



wwPDB X-ray Structure Validation Summary Report

May 6, 2014 – 09:27 AM EDT

PDB ID : 4N2O
Title : Structure of a novel autonomous cohesin protein from *Ruminococcus flavefaciens*
Authors : Frolow, F.; Voronov-Goldman, M.; Levy-Assaraf, M.; Lamed, R.; Bayer, E.; Shimon, L.
Deposited on : 2013-10-05
Resolution : 2.44 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>

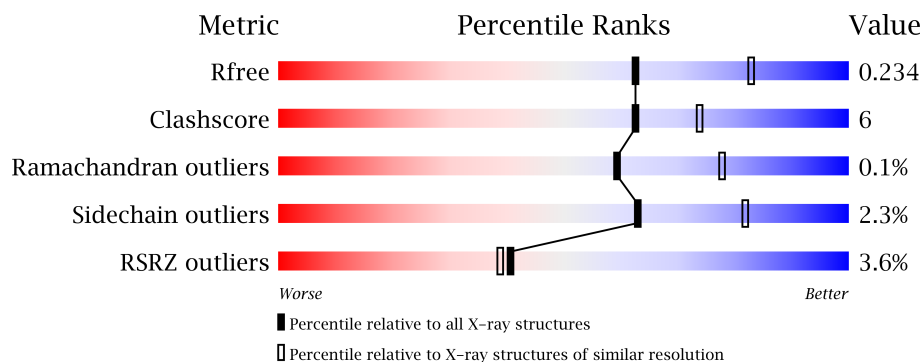
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable22978
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) : stable22978

1 Overall quality at a glance

The reported resolution of this entry is 2.44 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	2989 (2.48-2.40)
Clashscore	79885	3698 (2.48-2.40)
Ramachandran outliers	78287	3639 (2.48-2.40)
Sidechain outliers	78261	3640 (2.48-2.40)
RSRZ outliers	66119	2993 (2.48-2.40)

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. 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	201	
1	B	201	
1	C	201	
1	D	201	
1	E	201	
1	F	201	
1	G	201	
1	H	201	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12269 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Autonomous cohesin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	195	Total	C	N	O	S	Se	0	0	0
			1499	941	240	304	3	11			
1	B	193	Total	C	N	O	S	Se	0	0	0
			1489	936	238	301	3	11			
1	C	190	Total	C	N	O	S	Se	0	0	0
			1473	927	237	295	3	11			
1	D	191	Total	C	N	O	S	Se	0	0	0
			1470	925	234	297	3	11			
1	E	190	Total	C	N	O	S	Se	0	0	0
			1467	924	233	296	3	11			
1	F	193	Total	C	N	O	S	Se	0	1	0
			1508	948	245	300	3	12			
1	G	192	Total	C	N	O	S	Se	0	1	0
			1491	938	238	300	3	12			
1	H	191	Total	C	N	O	S	Se	0	1	0
			1485	935	237	298	3	12			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	1	Total	Cl	0	0
			1	1		
2	B	1	Total	Cl	0	0
			1	1		
2	A	2	Total	Cl	0	0
			2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	74	Total	O	0	0
			74	74		

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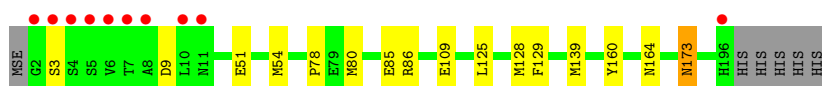
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	58	Total 58	O 58	0	0
3	C	51	Total 51	O 51	0	0
3	D	6	Total 6	O 6	0	0
3	E	8	Total 8	O 8	0	0
3	F	53	Total 53	O 53	0	0
3	G	69	Total 69	O 69	0	0
3	H	64	Total 64	O 64	0	0

3 Residue-property plots

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: Autonomous cohesin

Chain A: 



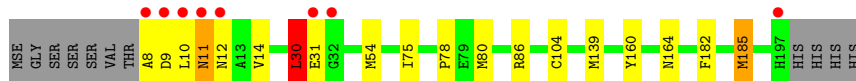
- Molecule 1: Autonomous cohesin

Chain B: 



- Molecule 1: Autonomous cohesin

Chain C: 



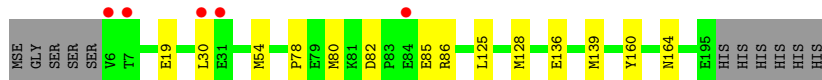
- Molecule 1: Autonomous cohesin

Chain D: 



- Molecule 1: Autonomous cohesin

Chain E: 

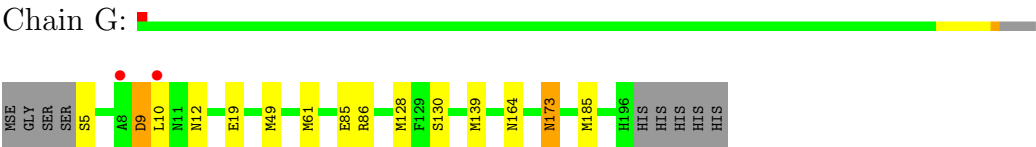


- Molecule 1: Autonomous cohesin

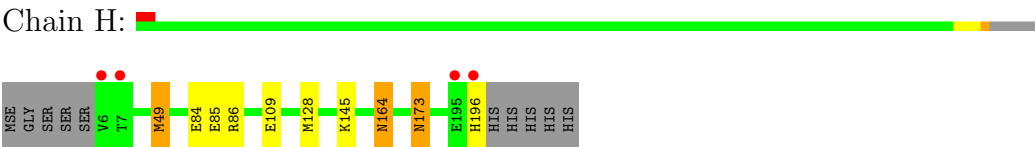
Chain F: 



● Molecule 1: Autonomous cohesin



● Molecule 1: Autonomous cohesin



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	116.24Å 67.73Å 258.91Å 90.00° 93.08° 90.00°	Depositor
Resolution (Å)	22.77 – 2.44 22.77 – 2.44	Depositor EDS
% Data completeness (in resolution range)	96.8 (22.77-2.44) 91.0 (22.77-2.44)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 2.44Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.205 , 0.229 0.214 , 0.234	Depositor DCC
R_{free} test set	3501 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	34.9	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 23.4	EDS
Estimated twinning fraction	0.022 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.024 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 72856 reflections	Xtriage
F_o , F_c correlation	0.92	EDS
Total number of atoms	12269	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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: CL

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	0.61	0/1520	0.78	2/2045 (0.1%)
1	B	0.58	0/1510	0.75	2/2032 (0.1%)
1	C	0.56	0/1495	0.78	3/2011 (0.1%)
1	D	0.52	0/1490	0.78	2/2005 (0.1%)
1	E	0.56	0/1487	0.80	3/2001 (0.1%)
1	F	0.57	0/1532	0.83	1/2061 (0.0%)
1	G	0.62	0/1512	0.83	4/2034 (0.2%)
1	H	0.55	0/1506	0.74	1/2026 (0.0%)
All	All	0.57	0/12052	0.79	18/16215 (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	C	0	2
1	G	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	49	MSE	CG-SE-CE	9.33	119.42	98.90
1	G	49	MSE	CG-SE-CE	8.54	117.70	98.90
1	B	49	MSE	CG-SE-CE	7.51	115.43	98.90
1	D	185	MSE	CG-SE-CE	-7.43	82.56	98.90
1	C	185	MSE	CG-SE-CE	-7.37	82.69	98.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	11	ASN	Peptide
1	C	12	ASN	Peptide
1	G	10	LEU	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	1499	0	0	11	0
1	B	1489	0	0	12	0
1	C	1473	0	0	12	0
1	D	1470	0	0	7	0
1	E	1467	0	0	8	0
1	F	1508	0	0	11	0
1	G	1491	0	0	9	0
1	H	1485	0	0	9	0
2	A	2	0	0	1	0
2	B	1	0	0	0	0
2	H	1	0	0	2	0
3	A	74	0	0	2	0
3	B	58	0	0	1	0
3	C	51	0	0	1	0
3	D	6	0	0	0	0
3	E	8	0	0	0	0
3	F	53	0	0	1	0
3	G	69	0	0	3	0
3	H	64	0	0	2	0
All	All	12269	0	0	67	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 6.

The worst 5 of 67 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:128[B]:MSE:CG	1:H:128[B]:MSE:CE	2.38	1.01
1:A:128:MSE:CE	1:A:129:PHE:O	2.19	0.91
1:A:54:MSE:CE	1:A:160:TYR:CE1	2.66	0.78
1:E:54:MSE:CE	1:E:160:TYR:CE1	2.67	0.78
1:B:54:MSE:CE	1:B:160:TYR:CE1	2.68	0.77

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	193/201 (96%)	186 (96%)	7 (4%)	0	100	100
1	B	191/201 (95%)	185 (97%)	6 (3%)	0	100	100
1	C	188/201 (94%)	180 (96%)	8 (4%)	0	100	100
1	D	189/201 (94%)	183 (97%)	6 (3%)	0	100	100
1	E	188/201 (94%)	183 (97%)	5 (3%)	0	100	100
1	F	192/201 (96%)	183 (95%)	8 (4%)	1 (0%)	38	51
1	G	191/201 (95%)	185 (97%)	6 (3%)	0	100	100
1	H	190/201 (94%)	185 (97%)	5 (3%)	0	100	100
All	All	1522/1608 (95%)	1470 (97%)	51 (3%)	1 (0%)	59	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	197	HIS

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	162/156 (104%)	158 (98%)	4 (2%)	60	79
1	B	161/156 (103%)	158 (98%)	3 (2%)	69	86
1	C	158/156 (101%)	154 (98%)	4 (2%)	60	79
1	D	159/156 (102%)	155 (98%)	4 (2%)	60	79
1	E	158/156 (101%)	156 (99%)	2 (1%)	80	92
1	F	162/156 (104%)	157 (97%)	5 (3%)	52	73
1	G	161/156 (103%)	156 (97%)	5 (3%)	52	73
1	H	160/156 (103%)	157 (98%)	3 (2%)	69	86
All	All	1281/1248 (103%)	1251 (98%)	30 (2%)	63	82

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	191	THR
1	E	164	ASN
1	H	164	ASN
1	E	125	LEU
1	F	31	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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	195/201 (97%)	-0.22	10 (5%) 27 25	22, 31, 63, 95	0
1	B	193/201 (96%)	-0.17	6 (3%) 47 45	24, 37, 64, 125	0
1	C	190/201 (94%)	-0.02	8 (4%) 35 33	27, 45, 89, 108	0
1	D	191/201 (95%)	0.34	10 (5%) 26 24	38, 57, 99, 126	0
1	E	190/201 (94%)	0.17	5 (2%) 53 51	40, 59, 86, 110	0
1	F	193/201 (96%)	0.05	10 (5%) 26 24	24, 46, 91, 132	0
1	G	192/201 (95%)	-0.36	2 (1%) 79 79	21, 30, 61, 90	0
1	H	191/201 (95%)	-0.23	4 (2%) 60 58	25, 37, 61, 114	0
All	All	1535/1608 (95%)	-0.05	55 (3%) 41 39	21, 42, 84, 132	0

The worst 5 of 55 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	194	LEU	8.0
1	B	4	SER	7.7
1	F	8	ALA	7.1
1	D	6	VAL	6.3
1	D	5	SER	6.1

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
2	CL	B	301	1/1	0.16	1.76	71,71,71,71	0
2	CL	H	301	1/1	0.16	0.76	78,78,78,78	0
2	CL	A	302	1/1	0.13	-0.17	56,56,56,56	0
2	CL	A	301	1/1	0.12	-0.64	53,53,53,53	0

6.5 Other polymers

There are no such residues in this entry.