.245 0.210 , 0.248	Depositor DCC
R_{free} test set	1521 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å^2)	44.6	Xtriage
Anisotropy	0.556	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 50.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4090	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.30	0/4076	0.48	0/5527

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	3989	0	3963	59	0
2	A	101	0	0	0	0
All	All	4090	0	3963	59	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 7.

All (59) 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:1305:ASP:HB2	1:A:1306:PRO:HD2	1.51	0.91
1:A:1520:THR:HG23	1:A:1525:MET:HE1	1.58	0.86
1:A:1305:ASP:HA	1:A:1422:TYR:CD1	2.19	0.77
1:A:1305:ASP:CB	1:A:1306:PRO:HD2	2.20	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1290:CYS:SG	1:A:1346:LYS:HE2	2.38	0.64
1:A:1305:ASP:HB2	1:A:1306:PRO:CD	2.31	0.59
1:A:995:PRO:C	1:A:996:ARG:HG2	2.23	0.58
1:A:1285:TYR:CZ	1:A:1289:ILE:HG21	2.39	0.58
1:A:1285:TYR:CE2	1:A:1289:ILE:HG21	2.39	0.57
1:A:1096:ASP:HB3	1:A:1100:ASP:CB	2.34	0.57
1:A:1310:ARG:HG3	1:A:1310:ARG:HH11	1.70	0.56
1:A:1329:GLU:O	1:A:1330:ASN:HB2	2.07	0.55
1:A:971:SER:H	1:A:981:MET:CE	2.21	0.54
1:A:1096:ASP:HB3	1:A:1100:ASP:HB2	1.90	0.54
1:A:1349:TYR:CZ	1:A:1401:PRO:HD3	2.43	0.53
1:A:1193:ARG:O	1:A:1194:ARG:HD3	2.11	0.50
1:A:1153:GLY:HA3	1:A:1198:LYS:HE3	1.93	0.50
1:A:1078:ASP:O	1:A:1112:ARG:NH2	2.45	0.49
1:A:1481:HIS:O	1:A:1485:ILE:HG13	2.12	0.49
1:A:1305:ASP:CB	1:A:1306:PRO:CD	2.89	0.49
1:A:1133:PRO:O	1:A:1152:GLU:HG3	2.12	0.49
1:A:1421:ILE:CG2	1:A:1422:TYR:N	2.76	0.49
1:A:964:GLU:HG3	1:A:965:PHE:CD2	2.48	0.49
1:A:1349:TYR:CE2	1:A:1400:GLU:HA	2.48	0.48
1:A:1520:THR:HG23	1:A:1525:MET:CE	2.36	0.48
1:A:1305:ASP:HA	1:A:1422:TYR:CG	2.48	0.48
1:A:1329:GLU:O	1:A:1330:ASN:CB	2.62	0.47
1:A:1096:ASP:HB3	1:A:1100:ASP:HB3	1.95	0.47
1:A:1521:LYS:O	1:A:1521:LYS:HD3	2.15	0.47
1:A:1145:GLN:HB2	1:A:1205:PRO:HG3	1.95	0.47
1:A:990:ARG:HD3	1:A:1047:GLU:OE1	2.14	0.46
1:A:1050:HIS:CD2	1:A:1061:LEU:HD11	2.50	0.46
1:A:1172:LEU:O	1:A:1176:ILE:HG13	2.16	0.46
1:A:968:PHE:HA	1:A:1007:ARG:HG2	1.97	0.45
1:A:1482:GLN:O	1:A:1486:GLU:HG3	2.16	0.45
1:A:1062:VAL:HG13	1:A:1121:VAL:HB	1.99	0.45
1:A:1319:ASP:O	1:A:1320:LYS:HB2	2.17	0.44
1:A:990:ARG:CD	1:A:992:ILE:HD11	2.48	0.44
1:A:1127:ASP:OD1	1:A:1140:SER:HA	2.18	0.44
1:A:1515:LEU:HD12	1:A:1515:LEU:HA	1.84	0.44
1:A:1168:MET:HG3	1:A:1183:PHE:HB2	2.00	0.43
1:A:1253:ASN:O	1:A:1254:GLU:HG2	2.18	0.43
1:A:1310:ARG:HG3	1:A:1310:ARG:NH1	2.33	0.43
1:A:1368:PHE:CD1	1:A:1368:PHE:N	2.87	0.43
1:A:964:GLU:HG3	1:A:965:PHE:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1462:LEU:O	1:A:1465:SER:HB2	2.20	0.42
1:A:1236:THR:HA	1:A:1237:PRO:HD3	1.91	0.42
1:A:991:ILE:HD11	1:A:1006:CYS:HB2	2.01	0.42
1:A:1101:LEU:HD11	1:A:1108:ARG:CZ	2.49	0.42
1:A:1396:SER:OG	1:A:1414:ASN:ND2	2.52	0.42
1:A:1315:CYS:O	1:A:1316:MET:HG3	2.20	0.42
1:A:1512:ASP:OD1	1:A:1512:ASP:N	2.52	0.42
1:A:1184:SER:HB2	1:A:1185:PRO:HD2	2.02	0.42
1:A:1304:HIS:CE1	1:A:1509:HIS:HB2	2.55	0.41
1:A:1140:SER:HB3	1:A:1143:VAL:O	2.20	0.41
1:A:1381:PHE:N	1:A:1381:PHE:CD1	2.88	0.41
1:A:1473:LEU:O	1:A:1474:ASP:HB2	2.21	0.41
1:A:1206:VAL:HG12	1:A:1256:VAL:CG2	2.51	0.40
1:A:1101:LEU:HD22	1:A:1106:ILE:HB	2.03	0.40

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	499/581 (86%)	477 (96%)	22 (4%)	0	100 100

There are no Ramachandran outliers to report.

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	434/519 (84%)	424 (98%)	10 (2%)	50 63

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	996	ARG
1	A	1139	SER
1	A	1286	ARG
1	A	1303	SER
1	A	1368	PHE
1	A	1400	GLU
1	A	1413	CYS
1	A	1454	ARG
1	A	1509	HIS
1	A	1512	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1239	GLN
1	A	1414	ASN
1	A	1514	ASN

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)

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	509/581 (87%)	0.16	30 (5%) 22 21	31, 54, 92, 112	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1015	ALA	11.5
1	A	1365	HIS	5.0
1	A	1511	THR	4.7
1	A	1012	HIS	3.9
1	A	1458	ILE	3.8
1	A	1093	GLU	3.4
1	A	1014	LEU	3.4
1	A	1409	HIS	3.2
1	A	1509	HIS	3.2
1	A	1513	THR	3.2
1	A	1454	ARG	3.0
1	A	1094	VAL	2.8
1	A	1512	ASP	2.7
1	A	1453	GLU	2.7
1	A	1401	PRO	2.7
1	A	1422	TYR	2.6
1	A	1423	THR	2.6
1	A	1457	TYR	2.5
1	A	1092	ASP	2.4
1	A	1003	ARG	2.3
1	A	972	PHE	2.3
1	A	1091	MET	2.3
1	A	1478	GLU	2.3
1	A	1508	LYS	2.2
1	A	1101	LEU	2.2
1	A	1196	PHE	2.2
1	A	1070	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1515	LEU	2.1
1	A	1387	THR	2.1
1	A	1100	ASP	2.0

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.