



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:49 PM UTC

PDB ID : 8JWL / pdb_00008jwl
Title : The first purified state crystal structure of AKRtyl
Authors : Lin, S.; Dai, S.; Xiao, Z.
Deposited on : 2023-06-29
Resolution : 2.30 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

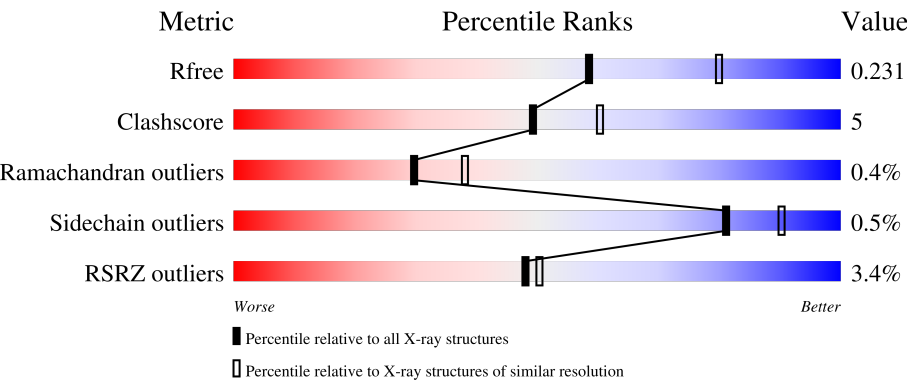
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	351	4% 80%9%9%
1	B	351	2% 85%9%6%
1	C	351	% 85%9%6%
1	D	351	8% 73%15%11%
1	E	351	4% 76%14%9%

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Mol	Chain	Length	Quality of chain
1	F	351	3% 80% 11% 9%
1	G	351	3% 81% 11% 8%
1	H	351	85% 8% 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 21051 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 Aldo/keto reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	0	0
			2455	1542	440	465	8			
1	B	330	Total	C	N	O	S	0	0	0
			2552	1600	462	482	8			
1	C	330	Total	C	N	O	S	0	0	0
			2548	1598	461	481	8			
1	D	312	Total	C	N	O	S	0	0	0
			2422	1525	434	455	8			
1	E	319	Total	C	N	O	S	0	0	0
			2469	1555	440	466	8			
1	F	321	Total	C	N	O	S	0	0	0
			2487	1565	443	471	8			
1	G	323	Total	C	N	O	S	0	0	0
			2499	1571	448	472	8			
1	H	328	Total	C	N	O	S	0	0	0
			2540	1594	459	479	8			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A3R7J519
A	-18	GLY	-	expression tag	UNP A0A3R7J519
A	-17	SER	-	expression tag	UNP A0A3R7J519
A	-16	SER	-	expression tag	UNP A0A3R7J519
A	-15	HIS	-	expression tag	UNP A0A3R7J519
A	-14	HIS	-	expression tag	UNP A0A3R7J519
A	-13	HIS	-	expression tag	UNP A0A3R7J519
A	-12	HIS	-	expression tag	UNP A0A3R7J519
A	-11	HIS	-	expression tag	UNP A0A3R7J519
A	-10	HIS	-	expression tag	UNP A0A3R7J519
A	-9	SER	-	expression tag	UNP A0A3R7J519
A	-8	SER	-	expression tag	UNP A0A3R7J519
A	-7	GLY	-	expression tag	UNP A0A3R7J519

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP A0A3R7J519
A	-5	VAL	-	expression tag	UNP A0A3R7J519
A	-4	PRO	-	expression tag	UNP A0A3R7J519
A	-3	ARG	-	expression tag	UNP A0A3R7J519
A	-2	GLY	-	expression tag	UNP A0A3R7J519
A	-1	SER	-	expression tag	UNP A0A3R7J519
A	0	HIS	-	expression tag	UNP A0A3R7J519
B	-19	MET	-	initiating methionine	UNP A0A3R7J519
B	-18	GLY	-	expression tag	UNP A0A3R7J519
B	-17	SER	-	expression tag	UNP A0A3R7J519
B	-16	SER	-	expression tag	UNP A0A3R7J519
B	-15	HIS	-	expression tag	UNP A0A3R7J519
B	-14	HIS	-	expression tag	UNP A0A3R7J519
B	-13	HIS	-	expression tag	UNP A0A3R7J519
B	-12	HIS	-	expression tag	UNP A0A3R7J519
B	-11	HIS	-	expression tag	UNP A0A3R7J519
B	-10	HIS	-	expression tag	UNP A0A3R7J519
B	-9	SER	-	expression tag	UNP A0A3R7J519
B	-8	SER	-	expression tag	UNP A0A3R7J519
B	-7	GLY	-	expression tag	UNP A0A3R7J519
B	-6	LEU	-	expression tag	UNP A0A3R7J519
B	-5	VAL	-	expression tag	UNP A0A3R7J519
B	-4	PRO	-	expression tag	UNP A0A3R7J519
B	-3	ARG	-	expression tag	UNP A0A3R7J519
B	-2	GLY	-	expression tag	UNP A0A3R7J519
B	-1	SER	-	expression tag	UNP A0A3R7J519
B	0	HIS	-	expression tag	UNP A0A3R7J519
C	-19	MET	-	initiating methionine	UNP A0A3R7J519
C	-18	GLY	-	expression tag	UNP A0A3R7J519
C	-17	SER	-	expression tag	UNP A0A3R7J519
C	-16	SER	-	expression tag	UNP A0A3R7J519
C	-15	HIS	-	expression tag	UNP A0A3R7J519
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C	-10	HIS	-	expression tag	UNP A0A3R7J519
C	-9	SER	-	expression tag	UNP A0A3R7J519
C	-8	SER	-	expression tag	UNP A0A3R7J519
C	-7	GLY	-	expression tag	UNP A0A3R7J519
C	-6	LEU	-	expression tag	UNP A0A3R7J519
C	-5	VAL	-	expression tag	UNP A0A3R7J519

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	PRO	-	expression tag	UNP A0A3R7J519
C	-3	ARG	-	expression tag	UNP A0A3R7J519
C	-2	GLY	-	expression tag	UNP A0A3R7J519
C	-1	SER	-	expression tag	UNP A0A3R7J519
C	0	HIS	-	expression tag	UNP A0A3R7J519
D	-19	MET	-	initiating methionine	UNP A0A3R7J519
D	-18	GLY	-	expression tag	UNP A0A3R7J519
D	-17	SER	-	expression tag	UNP A0A3R7J519
D	-16	SER	-	expression tag	UNP A0A3R7J519
D	-15	HIS	-	expression tag	UNP A0A3R7J519
D	-14	HIS	-	expression tag	UNP A0A3R7J519
D	-13	HIS	-	expression tag	UNP A0A3R7J519
D	-12	HIS	-	expression tag	UNP A0A3R7J519
D	-11	HIS	-	expression tag	UNP A0A3R7J519
D	-10	HIS	-	expression tag	UNP A0A3R7J519
D	-9	SER	-	expression tag	UNP A0A3R7J519
D	-8	SER	-	expression tag	UNP A0A3R7J519
D	-7	GLY	-	expression tag	UNP A0A3R7J519
D	-6	LEU	-	expression tag	UNP A0A3R7J519
D	-5	VAL	-	expression tag	UNP A0A3R7J519
D	-4	PRO	-	expression tag	UNP A0A3R7J519
D	-3	ARG	-	expression tag	UNP A0A3R7J519
D	-2	GLY	-	expression tag	UNP A0A3R7J519
D	-1	SER	-	expression tag	UNP A0A3R7J519
D	0	HIS	-	expression tag	UNP A0A3R7J519
E	-19	MET	-	initiating methionine	UNP A0A3R7J519
E	-18	GLY	-	expression tag	UNP A0A3R7J519
E	-17	SER	-	expression tag	UNP A0A3R7J519
E	-16	SER	-	expression tag	UNP A0A3R7J519
E	-15	HIS	-	expression tag	UNP A0A3R7J519
E	-14	HIS	-	expression tag	UNP A0A3R7J519
E	-13	HIS	-	expression tag	UNP A0A3R7J519
E	-12	HIS	-	expression tag	UNP A0A3R7J519
E	-11	HIS	-	expression tag	UNP A0A3R7J519
E	-10	HIS	-	expression tag	UNP A0A3R7J519
E	-9	SER	-	expression tag	UNP A0A3R7J519
E	-8	SER	-	expression tag	UNP A0A3R7J519
E	-7	GLY	-	expression tag	UNP A0A3R7J519
E	-6	LEU	-	expression tag	UNP A0A3R7J519
E	-5	VAL	-	expression tag	UNP A0A3R7J519
E	-4	PRO	-	expression tag	UNP A0A3R7J519
E	-3	ARG	-	expression tag	UNP A0A3R7J519

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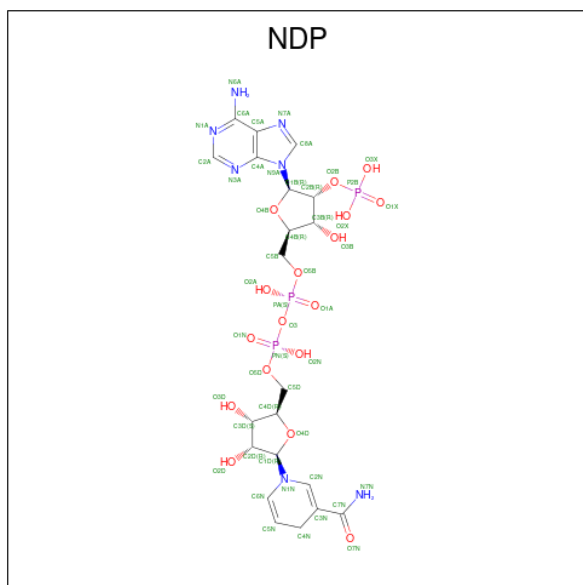
Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	GLY	-	expression tag	UNP A0A3R7J519
E	-1	SER	-	expression tag	UNP A0A3R7J519
E	0	HIS	-	expression tag	UNP A0A3R7J519
F	-19	MET	-	initiating methionine	UNP A0A3R7J519
F	-18	GLY	-	expression tag	UNP A0A3R7J519
F	-17	SER	-	expression tag	UNP A0A3R7J519
F	-16	SER	-	expression tag	UNP A0A3R7J519
F	-15	HIS	-	expression tag	UNP A0A3R7J519
F	-14	HIS	-	expression tag	UNP A0A3R7J519
F	-13	HIS	-	expression tag	UNP A0A3R7J519
F	-12	HIS	-	expression tag	UNP A0A3R7J519
F	-11	HIS	-	expression tag	UNP A0A3R7J519
F	-10	HIS	-	expression tag	UNP A0A3R7J519
F	-9	SER	-	expression tag	UNP A0A3R7J519
F	-8	SER	-	expression tag	UNP A0A3R7J519
F	-7	GLY	-	expression tag	UNP A0A3R7J519
F	-6	LEU	-	expression tag	UNP A0A3R7J519
F	-5	VAL	-	expression tag	UNP A0A3R7J519
F	-4	PRO	-	expression tag	UNP A0A3R7J519
F	-3	ARG	-	expression tag	UNP A0A3R7J519
F	-2	GLY	-	expression tag	UNP A0A3R7J519
F	-1	SER	-	expression tag	UNP A0A3R7J519
F	0	HIS	-	expression tag	UNP A0A3R7J519
G	-19	MET	-	initiating methionine	UNP A0A3R7J519
G	-18	GLY	-	expression tag	UNP A0A3R7J519
G	-17	SER	-	expression tag	UNP A0A3R7J519
G	-16	SER	-	expression tag	UNP A0A3R7J519
G	-15	HIS	-	expression tag	UNP A0A3R7J519
G	-14	HIS	-	expression tag	UNP A0A3R7J519
G	-13	HIS	-	expression tag	UNP A0A3R7J519
G	-12	HIS	-	expression tag	UNP A0A3R7J519
G	-11	HIS	-	expression tag	UNP A0A3R7J519
G	-10	HIS	-	expression tag	UNP A0A3R7J519
G	-9	SER	-	expression tag	UNP A0A3R7J519
G	-8	SER	-	expression tag	UNP A0A3R7J519
G	-7	GLY	-	expression tag	UNP A0A3R7J519
G	-6	LEU	-	expression tag	UNP A0A3R7J519
G	-5	VAL	-	expression tag	UNP A0A3R7J519
G	-4	PRO	-	expression tag	UNP A0A3R7J519
G	-3	ARG	-	expression tag	UNP A0A3R7J519
G	-2	GLY	-	expression tag	UNP A0A3R7J519
G	-1	SER	-	expression tag	UNP A0A3R7J519

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Chain	Residue	Modelled	Actual	Comment	Reference
G	0	HIS	-	expression tag	UNP A0A3R7J519
H	-19	MET	-	initiating methionine	UNP A0A3R7J519
H	-18	GLY	-	expression tag	UNP A0A3R7J519
H	-17	SER	-	expression tag	UNP A0A3R7J519
H	-16	SER	-	expression tag	UNP A0A3R7J519
H	-15	HIS	-	expression tag	UNP A0A3R7J519
H	-14	HIS	-	expression tag	UNP A0A3R7J519
H	-13	HIS	-	expression tag	UNP A0A3R7J519
H	-12	HIS	-	expression tag	UNP A0A3R7J519
H	-11	HIS	-	expression tag	UNP A0A3R7J519
H	-10	HIS	-	expression tag	UNP A0A3R7J519
H	-9	SER	-	expression tag	UNP A0A3R7J519
H	-8	SER	-	expression tag	UNP A0A3R7J519
H	-7	GLY	-	expression tag	UNP A0A3R7J519
H	-6	LEU	-	expression tag	UNP A0A3R7J519
H	-5	VAL	-	expression tag	UNP A0A3R7J519
H	-4	PRO	-	expression tag	UNP A0A3R7J519
H	-3	ARG	-	expression tag	UNP A0A3R7J519
H	-2	GLY	-	expression tag	UNP A0A3R7J519
H	-1	SER	-	expression tag	UNP A0A3R7J519
H	0	HIS	-	expression tag	UNP A0A3R7J519

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	H	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

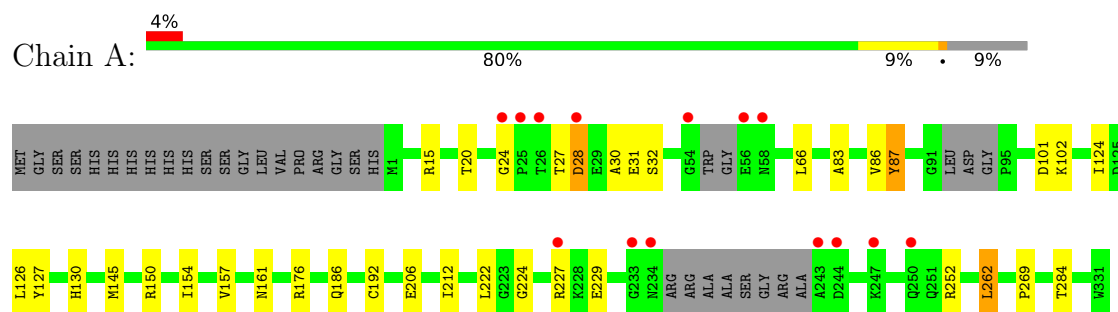
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	151	Total	O	0	0
			151	151		
3	B	131	Total	O	0	0
			131	131		
3	C	125	Total	O	0	0
			125	125		
3	D	98	Total	O	0	0
			98	98		
3	E	97	Total	O	0	0
			97	97		
3	F	123	Total	O	0	0
			123	123		
3	G	110	Total	O	0	0
			110	110		
3	H	148	Total	O	0	0
			148	148		

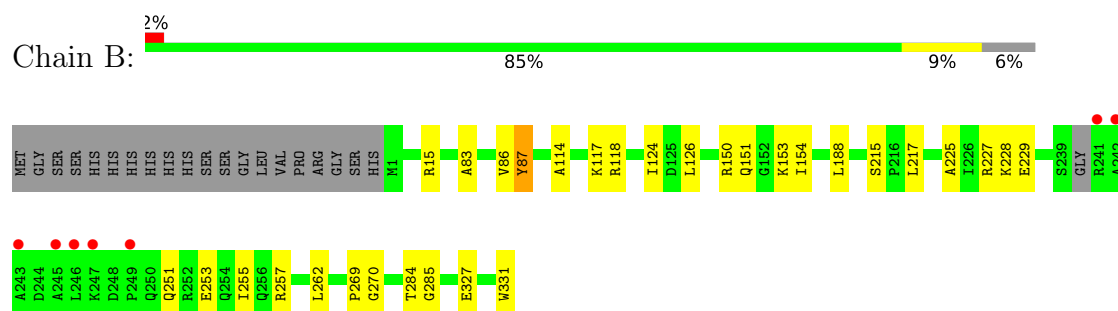
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

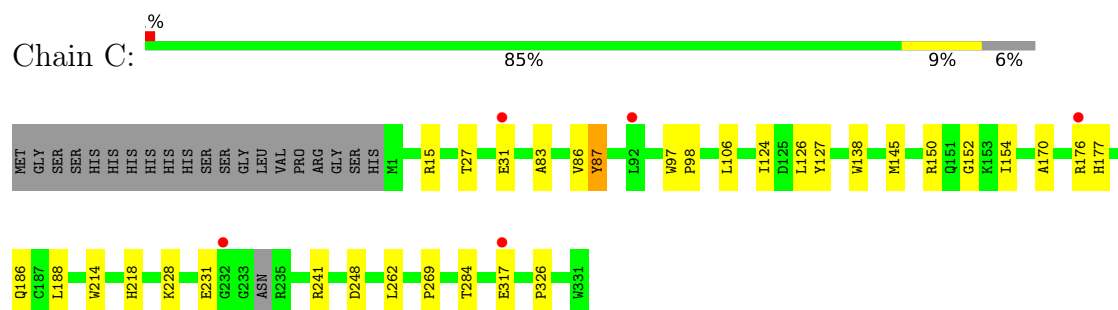
- Molecule 1: Aldo/keto reductase



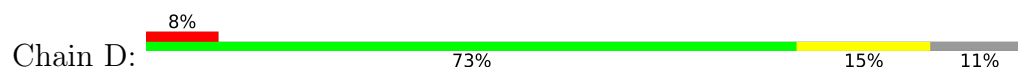
- Molecule 1: Aldo/keto reductase

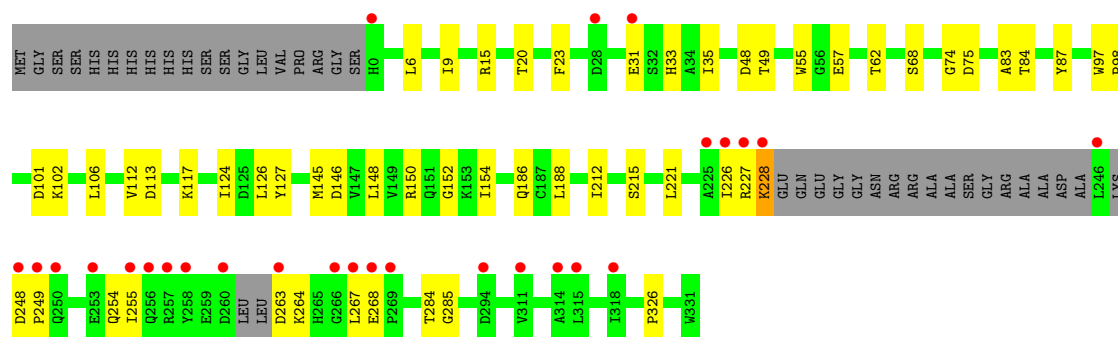


- Molecule 1: Aldo/keto reductase

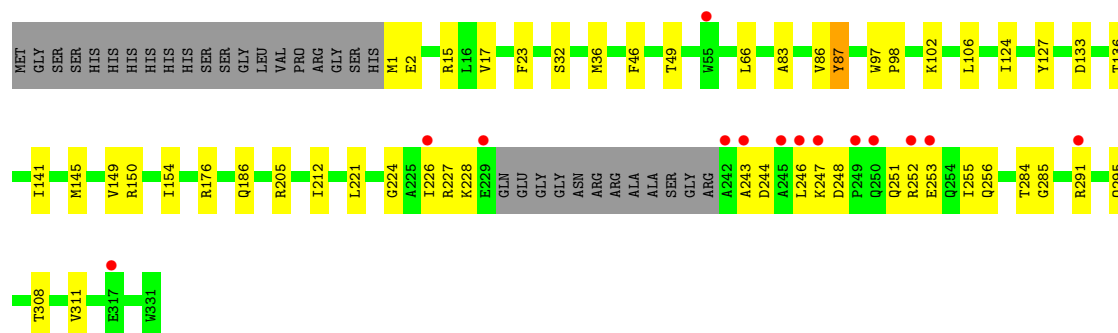
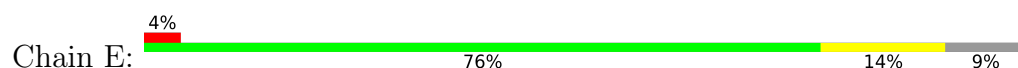


- Molecule 1: Aldo/keto reductase

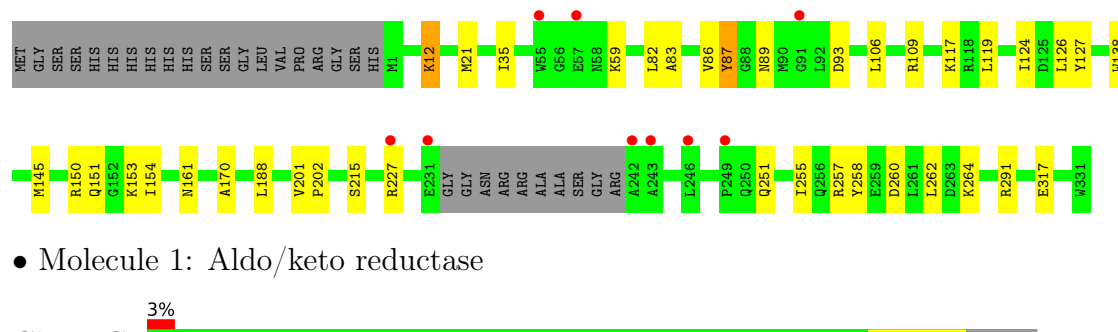
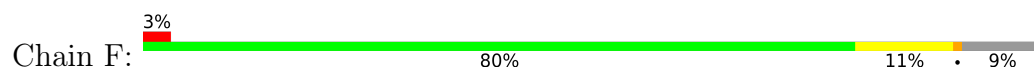




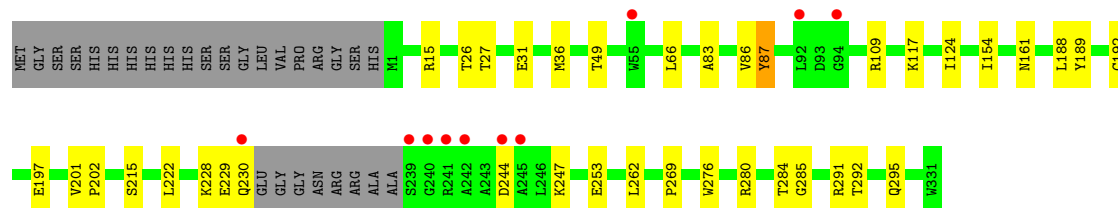
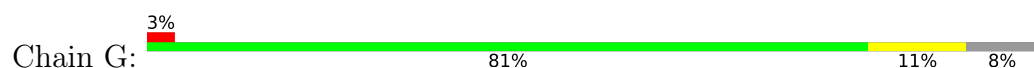
- Molecule 1: Aldo/keto reductase



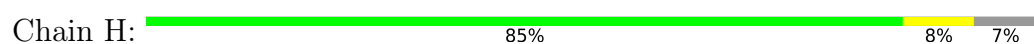
- Molecule 1: Aldo/keto reductase

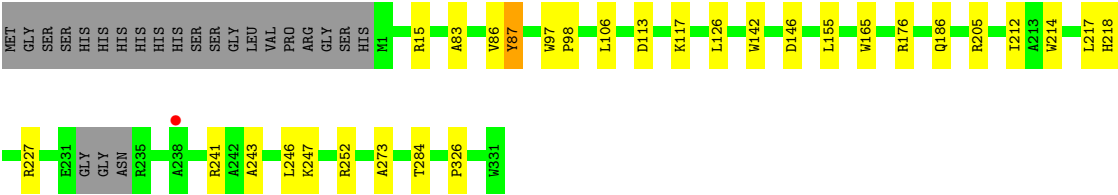


- Molecule 1: Aldo/keto reductase



- Molecule 1: Aldo/keto reductase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	167.97Å 183.09Å 102.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.17 – 2.30 38.17 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (38.17-2.30) 99.6 (38.17-2.30)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.187 , 0.231 0.187 , 0.231	Depositor DCC
R_{free} test set	6772 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	27.3	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 36.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	21051	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.27% 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: NDP

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	0.42	0/2506	0.60	0/3398
1	B	0.40	0/2607	0.60	0/3538
1	C	0.41	0/2603	0.57	0/3532
1	D	0.48	0/2476	0.68	3/3361 (0.1%)
1	E	0.38	0/2524	0.56	0/3429
1	F	0.45	0/2542	0.59	0/3453
1	G	0.41	0/2554	0.58	1/3468 (0.0%)
1	H	0.43	0/2595	0.59	0/3522
All	All	0.42	0/20407	0.60	4/27701 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	227	ARG	N-CA-C	-9.52	99.69	112.26
1	G	229	GLU	N-CA-C	-6.50	105.10	113.16
1	D	254	GLN	N-CA-C	-5.57	104.02	112.04
1	D	55	TRP	N-CA-C	5.24	121.95	110.80

There are no chirality outliers.

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	2455	0	2394	28	0
1	B	2552	0	2490	20	0
1	C	2548	0	2487	29	0
1	D	2422	0	2355	32	0
1	E	2469	0	2410	42	0
1	F	2487	0	2424	26	0
1	G	2499	0	2439	24	0
1	H	2540	0	2481	25	0
2	C	48	0	26	3	0
2	H	48	0	26	2	0
3	A	151	0	0	1	0
3	B	131	0	0	3	0
3	C	125	0	0	1	0
3	D	98	0	0	0	0
3	E	97	0	0	0	0
3	F	123	0	0	2	0
3	G	110	0	0	1	0
3	H	148	0	0	1	0
All	All	21051	0	19532	214	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 5.

All (214) 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:C:228:LYS:HB3	1:C:231:GLU:HG3	1.56	0.88
1:E:227:ARG:HG3	1:E:227:ARG:HH11	1.41	0.83
1:E:205:ARG:HH21	1:E:205:ARG:HG2	1.48	0.78
1:E:224:GLY:O	1:E:228:LYS:HD3	1.86	0.74
1:E:243:ALA:O	1:E:246:LEU:HD12	1.88	0.72
1:D:113:ASP:O	1:D:117:LYS:HE2	1.90	0.71
1:C:228:LYS:CB	1:C:231:GLU:HG3	2.21	0.70
1:A:28:ASP:HB2	1:A:31:GLU:H	1.56	0.70
1:B:117:LYS:NZ	3:B:401:HOH:O	2.25	0.69
1:D:20:THR:HG22	1:D:62:THR:HG21	1.74	0.69
1:G:26:THR:HG21	1:G:291:ARG:HE	1.57	0.69
1:H:205:ARG:HG2	1:H:205:ARG:HH21	1.59	0.68
1:B:15:ARG:HD2	1:B:284:THR:O	1.94	0.68
1:D:20:THR:HG22	1:D:62:THR:CG2	2.25	0.67
1:C:27:THR:HG23	1:C:31:GLU:HG2	1.79	0.65
1:G:36:MET:SD	1:G:66:LEU:HD22	2.37	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:291:ARG:HD2	1:E:295:GLN:OE1	1.98	0.64
1:B:114:ALA:HB1	3:B:402:HOH:O	1.96	0.64
1:F:117:LYS:HD3	1:F:117:LYS:N	2.13	0.64
1:A:150:ARG:HG2	1:A:150:ARG:HH21	1.63	0.64
1:A:28:ASP:CB	1:A:31:GLU:H	2.12	0.62
1:A:176:ARG:HD3	1:H:176:ARG:HG3	1.80	0.62
1:B:15:ARG:O	1:B:285:GLY:HA3	1.98	0.62
1:C:317:GLU:OE2	1:C:317:GLU:HA	1.99	0.62
1:E:308:THR:OG1	1:E:311:VAL:HG23	1.99	0.62
1:E:15:ARG:HD2	1:E:284:THR:O	2.00	0.61
1:B:118:ARG:NH2	3:B:402:HOH:O	2.33	0.61
1:D:152:GLY:O	1:F:109:ARG:NH1	2.34	0.61
1:E:251:GLN:O	1:E:255:ILE:HG12	2.01	0.60
1:F:257:ARG:NH1	1:F:317:GLU:OE1	2.33	0.60
1:B:227:ARG:HH21	1:B:228:LYS:HG3	1.66	0.60
1:E:226:ILE:HD12	1:E:256:GLN:HG2	1.84	0.59
1:B:225:ALA:O	1:B:229:GLU:HG3	2.02	0.59
1:F:59:LYS:HE3	1:F:89:ASN:O	2.04	0.58
1:G:15:ARG:HD2	1:G:284:THR:O	2.05	0.57
1:H:15:ARG:HD2	1:H:284:THR:O	2.05	0.56
1:C:152:GLY:O	1:G:109:ARG:NH1	2.37	0.56
1:E:227:ARG:HG3	1:E:227:ARG:NH1	2.15	0.56
1:E:36:MET:SD	1:E:66:LEU:HD22	2.46	0.56
1:D:31:GLU:O	1:D:35:ILE:HG13	2.06	0.56
1:B:327:GLU:HG3	1:B:331:TRP:O	2.06	0.55
1:C:218:HIS:CE1	1:C:241:ARG:HD3	2.42	0.55
1:A:262:LEU:HD23	1:A:269:PRO:HA	1.88	0.55
1:G:26:THR:HG21	1:G:291:ARG:HG2	1.88	0.54
1:G:262:LEU:HD23	1:G:269:PRO:HA	1.89	0.54
1:A:15:ARG:HD2	1:A:284:THR:O	2.07	0.54
1:A:20:THR:HG21	1:A:66:LEU:HD11	1.90	0.54
1:F:59:LYS:NZ	1:F:93:ASP:OD1	2.36	0.53
1:F:264:LYS:HD2	1:F:264:LYS:N	2.24	0.53
1:D:15:ARG:HD2	1:D:284:THR:O	2.09	0.53
1:D:20:THR:CG2	1:D:62:THR:CG2	2.86	0.53
1:C:150:ARG:NH2	1:E:150:ARG:HB3	2.24	0.53
1:D:97:TRP:CD2	1:D:98:PRO:HD2	2.44	0.52
1:H:113:ASP:O	1:H:117:LYS:HG3	2.09	0.52
1:B:253:GLU:O	1:B:257:ARG:HG3	2.09	0.52
1:C:262:LEU:HD23	1:C:269:PRO:HA	1.91	0.52
1:H:217:LEU:HD22	1:H:273:ALA:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:227:ARG:HH11	1:H:227:ARG:HB2	1.75	0.51
1:G:117:LYS:HE3	3:G:441:HOH:O	2.10	0.51
1:E:97:TRP:CD2	1:E:98:PRO:HD2	2.46	0.51
1:G:188:LEU:CD1	1:G:215:SER:HB3	2.41	0.51
1:A:86:VAL:O	1:A:87:TYR:HB2	2.09	0.51
1:B:217:LEU:HD11	1:B:270:GLY:HA2	1.91	0.51
3:A:405:HOH:O	1:E:106:LEU:HD21	2.10	0.51
1:B:262:LEU:HD23	1:B:269:PRO:HA	1.92	0.51
1:F:82:LEU:HD21	1:F:119:LEU:HD13	1.93	0.51
1:C:127:TYR:HD2	1:C:145:MET:HE1	1.76	0.51
1:H:205:ARG:HG2	1:H:205:ARG:NH2	2.24	0.51
1:E:23:PHE:CD2	1:E:32:SER:HB3	2.46	0.50
1:D:20:THR:HB	1:D:48:ASP:O	2.12	0.50
1:C:188:LEU:HB2	1:C:214:TRP:CZ2	2.46	0.50
1:C:186:GLN:OE1	2:C:401:NDP:H2N	2.11	0.50
1:G:26:THR:CG2	1:G:291:ARG:HG2	2.42	0.50
1:H:186:GLN:OE1	2:H:401:NDP:H2N	2.12	0.50
1:E:205:ARG:HH21	1:E:205:ARG:CG	2.23	0.50
1:B:150:ARG:HE	1:F:150:ARG:NH2	2.09	0.49
1:C:176:ARG:HB3	1:C:176:ARG:HH11	1.77	0.49
1:G:15:ARG:O	1:G:285:GLY:HA3	2.12	0.49
1:C:138:TRP:CZ2	1:C:170:ALA:HB2	2.48	0.49
1:C:15:ARG:HD2	1:C:284:THR:O	2.12	0.48
1:G:244:ASP:OD1	1:G:247:LYS:HD2	2.12	0.48
1:C:83:ALA:HA	1:C:126:LEU:O	2.13	0.48
1:A:24:GLY:H	1:A:27:THR:HB	1.79	0.48
1:A:150:ARG:HG2	1:A:150:ARG:NH2	2.27	0.48
1:E:102:LYS:HB3	1:E:133:ASP:OD2	2.14	0.48
1:C:326:PRO:HG3	1:F:161:ASN:O	2.13	0.48
1:G:86:VAL:O	1:G:87:TYR:HB2	2.14	0.48
1:C:97:TRP:CD2	1:C:98:PRO:HD2	2.49	0.47
1:D:106:LEU:HD23	1:H:155:LEU:CD1	2.43	0.47
1:B:86:VAL:O	1:B:87:TYR:HB2	2.15	0.47
1:E:17:VAL:HG22	1:E:46:PHE:CD2	2.48	0.47
1:F:124:ILE:O	1:F:154:ILE:HA	2.14	0.47
1:H:142:TRP:O	1:H:146:ASP:HB2	2.14	0.47
1:F:227:ARG:NH1	3:F:404:HOH:O	2.46	0.47
1:E:176:ARG:HG2	1:E:176:ARG:HH11	1.79	0.47
1:C:150:ARG:HH22	1:E:150:ARG:HB3	1.78	0.47
1:F:12:LYS:HB2	1:F:12:LYS:HE2	1.57	0.47
1:F:86:VAL:O	1:F:87:TYR:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:ALA:HA	1:A:126:LEU:O	2.15	0.47
1:B:124:ILE:O	1:B:154:ILE:HA	2.15	0.47
1:D:33:HIS:CE1	1:D:68:SER:HB3	2.50	0.47
1:C:214:TRP:CE3	2:C:401:NDP:H41N	2.50	0.47
1:E:244:ASP:C	1:E:246:LEU:H	2.23	0.47
1:E:86:VAL:HB	1:E:127:TYR:OH	2.14	0.46
1:E:86:VAL:O	1:E:87:TYR:CB	2.63	0.46
1:H:83:ALA:HA	1:H:126:LEU:O	2.16	0.46
1:A:27:THR:CG2	1:A:32:SER:OG	2.64	0.46
1:A:28:ASP:HB3	1:A:30:ALA:N	2.31	0.46
1:A:224:GLY:HA3	1:A:227:ARG:NH1	2.30	0.46
1:C:176:ARG:NH1	1:C:177:HIS:NE2	2.64	0.46
1:G:124:ILE:O	1:G:154:ILE:HA	2.16	0.46
1:C:86:VAL:O	1:C:87:TYR:CB	2.63	0.46
1:D:124:ILE:O	1:D:154:ILE:HA	2.16	0.46
1:A:28:ASP:HB2	1:A:31:GLU:HB2	1.98	0.46
1:E:1:MET:HE3	1:E:1:MET:HA	1.98	0.46
1:G:189:TYR:OH	1:G:197:GLU:OE2	2.23	0.46
1:B:83:ALA:HA	1:B:126:LEU:O	2.15	0.46
1:H:243:ALA:O	1:H:247:LYS:HG2	2.16	0.45
1:D:15:ARG:O	1:D:285:GLY:HA3	2.16	0.45
1:D:112:VAL:HG11	1:D:148:LEU:HD21	1.97	0.45
1:E:49:THR:HG22	1:E:83:ALA:O	2.17	0.45
1:E:291:ARG:HB2	1:E:295:GLN:HE22	1.81	0.45
1:E:145:MET:O	1:E:149:VAL:HG23	2.17	0.45
1:G:292:THR:OG1	1:G:295:GLN:HG3	2.17	0.45
1:H:205:ARG:NH2	3:H:506:HOH:O	2.49	0.45
1:A:28:ASP:HB3	1:A:30:ALA:H	1.82	0.45
1:A:145:MET:HE3	1:A:157:VAL:HG22	1.99	0.45
1:E:226:ILE:HG23	1:E:252:ARG:NH2	2.32	0.45
1:C:86:VAL:O	1:C:87:TYR:HB2	2.16	0.44
1:C:150:ARG:CZ	1:E:150:ARG:HD3	2.47	0.44
1:F:260:ASP:O	1:F:264:LYS:CD	2.65	0.44
1:F:188:LEU:CD1	1:F:215:SER:HB3	2.47	0.44
1:G:188:LEU:HD13	1:G:215:SER:HB3	1.99	0.44
1:D:228:LYS:HA	1:D:228:LYS:HD3	1.81	0.44
1:H:218:HIS:CE1	1:H:241:ARG:HD3	2.53	0.44
1:A:101:ASP:O	1:A:102:LYS:HB2	2.17	0.44
1:E:253:GLU:OE2	1:E:253:GLU:HA	2.17	0.44
1:E:1:MET:HE3	1:E:2:GLU:H	1.83	0.44
1:E:227:ARG:NH1	1:E:227:ARG:CG	2.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:20:THR:CG2	1:D:20:THR:O	2.66	0.44
1:F:258:TYR:CE1	1:F:262:LEU:HD11	2.53	0.44
1:H:86:VAL:O	1:H:87:TYR:HB2	2.17	0.44
1:H:227:ARG:HB2	1:H:227:ARG:NH1	2.33	0.44
1:D:101:ASP:OD1	1:D:102:LYS:HD2	2.17	0.44
1:E:124:ILE:O	1:E:154:ILE:HA	2.18	0.44
1:F:251:GLN:O	1:F:255:ILE:HG12	2.18	0.44
1:C:228:LYS:CA	1:C:231:GLU:HG3	2.48	0.43
1:E:252:ARG:HG2	1:E:252:ARG:HH11	1.83	0.43
1:D:186:GLN:HA	1:D:212:ILE:O	2.19	0.43
1:G:228:LYS:HA	1:G:228:LYS:HD3	1.78	0.43
1:B:188:LEU:HD13	1:B:215:SER:HB3	1.99	0.43
1:G:86:VAL:O	1:G:87:TYR:CB	2.66	0.43
1:F:21:MET:HB2	3:F:480:HOH:O	2.18	0.43
1:A:186:GLN:HG2	1:A:212:ILE:HB	2.00	0.43
1:F:151:GLN:OE1	1:F:153:LYS:HE3	2.19	0.43
1:E:247:LYS:HG3	1:E:248:ASP:N	2.33	0.43
1:C:27:THR:HG23	1:C:31:GLU:CG	2.48	0.43
1:E:97:TRP:CG	1:E:98:PRO:HD2	2.53	0.43
1:A:192:CYS:SG	1:A:222:LEU:HD21	2.59	0.43
1:A:206:GLU:HG2	1:H:165:TRP:CZ3	2.53	0.43
1:C:127:TYR:CD2	1:C:145:MET:HE1	2.54	0.43
1:D:221:LEU:HD11	1:D:255:ILE:HG13	2.01	0.43
1:E:15:ARG:O	1:E:285:GLY:HA3	2.19	0.43
1:A:24:GLY:O	1:A:27:THR:N	2.51	0.42
1:B:86:VAL:O	1:B:87:TYR:CB	2.67	0.42
1:D:23:PHE:N	1:D:23:PHE:CD1	2.85	0.42
1:D:83:ALA:HA	1:D:126:LEU:O	2.19	0.42
1:E:86:VAL:O	1:E:87:TYR:HB2	2.19	0.42
1:D:101:ASP:O	1:D:102:LYS:HB2	2.18	0.42
1:F:83:ALA:HA	1:F:126:LEU:O	2.19	0.42
1:F:138:TRP:CZ2	1:F:170:ALA:HB2	2.54	0.42
1:H:97:TRP:CD2	1:H:98:PRO:HD2	2.53	0.42
1:H:106:LEU:C	1:H:106:LEU:HD23	2.44	0.42
1:A:87:TYR:HB3	1:A:130:HIS:HB3	2.02	0.42
1:D:188:LEU:CD1	1:D:215:SER:HB3	2.50	0.42
1:H:214:TRP:CE3	2:H:401:NDP:H41N	2.55	0.42
1:A:86:VAL:HB	1:A:127:TYR:OH	2.20	0.42
1:F:106:LEU:C	1:F:106:LEU:HD23	2.45	0.42
1:F:35:ILE:HD11	1:F:291:ARG:O	2.19	0.41
1:C:106:LEU:C	1:C:106:LEU:HD23	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:127:TYR:HD2	1:F:145:MET:HE1	1.85	0.41
1:C:124:ILE:O	1:C:154:ILE:HA	2.20	0.41
1:D:127:TYR:CD2	1:D:145:MET:HE1	2.55	0.41
1:G:201:VAL:HB	1:G:202:PRO:HD3	2.02	0.41
1:B:117:LYS:HE3	1:B:117:LYS:HB3	1.72	0.41
1:B:251:GLN:O	1:B:255:ILE:HG12	2.20	0.41
1:D:6:LEU:O	1:D:9:ILE:HG12	2.19	0.41
1:G:27:THR:HB	1:G:31:GLU:HG3	2.02	0.41
1:A:229:GLU:CD	1:A:252:ARG:HH12	2.29	0.41
1:E:127:TYR:CD2	1:E:145:MET:HE1	2.54	0.41
1:H:86:VAL:O	1:H:87:TYR:CB	2.68	0.41
1:D:228:LYS:HZ2	1:D:228:LYS:HG2	1.65	0.41
1:G:192:CYS:SG	1:G:222:LEU:HD21	2.60	0.41
1:D:248:ASP:HB3	1:D:249:PRO:HD3	2.02	0.41
1:A:124:ILE:O	1:A:154:ILE:HA	2.21	0.41
1:A:161:ASN:O	1:H:326:PRO:HG3	2.21	0.41
1:A:206:GLU:HG2	1:H:165:TRP:HZ3	1.86	0.41
1:D:74:GLY:O	1:D:75:ASP:HB2	2.20	0.41
1:D:97:TRP:CG	1:D:98:PRO:HD2	2.55	0.41
1:D:146:ASP:OD2	1:D:150:ARG:HD2	2.21	0.41
1:D:326:PRO:HG3	1:G:161:ASN:O	2.21	0.41
1:G:276:TRP:CZ2	1:G:280:ARG:HD3	2.56	0.41
1:H:246:LEU:O	1:H:252:ARG:HD2	2.20	0.41
1:E:136:THR:HG22	1:E:141:ILE:HG13	2.02	0.41
1:F:201:VAL:HB	1:F:202:PRO:HD3	2.03	0.41
1:B:151:GLN:OE1	1:B:153:LYS:HE2	2.20	0.40
1:D:49:THR:O	1:D:84:THR:HA	2.21	0.40
1:C:248:ASP:OD1	1:C:248:ASP:C	2.64	0.40
1:F:86:VAL:O	1:F:87:TYR:CB	2.68	0.40
1:G:49:THR:HG22	1:G:83:ALA:O	2.22	0.40
1:E:186:GLN:HG2	1:E:212:ILE:HB	2.03	0.40
1:E:221:LEU:HD21	1:E:255:ILE:HD11	2.03	0.40
1:H:186:GLN:HA	1:H:212:ILE:O	2.22	0.40
2:C:401:NDP:H42N	3:C:581:HOH:O	2.20	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	310/351 (88%)	300 (97%)	8 (3%)	2 (1%)	21	27
1	B	326/351 (93%)	316 (97%)	9 (3%)	1 (0%)	36	46
1	C	326/351 (93%)	316 (97%)	9 (3%)	1 (0%)	36	46
1	D	305/351 (87%)	290 (95%)	14 (5%)	1 (0%)	36	46
1	E	315/351 (90%)	300 (95%)	14 (4%)	1 (0%)	36	46
1	F	317/351 (90%)	305 (96%)	11 (4%)	1 (0%)	36	46
1	G	319/351 (91%)	308 (97%)	10 (3%)	1 (0%)	36	46
1	H	324/351 (92%)	313 (97%)	10 (3%)	1 (0%)	36	46
All	All	2542/2808 (90%)	2448 (96%)	85 (3%)	9 (0%)	30	38

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28	ASP
1	A	87	TYR
1	B	87	TYR
1	C	87	TYR
1	D	87	TYR
1	E	87	TYR
1	F	87	TYR
1	G	87	TYR
1	H	87	TYR

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	250/275 (91%)	249 (100%)	1 (0%)	84	92
1	B	258/275 (94%)	258 (100%)	0	100	100
1	C	257/275 (94%)	257 (100%)	0	100	100
1	D	247/275 (90%)	240 (97%)	7 (3%)	38	56
1	E	251/275 (91%)	251 (100%)	0	100	100
1	F	253/275 (92%)	252 (100%)	1 (0%)	84	92
1	G	254/275 (92%)	252 (99%)	2 (1%)	73	86
1	H	257/275 (94%)	257 (100%)	0	100	100
All	All	2027/2200 (92%)	2016 (100%)	11 (0%)	81	90

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	262	LEU
1	D	57	GLU
1	D	226	ILE
1	D	228	LYS
1	D	263	ASP
1	D	264	LYS
1	D	267	LEU
1	D	268	GLU
1	F	12	LYS
1	G	230	GLN
1	G	253	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	HIS
1	A	58	ASN
1	A	72	GLN
1	A	177	HIS
1	A	234	ASN
1	D	22	ASN
1	D	128	GLN
1	E	128	GLN
1	E	177	HIS

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Mol	Chain	Res	Type
1	E	186	GLN
1	E	250	GLN
1	E	251	GLN
1	F	169	GLN
1	F	251	GLN
1	G	22	ASN
1	G	33	HIS
1	G	177	HIS
1	G	230	GLN
1	H	5	GLN
1	H	169	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NDP	H	401	-	51,52,52	1.23	4 (7%)	71,80,80	1.50	7 (9%)
2	NDP	C	401	-	51,52,52	1.24	4 (7%)	71,80,80	1.43	8 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NDP	H	401	-	-	3/34/77/77	0/5/5/5
2	NDP	C	401	-	-	3/34/77/77	0/5/5/5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	NDP	C5A-C4A	4.38	1.46	1.39
2	H	401	NDP	C5A-C4A	4.02	1.46	1.39
2	H	401	NDP	C5A-N7A	-3.40	1.32	1.39
2	C	401	NDP	C5A-N7A	-3.10	1.33	1.39
2	C	401	NDP	C4A-N9A	-2.53	1.32	1.37
2	H	401	NDP	C4A-N9A	-2.40	1.32	1.37
2	H	401	NDP	C5A-C6A	2.22	1.47	1.41
2	C	401	NDP	C5A-C6A	2.14	1.47	1.41

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	401	NDP	C5A-C4A-N3A	-6.02	118.43	126.72
2	C	401	NDP	C5A-C4A-N3A	-5.47	119.18	126.72
2	H	401	NDP	N3A-C4A-N9A	4.98	135.63	127.17
2	C	401	NDP	N3A-C4A-N9A	4.53	134.87	127.17
2	H	401	NDP	C2A-N3A-C4A	3.57	120.54	111.83
2	C	401	NDP	C2A-N3A-C4A	3.35	120.01	111.83
2	H	401	NDP	C4A-C5A-N7A	-3.31	106.80	110.58
2	H	401	NDP	N3A-C2A-N1A	-2.92	124.16	128.58
2	C	401	NDP	N3A-C2A-N1A	-2.90	124.20	128.58
2	H	401	NDP	C5A-N7A-C8A	2.73	107.74	103.45
2	C	401	NDP	C4A-C5A-N7A	-2.53	107.69	110.58
2	H	401	NDP	C4A-N9A-C8A	2.36	108.21	105.74
2	C	401	NDP	N6A-C6A-N1A	2.13	123.12	118.38
2	C	401	NDP	C3D-C2D-C1D	2.08	105.39	101.46
2	C	401	NDP	O2B-P2B-O1X	-2.03	102.09	109.33

There are no chirality outliers.

All (6) torsion outliers are listed below:

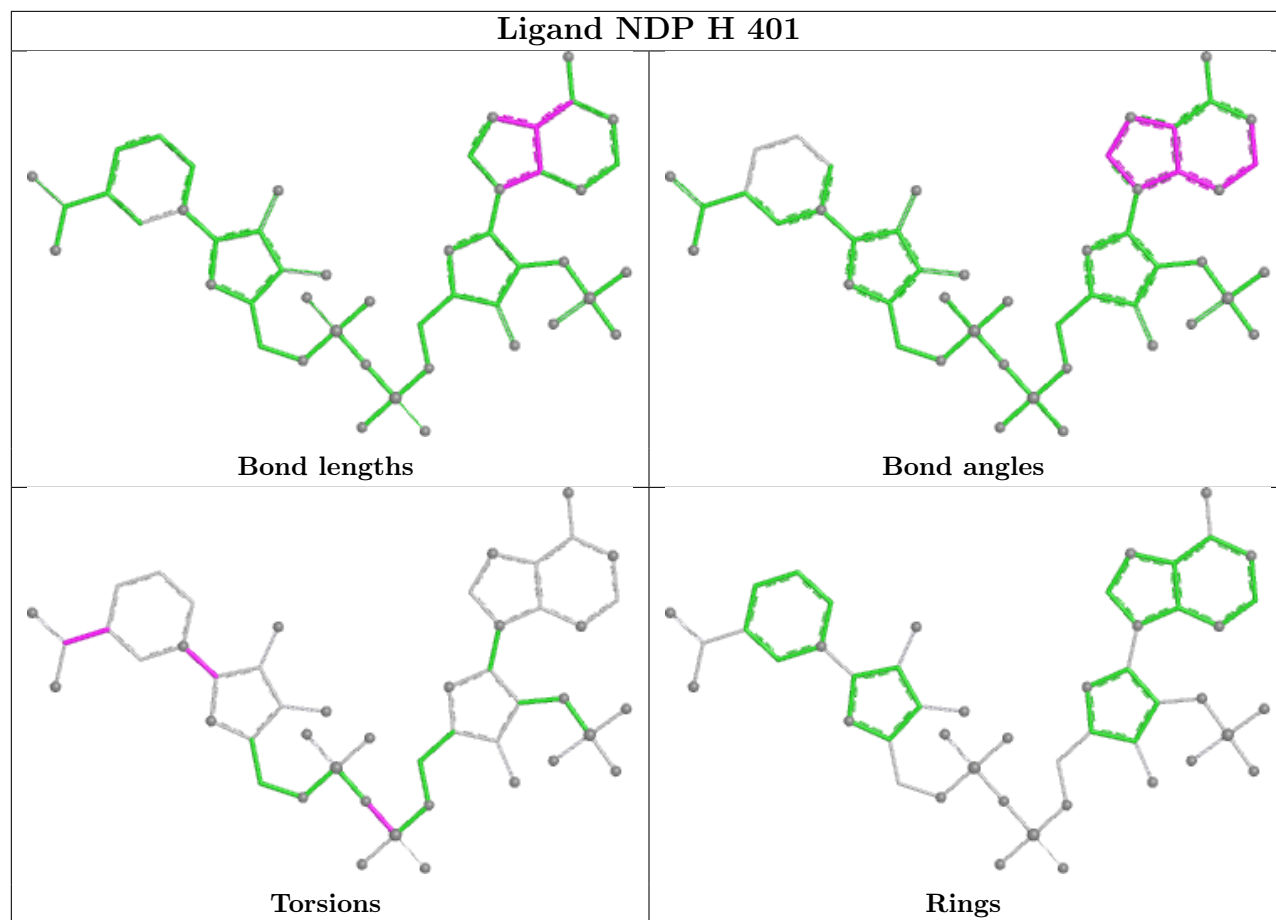
Mol	Chain	Res	Type	Atoms
2	C	401	NDP	PN-O3-PA-O5B
2	H	401	NDP	PN-O3-PA-O5B
2	H	401	NDP	O4D-C1D-N1N-C2N
2	C	401	NDP	O4D-C1D-N1N-C2N
2	C	401	NDP	C2B-O2B-P2B-O2X
2	H	401	NDP	C2N-C3N-C7N-N7N

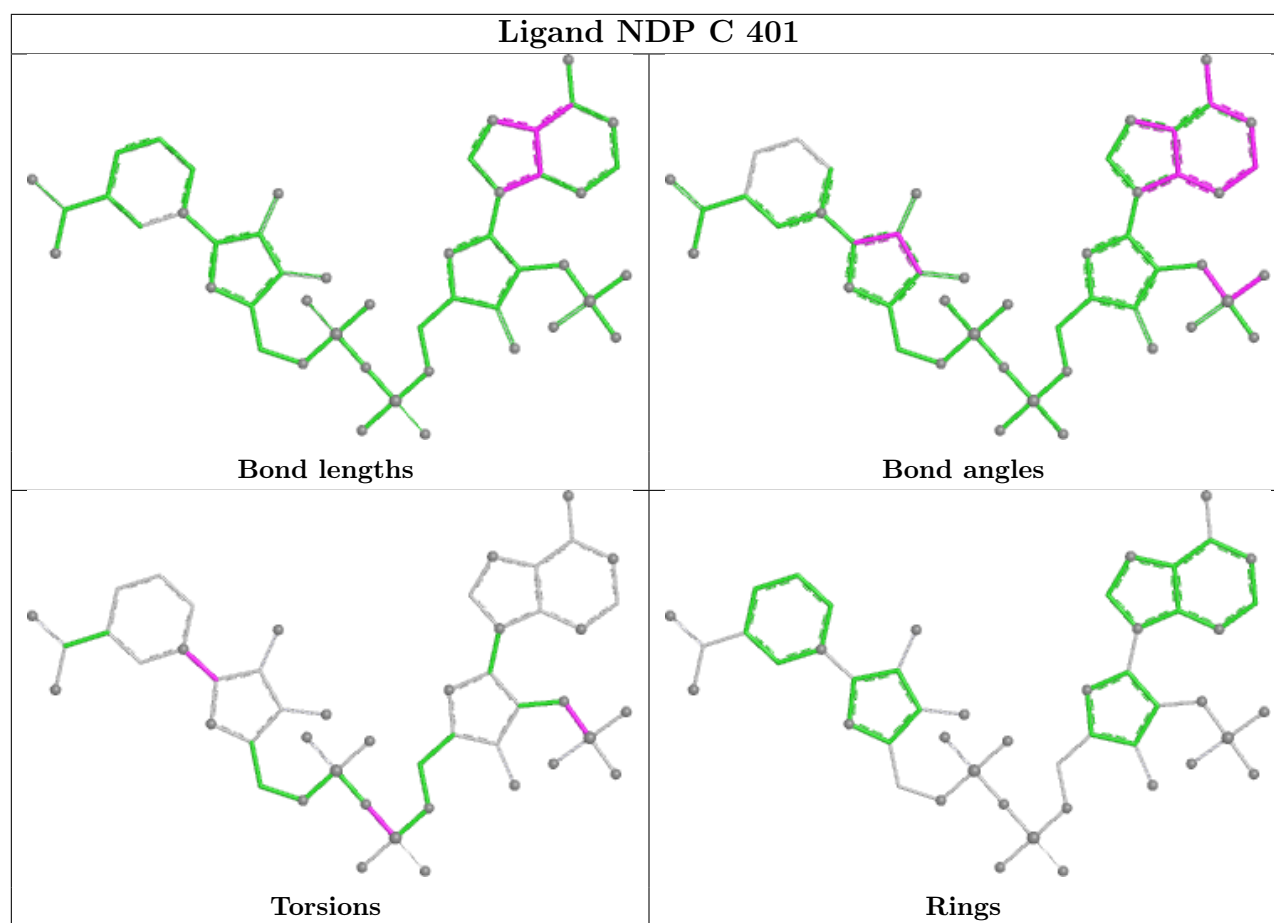
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	401	NDP	2	0
2	C	401	NDP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	318/351 (90%)	-0.08	14 (4%) 39 41	14, 24, 49, 68	0
1	B	330/351 (94%)	-0.05	7 (2%) 63 65	15, 26, 53, 82	0
1	C	330/351 (94%)	-0.12	5 (1%) 72 73	15, 25, 46, 68	0
1	D	312/351 (88%)	0.36	27 (8%) 16 17	14, 29, 64, 78	0
1	E	319/351 (90%)	0.24	14 (4%) 39 41	15, 30, 65, 93	0
1	F	321/351 (91%)	-0.05	9 (2%) 55 57	15, 25, 50, 80	0
1	G	323/351 (92%)	0.03	10 (3%) 51 53	16, 27, 56, 92	0
1	H	328/351 (93%)	-0.22	1 (0%) 90 90	14, 23, 45, 62	0
All	All	2581/2808 (91%)	0.01	87 (3%) 48 50	14, 26, 54, 93	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	246	LEU	7.2
1	E	242	ALA	5.8
1	A	243	ALA	5.5
1	D	260	ASP	5.0
1	A	58	ASN	4.9
1	E	245	ALA	4.5
1	A	56	GLU	4.5
1	D	253	GLU	4.2
1	C	232	GLY	4.0
1	B	245	ALA	4.0
1	F	242	ALA	3.9
1	D	263	ASP	3.8
1	G	239	SER	3.8
1	F	243	ALA	3.7
1	E	243	ALA	3.7
1	D	226	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	G	244	ASP	3.5
1	D	0	HIS	3.5
1	E	250	GLN	3.5
1	G	240	GLY	3.4
1	A	25	PRO	3.4
1	B	246	LEU	3.3
1	D	249	PRO	3.3
1	A	234	ASN	3.2
1	A	26	THR	3.2
1	D	250	GLN	3.2
1	D	225	ALA	3.2
1	G	92	LEU	3.2
1	B	242	ALA	3.1
1	B	249	PRO	3.1
1	E	246	LEU	3.1
1	C	317	GLU	3.0
1	A	233	GLY	3.0
1	D	314	ALA	3.0
1	A	28	ASP	3.0
1	D	258	TYR	2.9
1	G	230	GLN	2.9
1	E	247	LYS	2.8
1	A	54	GLY	2.8
1	F	57	GLU	2.8
1	D	311	VAL	2.8
1	D	266	GLY	2.7
1	F	55	TRP	2.7
1	D	228	LYS	2.7
1	G	242	ALA	2.7
1	A	244	ASP	2.7
1	D	31	GLU	2.6
1	D	248	ASP	2.6
1	E	317	GLU	2.6
1	G	55	TRP	2.6
1	D	269	PRO	2.6
1	B	247	LYS	2.6
1	D	267	LEU	2.5
1	E	249	PRO	2.5
1	E	229	GLU	2.5
1	D	255	ILE	2.4
1	B	241	ARG	2.4
1	E	55	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	291	ARG	2.4
1	E	226	ILE	2.4
1	D	227	ARG	2.4
1	G	245	ALA	2.3
1	D	318	ILE	2.3
1	F	91	GLY	2.3
1	G	241	ARG	2.3
1	A	250	GLN	2.3
1	H	238	ALA	2.3
1	C	31	GLU	2.3
1	D	315	LEU	2.2
1	A	227	ARG	2.2
1	F	231	GLU	2.2
1	D	28	ASP	2.2
1	A	24	GLY	2.2
1	E	252	ARG	2.2
1	F	227	ARG	2.2
1	C	176	ARG	2.2
1	D	268	GLU	2.2
1	B	243	ALA	2.2
1	F	249	PRO	2.1
1	C	92	LEU	2.1
1	D	294	ASP	2.1
1	F	246	LEU	2.1
1	A	247	LYS	2.1
1	D	257	ARG	2.1
1	E	253	GLU	2.0
1	G	94	GLY	2.0
1	D	256	GLN	2.0

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](#)

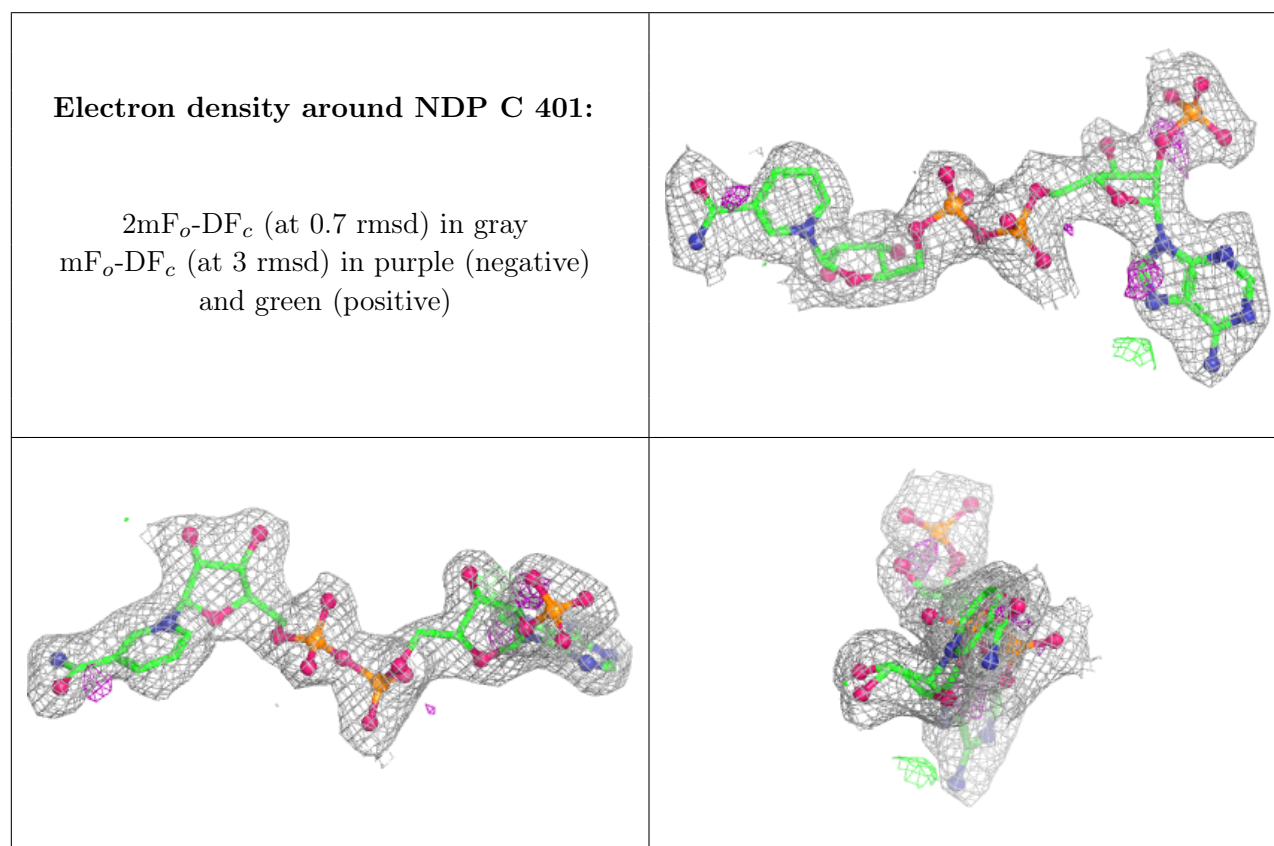
There are no oligosaccharides in this entry.

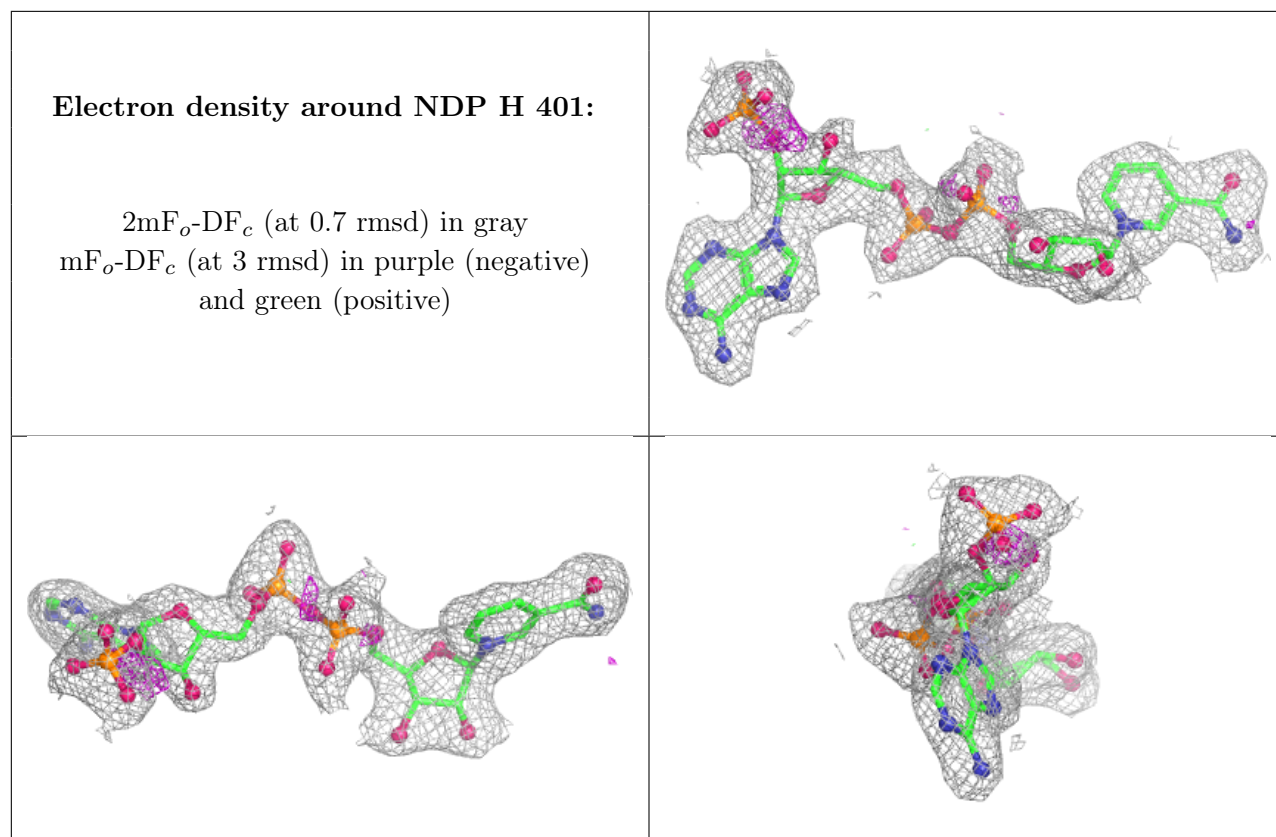
6.4 Ligands ⓘ

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. 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	B-factors(Å ²)	Q<0.9
2	NDP	C	401	48/48	0.95	0.08	21,29,35,40	0
2	NDP	H	401	48/48	0.95	0.08	18,27,34,40	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.