



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 26, 2018 – 12:51 PM EST

PDB ID : 3ZX2
Title : NTPDase1 in complex with Decavanadate
Authors : Zebisch, M.; Schaefer, P.; Straeter, N.
Deposited on : 2011-08-04
Resolution : 1.81 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030736

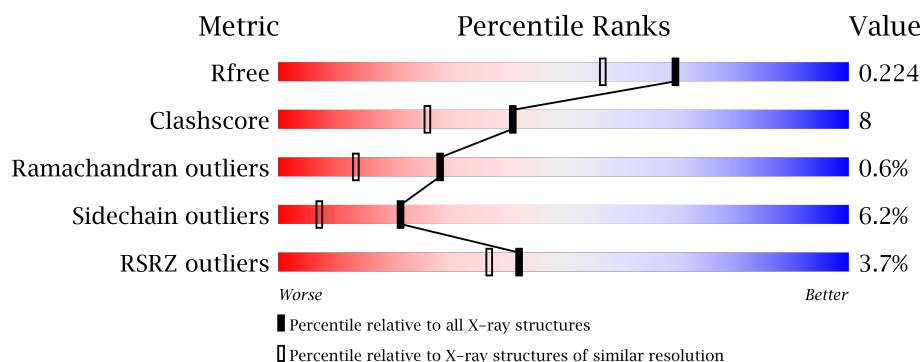
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.81 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}	100719	5868 (1.84-1.80)
Clashscore	112137	6856 (1.84-1.80)
Ramachandran outliers	110173	6780 (1.84-1.80)
Sidechain outliers	110143	6780 (1.84-1.80)
RSRZ outliers	101464	5947 (1.84-1.80)

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	452	<div> <div>2%</div> <div> <div></div> <div>73%</div> <div>13%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	452	<div> <div>3%</div> <div> <div></div> <div>67%</div> <div>19%</div> <div>•</div> <div>12%</div> </div> </div>
1	C	452	<div> <div>6%</div> <div> <div></div> <div>70%</div> <div>15%</div> <div>•</div> <div>13%</div> </div> </div>
1	D	452	<div> <div>2%</div> <div> <div></div> <div>71%</div> <div>15%</div> <div>•</div> <div>12%</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CL	D	503	-	-	X	-
3	ACY	A	511	-	-	X	X
3	ACY	B	511	-	-	X	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13563 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 ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	S	0	9	0
			3178	2051	512	595	20			
1	B	399	Total	C	N	O	S	0	4	0
			3172	2045	513	594	20			
1	C	393	Total	C	N	O	S	0	4	0
			3129	2024	502	583	20			
1	D	396	Total	C	N	O	S	0	7	0
			3166	2044	509	592	21			

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	MET	-	expression tag	UNP P97687
A	16	ALA	-	expression tag	UNP P97687
A	17	HIS	-	expression tag	UNP P97687
A	18	HIS	-	expression tag	UNP P97687
A	19	HIS	-	expression tag	UNP P97687
A	20	HIS	-	expression tag	UNP P97687
A	21	HIS	-	expression tag	UNP P97687
A	22	HIS	-	expression tag	UNP P97687
A	23	VAL	-	expression tag	UNP P97687
A	24	GLY	-	expression tag	UNP P97687
A	25	THR	-	expression tag	UNP P97687
A	26	GLY	-	expression tag	UNP P97687
A	27	SER	-	expression tag	UNP P97687
A	28	ASN	-	expression tag	UNP P97687
A	29	ASP	-	expression tag	UNP P97687
A	30	ASP	-	expression tag	UNP P97687
A	31	ASP	-	expression tag	UNP P97687
A	32	ASP	-	expression tag	UNP P97687
A	33	LYS	-	expression tag	UNP P97687
A	34	SER	-	expression tag	UNP P97687

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Chain	Residue	Modelled	Actual	Comment	Reference
A	35	PRO	-	expression tag	UNP P97687
A	36	ASP	-	expression tag	UNP P97687
A	37	PRO	-	expression tag	UNP P97687
A	80	GLN	LEU	SEE REMARK 999	UNP P97687
A	190	LYS	-	linker	UNP P97687
A	191	THR	-	linker	UNP P97687
A	192	PRO	-	linker	UNP P97687
A	204	GLY	-	linker	UNP P97687
A	205	GLY	-	linker	UNP P97687
A	206	SER	-	linker	UNP P97687
A	220	ILE	VAL	SEE REMARK 999	UNP P97687
A	227	SER	GLN	SEE REMARK 999	UNP P97687
A	331	ILE	PHE	conflict	UNP P97687
B	15	MET	-	expression tag	UNP P97687
B	16	ALA	-	expression tag	UNP P97687
B	17	HIS	-	expression tag	UNP P97687
B	18	HIS	-	expression tag	UNP P97687
B	19	HIS	-	expression tag	UNP P97687
B	20	HIS	-	expression tag	UNP P97687
B	21	HIS	-	expression tag	UNP P97687
B	22	HIS	-	expression tag	UNP P97687
B	23	VAL	-	expression tag	UNP P97687
B	24	GLY	-	expression tag	UNP P97687
B	25	THR	-	expression tag	UNP P97687
B	26	GLY	-	expression tag	UNP P97687
B	27	SER	-	expression tag	UNP P97687
B	28	ASN	-	expression tag	UNP P97687
B	29	ASP	-	expression tag	UNP P97687
B	30	ASP	-	expression tag	UNP P97687
B	31	ASP	-	expression tag	UNP P97687
B	32	ASP	-	expression tag	UNP P97687
B	33	LYS	-	expression tag	UNP P97687
B	34	SER	-	expression tag	UNP P97687
B	35	PRO	-	expression tag	UNP P97687
B	36	ASP	-	expression tag	UNP P97687
B	37	PRO	-	expression tag	UNP P97687
B	80	GLN	LEU	SEE REMARK 999	UNP P97687
B	190	LYS	-	linker	UNP P97687
B	191	THR	-	linker	UNP P97687
B	192	PRO	-	linker	UNP P97687
B	204	GLY	-	linker	UNP P97687
B	205	GLY	-	linker	UNP P97687

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Chain	Residue	Modelled	Actual	Comment	Reference
B	206	SER	-	linker	UNP P97687
B	220	ILE	VAL	SEE REMARK 999	UNP P97687
B	227	SER	GLN	SEE REMARK 999	UNP P97687
B	331	ILE	PHE	conflict	UNP P97687
C	15	MET	-	expression tag	UNP P97687
C	16	ALA	-	expression tag	UNP P97687
C	17	HIS	-	expression tag	UNP P97687
C	18	HIS	-	expression tag	UNP P97687
C	19	HIS	-	expression tag	UNP P97687
C	20	HIS	-	expression tag	UNP P97687
C	21	HIS	-	expression tag	UNP P97687
C	22	HIS	-	expression tag	UNP P97687
C	23	VAL	-	expression tag	UNP P97687
C	24	GLY	-	expression tag	UNP P97687
C	25	THR	-	expression tag	UNP P97687
C	26	GLY	-	expression tag	UNP P97687
C	27	SER	-	expression tag	UNP P97687
C	28	ASN	-	expression tag	UNP P97687
C	29	ASP	-	expression tag	UNP P97687
C	30	ASP	-	expression tag	UNP P97687
C	31	ASP	-	expression tag	UNP P97687
C	32	ASP	-	expression tag	UNP P97687
C	33	LYS	-	expression tag	UNP P97687
C	34	SER	-	expression tag	UNP P97687
C	35	PRO	-	expression tag	UNP P97687
C	36	ASP	-	expression tag	UNP P97687
C	37	PRO	-	expression tag	UNP P97687
C	80	GLN	LEU	SEE REMARK 999	UNP P97687
C	190	LYS	-	linker	UNP P97687
C	191	THR	-	linker	UNP P97687
C	192	PRO	-	linker	UNP P97687
C	204	GLY	-	linker	UNP P97687
C	205	GLY	-	linker	UNP P97687
C	206	SER	-	linker	UNP P97687
C	220	ILE	VAL	SEE REMARK 999	UNP P97687
C	227	SER	GLN	SEE REMARK 999	UNP P97687
C	331	ILE	PHE	conflict	UNP P97687
D	15	MET	-	expression tag	UNP P97687
D	16	ALA	-	expression tag	UNP P97687
D	17	HIS	-	expression tag	UNP P97687
D	18	HIS	-	expression tag	UNP P97687
D	19	HIS	-	expression tag	UNP P97687

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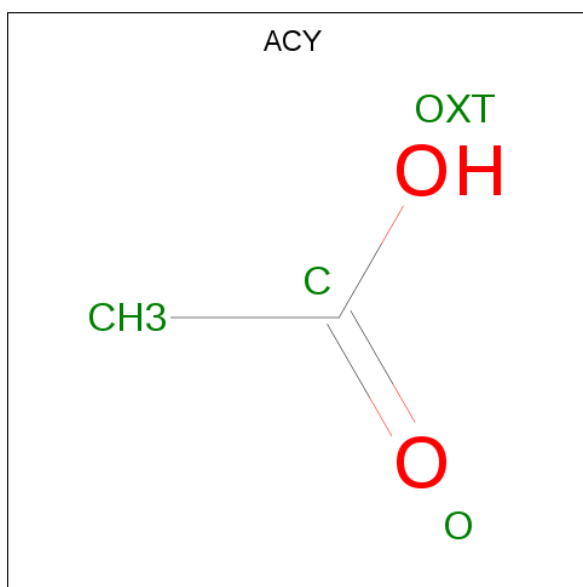
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Chain	Residue	Modelled	Actual	Comment	Reference
D	20	HIS	-	expression tag	UNP P97687
D	21	HIS	-	expression tag	UNP P97687
D	22	HIS	-	expression tag	UNP P97687
D	23	VAL	-	expression tag	UNP P97687
D	24	GLY	-	expression tag	UNP P97687
D	25	THR	-	expression tag	UNP P97687
D	26	GLY	-	expression tag	UNP P97687
D	27	SER	-	expression tag	UNP P97687
D	28	ASN	-	expression tag	UNP P97687
D	29	ASP	-	expression tag	UNP P97687
D	30	ASP	-	expression tag	UNP P97687
D	31	ASP	-	expression tag	UNP P97687
D	32	ASP	-	expression tag	UNP P97687
D	33	LYS	-	expression tag	UNP P97687
D	34	SER	-	expression tag	UNP P97687
D	35	PRO	-	expression tag	UNP P97687
D	36	ASP	-	expression tag	UNP P97687
D	37	PRO	-	expression tag	UNP P97687
D	80	GLN	LEU	SEE REMARK 999	UNP P97687
D	190	LYS	-	linker	UNP P97687
D	191	THR	-	linker	UNP P97687
D	192	PRO	-	linker	UNP P97687
D	204	GLY	-	linker	UNP P97687
D	205	GLY	-	linker	UNP P97687
D	206	SER	-	linker	UNP P97687
D	220	ILE	VAL	SEE REMARK 999	UNP P97687
D	227	SER	GLN	SEE REMARK 999	UNP P97687
D	331	ILE	PHE	conflict	UNP P97687

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

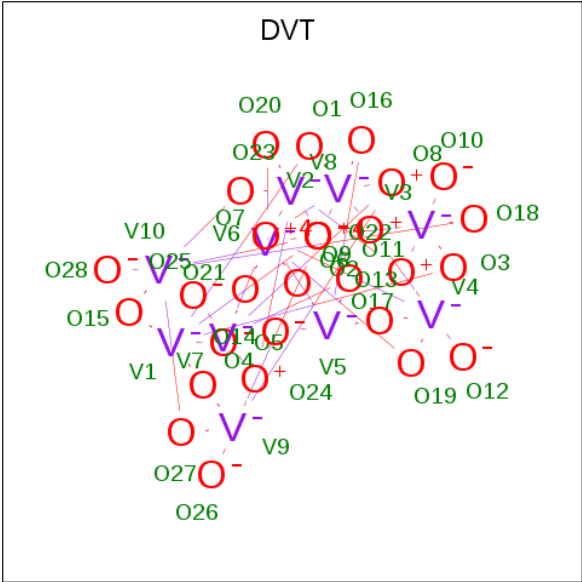
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	5	Total Cl 5 5	0	0
2	A	5	Total Cl 5 5	0	0
2	D	8	Total Cl 8 8	0	0
2	C	5	Total Cl 5 5	0	0

- Molecule 3 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is DECAVANADATE (three-letter code: DVT) (formula: $O_{28}V_{10}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	V	0	0
			38	28	10		
4	B	1	Total	O	V	0	1
			38	28	10		
4	C	1	Total	O	V	0	1
			38	28	10		
4	D	1	Total	O	V	0	0
			38	28	10		

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Na	0	0
			1	1		
5	D	3	Total	Na	0	0
			3	3		
5	C	2	Total	Na	0	0
			2	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	169	Total	O	0	1
			170	170		
6	B	130	Total	O	0	0
			130	130		

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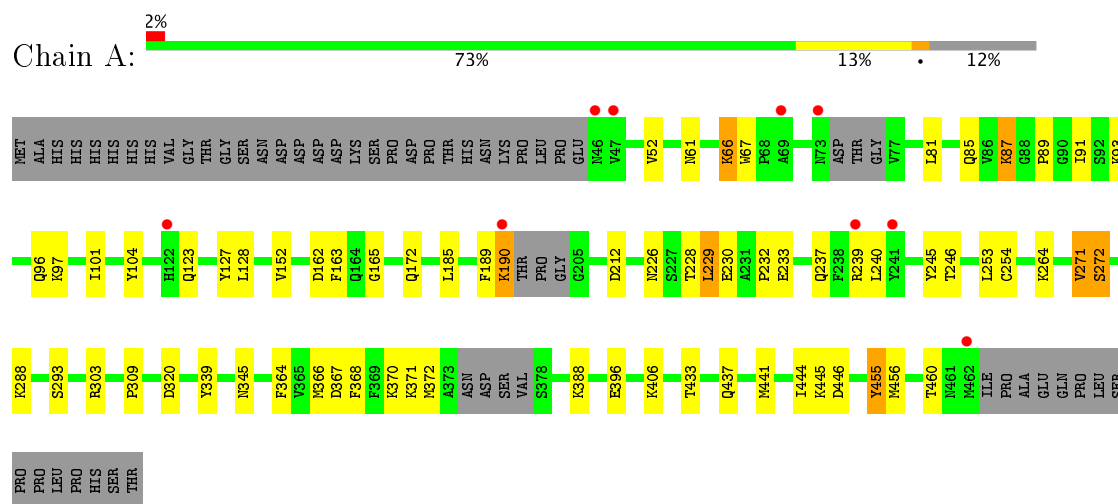
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	191	Total 191	O 191	0	0
6	D	218	Total 218	O 218	0	0

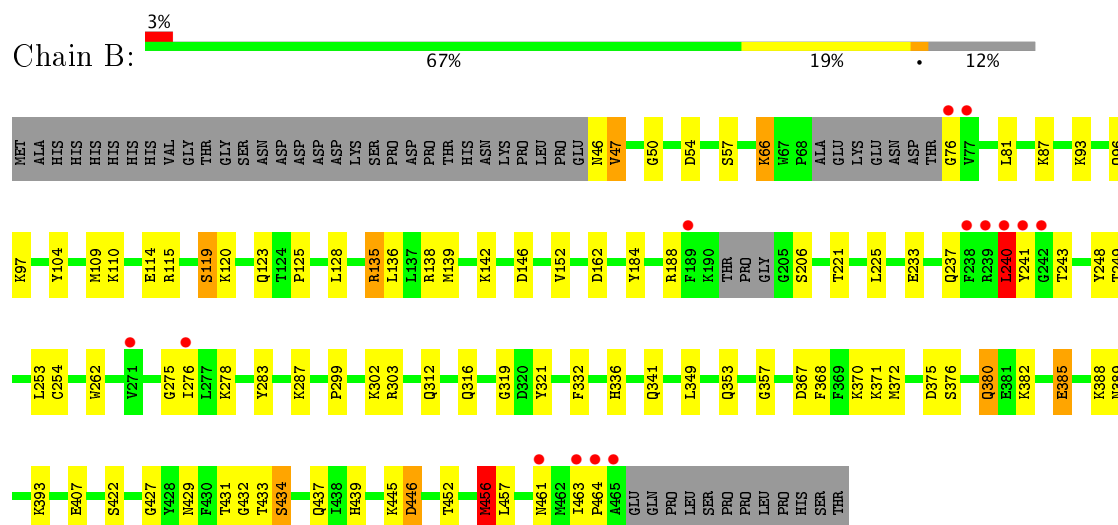
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1

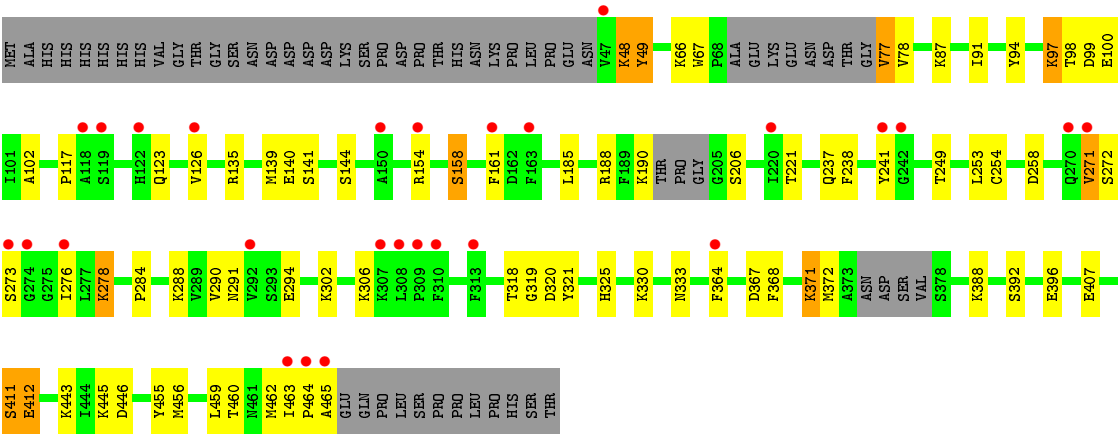


• Molecule 1: ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1

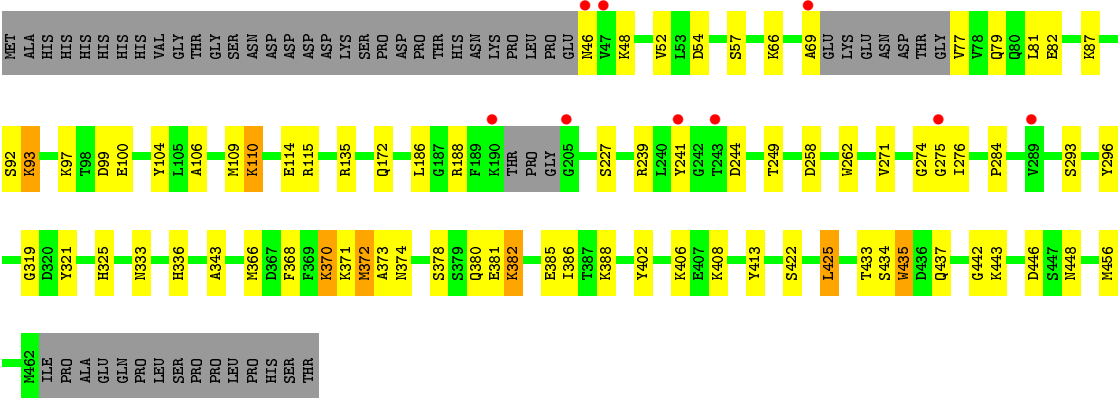


• Molecule 1: ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1





● Molecule 1: ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.92Å 80.98Å 165.52Å 90.00° 117.49° 90.00°	Depositor
Resolution (Å)	146.83 – 1.81 38.88 – 1.81	Depositor EDS
% Data completeness (in resolution range)	73.1 (146.83-1.81) 73.2 (38.88-1.81)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.98 (at 1.81Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.175 , 0.224 0.175 , 0.224	Depositor DCC
R_{free} test set	1270 reflections (1.01%)	DCC
Wilson B-factor (Å ²)	37.8	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 59.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.008 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13563	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: DVT, ACY, CL, NA

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	1.04	4/3285 (0.1%)	1.05	7/4436 (0.2%)
1	B	0.99	1/3262 (0.0%)	1.05	8/4408 (0.2%)
1	C	1.05	2/3221 (0.1%)	1.07	10/4351 (0.2%)
1	D	1.07	5/3267 (0.2%)	1.05	8/4414 (0.2%)
All	All	1.04	12/13035 (0.1%)	1.06	33/17609 (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
1	D	0	1
All	All	0	2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	233	GLU	CG-CD	6.60	1.61	1.51
1	D	413	TYR	CE2-CZ	-6.29	1.30	1.38
1	A	455	TYR	CE2-CZ	6.11	1.46	1.38
1	D	99	ASP	CB-CG	6.09	1.64	1.51
1	D	435	TRP	CD2-CE2	5.97	1.48	1.41
1	C	392	SER	CB-OG	-5.48	1.35	1.42
1	D	296	TYR	CG-CD2	5.36	1.46	1.39
1	D	262	TRP	CD2-CE2	5.36	1.47	1.41
1	B	262	TRP	CD2-CE2	5.31	1.47	1.41
1	A	230	GLU	CD-OE2	-5.30	1.19	1.25
1	A	67	TRP	CD2-CE2	5.28	1.47	1.41
1	C	396	GLU	CD-OE2	-5.14	1.20	1.25

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	ASP	CB-CG-OD2	-8.97	110.23	118.30
1	C	320	ASP	CB-CG-OD1	8.64	126.07	118.30
1	B	456	MET	CA-CB-CG	-8.45	98.93	113.30
1	D	99	ASP	CB-CG-OD1	8.28	125.75	118.30
1	B	240	LEU	CA-CB-CG	7.95	133.58	115.30
1	B	456	MET	CG-SD-CE	-7.66	87.94	100.20
1	B	135	ARG	NE-CZ-NH2	-7.25	116.67	120.30
1	A	212	ASP	CB-CG-OD2	7.07	124.67	118.30
1	D	408	LYS	CD-CE-NZ	-6.94	95.74	111.70
1	C	135	ARG	NE-CZ-NH1	6.82	123.71	120.30
1	A	455	TYR	CB-CG-CD1	-6.75	116.95	121.00
1	B	457	LEU	CB-CG-CD1	-6.47	100.00	111.00
1	D	135	ARG	NE-CZ-NH2	-6.24	117.18	120.30
1	A	162	ASP	CB-CG-OD1	6.22	123.90	118.30
1	B	104	TYR	CA-CB-CG	5.87	124.56	113.40
1	C	320	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	D	258	ASP	CB-CG-OD1	5.78	123.50	118.30
1	C	135	ARG	NE-CZ-NH2	-5.69	117.45	120.30
1	C	258	ASP	CB-CG-OD1	5.64	123.38	118.30
1	D	425	LEU	CA-CB-CG	5.63	128.25	115.30
1	A	388	LYS	CD-CE-NZ	5.62	124.64	111.70
1	A	396	GLU	OE1-CD-OE2	-5.59	116.59	123.30
1	C	49	TYR	CB-CA-C	-5.56	99.29	110.40
1	C	188	ARG	NE-CZ-NH2	-5.53	117.53	120.30
1	D	54	ASP	CB-CG-OD1	5.36	123.12	118.30
1	D	109	MET	CG-SD-CE	5.26	108.61	100.20
1	C	188	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	D	114	GLU	OE1-CD-OE2	-5.14	117.14	123.30
1	B	109	MET	CG-SD-CE	5.11	108.38	100.20
1	B	240	LEU	CB-CG-CD2	-5.11	102.32	111.00
1	C	272	SER	CB-CA-C	-5.09	100.42	110.10
1	C	392	SER	CB-CA-C	-5.04	100.53	110.10
1	A	320	ASP	CB-CG-OD1	5.00	122.80	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	272	SER	Peptide
1	D	274	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	3178	0	3094	63	0
1	B	3172	0	3093	70	0
1	C	3129	0	3064	42	0
1	D	3166	0	3102	43	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	8	0	0	4	0
3	A	4	0	3	8	0
3	B	8	0	6	4	0
3	C	8	0	6	0	0
3	D	8	0	6	0	0
4	A	38	0	0	2	0
4	B	38	0	0	0	0
4	C	38	0	0	1	0
4	D	38	0	0	5	0
5	B	1	0	0	0	0
5	C	2	0	0	0	0
5	D	3	0	0	0	0
6	A	170	0	0	6	0
6	B	130	0	0	4	0
6	C	191	0	0	4	0
6	D	218	0	0	3	0
All	All	13563	0	12374	204	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 8.

All (204) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:MET:CE	3:A:511:ACY:H1	1.39	1.48
1:A:366:MET:HE2	3:A:511:ACY:CH3	1.60	1.30
1:A:229:LEU:HD22	1:B:139:MET:SD	1.76	1.24
1:A:437[A]:GLN:OE1	6:A:2133:HOH:O	1.61	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:52:VAL:HG23	1:D:456:MET:CE	1.85	1.07
1:A:229:LEU:CD2	1:B:139:MET:SD	2.43	1.06
1:A:366:MET:CE	3:A:511:ACY:CH3	2.27	0.95
1:D:52:VAL:CG2	1:D:456:MET:HE2	2.07	0.83
1:D:52:VAL:HG23	1:D:456:MET:HE2	1.59	0.83
1:D:48:LYS:HG3	1:D:69:ALA:HA	1.60	0.82
1:C:185:LEU:O	1:C:445:LYS:HE3	1.81	0.79
1:B:371:LYS:HD2	1:C:371[B]:LYS:CD	2.14	0.77
1:A:455:TYR:C	1:A:455:TYR:CD1	2.57	0.77
1:C:407:GLU:O	1:C:411[A]:SER:HB2	1.84	0.76
1:A:366:MET:HE1	3:A:511:ACY:H1	1.63	0.75
1:B:371:LYS:HD2	1:C:371[B]:LYS:HD3	1.68	0.75
1:D:52:VAL:HG23	1:D:456:MET:HE3	1.69	0.75
1:A:271:VAL:CG1	1:A:309:PRO:HD3	2.18	0.74
1:D:373:ALA:O	1:D:374:ASN:HB2	1.88	0.74
1:B:138[B]:ARG:HG2	1:B:138[B]:ARG:HH11	1.52	0.74
1:C:49:TYR:OH	1:C:117:PRO:HD2	1.87	0.73
1:C:278:LYS:HG3	1:C:318:THR:HG21	1.71	0.72
1:C:412:GLU:HA	1:C:412:GLU:OE1	1.89	0.72
1:B:50:GLY:HA3	1:B:456:MET:HE1	1.72	0.72
1:B:275:GLY:O	1:B:276:ILE:HD13	1.89	0.71
1:A:366:MET:HE1	3:A:511:ACY:CH3	2.19	0.70
1:A:445:LYS:O	1:A:446:ASP:HB2	1.92	0.69
1:B:287[B]:LYS:HE3	6:B:2083:HOH:O	1.92	0.69
1:D:373:ALA:HB2	1:D:386:ILE:CD1	2.24	0.68
1:B:87:LYS:HE3	6:B:2024:HOH:O	1.92	0.68
1:A:228:THR:HG21	1:B:302:LYS:HZ3	1.59	0.67
1:A:229:LEU:HD21	1:B:139:MET:SD	2.34	0.67
1:A:172:GLN:HG3	6:A:2059:HOH:O	1.95	0.66
1:A:460:THR:O	1:A:460:THR:HG22	1.95	0.66
1:C:139:MET:O	1:D:227:SER:HA	1.96	0.66
1:D:437[A]:GLN:NE2	2:D:509:CL:CL	2.65	0.66
1:A:271:VAL:HG13	1:A:309:PRO:HD3	1.79	0.65
1:A:52:VAL:HG23	1:A:456:MET:CE	2.27	0.65
1:B:46:ASN:O	1:B:47:VAL:HB	1.97	0.65
1:C:241:TYR:O	1:C:465:ALA:HA	1.97	0.64
1:D:443:LYS:HA	1:D:448:ASN:HA	1.78	0.64
1:B:380:GLN:HE21	1:B:432:GLY:HA2	1.62	0.64
1:D:52:VAL:CG2	1:D:456:MET:CE	2.63	0.64
1:A:237:GLN:HG2	1:A:246:THR:OG1	1.99	0.63
1:A:66:LYS:HE2	1:A:81:LEU:HD13	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:THR:O	1:A:460:THR:CG2	2.46	0.63
1:A:127:TYR:CE2	1:A:455:TYR:CE2	2.86	0.63
4:D:531:DVT:O12	4:D:531:DVT:V4	1.56	0.63
6:C:2136:HOH:O	1:D:333:ASN:HB3	1.98	0.62
1:A:89:PRO:HB2	1:A:93:LYS:HG3	1.79	0.62
1:C:49:TYR:CZ	1:C:117:PRO:HD2	2.35	0.62
1:C:278:LYS:HG3	1:C:318:THR:CG2	2.30	0.61
1:D:442:GLY:O	1:D:448:ASN:HB2	2.00	0.61
4:D:531:DVT:V10	4:D:531:DVT:O28	1.58	0.61
1:A:366:MET:HE2	3:A:511:ACY:H1	0.64	0.61
1:A:127:TYR:CD2	1:A:455:TYR:CZ	2.89	0.61
1:B:371:LYS:HD2	1:C:371[B]:LYS:HD2	1.81	0.61
1:B:434:SER:O	1:B:437:GLN:HG2	2.02	0.60
1:A:52:VAL:HG23	1:A:456:MET:HE3	1.83	0.60
4:D:531:DVT:O26	4:D:531:DVT:V9	1.59	0.60
1:A:229:LEU:HD23	1:B:299:PRO:HB2	1.84	0.60
4:D:531:DVT:O14	4:D:531:DVT:V5	1.59	0.60
4:A:531:DVT:V10	4:A:531:DVT:O28	1.58	0.60
1:D:443:LYS:HG2	1:D:448:ASN:HB3	1.84	0.59
1:B:380:GLN:NE2	1:B:432:GLY:HA2	2.16	0.59
1:A:128:LEU:HD13	1:A:152:VAL:HG11	1.84	0.59
1:A:52:VAL:CG2	1:A:456:MET:CE	2.81	0.59
1:B:46:ASN:O	1:B:47:VAL:CB	2.50	0.59
1:A:52:VAL:CG2	1:A:456:MET:HE2	2.33	0.59
1:B:50:GLY:HA3	1:B:456:MET:CE	2.32	0.58
1:A:271:VAL:HG12	1:A:309:PRO:HD3	1.84	0.58
1:B:445:LYS:O	1:B:446:ASP:CB	2.51	0.58
1:D:382:LYS:HE3	1:D:382:LYS:HA	1.86	0.57
1:D:97:LYS:HD2	1:D:100:GLU:OE1	2.04	0.57
1:B:135:ARG:O	1:B:139:MET:HG3	2.04	0.57
1:B:240:LEU:HB3	1:B:241:TYR:CD1	2.39	0.57
1:A:229:LEU:HD12	1:A:232:PRO:HG3	1.85	0.57
1:A:406:LYS:HE2	4:A:531:DVT:O17	2.05	0.57
1:C:49:TYR:OH	1:C:117:PRO:CD	2.52	0.57
1:B:371:LYS:CD	1:C:371[B]:LYS:HD2	2.35	0.56
1:D:373:ALA:HB2	1:D:386:ILE:HD13	1.87	0.56
1:A:237:GLN:HA	1:A:245:TYR:O	2.06	0.55
1:A:228:THR:HG21	1:B:302:LYS:NZ	2.21	0.55
1:D:81:LEU:HD11	1:D:115[A]:ARG:NH2	2.22	0.55
1:A:61:ASN:HD22	1:A:85:GLN:HA	1.71	0.54
1:C:455:TYR:CZ	1:C:459:LEU:HD11	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:LYS:HE2	6:A:2007:HOH:O	2.06	0.54
1:A:229:LEU:CD2	1:B:136:LEU:HD23	2.37	0.54
1:B:241:TYR:CE2	1:B:464:PRO:HD2	2.43	0.53
1:B:125:PRO:HA	1:B:162:ASP:HB3	1.90	0.53
1:D:378:SER:HB2	1:D:382:LYS:HG2	1.91	0.53
1:C:87:LYS:HG2	6:C:2014:HOH:O	2.09	0.52
1:B:128:LEU:HD13	1:B:152:VAL:HG11	1.90	0.52
1:D:66:LYS:HE3	1:D:81:LEU:HD13	1.90	0.52
1:C:412:GLU:CA	1:C:412:GLU:OE1	2.58	0.52
1:C:77:VAL:HG23	1:C:78:VAL:N	2.25	0.51
1:A:185:LEU:O	1:A:445:LYS:HE3	2.10	0.51
1:D:271:VAL:HG23	6:D:2150:HOH:O	2.11	0.51
1:B:66:LYS:HD2	1:B:81:LEU:HD12	1.92	0.51
1:C:321:TYR:HB2	1:C:388:LYS:HA	1.92	0.51
1:B:349:LEU:HD23	1:B:429:ASN:ND2	2.25	0.50
1:A:189:PHE:C	1:A:190:LYS:HG3	2.31	0.50
1:A:366:MET:CE	3:A:511:ACY:C	2.90	0.50
1:A:229:LEU:HD23	1:B:136:LEU:CD2	2.41	0.50
1:B:46:ASN:O	1:B:47:VAL:HG12	2.12	0.50
1:C:460:THR:OG1	1:C:462:MET:HG3	2.12	0.50
1:C:126:VAL:HG21	1:C:161:PHE:HB2	1.94	0.49
1:D:172:GLN:HG2	1:D:249:THR:HG23	1.94	0.49
1:B:221:THR:HG23	1:B:249:THR:HB	1.93	0.49
1:C:94:TYR:HA	1:C:97:LYS:HG3	1.94	0.49
1:A:101:ILE:O	1:A:104:TYR:HB3	2.13	0.48
1:A:229:LEU:HD11	1:B:253:LEU:HD23	1.95	0.48
1:A:441:MET:SD	1:A:444:ILE:HD11	2.53	0.48
1:D:368:PHE:CE2	1:D:372:MET:HE3	2.49	0.48
1:D:321:TYR:HB2	1:D:388:LYS:HA	1.94	0.48
1:C:368:PHE:CE2	1:C:372:MET:CE	2.96	0.48
1:A:229:LEU:HD23	1:B:136:LEU:HD23	1.95	0.48
1:B:278:LYS:NZ	1:B:316:GLN:OE1	2.46	0.48
1:D:82:GLU:OE1	1:D:115[B]:ARG:HD3	2.14	0.48
1:A:339:TYR:HA	1:B:303:ARG:HB2	1.95	0.48
1:A:366:MET:HG3	1:A:370:LYS:HE2	1.96	0.48
1:D:52:VAL:HG22	1:D:456:MET:HE2	1.95	0.48
1:B:341:GLN:HG2	1:B:349:LEU:O	2.14	0.47
1:B:445:LYS:O	1:B:446:ASP:HB2	2.13	0.47
1:D:284:PRO:HD3	1:D:319:GLY:HA3	1.95	0.47
1:A:163:PHE:CE2	1:A:165:GLY:HA2	2.49	0.47
1:D:406:LYS:HE2	4:D:531:DVT:O17	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:PHE:CD2	3:B:511:ACY:H3	2.50	0.47
1:B:253:LEU:O	1:B:254:CYS:HB2	2.15	0.47
1:C:141:SER:HB3	1:C:144:SER:OG	2.15	0.47
1:C:443:LYS:HD3	1:C:446:ASP:HA	1.97	0.47
1:B:240:LEU:HB3	1:B:241:TYR:HD1	1.80	0.47
1:A:163:PHE:CZ	1:A:165:GLY:HA2	2.50	0.46
1:D:92:SER:OG	2:D:503:CL:CL	2.65	0.46
1:C:273:SER:HB3	1:C:276:ILE:O	2.16	0.46
1:C:333:ASN:ND2	1:D:336:HIS:HB3	2.30	0.46
1:D:402:TYR:HA	2:D:505:CL:CL	2.52	0.46
1:C:325:HIS:CD2	6:C:2121:HOH:O	2.68	0.46
1:A:303[B]:ARG:HG2	6:A:2106:HOH:O	2.15	0.46
1:C:253:LEU:O	1:C:254:CYS:HB2	2.15	0.46
1:D:57:SER:HA	2:D:503:CL:CL	2.53	0.46
1:B:54:ASP:HB2	1:B:452:THR:HG21	1.97	0.46
1:D:115[A]:ARG:NH1	6:D:2003:HOH:O	2.48	0.46
1:A:366:MET:HE1	3:A:511:ACY:C	2.46	0.46
1:B:332:PHE:CG	3:B:511:ACY:H3	2.51	0.46
1:B:367:ASP:O	1:B:371:LYS:HG3	2.15	0.46
1:C:48:LYS:N	1:C:67:TRP:O	2.42	0.46
1:C:98:THR:C	1:C:100:GLU:H	2.19	0.46
1:A:253:LEU:O	1:A:254:CYS:HB2	2.17	0.45
1:A:345:ASN:HB3	1:B:336:HIS:HE1	1.80	0.45
1:C:284:PRO:HD3	1:C:319:GLY:HA3	1.97	0.45
1:A:229:LEU:HD12	1:A:232:PRO:CG	2.47	0.45
1:A:264[B]:LYS:HE3	1:A:264[B]:LYS:HB3	1.62	0.45
1:B:110:LYS:HE3	1:B:114:GLU:HG2	1.98	0.45
1:A:85:GLN:NE2	6:A:2019:HOH:O	2.50	0.45
1:C:271:VAL:HG22	1:C:306:LYS:HD3	1.99	0.45
1:D:325:HIS:HD2	1:D:422:SER:OG	2.00	0.45
1:A:368:PHE:CE2	1:A:372:MET:CE	3.00	0.45
1:C:91:ILE:HG12	1:C:91:ILE:H	1.64	0.45
1:D:373:ALA:HB2	1:D:386:ILE:HD11	1.96	0.45
1:B:283:TYR:HB3	1:B:393:LYS:O	2.16	0.44
1:C:291:ASN:HB3	1:C:294:GLU:CG	2.47	0.44
1:B:385:GLU:O	1:B:389:ASN:ND2	2.51	0.44
1:B:142:LYS:HE2	1:B:142:LYS:HB3	1.63	0.44
1:A:52:VAL:HG22	1:A:456:MET:HE2	1.99	0.43
1:B:370:LYS:O	1:B:375:ASP:HA	2.17	0.43
1:A:367:ASP:O	1:A:371:LYS:HG2	2.17	0.43
1:B:46:ASN:O	1:B:47:VAL:CG1	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:96:GLN:H	1:B:97:LYS:NZ	2.17	0.43
1:D:368:PHE:CE2	1:D:372:MET:CE	3.01	0.43
1:B:225:LEU:HD12	6:B:2063:HOH:O	2.18	0.43
1:B:321:TYR:HB2	1:B:388:LYS:HA	2.00	0.43
1:C:221:THR:HG23	1:C:249:THR:HB	2.00	0.43
1:C:291:ASN:HB3	1:C:294:GLU:HG2	1.99	0.43
1:B:407:GLU:OE1	4:C:531[B]:DVT:O13	2.37	0.43
1:B:287[B]:LYS:HG3	6:B:2083:HOH:O	2.18	0.42
1:B:76:GLY:HA2	1:B:184:TYR:CZ	2.54	0.42
1:C:102:ALA:HB3	6:C:2022:HOH:O	2.19	0.42
1:C:367:ASP:O	1:C:371[B]:LYS:HG3	2.20	0.42
1:D:275:GLY:O	1:D:276:ILE:HD13	2.19	0.42
1:A:87:LYS:HD3	1:A:87:LYS:HA	1.66	0.42
1:A:91:ILE:HG21	1:A:91:ILE:HD13	1.83	0.42
1:B:54:ASP:HB2	1:B:452:THR:CG2	2.50	0.42
1:B:321:TYR:HB3	1:B:388:LYS:HG3	2.02	0.41
1:B:47:VAL:O	1:B:120:LYS:NZ	2.53	0.41
1:C:388:LYS:HE3	1:C:388:LYS:HB2	1.56	0.41
1:D:93:LYS:NZ	6:D:2044:HOH:O	2.51	0.41
1:B:93:LYS:O	1:B:97:LYS:HE3	2.19	0.41
1:D:366:MET:O	1:D:370:LYS:HB3	2.21	0.41
1:C:126:VAL:CG2	1:C:161:PHE:CB	2.99	0.41
1:D:321:TYR:HB3	1:D:388:LYS:HG3	2.03	0.41
1:A:229:LEU:HD21	1:B:136:LEU:HD23	2.02	0.41
1:B:368:PHE:CE2	1:B:372:MET:CE	3.04	0.41
1:D:106:ALA:O	1:D:110:LYS:HB2	2.21	0.41
1:B:357:GLY:HA2	1:B:439:HIS:O	2.20	0.41
1:B:240:LEU:HG	1:B:463:ILE:HG21	2.03	0.41
1:B:427:GLY:HA2	3:B:511:ACY:OXT	2.21	0.41
1:B:221:THR:HA	1:B:248:TYR:O	2.21	0.40
1:A:271:VAL:HG23	6:A:2097:HOH:O	2.21	0.40
1:B:248:TYR:CD1	1:B:248:TYR:C	2.94	0.40
1:B:332:PHE:CD1	3:B:511:ACY:H3	2.56	0.40
1:D:186:LEU:HB2	1:D:188:ARG:HG2	2.03	0.40

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	397/452 (88%)	376 (95%)	21 (5%)	0	100	100
1	B	397/452 (88%)	375 (94%)	17 (4%)	5 (1%)	14	3
1	C	389/452 (86%)	370 (95%)	17 (4%)	2 (0%)	32	17
1	D	397/452 (88%)	377 (95%)	17 (4%)	3 (1%)	22	8
All	All	1580/1808 (87%)	1498 (95%)	72 (5%)	10 (1%)	28	13

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	47	VAL
1	B	461	ASN
1	C	99	ASP
1	D	435	TRP
1	B	319	GLY
1	B	119	SER
1	B	431	THR
1	D	343	ALA
1	D	372	MET
1	C	464	PRO

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	344/390 (88%)	328 (95%)	16 (5%)	30	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	344/390 (88%)	320 (93%)	24 (7%)	18	5
1	C	340/390 (87%)	313 (92%)	27 (8%)	14	4
1	D	346/390 (89%)	325 (94%)	21 (6%)	22	7
All	All	1374/1560 (88%)	1286 (94%)	88 (6%)	21	7

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	LYS
1	A	87	LYS
1	A	96	GLN
1	A	97	LYS
1	A	123	GLN
1	A	190	LYS
1	A	226	ASN
1	A	229	LEU
1	A	239	ARG
1	A	240	LEU
1	A	271	VAL
1	A	272	SER
1	A	288	LYS
1	A	293	SER
1	A	364	PHE
1	A	433	THR
1	B	57[A]	SER
1	B	57[B]	SER
1	B	66	LYS
1	B	115	ARG
1	B	119	SER
1	B	123	GLN
1	B	146	ASP
1	B	188	ARG
1	B	206	SER
1	B	233	GLU
1	B	237	GLN
1	B	240	LEU
1	B	243	THR
1	B	312	GLN
1	B	353	GLN
1	B	376	SER
1	B	380	GLN

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Mol	Chain	Res	Type
1	B	382	LYS
1	B	385	GLU
1	B	422	SER
1	B	433	THR
1	B	434	SER
1	B	446	ASP
1	B	456	MET
1	C	48	LYS
1	C	66	LYS
1	C	77	VAL
1	C	97	LYS
1	C	123	GLN
1	C	140	GLU
1	C	154	ARG
1	C	158	SER
1	C	190	LYS
1	C	206	SER
1	C	237[A]	GLN
1	C	237[B]	GLN
1	C	238	PHE
1	C	271	VAL
1	C	278	LYS
1	C	288	LYS
1	C	290	VAL
1	C	302	LYS
1	C	330	LYS
1	C	364	PHE
1	C	371[A]	LYS
1	C	371[B]	LYS
1	C	411[A]	SER
1	C	411[B]	SER
1	C	412	GLU
1	C	456	MET
1	C	463	ILE
1	D	46	ASN
1	D	77	VAL
1	D	79	GLN
1	D	87	LYS
1	D	93	LYS
1	D	104	TYR
1	D	110	LYS
1	D	239	ARG

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Mol	Chain	Res	Type
1	D	241	TYR
1	D	244	ASP
1	D	293	SER
1	D	370	LYS
1	D	371	LYS
1	D	380	GLN
1	D	381	GLU
1	D	382	LYS
1	D	385	GLU
1	D	425	LEU
1	D	433	THR
1	D	434	SER
1	D	446	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	ASN
1	A	96	GLN
1	A	172	GLN
1	A	237	GLN
1	A	323	GLN
1	B	46	ASN
1	B	61	ASN
1	B	85	GLN
1	B	96	GLN
1	B	326	GLN
1	B	334	ASN
1	B	336	HIS
1	B	389	ASN
1	C	291	ASN
1	C	314	GLN
1	C	316	GLN
1	C	333	ASN
1	C	389	ASN
1	C	458	ASN
1	D	79	GLN
1	D	85	GLN
1	D	122	HIS
1	D	325	HIS
1	D	334	ASN
1	D	380	GLN

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Mol	Chain	Res	Type
1	D	458	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 40 ligands modelled in this entry, 29 are monoatomic - leaving 11 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	ACY	A	511	-	1,3,3	5.06	1 (100%)	0,3,3	0.00	-
4	DVT	A	531	-	20,60,60	0.78	0	0,206,206	0.00	-
3	ACY	B	511	-	1,3,3	3.84	1 (100%)	0,3,3	0.00	-
3	ACY	B	512	-	1,3,3	3.50	1 (100%)	0,3,3	0.00	-
4	DVT	B	531[A]	-	20,60,60	0.70	0	0,206,206	0.00	-
3	ACY	C	511	-	1,3,3	3.86	1 (100%)	0,3,3	0.00	-
3	ACY	C	512	-	1,3,3	3.24	1 (100%)	0,3,3	0.00	-
4	DVT	C	531[B]	-	20,60,60	0.69	0	0,206,206	0.00	-
3	ACY	D	511	-	1,3,3	1.22	0	0,3,3	0.00	-
3	ACY	D	512	-	1,3,3	2.95	1 (100%)	0,3,3	0.00	-
4	DVT	D	531	-	20,60,60	0.66	0	0,206,206	0.00	-

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	ACY	A	511	-	-	0/0/0/0	0/0/0/0
4	DVT	A	531	-	-	0/0/560/560	0/0/23/23
3	ACY	B	511	-	-	0/0/0/0	0/0/0/0
3	ACY	B	512	-	-	0/0/0/0	0/0/0/0
4	DVT	B	531[A]	-	-	0/0/560/560	0/0/23/23
3	ACY	C	511	-	-	0/0/0/0	0/0/0/0
3	ACY	C	512	-	-	0/0/0/0	0/0/0/0
4	DVT	C	531[B]	-	-	0/0/560/560	0/0/23/23
3	ACY	D	511	-	-	0/0/0/0	0/0/0/0
3	ACY	D	512	-	-	0/0/0/0	0/0/0/0
4	DVT	D	531	-	-	0/0/560/560	0/0/23/23

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	512	ACY	CH3-C	2.95	1.52	1.48
3	C	512	ACY	CH3-C	3.24	1.52	1.48
3	B	512	ACY	CH3-C	3.50	1.53	1.48
3	B	511	ACY	CH3-C	3.84	1.53	1.48
3	C	511	ACY	CH3-C	3.86	1.53	1.48
3	A	511	ACY	CH3-C	5.06	1.55	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	511	ACY	8	0
4	A	531	DVT	2	0
3	B	511	ACY	4	0
4	C	531[B]	DVT	1	0
4	D	531	DVT	5	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, 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	396/452 (87%)	-0.15	9 (2%) 61 57	29, 44, 79, 126	0
1	B	399/452 (88%)	-0.20	14 (3%) 44 39	30, 47, 80, 106	0
1	C	393/452 (86%)	0.21	27 (6%) 18 14	25, 46, 82, 100	0
1	D	396/452 (87%)	-0.19	9 (2%) 61 57	26, 40, 72, 95	0
All	All	1584/1808 (87%)	-0.08	59 (3%) 42 37	25, 44, 80, 126	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	271	VAL	7.6
1	C	276	ILE	5.4
1	C	310	PHE	5.4
1	D	241	TYR	5.4
1	C	273	SER	5.0
1	A	122[A]	HIS	4.8
1	A	73	ASN	4.8
1	B	241	TYR	4.5
1	C	274	GLY	4.5
1	C	241	TYR	3.8
1	B	464	PRO	3.7
1	C	465	ALA	3.7
1	D	69	ALA	3.6
1	C	463	ILE	3.6
1	A	69	ALA	3.6
1	B	77	VAL	3.5
1	B	465	ALA	3.3
1	C	150	ALA	3.3
1	B	76	GLY	3.2
1	B	463	ILE	3.2
1	C	154	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	270	GLN	2.9
1	A	241	TYR	2.9
1	C	464	PRO	2.8
1	C	163	PHE	2.7
1	B	240	LEU	2.6
1	C	309	PRO	2.5
1	D	243	THR	2.5
1	C	307	LYS	2.5
1	C	47	VAL	2.5
1	A	462	MET	2.5
1	C	242	GLY	2.4
1	D	289	VAL	2.4
1	C	308	LEU	2.4
1	C	313	PHE	2.4
1	D	47	VAL	2.4
1	A	46	ASN	2.4
1	C	122	HIS	2.3
1	B	189	PHE	2.3
1	B	238	PHE	2.3
1	A	47	VAL	2.3
1	B	271	VAL	2.3
1	B	461	ASN	2.3
1	C	220	ILE	2.2
1	B	239	ARG	2.2
1	C	364	PHE	2.2
1	D	46	ASN	2.1
1	C	119	SER	2.1
1	C	161	PHE	2.1
1	C	118	ALA	2.1
1	D	275	GLY	2.1
1	C	292	VAL	2.1
1	B	276	ILE	2.1
1	A	190	LYS	2.1
1	A	239	ARG	2.0
1	D	205	GLY	2.0
1	C	126	VAL	2.0
1	B	242	GLY	2.0
1	D	190	LYS	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	ACY	B	511	4/4	0.87	0.20	10.16	56,59,68,69	0
3	ACY	A	511	4/4	0.84	0.14	2.60	36,47,50,56	0
3	ACY	B	512	4/4	0.97	0.11	1.58	41,44,50,51	0
2	CL	B	506	1/1	0.97	0.08	1.17	58,58,58,58	0
5	NA	D	523	1/1	0.90	0.14	1.03	63,63,63,63	0
5	NA	D	521	1/1	0.99	0.09	0.36	38,38,38,38	0
5	NA	C	522	1/1	0.99	0.11	-0.27	32,32,32,32	0
2	CL	D	501	1/1	0.91	0.11	-0.41	47,47,47,47	0
2	CL	C	501	1/1	0.98	0.11	-0.44	44,44,44,44	0
2	CL	A	506	1/1	0.98	0.07	-0.61	60,60,60,60	0
3	ACY	C	512	4/4	0.98	0.06	-1.02	31,34,36,37	0
2	CL	D	503	1/1	1.00	0.05	-1.11	38,38,38,38	0
4	DVT	D	531	38/38	0.99	0.07	-1.15	30,37,41,43	38
5	NA	B	521	1/1	0.93	0.06	-1.32	59,59,59,59	0
3	ACY	C	511	4/4	0.98	0.06	-1.34	32,35,38,38	0
4	DVT	C	531[B]	38/38	0.98	0.08	-1.39	34,45,50,58	38
2	CL	C	505	1/1	0.99	0.10	-1.41	45,45,45,45	0
3	ACY	D	512	4/4	0.99	0.06	-1.47	40,41,42,43	0
4	DVT	A	531	38/38	0.99	0.06	-1.48	34,42,47,49	38
2	CL	C	502	1/1	0.98	0.06	-1.57	48,48,48,48	0
2	CL	B	503	1/1	0.99	0.05	-1.58	49,49,49,49	0
2	CL	A	501	1/1	0.97	0.06	-1.74	45,45,45,45	0
2	CL	D	508	1/1	0.97	0.05	-1.77	56,56,56,56	0
2	CL	A	503	1/1	0.99	0.05	-1.93	41,41,41,41	0
2	CL	A	505	1/1	0.99	0.11	-1.98	45,45,45,45	0
3	ACY	D	511	4/4	0.98	0.05	-2.05	36,37,40,43	0
2	CL	C	503	1/1	0.97	0.04	-2.10	48,48,48,48	0
2	CL	B	501	1/1	0.96	0.08	-2.33	48,48,48,48	0
2	CL	D	502	1/1	1.00	0.04	-2.48	43,43,43,43	0
4	DVT	B	531[A]	38/38	0.98	0.07	-2.52	40,49,58,62	38

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	CL	D	506	1/1	1.00	0.03	-3.08	46,46,46,46	0
2	CL	B	502	1/1	1.00	0.08	-3.91	43,43,43,43	0
5	NA	D	522	1/1	0.96	0.05	-	60,60,60,60	0
2	CL	A	502	1/1	0.99	0.06	-	44,44,44,44	0
2	CL	D	507	1/1	0.98	0.07	-	41,41,41,41	0
2	CL	D	505	1/1	1.00	0.11	-	43,43,43,43	0
2	CL	D	509	1/1	0.97	0.09	-	41,41,41,41	1
2	CL	B	505	1/1	0.96	0.08	-	47,47,47,47	0
2	CL	C	506	1/1	0.99	0.13	-	38,38,38,38	0
5	NA	C	521	1/1	0.98	0.09	-	53,53,53,53	0

6.5 Other polymers

There are no such residues in this entry.