



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:39 PM GMT

PDB ID : 1BW8
Title : MU2 ADAPTIN SUBUNIT (AP50) OF AP2 ADAPTOR (SECOND DOMAIN), COMPLEXED WITH EGFR INTERNALIZATION PEPTIDE FYRALM
Authors : Owen, D.J.; Evans, P.R.
Deposited on : 1998-09-30
Resolution : 2.65 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

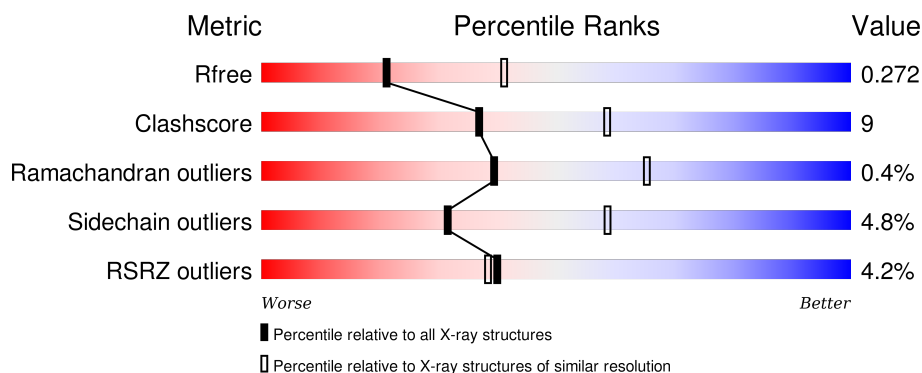
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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}	91344	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	321	
2	P	6	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2143 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 (MU2 ADAPTIN SUBUNIT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	256	Total	C	N	O	S	0	0	0
			2036	1312	349	361	14			

- Molecule 2 is a protein called PROTEIN (INTERNALIZATION SIGNAL FROM EGFR).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	6	Total	C	N	O	S	0	0	0
			56	38	9	8	1			

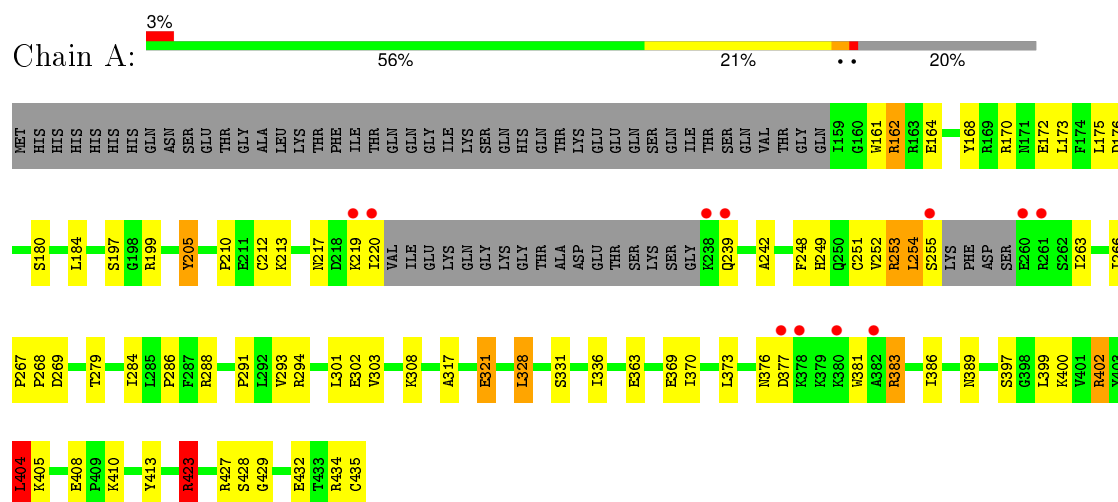
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	46	Total	O	0	0
			46	46		
3	P	5	Total	O	0	0
			5	5		

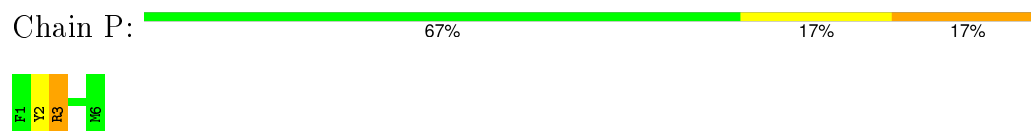
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: PROTEIN (MU2 ADAPTIN SUBUNIT)



- Molecule 2: PROTEIN (INTERNALIZATION SIGNAL FROM EGFR)



4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	125.68 Å 125.68 Å 73.16 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.00 – 2.65 34.67 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.6 (35.00-2.65) 99.6 (34.67-2.65)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 2.65 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.250 , 0.296 0.228 , 0.272	Depositor DCC
R_{free} test set	971 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	65.2	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.9	EDS
Estimated twinning fraction	0.027 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 19296 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2143	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.56	0/2077	1.54	26/2797 (0.9%)
2	P	0.64	0/57	1.51	1/73 (1.4%)
All	All	0.56	0/2134	1.54	27/2870 (0.9%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	199	ARG	NE-CZ-NH2	-15.66	112.47	120.30
1	A	162	ARG	NE-CZ-NH1	13.02	126.81	120.30
1	A	162	ARG	NE-CZ-NH2	-9.49	115.56	120.30
1	A	432	GLU	OE1-CD-OE2	8.06	132.97	123.30
1	A	199	ARG	NE-CZ-NH1	7.86	124.23	120.30
1	A	253	ARG	NE-CZ-NH1	7.81	124.21	120.30
1	A	176	ASP	CB-CG-OD2	7.14	124.72	118.30
2	P	3	ARG	NE-CZ-NH1	-6.85	116.88	120.30
1	A	321	GLU	OE1-CD-OE2	6.62	131.24	123.30
1	A	205	TYR	CB-CG-CD2	-6.59	117.05	121.00
1	A	269	ASP	CB-CG-OD1	6.54	124.18	118.30
1	A	162	ARG	CD-NE-CZ	6.51	132.71	123.60
1	A	402	ARG	NE-CZ-NH2	-6.43	117.09	120.30
1	A	170	ARG	NE-CZ-NH1	-6.27	117.17	120.30
1	A	423	ARG	CA-CB-CG	6.24	127.13	113.40
1	A	429	GLY	N-CA-C	-6.10	97.86	113.10
1	A	383	ARG	NE-CZ-NH2	-5.91	117.34	120.30
1	A	434	ARG	NE-CZ-NH2	-5.86	117.37	120.30
1	A	197	SER	N-CA-CB	5.85	119.27	110.50
1	A	317	ALA	N-CA-CB	5.70	118.09	110.10
1	A	427	ARG	CD-NE-CZ	5.67	131.54	123.60
1	A	427	ARG	NE-CZ-NH1	5.55	123.08	120.30
1	A	172	GLU	N-CA-CB	-5.43	100.82	110.60
1	A	336	ILE	N-CA-CB	5.26	122.91	110.80
1	A	404	LEU	CA-CB-CG	-5.17	103.41	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	266	ILE	N-CA-C	-5.11	97.20	111.00
1	A	413	TYR	CA-CB-CG	5.02	122.94	113.40

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	2036	0	2094	39	0
2	P	56	0	58	2	0
3	A	46	0	0	0	0
3	P	5	0	0	0	0
All	All	2143	0	2152	40	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 9.

All (40) 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:220:ILE:HG12	1:A:242:ALA:HA	1.56	0.86
1:A:291:PRO:HB3	1:A:386:ILE:HD12	1.68	0.75
1:A:328:LEU:HD12	1:A:328:LEU:H	1.51	0.74
1:A:217:ASN:HD22	1:A:239:GLN:HB3	1.55	0.71
1:A:252:VAL:HG13	1:A:263:ILE:HG23	1.78	0.65
1:A:331:SER:HB3	1:A:373:LEU:HG	1.83	0.60
1:A:254:LEU:H	1:A:254:LEU:HD22	1.69	0.58
1:A:284:ILE:O	1:A:286:PRO:HD3	2.05	0.57
1:A:328:LEU:HD12	1:A:328:LEU:N	2.19	0.56
1:A:301:LEU:HB2	1:A:370:ILE:HB	1.87	0.56
1:A:239:GLN:HB2	1:A:402:ARG:HH22	1.70	0.56
1:A:239:GLN:OE1	1:A:402:ARG:NH2	2.39	0.56
1:A:161:TRP:HH2	1:A:253:ARG:HH21	1.54	0.55
1:A:293:VAL:HG21	1:A:383:ARG:NH1	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:LYS:HB2	1:A:405:LYS:HB2	1.89	0.55
1:A:219:LYS:O	1:A:220:ILE:HB	2.09	0.52
1:A:279:THR:HG21	1:A:397:SER:HB2	1.92	0.51
1:A:212:CYS:HA	1:A:405:LYS:O	2.10	0.51
1:A:175:LEU:HD11	1:A:404:LEU:HD13	1.93	0.50
1:A:249:HIS:HD1	1:A:251:CYS:HG	1.61	0.48
1:A:293:VAL:HG12	1:A:303:VAL:HG22	1.94	0.48
1:A:294:ARG:HB3	1:A:302:GLU:HB2	1.96	0.48
1:A:321:GLU:HB3	1:A:389:ASN:HB2	1.95	0.48
1:A:399:LEU:HD23	1:A:400:LYS:N	2.29	0.47
1:A:253:ARG:HD3	1:A:253:ARG:HA	1.64	0.45
1:A:288:ARG:HG3	1:A:288:ARG:HH11	1.81	0.44
1:A:381:TRP:CE3	1:A:383:ARG:HG2	2.53	0.44
1:A:162:ARG:CZ	1:A:210:PRO:HD2	2.48	0.43
1:A:173:LEU:CD2	1:A:404:LEU:HD22	2.48	0.43
1:A:252:VAL:CG1	1:A:263:ILE:HG23	2.45	0.43
1:A:302:GLU:OE2	1:A:369:GLU:HG3	2.18	0.43
1:A:308:LYS:HG2	1:A:363:GLU:HG2	2.01	0.42
1:A:328:LEU:CD1	1:A:328:LEU:H	2.25	0.42
1:A:267:PRO:HA	1:A:268:PRO:HD3	1.87	0.42
1:A:408:GLU:OE2	1:A:410:LYS:HB2	2.20	0.42
1:A:423:ARG:HB3	2:P:2:TYR:CE1	2.55	0.41
2:P:2:TYR:O	2:P:3:ARG:HD3	2.21	0.41
1:A:248:PHE:CE2	1:A:263:ILE:HG12	2.55	0.41
1:A:168:TYR:CE2	1:A:205:TYR:HB3	2.55	0.41
1:A:248:PHE:HE2	1:A:263:ILE:HG12	1.86	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	250/321 (78%)	235 (94%)	14 (6%)	1 (0%)	39	65
2	P	4/6 (67%)	4 (100%)	0	0	100	100
All	All	254/327 (78%)	239 (94%)	14 (6%)	1 (0%)	39	65

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	254	LEU

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	225/289 (78%)	214 (95%)	11 (5%)	31	58
2	P	5/5 (100%)	5 (100%)	0	100	100
All	All	230/294 (78%)	219 (95%)	11 (5%)	31	59

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	164	GLU
1	A	180	SER
1	A	184	LEU
1	A	255	SER
1	A	328	LEU
1	A	376	ASN
1	A	377	ASP
1	A	404	LEU
1	A	423	ARG
1	A	428	SER
1	A	435	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	376	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 carbohydrates 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	256/321 (79%)	0.12	11 (4%) 39 37	36, 57, 94, 118	0
2	P	6/6 (100%)	0.21	0 100 100	46, 58, 68, 75	0
All	All	262/327 (80%)	0.13	11 (4%) 40 38	36, 57, 94, 118	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	220	ILE	5.6
1	A	378	LYS	4.4
1	A	382	ALA	3.3
1	A	260	GLU	3.0
1	A	377	ASP	3.0
1	A	261	ARG	2.9
1	A	255	SER	2.9
1	A	239	GLN	2.7
1	A	380	LYS	2.6
1	A	219	LYS	2.4
1	A	238	LYS	2.3

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 carbohydrates 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.