



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 08:00 AM BST

PDB ID : 6QB5
Title : Crystal structure of the N-terminal region of human cohesin subunit STAG1
Authors : Newman, J.A.; Katis, V.L.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.; Bountra, C.; Gileadi, O.
Deposited on : 2018-12-20
Resolution : 2.02 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

<https://www.wwpdb.org/validation/2017/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
Xtriage (Phenix) : 1.13
EDS : 2.13.1
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) : 2.13.1

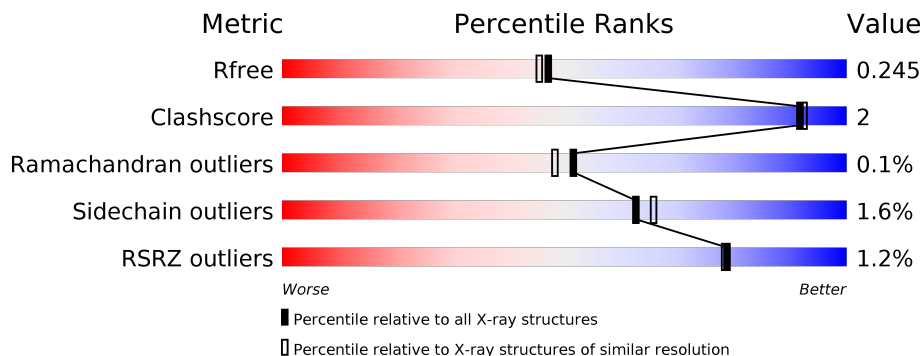
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.02 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	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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 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 $\leq 5\%$. 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	339	 % 85% 6% 7% 11%
1	B	339	 % 87% 6% 7%
1	C	339	 % 86% 6% 7%
1	D	339	 % 84% 6% 10%

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 10628 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 Cohesin subunit SA-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	C	315	2571	1637	434	480	20	0	1	0
1	A	303	2414	1540	404	450	20	0	0	0
1	B	316	2549	1623	432	474	20	0	0	0
1	D	305	2466	1569	416	461	20	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	82	SER	-	expression tag	UNP Q8WVM7
C	83	MET	-	expression tag	UNP Q8WVM7
C	84	GLY	-	expression tag	UNP Q8WVM7
C	85	GLY	-	expression tag	UNP Q8WVM7
A	82	SER	-	expression tag	UNP Q8WVM7
A	83	MET	-	expression tag	UNP Q8WVM7
A	84	GLY	-	expression tag	UNP Q8WVM7
A	85	GLY	-	expression tag	UNP Q8WVM7
B	82	SER	-	expression tag	UNP Q8WVM7
B	83	MET	-	expression tag	UNP Q8WVM7
B	84	GLY	-	expression tag	UNP Q8WVM7
B	85	GLY	-	expression tag	UNP Q8WVM7
D	82	SER	-	expression tag	UNP Q8WVM7
D	83	MET	-	expression tag	UNP Q8WVM7
D	84	GLY	-	expression tag	UNP Q8WVM7
D	85	GLY	-	expression tag	UNP Q8WVM7

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Na 1 1	0	0

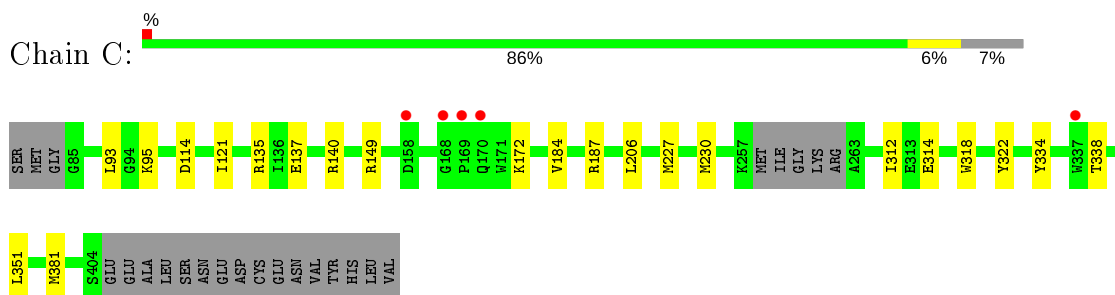
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	169	Total O 169 169	0	0
3	A	152	Total O 152 152	0	0
3	B	148	Total O 148 148	0	0
3	D	158	Total O 158 158	0	0

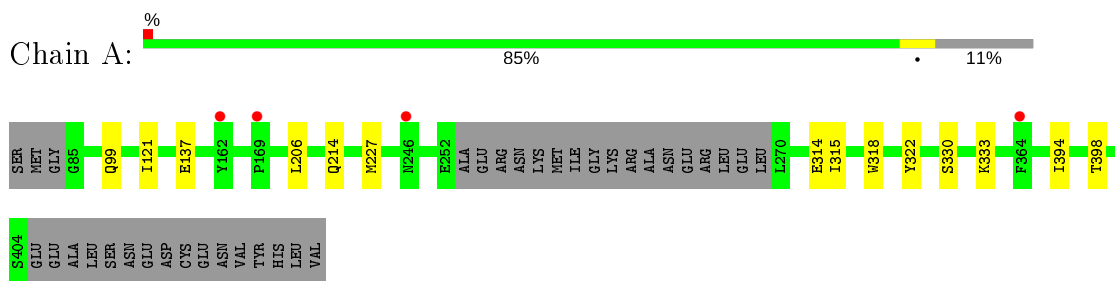
3 Residue-property plots [i](#)

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.

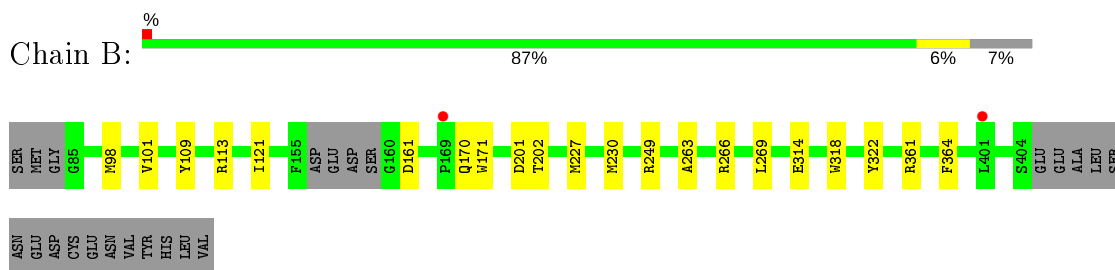
- Molecule 1: Cohesin subunit SA-1



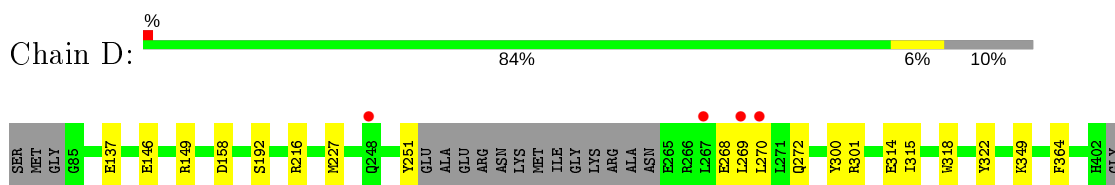
- Molecule 1: Cohesin subunit SA-1



- Molecule 1: Cohesin subunit SA-1



- Molecule 1: Cohesin subunit SA-1



SER
GLU
GLU
ALA
LEU
SER
ASN
GLU
ASP
CYS
GLU
ASN
VAL
TYR
HIS
LEU
VAL

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.61Å 124.98Å 231.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	85.00 – 2.02 85.00 – 2.02	Depositor EDS
% Data completeness (in resolution range)	99.5 (85.00-2.02) 99.7 (85.00-2.02)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.02Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.218 , 0.245 0.218 , 0.245	Depositor DCC
R_{free} test set	6239 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	36.4	Xtrriage
Anisotropy	0.644	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10628	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.34% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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](#)

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

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	0.23	0/2455	0.36	0/3313
1	B	0.23	0/2591	0.35	0/3492
1	C	0.23	0/2615	0.35	0/3523
1	D	0.23	0/2507	0.35	0/3381
All	All	0.23	0/10168	0.35	0/13709

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	2414	0	2369	5	0
1	B	2549	0	2522	8	0
1	C	2571	0	2550	11	0
1	D	2466	0	2433	7	0
2	D	1	0	0	0	0
3	A	152	0	0	0	0
3	B	148	0	0	0	0
3	C	169	0	0	1	0
3	D	158	0	0	1	0
All	All	10628	0	9874	31	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 2.

All (31) 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:D:300:TYR:OH	1:D:301:ARG:NH2	2.31	0.63
1:A:121:ILE:HG12	1:A:206:LEU:HD22	1.81	0.62
1:C:227:MET:HB3	1:C:314:GLU:HG2	1.83	0.61
1:D:227:MET:HB3	1:D:314:GLU:HG2	1.83	0.60
1:B:227:MET:HB3	1:B:314:GLU:HG2	1.83	0.59
1:C:135:ARG:NH1	1:C:137:GLU:OE2	2.38	0.57
1:A:227:MET:HB3	1:A:314:GLU:HG2	1.87	0.57
1:C:114:ASP:OD2	1:C:140:ARG:NH1	2.41	0.53
1:A:330:SER:O	1:A:333:LYS:NZ	2.39	0.52
1:B:121:ILE:HD11	1:B:202:THR:HG22	1.92	0.52
1:A:394:ILE:O	1:A:398:THR:HG23	2.11	0.51
1:C:312:ILE:HG13	1:C:338:THR:HG21	1.92	0.51
1:D:146:GLU:HG3	1:D:149:ARG:HH22	1.78	0.49
1:C:149:ARG:NH2	3:C:503:HOH:O	2.35	0.49
1:C:121:ILE:HG12	1:C:206:LEU:HD22	1.95	0.48
1:C:93:LEU:HD21	1:C:95:LYS:HE3	1.95	0.48
1:D:158:ASP:OD1	1:D:216:ARG:NE	2.47	0.47
1:B:109:TYR:CZ	1:B:113:ARG:HG2	2.51	0.46
1:D:251:TYR:HA	1:D:270:LEU:HD13	1.97	0.45
1:C:184:VAL:HG22	1:C:187:ARG:HH22	1.81	0.45
1:D:349:LYS:NZ	3:D:602:HOH:O	2.32	0.45
1:C:334:TYR:O	1:C:338:THR:OG1	2.31	0.43
1:C:230:MET:HG2	1:C:318:TRP:CE2	2.55	0.42
1:B:263:ALA:HB3	1:B:266:ARG:HB3	2.02	0.42
1:D:315:ILE:HA	1:D:318:TRP:CE3	2.55	0.42
1:B:98:MET:HA	1:B:101:VAL:HG12	2.02	0.41
1:B:170:GLN:HG2	1:B:171:TRP:CD1	2.56	0.41
1:B:361:ARG:HA	1:B:364:PHE:CD1	2.56	0.41
1:C:351:LEU:HD11	1:C:381:MET:HE2	2.03	0.41
1:B:230:MET:HG2	1:B:318:TRP:CZ2	2.56	0.40
1:A:315:ILE:HA	1:A:318:TRP:CE3	2.57	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	299/339 (88%)	293 (98%)	6 (2%)	0	100	100
1	B	312/339 (92%)	307 (98%)	5 (2%)	0	100	100
1	C	312/339 (92%)	307 (98%)	5 (2%)	0	100	100
1	D	301/339 (89%)	296 (98%)	4 (1%)	1 (0%)	41	36
All	All	1224/1356 (90%)	1203 (98%)	20 (2%)	1 (0%)	51	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	192	SER

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	260/306 (85%)	256 (98%)	4 (2%)	65	68
1	B	275/306 (90%)	270 (98%)	5 (2%)	59	61
1	C	281/306 (92%)	279 (99%)	2 (1%)	84	87
1	D	269/306 (88%)	263 (98%)	6 (2%)	52	53
All	All	1085/1224 (89%)	1068 (98%)	17 (2%)	62	66

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	172	LYS
1	C	322	TYR
1	A	99	GLN
1	A	137	GLU
1	A	214	GLN
1	A	322	TYR
1	B	161	ASP
1	B	201	ASP
1	B	249	ARG
1	B	269	LEU
1	B	322	TYR
1	D	137	GLU
1	D	268	GLU
1	D	269	LEU
1	D	272	GLN
1	D	322	TYR
1	D	364	PHE

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

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](#)

Of 1 ligands modelled in this entry, 1 is 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.

No monomer is involved in short contacts.

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	303/339 (89%)	-0.07	4 (1%) 77 76	28, 43, 80, 94	0
1	B	316/339 (93%)	-0.04	2 (0%) 89 89	28, 47, 74, 86	0
1	C	315/339 (92%)	0.06	5 (1%) 72 71	28, 42, 74, 100	0
1	D	305/339 (89%)	0.06	4 (1%) 77 76	29, 43, 81, 104	0
All	All	1239/1356 (91%)	0.00	15 (1%) 79 78	28, 44, 77, 104	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	169	PRO	5.3
1	C	170	GLN	3.8
1	C	158	ASP	3.4
1	D	267	LEU	3.3
1	D	269	LEU	3.0
1	A	169	PRO	2.7
1	A	246	ASN	2.7
1	D	270	LEU	2.7
1	C	168	GLY	2.6
1	B	401	LEU	2.6
1	A	162	TYR	2.5
1	A	364	PHE	2.5
1	C	337[A]	TRP	2.1
1	D	248	GLN	2.1
1	B	169	PRO	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 monosaccharides in this entry.

6.4 Ligands [i](#)

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. 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	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NA	D	501	1/1	0.91	0.12	45,45,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.