



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 6YZY / pdb_00006yzy
Title : Crystal structure of the M295V variant of Ssl1
Authors : Mielenbrink, S.; Olbrich, A.; Urlacher, V.; Span, I.
Deposited on : 2020-05-07
Resolution : 2.28 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	:	4-5-2 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

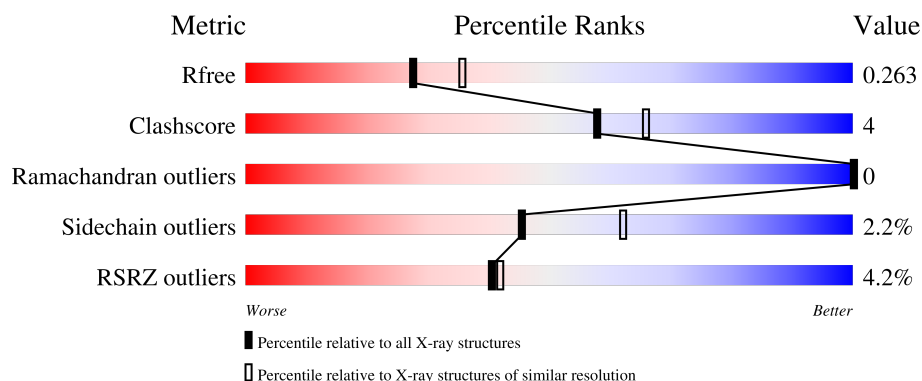
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	AAA	325	5% 73% 9% • 17%
1	BBB	325	4% 73% 10% 17%
1	CCC	325	2% 72% 10% • 17%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12346 atoms, of which 5985 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 Copper oxidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AAA	270	Total	C	H	N	O	S	96	0	0
			4093	1309	1998	383	394	9			
1	BBB	269	Total	C	H	N	O	S	97	0	0
			4078	1304	1992	382	391	9			
1	CCC	270	Total	C	H	N	O	S	96	0	0
			4085	1306	1995	383	392	9			

There are 24 discrepancies between the modelled and reference sequences:

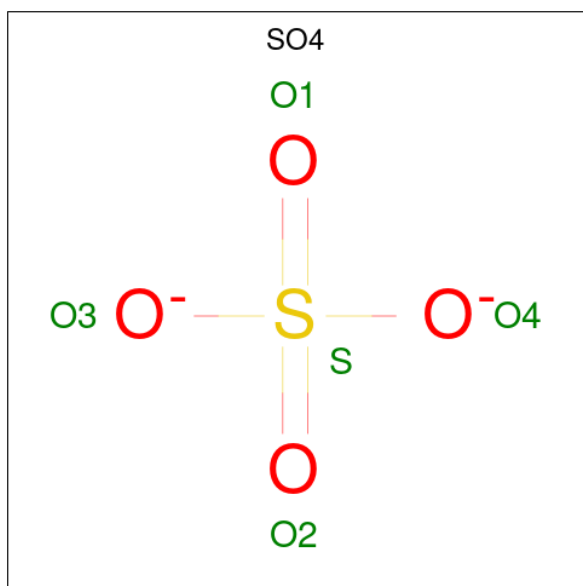
Chain	Residue	Modelled	Actual	Comment	Reference
AAA	1	MET	-	initiating methionine	UNP B5HSR1
AAA	2	HIS	-	expression tag	UNP B5HSR1
AAA	3	HIS	-	expression tag	UNP B5HSR1
AAA	4	HIS	-	expression tag	UNP B5HSR1
AAA	5	HIS	-	expression tag	UNP B5HSR1
AAA	6	HIS	-	expression tag	UNP B5HSR1
AAA	7	HIS	-	expression tag	UNP B5HSR1
AAA	295	VAL	MET	engineered mutation	UNP B5HSR1
BBB	1	MET	-	initiating methionine	UNP B5HSR1
BBB	2	HIS	-	expression tag	UNP B5HSR1
BBB	3	HIS	-	expression tag	UNP B5HSR1
BBB	4	HIS	-	expression tag	UNP B5HSR1
BBB	5	HIS	-	expression tag	UNP B5HSR1
BBB	6	HIS	-	expression tag	UNP B5HSR1
BBB	7	HIS	-	expression tag	UNP B5HSR1
BBB	295	VAL	MET	engineered mutation	UNP B5HSR1
CCC	1	MET	-	initiating methionine	UNP B5HSR1
CCC	2	HIS	-	expression tag	UNP B5HSR1
CCC	3	HIS	-	expression tag	UNP B5HSR1
CCC	4	HIS	-	expression tag	UNP B5HSR1
CCC	5	HIS	-	expression tag	UNP B5HSR1
CCC	6	HIS	-	expression tag	UNP B5HSR1
CCC	7	HIS	-	expression tag	UNP B5HSR1

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Chain	Residue	Modelled	Actual	Comment	Reference
CCC	295	VAL	MET	engineered mutation	UNP B5HSR1

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	AAA	1	Total O S 5 4 1	0	0
2	BBB	1	Total O S 5 4 1	0	0
2	CCC	1	Total O S 5 4 1	0	0
2	CCC	1	Total O S 5 4 1	0	0

- Molecule 3 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AAA	4	Total Cu 4 4	0	0
3	BBB	3	Total Cu 3 3	0	0
3	CCC	3	Total Cu 3 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	18	Total 18	O 18	0	0
4	BBB	16	Total 16	O 16	0	0
4	CCC	26	Total 26	O 26	0	0

GLN
ARG
ALA
GLU
HIS
HIS
HIS

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.35Å 103.96Å 161.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.99 – 2.28 48.99 – 2.28	Depositor EDS
% Data completeness (in resolution range)	98.6 (48.99-2.28) 98.7 (48.99-2.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.227 , 0.285 (Not available) , 0.263	Depositor DCC
R_{free} test set	1994 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	32.8	Xtriage
Anisotropy	0.302	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 25.2	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	0.93	EDS
Total number of atoms	12346	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 3.90% 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: SO4, CU

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	AAA	1.04	1/2153 (0.0%)	1.34	3/2922 (0.1%)
1	BBB	1.06	1/2144 (0.0%)	1.30	0/2910
1	CCC	1.03	0/2148	1.29	0/2915
All	All	1.04	2/6445 (0.0%)	1.31	3/8747 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	71	ILE	N-CA	5.34	1.50	1.45
1	BBB	248	PRO	C-O	-5.11	1.18	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	126	THR	CB-CA-C	6.07	120.49	110.78
1	AAA	163	THR	CA-C-N	5.33	125.75	119.94
1	AAA	163	THR	C-N-CA	5.33	125.75	119.94

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	AAA	2095	1998	1978	23	0
1	BBB	2086	1992	1972	19	0
1	CCC	2090	1995	1975	24	0
2	AAA	5	0	0	0	0
2	BBB	5	0	0	0	0
2	CCC	10	0	0	0	0
3	AAA	4	0	0	0	0
3	BBB	3	0	0	0	0
3	CCC	3	0	0	0	0
4	AAA	18	0	0	0	0
4	BBB	16	0	0	0	0
4	CCC	26	0	0	1	0
All	All	6361	5985	5925	55	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.

The worst 5 of 55 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:AAA:201:PRO:O	1:AAA:204:SER:OG	1.64	1.15
1:AAA:53:GLU:OE1	1:AAA:67:GLY:N	2.22	0.69
1:AAA:289:SER:N	1:CCC:225:GLU:OE2	2.24	0.65
1:BBB:86:ILE:O	1:BBB:126:THR:HA	2.01	0.61
1:AAA:201:PRO:C	1:AAA:204:SER:OG	2.45	0.58

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	AAA	268/325 (82%)	249 (93%)	19 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BBB	267/325 (82%)	254 (95%)	13 (5%)	0	100	100
1	CCC	268/325 (82%)	256 (96%)	12 (4%)	0	100	100
All	All	803/975 (82%)	759 (94%)	44 (6%)	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	AAA	217/256 (85%)	214 (99%)	3 (1%)	59	74
1	BBB	216/256 (84%)	212 (98%)	4 (2%)	50	66
1	CCC	216/256 (84%)	209 (97%)	7 (3%)	34	49
All	All	649/768 (84%)	635 (98%)	14 (2%)	45	62

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	CCC	99	HIS
1	CCC	107	VAL
1	CCC	311	TYR
1	CCC	227	TYR
1	CCC	236	ARG

Sometimes 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 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 14 ligands modelled in this entry, 10 are monoatomic - leaving 4 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	$\# Z > 2$
2	SO4	AAA	401	-	4,4,4	0.36	0	6,6,6	0.10	0
2	SO4	CCC	401	-	4,4,4	0.28	0	6,6,6	0.09	0
2	SO4	CCC	402	-	4,4,4	0.30	0	6,6,6	0.11	0
2	SO4	BBB	401	-	4,4,4	0.29	0	6,6,6	0.08	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.

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 ⓘ

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	AAA	270/325 (83%)	0.40	16 (5%) 28 29	23, 37, 67, 99	14 (5%)
1	BBB	269/325 (82%)	0.33	12 (4%) 38 39	25, 40, 69, 97	13 (4%)
1	CCC	270/325 (83%)	-0.06	6 (2%) 62 64	17, 30, 50, 81	12 (4%)
All	All	809/975 (82%)	0.22	34 (4%) 40 42	17, 36, 65, 99	39 (4%)

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	203	HIS	5.1
1	AAA	56	ALA	5.0
1	BBB	204	SER	3.8
1	BBB	202	ALA	3.8
1	BBB	205	GLY	3.7

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 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
2	SO4	CCC	402	5/5	0.86	0.12	59,60,62,64	0
2	SO4	BBB	401	5/5	0.92	0.09	50,60,61,62	0
2	SO4	AAA	401	5/5	0.93	0.09	52,53,57,64	0
2	SO4	CCC	401	5/5	0.94	0.07	47,49,50,51	0
3	CU	AAA	402	1/1	0.95	0.07	101,101,101,101	0
3	CU	BBB	404	1/1	0.98	0.03	37,37,37,37	0
3	CU	BBB	402	1/1	0.99	0.03	35,35,35,35	0
3	CU	BBB	403	1/1	0.99	0.03	44,44,44,44	0
3	CU	AAA	405	1/1	0.99	0.03	45,45,45,45	0
3	CU	CCC	404	1/1	0.99	0.03	37,37,37,37	0
3	CU	CCC	405	1/1	0.99	0.02	40,40,40,40	0
3	CU	CCC	403	1/1	1.00	0.03	27,27,27,27	0
3	CU	AAA	403	1/1	1.00	0.03	33,33,33,33	0
3	CU	AAA	404	1/1	1.00	0.01	26,26,26,26	0

6.5 Other polymers ⓘ

There are no such residues in this entry.