



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 23, 2019 – 11:12 AM EST

PDB ID : 5NX9  
Title : Crystal structure of Neanderthal Adenylosuccinate Lyase (ADSL) in complex with its products AMP and fumarate  
Authors : Van Laer, B.; Kapp, U.; Soler-Lopez, M.; Leonard, G.; Mueller-Dieckmann, C.  
Deposited on : 2017-05-09  
Resolution : 2.30 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](mailto: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.

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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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : rb-20031633  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20031633

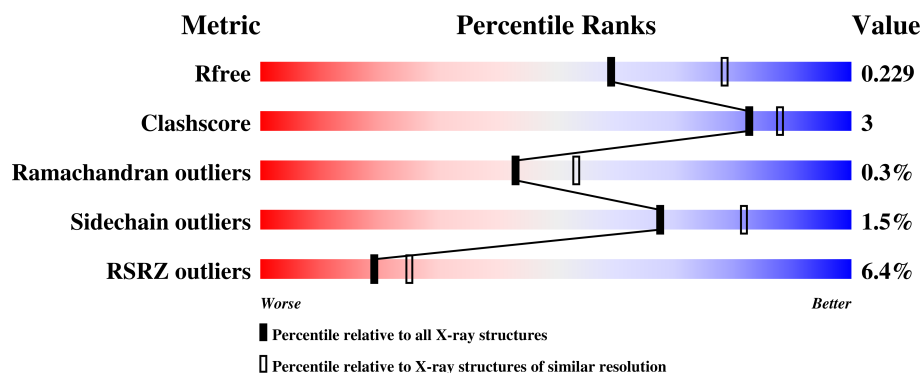
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

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	487	<div> <div>9%</div> <div>89%</div> <div>7%</div> <div>.</div> </div>
1	B	487	<div> <div>6%</div> <div>93%</div> <div>5%</div> <div>.</div> </div>
1	C	487	<div> <div>8%</div> <div>85%</div> <div>5%</div> <div>9%</div> </div>
1	D	487	<div> <div>2%</div> <div>90%</div> <div>8%</div> <div>.</div> </div>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 15464 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.

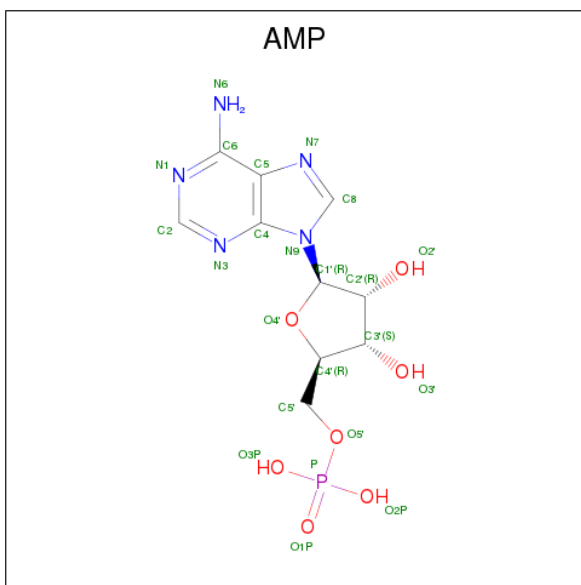
- Molecule 1 is a protein called Adenylosuccinate lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	466	Total	C	N	O	S	0	0	0
			3720	2344	662	688	26			
1	B	476	Total	C	N	O	S	0	0	0
			3791	2388	672	703	28			
1	C	441	Total	C	N	O	S	0	0	0
			3530	2228	626	652	24			
1	D	477	Total	C	N	O	S	0	0	0
			3799	2394	673	704	28			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

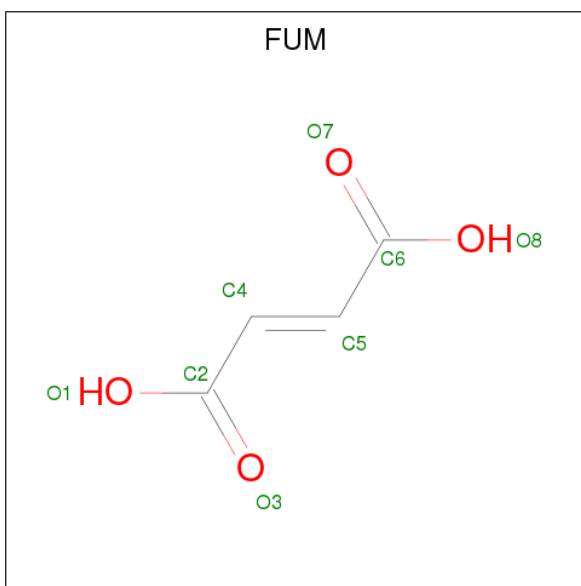
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		
2	A	2	Total	Cl	0	0
			2	2		
2	D	1	Total	Cl	0	0
			1	1		
2	C	2	Total	Cl	0	0
			2	2		

- Molecule 3 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>5</sub>O<sub>7</sub>P).



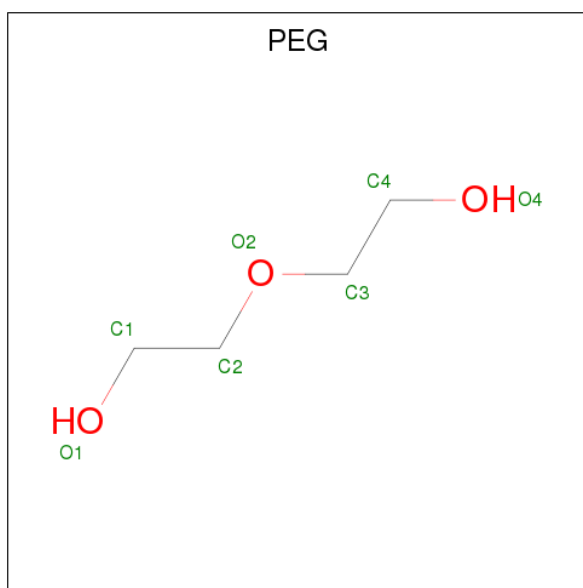
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
3	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 4 is FUMARIC ACID (three-letter code: FUM) (formula:  $C_4H_4O_4$ ).



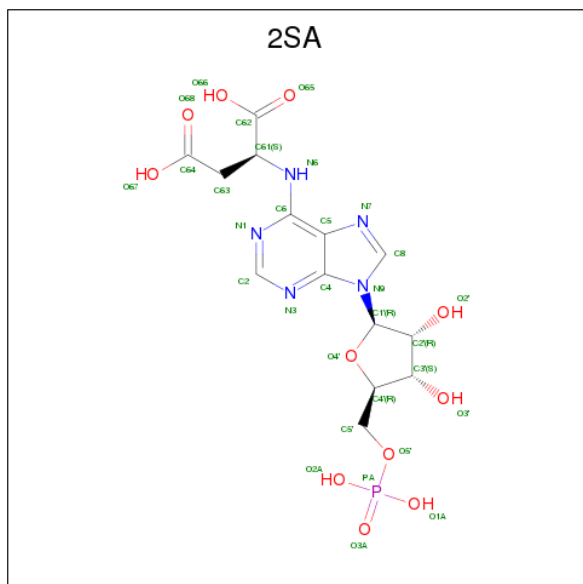
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	4	4		
4	D	1	Total	C	O	0	0
			8	4	4		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



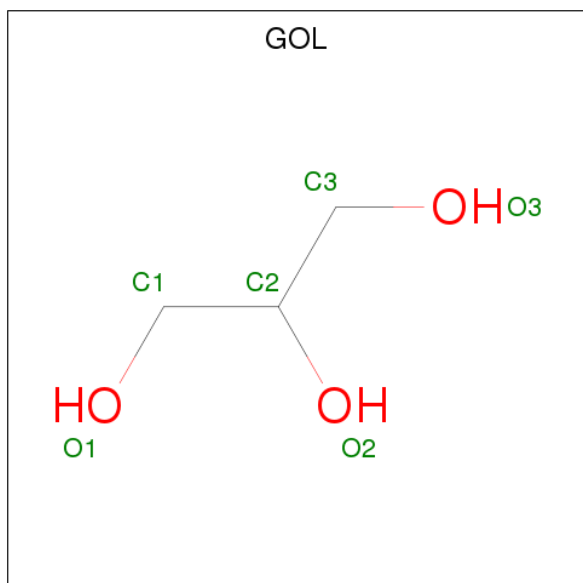
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is 2-[9-(3,4-DIHYDROXY-5-PHOSPHONOOXYMETHYL-TETRAHYDRO-FURAN-2-YL)-9H-PURIN-6-YLAMINO]-SUCCINIC ACID (three-letter code: 2SA) (formula:  $C_{14}H_{18}N_5O_{11}P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	P	0	0
			31	14	5	11	1		
6	C	1	Total	C	N	O	P	0	0
			31	14	5	11	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	99	Total	O	0	0
			99	99		
8	B	98	Total	O	0	0
			98	98		
8	C	98	Total	O	0	0
			98	98		
8	D	102	Total	O	0	0
			102	102		

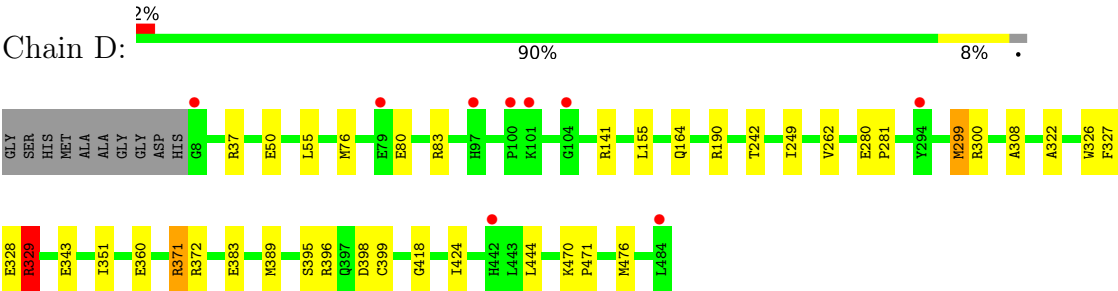


- Molecule 1: Adenylosuccinate lyase





● Molecule 1: Adenylosuccinate lyase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.74Å 107.49Å 209.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.38 – 2.30 48.38 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.38-2.30) 99.5 (48.38-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.48 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.193 , 0.227 0.198 , 0.229	Depositor DCC
$R_{free}$ test set	4317 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.8	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 40.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	15464	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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, 0.333 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: GOL, FUM, CL, 2SA, AMP, PEG

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	0.54	0/3786	0.63	0/5108
1	B	0.56	0/3860	0.65	0/5210
1	C	0.54	0/3594	0.61	0/4855
1	D	0.53	0/3868	0.63	2/5221 (0.0%)
All	All	0.54	0/15108	0.63	2/20394 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	300	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	D	398	ASP	CB-CG-OD1	5.01	122.81	118.30

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	3720	0	3752	22	0
1	B	3791	0	3818	17	0
1	C	3530	0	3552	21	0
1	D	3799	0	3829	24	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	1	0	0	0	0
3	A	23	0	12	3	0
3	D	23	0	12	0	0
4	A	8	0	2	3	0
4	D	8	0	2	0	0
5	A	35	0	50	1	0
5	B	7	0	10	1	0
5	C	28	0	40	0	0
5	D	21	0	30	0	0
6	B	31	0	14	0	0
6	C	31	0	14	0	0
7	C	6	0	8	0	0
8	A	99	0	0	0	0
8	B	98	0	0	1	0
8	C	98	0	0	3	0
8	D	102	0	0	1	0
All	All	15464	0	15145	80	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 3.

The worst 5 of 80 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:D:141:ARG:NH1	1:D:476:MET:O	2.14	0.81
1:A:141:ARG:NH1	1:A:476:MET:O	2.12	0.81
1:B:328:GLU:O	1:B:329:ARG:HB2	1.79	0.81
1:D:328:GLU:O	1:D:329:ARG:HB2	1.81	0.81
1:A:328:GLU:O	1:A:329:ARG:HB2	1.82	0.79

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	462/487 (95%)	458 (99%)	3 (1%)	1 (0%)	49	61
1	B	474/487 (97%)	469 (99%)	3 (1%)	2 (0%)	36	45
1	C	435/487 (89%)	432 (99%)	2 (0%)	1 (0%)	49	61
1	D	475/487 (98%)	473 (100%)	1 (0%)	1 (0%)	49	61
All	All	1846/1948 (95%)	1832 (99%)	9 (0%)	5 (0%)	43	53

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	329	ARG
1	B	9	SER
1	B	329	ARG
1	C	329	ARG
1	D	329	ARG

### 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	408/422 (97%)	400 (98%)	8 (2%)	58	75
1	B	416/422 (99%)	411 (99%)	5 (1%)	74	86
1	C	388/422 (92%)	383 (99%)	5 (1%)	71	84
1	D	417/422 (99%)	410 (98%)	7 (2%)	63	79
All	All	1629/1688 (96%)	1604 (98%)	25 (2%)	67	82

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	331	LEU
1	C	60	GLU
1	D	371	ARG

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Mol	Chain	Res	Type
1	B	425	GLU
1	C	93	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	439	GLN
1	D	161	GLN

### 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](#)

Of 26 ligands modelled in this entry, 6 are monoatomic - leaving 20 for Mogul analysis.

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	AMP	A	503	-	22,25,25	1.09	2 (9%)	23,38,38	1.99	5 (21%)
4	FUM	A	504	-	1,7,7	0.59	0	0,8,8	0.00	-
5	PEG	A	505	-	6,6,6	0.57	0	5,5,5	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	PEG	A	506	-	6,6,6	0.68	0	5,5,5	0.36	0
5	PEG	A	507	-	6,6,6	0.58	0	5,5,5	0.59	0
5	PEG	A	508	-	6,6,6	0.54	0	5,5,5	0.17	0
5	PEG	A	509	-	6,6,6	0.55	0	5,5,5	0.29	0
6	2SA	B	502	-	23,33,33	3.44	6 (26%)	25,49,49	2.26	4 (16%)
5	PEG	B	503	-	6,6,6	0.54	0	5,5,5	0.36	0
6	2SA	C	501	-	23,33,33	3.48	7 (30%)	25,49,49	2.60	6 (24%)
5	PEG	C	504	-	6,6,6	0.70	0	5,5,5	0.38	0
5	PEG	C	505	-	6,6,6	0.56	0	5,5,5	0.32	0
5	PEG	C	506	-	6,6,6	0.52	0	5,5,5	0.39	0
7	GOL	C	507	-	5,5,5	0.32	0	5,5,5	0.35	0
5	PEG	C	508	-	6,6,6	0.52	0	5,5,5	0.33	0
3	AMP	D	502	-	22,25,25	0.81	1 (4%)	23,38,38	1.95	2 (8%)
4	FUM	D	503	-	1,7,7	0.22	0	0,8,8	0.00	-
5	PEG	D	504	-	6,6,6	0.67	0	5,5,5	0.51	0
5	PEG	D	505	-	6,6,6	0.57	0	5,5,5	0.39	0
5	PEG	D	506	-	6,6,6	0.55	0	5,5,5	0.32	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
3	AMP	A	503	-	-	0/6/26/26	0/3/3/3
4	FUM	A	504	-	-	0/0/5/5	0/0/0/0
5	PEG	A	505	-	-	0/4/4/4	0/0/0/0
5	PEG	A	506	-	-	0/4/4/4	0/0/0/0
5	PEG	A	507	-	-	0/4/4/4	0/0/0/0
5	PEG	A	508	-	-	0/4/4/4	0/0/0/0
5	PEG	A	509	-	-	0/4/4/4	0/0/0/0
6	2SA	B	502	-	-	1/12/38/38	0/3/3/3
5	PEG	B	503	-	-	0/4/4/4	0/0/0/0
6	2SA	C	501	-	-	1/12/38/38	0/3/3/3
5	PEG	C	504	-	-	0/4/4/4	0/0/0/0
5	PEG	C	505	-	-	0/4/4/4	0/0/0/0
5	PEG	C	506	-	-	0/4/4/4	0/0/0/0
7	GOL	C	507	-	-	0/4/4/4	0/0/0/0
5	PEG	C	508	-	-	0/4/4/4	0/0/0/0
3	AMP	D	502	-	-	0/6/26/26	0/3/3/3
4	FUM	D	503	-	-	0/0/5/5	0/0/0/0
5	PEG	D	504	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEG	D	505	-	-	0/4/4/4	0/0/0/0
5	PEG	D	506	-	-	0/4/4/4	0/0/0/0

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	502	2SA	C3'-C2'	-9.62	1.28	1.53
6	C	501	2SA	C3'-C2'	-9.37	1.28	1.53
6	C	501	2SA	O4'-C4'	-6.78	1.29	1.45
6	B	502	2SA	O4'-C4'	-6.57	1.30	1.45
3	A	503	AMP	C8-N9	-2.14	1.34	1.36

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	501	2SA	N3-C2-N1	-8.01	122.00	128.86
3	D	502	AMP	N3-C2-N1	-7.46	122.48	128.86
3	A	503	AMP	N3-C2-N1	-7.29	122.62	128.86
6	B	502	2SA	N3-C2-N1	-7.13	122.76	128.86
6	C	501	2SA	C4'-O4'-C1'	-3.85	105.81	109.83

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	501	2SA	N1-C6-N6-C61
6	B	502	2SA	C62-C61-N6-C6

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	503	AMP	3	0
4	A	504	FUM	3	0
5	A	509	PEG	1	0
5	B	503	PEG	1	0

## 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 [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, 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	466/487 (95%)	0.22	44 (9%) 8 11	21, 36, 81, 110	0
1	B	476/487 (97%)	0.07	27 (5%) 24 30	21, 35, 76, 106	0
1	C	441/487 (90%)	0.18	39 (8%) 10 13	21, 34, 91, 130	0
1	D	477/487 (97%)	0.01	9 (1%) 66 73	22, 37, 63, 87	0
All	All	1860/1948 (95%)	0.12	119 (6%) 19 25	21, 35, 77, 130	0

The worst 5 of 119 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	432	TYR	9.3
1	C	436	ILE	7.4
1	C	437	HIS	6.5
1	A	282	PHE	6.0
1	B	392	ALA	6.0

### 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
5	PEG	D	505	7/7	0.73	0.30	57,67,74,75	0
7	GOL	C	507	6/6	0.78	0.22	60,63,65,67	0
5	PEG	A	509	7/7	0.80	0.22	63,64,68,71	0
5	PEG	D	506	7/7	0.81	0.15	56,61,68,70	0
5	PEG	A	508	7/7	0.81	0.13	61,65,67,68	0
5	PEG	C	505	7/7	0.84	0.14	64,67,68,68	0
5	PEG	C	504	7/7	0.87	0.11	37,45,47,48	0
5	PEG	A	507	7/7	0.88	0.17	53,55,58,58	0
5	PEG	C	508	7/7	0.89	0.15	51,54,61,67	0
5	PEG	A	506	7/7	0.90	0.13	50,51,57,57	0
5	PEG	B	503	7/7	0.91	0.12	49,53,55,56	0
5	PEG	D	504	7/7	0.92	0.13	46,47,50,51	0
5	PEG	C	506	7/7	0.92	0.15	42,48,63,64	0
5	PEG	A	505	7/7	0.93	0.14	44,48,52,52	0
4	FUM	D	503	8/8	0.94	0.10	33,34,36,38	0
6	2SA	C	501	31/31	0.96	0.11	24,28,48,54	0
4	FUM	A	504	8/8	0.96	0.13	33,35,36,38	0
2	CL	C	502	1/1	0.97	0.10	45,45,45,45	0
2	CL	A	501	1/1	0.97	0.08	49,49,49,49	0
3	AMP	D	502	23/23	0.98	0.09	30,34,38,44	0
6	2SA	B	502	31/31	0.98	0.09	26,31,37,38	0
2	CL	C	503	1/1	0.99	0.11	26,26,26,26	0
3	AMP	A	503	23/23	0.99	0.10	27,29,31,33	0
2	CL	B	501	1/1	1.00	0.09	24,24,24,24	0
2	CL	D	501	1/1	1.00	0.08	35,35,35,35	0
2	CL	A	502	1/1	1.00	0.10	27,27,27,27	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.