



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4KHO / pdb_00004kho
Title : Structure of the FACT complex Subunit Spt16M
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Deposited on : 2013-04-30
Resolution : 2.00 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 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

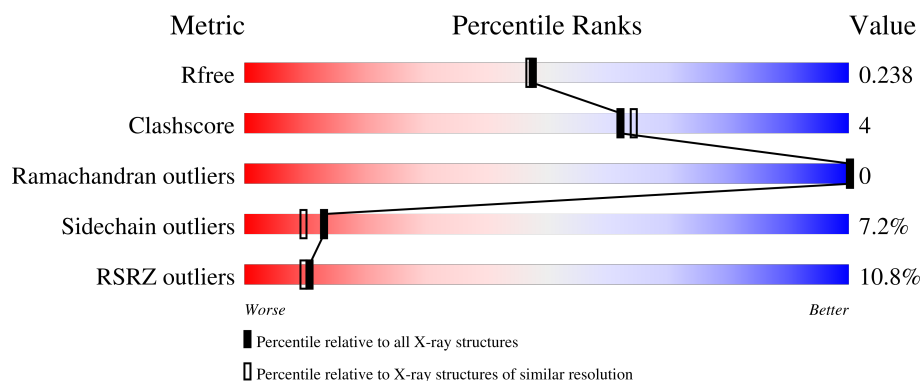
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 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 $\leq 5\%$. 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	299	9% 77% 12% 10%
1	B	299	10% 77% 8% 12%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4782 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 Uncharacterized protein Spt16M.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	S	0	0	0
			2196	1415	377	399	5			
1	B	262	Total	C	N	O	S	0	0	0
			2147	1382	370	390	5			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	647	GLY	-	expression tag	UNP G0SDN1
A	648	SER	-	expression tag	UNP G0SDN1
A	649	HIS	-	expression tag	UNP G0SDN1
A	650	MET	-	expression tag	UNP G0SDN1
B	647	GLY	-	expression tag	UNP G0SDN1
B	648	SER	-	expression tag	UNP G0SDN1
B	649	HIS	-	expression tag	UNP G0SDN1
B	650	MET	-	expression tag	UNP G0SDN1

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

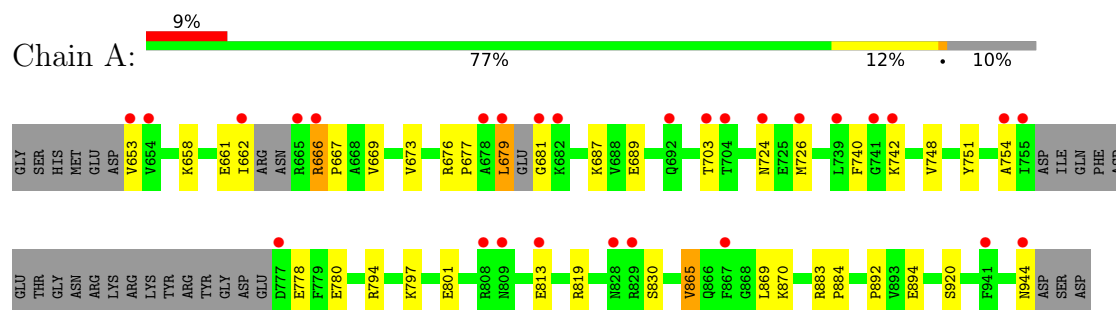
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	234	Total	O	0	0
			234	234		
4	B	196	Total	O	0	0
			196	196		

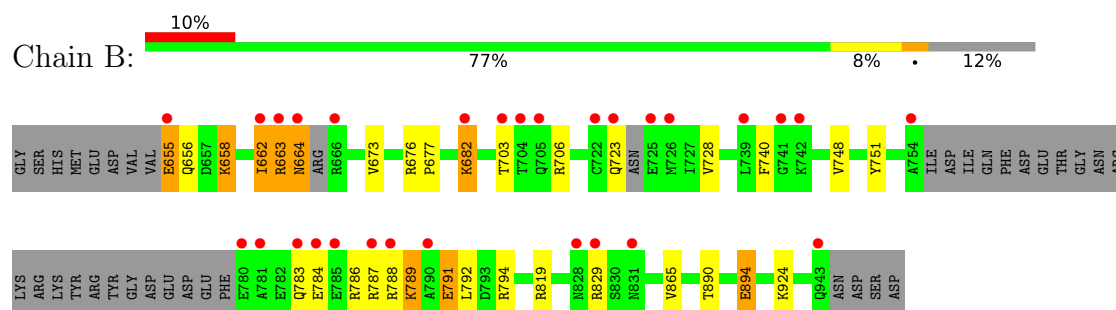
3 Residue-property plots [i](#)

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: Uncharacterized protein Spt16M



• Molecule 1: Uncharacterized protein Spt16M



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.55Å 75.03Å 142.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.14 – 2.00 45.14 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.14-2.00) 99.5 (45.14-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, R_{free}	0.208 , 0.236 0.210 , 0.238	Depositor DCC
R_{free} test set	1578 reflections (3.00%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4782	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% 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

5.1 Standard geometry

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

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	0.32	0/2245	0.75	0/3038
1	B	0.32	0/2195	0.75	0/2969
All	All	0.32	0/4440	0.75	0/6007

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

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	2196	0	2191	18	0
1	B	2147	0	2143	18	0
2	A	1	0	0	0	0
3	A	4	0	3	1	0
3	B	4	0	3	0	0
4	A	234	0	0	1	0
4	B	196	0	0	2	0
All	All	4782	0	4340	36	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 4.

All (36) 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:B:663:ARG:HD3	1:B:663:ARG:H	1.49	0.76
1:A:669:VAL:HG11	1:A:687:LYS:HE3	1.77	0.66
1:B:663:ARG:HD3	1:B:663:ARG:N	2.16	0.60
1:B:791:GLU:OE2	1:B:794:ARG:NH2	2.29	0.58
1:A:679:LEU:O	1:A:681:GLY:N	2.43	0.51
1:A:676:ARG:HG3	1:A:751:TYR:CE1	2.45	0.51
1:B:655:GLU:O	1:B:656:GLN:NE2	2.45	0.49
1:A:742:LYS:HE2	1:A:742:LYS:HB3	1.59	0.48
1:A:669:VAL:HG22	1:A:689:GLU:HG2	1.94	0.48
1:B:658:LYS:H	1:B:658:LYS:NZ	2.11	0.48
1:A:676:ARG:HA	1:A:677:PRO:C	2.39	0.47
1:B:894:GLU:OE2	4:B:1148:HOH:O	2.20	0.47
1:A:794:ARG:HH21	3:A:1002:ACT:H3	1.79	0.46
1:B:783:GLN:HB2	1:B:786:ARG:NH2	2.30	0.46
1:B:728:VAL:HG11	1:B:792:LEU:HG	1.97	0.45
1:A:661:GLU:HG2	1:A:662:ILE:N	2.31	0.45
1:A:676:ARG:HG3	1:A:751:TYR:HE1	1.82	0.45
1:B:786:ARG:NH2	4:B:1283:HOH:O	2.35	0.45
1:A:666:ARG:HA	1:A:667:PRO:HD3	1.83	0.45
1:A:778:GLU:OE2	4:A:1304:HOH:O	2.21	0.45
1:B:663:ARG:O	1:B:663:ARG:NE	2.50	0.45
1:A:797:LYS:O	1:A:801:GLU:HG2	2.17	0.44
1:A:865:VAL:HA	1:A:869:LEU:HD13	1.99	0.44
1:A:870:LYS:HE2	1:A:870:LYS:HB2	1.83	0.44
1:B:789:LYS:HB3	1:B:789:LYS:HE3	1.61	0.43
1:B:924:LYS:HB3	1:B:924:LYS:HE3	1.79	0.43
1:B:676:ARG:HA	1:B:677:PRO:C	2.43	0.43
1:A:726:MET:HG3	1:A:754:ALA:HB3	2.01	0.43
1:B:784:GLU:O	1:B:788:ARG:HG3	2.19	0.43
1:B:663:ARG:HA	1:B:664:ASN:OD1	2.18	0.42
1:B:676:ARG:HG3	1:B:751:TYR:CE1	2.55	0.42
1:B:682:LYS:N	1:B:682:LYS:HD2	2.33	0.42
1:B:662:ILE:HG12	1:B:663:ARG:HH21	1.84	0.41
1:A:883:ARG:HA	1:A:884:PRO:HD3	1.94	0.41
1:A:677:PRO:HG2	1:A:740:PHE:CE1	2.56	0.41
1:A:892:PRO:HB2	1:A:894:GLU:HG2	2.03	0.41

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	260/299 (87%)	252 (97%)	8 (3%)	0	100	100
1	B	254/299 (85%)	245 (96%)	9 (4%)	0	100	100
All	All	514/598 (86%)	497 (97%)	17 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	245/273 (90%)	230 (94%)	15 (6%)	17	14
1	B	239/273 (88%)	219 (92%)	20 (8%)	10	7
All	All	484/546 (89%)	449 (93%)	35 (7%)	13	10

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	653	VAL
1	A	658	LYS
1	A	666	ARG
1	A	673	VAL
1	A	679	LEU
1	A	703	THR
1	A	724	ASN
1	A	748	VAL

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Mol	Chain	Res	Type
1	A	780	GLU
1	A	813	GLU
1	A	819	ARG
1	A	830	SER
1	A	865	VAL
1	A	920	SER
1	A	944	ASN
1	B	655	GLU
1	B	658	LYS
1	B	662	ILE
1	B	663	ARG
1	B	664	ASN
1	B	673	VAL
1	B	682	LYS
1	B	703	THR
1	B	706	ARG
1	B	723	GLN
1	B	740	PHE
1	B	748	VAL
1	B	787	ARG
1	B	789	LYS
1	B	791	GLU
1	B	819	ARG
1	B	829	ARG
1	B	865	VAL
1	B	890	THR
1	B	894	GLU

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

Mol	Chain	Res	Type
1	A	692	GLN
1	B	656	GLN
1	B	866	GLN
1	B	932	GLN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
3	ACT	B	1001	-	3,3,3	0.79	0	3,3,3	1.35	0
3	ACT	A	1002	-	3,3,3	0.80	0	3,3,3	1.33	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1002	ACT	1	0

5.7 Other polymers [i](#)

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	268/299 (89%)	0.65	28 (10%)	11 10	25, 37, 59, 70	0
1	B	262/299 (87%)	0.67	29 (11%)	10 9	22, 36, 69, 90	0
All	All	530/598 (88%)	0.66	57 (10%)	11 10	22, 37, 65, 90	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	755	ILE	5.3
1	A	724	ASN	4.4
1	B	725	GLU	4.1
1	B	754	ALA	4.0
1	B	726	MET	4.0
1	B	787	ARG	4.0
1	B	783	GLN	3.9
1	B	704	THR	3.9
1	A	704	THR	3.8
1	A	741	GLY	3.6
1	A	829	ARG	3.6
1	B	781	ALA	3.6
1	B	739	LEU	3.5
1	A	681	GLY	3.4
1	B	664	ASN	3.2
1	A	813	GLU	3.1
1	A	678	ALA	3.1
1	B	655	GLU	3.1
1	A	742	LYS	3.1
1	B	829	ARG	2.9
1	A	754	ALA	2.9
1	B	785	GLU	2.8
1	B	943	GLN	2.8
1	B	780	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	722	CYS	2.7
1	A	739	LEU	2.7
1	A	665	ARG	2.7
1	B	741	GLY	2.7
1	B	705	GLN	2.6
1	B	663	ARG	2.6
1	A	944	ASN	2.5
1	B	784	GLU	2.5
1	B	828	ASN	2.5
1	A	808	ARG	2.4
1	B	742	LYS	2.4
1	A	654	VAL	2.4
1	A	666	ARG	2.4
1	B	790	ALA	2.3
1	A	679	LEU	2.3
1	A	653	VAL	2.3
1	A	703	THR	2.3
1	A	809	ASN	2.3
1	A	662	ILE	2.3
1	A	726	MET	2.2
1	B	723	GLN	2.2
1	B	666	ARG	2.2
1	B	682	LYS	2.2
1	A	777	ASP	2.2
1	A	941	PHE	2.1
1	B	703	THR	2.1
1	B	788	ARG	2.1
1	B	831	ASN	2.1
1	A	692	GLN	2.1
1	B	662	ILE	2.1
1	A	867	PHE	2.1
1	A	828	ASN	2.0
1	A	682	LYS	2.0

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	ACT	B	1001	4/4	0.74	0.24	38,46,46,48	0
3	ACT	A	1002	4/4	0.88	0.15	34,35,38,42	0
2	CA	A	1001	1/1	0.97	0.04	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.