



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 16, 2024 – 08:59 AM EDT

PDB ID : 2DOQ
Title : crystal structure of Sfi1p/Cdc31p complex
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Deposited on : 2006-05-03
Resolution : 3.00 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 ⓘ 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 ⓘ](#)) 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

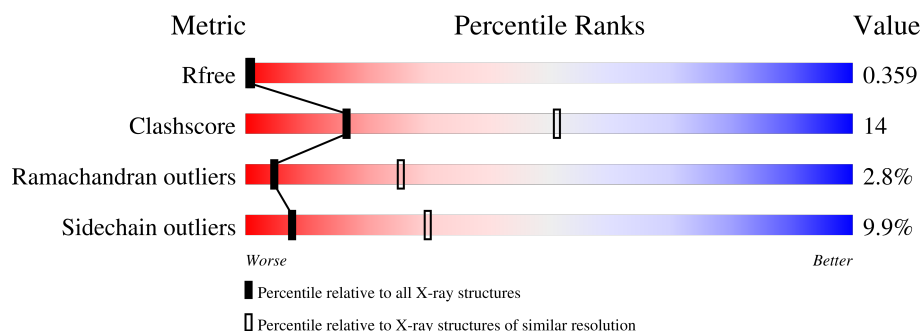
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

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 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	161	63% 25% 9%
1	B	161	57% 29% 7% 7%
1	C	161	48% 29% 19%
2	D	94	52% 28% 7% 12%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4230 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 Cell division control protein 31.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	146	Total	C	N	O	S	Se	0	0	0
			1205	762	192	245	1	5			
1	B	149	Total	C	N	O	S	Se	0	0	0
			1227	775	196	250	1	5			
1	C	130	Total	C	N	O	S	Se	0	0	0
			1083	691	174	213	5				

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP P06704
A	34	MSE	MET	MODIFIED RESIDUE	UNP P06704
A	49	MSE	MET	MODIFIED RESIDUE	UNP P06704
A	76	MSE	MET	MODIFIED RESIDUE	UNP P06704
A	85	MSE	MET	MODIFIED RESIDUE	UNP P06704
A	137	MSE	MET	MODIFIED RESIDUE	UNP P06704
B	1	MSE	MET	MODIFIED RESIDUE	UNP P06704
B	34	MSE	MET	MODIFIED RESIDUE	UNP P06704
B	49	MSE	MET	MODIFIED RESIDUE	UNP P06704
B	76	MSE	MET	MODIFIED RESIDUE	UNP P06704
B	85	MSE	MET	MODIFIED RESIDUE	UNP P06704
B	137	MSE	MET	MODIFIED RESIDUE	UNP P06704
C	1	MSE	MET	MODIFIED RESIDUE	UNP P06704
C	34	MSE	MET	MODIFIED RESIDUE	UNP P06704
C	49	MSE	MET	MODIFIED RESIDUE	UNP P06704
C	76	MSE	MET	MODIFIED RESIDUE	UNP P06704
C	85	MSE	MET	MODIFIED RESIDUE	UNP P06704
C	137	MSE	MET	MODIFIED RESIDUE	UNP P06704

- Molecule 2 is a protein called SFI1p.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	83	Total	C	N	O	Se	0	0	0
			704	450	124	128	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	213	GLY	-	CLONING ARTIFACT	UNP Q12369
D	214	PRO	-	CLONING ARTIFACT	UNP Q12369
D	215	LEU	-	CLONING ARTIFACT	UNP Q12369
D	216	GLY	-	CLONING ARTIFACT	UNP Q12369
D	217	SER	-	CLONING ARTIFACT	UNP Q12369
D	250	MSE	MET	MODIFIED RESIDUE	UNP Q12369
D	278	PHE	LEU	SEE REMARK 999	UNP Q12369
D	293	MSE	MET	MODIFIED RESIDUE	UNP Q12369

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Ca	0	0
			3	3		
3	B	3	Total	Ca	0	0
			3	3		
3	C	1	Total	Ca	0	0
			1	1		

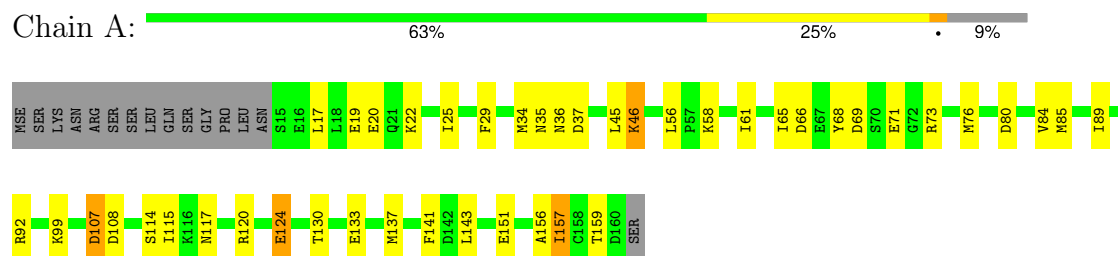
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O	0	0
			2	2		
4	D	2	Total	O	0	0
			2	2		

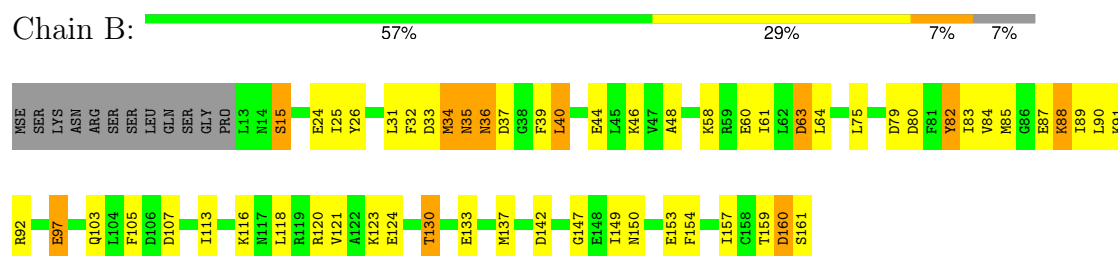
3 Residue-property plots

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. 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. 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.

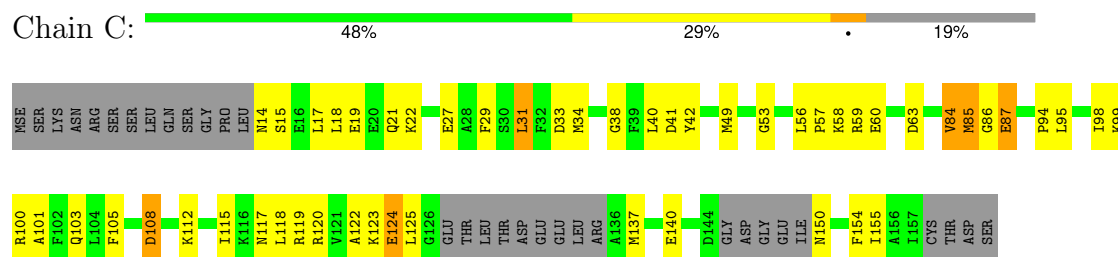
• Molecule 1: Cell division control protein 31



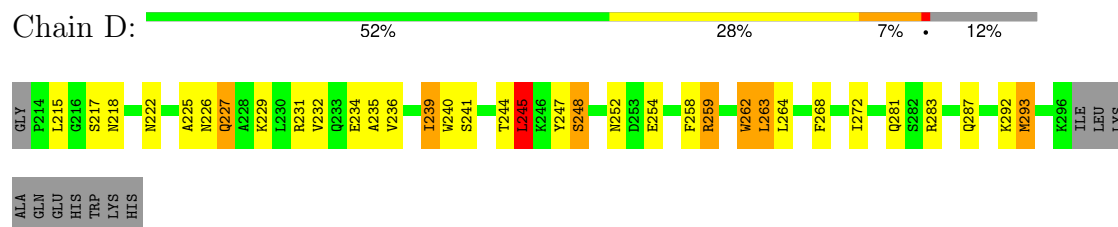
• Molecule 1: Cell division control protein 31



• Molecule 1: Cell division control protein 31



• Molecule 2: SFI1p



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	87.28Å 92.96Å 189.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	94.49 – 3.00 52.81 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (94.49-3.00) 99.5 (52.81-3.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.259 , 0.299 0.317 , 0.359	Depositor DCC
R_{free} test set	785 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	110.9	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 70.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4230	wwPDB-VP
Average B, all atoms (Å ²)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: CA

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	0.44	0/1218	0.57	0/1624
1	B	0.51	0/1240	0.71	1/1654 (0.1%)
1	C	0.44	0/1094	0.56	0/1453
2	D	0.59	0/718	0.69	1/961 (0.1%)
All	All	0.49	0/4270	0.63	2/5692 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	40	LEU	CA-CB-CG	6.04	129.19	115.30
2	D	245	LEU	CA-CB-CG	-5.15	103.46	115.30

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	1205	0	1160	31	1
1	B	1227	0	1181	38	0
1	C	1083	0	1050	35	0
2	D	704	0	685	32	1
3	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	3	0	0	0	0
3	C	1	0	0	0	0
4	A	2	0	0	0	0
4	D	2	0	0	0	0
All	All	4230	0	4076	118	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 14.

The worst 5 of 118 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:C:34:MSE:CE	2:D:281:GLN:HG3	2.05	0.86
1:C:49:MSE:HE1	1:C:56:LEU:HD11	1.59	0.84
1:B:24:GLU:HG3	2:D:262:TRP:HD1	1.47	0.79
1:C:60:GLU:O	1:C:63:ASP:HB2	1.83	0.79
1:A:137:MSE:HA	2:D:245:LEU:HD13	1.68	0.76

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)
1:A:19:GLU:OE1	2:D:247:TYR:OH[3_656]	2.14	0.06

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	144/161 (89%)	133 (92%)	8 (6%)	3 (2%)	7	33
1	B	147/161 (91%)	125 (85%)	16 (11%)	6 (4%)	3	16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	124/161 (77%)	105 (85%)	15 (12%)	4 (3%)	4	22
2	D	81/94 (86%)	63 (78%)	17 (21%)	1 (1%)	13	48
All	All	496/577 (86%)	426 (86%)	56 (11%)	14 (3%)	5	25

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	B	15	SER
1	B	33	ASP
1	C	84	VAL
1	B	36	ASN

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	131/139 (94%)	122 (93%)	9 (7%)	15	48
1	B	134/139 (96%)	120 (90%)	14 (10%)	7	27
1	C	117/139 (84%)	110 (94%)	7 (6%)	19	53
2	D	74/81 (91%)	59 (80%)	15 (20%)	1	6
All	All	456/498 (92%)	411 (90%)	45 (10%)	8	30

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	108	ASP
2	D	236	VAL
1	C	154	PHE
2	D	227	GLN
2	D	245	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	35	ASN
2	D	218	ASN
2	D	276	GLN
2	D	287	GLN

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 7 ligands modelled in this entry, 7 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.

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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.