



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:15 PM GMT

PDB ID : 4R87
Title : Crystal structure of spermidine N-acetyltransferase from *Vibrio cholerae* in complex with CoA and spermine
Authors : Filippova, E.V.; Minasov, G.; Kiryukhina, O.; Kuhn, M.L.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2014-08-29
Resolution : 2.61 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at 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.

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

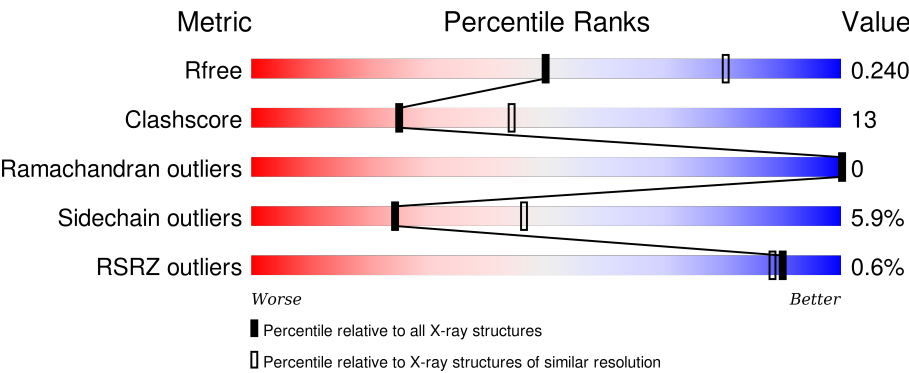
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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}	91344	2700 (2.64-2.60)
Clashscore	102246	3065 (2.64-2.60)
Ramachandran outliers	100387	3015 (2.64-2.60)
Sidechain outliers	100360	3015 (2.64-2.60)
RSRZ outliers	91569	2706 (2.64-2.60)

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. 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	176	<div><div>2%</div><div>64%</div><div>31%</div><div>• •</div></div>
1	B	176	<div><div>61%</div><div>34%</div><div>• •</div></div>
1	C	176	<div><div>%</div><div>68%</div><div>26%</div><div>• •</div></div>
1	D	176	<div><div>2%</div><div>61%</div><div>32%</div><div>• 5%</div></div>
1	E	176	<div><div>%</div><div>61%</div><div>32%</div><div>• •</div></div>

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Mol	Chain	Length	Quality of chain
1	F	176	
1	G	176	
1	H	176	
1	I	176	
1	J	176	
1	K	176	
1	L	176	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	COA	G	201	-	-	-	X
2	COA	I	201	-	-	-	X
3	SPM	I	202	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 18174 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 Spermidine n1-acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	170	Total	C	N	O	S	0	0	0
			1439	921	253	262	3			
1	B	169	Total	C	N	O	S	0	1	0
			1437	920	250	264	3			
1	C	169	Total	C	N	O	S	0	0	0
			1423	912	247	261	3			
1	D	168	Total	C	N	O	S	0	0	0
			1420	911	247	259	3			
1	E	170	Total	C	N	O	S	0	0	0
			1439	921	253	262	3			
1	F	169	Total	C	N	O	S	0	0	0
			1428	915	249	261	3			
1	G	170	Total	C	N	O	S	0	1	0
			1447	925	255	264	3			
1	H	169	Total	C	N	O	S	0	0	0
			1428	915	249	261	3			
1	I	169	Total	C	N	O	S	0	0	0
			1428	915	249	261	3			
1	J	169	Total	C	N	O	S	0	1	0
			1439	921	253	262	3			
1	K	170	Total	C	N	O	S	0	0	0
			1439	921	253	262	3			
1	L	169	Total	C	N	O	S	0	0	0
			1428	915	249	261	3			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
A	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
A	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
B	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
B	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03

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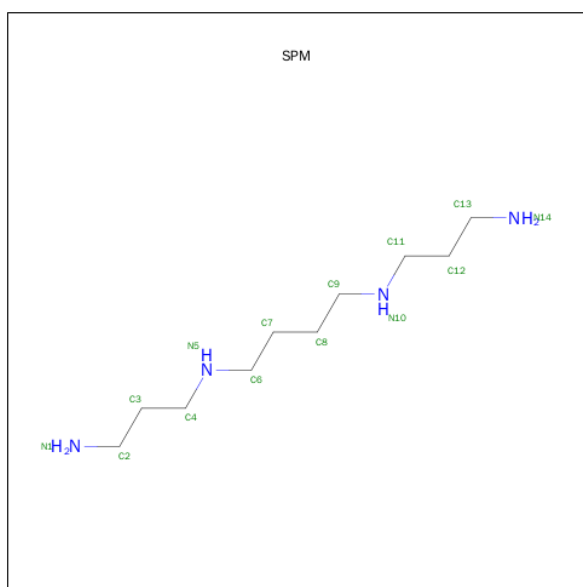
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
C	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
C	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
C	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
D	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
D	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
D	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
E	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
E	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
E	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
F	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
F	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
F	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
G	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
G	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
G	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
H	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
H	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
H	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
I	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
I	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
I	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
J	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
J	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
J	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
K	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
K	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
K	0	ALA	-	EXPRESSION TAG	UNP Q9KL03
L	-2	SER	-	EXPRESSION TAG	UNP Q9KL03
L	-1	ASN	-	EXPRESSION TAG	UNP Q9KL03
L	0	ALA	-	EXPRESSION TAG	UNP Q9KL03

- Molecule 2 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



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		0	0
			41	17	6	15	3			
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		0	0
			41	17	6	15	3			
2	E	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	F	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	G	1	Total	C	O	P			0	0
			21	5	13	3				
2	H	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	I	1	Total	C	N	O	P		0	0
			39	16	5	15	3			
2	J	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	K	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	L	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

- Molecule 3 is SPERMINE (three-letter code: SPM) (formula: C₁₀H₂₆N₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	C	N	0	0
			14	10	4		
3	G	1	Total	C	N	0	0
			14	10	4		
3	H	1	Total	C	N	0	0
			14	10	4		
3	I	1	Total	C	N	0	0
			14	10	4		
3	J	1	Total	C	N	0	0
			14	10	4		
3	K	1	Total	C	N	0	0
			14	10	4		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			7	4	3		
4	I	1	Total	C	O	0	0
			7	4	3		
4	L	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	21	Total	O	0	0
			21	21		
5	B	30	Total	O	0	1
			31	31		
5	C	29	Total	O	0	0
			29	29		
5	D	38	Total	O	0	0
			38	38		
5	E	32	Total	O	0	0
			32	32		
5	F	35	Total	O	0	0
			35	35		
5	G	21	Total	O	0	0
			21	21		
5	H	32	Total	O	0	0
			32	32		
5	I	25	Total	O	0	0
			25	25		

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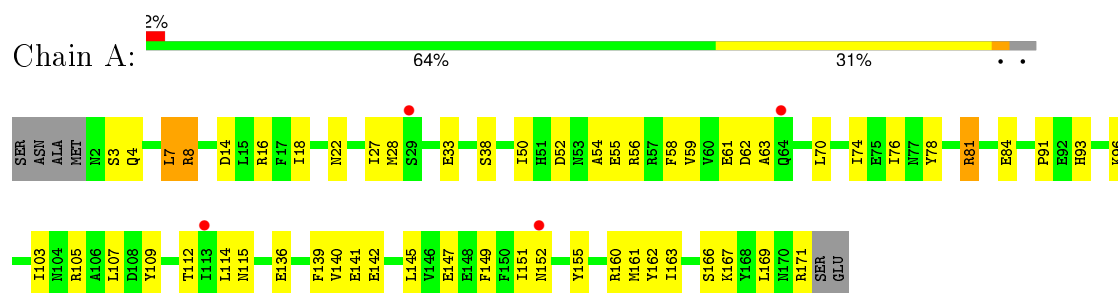
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	J	31	Total 31	O 31	0	0
5	K	31	Total 31	O 31	0	0
5	L	22	Total 22	O 22	0	0

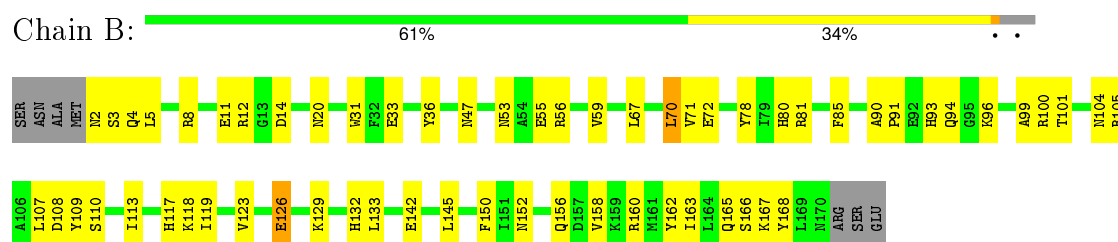
3 Residue-property plots [i](#)

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.

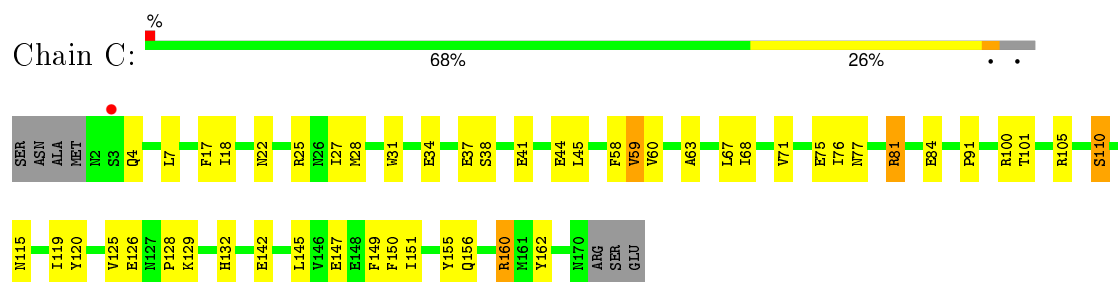
- Molecule 1: Spermidine n1-acetyltransferase



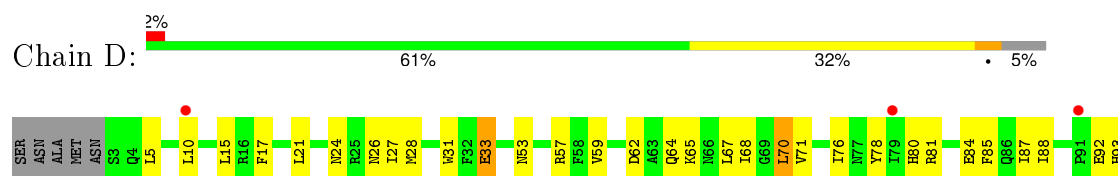
- Molecule 1: Spermidine n1-acetyltransferase



- Molecule 1: Spermidine n1-acetyltransferase



- Molecule 1: Spermidine n1-acetyltransferase

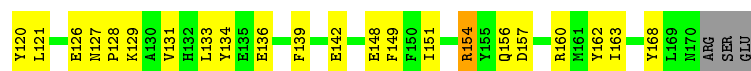




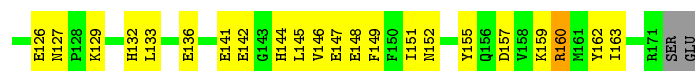
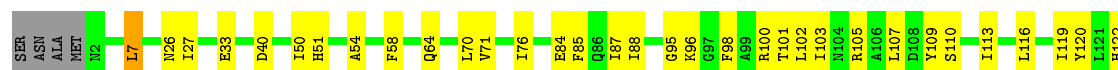
• Molecule 1: Spermidine n1-acetyltransferase



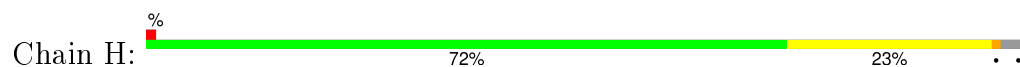
• Molecule 1: Spermidine n1-acetyltransferase



• Molecule 1: Spermidine n1-acetyltransferase



• Molecule 1: Spermidine n1-acetyltransferase



• Molecule 1: Spermidine n1-acetyltransferase





• Molecule 1: Spermidine n1-acetyltransferase

Chain J: 60% 33%



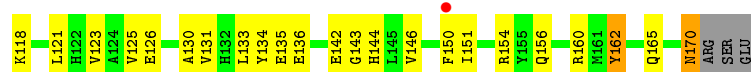
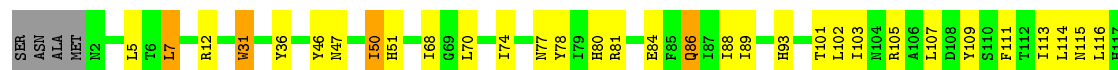
• Molecule 1: Spermidine n1-acetyltransferase

Chain K: 60% 32% 5%



• Molecule 1: Spermidine n1-acetyltransferase

Chain L: 65% 28%



4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α , β , γ	176.95Å 176.95Å 67.01Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.82 – 2.61 43.82 – 2.61	Depositor EDS
% Data completeness (in resolution range)	95.7 (43.82-2.61) 95.7 (43.82-2.61)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.53 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.185 , 0.238 0.188 , 0.240	Depositor DCC
R_{free} test set	3381 reflections (5.22%)	DCC
Wilson B-factor (Å ²)	36.5	Xtriage
Anisotropy	0.407	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.271 for H, K, L 0.215 for -K, -H, -L 0.289 for -H, -K, L 0.224 for K, H, -L 0.447 for -h,-k,l 0.440 for h,-h-k,-l 0.437 for -k,-h,-l	Xtriage
Reported twinning fraction	0.271 for H, K, L 0.215 for -K, -H, -L 0.289 for -H, -K, L 0.224 for K, H, -L	Depositor
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 68098 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18174	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.51% 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, 0.375 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, PEG, SPM

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	0.66	0/1472	0.88	2/1987 (0.1%)
1	B	0.71	0/1470	0.84	0/1985
1	C	0.69	0/1455	0.84	2/1965 (0.1%)
1	D	0.68	0/1453	0.82	1/1962 (0.1%)
1	E	0.75	0/1472	0.91	2/1987 (0.1%)
1	F	0.76	0/1461	0.86	1/1973 (0.1%)
1	G	0.78	0/1480	0.91	0/1998
1	H	0.75	0/1461	0.95	2/1973 (0.1%)
1	I	0.70	0/1461	0.86	1/1973 (0.1%)
1	J	0.68	0/1472	0.84	0/1987
1	K	0.70	0/1472	0.86	0/1987
1	L	0.67	0/1461	0.86	0/1973
All	All	0.71	0/17590	0.87	11/23750 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	1

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	40	ASP	CB-CG-OD1	-6.25	112.68	118.30
1	C	76	ILE	N-CA-C	-6.04	94.69	111.00
1	A	81	ARG	NE-CZ-NH2	5.84	123.22	120.30
1	E	123	VAL	CB-CA-C	-5.63	100.69	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	12	ARG	NE-CZ-NH2	5.35	122.97	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	169	LEU	Peptide

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	1439	0	1397	34	0
1	B	1437	0	1389	39	0
1	C	1423	0	1379	33	0
1	D	1420	0	1378	46	0
1	E	1439	0	1397	39	0
1	F	1428	0	1384	28	0
1	G	1447	0	1402	42	0
1	H	1428	0	1384	33	0
1	I	1428	0	1384	38	0
1	J	1439	0	1396	54	0
1	K	1439	0	1397	52	0
1	L	1428	0	1384	45	0
2	A	48	0	32	0	0
2	B	41	0	22	3	0
2	C	48	0	32	3	0
2	D	41	0	22	0	0
2	E	48	0	32	2	0
2	F	48	0	32	4	0
2	G	21	0	6	1	0
2	H	48	0	32	1	0
2	I	39	0	21	0	0
2	J	48	0	32	5	0
2	K	48	0	32	1	0
2	L	48	0	32	6	0
3	E	14	0	26	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	14	0	26	0	0
3	H	14	0	26	0	0
3	I	14	0	26	0	0
3	J	14	0	26	1	0
3	K	14	0	26	1	0
4	H	7	0	10	0	0
4	I	7	0	10	0	0
4	L	7	0	10	0	0
5	A	21	0	0	2	0
5	B	31	0	0	1	0
5	C	29	0	0	1	0
5	D	38	0	0	0	0
5	E	32	0	0	1	0
5	F	35	0	0	1	0
5	G	21	0	0	1	0
5	H	32	0	0	3	0
5	I	25	0	0	1	0
5	J	31	0	0	0	0
5	K	31	0	0	2	0
5	L	22	0	0	1	0
All	All	18174	0	17184	446	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 13.

The worst 5 of 446 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:K:129:LYS:HD3	2:K:201:COA:H8A	1.44	0.99
2:C:201:COA:H132	2:C:201:COA:O9P	1.77	0.84
2:L:201:COA:H132	2:L:201:COA:O9P	1.78	0.83
1:I:18:ILE:HD12	1:I:70:LEU:HD11	1.62	0.80
1:F:129:LYS:HG2	2:F:201:COA:O2B	1.83	0.78

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	168/176 (96%)	150 (89%)	18 (11%)	0	100	100
1	B	168/176 (96%)	148 (88%)	20 (12%)	0	100	100
1	C	167/176 (95%)	152 (91%)	15 (9%)	0	100	100
1	D	166/176 (94%)	150 (90%)	16 (10%)	0	100	100
1	E	168/176 (96%)	155 (92%)	13 (8%)	0	100	100
1	F	167/176 (95%)	156 (93%)	11 (7%)	0	100	100
1	G	169/176 (96%)	153 (90%)	16 (10%)	0	100	100
1	H	167/176 (95%)	150 (90%)	17 (10%)	0	100	100
1	I	167/176 (95%)	153 (92%)	14 (8%)	0	100	100
1	J	168/176 (96%)	145 (86%)	23 (14%)	0	100	100
1	K	168/176 (96%)	146 (87%)	22 (13%)	0	100	100
1	L	167/176 (95%)	148 (89%)	19 (11%)	0	100	100
All	All	2010/2112 (95%)	1806 (90%)	204 (10%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	154/159 (97%)	142 (92%)	12 (8%)	16	29
1	B	154/159 (97%)	143 (93%)	11 (7%)	18	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	152/159 (96%)	145 (95%)	7 (5%)	33	60
1	D	152/159 (96%)	141 (93%)	11 (7%)	18	34
1	E	154/159 (97%)	141 (92%)	13 (8%)	14	25
1	F	153/159 (96%)	146 (95%)	7 (5%)	33	60
1	G	155/159 (98%)	149 (96%)	6 (4%)	39	67
1	H	153/159 (96%)	150 (98%)	3 (2%)	63	85
1	I	153/159 (96%)	143 (94%)	10 (6%)	21	41
1	J	154/159 (97%)	147 (96%)	7 (4%)	34	61
1	K	154/159 (97%)	140 (91%)	14 (9%)	12	22
1	L	153/159 (96%)	146 (95%)	7 (5%)	33	60
All	All	1841/1908 (96%)	1733 (94%)	108 (6%)	24	46

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	110	SER
1	F	154	ARG
1	K	129	LYS
1	E	129	LYS
1	F	3	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	156	GLN
1	H	22	ASN
1	L	80	HIS
1	G	22	ASN
1	H	4	GLN

5.3.3 RNA ⓘ

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](#)

21 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	201	-	40,50,50	1.11	4 (10%)	50,75,75	3.32	16 (32%)
2	COA	B	201	-	33,43,50	1.13	2 (6%)	42,67,75	3.32	13 (30%)
2	COA	C	201	-	40,50,50	0.98	3 (7%)	50,75,75	2.94	12 (24%)
2	COA	D	201	-	33,43,50	1.09	2 (6%)	42,67,75	3.42	11 (26%)
2	COA	E	201	-	40,50,50	0.96	1 (2%)	50,75,75	3.56	20 (40%)
3	SPM	E	202	-	13,13,13	0.47	0	12,12,12	1.04	1 (8%)
2	COA	F	201	-	40,50,50	1.08	4 (10%)	50,75,75	2.88	14 (28%)
2	COA	G	201	-	19,21,50	0.75	0	26,33,75	1.36	3 (11%)
3	SPM	G	202	-	13,13,13	0.47	0	12,12,12	1.05	1 (8%)
2	COA	H	201	-	40,50,50	1.09	3 (7%)	50,75,75	2.96	15 (30%)
3	SPM	H	202	-	13,13,13	0.43	0	12,12,12	1.22	2 (16%)
4	PEG	H	203	-	6,6,6	0.45	0	5,5,5	0.31	0
2	COA	I	201	-	32,41,50	1.11	2 (6%)	42,64,75	3.28	14 (33%)
3	SPM	I	202	-	13,13,13	0.48	0	12,12,12	1.21	2 (16%)
4	PEG	I	203	-	6,6,6	0.45	0	5,5,5	0.18	0
2	COA	J	201	-	40,50,50	1.09	2 (5%)	50,75,75	3.35	13 (26%)
3	SPM	J	202	-	13,13,13	0.47	0	12,12,12	1.34	3 (25%)
2	COA	K	201	-	40,50,50	1.04	2 (5%)	50,75,75	3.02	15 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SPM	K	202	-	13,13,13	0.43	0	12,12,12	1.05	1 (8%)
2	COA	L	201	-	40,50,50	1.13	4 (10%)	50,75,75	2.95	10 (20%)
4	PEG	L	202	-	6,6,6	0.63	0	5,5,5	0.35	0

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	201	-	-	0/44/64/64	0/3/3/3
2	COA	B	201	-	-	0/36/56/64	0/3/3/3
2	COA	C	201	-	-	0/44/64/64	0/3/3/3
2	COA	D	201	-	-	0/36/56/64	0/3/3/3
2	COA	E	201	-	-	0/44/64/64	0/3/3/3
3	SPM	E	202	-	-	0/11/11/11	0/0/0/0
2	COA	F	201	-	-	0/44/64/64	0/3/3/3
2	COA	G	201	-	-	0/17/30/64	0/1/1/3
3	SPM	G	202	-	-	0/11/11/11	0/0/0/0
2	COA	H	201	-	-	0/44/64/64	0/3/3/3
3	SPM	H	202	-	-	0/11/11/11	0/0/0/0
4	PEG	H	203	-	-	0/4/4/4	0/0/0/0
2	COA	I	201	-	-	0/30/52/64	0/3/3/3
3	SPM	I	202	-	-	0/11/11/11	0/0/0/0
4	PEG	I	203	-	-	0/4/4/4	0/0/0/0
2	COA	J	201	-	-	0/44/64/64	0/3/3/3
3	SPM	J	202	-	-	0/11/11/11	0/0/0/0
2	COA	K	201	-	-	0/44/64/64	0/3/3/3
3	SPM	K	202	-	-	0/11/11/11	0/0/0/0
2	COA	L	201	-	-	0/44/64/64	0/3/3/3
4	PEG	L	202	-	-	0/4/4/4	0/0/0/0

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	201	COA	CDP-CBP	-2.80	1.47	1.53
2	B	201	COA	CEP-CBP	-2.66	1.48	1.53
2	F	201	COA	CDP-CBP	-2.26	1.49	1.53
2	A	201	COA	CDP-CBP	-2.18	1.49	1.53
2	H	201	COA	CEP-CBP	-2.14	1.49	1.53

The worst 5 of 166 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	201	COA	CDP-CBP-CAP	-10.75	89.72	109.34
2	E	201	COA	CDP-CBP-CAP	-10.12	90.86	109.34
2	D	201	COA	CDP-CBP-CAP	-9.77	91.51	109.34
2	E	201	COA	CEP-CBP-CAP	-9.23	92.49	109.34
2	K	201	COA	CEP-CBP-CAP	-9.06	92.81	109.34

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	201	COA	3	0
2	C	201	COA	3	0
2	E	201	COA	2	0
3	E	202	SPM	1	0
2	F	201	COA	4	0
2	G	201	COA	1	0
2	H	201	COA	1	0
2	J	201	COA	5	0
3	J	202	SPM	1	0
2	K	201	COA	1	0
3	K	202	SPM	1	0
2	L	201	COA	6	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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	170/176 (96%)	-0.04	4 (2%) 62 56	25, 41, 58, 70	0
1	B	169/176 (96%)	-0.10	0 100 100	26, 37, 55, 76	0
1	C	169/176 (96%)	-0.15	1 (0%) 90 88	28, 38, 55, 60	0
1	D	168/176 (95%)	-0.07	3 (1%) 71 66	29, 40, 61, 74	0
1	E	170/176 (96%)	-0.31	1 (0%) 90 88	20, 31, 47, 55	0
1	F	169/176 (96%)	-0.35	1 (0%) 90 88	20, 32, 47, 75	0
1	G	170/176 (96%)	-0.29	0 100 100	19, 32, 50, 79	0
1	H	169/176 (96%)	-0.37	1 (0%) 90 88	21, 30, 47, 72	0
1	I	169/176 (96%)	-0.29	0 100 100	25, 36, 46, 60	0
1	J	169/176 (96%)	-0.14	0 100 100	24, 37, 48, 66	0
1	K	170/176 (96%)	-0.15	1 (0%) 90 88	22, 38, 59, 70	0
1	L	169/176 (96%)	-0.17	1 (0%) 90 88	24, 37, 51, 58	0
All	All	2031/2112 (96%)	-0.20	13 (0%) 90 88	19, 36, 54, 79	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	29	SER	3.1
1	D	91	PRO	3.0
1	F	83	ALA	3.0
1	A	113	ILE	2.9
1	D	10	LEU	2.7

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 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, 95th 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(Å ²)	Q<0.9
2	COA	G	201	21/48	0.77	0.32	5.82	90,98,102,106	0
2	COA	I	201	39/48	0.81	0.27	4.09	45,80,90,91	0
3	SPM	I	202	14/14	0.87	0.27	2.73	34,39,42,42	0
3	SPM	J	202	14/14	0.92	0.20	1.70	26,34,47,50	0
3	SPM	H	202	14/14	0.91	0.20	1.63	39,45,49,51	0
3	SPM	K	202	14/14	0.90	0.19	1.56	39,42,45,45	0
2	COA	K	201	48/48	0.87	0.26	1.51	44,58,92,96	0
3	SPM	G	202	14/14	0.94	0.19	1.28	28,32,34,37	0
3	SPM	E	202	14/14	0.94	0.19	1.22	34,39,40,42	0
2	COA	A	201	48/48	0.87	0.23	0.80	49,68,85,93	0
2	COA	D	201	41/48	0.82	0.23	0.78	39,86,101,102	0
2	COA	B	201	41/48	0.90	0.22	0.71	39,54,72,75	0
2	COA	F	201	48/48	0.90	0.18	0.66	46,59,97,99	0
2	COA	C	201	48/48	0.90	0.20	0.48	45,61,88,94	0
2	COA	J	201	48/48	0.92	0.19	0.26	33,46,85,87	0
2	COA	E	201	48/48	0.92	0.19	0.15	34,50,97,105	0
2	COA	L	201	48/48	0.89	0.18	0.07	45,62,105,108	0
4	PEG	L	202	7/7	0.91	0.15	-0.30	45,45,47,48	0
2	COA	H	201	48/48	0.93	0.15	-0.40	38,50,59,60	0
4	PEG	H	203	7/7	0.91	0.17	-	38,40,45,47	0
4	PEG	I	203	7/7	0.93	0.15	-	56,58,60,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.