



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:37 AM GMT

PDB ID : 3BJ7  
Title : Spermine/spermidine N1-acetyltransferase from mouse: Crystal structure of a ternary complex reveals solvent-mediated spermine binding  
Authors : Montemayor, E.J.  
Deposited on : 2007-12-03  
Resolution : 2.20 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

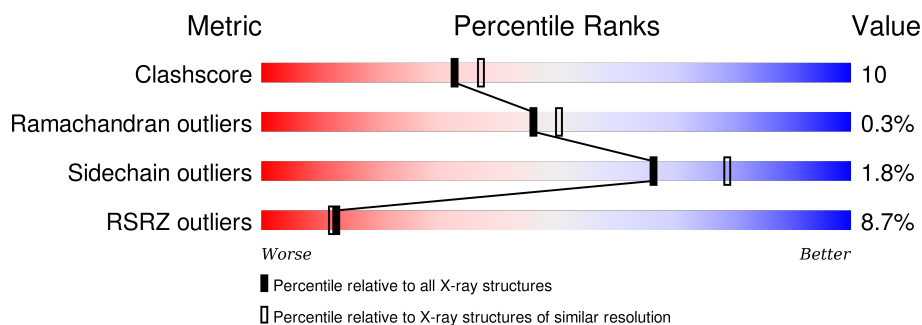
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	A	171	<div> <div>19%</div> <div> <div>66%</div> <div>26%</div> <div>• 5%</div> </div> </div>
1	B	171	<div> <div>6%</div> <div> <div>75%</div> <div>19%</div> <div>6%</div> </div> </div>
1	C	171	<div> <div>6%</div> <div> <div>75%</div> <div>19%</div> <div>• 5%</div> </div> </div>
1	D	171	<div> <div>2%</div> <div> <div>77%</div> <div>17%</div> <div>6%</div> </div> </div>

## 2 Entry composition [i](#)

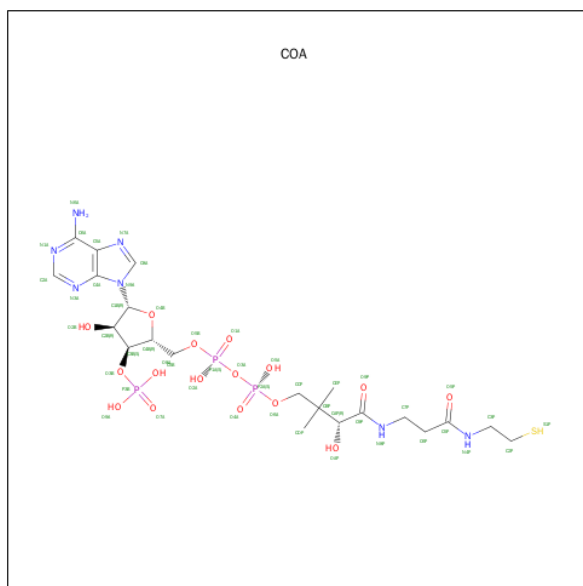
There are 3 unique types of molecules in this entry. The entry contains 5853 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
1	A	162	Total	C	N	O	S	0	0	0
			1328	863	212	243	10			
1	B	161	Total	C	N	O	S	0	0	0
			1337	873	215	239	10			
1	C	162	Total	C	N	O	S	0	0	0
			1328	863	212	243	10			
1	D	161	Total	C	N	O	S	0	0	0
			1337	873	215	239	10			

- Molecule 2 is COENZYME A (three-letter code: COA) (formula:  $C_{21}H_{36}N_7O_{16}P_3S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P S	0	0
			48	21	7	16	3 1		
2	B	1	Total	C	N	O	P S	0	0
			48	21	7	16	3 1		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

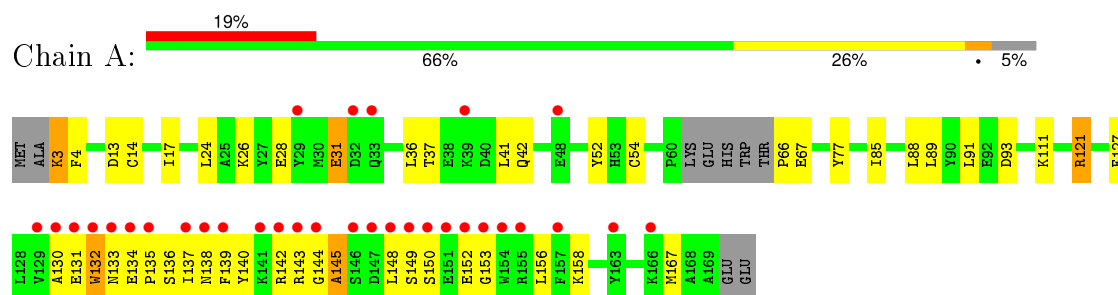
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	48	Total	O	0	0
			48	48		
3	B	86	Total	O	0	0
			86	86		
3	C	80	Total	O	0	0
			80	80		
3	D	117	Total	O	0	0
			117	117		

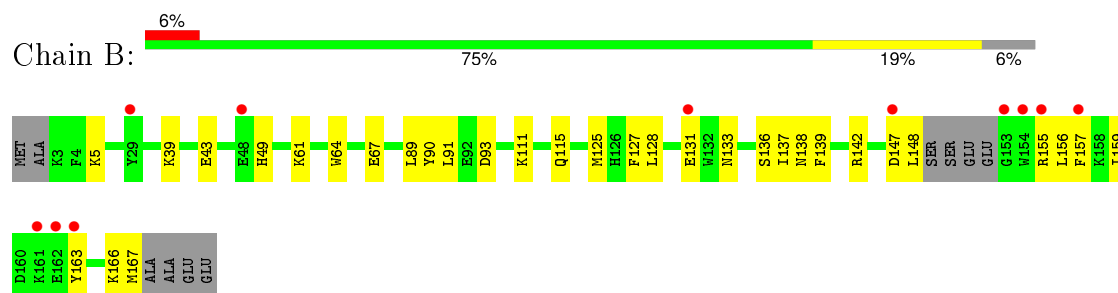
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

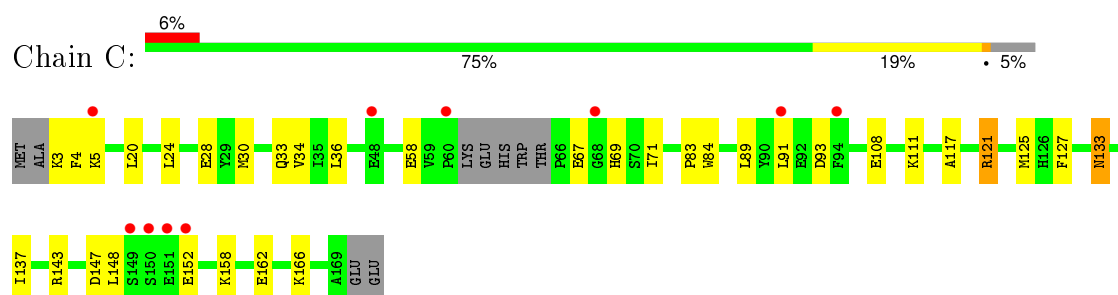
#### • Molecule 1: Diamine acetyltransferase 1



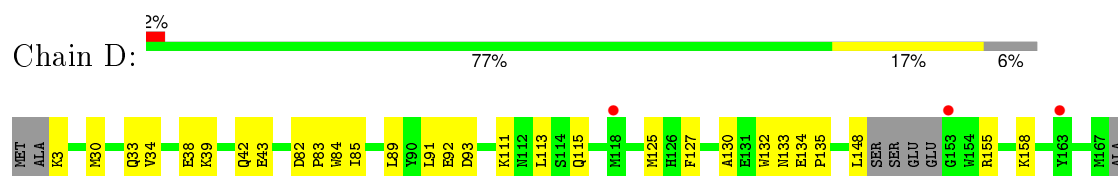
#### • Molecule 1: Diamine acetyltransferase 1



#### • Molecule 1: Diamine acetyltransferase 1



#### • Molecule 1: Diamine acetyltransferase 1



ALA  
GLU  
GLU

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.86Å 97.19Å 105.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.40 – 2.20 32.43 – 2.08	Depositor EDS
% Data completeness (in resolution range)	99.4 (32.40-2.20) 92.8 (32.43-2.08)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.60 (at 2.08Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.231 , 0.294 0.242 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	28.4	Xtriage
Anisotropy	0.344	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 50.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 46470 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5853	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: COA

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	0.34	0/1363	0.53	0/1833
1	B	0.36	0/1375	0.55	0/1851
1	C	0.34	0/1363	0.56	0/1833
1	D	0.37	0/1375	0.57	0/1851
All	All	0.36	0/5476	0.55	0/7368

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	A	1328	0	1291	55	0
1	B	1337	0	1301	33	0
1	C	1328	0	1291	27	0
1	D	1337	0	1301	24	0
2	A	48	0	31	0	0
2	B	48	0	31	0	0
2	C	48	0	31	0	0
2	D	48	0	31	1	0
3	A	48	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	86	0	0	1	0
3	C	80	0	0	0	0
3	D	117	0	0	1	0
All	All	5853	0	5308	113	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 10.

All (113) 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:C:121:ARG:HB3	1:C:121:ARG:HH11	1.32	0.93
1:C:121:ARG:NH1	1:C:121:ARG:HB3	1.93	0.83
1:A:121:ARG:HH11	1:A:121:ARG:HB3	1.45	0.82
1:C:148:LEU:HD13	1:D:158:LYS:HD3	1.62	0.81
1:C:158:LYS:HD3	1:D:148:LEU:HD21	1.64	0.80
1:A:131:GLU:HB3	1:B:155:ARG:HD2	1.72	0.72
1:A:131:GLU:HB3	1:B:155:ARG:CD	2.19	0.71
1:C:158:LYS:HB3	1:D:148:LEU:HD11	1.73	0.70
1:A:3:LYS:HD3	1:A:3:LYS:N	2.07	0.70
1:A:121:ARG:CB	1:A:121:ARG:HH11	2.04	0.70
1:A:158:LYS:HB3	1:B:148:LEU:HD11	1.72	0.69
1:A:85:ILE:HD11	1:A:88:LEU:HD21	1.74	0.68
1:A:14:CYS:SG	1:A:42:GLN:HG2	2.33	0.67
1:B:138:ASN:O	1:B:142:ARG:HG3	1.94	0.67
1:C:5:LYS:HE3	1:C:58:GLU:OE1	1.95	0.66
1:A:130:ALA:HB1	1:A:132:TRP:NE1	2.10	0.65
1:A:140:TYR:HB3	1:A:145:ALA:CB	2.27	0.65
1:A:91:LEU:HB3	1:A:127:PHE:HB3	1.79	0.64
1:C:89:LEU:HD12	1:C:117:ALA:HB2	1.79	0.64
1:A:149:SER:O	1:A:152:GLU:HB3	2.00	0.62
1:C:133:ASN:O	1:C:137:ILE:HG12	1.98	0.62
1:C:158:LYS:HB3	1:D:148:LEU:CD1	2.30	0.62
1:A:158:LYS:HD3	1:B:148:LEU:HD21	1.80	0.62
1:A:13:ASP:O	1:A:17:ILE:HG12	2.02	0.60
1:A:26:LYS:HB2	1:A:31:GLU:HG3	1.83	0.59
1:A:131:GLU:CB	1:B:155:ARG:HH11	2.15	0.59
1:A:138:ASN:HB3	1:A:142:ARG:NH1	2.18	0.58
1:D:38:GLU:O	1:D:42:GLN:HG3	2.04	0.57
1:A:36:LEU:CD2	1:A:41:LEU:HG	2.34	0.57
1:A:148:LEU:HD23	1:B:156:LEU:HG	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:LEU:HD23	1:A:37:THR:N	2.19	0.57
1:A:36:LEU:HD22	1:A:41:LEU:HG	1.86	0.56
1:B:89:LEU:C	1:B:89:LEU:HD23	2.26	0.56
1:B:39:LYS:O	1:B:43:GLU:HG3	2.05	0.56
1:D:111:LYS:O	1:D:115:GLN:HG3	2.05	0.56
1:A:148:LEU:C	1:A:150:SER:H	2.08	0.55
1:A:131:GLU:HB3	1:B:155:ARG:HD3	1.87	0.55
1:C:24:LEU:O	1:C:28:GLU:HG3	2.07	0.54
1:B:133:ASN:O	1:B:137:ILE:HG13	2.08	0.54
1:A:153:GLY:HA2	1:B:131:GLU:CD	2.27	0.54
1:A:158:LYS:CD	1:B:148:LEU:HD21	2.38	0.53
1:A:66:PRO:HG2	1:A:67:GLU:H	1.72	0.53
1:A:136:SER:HA	1:A:139:PHE:HB3	1.91	0.52
1:D:133:ASN:ND2	2:D:403:COA:O5P	2.42	0.52
1:A:130:ALA:HB1	1:A:132:TRP:CD1	2.45	0.51
1:A:24:LEU:O	1:A:28:GLU:HG3	2.11	0.50
1:A:127:PHE:O	1:B:156:LEU:HD12	2.12	0.49
1:A:111:LYS:HG3	1:B:167:MET:O	2.13	0.49
1:A:133:ASN:ND2	1:A:136:SER:H	2.10	0.49
1:A:134:GLU:N	1:A:135:PRO:CD	2.75	0.48
1:C:89:LEU:CD1	1:C:117:ALA:HB2	2.42	0.48
1:B:163:TYR:O	1:B:166:LYS:HB3	2.14	0.48
1:A:167:MET:O	1:B:111:LYS:HG3	2.13	0.48
1:B:147:ASP:O	1:B:148:LEU:HD23	2.12	0.48
1:A:145:ALA:HA	1:B:159:ILE:HG12	1.96	0.48
1:A:3:LYS:HG2	1:A:4:PHE:HD1	1.78	0.48
1:C:30:MET:HB3	1:C:33:GLN:NE2	2.29	0.48
1:C:34:VAL:HG22	1:D:84:TRP:CD1	2.48	0.48
1:D:39:LYS:HG2	3:D:455:HOH:O	2.13	0.48
1:A:3:LYS:HG2	1:A:4:PHE:CD1	2.49	0.47
1:A:140:TYR:HB3	1:A:145:ALA:HB3	1.94	0.47
1:A:17:ILE:HD12	1:A:54:CYS:SG	2.55	0.47
1:D:30:MET:HG3	1:D:33:GLN:HG3	1.95	0.47
1:A:138:ASN:HB3	1:A:142:ARG:HH12	1.78	0.47
1:B:91:LEU:HB3	1:B:127:PHE:HB3	1.97	0.47
1:C:162:GLU:O	1:C:166:LYS:HG3	2.15	0.47
1:B:89:LEU:HD23	1:B:90:TYR:N	2.30	0.47
1:A:130:ALA:HB1	1:A:132:TRP:CE2	2.50	0.46
1:C:67:GLU:HB2	1:C:69:HIS:CD2	2.51	0.46
1:B:89:LEU:HD22	1:B:125:MET:HG3	1.96	0.46
1:A:156:LEU:HA	1:B:128:LEU:HD23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:130:ALA:HB1	1:D:132:TRP:NE1	2.31	0.45
1:A:148:LEU:HB3	1:B:156:LEU:O	2.17	0.45
1:A:135:PRO:O	1:A:139:PHE:N	2.49	0.44
1:D:134:GLU:HB3	1:D:135:PRO:HD3	1.98	0.44
1:A:133:ASN:OD1	1:A:135:PRO:HD2	2.15	0.44
1:D:89:LEU:C	1:D:89:LEU:HD23	2.38	0.44
1:C:89:LEU:O	1:C:125:MET:HA	2.18	0.43
1:C:20:LEU:HD11	1:C:71:ILE:HG22	2.00	0.43
1:A:139:PHE:O	1:A:143:ARG:NH1	2.51	0.43
1:B:155:ARG:O	1:B:157:PHE:HD2	2.01	0.43
1:B:111:LYS:O	1:B:115:GLN:HG3	2.18	0.43
1:D:113:LEU:HB3	1:D:125:MET:CE	2.49	0.43
1:A:52:TYR:C	1:A:52:TYR:CD1	2.92	0.43
1:A:77:TYR:CD1	1:A:89:LEU:HD11	2.54	0.43
1:D:3:LYS:HA	1:D:3:LYS:HD2	1.87	0.43
1:B:5:LYS:CB	1:B:5:LYS:NZ	2.82	0.43
1:D:39:LYS:O	1:D:43:GLU:HG3	2.19	0.43
1:C:3:LYS:HG3	1:C:4:PHE:HD1	1.84	0.42
1:A:148:LEU:C	1:A:150:SER:N	2.72	0.42
1:B:67:GLU:CD	1:B:67:GLU:H	2.22	0.42
1:C:36:LEU:HD12	1:D:83:PRO:O	2.19	0.42
1:B:136:SER:O	1:B:139:PHE:HB3	2.19	0.42
1:A:131:GLU:C	1:A:133:ASN:H	2.23	0.42
1:C:84:TRP:CD1	1:D:34:VAL:HG22	2.55	0.41
1:A:36:LEU:HD23	1:A:37:THR:O	2.20	0.41
1:C:147:ASP:OD2	1:D:155:ARG:NH2	2.48	0.41
1:B:89:LEU:O	1:B:125:MET:HA	2.20	0.41
1:C:71:ILE:HD12	1:C:71:ILE:N	2.35	0.41
1:C:143:ARG:HG3	1:C:143:ARG:HH11	1.84	0.41
1:A:134:GLU:HA	1:A:137:ILE:HD12	2.02	0.41
1:C:108:GLU:O	1:C:111:LYS:HB3	2.20	0.41
1:A:140:TYR:C	1:A:145:ALA:HB3	2.41	0.41
1:B:49:HIS:HE1	3:B:479:HOH:O	2.04	0.41
1:A:42:GLN:HB3	1:A:42:GLN:HE21	1.59	0.41
1:C:83:PRO:HD3	1:D:92:GLU:CG	2.51	0.41
1:B:61:LYS:HA	1:B:64:TRP:CD1	2.56	0.40
1:C:91:LEU:HB3	1:C:127:PHE:HB3	2.03	0.40
1:C:158:LYS:HD3	1:D:148:LEU:CD2	2.45	0.40
1:D:113:LEU:HB3	1:D:125:MET:HE2	2.03	0.40
1:D:82:ASP:HB3	1:D:85:ILE:HG12	2.02	0.40
1:A:144:GLY:HA3	1:B:163:TYR:CG	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:91:LEU:HB3	1:D:127:PHE:HB3	2.03	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%)	148 (94%)	8 (5%)	2 (1%)	15	11
1	B	157/171 (92%)	152 (97%)	5 (3%)	0	100	100
1	C	158/171 (92%)	153 (97%)	5 (3%)	0	100	100
1	D	157/171 (92%)	155 (99%)	2 (1%)	0	100	100
All	All	630/684 (92%)	608 (96%)	20 (3%)	2 (0%)	46	50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	145	ALA
1	A	132	TRP

### 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	142/150 (95%)	138 (97%)	4 (3%)	51	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	143/150 (95%)	142 (99%)	1 (1%)	88	94
1	C	142/150 (95%)	138 (97%)	4 (3%)	51	63
1	D	143/150 (95%)	142 (99%)	1 (1%)	88	94
All	All	570/600 (95%)	560 (98%)	10 (2%)	66	79

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

Mol	Chain	Res	Type
1	A	3	LYS
1	A	31	GLU
1	A	93	ASP
1	A	121	ARG
1	B	93	ASP
1	C	93	ASP
1	C	121	ARG
1	C	133	ASN
1	C	152	GLU
1	D	93	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	42	GLN
1	A	115	GLN
1	A	133	ASN
1	B	33	GLN
1	B	69	HIS
1	B	112	ASN
1	C	33	GLN
1	C	115	GLN
1	C	133	ASN
1	C	138	ASN
1	D	112	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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	$\# Z  > 2$
2	COA	A	400	-	40,50,50	2.49	16 (40%)	50,75,75	2.37	14 (28%)
2	COA	B	401	-	40,50,50	2.47	16 (40%)	50,75,75	2.37	16 (32%)
2	COA	C	402	-	40,50,50	2.45	16 (40%)	50,75,75	2.32	15 (30%)
2	COA	D	403	-	40,50,50	2.40	16 (40%)	50,75,75	2.39	14 (28%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	COA	A	400	-	-	0/44/64/64	0/3/3/3
2	COA	B	401	-	-	0/44/64/64	0/3/3/3
2	COA	C	402	-	-	0/44/64/64	0/3/3/3
2	COA	D	403	-	-	0/44/64/64	0/3/3/3

All (64) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	403	COA	C2B-C3B	-2.09	1.48	1.53
2	D	403	COA	C4A-N3A	2.00	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	400	COA	C4A-N3A	2.02	1.38	1.35
2	B	401	COA	C4A-N3A	2.02	1.38	1.35
2	C	402	COA	O4B-C1B	2.04	1.43	1.41
2	C	402	COA	CDP-CBP	2.14	1.58	1.53
2	D	403	COA	OAP-CAP	2.14	1.46	1.42
2	C	402	COA	C4A-N3A	2.14	1.38	1.35
2	C	402	COA	P3B-O3B	2.16	1.66	1.60
2	A	400	COA	C2P-S1P	2.18	1.88	1.80
2	B	401	COA	OAP-CAP	2.18	1.46	1.42
2	C	402	COA	P3B-O7A	2.23	1.58	1.51
2	A	400	COA	P3B-O3B	2.23	1.66	1.60
2	B	401	COA	C2P-S1P	2.32	1.88	1.80
2	B	401	COA	P3B-O3B	2.36	1.67	1.60
2	B	401	COA	P3B-O7A	2.37	1.59	1.51
2	A	400	COA	P3B-O7A	2.38	1.59	1.51
2	D	403	COA	CDP-CBP	2.39	1.58	1.53
2	D	403	COA	P3B-O3B	2.40	1.67	1.60
2	D	403	COA	P3B-O7A	2.40	1.59	1.51
2	A	400	COA	OAP-CAP	2.40	1.47	1.42
2	B	401	COA	CDP-CBP	2.47	1.59	1.53
2	C	402	COA	OAP-CAP	2.48	1.47	1.42
2	D	403	COA	O4B-C1B	2.48	1.44	1.41
2	A	400	COA	O4B-C1B	2.64	1.44	1.41
2	A	400	COA	CDP-CBP	2.68	1.59	1.53
2	D	403	COA	C5A-C4A	2.96	1.47	1.40
2	C	402	COA	C2P-S1P	2.99	1.91	1.80
2	B	401	COA	O4B-C1B	3.00	1.45	1.41
2	C	402	COA	C5A-C4A	3.09	1.47	1.40
2	B	401	COA	C5A-C4A	3.14	1.47	1.40
2	A	400	COA	C5A-C4A	3.16	1.47	1.40
2	C	402	COA	C3B-C4B	3.19	1.62	1.52
2	A	400	COA	C3B-C4B	3.45	1.62	1.52
2	D	403	COA	O3B-C3B	3.46	1.54	1.44
2	B	401	COA	O3B-C3B	3.51	1.54	1.44
2	D	403	COA	O5P-C5P	3.56	1.30	1.23
2	A	400	COA	O4B-C4B	3.58	1.53	1.45
2	C	402	COA	O3B-C3B	3.73	1.55	1.44
2	C	402	COA	O4B-C4B	3.74	1.53	1.45
2	A	400	COA	O3B-C3B	3.85	1.55	1.44
2	B	401	COA	C3B-C4B	3.91	1.64	1.52
2	B	401	COA	O4B-C4B	3.97	1.54	1.45
2	D	403	COA	O4B-C4B	3.97	1.54	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	COA	C3P-N4P	3.98	1.55	1.46
2	D	403	COA	C3P-N4P	4.13	1.55	1.46
2	A	400	COA	C3P-N4P	4.15	1.55	1.46
2	D	403	COA	C3B-C4B	4.18	1.64	1.52
2	B	401	COA	O5P-C5P	4.20	1.32	1.23
2	C	402	COA	C3P-N4P	4.25	1.56	1.46
2	C	402	COA	O5P-C5P	4.27	1.32	1.23
2	A	400	COA	O5P-C5P	4.49	1.32	1.23
2	D	403	COA	C2A-N3A	4.76	1.40	1.32
2	B	401	COA	C2A-N3A	4.89	1.40	1.32
2	A	400	COA	C2A-N3A	4.95	1.40	1.32
2	C	402	COA	C2A-N3A	4.95	1.40	1.32
2	D	403	COA	C2A-N1A	5.25	1.43	1.33
2	B	401	COA	C2A-N1A	5.26	1.43	1.33
2	A	400	COA	C2A-N1A	5.26	1.43	1.33
2	C	402	COA	C2A-N1A	5.29	1.44	1.33
2	D	403	COA	O9P-C9P	5.39	1.34	1.23
2	C	402	COA	O9P-C9P	5.40	1.34	1.23
2	B	401	COA	O9P-C9P	5.69	1.34	1.23
2	A	400	COA	O9P-C9P	5.91	1.35	1.23

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	402	COA	N3A-C2A-N1A	-7.32	123.29	128.89
2	A	400	COA	N3A-C2A-N1A	-7.29	123.31	128.89
2	B	401	COA	N3A-C2A-N1A	-7.12	123.44	128.89
2	D	403	COA	N3A-C2A-N1A	-7.04	123.50	128.89
2	C	402	COA	C1B-N9A-C4A	-6.91	116.51	126.94
2	D	403	COA	C1B-N9A-C4A	-6.82	116.66	126.94
2	A	400	COA	C1B-N9A-C4A	-6.58	117.02	126.94
2	D	403	COA	C2B-C1B-N9A	-6.52	104.32	114.29
2	B	401	COA	C1B-N9A-C4A	-6.41	117.27	126.94
2	B	401	COA	C2B-C1B-N9A	-6.08	105.00	114.29
2	A	400	COA	O4B-C1B-N9A	-5.40	96.80	108.10
2	B	401	COA	O4B-C1B-N9A	-5.06	97.50	108.10
2	A	400	COA	C2B-C1B-N9A	-4.90	106.80	114.29
2	D	403	COA	O4B-C1B-N9A	-4.46	98.75	108.10
2	D	403	COA	CEP-CBP-CCP	-4.45	102.73	108.50
2	C	402	COA	O4B-C1B-N9A	-4.27	99.16	108.10
2	C	402	COA	CEP-CBP-CCP	-3.99	103.33	108.50
2	B	401	COA	CEP-CBP-CCP	-3.84	103.52	108.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	400	COA	CEP-CBP-CCP	-3.80	103.58	108.50
2	C	402	COA	C2B-C1B-N9A	-3.62	108.75	114.29
2	D	403	COA	C4B-O4B-C1B	-3.17	106.23	109.72
2	C	402	COA	O5B-C5B-C4B	-3.10	97.68	109.12
2	B	401	COA	P3B-O3B-C3B	-2.91	114.59	121.56
2	A	400	COA	P3B-O3B-C3B	-2.89	114.64	121.56
2	C	402	COA	P3B-O3B-C3B	-2.70	115.10	121.56
2	C	402	COA	O3B-C3B-C4B	-2.68	99.49	109.99
2	D	403	COA	O5B-C5B-C4B	-2.65	99.35	109.12
2	A	400	COA	O5B-C5B-C4B	-2.61	99.50	109.12
2	D	403	COA	P3B-O3B-C3B	-2.53	115.50	121.56
2	A	400	COA	O3B-C3B-C4B	-2.49	100.22	109.99
2	B	401	COA	O5B-C5B-C4B	-2.45	100.09	109.12
2	D	403	COA	O3B-C3B-C4B	-2.33	100.86	109.99
2	B	401	COA	O3B-C3B-C4B	-2.20	101.36	109.99
2	B	401	COA	C4B-O4B-C1B	-2.04	107.48	109.72
2	B	401	COA	CEP-CBP-CAP	2.05	113.09	109.34
2	D	403	COA	O2A-P1A-O3A	2.19	115.02	105.09
2	A	400	COA	CEP-CBP-CAP	2.19	113.34	109.34
2	C	402	COA	CEP-CBP-CAP	2.21	113.39	109.34
2	B	401	COA	O2A-P1A-O3A	2.22	115.17	105.09
2	C	402	COA	O2A-P1A-O3A	2.24	115.23	105.09
2	B	401	COA	C3B-C2B-C1B	2.25	105.37	99.98
2	B	401	COA	P2A-O3A-P1A	2.26	139.08	132.73
2	D	403	COA	CEP-CBP-CAP	2.43	113.79	109.34
2	C	402	COA	P2A-O3A-P1A	2.48	139.70	132.73
2	A	400	COA	O2A-P1A-O3A	2.65	117.13	105.09
2	A	400	COA	O3B-C3B-C2B	2.86	122.64	111.51
2	D	403	COA	O3B-C3B-C2B	2.86	122.65	111.51
2	B	401	COA	O3B-C3B-C2B	3.00	123.19	111.51
2	C	402	COA	O3B-C3B-C2B	3.07	123.43	111.51
2	A	400	COA	C3B-C2B-C1B	3.19	107.64	99.98
2	C	402	COA	C3B-C2B-C1B	3.22	107.69	99.98
2	D	403	COA	C4A-C5A-N7A	3.34	112.55	109.48
2	B	401	COA	C4A-C5A-N7A	3.46	112.67	109.48
2	A	400	COA	C4A-C5A-N7A	3.50	112.70	109.48
2	C	402	COA	C4A-C5A-N7A	3.56	112.75	109.48
2	A	400	COA	O4B-C4B-C5B	4.45	125.25	109.32
2	C	402	COA	O4B-C4B-C5B	4.58	125.71	109.32
2	D	403	COA	O4B-C4B-C5B	4.62	125.84	109.32
2	B	401	COA	O4B-C4B-C5B	4.81	126.51	109.32

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	403	COA	1	0

## 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 ⓘ

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	162/171 (94%)	1.05	32 (19%) 1 1	22, 39, 84, 92	0
1	B	161/171 (94%)	0.43	11 (6%) 20 20	18, 29, 60, 68	0
1	C	162/171 (94%)	0.44	10 (6%) 24 23	20, 33, 47, 57	0
1	D	161/171 (94%)	0.15	3 (1%) 70 68	17, 26, 43, 48	0
All	All	646/684 (94%)	0.52	56 (8%) 13 12	17, 32, 63, 92	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	150	SER	8.0
1	A	129	VAL	8.0
1	A	132	TRP	7.6
1	A	149	SER	7.5
1	B	163	TYR	7.0
1	A	135	PRO	6.0
1	A	137	ILE	5.7
1	A	144	GLY	5.3
1	A	134	GLU	5.2
1	A	139	PHE	4.5
1	A	48	GLU	4.4
1	B	157	PHE	4.4
1	A	138	ASN	4.4
1	A	151	GLU	4.3
1	A	155	ARG	4.2
1	A	130	ALA	4.1
1	A	133	ASN	4.1
1	B	153	GLY	3.9
1	B	161	LYS	3.8
1	A	131	GLU	3.6
1	A	32	ASP	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	155	ARG	3.3
1	A	39	LYS	3.2
1	C	152	GLU	3.1
1	A	148	LEU	3.1
1	C	91	LEU	3.1
1	C	60	PRO	2.9
1	A	142	ARG	2.9
1	C	48	GLU	2.8
1	A	163	TYR	2.8
1	A	154	TRP	2.7
1	A	147	ASP	2.7
1	D	153	GLY	2.7
1	C	149	SER	2.6
1	A	146	SER	2.6
1	B	162	GLU	2.6
1	A	29	TYR	2.5
1	A	153	GLY	2.5
1	A	152	GLU	2.5
1	C	68	GLY	2.4
1	A	33	GLN	2.4
1	B	147	ASP	2.3
1	C	151	GLU	2.2
1	A	157	PHE	2.1
1	D	163	TYR	2.1
1	A	166	LYS	2.1
1	B	154	TRP	2.1
1	B	29	TYR	2.1
1	D	118	MET	2.1
1	C	150	SER	2.1
1	B	131	GLU	2.0
1	C	5	LYS	2.0
1	B	48	GLU	2.0
1	A	141	LYS	2.0
1	C	94	PHE	2.0
1	A	143	ARG	2.0

## 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 [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	COA	B	401	48/48	0.84	0.23	1.78	13,39,66,67	0
2	COA	C	402	48/48	0.84	0.23	1.68	10,34,61,61	0
2	COA	D	403	48/48	0.80	0.18	0.41	20,32,40,52	0
2	COA	A	400	48/48	0.84	0.20	0.05	24,47,72,73	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.