



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 05:53 PM GMT

PDB ID : 2J0S
Title : THE CRYSTAL STRUCTURE OF THE EXON JUNCTION COMPLEX AT
2.2 Å RESOLUTION
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Deposited on : 2006-08-04
Resolution : 2.21 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

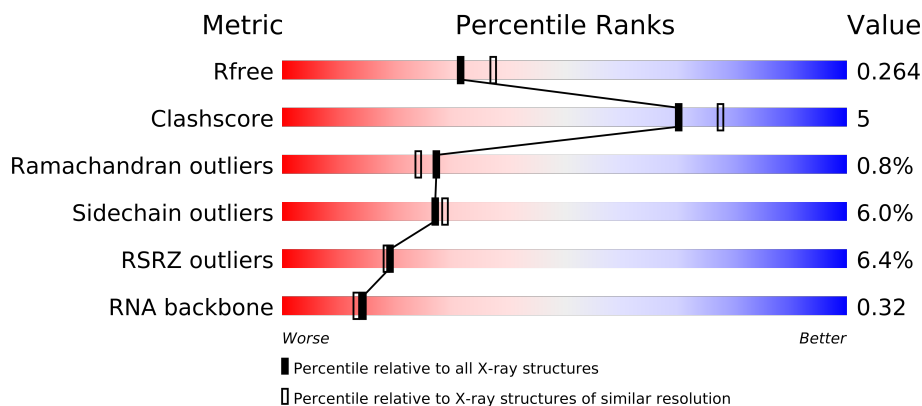
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance






The reported resolution of this entry is 2.21 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}	66092	3340 (2.24-2.20)
Clashscore	79885	4208 (2.24-2.20)
Ramachandran outliers	78287	4135 (2.24-2.20)
Sidechain outliers	78261	4136 (2.24-2.20)
RSRZ outliers	66119	3341 (2.24-2.20)
RNA backbone	1838	1109 (3.00-1.44)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	410	
2	C	146	
3	D	89	
4	E	15	
5	T	150	

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 2 is a protein called PROTEIN MAGO NASHI HOMOLOG.

- Molecule 3 is a protein called RNA-BINDING PROTEIN 8A.

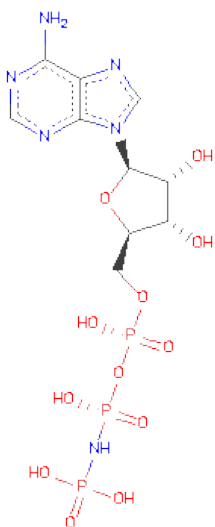
- Molecule 4 is a RNA chain called 5'-R(*UP*UP*UP*UP*UP*UP*UP*UP*UP*U
P*UP*UP*UP*UP*U)-3'.

- Molecule 5 is a protein called PROTEIN CASC3.

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		

- Molecule 7 is PHOSPHOAMINOPHOSPHONICACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	168	Total	O	0	0
			168	168		
8	C	117	Total	O	0	0
			117	117		
8	D	46	Total	O	0	0
			46	46		
8	E	4	Total	O	0	0
			4	4		
8	T	9	Total	O	0	0
			9	9		



4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	169.44Å 169.44Å 71.04Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.73 – 2.21 43.72 – 2.21	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.73-2.21) 99.7 (43.72-2.21)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.185 , 0.216 0.237 , 0.264	Depositor DCC
R_{free} test set	2930 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	35.6	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.3	EDS
Estimated twinning fraction	0.030 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 58630 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5906	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ANP

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	0.62	0/3211	0.75	2/4340 (0.0%)
2	C	0.80	1/1228 (0.1%)	0.84	3/1655 (0.2%)
3	D	0.65	0/730	0.67	0/989
4	E	1.33	1/132 (0.8%)	1.77	3/200 (1.5%)
5	T	0.66	0/379	0.72	0/510
All	All	0.69	2/5680 (0.0%)	0.80	8/7694 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1	U	OP3-P	-9.43	1.49	1.61
2	C	131	CYS	CB-SG	-6.91	1.70	1.82

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	27	ARG	NE-CZ-NH1	7.26	123.93	120.30
1	A	48	ASP	CB-CG-OD1	6.39	124.05	118.30
4	E	1	U	O4'-C1'-N1	6.33	113.26	108.20
2	C	27	ARG	NE-CZ-NH2	-5.86	117.37	120.30
2	C	82	ARG	NE-CZ-NH2	5.72	123.16	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	177	ARG	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3138	0	3166	35	0
2	C	1192	0	1173	8	0
3	D	710	0	662	6	0
4	E	121	0	61	0	0
5	T	369	0	308	4	0
6	A	1	0	0	0	0
7	A	31	0	13	0	0
8	A	168	0	0	0	0
8	C	117	0	0	2	0
8	D	46	0	0	0	0
8	E	4	0	0	0	0
8	T	9	0	0	0	0
All	All	5906	0	5383	50	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

The worst 5 of 50 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:121:GLN:HE22	1:A:342:ASP:H	1.29	0.80
1:A:121:GLN:HE21	1:A:324:ARG:HH22	1.35	0.72
1:A:275:LEU:HD23	1:A:348[B]:LEU:CD2	2.18	0.72
2:C:102[A]:SER:OG	8:C:2087:HOH:O	2.08	0.70
1:A:275:LEU:HD23	1:A:348[B]:LEU:HD21	1.74	0.68

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	397/410 (97%)	388 (98%)	6 (2%)	3 (1%)	27	24
2	C	143/146 (98%)	142 (99%)	1 (1%)	0	100	100
3	D	88/89 (99%)	86 (98%)	1 (1%)	1 (1%)	21	15
5	T	40/150 (27%)	36 (90%)	3 (8%)	1 (2%)	9	4
All	All	668/795 (84%)	652 (98%)	11 (2%)	5 (1%)	27	28

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	408	ALA
1	A	409	ASP
3	D	139	LEU
1	A	23	MET
5	T	216	GLY

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	345/360 (96%)	324 (94%)	21 (6%)	26	28
2	C	130/134 (97%)	122 (94%)	8 (6%)	26	27
3	D	72/75 (96%)	67 (93%)	5 (7%)	22	22
5	T	35/133 (26%)	33 (94%)	2 (6%)	29	31
All	All	582/702 (83%)	546 (94%)	36 (6%)	27	27

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	337	TRP
1	A	407	VAL
3	D	138	ASP
1	A	348[B]	LEU
2	C	7	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	356	ASN
2	C	13	HIS
3	D	103	HIS
1	A	351	ASN
3	D	90	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	E	5/15 (33%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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 ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	ANP	A	1413	6	33,33,33	2.89	8 (24%)	51,52,52	2.11	12 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	ANP	A	1413	6	-	0/18/38/38	0/1/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1413	ANP	PB-N3B	9.77	1.72	1.64
7	A	1413	ANP	PG-N3B	7.71	1.71	1.64
7	A	1413	ANP	PB-O1B	6.94	1.54	1.46
7	A	1413	ANP	PG-O1G	4.41	1.51	1.46
7	A	1413	ANP	C4-N9	-3.50	1.32	1.37

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1413	ANP	N3-C2-N1	-7.65	122.31	128.71
7	A	1413	ANP	PB-N3B-PG	-5.49	120.83	130.07
7	A	1413	ANP	N3-C4-N9	4.96	134.38	125.43
7	A	1413	ANP	O2B-PB-O1B	4.25	119.70	109.89
7	A	1413	ANP	C8-N9-C4	3.86	109.84	106.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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, 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	391/410 (95%)	0.36	25 (6%) 19 18	41, 47, 57, 85	0
2	C	143/146 (97%)	0.32	1 (0%) 84 86	41, 46, 53, 60	0
3	D	89/89 (100%)	0.42	12 (13%) 4 4	39, 46, 54, 58	0
4	E	6/15 (40%)	-0.60	0 100 100	45, 47, 60, 82	0
5	T	44/150 (29%)	0.32	5 (11%) 6 5	36, 61, 76, 77	0
All	All	673/810 (83%)	0.35	43 (6%) 19 18	36, 47, 62, 85	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	139	LEU	5.9
1	A	275	LEU	4.5
1	A	408	ALA	4.1
3	D	140	MET	4.0
1	A	173	ARG	3.4

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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
7	ANP	A	1413	31/31	0.10	-1.46	28,32,35,37	0
6	MG	A	1412	1/1	0.09	-2.31	30,30,30,30	0

6.5 Other polymers ⓘ

There are no such residues in this entry.