



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:24 AM GMT

PDB ID : 3APO
Title : Crystal structure of full-length ERdj5
Authors : Inaba, K.; Suzuki, M.; Nagata, K.
Deposited on : 2010-10-20
Resolution : 2.40 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

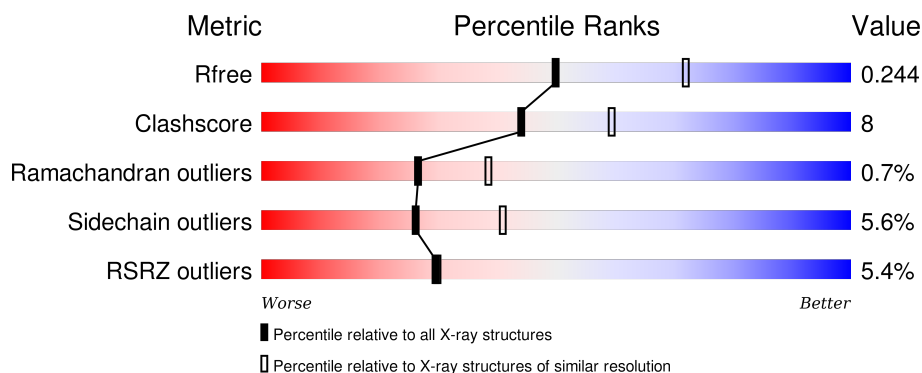
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	780	<div> <div>5%</div> <div>72%</div> <div>15%</div> <div>•</div> <div>12%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5768 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 DnaJ homolog subfamily C member 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	688	Total	C	N	O	S	0	0	0
			5547	3552	942	1029	24			

There are 31 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	MET	-	EXPRESSION TAG	UNP Q9DC23
A	15	GLY	-	EXPRESSION TAG	UNP Q9DC23
A	16	SER	-	EXPRESSION TAG	UNP Q9DC23
A	17	SER	-	EXPRESSION TAG	UNP Q9DC23
A	18	HIS	-	EXPRESSION TAG	UNP Q9DC23
A	19	HIS	-	EXPRESSION TAG	UNP Q9DC23
A	20	HIS	-	EXPRESSION TAG	UNP Q9DC23
A	21	HIS	-	EXPRESSION TAG	UNP Q9DC23
A	22	HIS	-	EXPRESSION TAG	UNP Q9DC23
A	23	HIS	-	EXPRESSION TAG	UNP Q9DC23
A	24	SER	-	EXPRESSION TAG	UNP Q9DC23
A	25	SER	-	EXPRESSION TAG	UNP Q9DC23
A	26	GLY	-	EXPRESSION TAG	UNP Q9DC23
A	27	HIS	-	EXPRESSION TAG	UNP Q9DC23
A	28	ILE	-	EXPRESSION TAG	UNP Q9DC23
A	29	GLU	-	EXPRESSION TAG	UNP Q9DC23
A	30	GLY	-	EXPRESSION TAG	UNP Q9DC23
A	31	ARG	-	EXPRESSION TAG	UNP Q9DC23
A	32	HIS	-	EXPRESSION TAG	UNP Q9DC23
A	91	ASP	HIS	ENGINEERED MUTATION	UNP Q9DC23
A	158	SER	CYS	ENGINEERED MUTATION	UNP Q9DC23
A	161	SER	CYS	ENGINEERED MUTATION	UNP Q9DC23
A	399	VAL	GLY	ENGINEERED MUTATION	UNP Q9DC23
A	419	SER	CYS	ENGINEERED MUTATION	UNP Q9DC23
A	480	SER	CYS	ENGINEERED MUTATION	UNP Q9DC23
A	483	SER	CYS	ENGINEERED MUTATION	UNP Q9DC23
A	588	SER	CYS	ENGINEERED MUTATION	UNP Q9DC23

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	591	SER	CYS	ENGINEERED MUTATION	UNP Q9DC23
A	617	GLY	GLN	SEE REMARK 999	UNP Q9DC23
A	700	SER	CYS	ENGINEERED MUTATION	UNP Q9DC23
A	703	SER	CYS	ENGINEERED MUTATION	UNP Q9DC23

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	221	Total O 221 221	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.10 Å 53.40 Å 92.30 Å 90.00° 113.40° 90.00°	Depositor
Resolution (Å)	45.83 – 2.40 45.83 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.83-2.40) 99.8 (45.83-2.40)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 2.39 Å)	Xtriage
Refinement program	REFMAC 5.5.0085	Depositor
R, R_{free}	0.197 , 0.246 0.198 , 0.244	Depositor DCC
R_{free} test set	1627 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	34.9	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.0	EDS
Estimated twinning fraction	0.013 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 32103 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5768	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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	0.57	0/5693	0.65	1/7711 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	304	LEU	CA-CB-CG	5.75	128.52	115.30

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	5547	0	5382	87	0
2	A	221	0	0	4	0
All	All	5768	0	5382	87	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 8.

All (87) 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:136:ARG:HG2	1:A:136:ARG:HH11	1.09	1.10

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:604:THR:CG2	1:A:661:ARG:HH11	1.76	0.98
1:A:323:ARG:HH11	1:A:323:ARG:HG3	1.28	0.96
1:A:53:GLN:HG2	1:A:126:ASP:HB3	1.57	0.86
1:A:604:THR:HG23	1:A:661:ARG:NH1	1.97	0.80
1:A:276:ARG:HH11	1:A:276:ARG:HG3	1.48	0.78
1:A:136:ARG:HH11	1:A:136:ARG:CG	1.94	0.76
1:A:604:THR:CG2	1:A:661:ARG:NH1	2.48	0.76
1:A:604:THR:HG23	1:A:661:ARG:HH11	1.53	0.73
1:A:604:THR:HG21	1:A:661:ARG:HD2	1.69	0.72
1:A:604:THR:HG22	1:A:661:ARG:HH11	1.54	0.72
1:A:537:TYR:O	2:A:865:HOH:O	2.11	0.69
1:A:226:VAL:O	1:A:230:MET:HG2	1.93	0.68
1:A:272:THR:HG22	1:A:275:THR:H	1.59	0.67
1:A:136:ARG:HG2	1:A:136:ARG:NH1	1.88	0.65
1:A:323:ARG:NH1	1:A:323:ARG:HG3	2.05	0.65
1:A:690:HIS:HD2	1:A:751:TYR:H	1.43	0.64
1:A:231:GLN:HA	1:A:231:GLN:HE21	1.63	0.64
1:A:36:PHE:HB3	1:A:96:TYR:OH	1.99	0.62
1:A:49:ARG:O	1:A:53:GLN:HG3	2.02	0.60
1:A:389:THR:O	1:A:392:LYS:HB2	2.02	0.59
1:A:576:ASP:HA	1:A:639:GLN:HG2	1.84	0.59
1:A:264:CYS:HG	1:A:270:CYS:HG	1.52	0.57
1:A:497:LEU:HD13	1:A:501:LEU:HD11	1.87	0.57
1:A:690:HIS:CD2	1:A:751:TYR:H	2.23	0.56
1:A:36:PHE:CB	1:A:96:TYR:OH	2.56	0.54
1:A:424:LYS:HE2	1:A:453:SER:O	2.08	0.54
1:A:590:PRO:HB2	1:A:632:PRO:HD3	1.90	0.53
1:A:264:CYS:SG	1:A:270:CYS:SG	3.04	0.53
1:A:272:THR:CG2	1:A:275:THR:H	2.21	0.53
1:A:604:THR:CG2	1:A:661:ARG:HD2	2.37	0.53
1:A:601:MET:O	1:A:604:THR:HB	2.08	0.52
1:A:276:ARG:CG	1:A:276:ARG:HH11	2.20	0.52
1:A:264:CYS:HB3	1:A:270:CYS:SG	2.50	0.52
1:A:171:PHE:O	1:A:175:VAL:HG22	2.10	0.52
1:A:272:THR:HG23	1:A:274:GLN:H	1.74	0.51
1:A:164:LEU:HD13	1:A:220:ARG:HD2	1.92	0.51
1:A:396:ILE:HD11	1:A:451:VAL:HG21	1.93	0.51
1:A:366:ARG:HD3	2:A:824:HOH:O	2.11	0.51
1:A:206:ILE:HG22	1:A:214:VAL:HB	1.94	0.49
1:A:733:GLN:HE21	1:A:734:THR:N	2.11	0.49
1:A:463:PHE:O	1:A:465:ALA:N	2.43	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:GLU:HB3	2:A:962:HOH:O	2.12	0.48
1:A:688:LYS:HG2	1:A:751:TYR:CZ	2.49	0.48
1:A:464:PRO:HB3	1:A:471:TRP:CE2	2.49	0.48
1:A:507:ASP:OD1	1:A:509:THR:HB	2.13	0.47
1:A:733:GLN:HE21	1:A:734:THR:H	1.62	0.47
1:A:537:TYR:OH	1:A:545:GLN:HB2	2.15	0.47
1:A:353:LEU:HD11	1:A:399:VAL:HG21	1.97	0.47
1:A:391:LEU:HD23	1:A:448:LYS:HE3	1.97	0.47
1:A:277:LEU:O	1:A:280:SER:HB3	2.16	0.46
1:A:470:PRO:HB2	1:A:501:LEU:HB3	1.98	0.46
1:A:578:VAL:HG23	1:A:609:ILE:HG23	1.98	0.46
1:A:276:ARG:NH1	1:A:276:ARG:HG3	2.25	0.45
1:A:415:VAL:HG13	1:A:419:SER:OG	2.17	0.45
1:A:313:TYR:HB3	1:A:329:LEU:HB3	1.98	0.45
1:A:266:LYS:HA	1:A:266:LYS:HD2	1.64	0.45
1:A:136:ARG:NH1	1:A:136:ARG:CG	2.63	0.45
1:A:49:ARG:HG2	1:A:53:GLN:NE2	2.30	0.45
1:A:174:GLU:OE2	1:A:278:ARG:NH1	2.42	0.44
1:A:278:ARG:O	1:A:282:MET:HG3	2.18	0.44
1:A:589:HIS:N	1:A:590:PRO:HD2	2.33	0.43
1:A:81:ASN:O	1:A:83:ALA:N	2.51	0.43
1:A:266:LYS:HE3	1:A:267:GLY:H	1.83	0.43
1:A:53:GLN:CG	1:A:126:ASP:HB3	2.36	0.43
1:A:189:ASP:OD1	1:A:191:MET:HB3	2.18	0.43
1:A:276:ARG:CG	1:A:276:ARG:NH1	2.81	0.43
1:A:272:THR:HG23	1:A:274:GLN:N	2.34	0.43
1:A:565:THR:O	1:A:569:LEU:HB2	2.19	0.42
1:A:266:LYS:C	1:A:268:GLU:H	2.22	0.42
1:A:365:HIS:HB2	1:A:367:TRP:HE1	1.85	0.42
1:A:138:GLU:HG3	1:A:138:GLU:H	1.73	0.42
1:A:265:SER:O	1:A:268:GLU:HB2	2.18	0.42
1:A:120:TYR:O	1:A:121:ASP:HB2	2.19	0.42
1:A:49:ARG:HG2	1:A:53:GLN:HE21	1.85	0.42
1:A:683:LYS:NZ	2:A:809:HOH:O	2.52	0.42
1:A:533:SER:C	1:A:534:ILE:HG13	2.40	0.42
1:A:42:VAL:HG21	1:A:51:ILE:HD13	2.01	0.42
1:A:242:THR:OG1	1:A:297:GLN:NE2	2.43	0.42
1:A:453:SER:HA	1:A:495:THR:HG22	2.02	0.42
1:A:713:LEU:O	1:A:717:ILE:HG12	2.19	0.41
1:A:523:TYR:HA	1:A:524:PRO:HA	1.93	0.41
1:A:562:THR:HG1	1:A:565:THR:H	1.67	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:PHE:HE1	1:A:81:ASN:HA	1.86	0.40
1:A:339:ILE:O	1:A:343:ILE:HG12	2.21	0.40
1:A:429:LYS:HD3	1:A:429:LYS:HA	1.81	0.40
1:A:249:ILE:HA	1:A:249:ILE:HD13	1.94	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	676/780 (87%)	653 (97%)	18 (3%)	5 (1%)	26	38

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	121	ASP
1	A	541	HIS
1	A	56	LYS
1	A	464	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	602/681 (88%)	568 (94%)	34 (6%)	26	41

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	LYS
1	A	98	LYS
1	A	127	ASP
1	A	135	GLU
1	A	136	ARG
1	A	138	GLU
1	A	150	PHE
1	A	167	THR
1	A	192	LEU
1	A	206	ILE
1	A	208	ARG
1	A	209	SER
1	A	211	MET
1	A	223	GLU
1	A	231	GLN
1	A	264	CYS
1	A	266	LYS
1	A	272	THR
1	A	298	ASP
1	A	304	LEU
1	A	323	ARG
1	A	337	LYS
1	A	399	VAL
1	A	419	SER
1	A	439	ILE
1	A	461	GLN
1	A	538	GLU
1	A	555	ASN
1	A	577	GLU
1	A	595	MET
1	A	633	GLU
1	A	733	GLN
1	A	762	GLN
1	A	780	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	GLN
1	A	231	GLN
1	A	244	ASN
1	A	297	GLN
1	A	346	ASN
1	A	380	ASN
1	A	618	GLN
1	A	654	ASN
1	A	681	ASN
1	A	686	GLN
1	A	690	HIS
1	A	705	ASN
1	A	733	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 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

6.1 Protein, DNA and RNA chains

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	688/780 (88%)	-0.00	37 (5%)	29 30	22, 41, 87, 119	3 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	161	SER	5.3
1	A	160	HIS	4.8
1	A	162	HIS	4.6
1	A	122	PHE	4.5
1	A	118	TYR	4.5
1	A	190	ARG	4.3
1	A	191	MET	4.1
1	A	153	PHE	4.0
1	A	120	TYR	3.8
1	A	215	LYS	3.6
1	A	157	GLY	3.5
1	A	159	SER	3.4
1	A	184	VAL	3.2
1	A	55	PHE	3.2
1	A	216	TYR	3.1
1	A	220	ARG	3.1
1	A	156	PRO	3.1
1	A	192	LEU	3.0
1	A	40	LEU	3.0
1	A	183	ALA	3.0
1	A	158	SER	2.9
1	A	205	PHE	2.8
1	A	163	ASP	2.7
1	A	93	ARG	2.7
1	A	119	ARG	2.7
1	A	117	TYR	2.7
1	A	92	LEU	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	84	TYR	2.4
1	A	98	LYS	2.3
1	A	222	LYS	2.2
1	A	121	ASP	2.2
1	A	36	PHE	2.1
1	A	645	TYR	2.1
1	A	170	GLU	2.0
1	A	167	THR	2.0
1	A	217	ASN	2.0
1	A	154	TYR	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 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.