Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 05:30 PM GMT

PDB ID	:	4ILH
Title	:	Crystal structure of an Aar2p C-terminal deletion mutant in conplex with Prp8p RNaseH
Authors	:	Weber, G.; Heroven, A.C.; Santos, K.F.; Wahl, M.C.
Deposited on	:	2012-12-31
Resolution	:	1.85 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

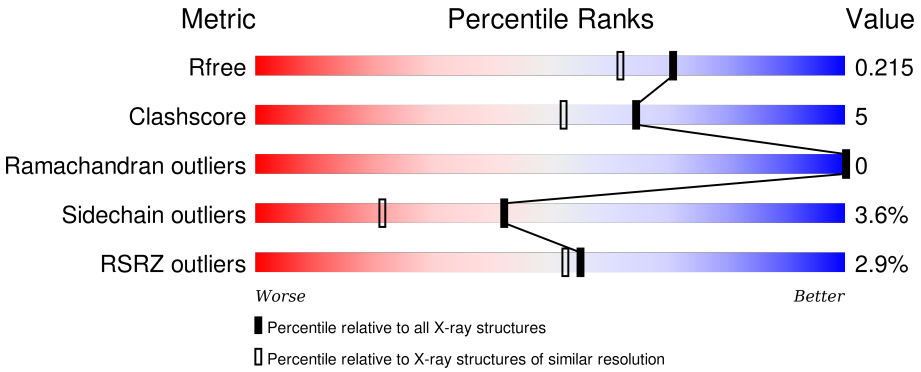
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.85 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	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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 <=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	258	3%, 90%, 8%
2	B	339	3%, 72%, 14%, 13%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5142 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	10	0
			2121	1358	355	398	10			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1833	GLY	-	EXPRESSION TAG	UNP P33334
A	1834	ALA	-	EXPRESSION TAG	UNP P33334
A	1835	MET	-	EXPRESSION TAG	UNP P33334

- Molecule 2 is a protein called A1 cistron-splicing factor AAR2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	295	Total	C	N	O	S	0	6	0
			2506	1605	411	471	19			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	332	LEU	-	EXPRESSION TAG	UNP P32357
B	333	GLU	-	EXPRESSION TAG	UNP P32357
B	334	HIS	-	EXPRESSION TAG	UNP P32357
B	335	HIS	-	EXPRESSION TAG	UNP P32357
B	336	HIS	-	EXPRESSION TAG	UNP P32357
B	337	HIS	-	EXPRESSION TAG	UNP P32357
B	338	HIS	-	EXPRESSION TAG	UNP P32357
B	339	HIS	-	EXPRESSION TAG	UNP P32357

- Molecule 3 is water.

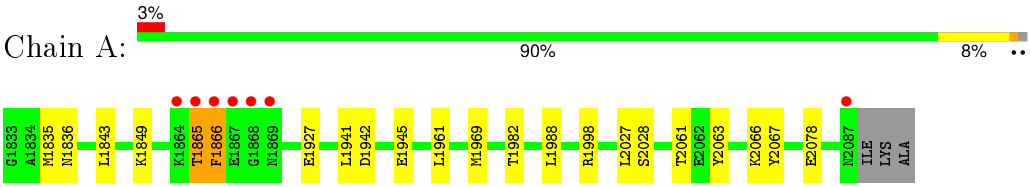
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	250	Total O 252 252	0	2
3	B	263	Total O 263 263	0	0

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.

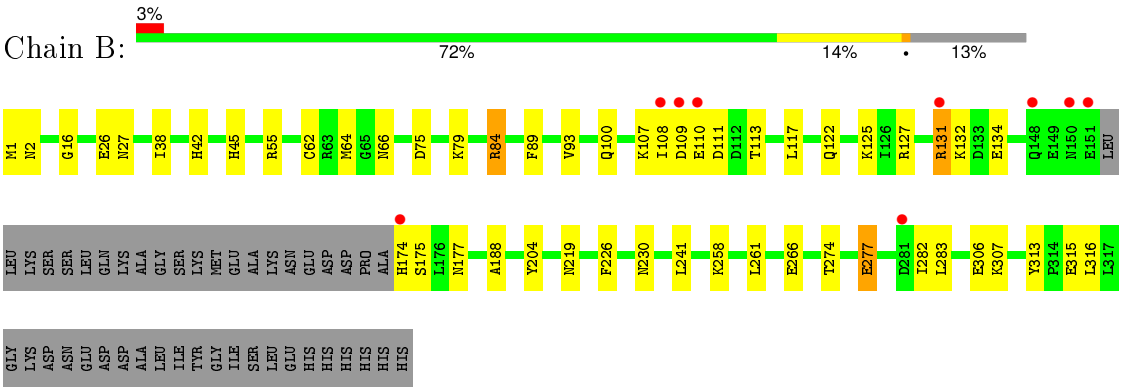
- Molecule 1: Pre-mRNA-splicing factor 8

Chain A:



- Molecule 2: A1 cistron-splicing factor AAR2

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	79.89Å 76.76Å 91.86Å 90.00° 105.88° 90.00°	Depositor
Resolution (Å)	33.95 – 1.85 33.95 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (33.95-1.85) 99.8 (33.95-1.85)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.30 (at 1.85Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.168 , 0.217 0.167 , 0.215	Depositor DCC
R_{free} test set	2274 reflections (5.00%)	DCC
Wilson B-factor (Å^2)	20.6	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 53.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 45500 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5142	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.86% 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, 0.375 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	0.45	0/2168	0.60	0/2940
2	B	0.47	0/2577	0.58	0/3477
All	All	0.46	0/4745	0.59	0/6417

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

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	2121	0	2160	16	0
2	B	2506	0	2397	31	0
3	A	252	0	0	8	0
3	B	263	0	0	9	1
All	All	5142	0	4557	47	1

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 5.

All (47) 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:1836:ASN:ND2	3:A:2348:HOH:O	2.13	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:261:LEU:O	3:B:586:HOH:O	2.01	0.78
1:A:1843:LEU:HA	1:A:1849:LYS:HD2	1.71	0.72
1:A:1982:THR:OG1	3:A:2301:HOH:O	2.09	0.68
2:B:174:HIS:O	3:B:626:HOH:O	2.10	0.67
2:B:313:TYR:HB3	2:B:316:LEU:HD23	1.77	0.65
2:B:177:ASN:O	3:B:658:HOH:O	2.16	0.60
2:B:266:GLU:OE2	3:B:590:HOH:O	2.16	0.60
2:B:122:GLN:H	2:B:125[B]:LYS:HD3	1.72	0.54
1:A:1961:LEU:O	3:A:2287:HOH:O	2.19	0.53
2:B:1:MET:N	3:B:408:HOH:O	2.42	0.51
2:B:226:PHE:CE2	2:B:230[A]:ASN:ND2	2.79	0.51
1:A:1941[A]:LEU:HG	1:A:1945:GLU:OE2	2.12	0.49
1:A:1927:GLU:H	1:A:1927:GLU:CD	2.16	0.48
2:B:315:GLU:HG2	2:B:316:LEU:HD22	1.94	0.48
2:B:64[A]:MET:CE	2:B:127:ARG:HH12	2.26	0.48
2:B:93:VAL:O	2:B:100:GLN:NE2	2.38	0.48
2:B:42:HIS:HD2	3:B:633:HOH:O	1.96	0.48
1:A:2066:LYS:HD2	1:A:2067:TYR:CE1	2.50	0.47
1:A:1998:ARG:HD2	3:A:2314:HOH:O	2.16	0.46
2:B:16:GLY:HA3	2:B:45:HIS:CE1	2.50	0.46
2:B:131:ARG:HA	2:B:131:ARG:HD2	1.71	0.46
2:B:107:LYS:HD3	2:B:108:ILE:N	2.30	0.46
2:B:2:ASN:ND2	2:B:62:CYS:HB3	2.32	0.46
2:B:277:GLU:OE2	3:B:599:HOH:O	2.20	0.45
2:B:282:ILE:HD12	2:B:283:LEU:HG	1.98	0.45
1:A:1835:MET:HG2	3:A:2310:HOH:O	2.16	0.45
2:B:27:ASN:HA	3:B:627:HOH:O	2.17	0.44
2:B:75:ASP:OD2	2:B:79:LYS:NZ	2.39	0.44
1:A:1865:THR:HG22	1:A:1866:PHE:H	1.82	0.43
2:B:66:ASN:HB3	2:B:89:PHE:CD1	2.54	0.43
2:B:125[A]:LYS:HE3	2:B:219:ASN:OD1	2.18	0.43
2:B:188:ALA:HA	2:B:204:TYR:CD1	2.54	0.42
2:B:107:LYS:HD3	2:B:108:ILE:H	1.85	0.42
1:A:1969:MET:HB2	3:A:2219:HOH:O	2.19	0.42
2:B:2:ASN:HD22	2:B:62:CYS:HB3	1.84	0.42
2:B:111:ASP:C	2:B:113:THR:H	2.23	0.42
2:B:282:ILE:H	2:B:282:ILE:HG13	1.75	0.41
1:A:2078:GLU:OE2	3:A:2347:HOH:O	2.22	0.41
1:A:1942:ASP:OD2	3:A:2216:HOH:O	2.22	0.41
2:B:127:ARG:HD3	2:B:132:LYS:HG2	2.02	0.41
2:B:66:ASN:HB3	2:B:89:PHE:CG	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:84:ARG:NH1	3:B:549:HOH:O	2.55	0.40
1:A:2063:TYR:HA	1:A:2066:LYS:HE3	2.03	0.40
2:B:117:LEU:HD11	2:B:274:THR:HG21	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:615:HOH:O	3:B:645:HOH:O[2_454]	2.05	0.15

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	263/258 (102%)	261 (99%)	2 (1%)	0	100	100
2	B	297/339 (88%)	284 (96%)	13 (4%)	0	100	100
All	All	560/597 (94%)	545 (97%)	15 (3%)	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	241/233 (103%)	237 (98%)	4 (2%)	68	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	281/312 (90%)	267 (95%)	14 (5%)	30 11
All	All	522/545 (96%)	504 (97%)	18 (3%)	42 24

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1865	THR
1	A	1866	PHE
1	A	1988	LEU
1	A	2027	LEU
2	B	26	GLU
2	B	38	ILE
2	B	55	ARG
2	B	84	ARG
2	B	109	ASP
2	B	110	GLU
2	B	131	ARG
2	B	134	GLU
2	B	175	SER
2	B	241	LEU
2	B	258	LYS
2	B	277	GLU
2	B	306	GLU
2	B	307	LYS

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

Mol	Chain	Res	Type
2	B	116	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	255/258 (98%)	-0.35	7 (2%) 58 55	3, 13, 38, 78	0
2	B	295/339 (87%)	-0.23	9 (3%) 52 49	3, 14, 43, 71	0
All	All	550/597 (92%)	-0.29	16 (2%) 55 52	3, 14, 39, 78	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1866	PHE	6.8
2	B	109	ASP	5.1
2	B	151	GLU	3.9
1	A	2087	ASN	3.8
1	A	1865	THR	3.6
2	B	131	ARG	2.8
1	A	1868	GLY	2.8
2	B	174	HIS	2.7
1	A	1864	LYS	2.7
2	B	150	ASN	2.6
2	B	108	ILE	2.6
2	B	148	GLN	2.6
2	B	110	GLU	2.5
1	A	1869	ASN	2.4
2	B	281	ASP	2.2
1	A	1867	GLU	2.2

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.