



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:58 PM GMT

PDB ID : 1I3N
Title : MOLECULAR BASIS FOR SEVERE EPIMERASE-DEFICIENCY GALACTOSEMIA: X-RAY STRUCTURE OF THE HUMAN V94M-SUBSTITUTED UDP-GALACTOSE 4-EPIMERASE
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Deposited on : 2001-02-15
Resolution : 1.50 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

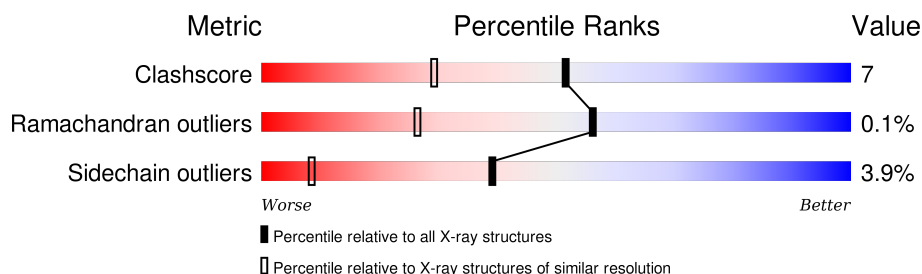
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2274 (1.50-1.50)
Ramachandran outliers	100387	2218 (1.50-1.50)
Sidechain outliers	100360	2216 (1.50-1.50)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	348	
1	B	348	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6500 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 UDP-GLUCOSE 4-EPIMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	347	Total	C	N	O	S	0	2	0
			2697	1707	471	503	16			
1	B	345	Total	C	N	O	S	0	8	0
			2706	1714	467	509	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	94	MET	VAL	ENGINEERED	UNP Q14376
B	94	MET	VAL	ENGINEERED	UNP Q14376

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

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

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

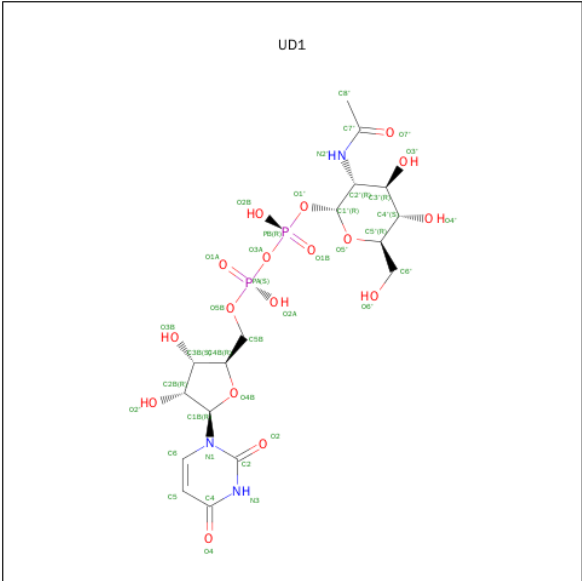
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
4	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 5 is URIDINE-DIPHOSPHATE-N-ACETYLGLUCOSAMINE (three-letter code: UD1) (formula: C₁₇H₂₇N₃O₁₇P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	1
			40	17	3	18	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P	0	0
			39	17	3	17	2		

- Molecule 6 is water.

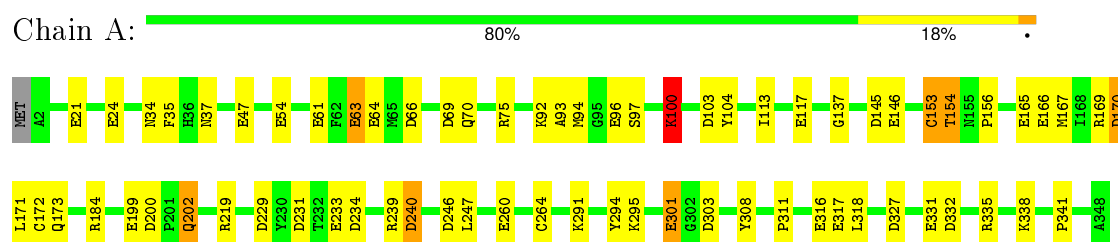
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	498	Total	O	0	0
			498	498		
6	B	427	Total	O	0	0
			427	427		

3 Residue-property plots

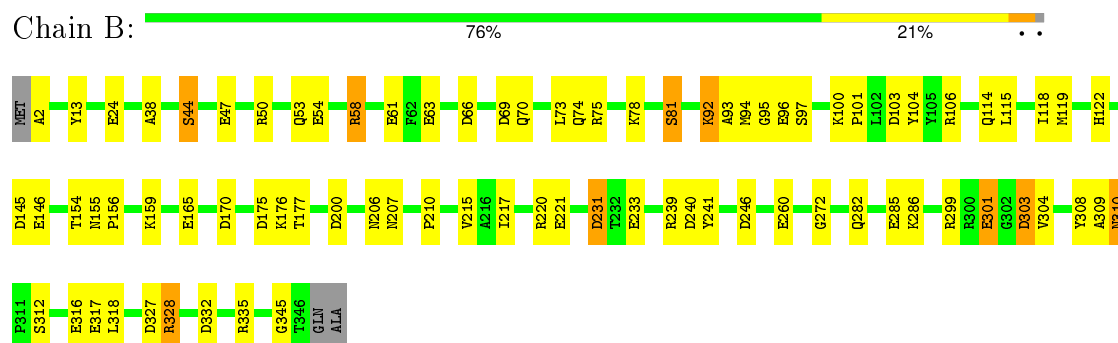
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

• Molecule 1: UDP-GLUCOSE 4-EPIMERASE



• Molecule 1: UDP-GLUCOSE 4-EPIMERASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.10 Å 90.00 Å 96.80 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.50	Depositor
% Data completeness (in resolution range)	97.3 (50.00-1.50)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.180 , 0.215	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6500	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

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: MG, UD1, NAD, CL

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	0.89	18/2762 (0.7%)	1.23	31/3733 (0.8%)
1	B	0.90	13/2799 (0.5%)	1.28	34/3787 (0.9%)
All	All	0.90	31/5561 (0.6%)	1.25	65/7520 (0.9%)

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	1	0

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	54	GLU	CD-OE2	8.47	1.34	1.25
1	A	117	GLU	CD-OE2	8.28	1.34	1.25
1	B	285	GLU	CD-OE2	6.89	1.33	1.25
1	B	146	GLU	CD-OE2	6.89	1.33	1.25
1	B	317	GLU	CD-OE2	6.89	1.33	1.25
1	A	146	GLU	CD-OE2	6.85	1.33	1.25
1	A	316	GLU	CD-OE2	6.83	1.33	1.25
1	A	63	GLU	CD-OE2	6.76	1.33	1.25
1	A	317	GLU	CD-OE2	6.63	1.32	1.25
1	A	21	GLU	CD-OE2	6.63	1.32	1.25
1	B	221	GLU	CD-OE2	6.29	1.32	1.25
1	B	54	GLU	CD-OE2	6.14	1.32	1.25
1	A	301	GLU	CD-OE2	6.01	1.32	1.25
1	B	165	GLU	CD-OE2	6.01	1.32	1.25
1	A	61	GLU	CD-OE2	5.92	1.32	1.25
1	A	165	GLU	CD-OE2	5.91	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	301	GLU	CD-OE2	5.90	1.32	1.25
1	B	260	GLU	CD-OE2	5.77	1.31	1.25
1	A	47	GLU	CD-OE2	5.76	1.31	1.25
1	A	64	GLU	CD-OE2	5.59	1.31	1.25
1	B	63	GLU	CD-OE2	5.59	1.31	1.25
1	B	47	GLU	CD-OE2	5.49	1.31	1.25
1	A	331	GLU	CD-OE2	5.40	1.31	1.25
1	B	24[A]	GLU	CD-OE2	5.40	1.31	1.25
1	B	24[B]	GLU	CD-OE2	5.40	1.31	1.25
1	A	233	GLU	CD-OE2	5.36	1.31	1.25
1	A	260	GLU	CD-OE2	5.30	1.31	1.25
1	A	24	GLU	CD-OE2	5.27	1.31	1.25
1	A	166	GLU	CD-OE2	5.19	1.31	1.25
1	A	199	GLU	CD-OE2	5.09	1.31	1.25
1	B	316	GLU	CD-OE2	5.04	1.31	1.25

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	328	ARG	NE-CZ-NH1	13.31	126.96	120.30
1	B	328	ARG	NE-CZ-NH2	-10.92	114.84	120.30
1	B	69	ASP	CB-CG-OD2	-9.35	109.88	118.30
1	B	145	ASP	CB-CG-OD2	-9.10	110.11	118.30
1	B	200	ASP	CB-CG-OD1	8.86	126.27	118.30
1	B	75	ARG	NE-CZ-NH1	8.33	124.46	120.30
1	A	153	CYS	C-N-CA	7.81	141.24	121.70
1	B	69	ASP	CB-CG-OD1	7.64	125.17	118.30
1	A	335	ARG	NE-CZ-NH1	7.23	123.92	120.30
1	A	154	THR	N-CA-C	7.18	130.39	111.00
1	A	145	ASP	CB-CG-OD2	-7.15	111.87	118.30
1	B	332	ASP	CB-CG-OD1	7.13	124.72	118.30
1	B	170	ASP	CB-CG-OD2	-7.05	111.95	118.30
1	A	170	ASP	CB-CG-OD2	-7.02	111.98	118.30
1	A	234	ASP	CB-CG-OD2	-7.02	111.98	118.30
1	A	327	ASP	CB-CG-OD2	-7.01	111.99	118.30
1	B	145	ASP	CB-CG-OD1	6.99	124.59	118.30
1	A	239	ARG	NE-CZ-NH1	6.95	123.77	120.30
1	A	327	ASP	CB-CG-OD1	6.91	124.52	118.30
1	B	246	ASP	CB-CG-OD1	6.75	124.37	118.30
1	A	69	ASP	CB-CG-OD2	-6.71	112.27	118.30
1	B	200	ASP	CB-CG-OD2	-6.57	112.39	118.30
1	A	246	ASP	CB-CG-OD2	-6.53	112.43	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	66	ASP	CB-CG-OD2	-6.53	112.43	118.30
1	A	66	ASP	CB-CG-OD2	-6.52	112.43	118.30
1	A	231	ASP	CB-CG-OD2	-6.48	112.47	118.30
1	B	246	ASP	CB-CG-OD2	-6.44	112.50	118.30
1	B	58	ARG	NE-CZ-NH2	-6.41	117.10	120.30
1	A	100	LYS	CB-CA-C	-6.40	97.61	110.40
1	A	69	ASP	CB-CG-OD1	6.35	124.02	118.30
1	B	170	ASP	CB-CG-OD1	6.35	124.02	118.30
1	A	184	ARG	NE-CZ-NH2	-6.29	117.15	120.30
1	B	332	ASP	CB-CG-OD2	-6.29	112.64	118.30
1	B	106	ARG	NE-CZ-NH1	6.19	123.39	120.30
1	A	66	ASP	CB-CG-OD1	6.18	123.86	118.30
1	B	75	ARG	NE-CZ-NH2	-6.17	117.22	120.30
1	A	219	ARG	NE-CZ-NH1	6.14	123.37	120.30
1	A	246	ASP	CB-CG-OD1	6.08	123.77	118.30
1	B	303	ASP	CB-CG-OD2	-6.04	112.86	118.30
1	B	335	ARG	NE-CZ-NH1	6.02	123.31	120.30
1	B	231[A]	ASP	CB-CG-OD1	5.81	123.53	118.30
1	B	231[B]	ASP	CB-CG-OD1	5.81	123.53	118.30
1	A	145	ASP	CB-CG-OD1	5.67	123.40	118.30
1	A	332	ASP	CB-CG-OD1	5.63	123.37	118.30
1	B	231[A]	ASP	CB-CG-OD2	-5.61	113.25	118.30
1	B	231[B]	ASP	CB-CG-OD2	-5.61	113.25	118.30
1	A	75	ARG	NE-CZ-NH1	5.57	123.08	120.30
1	A	229	ASP	CB-CG-OD2	-5.56	113.30	118.30
1	A	153	CYS	CA-C-N	-5.55	104.99	117.20
1	B	13	TYR	CB-CG-CD2	-5.53	117.68	121.00
1	A	240	ASP	CB-CG-OD1	5.46	123.21	118.30
1	A	294	TYR	CB-CG-CD1	-5.44	117.73	121.00
1	B	335	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	B	106	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	A	153	CYS	N-CA-C	5.26	125.21	111.00
1	B	66	ASP	CB-CG-OD1	5.26	123.03	118.30
1	A	231	ASP	CB-CG-OD1	5.24	123.02	118.30
1	B	318	LEU	CB-CA-C	-5.21	100.31	110.20
1	B	38	ALA	N-CA-CB	5.18	117.36	110.10
1	A	200	ASP	CB-CG-OD2	-5.13	113.69	118.30
1	B	92	LYS	N-CA-CB	5.12	119.81	110.60
1	A	170	ASP	CB-CG-OD1	5.12	122.90	118.30
1	A	200	ASP	CB-CG-OD1	5.09	122.88	118.30
1	B	299	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	B	327	ASP	CB-CG-OD2	-5.03	113.78	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	154	THR	CA

There are no planarity outliers.

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	2697	0	2661	24	0
1	B	2706	0	2655	50	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
4	A	44	0	26	0	0
4	B	44	0	26	0	0
5	A	40	0	6	0	0
5	B	39	0	25	3	0
6	A	498	0	0	4	0
6	B	427	0	0	12	0
All	All	6500	0	5399	75	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 7.

All (75) 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:73:LEU:HD13	1:B:118[A]:ILE:HD13	1.40	1.03
5:B:901:UD1:H5'	6:B:1985:HOH:O	1.84	0.78
1:B:70:GLN:HG3	6:B:1270:HOH:O	1.83	0.77
1:B:155:ASN:HB3	1:B:156:PRO:HD2	1.66	0.76
1:A:63:GLU:HG3	6:A:1961:HOH:O	1.84	0.76
1:B:73:LEU:HD13	1:B:118[A]:ILE:CD1	2.20	0.68
1:B:73:LEU:HD22	1:B:118[A]:ILE:CD1	2.24	0.67
1:B:73:LEU:HB3	1:B:118[A]:ILE:HD12	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:SER:HA	1:A:104:TYR:CE1	2.34	0.63
1:A:97:SER:O	1:A:156:PRO:HG2	1.98	0.62
1:B:154:THR:HB	6:B:1939:HOH:O	1.99	0.62
1:B:94:MET:HB2	1:B:96:GLU:HG3	1.83	0.60
1:B:97:SER:HA	1:B:104:TYR:CE1	2.36	0.59
1:B:345:GLY:HA2	6:B:1338:HOH:O	2.02	0.58
1:B:215:VAL:HG22	1:B:220:ARG:HB2	1.84	0.57
1:B:286:LYS:HE2	6:B:1761:HOH:O	2.05	0.57
1:A:94:MET:HB2	1:A:96:GLU:HG3	1.85	0.57
1:A:37:ASN:OD1	1:A:202:GLN:NE2	2.37	0.56
1:B:310:ASN:C	1:B:310:ASN:HD22	2.09	0.56
1:A:113:ILE:HG12	1:A:167:MET:HE1	1.88	0.56
1:B:53:GLN:HG3	1:B:58:ARG:O	2.05	0.56
1:B:44:SER:HB2	6:B:1613:HOH:O	2.06	0.55
1:B:73:LEU:HD22	1:B:118[A]:ILE:HD11	1.86	0.55
1:A:100:LYS:HD3	1:A:103:ASP:HB2	1.87	0.55
1:B:310:ASN:HD22	1:B:312:SER:H	1.55	0.55
1:B:282[B]:GLN:HG3	6:B:1760:HOH:O	2.07	0.55
1:B:93:ALA:C	1:B:95:GLY:H	2.10	0.53
1:B:70:GLN:NE2	1:B:114[A]:GLN:OE1	2.43	0.52
5:B:901:UD1:O7'	5:B:901:UD1:O1'	2.28	0.52
1:B:310:ASN:ND2	1:B:312:SER:H	2.08	0.51
1:B:73:LEU:HB3	1:B:118[A]:ILE:CD1	2.41	0.51
1:B:94:MET:HB2	1:B:96:GLU:OE2	2.09	0.51
1:A:338:LYS:HE3	6:A:1573:HOH:O	2.11	0.51
1:B:74:GLN:O	1:B:78:LYS:HG3	2.12	0.50
1:B:73:LEU:CD1	1:B:114[A]:GLN:HG3	2.42	0.50
1:B:70:GLN:HG2	1:B:114[A]:GLN:OE1	2.12	0.50
1:A:70:GLN:OE1	6:A:1996:HOH:O	2.19	0.50
1:A:100:LYS:HD2	1:A:104:TYR:HE1	1.77	0.49
1:A:240:ASP:HB2	1:A:308:TYR:HA	1.94	0.49
1:B:94:MET:HB2	1:B:96:GLU:CG	2.43	0.49
1:A:100:LYS:HD2	1:A:104:TYR:CE1	2.49	0.48
1:B:239:ARG:HB2	1:B:241:TYR:CE1	2.49	0.48
1:B:61:GLU:HG2	6:B:1598:HOH:O	2.13	0.47
1:B:240:ASP:HB2	1:B:308:TYR:HA	1.96	0.47
5:B:901:UD1:H6'1	6:B:1940:HOH:O	2.14	0.46
1:A:311:PRO:HD2	6:A:1545:HOH:O	2.14	0.46
1:B:73:LEU:HD12	1:B:114[A]:GLN:HG3	1.98	0.46
1:A:171:LEU:HA	1:B:101:PRO:HG2	1.98	0.45
1:B:115:LEU:O	1:B:118[A]:ILE:HG12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:LEU:HD22	1:B:118[A]:ILE:HD12	1.98	0.45
1:A:94:MET:HB2	1:A:96:GLU:CG	2.47	0.44
1:A:167:MET:HB3	1:A:167:MET:HE3	1.82	0.44
1:B:328:ARG:NH2	6:B:1989:HOH:O	2.30	0.44
1:B:2:ALA:N	1:B:81:SER:HB3	2.32	0.44
1:B:115:LEU:O	1:B:118[B]:ILE:HG22	2.18	0.44
1:A:318:LEU:HA	1:A:318:LEU:HD12	1.80	0.44
1:B:122:HIS:ND1	6:B:1632:HOH:O	2.36	0.43
1:B:272:GLY:HA2	1:B:309:ALA:O	2.18	0.43
1:A:100:LYS:HE2	1:A:103:ASP:OD1	2.19	0.43
1:A:93:ALA:HA	1:A:104:TYR:OH	2.18	0.43
1:A:170:ASP:OD2	1:B:159:LYS:NZ	2.51	0.43
1:B:100:LYS:HE3	1:B:103:ASP:HB2	2.00	0.43
1:B:73:LEU:CD1	1:B:118[A]:ILE:HD13	2.29	0.42
1:B:207[B]:ASN:CG	1:B:210:PRO:HG2	2.39	0.42
1:B:118[B]:ILE:CG2	1:B:119:MET:N	2.82	0.42
1:B:70:GLN:HB3	6:B:1854:HOH:O	2.19	0.42
1:B:155:ASN:HB3	1:B:156:PRO:CD	2.36	0.42
1:A:172:CYS:SG	1:A:264:CYS:HB2	2.60	0.41
1:B:94:MET:HA	1:B:206:ASN:ND2	2.36	0.41
1:A:137:GLY:HA2	1:A:153:CYS:HB2	2.02	0.41
1:B:215:VAL:CG2	1:B:220:ARG:HB2	2.50	0.41
1:B:175:ASP:OD2	1:B:177:THR:OG1	2.30	0.41
1:A:34:ASN:O	1:A:35:PHE:HB2	2.21	0.41
1:A:173:GLN:NE2	1:A:173:GLN:HA	2.37	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	347/348 (100%)	340 (98%)	6 (2%)	1 (0%)	46 19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	352/348 (101%)	341 (97%)	11 (3%)	0	100	100
All	All	699/696 (100%)	681 (97%)	17 (2%)	1 (0%)	56	26

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	154	THR

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	282/282 (100%)	272 (96%)	10 (4%)	43	11
1	B	287/282 (102%)	274 (96%)	13 (4%)	34	6
All	All	569/564 (101%)	546 (96%)	23 (4%)	39	8

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	92	LYS
1	A	100	LYS
1	A	169	ARG
1	A	202	GLN
1	A	247	LEU
1	A	291	LYS
1	A	295	LYS
1	A	301	GLU
1	A	303	ASP
1	A	341	PRO
1	B	44	SER
1	B	50	ARG
1	B	81	SER
1	B	92	LYS
1	B	176	LYS

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Mol	Chain	Res	Type
1	B	217	ILE
1	B	231[A]	ASP
1	B	231[B]	ASP
1	B	233	GLU
1	B	301	GLU
1	B	303	ASP
1	B	304	VAL
1	B	310	ASN

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

Mol	Chain	Res	Type
1	A	74	GLN
1	A	138	ASN
1	A	173	GLN
1	A	202	GLN
1	A	224	ASN
1	A	339	GLN
1	B	74	GLN
1	B	138	ASN
1	B	206	ASN
1	B	224	ASN
1	B	310	ASN
1	B	339	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 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
4	NAD	A	400	-	38,48,48	1.00	3 (7%)	47,73,73	1.60	5 (10%)
5	UD1	A	401[A]	-	32,41,41	1.27	3 (9%)	46,62,62	2.29	5 (10%)
5	UD1	A	401[B]	-	32,41,41	1.27	3 (9%)	46,62,62	2.29	5 (10%)
4	NAD	B	900	-	38,48,48	0.99	2 (5%)	47,73,73	1.61	6 (12%)
5	UD1	B	901	-	32,41,41	1.22	4 (12%)	46,62,62	2.25	8 (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
4	NAD	A	400	-	-	0/22/62/62	0/5/5/5
5	UD1	A	401[A]	-	-	0/22/63/63	0/3/3/3
5	UD1	A	401[B]	-	-	0/22/63/63	0/3/3/3
4	NAD	B	900	-	-	0/22/62/62	0/5/5/5
5	UD1	B	901	-	-	0/22/63/63	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	901	UD1	C6-C5	-2.70	1.32	1.38
5	A	401[A]	UD1	C6-C5	-2.69	1.32	1.38
5	A	401[B]	UD1	C6-C5	-2.69	1.32	1.38
4	B	900	NAD	PA-O2A	-2.56	1.44	1.54
4	A	400	NAD	C3N-C7N	2.19	1.54	1.50
4	A	400	NAD	C4N-C3N	2.21	1.43	1.39
4	A	400	NAD	C2A-N1A	2.29	1.38	1.33
5	A	401[A]	UD1	C6-N1	2.60	1.39	1.35
5	A	401[B]	UD1	C6-N1	2.60	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	901	UD1	C2'-N2'	2.60	1.50	1.45
5	B	901	UD1	C6-N1	2.68	1.39	1.35
4	B	900	NAD	C4N-C3N	2.82	1.44	1.39
5	B	901	UD1	C4-N3	3.27	1.39	1.33
5	A	401[A]	UD1	C4-N3	4.36	1.41	1.33
5	A	401[B]	UD1	C4-N3	4.36	1.41	1.33

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	400	NAD	C5N-C4N-C3N	-5.07	113.96	120.33
4	B	900	NAD	C5N-C4N-C3N	-4.75	114.36	120.33
4	B	900	NAD	C5N-C6N-N1N	-4.74	112.26	120.47
4	A	400	NAD	C5N-C6N-N1N	-3.80	113.90	120.47
5	B	901	UD1	C5-C4-N3	-3.69	113.65	123.12
5	A	401[A]	UD1	C5-C4-N3	-3.51	114.13	123.12
5	A	401[B]	UD1	C5-C4-N3	-3.51	114.13	123.12
4	B	900	NAD	C3N-C2N-N1N	-3.30	116.56	120.36
5	A	401[A]	UD1	O5'-C1'-O1'	-2.94	107.48	111.36
5	A	401[B]	UD1	O5'-C1'-O1'	-2.94	107.48	111.36
5	A	401[A]	UD1	C2'-N2'-C7'	-2.86	115.77	123.10
5	A	401[B]	UD1	C2'-N2'-C7'	-2.86	115.77	123.10
5	B	901	UD1	O3'-C3'-C4'	-2.08	105.65	110.34
5	B	901	UD1	C4B-O4B-C1B	2.08	112.00	109.72
5	B	901	UD1	O5'-C5'-C6'	2.08	111.61	106.36
4	B	900	NAD	C2N-C3N-C4N	2.15	120.68	118.29
5	A	401[A]	UD1	C8'-C7'-N2'	2.27	120.45	116.11
5	A	401[B]	UD1	C8'-C7'-N2'	2.27	120.45	116.11
5	B	901	UD1	C6-C5-C4	2.27	121.53	117.28
5	B	901	UD1	C4'-C3'-C2'	2.53	113.93	110.43
5	B	901	UD1	O5'-C5'-C4'	2.61	114.59	109.68
4	A	400	NAD	C2N-C3N-C4N	2.62	121.20	118.29
4	A	400	NAD	C3N-C7N-N7N	2.84	120.92	117.82
4	B	900	NAD	C3N-C7N-N7N	3.45	121.60	117.82
4	B	900	NAD	C6N-C5N-C4N	4.26	125.87	119.44
4	A	400	NAD	C6N-C5N-C4N	5.66	127.99	119.44
5	B	901	UD1	C4-N3-C2	12.68	126.69	114.14
5	A	401[A]	UD1	C4-N3-C2	13.20	127.21	114.14
5	A	401[B]	UD1	C4-N3-C2	13.20	127.21	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	901	UD1	3	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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.