



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 3, 2020 – 07:20 pm BST

PDB ID : 5LUM
Title : Alpha-crystallin domain of human HSPB6 patched with its N-terminal peptide
Authors : Sluchanko, N.N.; Beelen, S.; Kulikova, A.A.; Weeks, S.D.; Antson, A.A.; Gusev, N.B.; Strelkov, S.V.
Deposited on : 2016-09-09
Resolution : 2.60 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 : **FAILED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

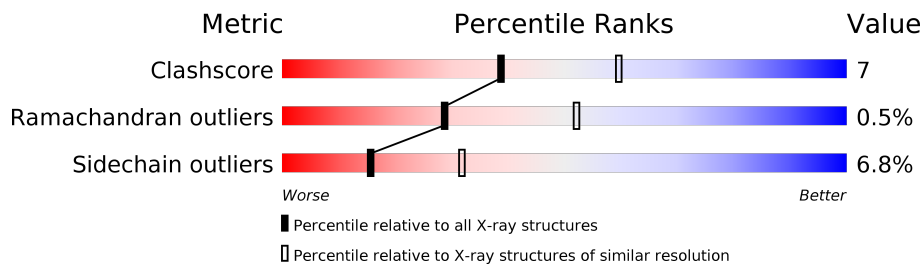
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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))
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)



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 $\leq 5\%$.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	F	9	
1	G	9	
1	H	9	
1	I	9	
1	J	9	
2	A	78	
2	B	78	
2	C	78	

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Mol	Chain	Length	Quality of chain
2	D	78	 85% 13%
2	E	78	 90% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3416 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 Heat shock protein beta-6.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	F	9	67	44	10	13	0	0	0
1	G	9	67	44	10	13	0	0	0
1	H	9	67	44	10	13	0	0	0
1	I	9	67	44	10	13	0	0	0
1	J	9	67	44	10	13	0	0	0

- Molecule 2 is a protein called Heat shock protein beta-6.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	A	78	615	390	115	110	0	1	0
2	B	78	608	385	113	110	0	0	0
2	C	78	608	385	113	110	0	0	0
2	D	78	608	385	113	110	0	0	0
2	E	78	608	385	113	110	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.


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

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.

Note EDS failed to run properly.

- Molecule 1: Heat shock protein beta-6

Chain F:  78% 22%



- Molecule 1: Heat shock protein beta-6

Chain G:  44% 44% 11%



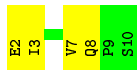
- Molecule 1: Heat shock protein beta-6

Chain H:  78% 22%



- Molecule 1: Heat shock protein beta-6

Chain I:  56% 44%




- Molecule 1: Heat shock protein beta-6

Chain J:  67% 33%



- Molecule 2: Heat shock protein beta-6

Chain A:  86% 14%



• Molecule 2: Heat shock protein beta-6

Chain B:  62% 37%




• Molecule 2: Heat shock protein beta-6

Chain C:  68% 29%



• Molecule 2: Heat shock protein beta-6

Chain D:  85% 13%



• Molecule 2: Heat shock protein beta-6

Chain E:  90% 10%



4 Data and refinement statistics i

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	105.69Å 105.69Å 111.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.61 – 2.60	Depositor
% Data completeness (in resolution range)	100.0 (28.61-2.60)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 2.61Å)	Xtrriage
Refinement program	BUSTER-TNT 2.10.2	Depositor
R, R_{free}	0.207 , 0.227	Depositor
Wilson B-factor (Å ²)	82.5	Xtrriage
Anisotropy	0.357	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.036 for -h,-k,l	Xtrriage
Total number of atoms	3416	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	F	0.55	0/69	0.77	0/96
1	G	0.69	0/69	1.01	0/96
1	H	0.57	0/69	0.94	0/96
1	I	0.57	0/69	0.78	0/96
1	J	0.58	0/69	0.77	0/96
2	A	0.54	0/637	0.80	0/867
2	B	0.53	0/626	0.78	0/852
2	C	0.53	0/626	0.76	0/852
2	D	0.48	0/626	0.75	0/852
2	E	0.45	0/626	0.72	0/852
All	All	0.52	0/3486	0.77	0/4755

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 [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	F	67	0	68	1	0
1	G	67	0	68	3	0
1	H	67	0	68	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	67	0	68	1	0
1	J	67	0	68	0	0
2	A	615	0	595	4	0
2	B	608	0	588	18	0
2	C	608	0	588	23	0
2	D	608	0	588	7	0
2	E	608	0	588	3	0
3	A	10	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
4	A	3	0	0	0	0
4	B	3	0	0	0	0
4	C	2	0	0	0	0
4	D	1	0	0	0	0
4	E	3	0	0	0	0
4	G	2	0	0	0	0
All	All	3416	0	3287	50	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 7.

All (50) 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)
2:B:130:ALA:HB2	2:D:138:PRO:HB3	1.61	0.81
2:C:92:VAL:HG11	2:C:129:PRO:HB3	1.71	0.72
2:B:74:PHE:HB3	2:B:146:ALA:HB3	1.72	0.72
2:D:78:LEU:HD11	2:D:119:ARG:HD2	1.75	0.68
1:F:7:VAL:H	1:G:8:GLN:HE22	1.39	0.68
2:B:100:HIS:HD2	2:B:118:HIS:ND1	1.94	0.66
2:C:119:ARG:HG3	2:C:119:ARG:HH11	1.61	0.65
2:B:116:GLU:HG2	2:C:116:GLU:HG2	1.77	0.64
2:C:110:HIS:CD2	2:C:111:GLY:H	2.16	0.64
2:C:128:ASP:HB2	2:C:149:ALA:HB2	1.79	0.64
2:B:122:ARG:HE	2:C:110:HIS:HB2	1.64	0.63
2:C:110:HIS:HD2	2:C:111:GLY:H	1.46	0.63
2:C:78:LEU:HD23	2:C:117:PHE:HE2	1.66	0.60
2:E:92:VAL:HG11	2:E:129:PRO:HB3	1.84	0.58
2:D:92:VAL:HG11	2:D:129:PRO:HB3	1.84	0.58
2:C:78:LEU:HD23	2:C:117:PHE:CE2	2.38	0.58
2:B:97:VAL:HG23	2:B:123:LEU:HG	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:126:GLY:O	2:B:127:VAL:HG23	2.05	0.56
2:B:106:ARG:HH21	2:E:95:GLU:H	1.52	0.55
2:C:106:ARG:HG3	2:C:112:PHE:HD1	1.72	0.54
2:B:122:ARG:HE	2:C:110:HIS:CB	2.22	0.52
2:B:76:VAL:HG11	2:B:121:TYR:CE1	2.45	0.52
2:D:108:ASP:HB3	2:D:111:GLY:H	1.76	0.51
2:A:100[B]:HIS:CE1	2:A:118:HIS:CE1	3.00	0.49
2:D:74:PHE:HB3	2:D:146:ALA:HB3	1.94	0.49
2:E:97:VAL:HG23	2:E:123:LEU:HG	1.94	0.49
2:C:119:ARG:HD3	2:C:120:ARG:H	1.77	0.48
2:C:119:ARG:CG	2:C:119:ARG:HH11	2.26	0.48
1:G:2:GLU:HG3	2:D:81:LYS:HB2	1.95	0.48
2:D:85:PRO:HG3	2:D:136:LEU:HD23	1.95	0.48
2:A:92:VAL:HG11	2:A:129:PRO:HB3	1.96	0.47
2:C:131:ALA:HB1	2:C:147:ALA:HB3	1.97	0.47
2:A:105:GLU:HG3	2:A:112:PHE:HB3	1.97	0.46
2:C:106:ARG:HG3	2:C:112:PHE:CD1	2.49	0.46
2:B:92:VAL:HG11	2:B:129:PRO:HB3	1.98	0.46
1:G:10:SER:HB2	2:B:135:ALA:HB1	1.98	0.45
2:A:85:PRO:HG3	2:A:136:LEU:HD23	1.99	0.44
2:B:91:LYS:HE3	2:B:93:VAL:HG21	2.00	0.44
2:B:115:ARG:HG2	2:C:117:PHE:HD1	1.82	0.43
2:C:87:GLU:O	2:C:101:ALA:HA	2.18	0.43
2:C:119:ARG:HD2	2:C:121:TYR:CZ	2.54	0.43
2:B:87:GLU:O	2:B:101:ALA:HA	2.18	0.42
2:B:110:HIS:HA	2:B:111:GLY:HA2	1.93	0.41
2:B:78:LEU:HD23	2:B:117:PHE:CE2	2.55	0.41
2:C:119:ARG:HD3	2:C:120:ARG:N	2.35	0.41
2:C:123:LEU:HD22	2:C:127:VAL:HG11	2.03	0.41
2:B:122:ARG:HH21	2:C:110:HIS:HB2	1.86	0.40
2:C:72:GLY:O	2:C:148:PRO:HG3	2.22	0.40
1:I:2:GLU:O	1:I:3:ILE:HG13	2.22	0.40
2:C:75:SER:OG	2:C:145:GLN:HG2	2.20	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	F	7/9 (78%)	7 (100%)	0	0	100	100
1	G	7/9 (78%)	7 (100%)	0	0	100	100
1	H	7/9 (78%)	7 (100%)	0	0	100	100
1	I	7/9 (78%)	7 (100%)	0	0	100	100
1	J	7/9 (78%)	7 (100%)	0	0	100	100
2	A	77/78 (99%)	75 (97%)	2 (3%)	0	100	100
2	B	76/78 (97%)	71 (93%)	4 (5%)	1 (1%)	12	24
2	C	76/78 (97%)	72 (95%)	4 (5%)	0	100	100
2	D	76/78 (97%)	72 (95%)	4 (5%)	0	100	100
2	E	76/78 (97%)	72 (95%)	3 (4%)	1 (1%)	12	24
All	All	416/435 (96%)	397 (95%)	17 (4%)	2 (0%)	29	52

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	109	GLU
2	B	108	ASP

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	F	9/9 (100%)	8 (89%)	1 (11%)	6	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	9/9 (100%)	6 (67%)	3 (33%)	0	0
1	H	9/9 (100%)	7 (78%)	2 (22%)	1	1
1	I	9/9 (100%)	7 (78%)	2 (22%)	1	1
1	J	9/9 (100%)	6 (67%)	3 (33%)	0	0
2	A	65/64 (102%)	62 (95%)	3 (5%)	27	51
2	B	64/64 (100%)	60 (94%)	4 (6%)	18	36
2	C	64/64 (100%)	61 (95%)	3 (5%)	26	50
2	D	64/64 (100%)	62 (97%)	2 (3%)	40	66
2	E	64/64 (100%)	62 (97%)	2 (3%)	40	66
All	All	366/365 (100%)	341 (93%)	25 (7%)	16	32

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

Mol	Chain	Res	Type
1	F	3	ILE
2	A	78	LEU
2	A	104	GLU
2	A	123	LEU
1	G	3	ILE
1	G	7	VAL
1	G	10	SER
2	B	104	GLU
2	B	110	HIS
2	B	119	ARG
2	B	120	ARG
1	H	7	VAL
1	H	10	SER
2	C	106	ARG
2	C	115	ARG
2	C	119	ARG
1	I	7	VAL
1	I	8	GLN
2	D	78	LEU
2	D	108	ASP
1	J	2	GLU
1	J	7	VAL
1	J	8	GLN
2	E	103	HIS
2	E	110	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	8	GLN
1	G	8	GLN
2	B	100	HIS
2	B	103	HIS
1	H	8	GLN
2	C	103	HIS
2	C	110	HIS
2	D	100	HIS
2	D	118	HIS
2	E	100	HIS

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 [i](#)

4 ligands 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	$\# Z > 2$
3	SO4	D	201	-	4,4,4	0.27	0	6,6,6	0.43	0
3	SO4	A	201	-	4,4,4	0.24	0	6,6,6	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	E	201	-	4,4,4	0.23	0	6,6,6	0.23	0
3	SO4	A	202	-	4,4,4	0.32	0	6,6,6	0.15	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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.