Full wwPDB X-ray Structure Validation Report (i)

May 22, 2020 – 02:30 pm BST

PDB ID	:	6DU3
Title	:	Structure of Scp1 D96N bound to REST-pS861/4 peptide
Authors	:	Burkholder, N.T.; Mayfield, J.E.; Yu, X.; Irani, S.; Arce, D.K.; Jiang, F.; Matthews, W.; Xue, Y.; Zhang, Y.J.
Deposited on	:	2018-06-19
Resolution	:	2.58 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

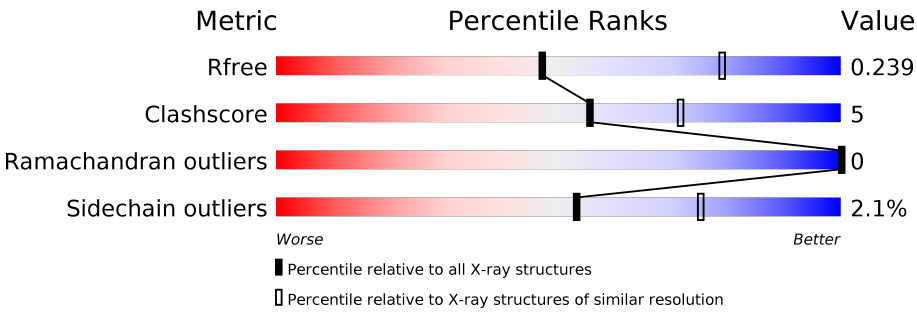
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.58 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	3676 (2.60-2.56)
Clashscore	141614	4049 (2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	180	87% 12% •
1	B	180	84% 15% •
2	C	12	42% 17% 42%
2	D	12	17% 25% 58%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3016 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 Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	180	1457	937	247	268	5	0	0	0
1	B	180	1449	932	246	266	5	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	96	ASN	ASP	engineered mutation	UNP Q9GZU7
B	96	ASN	ASP	engineered mutation	UNP Q9GZU7

- Molecule 2 is a protein called REST-pS861.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	C	7	53	31	7	14	1	0	0	0
2	D	5	37	22	5	9	1	0	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is water.

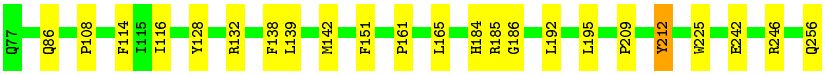
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	9	9	9	0	0
			Total	O		
4	B	6	6	6	0	0
			Total	O		
4	C	2	2	2	0	0
			Total	O		
4	D	1	1	1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1

Chain A:

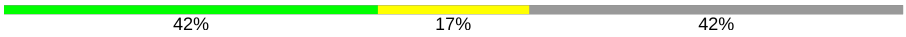


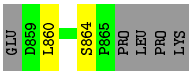
• Molecule 1: Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1

Chain B:

• Molecule 2: REST-pS861

Chain C:





• Molecule 2: REST-pS861

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	125.41Å 78.73Å 63.00Å 90.00° 112.42° 90.00°	Depositor
Resolution (Å)	39.20 – 2.58 48.94 – 2.58	Depositor EDS
% Data completeness (in resolution range)	98.0 (39.20-2.58) 98.8 (48.94-2.58)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.36 (at 2.58Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	(Not available) , (Not available) 0.202 , 0.239	Depositor DCC
R_{free} test set	1787 reflections (10.01%)	wwPDB-VP
Wilson B-factor (Å^2)	34.6	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 45.7	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	0.93	EDS
Total number of atoms	3016	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.11% 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)

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

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	0/1493	0.60	0/2031
1	B	0.40	0/1485	0.60	0/2022
2	C	0.37	0/44	1.07	1/59 (1.7%)
2	D	0.35	0/27	0.60	0/35
All	All	0.42	0/3049	0.61	1/4147 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	860	LEU	CA-CB-CG	-6.51	100.33	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	1457	0	1424	13	0
1	B	1449	0	1409	18	0
2	C	53	0	43	1	0
2	D	37	0	30	3	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	9	0	0	0	0
4	B	6	0	0	0	0
4	C	2	0	0	0	0
4	D	1	0	0	0	0
All	All	3016	0	2906	30	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.

All (30) 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:A:116:ILE:HD13	1:A:161:PRO:HB2	1.65	0.78
1:B:155:LEU:HD12	2:D:859:ASP:HA	1.76	0.66
1:B:96:ASN:HD21	2:D:861:SEP:P	2.23	0.61
1:B:251:TYR:O	1:B:255:ARG:N	2.28	0.58
1:A:192:LEU:HD22	1:A:195:LEU:HD11	1.92	0.52
1:B:209:PRO:HA	1:B:212:TYR:CZ	2.46	0.51
1:A:209:PRO:HA	1:A:212:TYR:CZ	2.45	0.51
1:B:244:LEU:O	1:B:247:VAL:HG22	2.11	0.50
1:A:186:GLY:O	2:C:864:SER:HB3	2.12	0.49
1:A:184:HIS:NE2	1:A:185:ARG:HD3	2.28	0.49
1:B:87:ASP:HA	1:B:90:LYS:HE3	1.94	0.49
1:A:242:GLU:O	1:A:246:ARG:NH1	2.47	0.48
1:B:240:PHE:CZ	1:B:244:LEU:HD11	2.48	0.48
1:B:243:GLN:HA	1:B:246:ARG:NH1	2.28	0.48
1:B:132:ARG:HH21	1:B:233:GLU:HB3	1.79	0.47
1:B:151:PHE:CD1	1:B:176:LEU:HB2	2.50	0.46
1:A:108:PRO:HA	1:A:128:TYR:CE1	2.51	0.46
1:A:132:ARG:CZ	1:A:225:TRP:HB2	2.45	0.46
1:A:139:LEU:HA	1:A:139:LEU:HD23	1.73	0.46
1:A:86:GLN:HG3	1:B:125:HIS:NE2	2.32	0.45
1:B:116:ILE:CD1	1:B:161:PRO:HB2	2.46	0.45
1:B:140:GLN:HG2	1:B:169:TRP:CD2	2.53	0.44
2:D:861:SEP:HA	2:D:862:PRO:HD3	1.77	0.43
1:A:138:PHE:O	1:A:142:MET:HG2	2.18	0.42
1:A:165:LEU:HD23	1:A:165:LEU:HA	1.88	0.42
1:B:116:ILE:CG2	1:B:127:VAL:HB	2.50	0.42
1:A:86:GLN:HG3	1:B:125:HIS:CE1	2.56	0.41
1:B:201:ARG:HH11	1:B:201:ARG:HG2	1.86	0.40
1:B:239:PRO:O	1:B:242:GLU:HB2	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:ILE:HG23	1:B:127:VAL:HB	2.04	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	178/180 (99%)	171 (96%)	7 (4%)	0	100	100
1	B	178/180 (99%)	165 (93%)	13 (7%)	0	100	100
2	C	4/12 (33%)	4 (100%)	0	0	100	100
2	D	2/12 (17%)	2 (100%)	0	0	100	100
All	All	362/384 (94%)	342 (94%)	20 (6%)	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	162/163 (99%)	158 (98%)	4 (2%)	47	70
1	B	160/163 (98%)	157 (98%)	3 (2%)	57	77
2	C	6/11 (54%)	6 (100%)	0	100	100
2	D	3/11 (27%)	3 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	331/348 (95%)	324 (98%)	7 (2%)	53 75

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	PHE
1	A	151	PHE
1	A	212	TYR
1	A	256	GLN
1	B	151	PHE
1	B	166	LEU
1	B	256	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	243	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)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\#\|Z\| > 2$
2	SEP	C	861	3,2	8,9,10	1.60	1 (12%)	8,12,14	1.28	1 (12%)
2	SEP	D	861	3,2	8,9,10	1.68	2 (25%)	8,12,14	2.10	2 (25%)

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
2	SEP	C	861	3,2	-	3/5/8/10	-
2	SEP	D	861	3,2	-	2/5/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	861	SEP	P-O1P	3.59	1.62	1.50
2	C	861	SEP	P-O1P	3.40	1.61	1.50
2	D	861	SEP	P-O2P	2.00	1.62	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	861	SEP	OG-CB-CA	4.81	112.83	108.14
2	D	861	SEP	P-OG-CB	-2.56	111.25	118.30
2	C	861	SEP	OG-CB-CA	2.48	110.56	108.14

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	861	SEP	N-CA-CB-OG
2	C	861	SEP	CB-OG-P-O3P
2	C	861	SEP	CB-OG-P-O2P
2	D	861	SEP	CB-OG-P-O3P
2	D	861	SEP	N-CA-CB-OG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	861	SEP	2	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 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 (i)

6.1 Protein, DNA and RNA chains (i)

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

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

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

6.4 Ligands (i)

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

6.5 Other polymers (i)

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