Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 10:53 AM EDT

PDB ID	:	2B3U
Title	:	Human Spermine spermidine acetyltransferase K26R mutant
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Deposited on	:	2005-09-21
Resolution	:	1.85 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 (i) 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 (i)) were used in the production of this report:

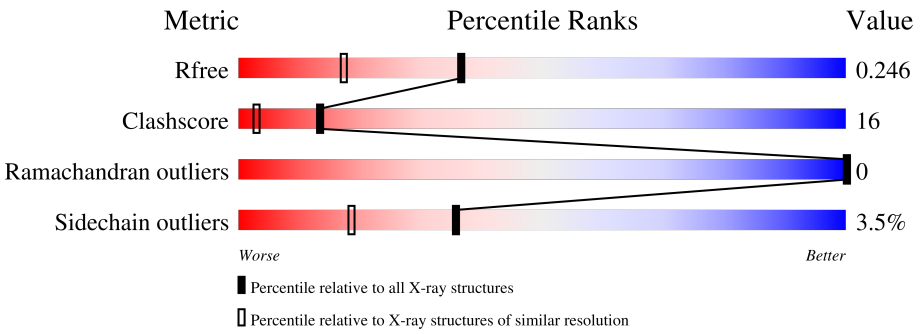
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 1.85 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)

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%

Mol	Chain	Length	Quality of chain
1	A	171	76% 16% • 5%
1	B	171	72% 20% • •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2848 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.

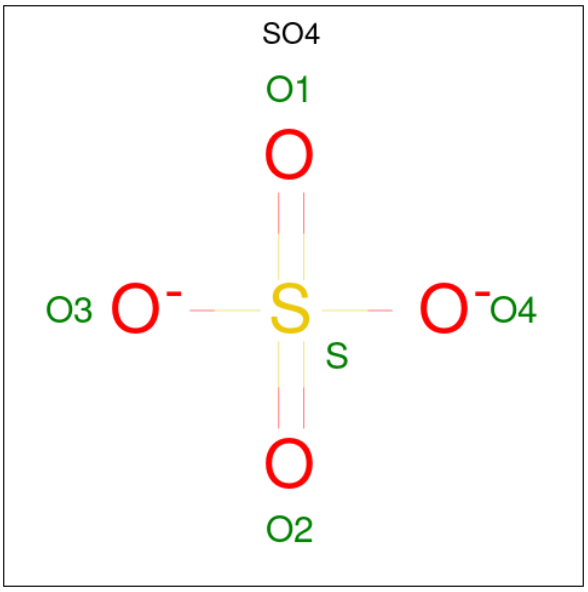
- Molecule 1 is a protein called Diamine acetyltransferase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	162	1324	861	215	239	4	5	0	0	0
1	B	164	1357	883	217	247	4	6	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	ARG	LYS	engineered mutation	UNP P21673
B	26	ARG	LYS	engineered mutation	UNP P21673

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	B	1	5	4	1	0	0

- Molecule 3 is water.

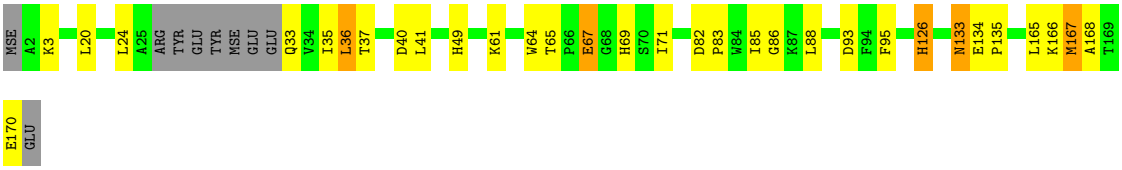
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	87	87	87	0	0
			Total	O		
3	B	70	70	70	0	0

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. 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.

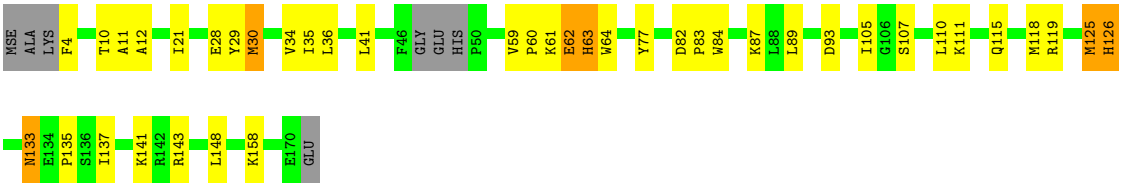
• Molecule 1: Diamine acetyltransferase 1

Chain A:



• Molecule 1: Diamine acetyltransferase 1

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	74.30Å 74.30Å 63.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.85 29.42 – 1.85	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-1.85) 99.3 (29.42-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.67 (at 1.85Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.210 , 0.240 0.230 , 0.246	Depositor DCC
R_{free} test set	1190 reflections (2.08%)	wwPDB-VP
Wilson B-factor (Å^2)	19.0	Xtriage
Anisotropy	0.468	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 47.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	2848	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.94% 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 (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	A	0.63	1/1355 (0.1%)	0.75	1/1820 (0.1%)
1	B	0.66	2/1388 (0.1%)	0.72	0/1862
All	All	0.65	3/2743 (0.1%)	0.73	1/3682 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	167	MSE	SE-CE	-9.59	1.38	1.95
1	B	125	MSE	SE-CE	-7.94	1.48	1.95
1	B	30	MSE	CG-SE	-5.99	1.75	1.95

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	33	GLN	N-CA-C	7.62	131.59	111.00

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	A	1324	0	1289	33	0
1	B	1357	0	1314	60	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	87	0	0	4	0
3	B	70	0	0	2	0
All	All	2848	0	2603	85	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 16.

All (85) 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:82:ASP:HB3	1:A:85:ILE:HG22	1.24	1.11
1:A:82:ASP:HB3	1:A:85:ILE:CG2	1.96	0.95
1:B:36:LEU:HD21	1:B:41:LEU:HD21	1.53	0.91
1:A:167:MSE:HE1	1:B:143:ARG:HD3	1.58	0.86
1:A:82:ASP:CB	1:A:85:ILE:HG22	2.12	0.78
1:A:167:MSE:HE1	1:B:143:ARG:CD	2.14	0.78
1:B:83:PRO:HG2	1:B:84:TRP:CE3	2.20	0.76
1:B:62:GLU:OE1	1:B:63:HIS:ND1	2.20	0.74
1:A:67:GLU:HG3	1:A:69:HIS:ND1	2.02	0.73
1:B:83:PRO:HG2	1:B:84:TRP:CZ3	2.23	0.73
1:A:168:ALA:O	1:B:115:GLN:NE2	2.25	0.69
1:A:20:LEU:HD11	1:A:71:ILE:HG22	1.74	0.69
3:A:216:HOH:O	1:B:158:LYS:HE3	1.93	0.68
1:B:110:LEU:HD13	1:B:143:ARG:HD3	1.74	0.68
1:A:167:MSE:HE2	3:B:178:HOH:O	1.94	0.67
1:B:61:LYS:HA	1:B:64:TRP:CD1	2.31	0.65
1:A:85:ILE:HG23	1:A:86:GLY:N	2.11	0.65
1:A:83:PRO:HG3	1:B:93:ASP:OD2	1.98	0.63
1:B:10:THR:HG22	1:B:12:ALA:H	1.62	0.63
1:B:36:LEU:HD21	1:B:41:LEU:CD2	2.26	0.63
1:B:62:GLU:H	1:B:62:GLU:CD	2.02	0.62
1:A:133:ASN:HD22	1:A:135:PRO:HD2	1.64	0.62
1:A:126:HIS:HD2	3:B:173:HOH:O	1.83	0.62
1:B:77:TYR:CD1	1:B:89:LEU:HD11	2.35	0.62
1:B:29:TYR:O	1:B:30:MSE:HG3	2.00	0.60
1:B:59:VAL:HB	1:B:63:HIS:HB2	1.84	0.59
1:B:36:LEU:HD11	1:B:41:LEU:CD2	2.33	0.59
1:B:110:LEU:HD21	1:B:125:MSE:HE1	1.85	0.58
1:B:111:LYS:O	1:B:115:GLN:HG3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:LEU:CD1	1:B:143:ARG:HD3	2.34	0.58
1:A:85:ILE:HG23	1:A:86:GLY:H	1.70	0.57
1:B:36:LEU:HD11	1:B:41:LEU:HG	1.88	0.56
1:B:4:PHE:CE2	1:B:105:ILE:HG12	2.44	0.53
1:A:166:LYS:O	1:A:170:GLU:HB2	2.09	0.53
1:B:60:PRO:HD2	1:B:63:HIS:CD2	2.43	0.53
3:A:177:HOH:O	1:B:126:HIS:HD2	1.92	0.53
1:B:21:ILE:HD12	1:B:36:LEU:CD2	2.39	0.53
1:A:93:ASP:OD2	1:B:83:PRO:HG3	2.09	0.52
1:B:34:VAL:O	1:B:35:ILE:HD13	2.09	0.52
1:A:36:LEU:HD13	1:A:40:ASP:HB2	1.92	0.52
1:B:36:LEU:CD2	1:B:41:LEU:HD21	2.35	0.52
1:B:110:LEU:CD2	1:B:125:MSE:HE1	2.39	0.51
1:B:115:GLN:O	1:B:119:ARG:HG3	2.11	0.51
1:B:21:ILE:CD1	1:B:36:LEU:CD2	2.89	0.50
1:A:85:ILE:CG2	1:A:86:GLY:N	2.75	0.50
1:B:21:ILE:HD12	1:B:36:LEU:HD23	1.93	0.50
1:A:35:ILE:O	1:A:35:ILE:HG22	2.12	0.50
1:B:60:PRO:HD2	1:B:63:HIS:CG	2.47	0.49
1:A:65:THR:OG1	1:A:67:GLU:HG2	2.13	0.49
1:B:133:ASN:HD22	1:B:135:PRO:HD2	1.77	0.49
1:A:36:LEU:HD13	1:A:37:THR:N	2.29	0.48
1:A:85:ILE:CG2	1:A:86:GLY:H	2.27	0.47
1:B:62:GLU:OE1	1:B:63:HIS:CE1	2.66	0.47
1:B:83:PRO:HG2	1:B:84:TRP:HE3	1.76	0.47
1:B:10:THR:CG2	1:B:11:ALA:N	2.78	0.47
1:A:85:ILE:CG2	1:A:88:LEU:HD21	2.45	0.46
1:A:49:HIS:HB3	3:A:241:HOH:O	2.16	0.46
1:B:36:LEU:HD21	1:B:41:LEU:CG	2.45	0.45
1:B:36:LEU:HD21	1:B:41:LEU:HD11	1.98	0.45
1:A:24:LEU:HD13	1:A:95:PHE:HB2	1.97	0.45
1:B:28:GLU:O	1:B:30:MSE:HE2	2.17	0.45
1:B:61:LYS:HG3	1:B:64:TRP:CE2	2.52	0.45
3:A:179:HOH:O	1:B:87:LYS:HE2	2.16	0.45
1:B:36:LEU:HD11	1:B:41:LEU:CG	2.47	0.45
1:A:61:LYS:HA	1:A:64:TRP:CD1	2.52	0.45
1:B:61:LYS:HE3	1:B:64:TRP:CZ3	2.52	0.44
1:B:63:HIS:N	1:B:63:HIS:HD1	2.16	0.44
1:B:83:PRO:HG2	1:B:84:TRP:HZ3	1.80	0.44
1:A:165:LEU:HD13	1:B:118:MSE:HE2	2.00	0.43
1:A:85:ILE:HG23	1:A:88:LEU:HD21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:ASP:OD1	1:B:84:TRP:HB2	2.18	0.43
1:B:30:MSE:HE3	1:B:30:MSE:HB2	1.61	0.43
1:A:168:ALA:C	1:B:115:GLN:HE21	2.22	0.43
1:B:62:GLU:OE1	1:B:62:GLU:N	2.51	0.43
1:A:134:GLU:N	1:A:135:PRO:CD	2.82	0.42
1:B:89:LEU:O	1:B:125:MSE:HA	2.20	0.42
1:A:65:THR:HG1	1:A:69:HIS:H	1.68	0.42
1:A:167:MSE:HE3	1:B:143:ARG:HG2	2.02	0.42
1:B:35:ILE:HG22	1:B:35:ILE:O	2.20	0.41
1:B:36:LEU:HD11	1:B:41:LEU:HD23	2.02	0.41
1:A:36:LEU:HD11	1:A:41:LEU:HG	2.03	0.41
1:B:61:LYS:HE3	1:B:64:TRP:CH2	2.56	0.41
1:B:107:SER:O	1:B:111:LYS:HG3	2.21	0.40
1:B:137:ILE:O	1:B:141:LYS:HG3	2.21	0.40
1:B:110:LEU:CD1	1:B:143:ARG:CD	2.98	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	158/171 (92%)	156 (99%)	2 (1%)	0	100	100
1	B	160/171 (94%)	156 (98%)	4 (2%)	0	100	100
All	All	318/342 (93%)	312 (98%)	6 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	141/143 (99%)	136 (96%)	5 (4%)	36	18
1	B	145/143 (101%)	140 (97%)	5 (3%)	37	19
All	All	286/286 (100%)	276 (96%)	10 (4%)	36	18

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	36	LEU
1	A	67	GLU
1	A	126	HIS
1	A	133	ASN
1	B	62	GLU
1	B	63	HIS
1	B	126	HIS
1	B	133	ASN
1	B	148	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	126	HIS
1	A	133	ASN
1	B	115	GLN
1	B	126	HIS
1	B	133	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	$\#\|Z\| > 2$
2	SO4	B	172	-	4,4,4	1.85	1 (25%)	6,6,6	0.81	0
2	SO4	A	172	-	4,4,4	1.62	1 (25%)	6,6,6	0.84	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	172	SO4	O1-S	3.25	1.64	1.44
2	A	172	SO4	O1-S	2.69	1.60	1.44

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 (i)

6.1 Protein, DNA and RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.