Full wwPDB X-ray Structure Validation Report (i)

Jun 17, 2024 – 12:23 AM EDT

PDB ID	:	5K50
Title	:	Three-dimensional structure of L-threonine 3-dehydrogenase from Trypanosoma brucei bound to NAD+ and L-allo-threonine refined to 2.23 angstroms
Authors	:	Adjogatse, E.A.; Erskine, P.T.; Cooper, J.B.
Deposited on	:	2016-05-22
Resolution	:	2.26 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 (i) 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 (i)) were used in the production of this report:

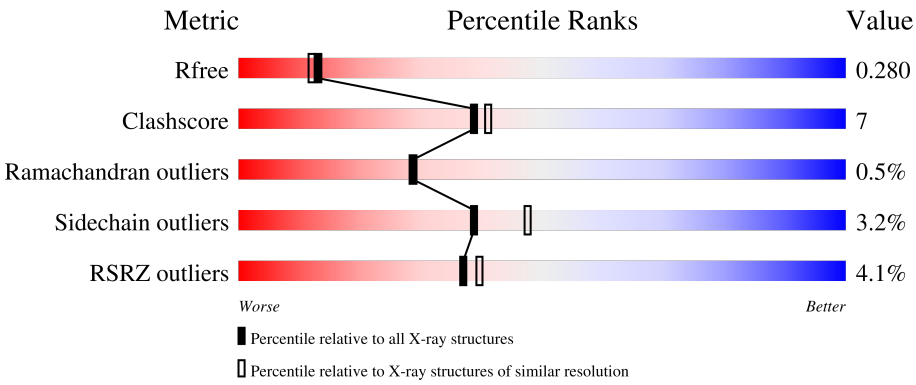
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.26 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}	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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 <=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	319	5% 80% 19%
1	C	319	3% 85% 12% • •
1	E	319	3% 85% 14% •
1	G	319	4% 88% 12% •

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Mol	Chain	Length	Quality of chain
1	I	319	4% 87% 12%
1	J	319	6% 81% 18%

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
3	GOL	J	1402	-	-	X	-
4	ACT	A	1403	-	-	X	-
4	ACT	C	1403	-	-	X	-

2 Entry composition (i)

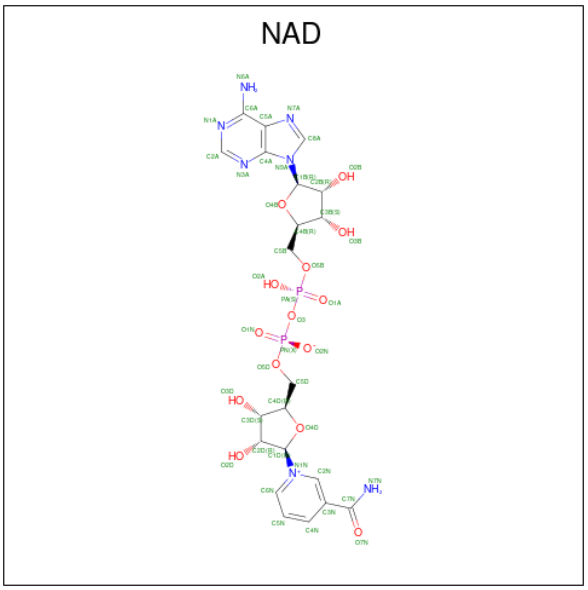
There are 6 unique types of molecules in this entry. The entry contains 15781 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 L-threonine 3-dehydrogenase.

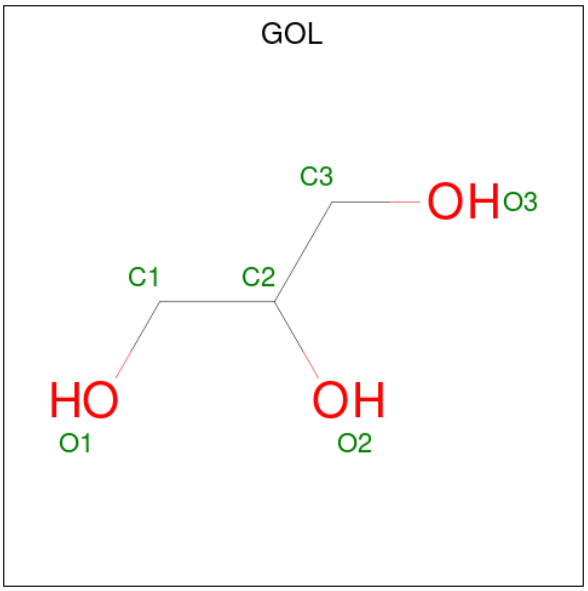
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	319	2493	1590	415	470	18	0	0	0
1	C	319	2493	1590	415	470	18	0	0	0
1	E	319	2493	1590	415	470	18	0	0	0
1	G	319	2532	1614	422	478	18	0	7	0
1	I	319	2493	1590	415	470	18	0	0	0
1	J	319	2493	1590	415	470	18	0	0	0

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
3	E	1	6	3	3	0	0
3	E	1	6	3	3	0	0
3	G	1	6	3	3	0	0
3	I	1	6	3	3	0	0
3	I	1	6	3	3	0	0

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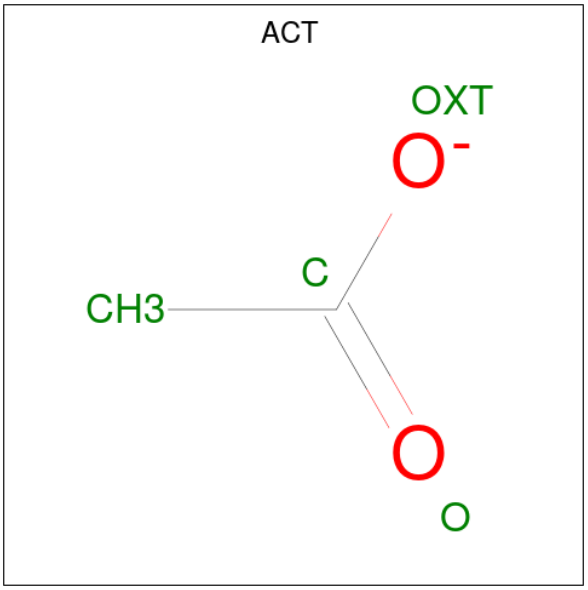
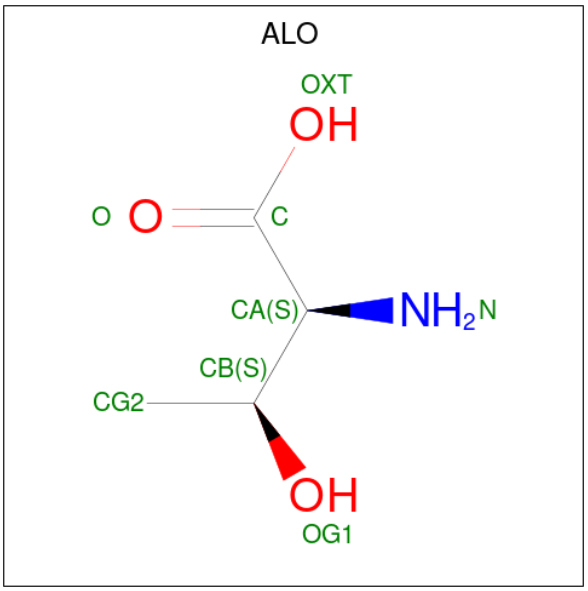
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	J	1	6	3	3	0	0
			Total	C	O		
3	J	1	6	3	3	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	4	2	2	0	0
			Total	C	O		
4	C	1	4	2	2	0	0
			Total	C	O		
4	C	1	4	2	2	0	0
			Total	C	O		
4	J	1	4	2	2	0	0

- Molecule 5 is ALLO-THREONINE (three-letter code: ALO) (formula: $C_4H_9NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	C	1	8	4	1	3	0	0
			Total	C	N	O		
5	G	1	8	4	1	3	0	0

- Molecule 6 is water.

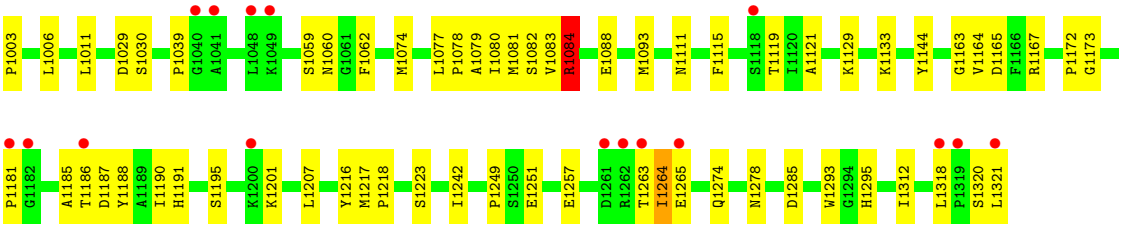
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	60	60	60	0	0
			Total	O		
6	C	65	65	65	0	0
			Total	O		
6	E	82	82	82	0	0
			Total	O		
6	G	79	79	79	0	0
			Total	O		
6	I	79	79	79	0	0
			Total	O		
6	J	75	75	75	0	0

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.

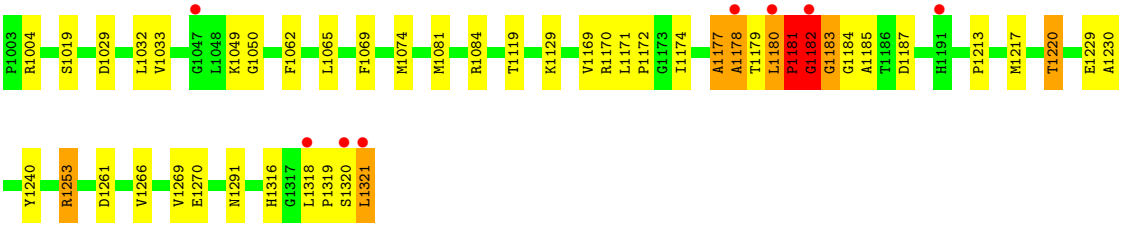
• Molecule 1: L-threonine 3-dehydrogenase

Chain A:



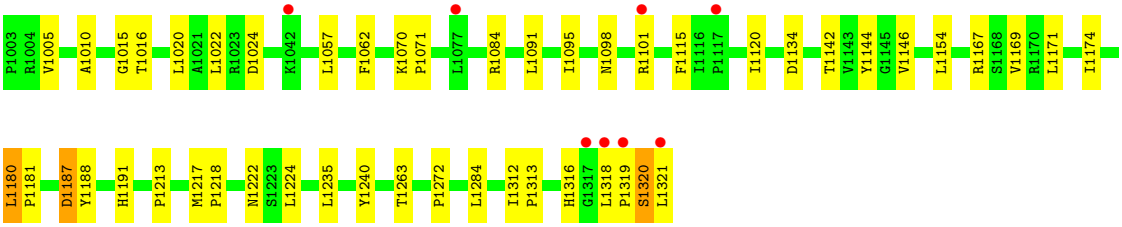
• Molecule 1: L-threonine 3-dehydrogenase

Chain C:



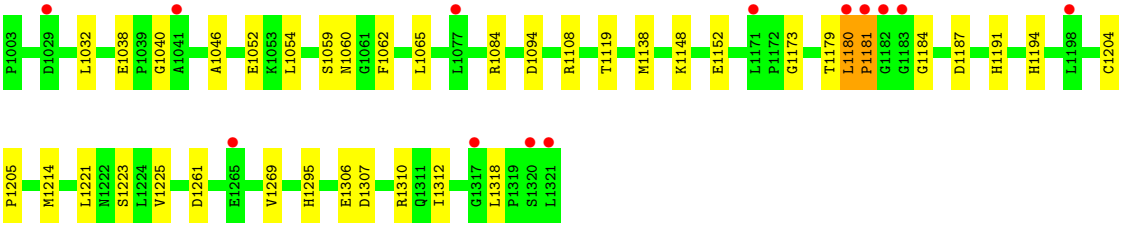
• Molecule 1: L-threonine 3-dehydrogenase

Chain E:



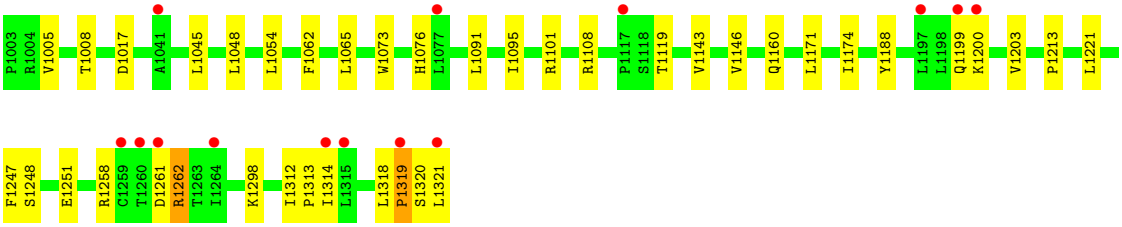
• Molecule 1: L-threonine 3-dehydrogenase

Chain G:



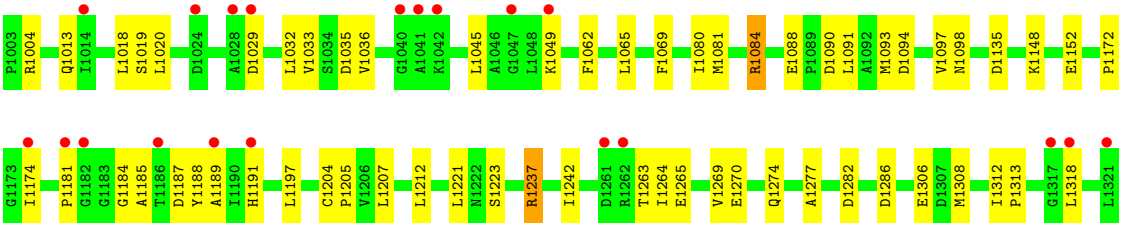
- Molecule 1: L-threonine 3-dehydrogenase

Chain I:



- Molecule 1: L-threonine 3-dehydrogenase

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	133.03Å 273.06Å 55.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.09 – 2.26 31.09 – 2.26	Depositor EDS
% Data completeness (in resolution range)	99.7 (31.09-2.26) 99.7 (31.09-2.26)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.82 (at 2.26Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.207 , 0.281 0.214 , 0.280	Depositor DCC
R_{free} test set	4815 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	31.2	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 39.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.40$, $< L^2 > = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	15781	wwPDB-VP
Average B, all atoms (Å^2)	33.0	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 38.79 % 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 3.4958e-04.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: ALO, NAD, GOL, ACT

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	0.66	1/2549 (0.0%)	0.79	2/3458 (0.1%)
1	C	0.71	1/2549 (0.0%)	0.87	5/3458 (0.1%)
1	E	0.66	0/2549	0.79	0/3458
1	G	0.67	0/2589	0.83	2/3513 (0.1%)
1	I	0.67	0/2549	0.81	1/3458 (0.0%)
1	J	0.61	0/2549	0.82	4/3458 (0.1%)
All	All	0.66	2/15334 (0.0%)	0.82	14/20803 (0.1%)

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	C	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1181	PRO	N-CD	5.78	1.55	1.47
1	A	1251	GLU	CD-OE2	-5.27	1.19	1.25

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	1183	GLY	N-CA-C	7.40	131.61	113.10
1	J	1237	ARG	NE-CZ-NH1	6.72	123.66	120.30
1	I	1108	ARG	NE-CZ-NH2	-6.33	117.13	120.30
1	G	1108	ARG	NE-CZ-NH2	-6.19	117.21	120.30
1	J	1237	ARG	NE-CZ-NH2	-6.12	117.24	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	J	1286	ASP	CB-CG-OD1	5.53	123.28	118.30
1	C	1084	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	C	1181	PRO	CA-N-CD	-5.50	103.81	111.50
1	G	1084	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	C	1170	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	J	1282	ASP	CB-CG-OD1	5.33	123.10	118.30
1	C	1084	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	A	1084	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	A	1165	ASP	CB-CG-OD2	-5.04	113.77	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	1182	GLY	Peptide

5.2 Too-close contacts (i)

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	2493	0	2504	39	0
1	C	2493	0	2504	46	0
1	E	2493	0	2504	36	0
1	G	2532	0	2542	35	0
1	I	2493	0	2504	25	0
1	J	2493	0	2504	46	0
2	A	44	0	26	3	0
2	C	44	0	26	1	0
2	E	44	0	26	1	0
2	G	44	0	26	0	0
2	I	44	0	26	1	0
2	J	44	0	26	1	0
3	A	6	0	8	1	0
3	E	12	0	16	2	0
3	G	6	0	8	0	0
3	I	12	0	16	1	0
3	J	12	0	16	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	4	0	3	7	0
4	C	8	0	6	2	0
4	J	4	0	3	0	0
5	C	8	0	8	3	0
5	G	8	0	8	0	0
6	A	60	0	0	2	0
6	C	65	0	0	2	0
6	E	82	0	0	3	0
6	G	79	0	0	2	0
6	I	79	0	0	2	0
6	J	75	0	0	2	0
All	All	15781	0	15310	229	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 (229) 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:G:1180[B]:LEU:HD12	1:G:1181[B]:PRO:CD	1.12	1.56
1:G:1180[B]:LEU:CD1	1:G:1181[B]:PRO:HD3	1.00	1.48
1:J:1080:ILE:HD11	1:J:1091:LEU:HG	1.25	1.15
1:J:1080:ILE:CD1	1:J:1091:LEU:HG	1.78	1.14
1:J:1181:PRO:HB2	1:J:1191:HIS:ND1	1.63	1.14
1:G:1180[B]:LEU:HD13	1:G:1181[B]:PRO:HD3	1.30	1.12
1:C:1179:THR:O	1:C:1180:LEU:CB	1.92	1.11
1:C:1179:THR:O	1:C:1180:LEU:HB3	1.58	1.04
1:G:1180[B]:LEU:HD12	1:G:1181[B]:PRO:HD2	1.48	0.93
1:J:1181:PRO:HB2	1:J:1191:HIS:CE1	2.02	0.93
1:C:1180:LEU:HG	1:C:1181:PRO:HD2	1.50	0.92
1:C:1180:LEU:CD1	1:C:1181:PRO:HD2	1.99	0.91
1:C:1291:ASN:HB3	6:C:1541:HOH:O	1.73	0.89
1:G:1179[B]:THR:O	1:G:1180[B]:LEU:O	1.91	0.89
1:G:1180[B]:LEU:HD12	1:G:1181[B]:PRO:CG	2.02	0.88
1:G:1180[B]:LEU:CD1	1:G:1181[B]:PRO:CD	1.94	0.88
1:J:1032:LEU:HD21	1:J:1065:LEU:HD11	1.53	0.88
1:G:1032:LEU:HD21	1:G:1065:LEU:HD11	1.54	0.88
1:C:1180:LEU:HG	1:C:1181:PRO:CD	2.03	0.87
1:G:1180[B]:LEU:CG	1:G:1181[B]:PRO:HD3	2.05	0.86
1:E:1318:LEU:HB2	1:E:1319:PRO:CD	2.06	0.85
1:C:1179:THR:O	1:C:1180:LEU:HB2	1.74	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1178:ALA:HB1	1:C:1316:HIS:NE2	1.95	0.81
1:G:1180[B]:LEU:HD11	1:G:1194:HIS:CE1	2.15	0.81
1:G:1180[B]:LEU:CB	1:G:1181[B]:PRO:CD	2.59	0.80
1:A:1083:VAL:H	4:A:1403:ACT:H2	1.46	0.80
1:C:1180:LEU:CG	1:C:1181:PRO:HD2	2.12	0.79
1:G:1032:LEU:CD2	1:G:1065:LEU:HD11	2.14	0.77
1:E:1318:LEU:HB2	1:E:1319:PRO:HD3	1.65	0.77
1:J:1181:PRO:O	1:J:1191:HIS:HE1	1.66	0.76
1:G:1180[B]:LEU:HB3	1:G:1181[B]:PRO:CD	2.15	0.76
1:C:1180:LEU:HD12	1:C:1181:PRO:HD2	1.67	0.76
1:C:1185:ALA:HB3	5:C:1402:ALO:OXT	1.86	0.75
1:C:1320:SER:O	1:C:1321:LEU:HD23	1.87	0.74
1:J:1187:ASP:O	1:J:1191:HIS:CD2	2.41	0.73
1:A:1060:ASN:ND2	6:A:1501:HOH:O	2.20	0.73
1:E:1180:LEU:HG	1:E:1181:PRO:HD2	1.71	0.71
1:G:1181[B]:PRO:HB2	1:G:1191:HIS:NE2	2.06	0.70
1:C:1184:GLY:HA2	4:C:1403:ACT:H3	1.75	0.67
1:J:1184:GLY:HA2	3:J:1402:GOL:H2	1.77	0.67
1:I:1298:LYS:NZ	1:J:1265:GLU:OE1	2.28	0.66
1:A:1257:GLU:HG3	1:A:1264:ILE:HG22	1.77	0.66
1:J:1269:VAL:HG12	1:J:1270:GLU:H	1.62	0.65
1:A:1129:LYS:NZ	1:A:1278:ASN:O	2.29	0.65
1:E:1120:ILE:HG22	1:E:1284:LEU:HD21	1.77	0.65
1:C:1004:ARG:NH1	1:C:1069:PHE:O	2.29	0.65
1:C:1180:LEU:HG	1:C:1181:PRO:N	2.08	0.64
1:J:1013:GLN:NE2	1:J:1174:ILE:O	2.30	0.64
1:A:1257:GLU:CG	1:A:1264:ILE:HG22	2.27	0.64
1:C:1178:ALA:HB1	1:C:1316:HIS:CD2	2.33	0.64
1:I:1017:ASP:HB3	1:I:1221:LEU:HD11	1.79	0.64
1:C:1217:MET:HA	1:C:1220:THR:HG23	1.80	0.63
1:J:1181:PRO:O	1:J:1191:HIS:CE1	2.50	0.63
1:C:1320:SER:O	1:C:1321:LEU:CD2	2.47	0.62
1:E:1098:ASN:CG	1:E:1101:ARG:HH21	2.04	0.61
1:G:1180[B]:LEU:HB3	1:G:1181[B]:PRO:HD2	1.81	0.61
1:I:1045:LEU:HA	1:I:1048:LEU:HD12	1.81	0.61
1:C:1320:SER:C	1:C:1321:LEU:HD23	2.20	0.61
1:G:1180[B]:LEU:CG	1:G:1181[B]:PRO:CD	2.72	0.61
1:A:1181:PRO:HB3	1:A:1191:HIS:CD2	2.37	0.59
1:G:1223:SER:OG	1:G:1295:HIS:ND1	2.34	0.59
1:C:1184:GLY:HA2	4:C:1403:ACT:CH3	2.33	0.58
1:I:1101:ARG:HG3	6:I:1504:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1320:SER:O	1:C:1321:LEU:CG	2.52	0.58
1:C:1178:ALA:HB1	1:C:1316:HIS:CE1	2.38	0.58
1:E:1222:ASN:ND2	6:E:1503:HOH:O	2.33	0.58
1:J:1181:PRO:C	1:J:1191:HIS:CE1	2.77	0.58
1:J:1080:ILE:CD1	1:J:1091:LEU:CG	2.70	0.58
1:J:1081:MET:HB2	3:J:1402:GOL:H32	1.85	0.58
1:E:1098:ASN:OD1	1:E:1101:ARG:NH2	2.36	0.57
1:I:1258:ARG:HG3	1:I:1258:ARG:HH11	1.68	0.57
1:J:1185:ALA:HB2	3:J:1402:GOL:O1	2.04	0.57
1:E:1101:ARG:HG2	1:E:1154:LEU:HD21	1.87	0.57
1:G:1054:LEU:HD22	1:G:1065:LEU:HD23	1.87	0.56
1:C:1029:ASP:OD1	1:C:1029:ASP:N	2.32	0.56
1:C:1320:SER:O	1:C:1321:LEU:HG	2.06	0.56
1:A:1216:TYR:CD2	1:A:1218:PRO:HD2	2.40	0.56
1:E:1312:ILE:O	1:E:1316:HIS:N	2.36	0.56
1:A:1320:SER:O	1:A:1321:LEU:HB2	2.06	0.55
1:C:1174:ILE:HD12	1:C:1220:THR:HG21	1.87	0.55
1:I:1258:ARG:HG3	1:I:1258:ARG:NH1	2.21	0.55
1:G:1184[B]:GLY:N	1:G:1187:ASP:OD2	2.36	0.55
1:I:1320:SER:O	1:I:1321:LEU:OXT	2.24	0.55
1:G:1179[B]:THR:C	1:G:1180[B]:LEU:O	2.45	0.55
1:C:1316:HIS:HB3	1:C:1318:LEU:CD1	2.36	0.55
1:E:1171:LEU:HD22	1:E:1174:ILE:HD11	1.89	0.55
1:C:1178:ALA:CB	1:C:1316:HIS:CD2	2.90	0.55
1:I:1054:LEU:HD22	1:I:1065:LEU:HD22	1.90	0.54
1:J:1084:ARG:HD2	1:J:1088:GLU:OE1	2.08	0.54
1:J:1181:PRO:CB	1:J:1191:HIS:CE1	2.86	0.54
1:J:1269:VAL:HG12	1:J:1270:GLU:N	2.22	0.54
1:J:1207:LEU:HG	1:J:1274:GLN:CD	2.28	0.53
1:A:1081:MET:HA	1:A:1144:TYR:CD1	2.43	0.53
1:E:1120:ILE:HG21	1:E:1213:PRO:HG2	1.90	0.53
1:A:1083:VAL:HG23	4:A:1403:ACT:H3	1.90	0.53
1:A:1207:LEU:HD12	1:A:1274:GLN:NE2	2.24	0.53
1:I:1312:ILE:N	1:I:1313:PRO:HD2	2.24	0.52
1:I:1200:LYS:HA	1:I:1200:LYS:CE	2.39	0.52
1:A:1006:LEU:O	1:A:1074:MET:HA	2.08	0.52
1:E:1180:LEU:HD21	1:E:1191:HIS:HE1	1.74	0.52
1:I:1171:LEU:HD22	1:I:1174:ILE:HD11	1.90	0.52
1:A:1084:ARG:HD2	1:A:1088:GLU:OE1	2.10	0.52
1:G:1194:HIS:CD2	1:G:1312:ILE:HD13	2.45	0.52
1:C:1177:ALA:O	1:C:1178:ALA:HB3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1138:MET:HG2	6:G:1515:HOH:O	2.10	0.51
1:E:1005:VAL:HG11	1:E:1022:LEU:HD13	1.91	0.51
1:E:1057:LEU:HD11	1:E:1095:ILE:HD13	1.91	0.51
1:I:1005:VAL:HG22	1:I:1073:TRP:HB2	1.93	0.51
1:J:1018:LEU:HA	1:J:1221:LEU:HD22	1.91	0.51
1:A:1163:GLY:O	1:A:1164:VAL:C	2.48	0.51
1:E:1134:ASP:OD2	6:E:1501:HOH:O	2.19	0.51
1:G:1032:LEU:HD11	1:G:1052:GLU:HG2	1.92	0.51
1:A:1079:ALA:HB3	2:A:1401:NAD:H3D	1.93	0.51
1:A:1173:GLY:HA3	1:A:1186:THR:HG21	1.93	0.51
1:C:1172:PRO:HB3	1:C:1213:PRO:HB2	1.93	0.51
2:I:1401:NAD:C5N	3:I:1402:GOL:O1	2.59	0.51
1:A:1083:VAL:HG23	4:A:1403:ACT:CH3	2.41	0.51
1:J:1181:PRO:CB	1:J:1191:HIS:ND1	2.55	0.51
1:J:1004:ARG:NH1	1:J:1069:PHE:O	2.34	0.50
1:J:1080:ILE:HD11	1:J:1091:LEU:CG	2.18	0.50
1:A:1093:MET:HB3	1:E:1101:ARG:HH11	1.77	0.50
1:A:1011:LEU:HD11	1:A:1039:PRO:HD3	1.93	0.50
1:G:1181[B]:PRO:HB2	1:G:1191:HIS:CE1	2.47	0.49
1:A:1082:SER:HB2	4:A:1403:ACT:H2	1.93	0.49
2:A:1401:NAD:C4N	3:A:1402:GOL:H2	2.42	0.49
1:A:1111:ASN:HA	6:A:1529:HOH:O	2.11	0.49
1:J:1270:GLU:HA	1:J:1270:GLU:OE1	2.13	0.49
1:G:1181[B]:PRO:HB2	1:G:1191:HIS:CD2	2.47	0.49
1:I:1247:PHE:HA	1:I:1251:GLU:OE2	2.12	0.49
1:C:1033:VAL:HG22	1:C:1050:GLY:O	2.13	0.48
1:C:1316:HIS:HB3	1:C:1318:LEU:HD13	1.94	0.48
1:J:1032:LEU:CD2	1:J:1065:LEU:HD11	2.36	0.48
1:A:1003:PRO:O	1:A:1030:SER:OG	2.29	0.48
1:A:1185:ALA:N	4:A:1403:ACT:H3	2.28	0.48
2:E:1401:NAD:C4N	3:E:1403:GOL:H2	2.44	0.48
1:I:1298:LYS:NZ	1:J:1265:GLU:CD	2.67	0.48
1:A:1172:PRO:HD3	1:A:1242:ILE:O	2.14	0.48
1:A:1201:LYS:HA	1:A:1265:GLU:O	2.14	0.47
1:E:1320:SER:O	1:E:1321:LEU:C	2.52	0.47
1:G:1181[B]:PRO:HG2	1:G:1191:HIS:CE1	2.49	0.47
1:C:1081:MET:CE	5:C:1402:ALO:HA	2.45	0.47
1:A:1181:PRO:HG3	1:A:1190:ILE:HG22	1.97	0.47
1:E:1144:TYR:OH	3:E:1403:GOL:O2	2.29	0.47
1:J:1188:TYR:CG	1:J:1189:ALA:N	2.83	0.47
1:E:1180:LEU:HD21	1:E:1191:HIS:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1094:ASP:O	1:J:1098:ASN:HB2	2.15	0.46
1:A:1115:PHE:HA	1:A:1167:ARG:O	2.15	0.46
1:G:1065:LEU:HD12	6:G:1546:HOH:O	2.15	0.46
1:E:1169:VAL:HA	1:E:1240:TYR:O	2.15	0.46
1:E:1142:THR:O	1:E:1146:VAL:HG23	2.16	0.46
1:C:1318:LEU:HB3	1:C:1319:PRO:CD	2.44	0.46
1:C:1318:LEU:CB	1:C:1319:PRO:CD	2.94	0.46
1:C:1269:VAL:CG1	1:C:1270:GLU:N	2.79	0.46
1:C:1019:SER:HB3	1:C:1033:VAL:HG11	1.97	0.46
1:A:1312:ILE:HG22	1:A:1318:LEU:HD13	1.98	0.45
1:C:1169:VAL:HA	1:C:1240:TYR:O	2.15	0.45
1:E:1101:ARG:HG2	1:E:1154:LEU:CD2	2.46	0.45
1:I:1008:THR:OG1	1:I:1076:HIS:HA	2.17	0.45
1:E:1217:MET:N	1:E:1218:PRO:CD	2.79	0.45
1:A:1285:ASP:OD1	1:A:1285:ASP:C	2.55	0.45
1:E:1115:PHE:HA	1:E:1167:ARG:O	2.16	0.45
1:E:1224:LEU:HD23	1:E:1224:LEU:HA	1.82	0.45
1:I:1248:SER:OG	6:I:1501:HOH:O	2.15	0.44
1:J:1148:LYS:O	1:J:1152:GLU:HG3	2.17	0.44
1:J:1191:HIS:CD2	6:J:1529:HOH:O	2.69	0.44
2:J:1401:NAD:O2B	6:J:1501:HOH:O	2.21	0.44
1:E:1318:LEU:HB2	1:E:1319:PRO:HD2	1.94	0.44
1:J:1135:ASP:OD1	1:J:1237:ARG:NH2	2.50	0.44
1:C:1032:LEU:HD21	1:C:1065:LEU:HD11	1.98	0.44
1:A:1080:ILE:HG23	1:A:1084:ARG:HG2	1.99	0.44
1:E:1010:ALA:HA	1:E:1015:GLY:HA3	2.00	0.44
1:C:1081:MET:HE3	5:C:1402:ALO:HA	2.00	0.44
1:C:1253:ARG:HG3	1:C:1266:VAL:HG21	1.99	0.44
1:E:1318:LEU:CD1	1:E:1319:PRO:HD2	2.48	0.44
1:I:1045:LEU:HA	1:I:1048:LEU:CD1	2.47	0.44
1:G:1221:LEU:O	1:G:1225:VAL:HG23	2.17	0.43
1:A:1077:LEU:N	1:A:1078:PRO:HD3	2.33	0.43
1:G:1205:PRO:HA	1:G:1269:VAL:O	2.17	0.43
1:I:1091:LEU:O	1:I:1095:ILE:HG12	2.18	0.43
1:J:1188:TYR:CD1	1:J:1188:TYR:C	2.91	0.43
1:J:1313:PRO:HB3	1:J:1318:LEU:O	2.18	0.43
1:A:1181:PRO:CB	1:A:1191:HIS:CD2	3.01	0.43
1:E:1272:PRO:HD2	6:E:1539:HOH:O	2.18	0.43
1:J:1093:MET:O	1:J:1097:VAL:HB	2.19	0.43
1:A:1185:ALA:H	4:A:1403:ACT:CH3	2.31	0.43
1:A:1119:THR:CG2	1:A:1121:ALA:HB3	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1212:LEU:HD11	1:J:1277:ALA:HB1	2.01	0.43
1:J:1312:ILE:N	1:J:1313:PRO:HD2	2.34	0.43
1:A:1217:MET:O	1:A:1218:PRO:C	2.57	0.42
1:E:1091:LEU:O	1:E:1095:ILE:HG12	2.19	0.42
1:I:1318:LEU:HB3	1:I:1319:PRO:HD2	2.00	0.42
1:E:1070:LYS:N	1:E:1071:PRO:CD	2.81	0.42
1:G:1148:LYS:O	1:G:1152:GLU:HG3	2.19	0.42
1:G:1307:ASP:OD1	1:G:1310:ARG:NH2	2.52	0.42
1:J:1019:SER:HB3	1:J:1033:VAL:HG11	1.99	0.42
1:G:1204:CYS:HA	1:G:1205:PRO:HD3	1.85	0.42
1:A:1185:ALA:N	4:A:1403:ACT:CH3	2.82	0.42
1:I:1200:LYS:HA	1:I:1200:LYS:HE3	2.01	0.42
1:A:1293:TRP:CH2	1:A:1295:HIS:HB2	2.55	0.42
1:E:1187:ASP:OD1	1:E:1187:ASP:N	2.53	0.42
1:I:1143:VAL:O	1:I:1146:VAL:HB	2.20	0.42
1:E:1312:ILE:N	1:E:1313:PRO:HD2	2.35	0.42
1:C:1269:VAL:HG12	1:C:1270:GLU:N	2.35	0.42
1:E:1318:LEU:HD13	1:E:1319:PRO:HD2	2.01	0.42
1:G:1040:GLY:O	1:G:1046:ALA:HB2	2.20	0.41
1:G:1180[B]:LEU:HD13	1:G:1180[B]:LEU:HA	1.54	0.41
1:I:1199:GLN:OE1	1:I:1262:ARG:NH1	2.52	0.41
1:I:1321:LEU:O	1:I:1321:LEU:HG	2.20	0.41
1:J:1035:ASP:OD1	1:J:1036:VAL:N	2.53	0.41
1:J:1172:PRO:HD3	1:J:1242:ILE:O	2.20	0.41
1:C:1129:LYS:NZ	6:C:1504:HOH:O	2.46	0.41
1:C:1316:HIS:CB	1:C:1318:LEU:HD13	2.50	0.41
1:I:1258:ARG:HH11	1:I:1258:ARG:CG	2.32	0.41
1:J:1188:TYR:CD1	1:J:1189:ALA:N	2.89	0.41
2:A:1401:NAD:O2N	2:A:1401:NAD:N7N	2.54	0.41
1:G:1173:GLY:HA3	1:G:1214:MET:SD	2.60	0.41
1:I:1188:TYR:CD1	1:I:1188:TYR:C	2.93	0.41
1:J:1197:LEU:HD13	1:J:1313:PRO:HD3	2.02	0.41
1:A:1188:TYR:CE1	1:A:1249:PRO:HG3	2.56	0.41
1:C:1180:LEU:O	1:C:1182:GLY:N	2.54	0.41
1:E:1016:THR:O	1:E:1020:LEU:HD12	2.21	0.41
1:J:1204:CYS:HA	1:J:1205:PRO:HD2	1.93	0.41
1:C:1171:LEU:HB2	2:C:1401:NAD:C5N	2.51	0.40
1:J:1308:MET:HB3	1:J:1308:MET:HE3	1.91	0.40
1:A:1188:TYR:CZ	1:A:1249:PRO:HG3	2.56	0.40
1:J:1185:ALA:HB2	3:J:1402:GOL:HO1	1.85	0.40
1:C:1229:GLU:O	1:C:1230:ALA:C	2.58	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:1020:LEU:HD21	1:J:1045:LEU:HD23	2.02	0.40
1:E:1188:TYR:CD1	1:E:1188:TYR:C	2.94	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	317/319 (99%)	303 (96%)	14 (4%)	0	100 100
1	C	317/319 (99%)	294 (93%)	17 (5%)	6 (2%)	8 4
1	E	317/319 (99%)	303 (96%)	14 (4%)	0	100 100
1	G	324/319 (102%)	299 (92%)	21 (6%)	4 (1%)	13 9
1	I	317/319 (99%)	297 (94%)	19 (6%)	1 (0%)	41 46
1	J	317/319 (99%)	303 (96%)	14 (4%)	0	100 100
All	All	1909/1914 (100%)	1799 (94%)	99 (5%)	11 (1%)	29 25

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	1180	LEU
1	G	1180[A]	LEU
1	G	1180[B]	LEU
1	C	1183	GLY
1	C	1178	ALA
1	C	1181	PRO
1	C	1182	GLY
1	G	1181[A]	PRO
1	G	1181[B]	PRO
1	C	1177	ALA
1	I	1314	ILE

5.3.2 Protein sidechains (i)

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	276/276 (100%)	266 (96%)	10 (4%)	35	42
1	C	276/276 (100%)	267 (97%)	9 (3%)	38	46
1	E	276/276 (100%)	268 (97%)	8 (3%)	42	51
1	G	279/276 (101%)	270 (97%)	9 (3%)	39	47
1	I	276/276 (100%)	268 (97%)	8 (3%)	42	51
1	J	276/276 (100%)	267 (97%)	9 (3%)	38	46
All	All	1659/1656 (100%)	1606 (97%)	53 (3%)	39	47

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1029	ASP
1	A	1059	SER
1	A	1062	PHE
1	A	1084	ARG
1	A	1133	LYS
1	A	1187	ASP
1	A	1195	SER
1	A	1223	SER
1	A	1263	THR
1	A	1264	ILE
1	C	1049	LYS
1	C	1062	PHE
1	C	1074	MET
1	C	1119	THR
1	C	1187	ASP
1	C	1220	THR
1	C	1253	ARG
1	C	1261	ASP
1	C	1321	LEU
1	E	1024	ASP
1	E	1062	PHE
1	E	1084	ARG

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Mol	Chain	Res	Type
1	E	1180	LEU
1	E	1187	ASP
1	E	1235	LEU
1	E	1263	THR
1	E	1320	SER
1	G	1038	GLU
1	G	1059	SER
1	G	1060	ASN
1	G	1062	PHE
1	G	1094	ASP
1	G	1119	THR
1	G	1261	ASP
1	G	1306	GLU
1	G	1318	LEU
1	I	1062	PHE
1	I	1119	THR
1	I	1160	GLN
1	I	1203	VAL
1	I	1213	PRO
1	I	1261	ASP
1	I	1262	ARG
1	I	1319	PRO
1	J	1029	ASP
1	J	1049	LYS
1	J	1062	PHE
1	J	1084	ARG
1	J	1090	ASP
1	J	1223	SER
1	J	1263	THR
1	J	1264	ILE
1	J	1306	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1060	ASN
1	A	1199	GLN
1	A	1278	ASN
1	C	1060	ASN
1	C	1278	ASN
1	E	1060	ASN
1	E	1191	HIS

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Mol	Chain	Res	Type
1	G	1060	ASN
1	G	1194	HIS
1	I	1060	ASN
1	I	1278	ASN
1	J	1060	ASN
1	J	1191	HIS
1	J	1194	HIS
1	J	1278	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

20 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	$\#\|Z\| > 2$
3	GOL	G	1402	-	5,5,5	0.61	0	5,5,5	0.61	0
3	GOL	J	1403	-	5,5,5	0.40	0	5,5,5	0.40	0
2	NAD	A	1401	-	42,48,48	1.48	4 (9%)	50,73,73	1.54	8 (16%)
3	GOL	J	1402	-	5,5,5	0.24	0	5,5,5	0.77	0
3	GOL	E	1403	-	5,5,5	0.51	0	5,5,5	1.18	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAD	C	1401	-	42,48,48	1.66	7 (16%)	50,73,73	1.52	8 (16%)
5	ALO	G	1403	-	6,7,7	0.87	0	7,9,9	0.46	0
3	GOL	I	1402	-	5,5,5	0.53	0	5,5,5	0.83	0
5	ALO	C	1402	-	6,7,7	1.29	1 (16%)	7,9,9	1.23	2 (28%)
2	NAD	G	1401	-	42,48,48	1.56	8 (19%)	50,73,73	1.26	5 (10%)
3	GOL	E	1402	-	5,5,5	0.39	0	5,5,5	0.43	0
4	ACT	C	1404	-	3,3,3	1.05	0	3,3,3	0.34	0
2	NAD	I	1401	-	42,48,48	1.53	5 (11%)	50,73,73	1.26	6 (12%)
4	ACT	C	1403	-	3,3,3	1.02	0	3,3,3	0.22	0
2	NAD	E	1401	-	42,48,48	2.16	6 (14%)	50,73,73	1.35	5 (10%)
3	GOL	A	1402	-	5,5,5	0.52	0	5,5,5	1.27	1 (20%)
4	ACT	A	1403	-	3,3,3	0.89	0	3,3,3	0.56	0
4	ACT	J	1404	-	3,3,3	0.90	0	3,3,3	0.36	0
2	NAD	J	1401	-	42,48,48	1.61	6 (14%)	50,73,73	1.58	8 (16%)
3	GOL	I	1403	-	5,5,5	0.38	0	5,5,5	0.80	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	I	1401	-	-	5/26/62/62	0/5/5/5
3	GOL	J	1402	-	-	2/4/4/4	-
2	NAD	J	1401	-	-	4/26/62/62	0/5/5/5
3	GOL	I	1403	-	-	2/4/4/4	-
5	ALO	G	1403	-	-	1/8/8/8	-
2	NAD	E	1401	-	-	3/26/62/62	0/5/5/5
3	GOL	A	1402	-	-	3/4/4/4	-
3	GOL	G	1402	-	-	2/4/4/4	-
3	GOL	J	1403	-	-	0/4/4/4	-
3	GOL	E	1403	-	-	0/4/4/4	-
3	GOL	I	1402	-	-	2/4/4/4	-
5	ALO	C	1402	-	-	5/8/8/8	-
2	NAD	A	1401	-	-	5/26/62/62	0/5/5/5
2	NAD	G	1401	-	-	2/26/62/62	0/5/5/5
3	GOL	E	1402	-	-	4/4/4/4	-
2	NAD	C	1401	-	-	6/26/62/62	0/5/5/5

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1401	NAD	O7N-C7N	8.45	1.40	1.24
2	A	1401	NAD	O7N-C7N	6.20	1.36	1.24
2	I	1401	NAD	O7N-C7N	6.10	1.35	1.24
2	C	1401	NAD	O7N-C7N	5.89	1.35	1.24
2	J	1401	NAD	O7N-C7N	5.76	1.35	1.24
2	E	1401	NAD	C2N-N1N	5.49	1.41	1.35
2	E	1401	NAD	O4B-C1B	5.16	1.48	1.41
2	J	1401	NAD	C2N-N1N	5.02	1.41	1.35
2	G	1401	NAD	O4B-C1B	4.36	1.47	1.41
2	G	1401	NAD	O7N-C7N	4.04	1.31	1.24
2	E	1401	NAD	O4D-C1D	3.85	1.46	1.41
2	C	1401	NAD	C2N-N1N	3.75	1.39	1.35
2	G	1401	NAD	C2N-N1N	3.46	1.39	1.35
2	C	1401	NAD	C3N-C7N	3.31	1.55	1.50
2	I	1401	NAD	C2N-N1N	3.18	1.38	1.35
2	C	1401	NAD	O4D-C1D	3.11	1.45	1.41
2	C	1401	NAD	O4D-C4D	3.01	1.51	1.45
2	E	1401	NAD	C3N-C7N	2.91	1.54	1.50
2	J	1401	NAD	C3N-C7N	2.88	1.54	1.50
2	G	1401	NAD	C2D-C1D	-2.63	1.49	1.53
2	E	1401	NAD	PN-O5D	2.61	1.69	1.59
2	A	1401	NAD	C2N-N1N	2.51	1.38	1.35
2	I	1401	NAD	C3N-C7N	2.48	1.54	1.50
2	A	1401	NAD	C6N-N1N	2.41	1.41	1.35
2	J	1401	NAD	PA-O2A	-2.40	1.44	1.55
2	I	1401	NAD	PN-O2N	-2.39	1.44	1.55
2	C	1401	NAD	O4B-C1B	-2.37	1.37	1.41
2	A	1401	NAD	C3N-C7N	2.31	1.54	1.50
2	G	1401	NAD	C3B-C4B	2.28	1.58	1.53
2	J	1401	NAD	O4B-C1B	-2.27	1.37	1.41
2	G	1401	NAD	C6N-N1N	2.26	1.40	1.35
5	C	1402	ALO	OXT-C	-2.16	1.23	1.30
2	C	1401	NAD	C2B-C1B	-2.16	1.50	1.53
2	I	1401	NAD	C6N-N1N	2.11	1.40	1.35
2	G	1401	NAD	C3N-C7N	2.08	1.53	1.50
2	J	1401	NAD	C5D-C4D	2.05	1.58	1.51
2	G	1401	NAD	O4D-C1D	2.01	1.43	1.41

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	J	1401	NAD	O4B-C1B-C2B	-5.93	98.26	106.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	1401	NAD	N3A-C2A-N1A	-4.97	120.91	128.68
2	E	1401	NAD	N3A-C2A-N1A	-4.47	121.69	128.68
2	A	1401	NAD	N3A-C2A-N1A	-4.47	121.69	128.68
2	C	1401	NAD	C4A-C5A-N7A	-4.17	105.05	109.40
2	G	1401	NAD	N3A-C2A-N1A	-4.04	122.37	128.68
2	A	1401	NAD	C6N-N1N-C2N	-3.95	118.38	121.97
2	A	1401	NAD	PN-O3-PA	-3.55	120.63	132.83
2	J	1401	NAD	C6N-N1N-C2N	-3.33	118.94	121.97
2	I	1401	NAD	N3A-C2A-N1A	-3.23	123.64	128.68
2	J	1401	NAD	O3D-C3D-C2D	-3.17	101.58	111.82
2	A	1401	NAD	C1B-N9A-C4A	-3.09	121.20	126.64
2	E	1401	NAD	C1B-N9A-C4A	-3.03	121.31	126.64
2	A	1401	NAD	C2N-C3N-C4N	3.01	121.67	118.26
2	A	1401	NAD	C5N-C4N-C3N	-2.95	116.85	120.34
2	C	1401	NAD	C6N-N1N-C2N	-2.95	119.29	121.97
2	J	1401	NAD	C5B-C4B-C3B	-2.87	104.43	115.18
2	G	1401	NAD	C6N-N1N-C2N	-2.86	119.36	121.97
2	C	1401	NAD	O3D-C3D-C2D	-2.81	102.72	111.82
2	J	1401	NAD	N3A-C2A-N1A	-2.78	124.34	128.68
2	J	1401	NAD	PN-O3-PA	-2.70	123.57	132.83
2	A	1401	NAD	C4A-C5A-N7A	-2.66	106.63	109.40
2	E	1401	NAD	C4A-C5A-N7A	-2.59	106.70	109.40
2	E	1401	NAD	C3N-C2N-N1N	-2.59	117.90	120.43
2	I	1401	NAD	C1B-N9A-C4A	-2.58	122.10	126.64
2	C	1401	NAD	C5B-C4B-C3B	-2.56	105.58	115.18
2	E	1401	NAD	C5D-C4D-C3D	-2.49	105.84	115.18
2	J	1401	NAD	O5B-C5B-C4B	2.46	117.45	108.99
2	C	1401	NAD	C1B-N9A-C4A	-2.37	122.48	126.64
2	G	1401	NAD	C3N-C7N-N7N	2.32	120.53	117.75
5	C	1402	ALO	OG1-CB-CA	-2.32	104.09	109.04
2	I	1401	NAD	C3N-C2N-N1N	-2.27	118.21	120.43
3	A	1402	GOL	O2-C2-C1	2.19	118.78	109.12
2	J	1401	NAD	O4D-C1D-C2D	-2.19	103.72	106.93
2	I	1401	NAD	O3B-C3B-C4B	-2.15	104.83	111.05
2	I	1401	NAD	O7N-C7N-C3N	2.15	122.21	119.63
2	A	1401	NAD	C5D-C4D-C3D	-2.14	107.17	115.18
2	C	1401	NAD	O2N-PN-O1N	2.13	122.75	112.24
2	I	1401	NAD	O2N-PN-O1N	2.11	122.66	112.24
2	G	1401	NAD	C5D-C4D-C3D	-2.07	107.43	115.18
5	C	1402	ALO	CG2-CB-CA	2.06	117.02	112.16
2	G	1401	NAD	PN-O3-PA	-2.06	125.76	132.83
2	C	1401	NAD	C5A-C6A-N6A	2.03	123.43	120.35

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1401	NAD	O4D-C4D-C5D-O5D
2	C	1401	NAD	C5D-O5D-PN-O1N
2	J	1401	NAD	C5D-O5D-PN-O1N
3	I	1402	GOL	C1-C2-C3-O3
3	I	1403	GOL	O1-C1-C2-C3
5	C	1402	ALO	N-CA-CB-CG2
5	C	1402	ALO	N-CA-CB-OG1
5	C	1402	ALO	C-CA-CB-CG2
5	C	1402	ALO	C-CA-CB-OG1
2	A	1401	NAD	C3D-C4D-C5D-O5D
3	G	1402	GOL	O1-C1-C2-O2
3	I	1402	GOL	O2-C2-C3-O3
2	I	1401	NAD	O4D-C4D-C5D-O5D
3	A	1402	GOL	O1-C1-C2-C3
3	E	1402	GOL	O1-C1-C2-C3
3	E	1402	GOL	C1-C2-C3-O3
3	G	1402	GOL	O1-C1-C2-C3
3	J	1402	GOL	O1-C1-C2-C3
3	E	1402	GOL	O1-C1-C2-O2
3	I	1403	GOL	O1-C1-C2-O2
3	J	1402	GOL	O1-C1-C2-O2
2	A	1401	NAD	C5D-O5D-PN-O3
2	C	1401	NAD	C5D-O5D-PN-O3
2	J	1401	NAD	C5D-O5D-PN-O3
3	A	1402	GOL	C1-C2-C3-O3
2	J	1401	NAD	C5D-O5D-PN-O2N
2	G	1401	NAD	O4D-C4D-C5D-O5D
3	A	1402	GOL	O1-C1-C2-O2
3	E	1402	GOL	O2-C2-C3-O3
2	C	1401	NAD	O4B-C4B-C5B-O5B
5	C	1402	ALO	OXT-C-CA-N
2	I	1401	NAD	O4B-C4B-C5B-O5B
2	J	1401	NAD	O4B-C4B-C5B-O5B
2	C	1401	NAD	C3B-C4B-C5B-O5B
2	I	1401	NAD	C3D-C4D-C5D-O5D
2	E	1401	NAD	O4B-C4B-C5B-O5B
5	G	1403	ALO	N-CA-CB-OG1
2	E	1401	NAD	C5D-O5D-PN-O3
2	G	1401	NAD	O4B-C4B-C5B-O5B
2	I	1401	NAD	PN-O3-PA-O1A

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Mol	Chain	Res	Type	Atoms
2	I	1401	NAD	PN-O3-PA-O2A
2	A	1401	NAD	C5D-O5D-PN-O1N
2	C	1401	NAD	C5B-O5B-PA-O1A
2	C	1401	NAD	C5D-O5D-PN-O2N
2	E	1401	NAD	C5D-O5D-PN-O1N
2	A	1401	NAD	O4B-C4B-C5B-O5B

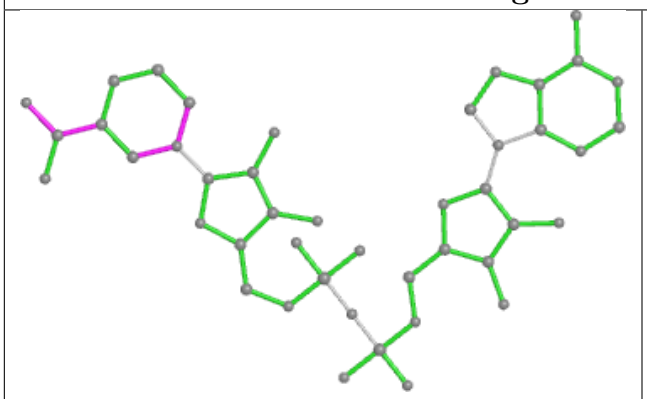
There are no ring outliers.

12 monomers are involved in 24 short contacts:

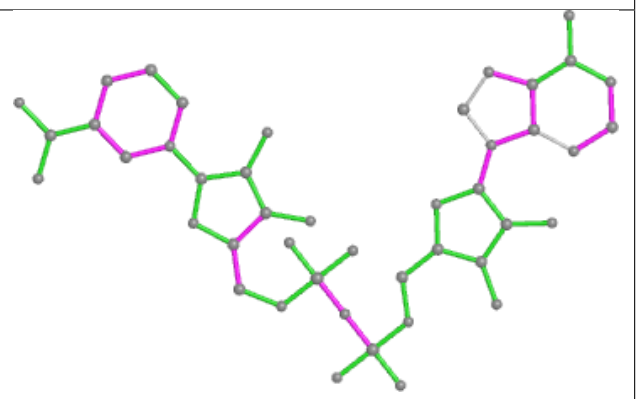
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1401	NAD	3	0
3	J	1402	GOL	4	0
3	E	1403	GOL	2	0
2	C	1401	NAD	1	0
3	I	1402	GOL	1	0
5	C	1402	ALO	3	0
2	I	1401	NAD	1	0
4	C	1403	ACT	2	0
2	E	1401	NAD	1	0
3	A	1402	GOL	1	0
4	A	1403	ACT	7	0
2	J	1401	NAD	1	0

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 then 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.

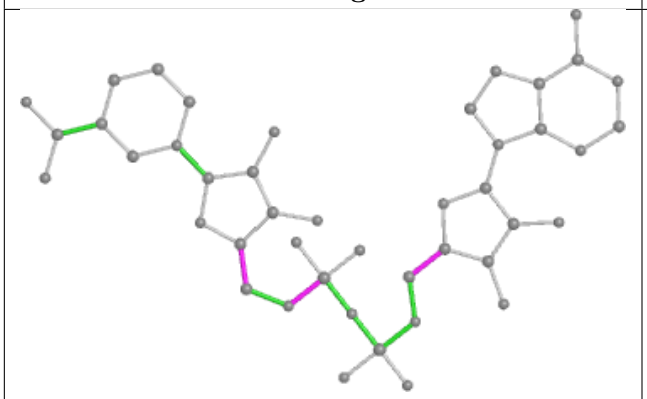
Ligand NAD A 1401



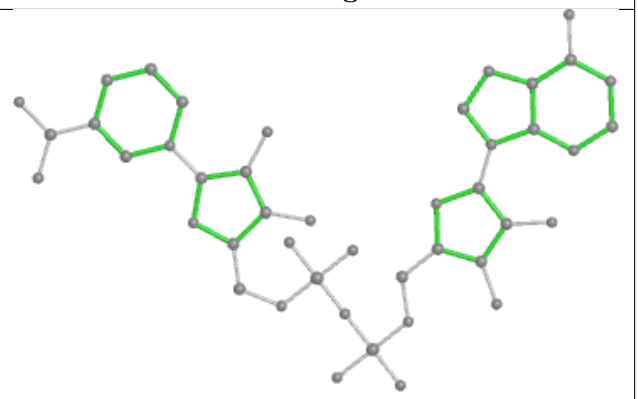
Bond lengths



Bond angles

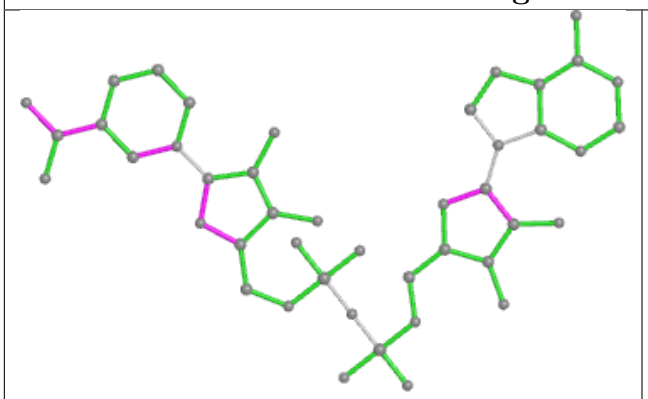


Torsions

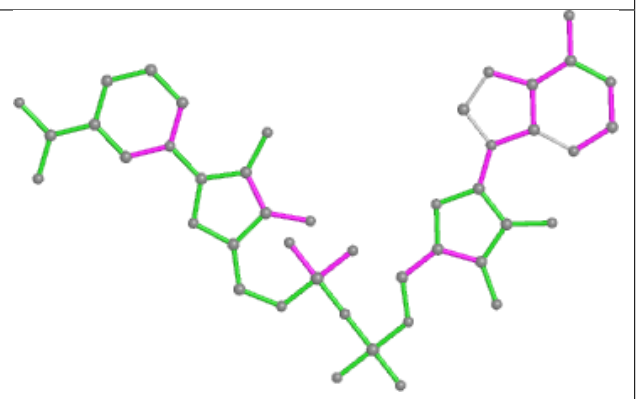


Rings

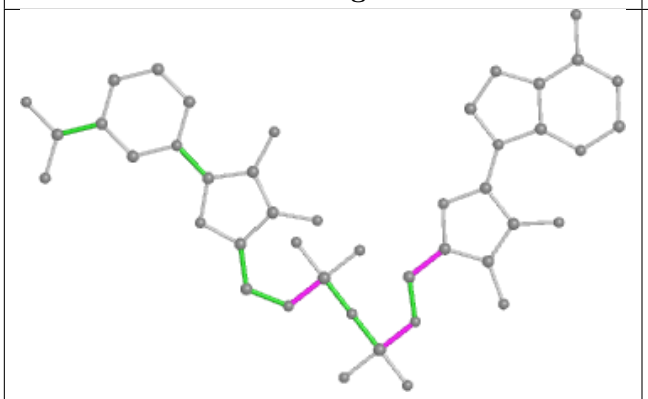
Ligand NAD C 1401



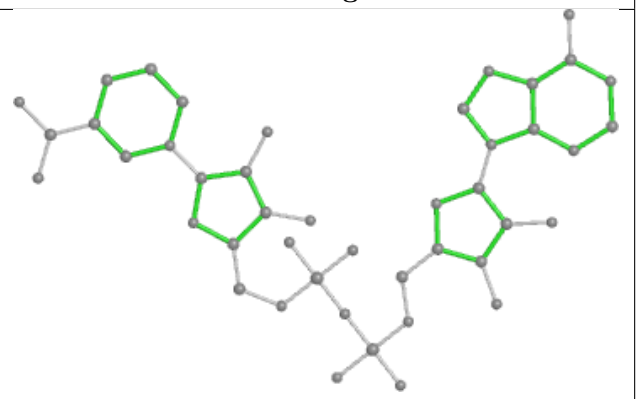
Bond lengths



Bond angles

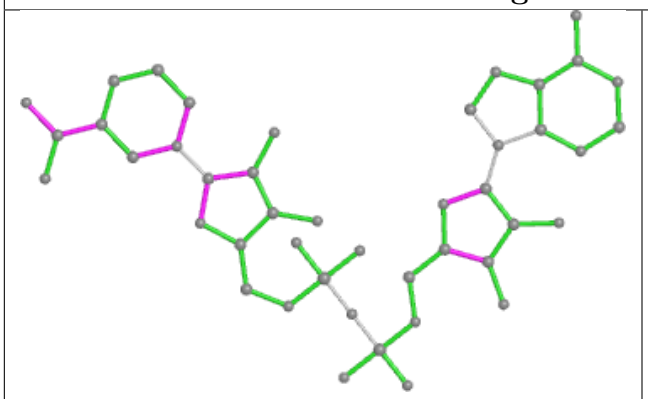


Torsions

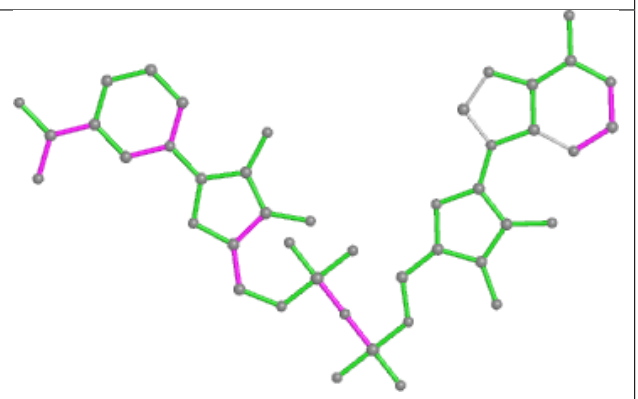


Rings

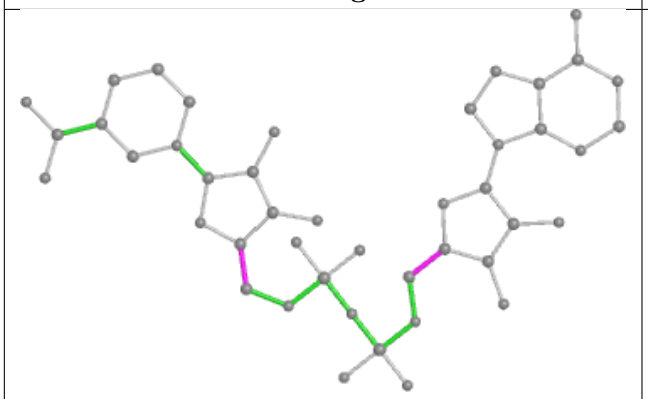
Ligand NAD G 1401



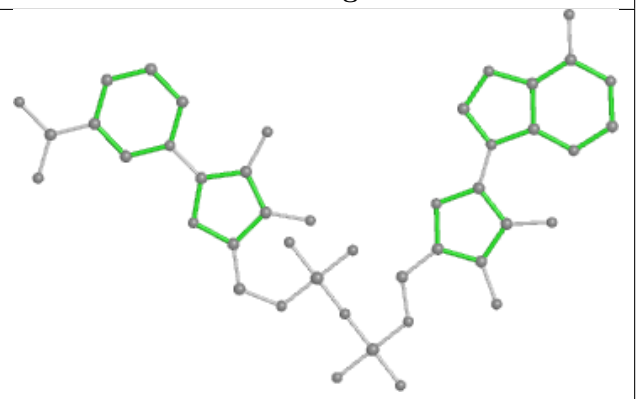
Bond lengths



Bond angles

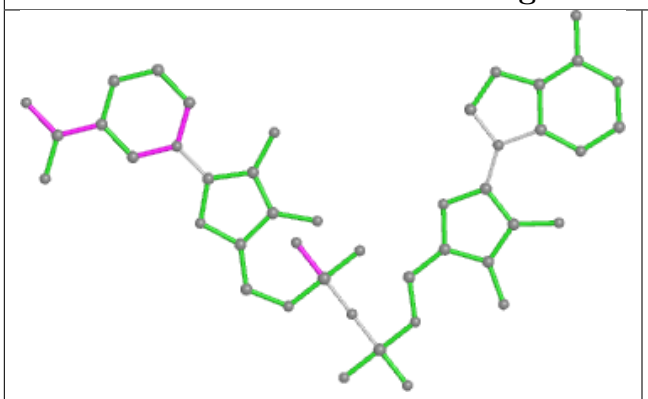


Torsions

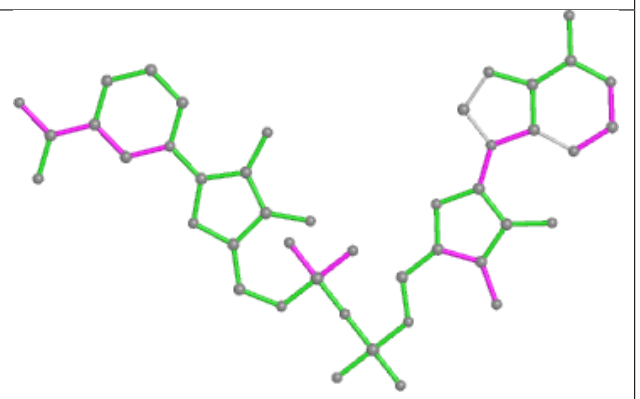


Rings

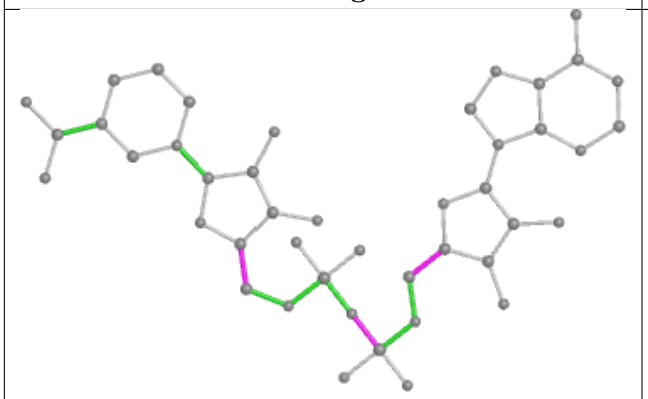
Ligand NAD I 1401



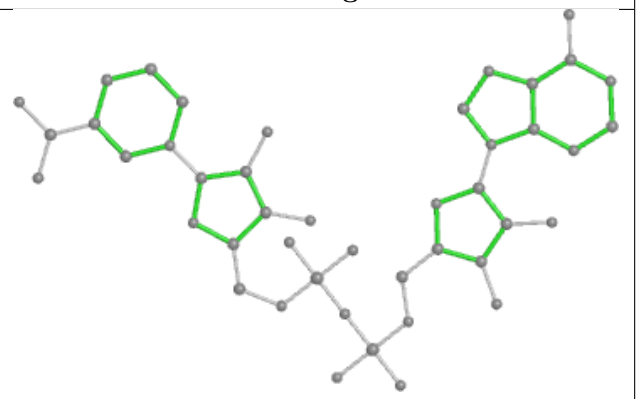
Bond lengths



Bond angles

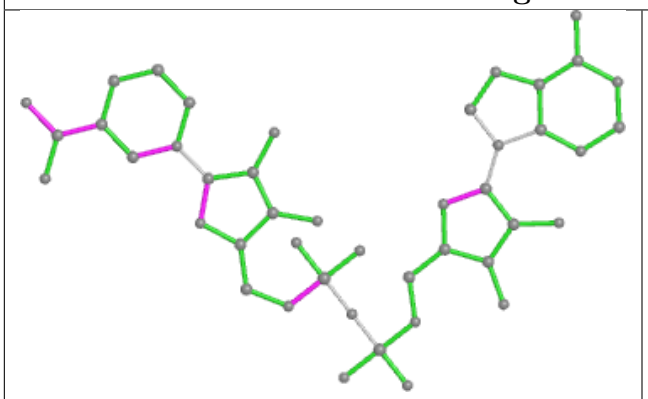


Torsions

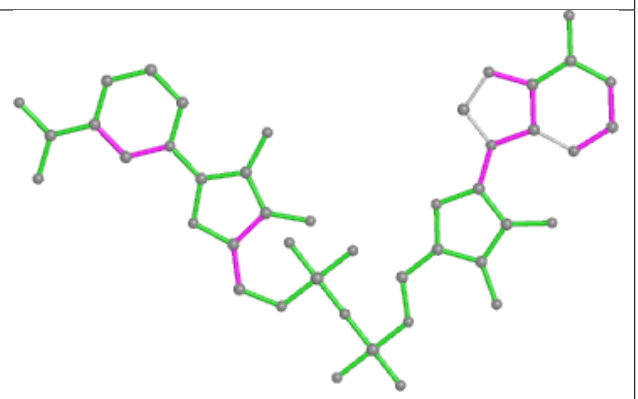


Rings

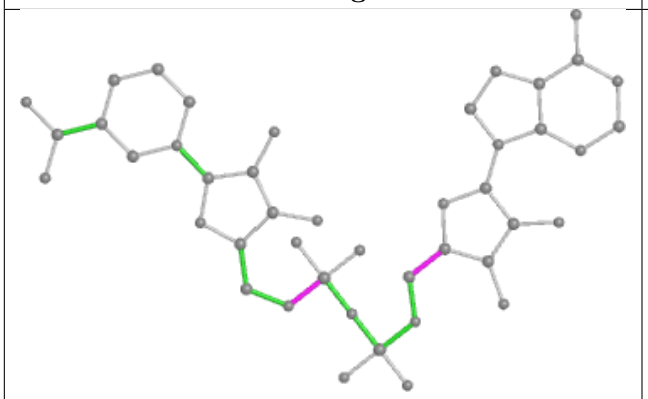
Ligand NAD E 1401



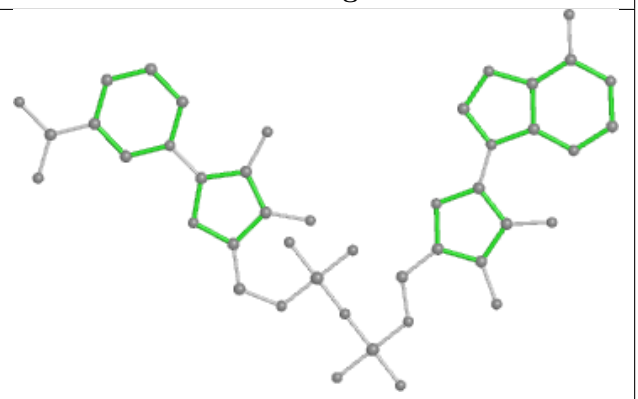
Bond lengths



Bond angles

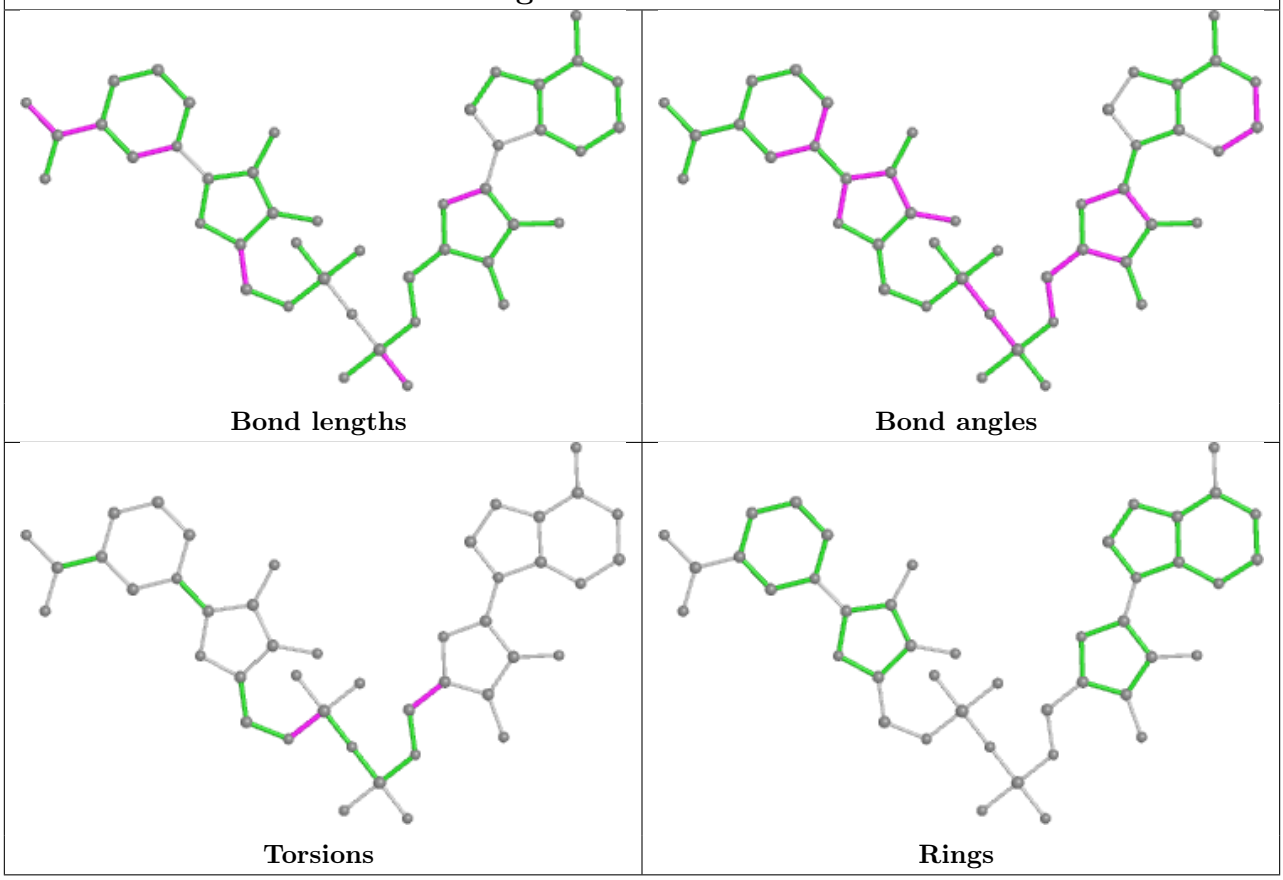


Torsions



Rings

Ligand NAD J 1401



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	319/319 (100%)	0.14	16 (5%)	28	31	18, 34, 61, 91	0
1	C	319/319 (100%)	0.01	8 (2%)	57	60	14, 27, 60, 77	0
1	E	319/319 (100%)	-0.04	8 (2%)	57	60	19, 31, 56, 86	0
1	G	319/319 (100%)	-0.04	13 (4%)	37	40	17, 29, 50, 74	0
1	I	319/319 (100%)	0.07	14 (4%)	34	37	15, 30, 67, 96	0
1	J	319/319 (100%)	0.20	20 (6%)	20	22	16, 33, 63, 83	0
All	All	1914/1914 (100%)	0.06	79 (4%)	37	40	14, 31, 60, 96	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	1321	LEU	7.2
1	C	1321	LEU	6.1
1	E	1321	LEU	5.9
1	J	1182	GLY	5.2
1	A	1182	GLY	5.0
1	C	1180	LEU	4.5
1	J	1317	GLY	4.5
1	J	1191	HIS	4.2
1	G	1182[A]	GLY	4.1
1	J	1041	ALA	4.1
1	I	1264	ILE	4.1
1	J	1321	LEU	4.1
1	C	1178	ALA	4.0
1	A	1181	PRO	3.8
1	I	1259	CYS	3.7
1	G	1321	LEU	3.6
1	G	1183[A]	GLY	3.6
1	J	1181	PRO	3.5
1	G	1181[A]	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	G	1265	GLU	3.4
1	I	1260	THR	3.4
1	J	1047	GLY	3.3
1	E	1042	LYS	3.3
1	I	1319	PRO	3.3
1	A	1318	LEU	3.2
1	C	1320	SER	2.9
1	A	1321	LEU	2.9
1	G	1317	GLY	2.9
1	A	1041	ALA	2.9
1	J	1261	ASP	2.8
1	G	1320	SER	2.8
1	A	1040	GLY	2.7
1	A	1319	PRO	2.6
1	A	1186	THR	2.6
1	J	1042	LYS	2.6
1	A	1261	ASP	2.6
1	J	1318	LEU	2.5
1	I	1315	LEU	2.5
1	C	1191	HIS	2.5
1	G	1077	LEU	2.5
1	G	1198	LEU	2.5
1	E	1101	ARG	2.5
1	J	1040	GLY	2.5
1	I	1199	GLN	2.4
1	J	1262	ARG	2.4
1	C	1047	GLY	2.4
1	J	1029	ASP	2.4
1	J	1186	THR	2.4
1	G	1180[A]	LEU	2.4
1	I	1077	LEU	2.4
1	E	1077	LEU	2.3
1	J	1189	ALA	2.3
1	C	1182	GLY	2.3
1	G	1041	ALA	2.3
1	I	1197	LEU	2.3
1	E	1319	PRO	2.3
1	I	1117	PRO	2.3
1	I	1200	LYS	2.3
1	C	1318	LEU	2.2
1	E	1318	LEU	2.2
1	I	1261	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	I	1041	ALA	2.2
1	E	1317	GLY	2.2
1	I	1314	ILE	2.1
1	A	1118	SER	2.1
1	E	1117	PRO	2.1
1	A	1262	ARG	2.1
1	G	1171	LEU	2.1
1	G	1029	ASP	2.1
1	J	1014	ILE	2.1
1	J	1049	LYS	2.1
1	A	1265	GLU	2.0
1	A	1263	THR	2.0
1	J	1028	ALA	2.0
1	A	1049	LYS	2.0
1	A	1048	LEU	2.0
1	J	1174	ILE	2.0
1	A	1200	LYS	2.0
1	J	1024	ASP	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 monosaccharides 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. 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
3	GOL	J	1402	6/6	0.80	0.25	49,51,52,56	0
3	GOL	G	1402	6/6	0.82	0.27	41,43,45,45	0
5	ALO	C	1402	8/8	0.84	0.22	22,25,29,32	0
5	ALO	G	1403	8/8	0.85	0.20	32,39,41,52	0
4	ACT	C	1403	4/4	0.86	0.20	39,47,49,50	0

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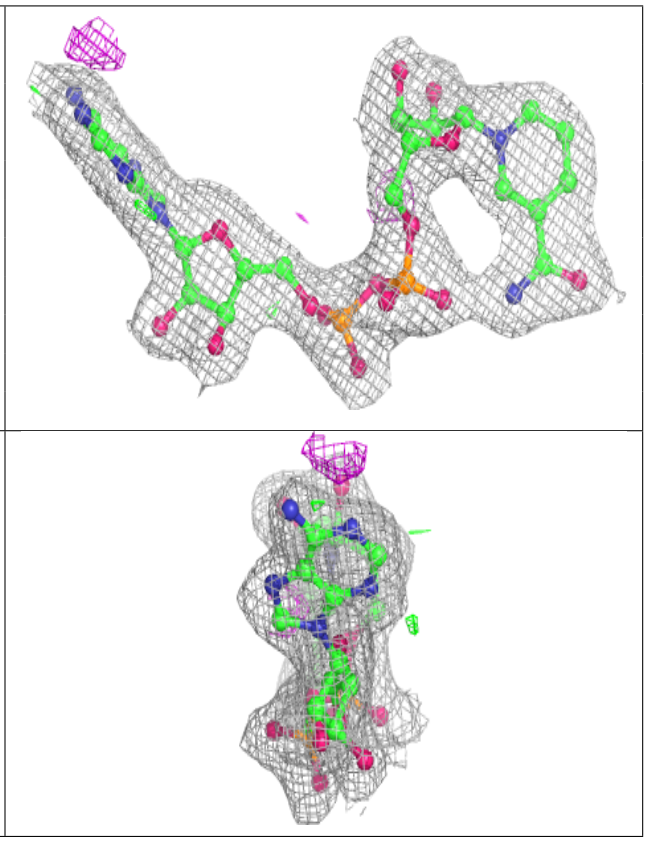
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GOL	I	1403	6/6	0.86	0.15	45,48,48,49	0
4	ACT	A	1403	4/4	0.86	0.19	51,52,56,59	0
3	GOL	J	1403	6/6	0.89	0.14	47,49,51,52	0
4	ACT	C	1404	4/4	0.89	0.23	49,50,52,54	0
3	GOL	E	1403	6/6	0.90	0.20	32,35,36,39	0
3	GOL	E	1402	6/6	0.90	0.13	37,39,40,41	0
3	GOL	A	1402	6/6	0.93	0.23	30,31,35,39	0
3	GOL	I	1402	6/6	0.93	0.17	32,33,36,36	0
2	NAD	J	1401	44/44	0.94	0.15	19,24,27,30	0
2	NAD	G	1401	44/44	0.94	0.14	19,24,27,30	0
2	NAD	A	1401	44/44	0.95	0.14	20,26,30,34	0
2	NAD	I	1401	44/44	0.95	0.12	21,24,27,28	0
2	NAD	E	1401	44/44	0.96	0.12	16,22,25,29	0
4	ACT	J	1404	4/4	0.96	0.34	25,27,28,29	0
2	NAD	C	1401	44/44	0.97	0.13	17,20,23,25	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.

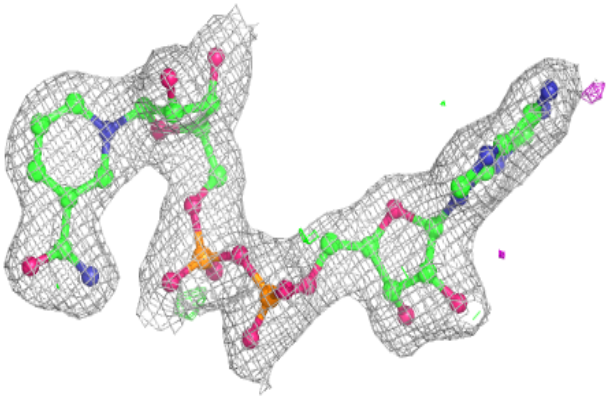
Electron density around NAD J 1401:

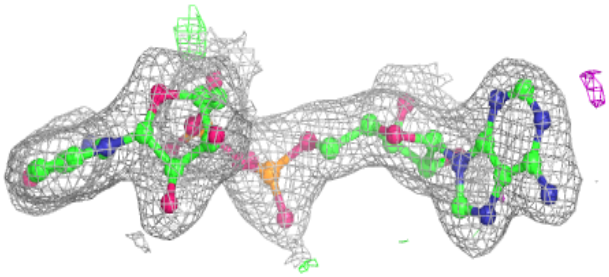
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

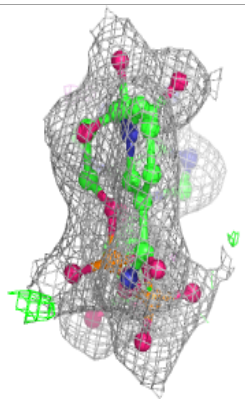


Electron density around NAD G 1401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

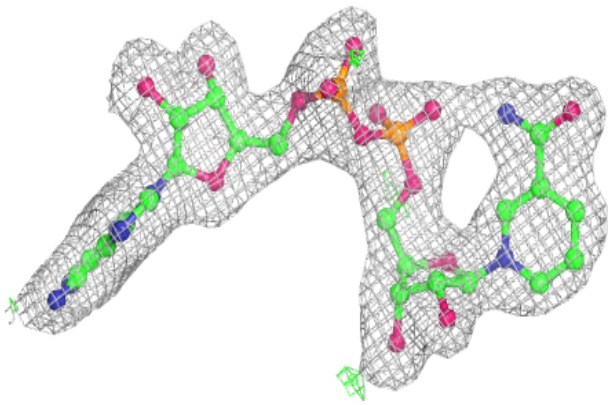


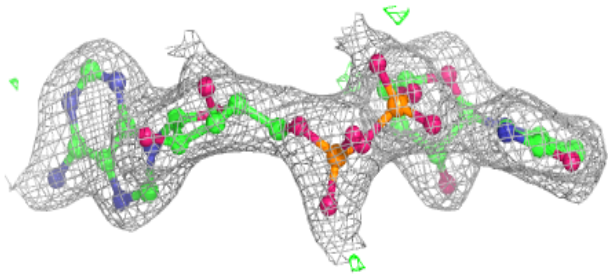


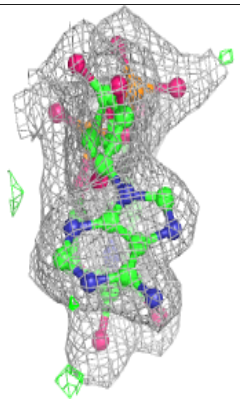


Electron density around NAD A 1401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

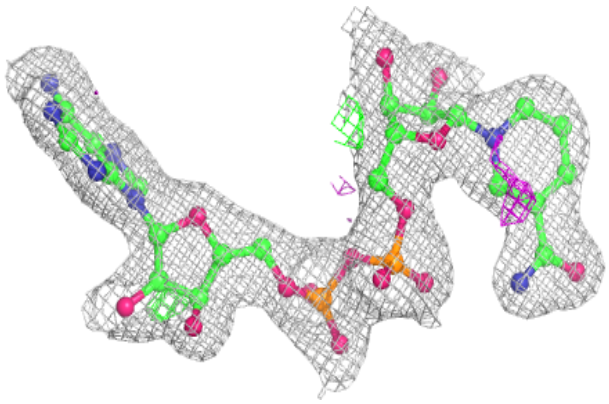


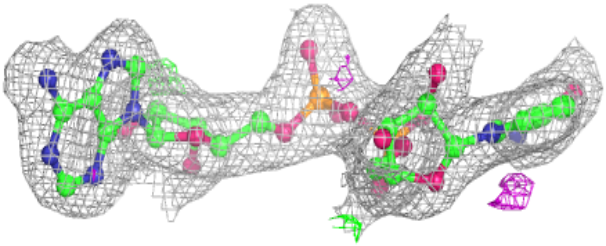


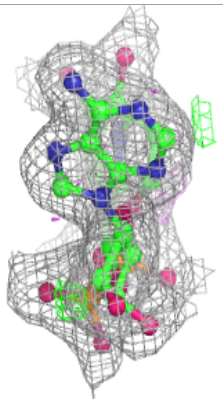


Electron density around NAD I 1401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

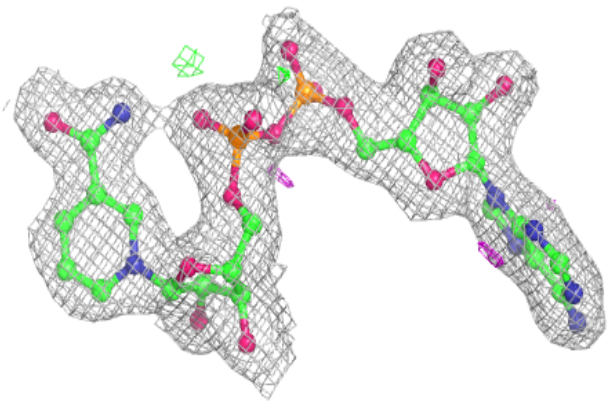


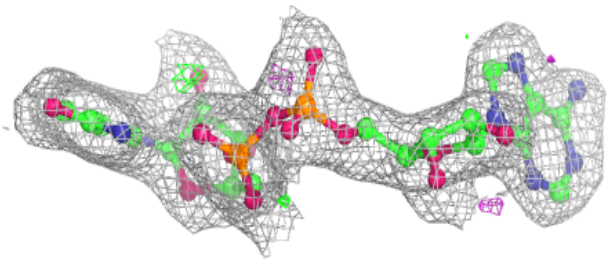


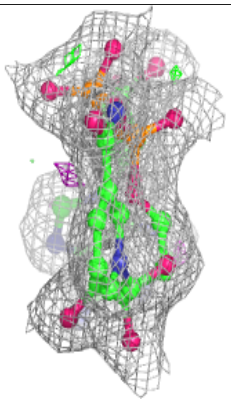


Electron density around NAD E 1401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

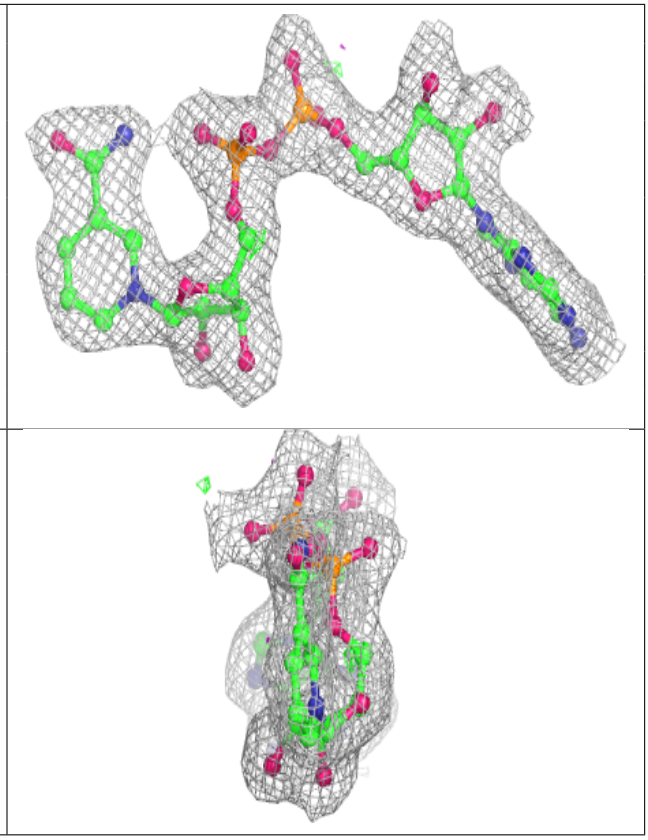






Electron density around NAD C 1401:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.