wwPDB X-ray Structure Validation Summary Report (i)

Jun 18, 2024 – 08:58 AM EDT

PDB ID	:	4C0G
Title	:	Structure of the NOT-box domain of human CNOT3
Authors	:	Boland, A.; Chen, Y.; Raisch, T.; Jonas, S.; Izaurralde, E.; Weichenrieder, O.
Deposited on	:	2013-08-01
Resolution	:	2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i)) were used in the production of this report:

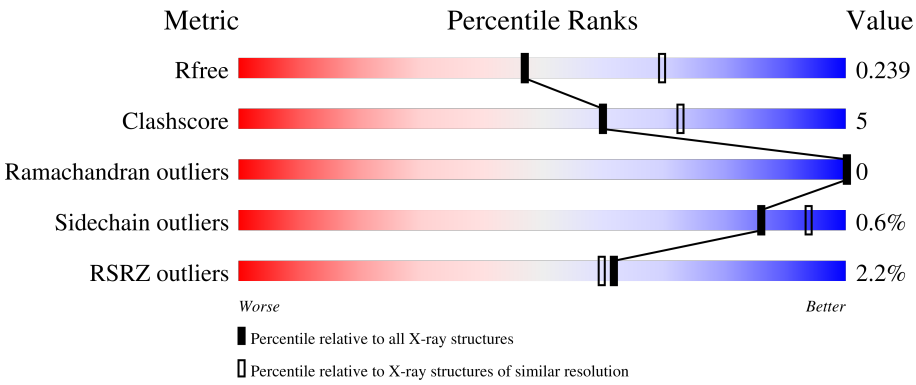
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.40 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (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 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	102	% 76% 12% 12%
1	B	102	% 80% 15% 5%
1	C	102	5% 83% 11% 6%
1	D	102	2% 88% 6% 6%
1	E	102	77% 12% 11%

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Mol	Chain	Length	Quality of chain
1	F	102	3% 76% 15% 9%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 9619 atoms, of which 4559 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 CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	Se			
1	A	90	1562	535	756	126	143	2	0	0	0
1	B	97	1643	564	787	139	151	2	0	0	0
1	C	96	1591	550	753	135	151	2	0	0	0
1	D	96	1618	562	766	138	150	2	0	0	0
1	E	91	1572	539	761	128	142	2	0	0	0
1	F	93	1557	543	736	126	150	2	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	652	GLY	-	expression tag	UNP O75175
A	653	ALA	-	expression tag	UNP O75175
A	654	MSE	-	expression tag	UNP O75175
A	655	ALA	-	expression tag	UNP O75175
B	652	GLY	-	expression tag	UNP O75175
B	653	ALA	-	expression tag	UNP O75175
B	654	MSE	-	expression tag	UNP O75175
B	655	ALA	-	expression tag	UNP O75175
C	652	GLY	-	expression tag	UNP O75175
C	653	ALA	-	expression tag	UNP O75175
C	654	MSE	-	expression tag	UNP O75175
C	655	ALA	-	expression tag	UNP O75175
D	652	GLY	-	expression tag	UNP O75175
D	653	ALA	-	expression tag	UNP O75175
D	654	MSE	-	expression tag	UNP O75175
D	655	ALA	-	expression tag	UNP O75175
E	652	GLY	-	expression tag	UNP O75175

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Chain	Residue	Modelled	Actual	Comment	Reference
E	653	ALA	-	expression tag	UNP O75175
E	654	MSE	-	expression tag	UNP O75175
E	655	ALA	-	expression tag	UNP O75175
F	652	GLY	-	expression tag	UNP O75175
F	653	ALA	-	expression tag	UNP O75175
F	654	MSE	-	expression tag	UNP O75175
F	655	ALA	-	expression tag	UNP O75175

- Molecule 2 is water.

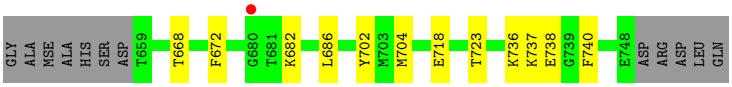
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	10	10	10	0	0
			Total	O		
2	B	14	14	14	0	0
			Total	O		
2	C	13	13	13	0	0
			Total	O		
2	D	10	10	10	0	0
			Total	O		
2	E	15	15	15	0	0
			Total	O		
2	F	14	14	14	0	0

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: CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 3

Chain A:



• Molecule 1: CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 3

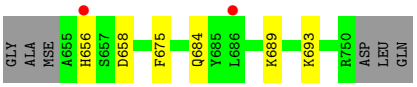
Chain B:

• Molecule 1: CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 3

Chain C:

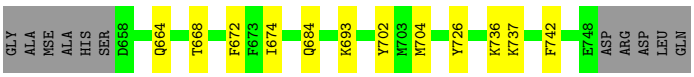
• Molecule 1: CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 3

Chain D:



• Molecule 1: CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 3

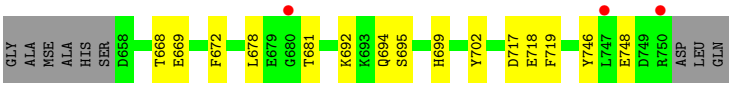
Chain E:



• Molecule 1: CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 3

Chain F:

3%
76%
15%
9%


GLY
ALA
MSE
ALA
HIS
SER
D658
T668
E669
F672
L678
E679
G680
T681
K692
K693
Q694
S695
H699
Y702
D717
E718
F719
Y746
L747
E748
D749
R750
ASP
LEU
GLN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	52.30Å 97.57Å 141.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.06 – 2.40 49.06 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.06-2.40) 99.6 (49.06-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	2.86 (at 2.39Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.221 , 0.257 0.211 , 0.239	Depositor DCC
R_{free} test set	1479 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	54.6	Xtriage
Anisotropy	0.657	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 41.4	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	9619	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.62% 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	0.25	0/832	0.40	0/1116
1	B	0.24	0/883	0.37	0/1184
1	C	0.24	0/863	0.37	0/1158
1	D	0.25	0/879	0.38	0/1178
1	E	0.26	0/837	0.39	0/1122
1	F	0.25	0/847	0.37	0/1138
All	All	0.25	0/5141	0.38	0/6896

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	806	756	754	9	0
1	B	856	787	799	10	0
1	C	838	753	776	8	0
1	D	852	766	799	3	0
1	E	811	761	763	6	0
1	F	821	736	753	10	0
2	A	10	0	0	0	0
2	B	14	0	0	0	0
2	C	13	0	0	0	0
2	D	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	15	0	0	0	0
2	F	14	0	0	0	0
All	All	5060	4559	4644	44	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 5.

The worst 5 of 44 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:F:694:GLN:O	1:F:695:SER:HB2	1.94	0.67
1:C:659:THR:OG1	1:C:661:GLU:OE1	2.15	0.63
1:B:656:HIS:O	1:B:659:THR:OG1	2.17	0.59
1:B:749:ASP:O	1:B:750:ARG:HG2	2.03	0.59
1:B:700:THR:CG2	1:B:748:GLU:HG2	2.34	0.58

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	88/102 (86%)	84 (96%)	4 (4%)	0	100	100
1	B	95/102 (93%)	92 (97%)	3 (3%)	0	100	100
1	C	94/102 (92%)	93 (99%)	1 (1%)	0	100	100
1	D	94/102 (92%)	91 (97%)	3 (3%)	0	100	100
1	E	89/102 (87%)	87 (98%)	2 (2%)	0	100	100
1	F	91/102 (89%)	89 (98%)	2 (2%)	0	100	100
All	All	551/612 (90%)	536 (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	81/88 (92%)	81 (100%)	0	100	100
1	B	85/88 (97%)	84 (99%)	1 (1%)	71	85
1	C	83/88 (94%)	82 (99%)	1 (1%)	71	85
1	D	85/88 (97%)	85 (100%)	0	100	100
1	E	81/88 (92%)	80 (99%)	1 (1%)	71	85
1	F	82/88 (93%)	82 (100%)	0	100	100
All	All	497/528 (94%)	494 (99%)	3 (1%)	86	94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	742	PHE
1	C	742	PHE
1	E	742	PHE

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

Mol	Chain	Res	Type
1	C	699	HIS
1	D	656	HIS
1	F	699	HIS

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	88/102 (86%)	-0.12	1 (1%)	80	79	39, 61, 99, 124	0
1	B	95/102 (93%)	-0.03	1 (1%)	80	79	40, 63, 115, 135	0
1	C	94/102 (92%)	0.23	5 (5%)	26	25	42, 69, 119, 150	0
1	D	94/102 (92%)	0.18	2 (2%)	63	61	38, 63, 109, 145	0
1	E	89/102 (87%)	-0.06	0	100	100	39, 58, 100, 138	0
1	F	91/102 (89%)	0.27	3 (3%)	46	45	40, 64, 135, 149	0
All	All	551/612 (90%)	0.08	12 (2%)	62	60	38, 64, 117, 150	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	659	THR	5.1
1	D	656	HIS	4.7
1	C	660	VAL	4.2
1	C	658	ASP	3.7
1	D	686	LEU	3.6

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.