Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 09:17 pm BST

PDB ID	:	4KGO
Title	:	Crystal Structure of double Leucine to Methionine mutant human splunc1 lacking the secretion signal sequence
Authors	:	Betts, L.; Walton, W.G.
Deposited on	:	2013-04-29
Resolution	:	3.19 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 following versions of software and data (see references ⓘ) were used in the production of this report:

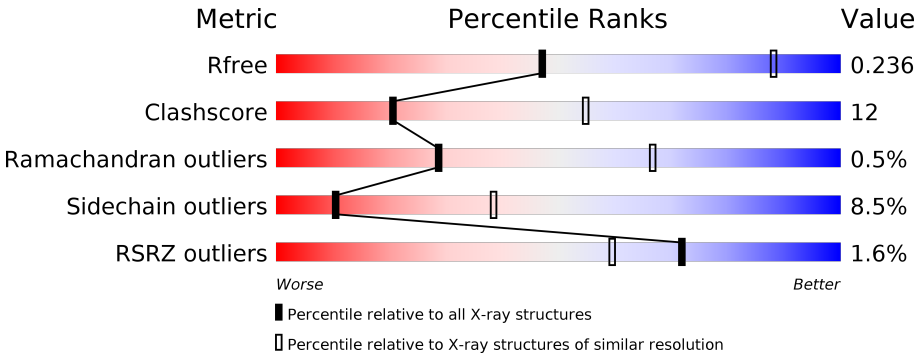
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 3.19 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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% 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	240	2% 58% 17% • 24%
1	B	240	56% 26% • 15%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2735 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 BPI fold-containing family A member 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	203	Total	C	N	O	S	Se	0	0	0
			1459	932	248	274	2	3			
1	A	183	Total	C	N	O	S	Se	0	0	0
			1276	817	214	240	2	3			

There are 10 discrepancies between the modelled and reference sequences:

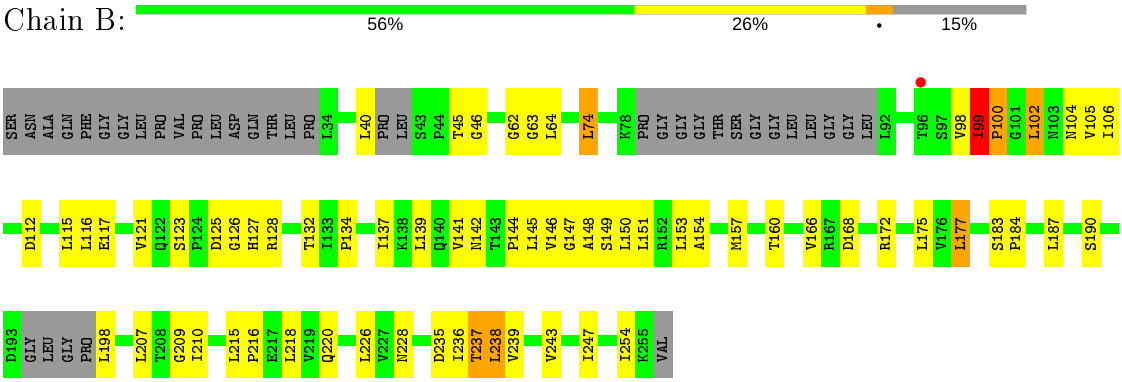
Chain	Residue	Modelled	Actual	Comment	Reference
B	17	SER	-	EXPRESSION TAG	UNP Q9NP55
B	18	ASN	-	EXPRESSION TAG	UNP Q9NP55
B	68	MSE	LEU	ENGINEERED MUTATION	UNP Q9NP55
B	105	VAL	ILE	SEE REMARK 999	UNP Q9NP55
B	157	MSE	LEU	ENGINEERED MUTATION	UNP Q9NP55
A	17	SER	-	EXPRESSION TAG	UNP Q9NP55
A	18	ASN	-	EXPRESSION TAG	UNP Q9NP55
A	68	MSE	LEU	ENGINEERED MUTATION	UNP Q9NP55
A	105	VAL	ILE	SEE REMARK 999	UNP Q9NP55
A	157	MSE	LEU	ENGINEERED MUTATION	UNP Q9NP55

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 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.

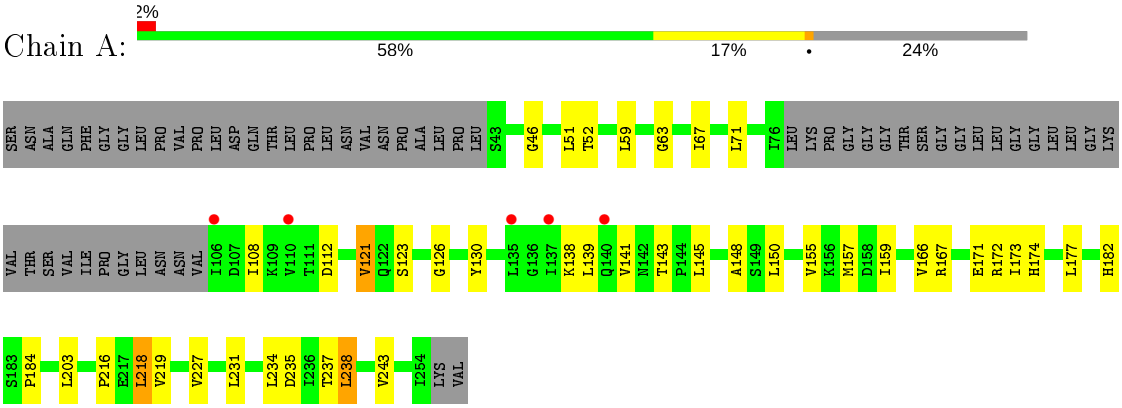
- Molecule 1: BPI fold-containing family A member 1

Chain B:



- Molecule 1: BPI fold-containing family A member 1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α, β, γ	151.83Å 151.83Å 35.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.01 – 3.19 48.01 – 3.19	Depositor EDS
% Data completeness (in resolution range)	97.0 (48.01-3.19) 91.4 (48.01-3.19)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.24 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.7.1_743	Depositor
R, R_{free}	0.229 , 0.256 0.217 , 0.236	Depositor DCC
R_{free} test set	702 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	97.7	Xtriage
Anisotropy	0.518	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 102.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	2735	wwPDB-VP
Average B, all atoms (Å^2)	132.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.31% 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	0.28	0/1287	0.45	0/1759
1	B	0.36	1/1469 (0.1%)	0.49	1/2000 (0.1%)
All	All	0.32	1/2756 (0.0%)	0.47	1/3759 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	100	PRO	N-CD	5.02	1.54	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	99	ILE	C-N-CD	5.95	140.90	128.40

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	1276	0	1281	24	0
1	B	1459	0	1501	45	1
All	All	2735	0	2782	68	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 12.

All (68) 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:99:ILE:HB	1:B:100:PRO:HD2	1.58	0.84
1:B:40:LEU:H	1:B:117:GLU:HG3	1.45	0.81
1:B:102:LEU:O	1:B:105:VAL:HG22	1.80	0.81
1:B:98:VAL:HG12	1:B:99:ILE:HD12	1.65	0.79
1:B:116:LEU:HB2	1:B:134:PRO:HB2	1.71	0.72
1:A:108:ILE:HG12	1:A:141:VAL:HG12	1.75	0.68
1:B:99:ILE:HB	1:B:100:PRO:CD	2.26	0.66
1:B:102:LEU:HD23	1:B:210:ILE:HG13	1.79	0.64
1:B:157:MSE:HE1	1:B:216:PRO:HA	1.78	0.64
1:A:143:THR:OG1	1:A:148:ALA:O	2.15	0.64
1:B:99:ILE:HG22	1:B:100:PRO:CD	2.29	0.63
1:B:177:LEU:HD12	1:B:228:ASN:HB2	1.81	0.62
1:A:235:ASP:HB3	1:A:238:LEU:HB2	1.81	0.62
1:B:99:ILE:HG22	1:B:100:PRO:HD3	1.81	0.62
1:B:175:LEU:HG	1:B:239:VAL:HG13	1.83	0.60
1:A:172:ARG:O	1:A:173:ILE:HG22	2.01	0.60
1:A:173:ILE:HD11	1:A:243:VAL:HG11	1.83	0.60
1:A:235:ASP:OD1	1:A:237:THR:OG1	2.17	0.58
1:B:105:VAL:HG23	1:B:105:VAL:O	2.03	0.57
1:A:166:VAL:O	1:A:173:ILE:HA	2.04	0.57
1:B:98:VAL:CG1	1:B:99:ILE:HD12	2.32	0.57
1:A:173:ILE:HG12	1:A:173:ILE:O	2.07	0.55
1:B:45:THR:OG1	1:B:46:GLY:N	2.40	0.55
1:B:62:GLY:N	1:B:63:GLY:HA2	2.21	0.54
1:B:99:ILE:CG2	1:B:100:PRO:CD	2.86	0.54
1:B:98:VAL:C	1:B:99:ILE:HD12	2.28	0.54
1:B:99:ILE:CB	1:B:100:PRO:CD	2.85	0.54
1:B:123:SER:HB2	1:B:128:ARG:HB2	1.90	0.53
1:B:168:ASP:OD1	1:B:172:ARG:HG2	2.10	0.52
1:B:139:LEU:HB2	1:B:153:LEU:HB2	1.92	0.51
1:B:160:THR:HG23	1:B:183:SER:HB2	1.93	0.51
1:B:235:ASP:HB3	1:B:238:LEU:HB2	1.93	0.51
1:A:157:MSE:HE3	1:A:219:VAL:HG21	1.93	0.51
1:A:121:VAL:HG23	1:A:130:TYR:HB2	1.93	0.50
1:B:237:THR:HG23	1:A:46:GLY:H	1.76	0.50
1:A:231:LEU:HA	1:A:234:LEU:HD13	1.92	0.50
1:B:243:VAL:O	1:B:247:ILE:HG12	2.12	0.50
1:A:173:ILE:HG23	1:A:173:ILE:O	2.12	0.50
1:A:172:ARG:CB	1:A:174:HIS:CE1	2.96	0.48
1:A:123:SER:O	1:A:126:GLY:N	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:ASP:HB2	1:A:138:LYS:HB2	1.96	0.47
1:A:182:HIS:CG	1:A:216:PRO:HB3	2.49	0.47
1:B:74:LEU:HD23	1:B:74:LEU:HA	1.73	0.47
1:B:142:ASN:ND2	1:B:150:LEU:HD23	2.29	0.46
1:B:236:ILE:HD12	1:B:236:ILE:H	1.81	0.46
1:B:132:THR:O	1:B:134:PRO:HD3	2.16	0.45
1:B:141:VAL:HG11	1:B:207:LEU:HD11	1.99	0.45
1:B:99:ILE:CB	1:B:100:PRO:HD2	2.36	0.45
1:B:125:ASP:OD1	1:B:126:GLY:N	2.49	0.45
1:B:141:VAL:HB	1:B:151:LEU:HB2	1.99	0.44
1:A:167:ARG:HG3	1:A:171:GLU:HA	2.00	0.44
1:B:146:VAL:HA	1:B:147:GLY:HA2	1.41	0.43
1:B:106:ILE:HD11	1:B:144:PRO:HB3	2.00	0.43
1:B:45:THR:HG1	1:B:46:GLY:H	1.62	0.42
1:B:98:VAL:HG12	1:B:99:ILE:CD1	2.41	0.42
1:A:177:LEU:HD11	1:A:227:VAL:HB	2.01	0.42
1:A:59:LEU:HD21	1:A:227:VAL:HG22	2.01	0.42
1:A:145:LEU:HD12	1:A:203:LEU:HG	2.01	0.42
1:A:159:ILE:HD11	1:A:219:VAL:HG12	2.02	0.41
1:A:63:GLY:O	1:A:67:ILE:HG12	2.20	0.41
1:B:125:ASP:OD1	1:B:127:HIS:N	2.47	0.41
1:B:183:SER:HA	1:B:184:PRO:HD3	1.89	0.41
1:B:215:LEU:HD23	1:B:215:LEU:HA	1.90	0.41
1:B:148:ALA:O	1:B:149:SER:HB2	2.21	0.41
1:B:254:ILE:H	1:B:254:ILE:HG13	1.64	0.41
1:B:154:ALA:HB3	1:B:190:SER:HB2	2.02	0.41
1:B:216:PRO:O	1:B:220:GLN:HB3	2.21	0.41
1:A:71:LEU:HD22	1:A:218:LEU:HD22	2.03	0.40

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:B:104:ASN:OD1	1:B:209:GLY:CA[3_455]	2.00	0.20

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	179/240 (75%)	166 (93%)	12 (7%)	1 (1%)	25 64
1	B	195/240 (81%)	182 (93%)	12 (6%)	1 (0%)	29 67
All	All	374/480 (78%)	348 (93%)	24 (6%)	2 (0%)	29 67

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	99	ILE
1	A	184	PRO

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	135/199 (68%)	127 (94%)	8 (6%)	19 54
1	B	160/199 (80%)	143 (89%)	17 (11%)	6 27
All	All	295/398 (74%)	270 (92%)	25 (8%)	10 38

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	64	LEU
1	B	74	LEU
1	B	99	ILE
1	B	102	LEU

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Mol	Chain	Res	Type
1	B	112	ASP
1	B	115	LEU
1	B	121	VAL
1	B	137	ILE
1	B	145	LEU
1	B	166	VAL
1	B	177	LEU
1	B	187	LEU
1	B	198	LEU
1	B	218	LEU
1	B	226	LEU
1	B	237	THR
1	B	238	LEU
1	A	51	LEU
1	A	52	THR
1	A	121	VAL
1	A	139	LEU
1	A	150	LEU
1	A	155	VAL
1	A	218	LEU
1	A	238	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	140	GLN
1	B	142	ASN

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 carbohydrates 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	180/240 (75%)	0.07	5 (2%)	53	37	95, 146, 192, 206	0
1	B	200/240 (83%)	-0.08	1 (0%)	91	86	79, 119, 167, 225	0
All	All	380/480 (79%)	-0.01	6 (1%)	72	59	79, 130, 183, 225	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	96	THR	3.3
1	A	110	VAL	3.3
1	A	135	LEU	2.9
1	A	137	ILE	2.2
1	A	140	GLN	2.2
1	A	106	ILE	2.1

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 carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.