Full wwPDB X-ray Structure Validation Report ⓘ

Sep 6, 2022 – 08:08 AM JST

PDB ID	:	7EL5
Title	:	Crystal structure of Sizzled protein from Xenopus Laevis
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Deposited on	:	2021-04-08
Resolution	:	1.95 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:

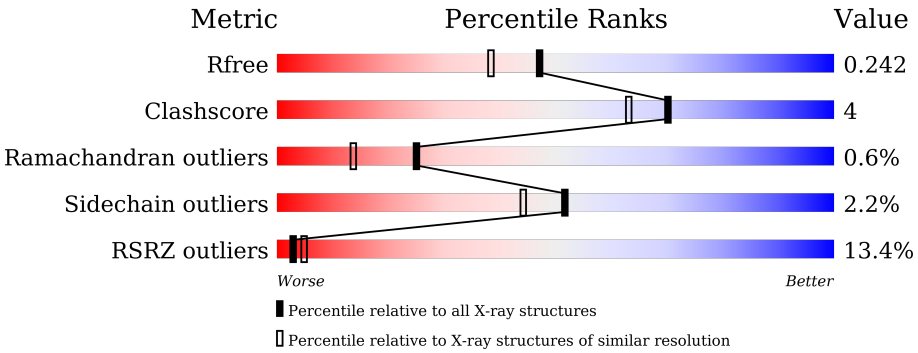
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.30
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.30

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 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 <=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	275	12% 76% 9% 15%
1	B	275	12% 76% 12% 12%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3880 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 Secreted Xwnt8 inhibitor sizzled.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	235	Total	C	N	O	S	0	0	0
			1840	1166	321	329	24			
1	B	241	Total	C	N	O	S	0	1	0
			1916	1214	336	342	24			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	GLU	-	expression tag	UNP O73821
A	17	THR	-	expression tag	UNP O73821
A	18	GLY	-	expression tag	UNP O73821
A	248	ASP	GLU	conflict	UNP O73821
A	282	GLY	-	expression tag	UNP O73821
A	283	THR	-	expression tag	UNP O73821
A	284	LYS	-	expression tag	UNP O73821
A	285	HIS	-	expression tag	UNP O73821
A	286	HIS	-	expression tag	UNP O73821
A	287	HIS	-	expression tag	UNP O73821
A	288	HIS	-	expression tag	UNP O73821
A	289	HIS	-	expression tag	UNP O73821
A	290	HIS	-	expression tag	UNP O73821
B	16	GLU	-	expression tag	UNP O73821
B	17	THR	-	expression tag	UNP O73821
B	18	GLY	-	expression tag	UNP O73821
B	248	ASP	GLU	conflict	UNP O73821
B	282	GLY	-	expression tag	UNP O73821
B	283	THR	-	expression tag	UNP O73821
B	284	LYS	-	expression tag	UNP O73821
B	285	HIS	-	expression tag	UNP O73821
B	286	HIS	-	expression tag	UNP O73821
B	287	HIS	-	expression tag	UNP O73821
B	288	HIS	-	expression tag	UNP O73821
B	289	HIS	-	expression tag	UNP O73821

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Chain	Residue	Modelled	Actual	Comment	Reference
B	290	HIS	-	expression tag	UNP O73821

- Molecule 2 is water.

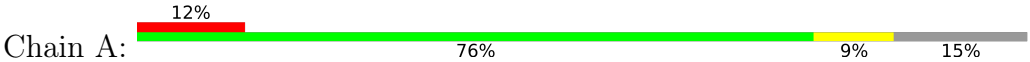
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	64	Total O 64 64	0	0
2	B	60	Total O 60 60	0	0

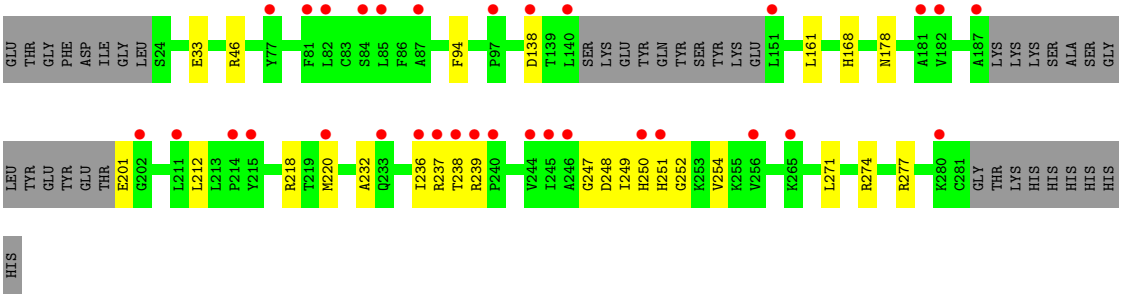
3 Residue-property plots (i)

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: Secreted Xwnt8 inhibitor sizzled

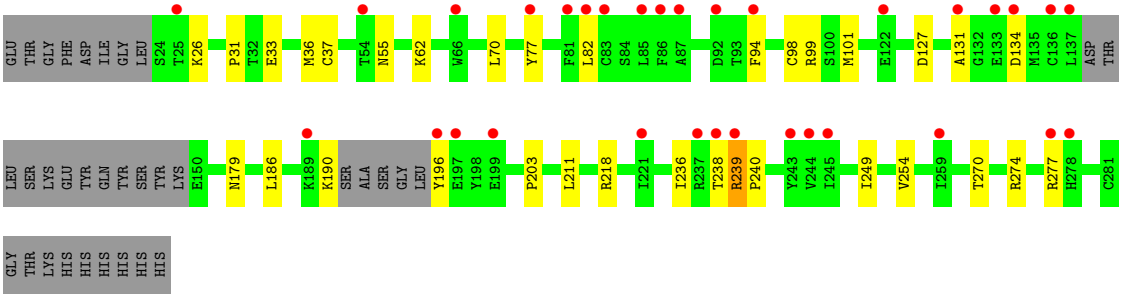
Chain A:





• Molecule 1: Secreted Xwnt8 inhibitor sizzled

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	63.88Å 77.48Å 107.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.91 – 1.95 19.91 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.0 (19.91-1.95) 98.9 (19.91-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.50 (at 1.94Å)	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
R, R_{free}	0.205 , 0.243 0.206 , 0.242	Depositor DCC
R_{free} test set	1957 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	36.0	Xtriage
Anisotropy	0.673	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 49.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3880	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.63% 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

5.1 Standard geometry

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	0/1885	0.65	2/2559 (0.1%)
1	B	0.39	0/1967	0.61	0/2666
All	All	0.41	0/3852	0.63	2/5225 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	161	LEU	CA-CB-CG	6.38	129.97	115.30
1	A	161	LEU	CB-CG-CD2	-5.89	100.98	111.00

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	1840	0	1789	11	0
1	B	1916	0	1867	16	0
2	A	64	0	0	1	0
2	B	60	0	0	1	0
All	All	3880	0	3656	27	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 (27) 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:201:GLU:O	1:A:218:ARG:NH1	2.02	0.92
1:A:232:ALA:O	1:A:236:ILE:HG12	1.90	0.72
1:B:190:LYS:HA	1:B:196:TYR:HA	1.79	0.64
1:A:138:ASP:OD1	2:A:301:HOH:O	2.15	0.64
1:B:98:CYS:SG	2:B:341:HOH:O	2.56	0.61
1:A:212:LEU:HD11	1:A:249:ILE:HD12	1.85	0.58
1:B:36:MET:HG2	1:B:37:CYS:SG	2.44	0.57
1:B:186:LEU:HB3	1:B:236:ILE:HD11	1.92	0.52
1:B:134:ASP:OD1	1:B:134:ASP:N	2.41	0.50
1:B:179:ASN:HD21	1:B:211:LEU:HD22	1.77	0.50
1:B:270:THR:O	1:B:274:ARG:HG3	2.12	0.50
1:A:168:HIS:CG	1:A:271:LEU:HD23	2.47	0.49
1:B:239:ARG:HG2	1:B:240:PRO:HD2	1.96	0.48
1:B:31:PRO:HB2	1:B:33:GLU:HG2	1.96	0.47
1:B:203:PRO:HA	1:B:218:ARG:HD2	1.96	0.47
1:A:238:THR:HG22	1:A:239:ARG:HA	1.98	0.46
1:A:220:MET:SD	1:A:254:VAL:HG21	2.55	0.46
1:B:99:ARG:HE	1:B:131:ALA:HB2	1.81	0.45
1:B:99:ARG:NH1	1:B:127:ASP:HA	2.32	0.45
1:B:249:ILE:HG12	1:B:254:VAL:HG22	1.99	0.45
1:A:46:ARG:HD3	1:A:94:PHE:CE1	2.54	0.43
1:B:77:TYR:HB3	1:B:101:MET:HE3	2.01	0.42
1:A:178:ASN:HB3	1:A:247:GLY:O	2.20	0.42
1:A:251:HIS:HA	1:A:252:GLY:HA2	1.78	0.42
1:B:238:THR:HA	1:B:239:ARG:HA	1.87	0.41
1:B:70:LEU:HD21	1:B:82:LEU:HD12	2.03	0.41
1:A:238:THR:CG2	1:A:239:ARG:HA	2.52	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	229/275 (83%)	219 (96%)	8 (4%)	2 (1%)	17 8
1	B	236/275 (86%)	231 (98%)	4 (2%)	1 (0%)	34 22
All	All	465/550 (84%)	450 (97%)	12 (3%)	3 (1%)	25 14

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	237	ARG
1	B	239	ARG
1	A	250	HIS

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	205/245 (84%)	201 (98%)	4 (2%)	55 48
1	B	214/245 (87%)	209 (98%)	5 (2%)	50 42
All	All	419/490 (86%)	410 (98%)	9 (2%)	52 46

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	GLU
1	A	248	ASP
1	A	274	ARG
1	A	277	ARG
1	B	26	LYS
1	B	55	ASN
1	B	62	LYS
1	B	94	PHE
1	B	277	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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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, 95^{th} 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	235/275 (85%)	0.84	32 (13%)	3	4	30, 41, 68, 92	0
1	B	241/275 (87%)	0.79	32 (13%)	3	5	28, 44, 74, 87	0
All	All	476/550 (86%)	0.82	64 (13%)	3	5	28, 43, 72, 92	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	LEU	8.0
1	A	202	GLY	6.9
1	B	94	PHE	6.6
1	A	215	TYR	5.3
1	A	238	THR	4.8
1	B	239	ARG	4.6
1	A	250	HIS	4.6
1	B	77	TYR	4.5
1	A	236	ILE	4.4
1	B	82	LEU	3.8
1	B	134	ASP	3.8
1	B	25	THR	3.7
1	B	189	LYS	3.7
1	B	83	CYS	3.7
1	B	278	HIS	3.7
1	B	238	THR	3.6
1	B	85	LEU	3.6
1	A	181	ALA	3.5
1	B	122	GLU	3.5
1	B	197	GLU	3.4
1	A	244	VAL	3.4
1	B	237	ARG	3.3
1	A	251	HIS	3.3
1	A	239	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	245	ILE	3.2
1	A	237	ARG	3.2
1	A	187	ALA	3.0
1	B	245	ILE	2.9
1	B	137	LEU	2.9
1	B	92	ASP	2.9
1	A	211	LEU	2.9
1	B	87	ALA	2.8
1	A	214	PRO	2.8
1	A	81	PHE	2.7
1	B	54	THR	2.7
1	A	85	LEU	2.7
1	A	97	PRO	2.7
1	A	82	LEU	2.7
1	B	81	PHE	2.7
1	B	86	PHE	2.7
1	B	243	TYR	2.6
1	A	151	LEU	2.6
1	B	277	ARG	2.6
1	B	244	VAL	2.6
1	B	199	GLU	2.6
1	A	233	GLN	2.6
1	A	77	TYR	2.6
1	B	259	ILE	2.5
1	B	66	TRP	2.5
1	B	221	ILE	2.5
1	A	246	ALA	2.5
1	A	256	VAL	2.4
1	B	131	ALA	2.4
1	A	280	LYS	2.3
1	B	136	CYS	2.2
1	A	182	VAL	2.2
1	B	196	TYR	2.2
1	A	84	SER	2.2
1	A	87	ALA	2.2
1	A	240	PRO	2.1
1	A	265	LYS	2.1
1	B	133	GLU	2.1
1	A	138	ASP	2.0
1	A	220	MET	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.