



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:44 PM GMT

PDB ID : 4JBN
Title : Crystal structure of O-Acetyl Serine Sulphydrylase from *Entamoeba histolytica* in complex with Serine acetyl transferase derived tetrapeptide, SPSI
Authors : Raj, I.; Gourinath, S.
Deposited on : 2013-02-20
Resolution : 1.87 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
<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

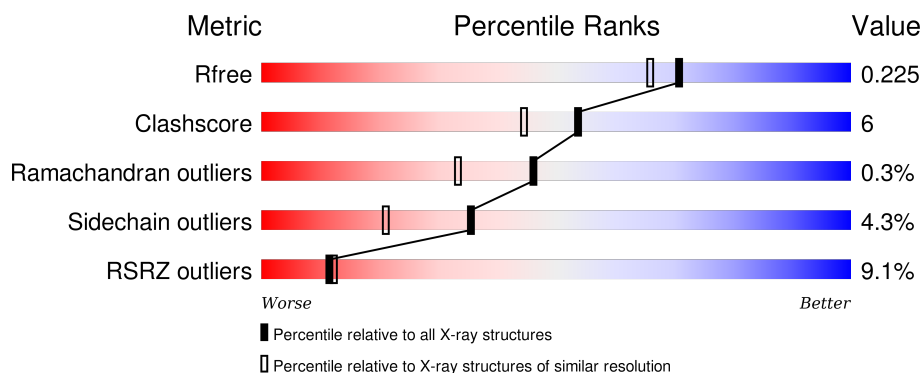
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.87 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	6965 (1.90-1.86)
Clashscore	102246	7778 (1.90-1.86)
Ramachandran outliers	100387	7691 (1.90-1.86)
Sidechain outliers	100360	7692 (1.90-1.86)
RSRZ outliers	91569	6979 (1.90-1.86)

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 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	338	<div> <div>12%</div> <div> <div></div> <div>85%</div> <div>12%</div> <div>..</div> </div> </div>
1	B	338	<div> <div>5%</div> <div> <div></div> <div>83%</div> <div>15%</div> <div>.</div> </div> </div>
2	C	4	<div> <div>75%</div> <div> <div>25%</div> <div>25%</div> <div>25%</div> <div>25%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5448 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 Cysteine synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	P	S	0	0	0
			2581	1638	434	494	1	14			
1	B	337	Total	C	N	O	P	S	0	0	0
			2591	1644	437	495	1	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	338	HIS	-	EXPRESSION TAG	UNP O15570
B	338	HIS	-	EXPRESSION TAG	UNP O15570

- Molecule 2 is a protein called SAT derived tetrapeptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			20	12	3	5			

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



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

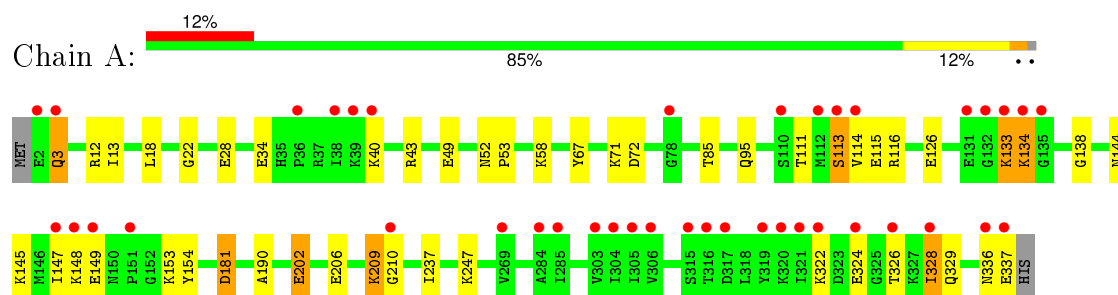
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	121	Total	O	0	0
			121	121		
4	B	130	Total	O	0	0
			130	130		

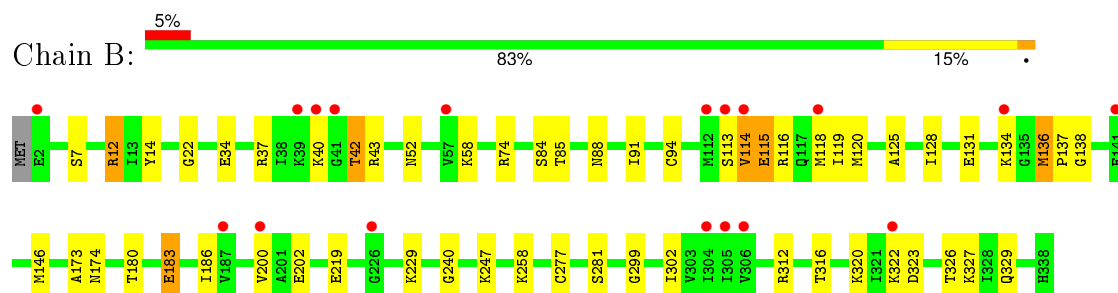
3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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.

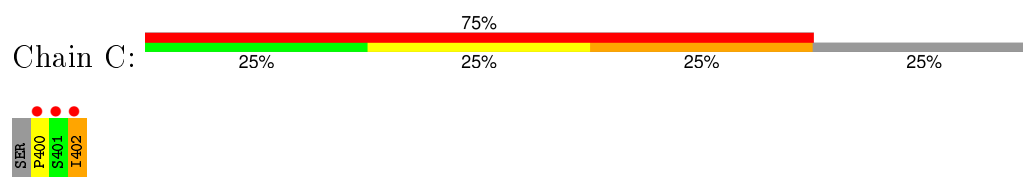
• Molecule 1: Cysteine synthase



• Molecule 1: Cysteine synthase



• Molecule 2: SAT derived tetrapeptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	80.52Å 80.52Å 112.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.47 – 1.87 27.46 – 1.87	Depositor EDS
% Data completeness (in resolution range)	98.8 (27.47-1.87) 98.8 (27.46-1.87)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.74 (at 1.87Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.184 , 0.222 0.189 , 0.225	Depositor DCC
R_{free} test set	2872 reflections (5.15%)	DCC
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 47.2	EDS
Estimated twinning fraction	0.021 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 58645 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5448	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: LLP, 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	1.09	2/2598 (0.1%)	0.99	8/3499 (0.2%)
1	B	1.14	1/2609 (0.0%)	1.03	5/3514 (0.1%)
2	C	1.60	0/19	2.01	1/23 (4.3%)
All	All	1.12	3/5226 (0.1%)	1.01	14/7036 (0.2%)

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	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	181	ASP	CB-CG	-5.94	1.39	1.51
1	B	7	SER	CB-OG	-5.30	1.35	1.42
1	A	49	GLU	CD-OE1	-5.17	1.20	1.25

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	37	ARG	NE-CZ-NH2	-15.04	112.78	120.30
1	B	37	ARG	NE-CZ-NH1	10.80	125.70	120.30
1	B	12	ARG	NE-CZ-NH1	9.20	124.90	120.30
1	A	12	ARG	NE-CZ-NH1	7.99	124.29	120.30
1	A	209	LYS	C-N-CA	-6.44	108.77	122.30
1	A	72	ASP	CB-CG-OD2	6.41	124.07	118.30
2	C	400	PRO	N-CA-CB	6.24	110.79	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	ARG	NE-CZ-NH2	-6.09	117.25	120.30
1	B	74	ARG	NE-CZ-NH2	-5.65	117.48	120.30
1	B	12	ARG	NE-CZ-NH2	-5.57	117.52	120.30
1	A	72	ASP	CB-CG-OD1	-5.52	113.33	118.30
1	A	202	GLU	CG-CD-OE1	5.42	129.14	118.30
1	A	18	LEU	CB-CG-CD1	-5.29	102.00	111.00
1	A	202	GLU	CG-CD-OE2	-5.13	108.04	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	210	GLY	Peptide

5.2 Too-close contacts ⓘ

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	2581	0	2640	27	0
1	B	2591	0	2647	42	0
2	C	20	0	17	1	0
3	A	5	0	0	0	0
4	A	121	0	0	2	0
4	B	130	0	0	4	0
All	All	5448	0	5304	68	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 6.

All (68) 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:B:174:ASN:HB2	4:B:520:HOH:O	1.81	0.80
1:B:115:GLU:HA	1:B:118:MET:HE3	1.65	0.79
1:B:180:THR:O	1:B:183:GLU:HG2	1.84	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:GLU:HA	1:B:118:MET:CE	2.15	0.76
1:B:42:THR:HG21	4:B:473:HOH:O	1.86	0.74
1:B:322:LYS:HG3	1:B:322:LYS:O	1.92	0.69
1:A:145:LYS:O	1:A:149:GLU:HG3	1.94	0.68
1:B:42:THR:HG22	1:B:299:GLY:H	1.59	0.68
1:A:113:SER:HB3	1:A:116:ARG:HB2	1.77	0.66
1:A:336:ASN:O	1:A:337:GLU:C	2.35	0.65
1:B:22:GLY:H	1:B:52:ASN:HD21	1.42	0.65
1:B:114:VAL:O	1:B:118:MET:HG3	1.96	0.65
1:A:22:GLY:H	1:A:52:ASN:ND2	1.95	0.64
1:B:219:GLU:HG3	1:B:258:LYS:HG3	1.80	0.64
1:B:131:GLU:HB3	1:B:134:LYS:HG3	1.80	0.63
1:A:22:GLY:H	1:A:52:ASN:HD21	1.47	0.63
1:A:326:THR:HG23	1:A:329:GLN:H	1.64	0.63
1:B:131:GLU:HB3	1:B:134:LYS:CG	2.28	0.62
1:B:131:GLU:CB	1:B:134:LYS:HG3	2.34	0.58
1:B:229:LYS:HD2	1:B:240:GLY:HA3	1.84	0.58
1:B:22:GLY:H	1:B:52:ASN:ND2	2.02	0.57
1:B:91:ILE:HD12	1:B:119:ILE:HG21	1.86	0.56
1:B:91:ILE:HD12	1:B:119:ILE:CG2	2.36	0.55
1:A:144:ASN:HA	1:A:147:ILE:HG12	1.87	0.55
1:B:180:THR:O	1:B:183:GLU:CG	2.55	0.54
1:B:316:THR:O	1:B:320:LYS:HE2	2.07	0.54
1:B:34:GLU:OE1	1:B:327:LYS:NZ	2.42	0.53
1:B:88:ASN:ND2	1:B:312:ARG:HH11	2.06	0.52
1:B:326:THR:HG23	1:B:329:GLN:H	1.75	0.51
1:A:147:ILE:HG13	1:A:148:LYS:H	1.74	0.51
1:A:147:ILE:HG13	1:A:148:LYS:N	2.27	0.50
1:A:202:GLU:OE2	1:A:247:LYS:NZ	2.36	0.50
1:A:144:ASN:O	1:A:147:ILE:HG13	2.13	0.48
1:B:173:ALA:HB2	1:B:200:VAL:HA	1.95	0.47
1:A:144:ASN:O	1:A:147:ILE:CG1	2.62	0.47
1:B:85:THR:HG23	1:B:85:THR:O	2.15	0.47
1:A:133:LYS:HG3	1:A:133:LYS:H	1.49	0.47
1:A:58:LLP:H4'1	2:C:402:ILE:HD11	1.98	0.47
1:B:42:THR:CG2	4:B:473:HOH:O	2.54	0.46
1:A:28:GLU:OE2	1:A:43:ARG:NH2	2.48	0.46
1:A:153:LYS:HD3	1:A:154:TYR:CZ	2.49	0.46
1:B:131:GLU:OE1	1:B:134:LYS:HE2	2.15	0.46
1:B:113:SER:OG	1:B:116:ARG:NH1	2.49	0.46
1:B:12:ARG:HD3	1:B:14:TYR:CE1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:277:CYS:HB2	1:B:281:SER:CB	2.47	0.45
1:B:174:ASN:CB	4:B:520:HOH:O	2.51	0.44
1:B:322:LYS:O	1:B:322:LYS:CG	2.62	0.44
1:B:128:ILE:HD13	1:B:146:MET:SD	2.57	0.44
1:B:113:SER:HB3	1:B:116:ARG:HB2	2.00	0.43
1:B:136:MET:CB	1:B:137:PRO:HD3	2.48	0.43
1:A:67:TYR:CE1	1:A:71:LYS:HD2	2.53	0.43
1:B:94:CYS:SG	1:B:125:ALA:HB2	2.58	0.43
1:A:3:GLN:HG2	1:A:3:GLN:H	1.64	0.43
1:B:91:ILE:HD13	1:B:120:MET:HG3	2.00	0.43
1:A:116:ARG:NH2	4:A:555:HOH:O	2.52	0.42
1:B:202:GLU:OE2	1:B:247:LYS:NZ	2.51	0.42
1:A:134:LYS:HB3	1:A:138:GLY:HA3	2.01	0.42
1:A:53:PRO:HB2	1:A:95:GLN:HE22	1.84	0.41
1:B:134:LYS:HB3	1:B:138:GLY:HA3	2.02	0.41
1:B:58:LLP:O3	1:B:58:LLP:NZ	2.53	0.41
1:A:326:THR:HG22	1:A:329:GLN:HB2	2.01	0.41
1:B:186:ILE:HD12	1:B:302:ILE:HG12	2.02	0.41
1:B:131:GLU:O	1:B:134:LYS:HB2	2.21	0.40
1:A:190:ALA:HB1	1:A:237:ILE:HG21	2.03	0.40
1:A:328:ILE:HG13	1:A:328:ILE:O	2.20	0.40
1:A:134:LYS:HB3	4:A:553:HOH:O	2.21	0.40
1:A:326:THR:CG2	1:A:328:ILE:HG23	2.51	0.40
1:A:13:ILE:HG21	1:B:43:ARG:HH22	1.85	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	333/338 (98%)	321 (96%)	11 (3%)	1 (0%)	46 33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	334/338 (99%)	326 (98%)	7 (2%)	1 (0%)	46	33
2	C	1/4 (25%)	0	1 (100%)	0	100	100
All	All	668/680 (98%)	647 (97%)	19 (3%)	2 (0%)	46	33

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	113	SER
1	B	323	ASP

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	275/277 (99%)	259 (94%)	16 (6%)	25	11
1	B	276/277 (100%)	269 (98%)	7 (2%)	55	44
2	C	2/4 (50%)	1 (50%)	1 (50%)	0	0
All	All	553/558 (99%)	529 (96%)	24 (4%)	35	21

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	34	GLU
1	A	40	LYS
1	A	85	THR
1	A	111	THR
1	A	114	VAL
1	A	115	GLU
1	A	126	GLU
1	A	133	LYS
1	A	134	LYS
1	A	181	ASP
1	A	206	GLU

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Mol	Chain	Res	Type
1	A	209	LYS
1	A	322	LYS
1	A	324	GLU
1	A	328	ILE
2	C	402	ILE
1	B	40	LYS
1	B	42	THR
1	B	84	SER
1	B	114	VAL
1	B	115	GLU
1	B	136	MET
1	B	183	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	68	GLN
1	A	88	ASN
1	A	95	GLN
1	A	144	ASN
1	A	260	GLN
1	B	52	ASN
1	B	88	ASN
1	B	144	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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
1	LLP	A	58	1	23,24,25	3.11	6 (26%)	28,32,34	1.44	5 (17%)
1	LLP	B	58	1	23,24,25	3.14	4 (17%)	28,32,34	1.54	5 (17%)

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
1	LLP	A	58	1	-	0/15/17/19	0/1/1/1
1	LLP	B	58	1	-	0/15/17/19	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	58	LLP	CB-CA	-2.20	1.51	1.53
1	A	58	LLP	C2'-C2	3.13	1.56	1.50
1	A	58	LLP	C4-C5	3.50	1.46	1.42
1	A	58	LLP	C4'-NZ	3.53	1.38	1.27
1	A	58	LLP	C4-C3	4.23	1.46	1.40
1	B	58	LLP	C4'-NZ	4.82	1.41	1.27
1	B	58	LLP	C4-C3	5.16	1.47	1.40
1	B	58	LLP	C4-C5	5.24	1.49	1.42
1	B	58	LLP	C3-C2	11.39	1.48	1.40
1	A	58	LLP	C3-C2	11.98	1.49	1.40

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	58	LLP	OP4-P-OP1	-2.85	99.90	107.14
1	B	58	LLP	CE-NZ-C4'	-2.37	112.12	118.97
1	B	58	LLP	C5-C4-C4'	-2.37	118.11	121.52
1	A	58	LLP	CD-CE-NZ	-2.30	107.21	110.98
1	B	58	LLP	OP3-P-OP2	2.07	115.27	107.38
1	A	58	LLP	O3-C3-C2	2.16	121.41	117.66
1	A	58	LLP	OP3-P-OP1	2.33	118.07	110.58
1	B	58	LLP	C6-N1-C2	2.65	124.68	119.28
1	A	58	LLP	OP4-C5'-C5	3.19	114.26	108.99
1	B	58	LLP	O3-C3-C2	3.60	123.92	117.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	58	LLP	1	0
1	B	58	LLP	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	401	-	4,4,4	1.02	0	6,6,6	0.45	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	SO4	A	401	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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 ⓘ

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, 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	335/338 (99%)	0.57	40 (11%) 6 6	14, 24, 53, 87	0
1	B	336/338 (99%)	0.31	18 (5%) 29 31	14, 23, 43, 75	0
2	C	3/4 (75%)	6.73	3 (100%) 0 0	50, 50, 75, 96	0
All	All	674/680 (99%)	0.47	61 (9%) 11 12	14, 24, 50, 96	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	400	PRO	10.8
1	A	337	GLU	9.4
1	A	40	LYS	5.7
2	C	401	SER	5.3
1	A	315	SER	5.2
1	A	113	SER	5.0
1	A	133	LYS	5.0
1	A	148	LYS	4.7
1	B	40	LYS	4.7
1	A	134	LYS	4.4
1	A	39	LYS	4.2
2	C	402	ILE	4.1
1	A	110	SER	4.1
1	A	112	MET	3.9
1	A	2	GLU	3.8
1	A	336	ASN	3.8
1	A	317	ASP	3.8
1	B	134	LYS	3.8
1	A	147	ILE	3.7
1	A	135	GLY	3.7
1	A	151	PRO	3.5
1	A	3	GLN	3.4
1	B	113	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	39	LYS	3.1
1	B	2	GLU	3.1
1	A	316	THR	3.0
1	A	321	ILE	3.0
1	B	304	ILE	2.8
1	B	322	LYS	2.8
1	A	304	ILE	2.7
1	B	226	GLY	2.7
1	A	285	ILE	2.6
1	A	131	GLU	2.6
1	A	36	PRO	2.6
1	A	149	GLU	2.6
1	B	305	ILE	2.6
1	B	187	VAL	2.6
1	A	303	VAL	2.5
1	A	322	LYS	2.5
1	A	320	LYS	2.5
1	A	269	VAL	2.4
1	A	210	GLY	2.4
1	A	114	VAL	2.4
1	B	118	MET	2.4
1	A	319	TYR	2.3
1	B	41	GLY	2.3
1	A	305	ILE	2.2
1	A	328	ILE	2.2
1	A	326	THR	2.2
1	A	284	ALA	2.2
1	B	57	VAL	2.2
1	B	200	VAL	2.2
1	A	324	GLU	2.1
1	B	141	GLU	2.1
1	B	114	VAL	2.1
1	A	38	ILE	2.1
1	A	306	VAL	2.1
1	A	78	GLY	2.1
1	B	112	MET	2.1
1	A	132	GLY	2.0
1	B	306	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	LLP	A	58	24/25	0.98	0.14	-	14,15,17,18	0
1	LLP	B	58	24/25	0.98	0.12	-	14,16,17,17	0

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
3	SO4	A	401	5/5	0.94	0.23	0.59	88,88,89,90	0

6.5 Other polymers [i](#)

There are no such residues in this entry.