



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:35 PM GMT

PDB ID : 4FBG
Title : Crystal structure of Treponema denticola trans-2-enoyl-CoA reductase in complex with NAD
Authors : Hu, K.; Zhao, M.; Zhang, T.; Yang, S.; Ding, J.
Deposited on : 2012-05-23
Resolution : 3.02 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

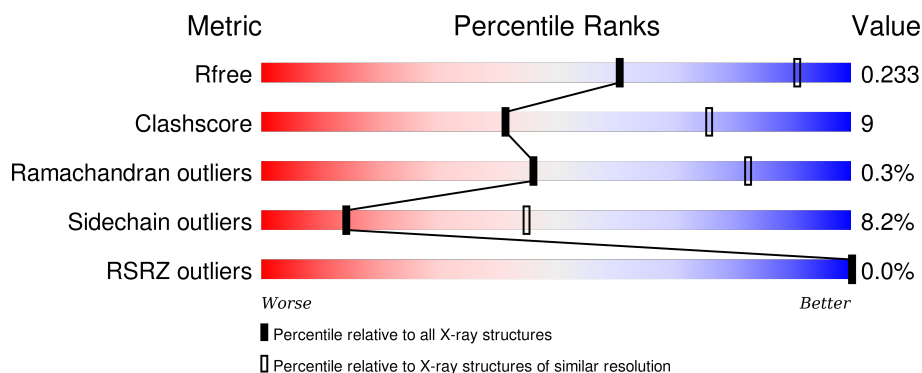
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.02 Å.

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














Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1773 (3.04-3.00)
Clashscore	102246	2117 (3.04-3.00)
Ramachandran outliers	100387	2050 (3.04-3.00)
Sidechain outliers	100360	2053 (3.04-3.00)
RSRZ outliers	91569	1788 (3.04-3.00)

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	405	<div> <div>73%</div> <div>22%</div> <div>..</div> </div>
1	B	405	<div> <div>75%</div> <div>20%</div> <div>..</div> </div>
1	C	405	<div> <div>77%</div> <div>18%</div> <div>..</div> </div>
1	D	405	<div> <div>78%</div> <div>20%</div> <div>..</div> </div>
1	E	405	<div> <div>76%</div> <div>20%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	405	
1	G	405	
1	H	405	
1	I	405	
1	J	405	
1	K	405	
1	L	405	
1	M	405	
1	N	405	
1	O	405	
1	P	405	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAD	A	1001	-	-	-	X
2	NAD	E	1001	-	-	-	X
2	NAD	I	1001	-	-	-	X
2	NAD	K	1001	-	-	-	X
2	NAD	M	1001	-	-	-	X

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 49790 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 Putative reductase TDE_0597.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	Se	0	0	0
			3096	1957	527	601	5	6			
1	B	397	Total	C	N	O	S	Se	0	0	0
			3079	1946	525	597	5	6			
1	C	399	Total	C	N	O	S	Se	0	0	0
			3096	1957	527	601	5	6			
1	D	401	Total	C	N	O	S	Se	0	0	0
			3116	1969	533	603	5	6			
1	E	397	Total	C	N	O	S	Se	0	0	0
			3079	1946	525	597	5	6			
1	F	398	Total	C	N	O	S	Se	0	0	0
			3087	1952	526	598	5	6			
1	G	398	Total	C	N	O	S	Se	0	0	0
			3087	1952	526	598	5	6			
1	H	399	Total	C	N	O	S	Se	0	0	0
			3096	1957	527	601	5	6			
1	I	399	Total	C	N	O	S	Se	0	0	0
			3096	1957	527	601	5	6			
1	J	397	Total	C	N	O	S	Se	0	0	0
			3079	1946	525	597	5	6			
1	K	397	Total	C	N	O	S	Se	0	0	0
			3079	1946	525	597	5	6			
1	L	401	Total	C	N	O	S	Se	0	0	0
			3116	1969	533	603	5	6			
1	M	397	Total	C	N	O	S	Se	0	0	0
			3079	1946	525	597	5	6			
1	N	398	Total	C	N	O	S	Se	0	0	0
			3087	1952	526	598	5	6			
1	O	397	Total	C	N	O	S	Se	0	0	0
			3079	1946	525	597	5	6			
1	P	398	Total	C	N	O	S	Se	0	0	0
			3087	1952	526	598	5	6			

There are 128 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
A	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
A	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
A	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
A	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
A	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
A	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
A	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
B	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
B	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
B	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
B	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
B	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
B	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
B	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
B	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
C	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
C	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
C	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
C	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
C	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
C	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
C	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
C	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
D	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
D	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
D	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
D	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
D	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
D	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
D	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
D	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
E	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
E	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
E	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
E	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
E	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
E	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
E	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
E	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
F	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
F	399	GLU	-	EXPRESSION TAG	UNP Q73Q47

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Chain	Residue	Modelled	Actual	Comment	Reference
F	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
F	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
F	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
F	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
F	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
F	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
G	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
G	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
G	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
G	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
G	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
G	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
G	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
G	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
H	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
H	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
H	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
H	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
H	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
H	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
H	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
H	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
I	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
I	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
I	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
I	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
I	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
I	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
I	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
I	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
J	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
J	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
J	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
J	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
J	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
J	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
J	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
J	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
K	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
K	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
K	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
K	401	HIS	-	EXPRESSION TAG	UNP Q73Q47

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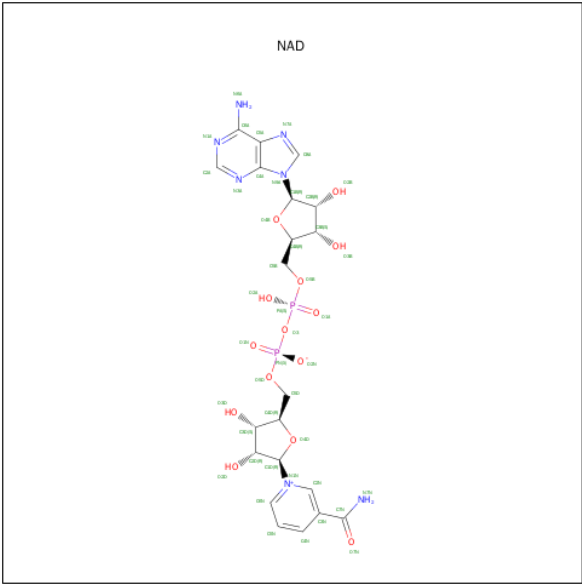
Chain	Residue	Modelled	Actual	Comment	Reference
K	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
K	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
K	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
K	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
L	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
L	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
L	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
L	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
L	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
L	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
L	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
L	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
M	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
M	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
M	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
M	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
M	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
M	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
M	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
M	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
N	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
N	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
N	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
N	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
N	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
N	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
N	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
N	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
O	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
O	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
O	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
O	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
O	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
O	403	HIS	-	EXPRESSION TAG	UNP Q73Q47
O	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
O	405	HIS	-	EXPRESSION TAG	UNP Q73Q47
P	398	LEU	-	EXPRESSION TAG	UNP Q73Q47
P	399	GLU	-	EXPRESSION TAG	UNP Q73Q47
P	400	HIS	-	EXPRESSION TAG	UNP Q73Q47
P	401	HIS	-	EXPRESSION TAG	UNP Q73Q47
P	402	HIS	-	EXPRESSION TAG	UNP Q73Q47
P	403	HIS	-	EXPRESSION TAG	UNP Q73Q47

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Chain	Residue	Modelled	Actual	Comment	Reference
P	404	HIS	-	EXPRESSION TAG	UNP Q73Q47
P	405	HIS	-	EXPRESSION TAG	UNP Q73Q47

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).

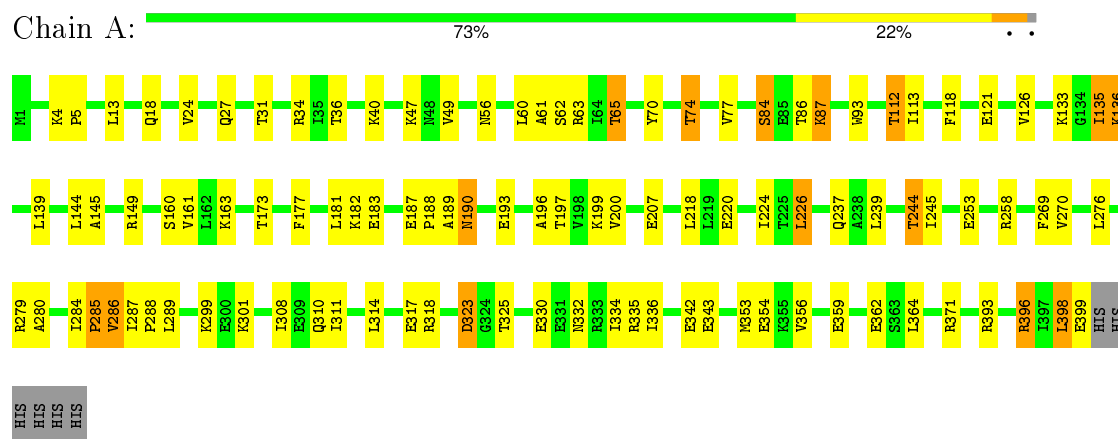


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	I	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	K	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	M	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	P	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

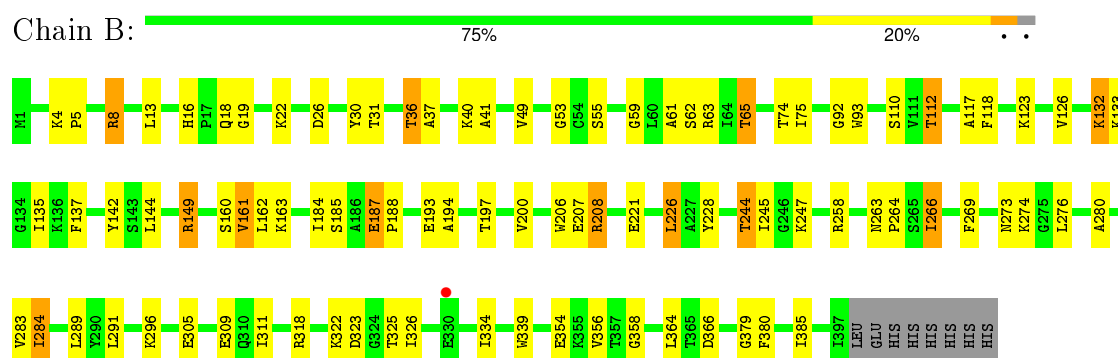
3 Residue-property plots

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 ($RSRZ > 2$). 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.

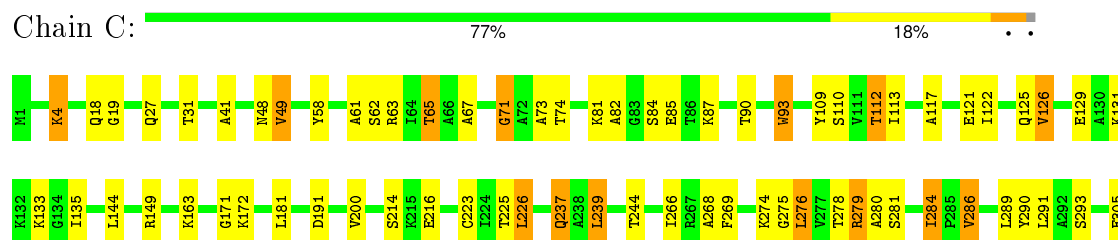
• Molecule 1: Putative reductase TDE_0597



• Molecule 1: Putative reductase TDE_0597

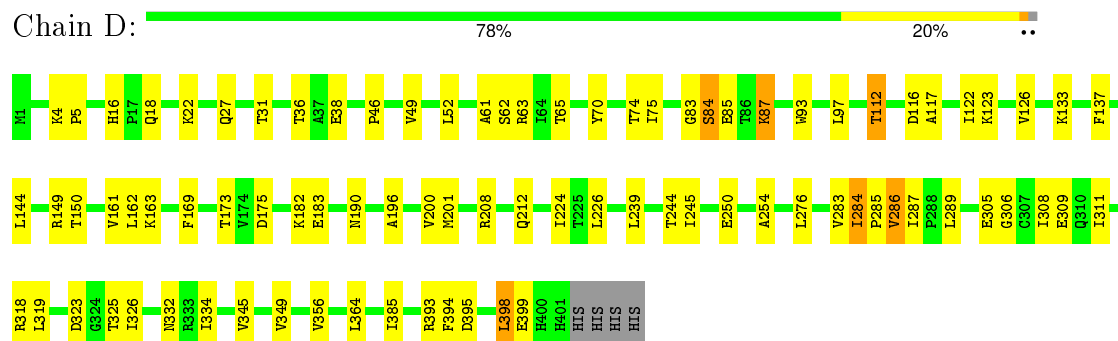


• Molecule 1: Putative reductase TDE_0597

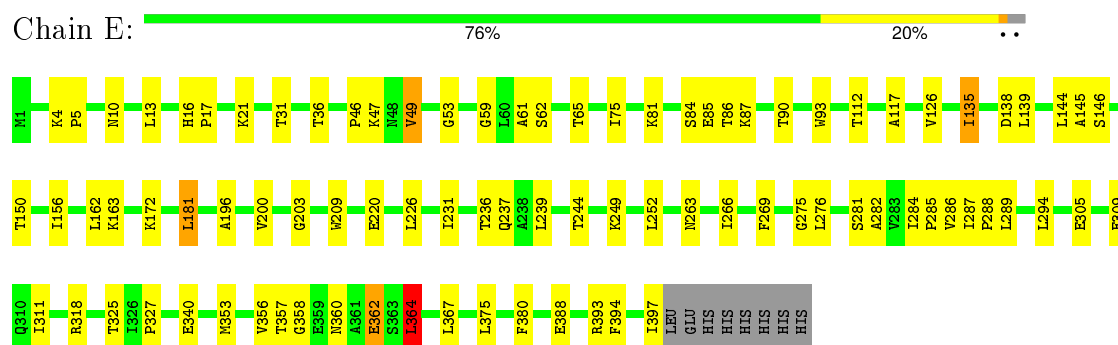




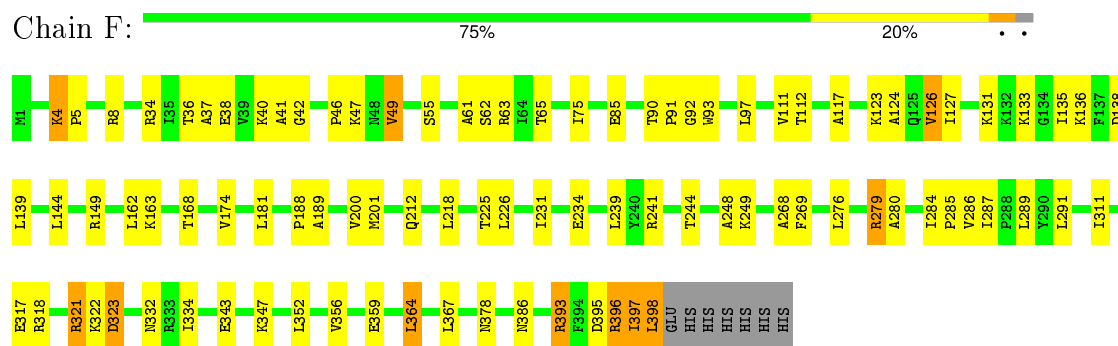
• Molecule 1: Putative reductase TDE_0597



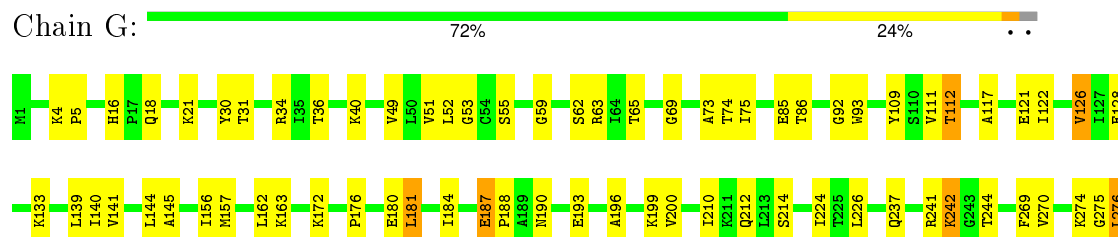
• Molecule 1: Putative reductase TDE_0597



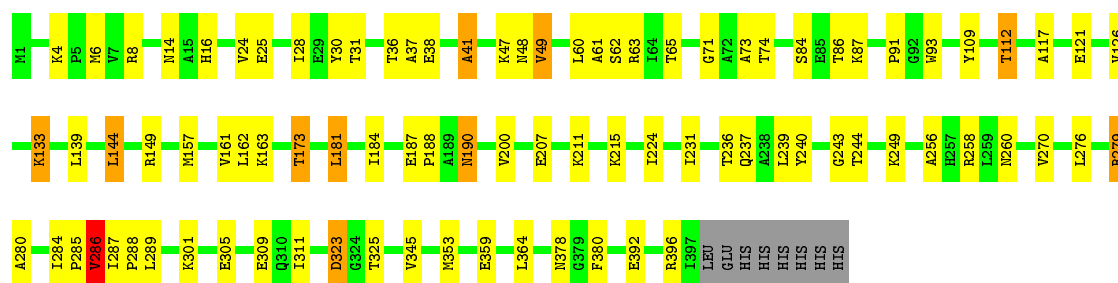
• Molecule 1: Putative reductase TDE_0597



• Molecule 1: Putative reductase TDE_0597

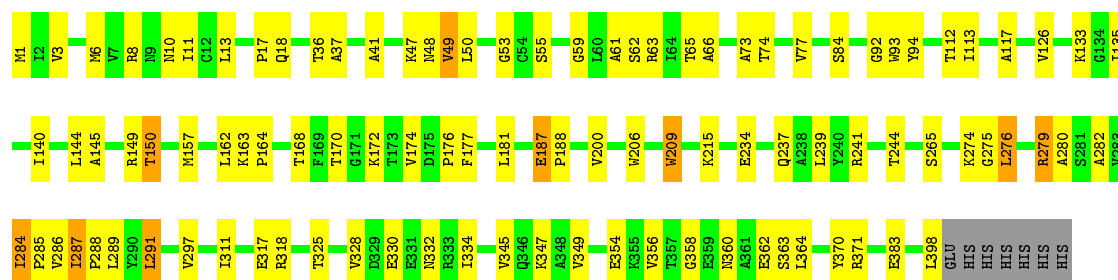






- Molecule 1: Putative reductase TDE_0597

Chain P: 73% 23% . .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	100.79Å 120.03Å 171.29Å 90.80° 104.96° 112.75°	Depositor
Resolution (Å)	50.00 – 3.02 41.07 – 3.02	Depositor EDS
% Data completeness (in resolution range)	94.8 (50.00-3.02) 90.9 (41.07-3.02)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.235 , 0.292 0.237 , 0.233	Depositor DCC
R_{free} test set	6668 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	62.4	Xtriage
Anisotropy	0.288	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 10.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 132077 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	49790	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.31 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 5.9504e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAD

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	0.47	2/3146 (0.1%)	0.55	0/4237
1	B	0.48	3/3129 (0.1%)	0.54	0/4214
1	C	0.46	1/3146 (0.0%)	0.55	0/4237
1	D	0.46	1/3168 (0.0%)	0.54	0/4267
1	E	0.48	1/3129 (0.0%)	0.55	1/4214 (0.0%)
1	F	0.48	1/3137 (0.0%)	0.55	0/4225
1	G	0.48	2/3137 (0.1%)	0.55	0/4225
1	H	0.55	3/3146 (0.1%)	0.56	0/4237
1	I	0.51	3/3146 (0.1%)	0.54	0/4237
1	J	0.46	2/3129 (0.1%)	0.54	0/4214
1	K	0.48	2/3129 (0.1%)	0.55	0/4214
1	L	0.47	1/3168 (0.0%)	0.54	0/4267
1	M	0.46	1/3129 (0.0%)	0.53	0/4214
1	N	0.50	1/3137 (0.0%)	0.55	0/4225
1	O	0.57	3/3129 (0.1%)	0.57	1/4214 (0.0%)
1	P	0.49	4/3137 (0.1%)	0.55	0/4225
All	All	0.49	31/50242 (0.1%)	0.55	2/67666 (0.0%)

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	4	LYS	CD-CE	5.90	1.66	1.51
1	A	285	PRO	N-CD	5.58	1.55	1.47
1	I	285	PRO	N-CD	5.57	1.55	1.47
1	O	41	ALA	C-O	5.56	1.33	1.23
1	P	93	TRP	CD2-CE2	5.55	1.48	1.41

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	O	181	LEU	CA-CB-CG	5.82	128.69	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	364	LEU	CA-CB-CG	5.21	127.29	115.30

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	3096	0	3097	61	0
1	B	3079	0	3080	53	0
1	C	3096	0	3097	60	0
1	D	3116	0	3111	44	0
1	E	3079	0	3080	50	0
1	F	3087	0	3091	58	0
1	G	3087	0	3091	64	0
1	H	3096	0	3097	51	0
1	I	3096	0	3097	45	0
1	J	3079	0	3080	40	0
1	K	3079	0	3080	54	0
1	L	3116	0	3111	62	0
1	M	3079	0	3080	45	0
1	N	3087	0	3091	54	0
1	O	3079	0	3080	47	0
1	P	3087	0	3091	68	0
2	A	44	0	26	2	0
2	E	44	0	26	3	0
2	G	44	0	26	4	0
2	H	44	0	26	2	0
2	I	44	0	26	1	0
2	K	44	0	26	2	0
2	M	44	0	26	4	0
2	P	44	0	26	3	0
All	All	49790	0	49662	847	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 9.

The worst 5 of 847 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:N:393:ARG:HH11	1:N:393:ARG:HG2	1.18	1.08
1:K:63:ARG:HH12	1:K:112:THR:HG22	1.20	1.02
1:G:396:ARG:HH11	1:G:396:ARG:HG2	1.34	0.92
1:B:8:ARG:HH11	1:B:8:ARG:HG3	1.36	0.91
1:K:258:ARG:O	1:K:262:GLU:HG2	1.71	0.90

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	397/405 (98%)	370 (93%)	26 (6%)	1 (0%)	46	82
1	B	395/405 (98%)	378 (96%)	16 (4%)	1 (0%)	46	82
1	C	397/405 (98%)	368 (93%)	26 (6%)	3 (1%)	24	65
1	D	399/405 (98%)	378 (95%)	20 (5%)	1 (0%)	46	82
1	E	395/405 (98%)	372 (94%)	22 (6%)	1 (0%)	46	82
1	F	396/405 (98%)	369 (93%)	27 (7%)	0	100	100
1	G	396/405 (98%)	369 (93%)	26 (7%)	1 (0%)	46	82
1	H	397/405 (98%)	365 (92%)	29 (7%)	3 (1%)	24	65
1	I	397/405 (98%)	370 (93%)	26 (6%)	1 (0%)	46	82
1	J	395/405 (98%)	373 (94%)	21 (5%)	1 (0%)	46	82
1	K	395/405 (98%)	366 (93%)	29 (7%)	0	100	100
1	L	399/405 (98%)	367 (92%)	31 (8%)	1 (0%)	46	82
1	M	395/405 (98%)	374 (95%)	20 (5%)	1 (0%)	46	82
1	N	396/405 (98%)	375 (95%)	20 (5%)	1 (0%)	46	82

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	O	395/405 (98%)	370 (94%)	23 (6%)	2 (0%)	34	75
1	P	396/405 (98%)	366 (92%)	30 (8%)	0	100	100
All	All	6340/6480 (98%)	5930 (94%)	392 (6%)	18 (0%)	46	82

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	286	VAL
1	E	286	VAL
1	G	286	VAL
1	I	286	VAL
1	M	286	VAL

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	325/325 (100%)	291 (90%)	34 (10%)	8	31
1	B	323/325 (99%)	296 (92%)	27 (8%)	14	43
1	C	325/325 (100%)	302 (93%)	23 (7%)	18	53
1	D	327/325 (101%)	300 (92%)	27 (8%)	14	44
1	E	323/325 (99%)	306 (95%)	17 (5%)	28	66
1	F	324/325 (100%)	300 (93%)	24 (7%)	17	50
1	G	324/325 (100%)	298 (92%)	26 (8%)	15	46
1	H	325/325 (100%)	298 (92%)	27 (8%)	14	44
1	I	325/325 (100%)	301 (93%)	24 (7%)	17	50
1	J	323/325 (99%)	304 (94%)	19 (6%)	24	61
1	K	323/325 (99%)	292 (90%)	31 (10%)	10	36
1	L	327/325 (101%)	289 (88%)	38 (12%)	7	26
1	M	323/325 (99%)	296 (92%)	27 (8%)	14	43
1	N	324/325 (100%)	298 (92%)	26 (8%)	15	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	323/325 (99%)	297 (92%)	26 (8%)	15	46
1	P	324/325 (100%)	297 (92%)	27 (8%)	14	44
All	All	5188/5200 (100%)	4765 (92%)	423 (8%)	14	45

5 of 423 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	156	ILE
1	J	135	ILE
1	O	323	ASP
1	H	286	VAL
1	I	162	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	212	GLN
1	H	304	HIS
1	O	304	HIS
1	G	304	HIS
1	H	125	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 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	NAD	A	1001	-	38,48,48	3.38	8 (21%)	47,73,73	3.47	8 (17%)
2	NAD	E	1001	-	38,48,48	3.75	8 (21%)	47,73,73	3.31	10 (21%)
2	NAD	G	1001	-	38,48,48	3.24	9 (23%)	47,73,73	4.01	7 (14%)
2	NAD	H	1001	-	38,48,48	3.45	8 (21%)	47,73,73	3.70	9 (19%)
2	NAD	I	1001	-	38,48,48	3.37	8 (21%)	47,73,73	3.67	7 (14%)
2	NAD	K	1001	-	38,48,48	3.68	9 (23%)	47,73,73	3.31	8 (17%)
2	NAD	M	1001	-	38,48,48	3.63	8 (21%)	47,73,73	3.40	10 (21%)
2	NAD	P	1001	-	38,48,48	3.37	7 (18%)	47,73,73	3.66	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
2	NAD	A	1001	-	-	0/22/62/62	0/5/5/5
2	NAD	E	1001	-	-	0/22/62/62	0/5/5/5
2	NAD	G	1001	-	-	0/22/62/62	0/5/5/5
2	NAD	H	1001	-	-	0/22/62/62	0/5/5/5
2	NAD	I	1001	-	-	0/22/62/62	0/5/5/5
2	NAD	K	1001	-	-	0/22/62/62	0/5/5/5
2	NAD	M	1001	-	-	0/22/62/62	0/5/5/5
2	NAD	P	1001	-	-	0/22/62/62	0/5/5/5

The worst 5 of 65 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1001	NAD	C3N-C7N	-7.06	1.39	1.50
2	H	1001	NAD	C3N-C7N	-7.05	1.39	1.50
2	I	1001	NAD	C3N-C7N	-6.89	1.39	1.50
2	P	1001	NAD	C3N-C7N	-6.88	1.39	1.50
2	A	1001	NAD	C3N-C7N	-6.87	1.39	1.50

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	G	1001	NAD	N3A-C2A-N1A	-24.85	109.87	128.89
2	I	1001	NAD	N3A-C2A-N1A	-22.96	111.32	128.89
2	P	1001	NAD	N3A-C2A-N1A	-21.11	112.73	128.89
2	H	1001	NAD	N3A-C2A-N1A	-20.97	112.84	128.89
2	A	1001	NAD	N3A-C2A-N1A	-20.89	112.90	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	NAD	2	0
2	E	1001	NAD	3	0
2	G	1001	NAD	4	0
2	H	1001	NAD	2	0
2	I	1001	NAD	1	0
2	K	1001	NAD	2	0
2	M	1001	NAD	4	0
2	P	1001	NAD	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	393/405 (97%)	-0.47	0 100 100	38, 62, 77, 109	0
1	B	391/405 (96%)	-0.48	1 (0%) 94 84	42, 61, 83, 97	0
1	C	393/405 (97%)	-0.44	0 100 100	41, 64, 86, 100	0
1	D	395/405 (97%)	-0.47	0 100 100	44, 64, 85, 109	0
1	E	391/405 (96%)	-0.44	0 100 100	41, 65, 85, 104	0
1	F	392/405 (96%)	-0.44	0 100 100	40, 68, 87, 103	0
1	G	392/405 (96%)	-0.48	0 100 100	46, 68, 89, 103	0
1	H	393/405 (97%)	-0.27	0 100 100	43, 76, 98, 116	0
1	I	393/405 (97%)	-0.35	1 (0%) 94 84	49, 75, 100, 138	0
1	J	391/405 (96%)	-0.44	0 100 100	38, 62, 93, 107	0
1	K	391/405 (96%)	-0.42	0 100 100	38, 61, 90, 111	0
1	L	395/405 (97%)	-0.43	0 100 100	45, 66, 89, 123	0
1	M	391/405 (96%)	-0.42	0 100 100	38, 63, 84, 98	0
1	N	392/405 (96%)	-0.36	1 (0%) 94 84	48, 72, 92, 115	0
1	O	391/405 (96%)	-0.40	0 100 100	43, 70, 100, 123	0
1	P	392/405 (96%)	-0.42	0 100 100	40, 65, 86, 112	0
All	All	6276/6480 (96%)	-0.42	3 (0%) 100 100	38, 66, 91, 138	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	354	GLU	2.6
1	B	330	GLU	2.3
1	I	2	ILE	2.3

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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(\AA^2)	Q<0.9
2	NAD	K	1001	44/44	0.72	0.41	6.65	72,95,105,111	44
2	NAD	E	1001	44/44	0.74	0.39	4.53	83,97,115,117	44
2	NAD	M	1001	44/44	0.70	0.42	3.84	113,116,133,136	44
2	NAD	I	1001	44/44	0.81	0.32	2.70	83,92,103,105	44
2	NAD	A	1001	44/44	0.85	0.30	2.57	65,85,96,99	44
2	NAD	G	1001	44/44	0.84	0.29	1.99	80,89,100,101	44
2	NAD	P	1001	44/44	0.87	0.25	1.18	77,83,93,96	44
2	NAD	H	1001	44/44	0.87	0.24	0.65	76,88,95,97	44

6.5 Other polymers [i](#)

There are no such residues in this entry.