



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2020 – 08:50 am BST

PDB ID : 1PJ3
Title : Crystal structure of human mitochondrial NAD(P)⁺-dependent malic enzyme in a pentary complex with natural substrate pyruvate, cofactor NAD⁺, Mn⁺⁺, and allosteric activator fumarate.
Authors : Tao, X.; Yang, Z.; Tong, L.
Deposited on : 2003-05-30
Resolution : 2.10 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.11
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) : 2.11

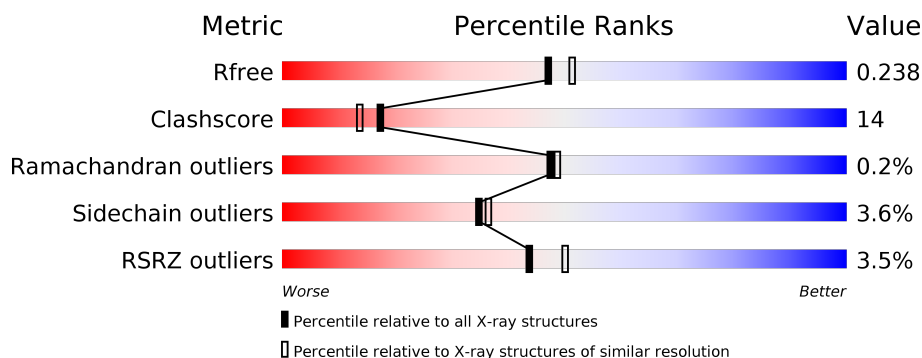
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 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	564	<div> <div>3%</div> <div> <div></div> <div>74%</div> <div>22%</div> <div>..</div> </div> </div>
1	B	564	<div> <div>4%</div> <div> <div></div> <div>65%</div> <div>32%</div> <div>..</div> </div> </div>
1	C	564	<div> <div>2%</div> <div> <div></div> <div>73%</div> <div>24%</div> <div>..</div> </div> </div>
1	D	564	<div> <div>4%</div> <div> <div></div> <div>71%</div> <div>25%</div> <div>..</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 19265 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 NAD-dependent malic enzyme, mitochondrial.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	553	Total	C	N	O	S	Se	0	0	0
			4367	2796	744	804	9	14			
1	B	553	Total	C	N	O	S	Se	0	0	0
			4367	2796	744	804	9	14			
1	C	553	Total	C	N	O	S	Se	0	0	0
			4367	2796	744	804	9	14			
1	D	553	Total	C	N	O	S	Se	0	0	0
			4367	2796	744	804	9	14			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	38	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	47	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	75	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	86	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	108	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	177	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	219	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	239	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	325	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	327	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	343	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	407	MSE	MET	MODIFIED RESIDUE	UNP P23368
A	539	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1029	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1038	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1047	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1075	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1086	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1108	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1177	MSE	MET	MODIFIED RESIDUE	UNP P23368

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1219	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1239	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1325	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1327	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1343	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1407	MSE	MET	MODIFIED RESIDUE	UNP P23368
B	1539	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2029	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2038	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2047	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2075	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2086	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2108	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2177	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2219	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2239	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2325	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2327	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2343	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2407	MSE	MET	MODIFIED RESIDUE	UNP P23368
C	2539	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3029	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3038	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3047	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3075	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3086	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3108	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3177	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3219	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3239	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3325	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3327	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3343	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3407	MSE	MET	MODIFIED RESIDUE	UNP P23368
D	3539	MSE	MET	MODIFIED RESIDUE	UNP P23368

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

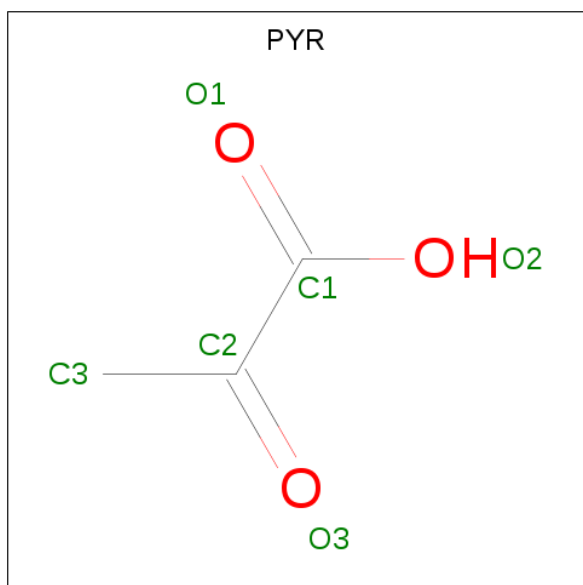
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Mn 1 1	0	0
2	A	1	Total Mn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total	Mn	0	0
			1	1		
2	C	1	Total	Mn	0	0
			1	1		

- Molecule 3 is PYRUVIC ACID (three-letter code: PYR) (formula: $C_3H_4O_3$).



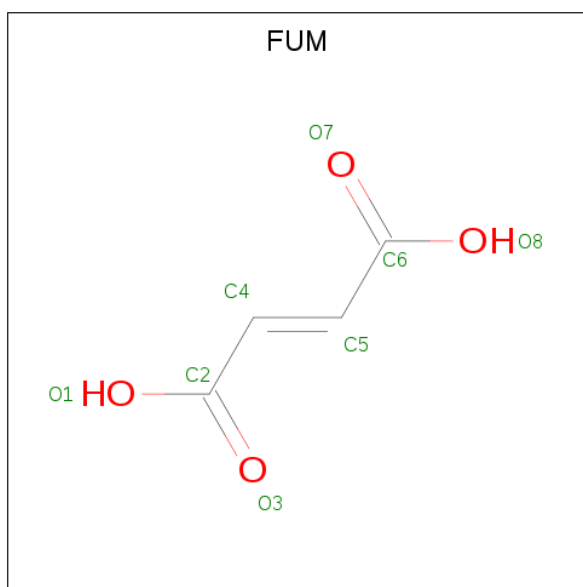
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
4	A	1	Total	C	N	O	P	9	0
			44	21	7	14	2		
4	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
4	B	1	Total	C	N	O	P	9	0
			44	21	7	14	2		
4	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
4	C	1	Total	C	N	O	P	9	0
			44	21	7	14	2		
4	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
4	D	1	Total	C	N	O	P	9	0
			44	21	7	14	2		

- Molecule 5 is FUMARIC ACID (three-letter code: FUM) (formula: C₄H₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			8	4	4		
5	B	1	Total	C	O	0	0
			8	4	4		
5	C	1	Total	C	O	0	0
			8	4	4		
5	D	1	Total	C	O	0	0
			8	4	4		

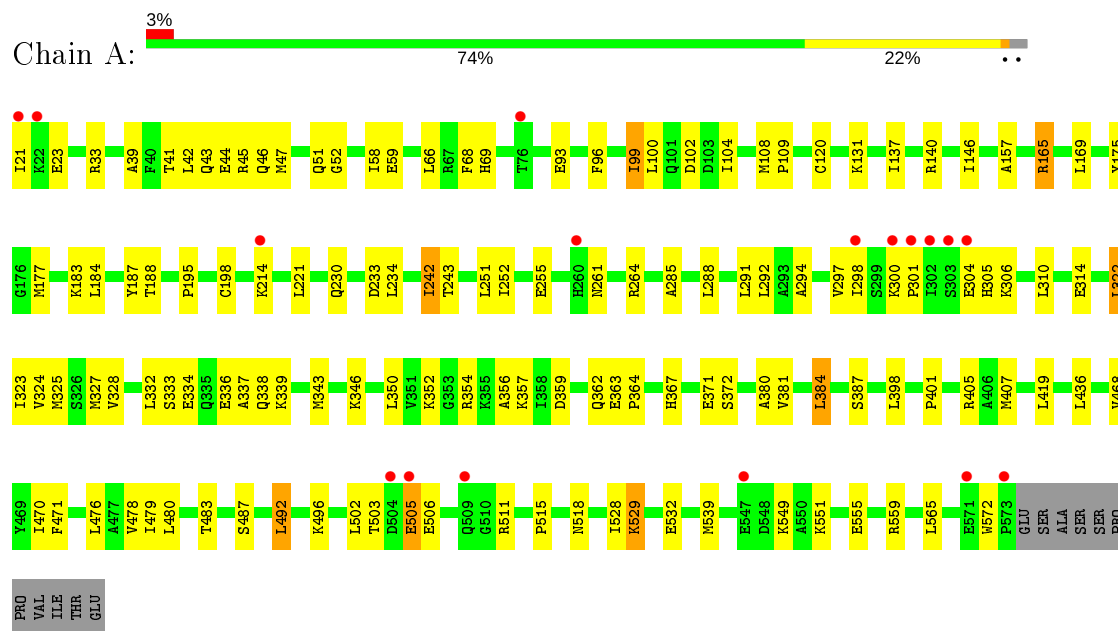
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	364	Total	O	0	0
			364	364		
6	B	319	Total	O	0	0
			319	319		
6	C	384	Total	O	0	0
			384	384		
6	D	318	Total	O	0	0
			318	318		

3 Residue-property plots

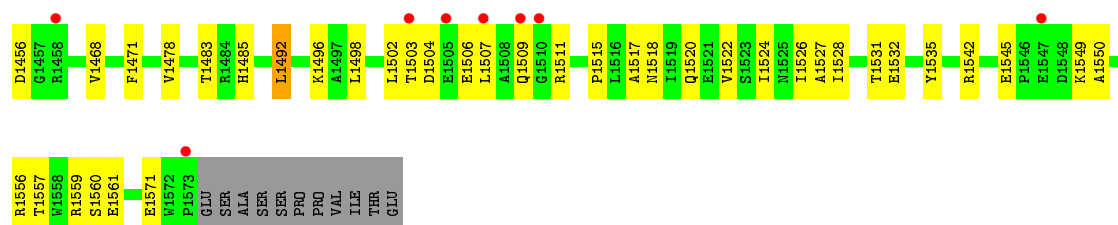
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: NAD-dependent malic enzyme, mitochondrial

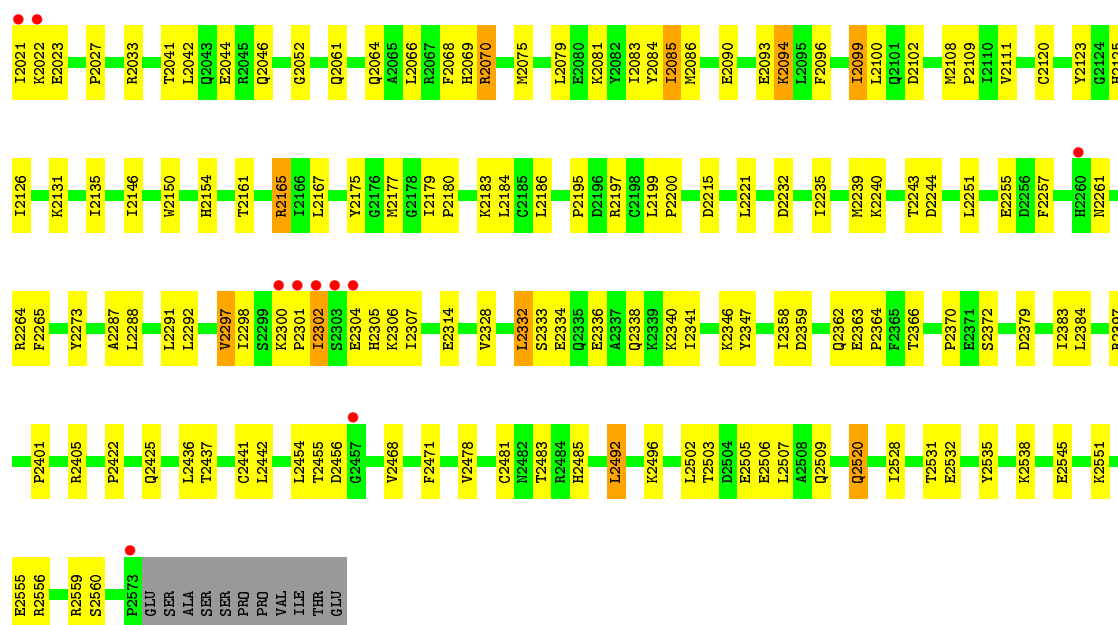
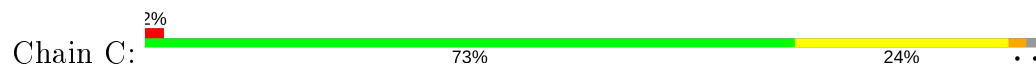


- Molecule 1: NAD-dependent malic enzyme, mitochondrial

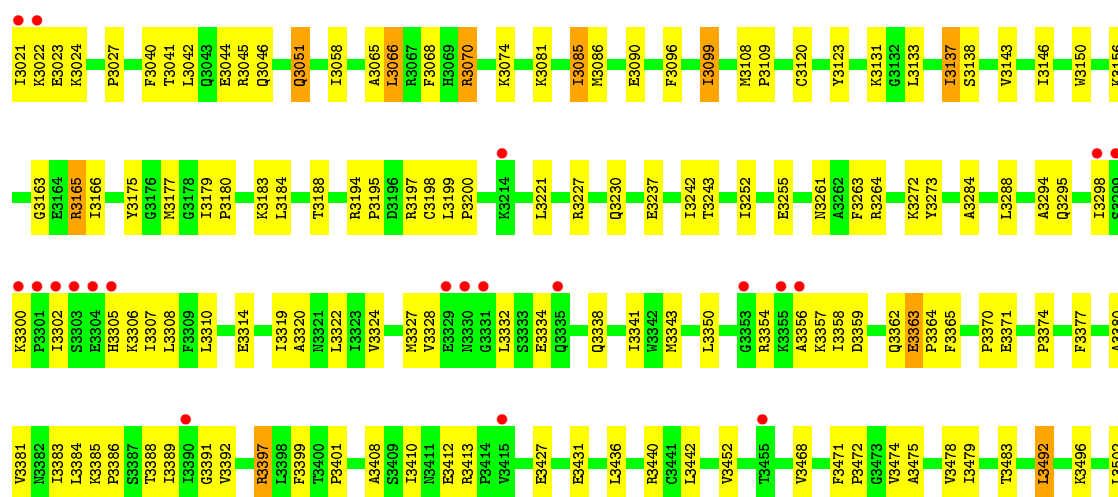




- Molecule 1: NAD-dependent malic enzyme, mitochondrial



- Molecule 1: NAD-dependent malic enzyme, mitochondrial





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	225.83Å 117.05Å 111.85Å 90.00° 109.57° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 27.18 – 2.09	Depositor EDS
% Data completeness (in resolution range)	90.6 (20.00-2.10) 91.6 (27.18-2.09)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.24 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.192 , 0.236 0.195 , 0.238	Depositor DCC
R_{free} test set	11059 reflections (7.49%)	wwPDB-VP
Wilson B-factor (Å ²)	25.9	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19265	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.32	0/4447	0.58	0/5998
1	B	0.31	0/4447	0.57	0/5998
1	C	0.32	0/4447	0.58	0/5998
1	D	0.31	0/4447	0.56	0/5998
All	All	0.31	0/17788	0.57	0/23992

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	4367	0	4407	107	0
1	B	4367	0	4407	140	0
1	C	4367	0	4407	108	0
1	D	4367	0	4407	138	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	6	0	3	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	6	0	3	2	0
3	C	6	0	3	0	0
3	D	6	0	3	2	0
4	A	88	0	52	2	0
4	B	88	0	52	1	0
4	C	88	0	52	1	0
4	D	88	0	52	1	0
5	A	8	0	2	0	0
5	B	8	0	2	0	0
5	C	8	0	2	0	0
5	D	8	0	2	0	0
6	A	364	0	0	6	0
6	B	319	0	0	8	0
6	C	384	0	0	4	0
6	D	318	0	0	4	0
All	All	19265	0	17856	491	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 14.

All (491) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1357:LYS:HD3	1:B:1357:LYS:H	1.24	1.02
1:A:43:GLN:HG2	1:A:47:MSE:HE3	1.47	0.97
1:B:1358:ILE:HD13	1:B:1366:THR:HG21	1.46	0.94
1:A:407:MSE:HE2	1:A:407:MSE:HA	1.51	0.93
1:A:140:ARG:HH22	1:A:234:LEU:N	1.67	0.92
1:D:3343:MSE:HE2	1:D:3365:PHE:HB2	1.53	0.90
1:B:1343:MSE:HE2	1:B:1365:PHE:HB2	1.55	0.86
1:A:532:GLU:HG2	1:A:549:LYS:HG3	1.57	0.86
1:B:1504:ASP:HA	1:B:1507:LEU:HD13	1.58	0.84
1:C:2332:LEU:H	1:C:2332:LEU:HD12	1.43	0.84
1:D:3374:PRO:HG3	1:D:3383:ILE:HD12	1.58	0.84
1:A:323:ILE:HG22	1:A:327:MSE:HE2	1.57	0.84
1:A:381:VAL:HG13	1:A:407:MSE:HE3	1.58	0.83
1:D:3261:ASN:HD22	1:D:3264:ARG:HE	1.25	0.83
1:B:1492:LEU:HD22	1:B:1496:LYS:HE3	1.59	0.83
1:C:2492:LEU:HD22	1:C:2496:LYS:HE3	1.62	0.81
1:B:1043:GLN:HG2	1:B:1047:MSE:HE3	1.61	0.80
1:A:261:ASN:HD22	1:A:264:ARG:HE	1.29	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2096:PHE:O	1:C:2100:LEU:HD13	1.82	0.80
1:C:2520:GLN:HE21	1:C:2520:GLN:H	1.30	0.79
1:B:1261:ASN:HD22	1:B:1264:ARG:HD3	1.47	0.79
1:B:1323:ILE:HG22	1:B:1327:MSE:HE2	1.65	0.78
1:B:1079:LEU:O	1:B:1083:ILE:HD13	1.83	0.78
1:B:1369:ALA:HB1	1:B:1373:ILE:HD11	1.64	0.78
1:D:3302:ILE:HD11	1:D:3327:MSE:HE2	1.66	0.78
1:B:1357:LYS:HD3	1:B:1357:LYS:N	1.98	0.77
1:C:2520:GLN:HG2	6:C:4941:HOH:O	1.85	0.77
1:B:1527:ALA:O	1:B:1531:THR:HG23	1.86	0.76
1:B:1343:MSE:HE3	1:B:1350:LEU:HD12	1.66	0.75
1:D:3085:ILE:HD12	1:D:3096:PHE:HE1	1.50	0.74
1:A:381:VAL:CG1	1:A:407:MSE:HE3	2.18	0.74
1:C:2021:ILE:HG13	1:C:2023:GLU:H	1.52	0.73
1:D:3308:LEU:HD23	1:D:3389:ILE:HD11	1.72	0.72
1:A:140:ARG:NH2	1:A:230:GLN:O	2.23	0.71
1:D:3363:GLU:HB3	1:D:3364:PRO:HD3	1.74	0.70
1:C:2081:LYS:O	1:C:2085:ILE:HG23	1.93	0.69
1:A:140:ARG:HH11	1:A:140:ARG:HG3	1.58	0.69
1:B:1377:PHE:O	1:B:1381:VAL:HG23	1.92	0.69
1:B:1478:VAL:HG13	1:B:1483:THR:HB	1.74	0.69
1:C:2520:GLN:NE2	1:C:2520:GLN:H	1.90	0.69
1:C:2085:ILE:HD12	1:C:2096:PHE:HE1	1.58	0.69
1:B:1522:VAL:O	1:B:1526:ILE:HG12	1.93	0.68
1:B:1334:GLU:O	1:B:1338:GLN:HG3	1.93	0.68
1:D:3520:GLN:H	1:D:3520:GLN:HE21	1.39	0.68
1:A:371:GLU:H	1:A:371:GLU:CD	1.97	0.68
1:B:1305:HIS:HD2	1:B:1387:SER:OG	1.77	0.67
1:D:3179:ILE:HB	1:D:3180:PRO:HD3	1.77	0.67
1:B:1066:LEU:HD22	1:B:1070:ARG:NH1	2.09	0.67
1:A:551:LYS:O	1:A:555:GLU:HG3	1.95	0.67
1:A:261:ASN:ND2	1:A:264:ARG:HE	1.93	0.66
1:C:2154:HIS:O	1:C:2197:ARG:HD2	1.94	0.66
1:A:407:MSE:CE	1:A:407:MSE:HA	2.25	0.66
1:D:3371:GLU:CD	1:D:3371:GLU:H	1.99	0.66
1:D:3308:LEU:HB3	1:D:3389:ILE:HD12	1.78	0.66
1:D:3021:ILE:HD12	1:D:3021:ILE:N	2.11	0.66
1:B:1301:PRO:HD2	1:B:1304:GLU:OE2	1.96	0.65
3:B:1603:PYR:H33	6:B:4964:HOH:O	1.97	0.65
1:B:1332:LEU:HD12	1:B:1332:LEU:H	1.61	0.65
1:C:2288:LEU:O	1:C:2292:LEU:HD13	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2298:ILE:HG22	1:C:2300:LYS:H	1.62	0.65
1:A:96:PHE:O	1:A:100:LEU:HD13	1.96	0.65
1:D:3068:PHE:CD2	1:D:3099:ILE:HG13	2.32	0.64
1:B:1261:ASN:HA	1:B:1264:ARG:HD3	1.78	0.64
1:C:2099:ILE:HG22	1:C:2100:LEU:HD12	1.79	0.64
1:D:3332:LEU:HD12	1:D:3332:LEU:H	1.63	0.64
1:D:3359:ASP:OD2	1:D:3362:GLN:HG3	1.98	0.64
1:D:3475:ALA:O	1:D:3479:ILE:HG12	1.96	0.64
1:B:1377:PHE:CZ	1:B:1389:ILE:HD11	2.32	0.64
1:C:2397:ARG:NH1	6:C:5346:HOH:O	2.29	0.64
1:B:1068:PHE:CD2	1:B:1099:ILE:HG13	2.32	0.64
1:D:3492:LEU:HD22	1:D:3496:LYS:HE3	1.79	0.64
1:D:3520:GLN:NE2	1:D:3520:GLN:H	1.95	0.64
1:B:1354:ARG:CZ	1:B:1356:ALA:HB3	2.27	0.64
1:C:2297:VAL:HG12	1:C:2507:LEU:HD11	1.79	0.64
1:D:3066:LEU:HD22	1:D:3070:ARG:HE	1.62	0.64
1:C:2358:ILE:HD13	1:C:2366:THR:HG21	1.80	0.63
1:D:3334:GLU:O	1:D:3338:GLN:HG3	1.97	0.63
1:A:333:SER:H	1:A:336:GLU:CD	2.01	0.63
1:B:1288:LEU:O	1:B:1292:LEU:HD13	1.99	0.63
1:D:3551:LYS:O	1:D:3555:GLU:HG3	1.98	0.63
1:B:1437:THR:HG21	1:B:1441:CYS:HB3	1.80	0.63
1:A:505:GLU:H	1:A:505:GLU:CD	2.02	0.63
1:A:99:ILE:HG22	1:A:100:LEU:HD12	1.80	0.62
1:C:2301:PRO:HD2	1:C:2304:GLU:OE1	1.99	0.62
1:D:3184:LEU:HD12	1:D:3200:PRO:HG3	1.80	0.62
1:A:146:ILE:HG23	1:B:1052:GLY:HA3	1.81	0.62
1:C:2478:VAL:HG13	1:C:2483:THR:HB	1.82	0.62
1:D:3261:ASN:ND2	1:D:3264:ARG:HE	1.94	0.62
1:B:1154:HIS:HD2	6:B:4910:HOH:O	1.82	0.62
1:D:3478:VAL:HG13	1:D:3483:THR:HB	1.79	0.62
1:A:285:ALA:HB3	1:A:470:ILE:HD13	1.82	0.62
1:B:1363:GLU:HB3	1:B:1364:PRO:HD3	1.81	0.62
1:D:3081:LYS:O	1:D:3085:ILE:HG23	2.01	0.61
1:D:3183:LYS:HE3	1:D:3255:GLU:CD	2.21	0.61
1:D:3354:ARG:NE	1:D:3358:ILE:HD11	2.15	0.61
1:B:1357:LYS:CD	1:B:1357:LYS:H	1.92	0.61
1:A:68:PHE:CD2	1:A:99:ILE:HG13	2.35	0.61
1:D:3357:LYS:C	1:D:3358:ILE:HD12	2.20	0.61
1:A:242:ILE:HG21	1:A:252:ILE:HD11	1.83	0.61
1:D:3308:LEU:HB3	1:D:3389:ILE:CD1	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:PRO:HB2	1:A:518:ASN:ND2	2.16	0.61
1:B:1432:GLU:O	1:B:1436:LEU:HB2	2.01	0.61
1:A:324:VAL:HA	1:A:327:MSE:HE3	1.83	0.60
1:C:2184:LEU:HD12	1:C:2200:PRO:HG3	1.81	0.60
1:C:2052:GLY:HA3	1:D:3146:ILE:HG23	1.82	0.60
1:C:2346:LYS:HE2	1:C:2347:TYR:CE1	2.37	0.60
1:D:3066:LEU:CD2	1:D:3070:ARG:HE	2.15	0.60
1:C:2066:LEU:HD11	1:C:2070:ARG:NH1	2.17	0.59
1:C:2085:ILE:HD11	1:C:2111:VAL:HG12	1.84	0.59
1:D:3357:LYS:O	1:D:3358:ILE:HD12	2.02	0.59
1:C:2261:ASN:ND2	1:C:2264:ARG:HH21	1.99	0.59
1:D:3041:THR:O	1:D:3045:ARG:HG3	2.02	0.59
1:A:492:LEU:HD22	1:A:496:LYS:HE2	1.84	0.59
1:C:2179:ILE:HB	1:C:2180:PRO:HD3	1.84	0.59
1:A:503:THR:OG1	1:A:506:GLU:HG3	2.02	0.59
1:B:1324:VAL:HA	1:B:1327:MSE:HE3	1.84	0.59
1:D:3261:ASN:HD22	1:D:3264:ARG:NE	1.97	0.58
1:D:3298:ILE:HG22	1:D:3300:LYS:HG3	1.84	0.58
1:A:346:LYS:HE2	6:A:4186:HOH:O	2.02	0.58
1:B:1177:MSE:O	1:B:1180:PRO:HD2	2.02	0.58
1:C:2068:PHE:CD2	1:C:2099:ILE:HG13	2.36	0.58
1:D:3306:LYS:HG2	1:D:3386:PRO:HA	1.85	0.58
3:A:603:PYR:H33	6:A:5000:HOH:O	2.03	0.58
1:A:352:LYS:HZ2	1:A:367:HIS:HA	1.67	0.58
1:A:41:THR:O	1:A:45:ARG:HG3	2.03	0.58
1:D:3184:LEU:HD22	1:D:3198:CYS:HB3	1.84	0.58
1:C:2505:GLU:O	1:C:2509:GLN:HG3	2.03	0.58
1:D:3051:GLN:HE21	1:D:3051:GLN:HA	1.69	0.58
1:B:1065:ALA:HA	1:B:1099:ILE:HD11	1.86	0.57
1:A:43:GLN:CG	1:A:47:MSE:HE3	2.30	0.57
1:C:2332:LEU:CD1	1:C:2332:LEU:H	2.15	0.57
1:D:3306:LYS:HE3	1:D:3384:LEU:O	2.04	0.57
1:B:1358:ILE:CD1	1:B:1366:THR:HG21	2.28	0.57
1:A:325:MSE:HE2	1:A:492:LEU:HD12	1.85	0.57
1:B:1288:LEU:HD22	1:B:1322:LEU:HG	1.86	0.57
1:D:3350:LEU:HD12	1:D:3358:ILE:HG13	1.87	0.57
1:A:140:ARG:NH2	1:A:233:ASP:HB2	2.19	0.57
1:B:1422:PRO:HD2	1:B:1425:GLN:HE21	1.69	0.57
1:A:327:MSE:HE3	1:A:337:ALA:HB1	1.86	0.57
1:D:3194:ARG:HH11	1:D:3194:ARG:HG2	1.69	0.57
1:A:301:PRO:HB2	1:A:304:GLU:OE1	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:PRO:HA	1:A:436:LEU:HD13	1.86	0.56
1:A:285:ALA:CB	1:A:470:ILE:HD13	2.35	0.56
1:D:3528:ILE:O	1:D:3532:GLU:HG3	2.06	0.56
1:D:3272:LYS:NZ	1:D:3272:LYS:HB3	2.20	0.56
1:A:140:ARG:HD3	6:A:5264:HOH:O	2.06	0.56
1:D:3137:ILE:HD11	1:D:3230:GLN:NE2	2.19	0.56
1:D:3354:ARG:NE	1:D:3356:ALA:HB3	2.20	0.56
1:B:1295:GLN:HG3	6:B:4795:HOH:O	2.06	0.56
1:C:2503:THR:OG1	1:C:2506:GLU:HG3	2.06	0.56
1:D:3272:LYS:HZ3	1:D:3272:LYS:HB3	1.69	0.56
1:D:3298:ILE:CG2	1:D:3300:LYS:HE3	2.35	0.56
1:D:3085:ILE:HD12	1:D:3096:PHE:CE1	2.36	0.56
1:B:1120:CYS:O	1:B:1175:TYR:HB3	2.06	0.56
1:B:1261:ASN:HA	1:B:1264:ARG:CD	2.34	0.56
1:A:108:MSE:HB3	1:A:109:PRO:HD3	1.89	0.55
1:D:3300:LYS:HB2	1:D:3300:LYS:NZ	2.21	0.55
1:B:1315:ALA:O	1:B:1319:ILE:HG13	2.06	0.55
1:A:300:LYS:HE3	1:A:305:HIS:CD2	2.41	0.55
1:B:1132:GLY:CA	1:B:1200:PRO:HG2	2.36	0.55
1:B:1302:ILE:O	1:B:1340:LYS:HE2	2.06	0.55
1:C:2363:GLU:HB3	1:C:2364:PRO:HD3	1.87	0.55
1:D:3389:ILE:HG23	1:D:3399:PHE:CZ	2.42	0.55
1:D:3503:THR:OG1	1:D:3506:GLU:HG3	2.07	0.55
1:B:1036:LYS:HB3	1:B:1039:ALA:HB3	1.89	0.54
1:C:2022:LYS:NZ	1:C:2022:LYS:HB3	2.22	0.54
1:C:2297:VAL:CG2	1:C:2442:LEU:HD11	2.37	0.54
1:A:104:ILE:HG13	1:A:108:MSE:HE2	1.90	0.54
1:A:354:ARG:NE	1:A:356:ALA:HB3	2.23	0.54
1:C:2468:VAL:HA	1:C:2471:PHE:CE2	2.43	0.54
3:D:3603:PYR:H33	6:D:5039:HOH:O	2.07	0.54
1:A:120:CYS:O	1:A:175:TYR:HB3	2.08	0.54
1:D:3120:CYS:O	1:D:3175:TYR:HB3	2.07	0.54
1:D:3535:TYR:CD2	1:D:3545:GLU:HG3	2.42	0.54
1:A:328:VAL:HA	1:A:332:LEU:O	2.08	0.54
1:B:1022:LYS:HE2	6:D:4559:HOH:O	2.06	0.54
1:B:1108:MSE:HB3	1:B:1109:PRO:HD3	1.90	0.54
1:B:1559:ARG:HB3	1:B:1561:GLU:OE1	2.08	0.54
1:C:2041:THR:OG1	1:C:2044:GLU:HG3	2.07	0.54
1:D:3354:ARG:HD2	6:D:4693:HOH:O	2.08	0.54
1:D:3085:ILE:HG13	1:D:3086:MSE:N	2.23	0.54
1:D:3532:GLU:HG2	1:D:3549:LYS:HG2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1179:ILE:HB	1:B:1180:PRO:HD3	1.90	0.53
1:D:3350:LEU:HD13	1:D:3354:ARG:CZ	2.38	0.53
1:D:3571:GLU:HG3	6:D:5047:HOH:O	2.07	0.53
1:B:1300:LYS:HD2	1:B:1304:GLU:OE1	2.08	0.53
1:D:3065:ALA:HA	1:D:3099:ILE:HD11	1.89	0.53
1:B:1140:ARG:NH2	1:B:1230:GLN:HG2	2.23	0.53
1:B:1518:ASN:HD22	1:B:1518:ASN:N	2.06	0.53
1:C:2485:HIS:HE1	6:C:4932:HOH:O	1.92	0.53
1:D:3307:ILE:CD1	1:D:3388:THR:HB	2.39	0.53
1:B:1359:ASP:OD2	1:B:1362:GLN:HG3	2.08	0.53
1:B:1571:GLU:HG3	6:B:4517:HOH:O	2.09	0.53
1:D:3041:THR:OG1	1:D:3044:GLU:HG3	2.08	0.53
1:D:3354:ARG:HE	1:D:3358:ILE:HD11	1.73	0.53
1:C:2328:VAL:HA	1:C:2332:LEU:O	2.08	0.53
1:C:2085:ILE:HD11	1:C:2086:MSE:SE	2.59	0.53
1:C:2033:ARG:HD3	1:C:2093:GLU:OE2	2.09	0.53
1:C:2437:THR:HG21	1:C:2441:CYS:HB3	1.89	0.53
1:C:2535:TYR:CD2	1:C:2545:GLU:HG3	2.44	0.53
1:C:2307:ILE:HD12	1:C:2307:ILE:N	2.24	0.52
1:D:3310:LEU:HB3	1:D:3391:GLY:HA2	1.91	0.52
1:A:478:VAL:HG13	1:A:483:THR:HB	1.90	0.52
1:B:1454:LEU:C	1:B:1456:ASP:N	2.62	0.52
1:D:3243:THR:HG21	1:D:3273:TYR:CD2	2.44	0.52
1:B:1468:VAL:HA	1:B:1471:PHE:CE2	2.44	0.52
1:D:3307:ILE:HB	1:D:3341:ILE:HD13	1.90	0.52
1:B:1188:THR:HG21	1:B:1195:PRO:HG3	1.92	0.52
1:C:2183:LYS:HE3	1:C:2255:GLU:CD	2.30	0.52
1:B:1021:ILE:HD13	1:B:1021:ILE:N	2.24	0.52
1:B:1165:ARG:NH2	3:B:1603:PYR:O1	2.41	0.52
1:A:188:THR:HG21	1:A:195:PRO:HG3	1.91	0.52
1:D:3401:PRO:HA	1:D:3436:LEU:HD13	1.92	0.52
1:C:2297:VAL:HG21	1:C:2442:LEU:HD11	1.91	0.52
1:B:1382:ASN:O	1:B:1385:LYS:HG3	2.10	0.51
1:B:1297:VAL:HG21	1:B:1442:LEU:HD21	1.92	0.51
1:D:3108:MSE:HB3	1:D:3109:PRO:HD3	1.93	0.51
1:D:3143:VAL:HB	1:D:3237:GLU:HG2	1.93	0.51
1:D:3492:LEU:CD2	1:D:3496:LYS:HE3	2.40	0.51
1:A:157:ALA:HB2	1:A:479:ILE:HD11	1.92	0.51
1:A:401:PRO:O	1:A:405:ARG:HG3	2.10	0.51
1:A:41:THR:OG1	1:A:44:GLU:HG3	2.11	0.51
1:A:529:LYS:HB3	1:A:529:LYS:NZ	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1166:ILE:HG21	1:B:1172:LEU:HD12	1.92	0.51
1:A:140:ARG:HG3	1:A:140:ARG:NH1	2.25	0.51
1:C:2090:GLU:OE1	1:C:2131:LYS:HE2	2.09	0.51
1:C:2302:ILE:HA	1:C:2305:HIS:ND1	2.25	0.51
1:B:1022:LYS:HB3	1:B:1022:LYS:NZ	2.25	0.51
1:B:1504:ASP:CA	1:B:1507:LEU:HD13	2.35	0.51
1:D:3314:GLU:HB2	4:D:3601:NAD:O1N	2.10	0.51
1:D:3165:ARG:NH2	3:D:3603:PYR:O1	2.39	0.51
1:A:294:ALA:O	1:A:298:ILE:HG12	2.11	0.51
1:B:1389:ILE:HG22	1:B:1416:ILE:HA	1.93	0.51
1:B:1520:GLN:HB2	6:B:4705:HOH:O	2.11	0.50
1:A:288:LEU:HD22	1:A:322:LEU:HD13	1.92	0.50
1:C:2300:LYS:HG3	1:C:2304:GLU:OE1	2.11	0.50
1:B:1024:LYS:O	1:D:3022:LYS:NZ	2.45	0.50
1:D:3385:LYS:HA	1:D:3410:ILE:HD13	1.91	0.50
1:A:487:SER:OG	1:A:539:MSE:HE1	2.12	0.50
1:D:3391:GLY:HA3	1:D:3427:GLU:HG2	1.92	0.50
1:D:3556:ARG:HH11	1:D:3556:ARG:HG3	1.76	0.50
1:B:1524:ILE:O	1:B:1528:ILE:HG13	2.12	0.50
1:C:2154:HIS:O	1:C:2197:ARG:CD	2.59	0.50
1:D:3090:GLU:OE1	1:D:3131:LYS:HG2	2.10	0.50
1:B:1159:VAL:HG23	1:B:1184:LEU:HD21	1.94	0.50
1:B:1406:ALA:O	1:B:1410:ILE:HG12	2.11	0.50
1:B:1343:MSE:HE3	1:B:1350:LEU:CD1	2.38	0.50
1:B:1532:GLU:HG2	1:B:1549:LYS:HG2	1.94	0.50
1:C:2186:LEU:HD13	1:C:2468:VAL:HG23	1.94	0.50
1:C:2507:LEU:HD13	1:C:2507:LEU:C	2.32	0.50
1:D:3263:PHE:CZ	1:D:3314:GLU:HA	2.47	0.50
1:B:1535:TYR:CD2	1:B:1545:GLU:HG3	2.47	0.50
1:D:3156:LYS:HA	1:D:3156:LYS:HE2	1.93	0.50
1:D:3188:THR:HG21	1:D:3195:PRO:HG3	1.94	0.50
1:C:2379:ASP:O	1:C:2383:ILE:HD13	2.11	0.49
1:A:140:ARG:NH2	1:A:234:LEU:N	2.48	0.49
1:D:3341:ILE:HB	1:D:3365:PHE:HD2	1.77	0.49
1:A:310:LEU:HD21	1:A:398:LEU:HD12	1.93	0.49
1:B:1069:HIS:HE1	1:B:1102:ASP:OD2	1.96	0.49
1:A:184:LEU:HD22	1:A:198:CYS:HB3	1.95	0.49
1:A:21:ILE:HD12	1:A:565:LEU:HD22	1.95	0.49
1:B:1132:GLY:HA3	1:B:1200:PRO:HG2	1.94	0.49
1:C:2334:GLU:O	1:C:2338:GLN:HG3	2.12	0.49
1:C:2346:LYS:HE2	1:C:2347:TYR:HE1	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:LEU:CD2	1:A:322:LEU:HD13	2.41	0.49
1:D:3302:ILE:CD1	1:D:3327:MSE:HE2	2.38	0.49
1:B:1485:HIS:HE1	6:B:5361:HOH:O	1.95	0.49
1:C:2108:MSE:HB3	1:C:2109:PRO:HD3	1.93	0.49
1:D:3021:ILE:CD1	1:D:3021:ILE:N	2.76	0.49
1:A:42:LEU:HB2	1:A:58:ILE:HD11	1.96	0.48
1:A:69:HIS:HE1	1:A:102:ASP:OD2	1.96	0.48
1:C:2243:THR:HG21	1:C:2273:TYR:CD2	2.48	0.48
1:C:2422:PRO:HD2	1:C:2425:GLN:HE21	1.79	0.48
1:A:371:GLU:HG2	1:A:372:SER:H	1.78	0.48
1:C:2023:GLU:CG	1:C:2027:PRO:HB2	2.43	0.48
1:D:3085:ILE:CD1	1:D:3096:PHE:HE1	2.23	0.48
1:B:1033:ARG:HD3	1:B:1093:GLU:OE2	2.13	0.48
1:B:1503:THR:OG1	1:B:1506:GLU:HG3	2.14	0.48
1:B:1528:ILE:HD13	1:B:1550:ALA:HA	1.95	0.48
1:B:1389:ILE:HG22	1:B:1416:ILE:HD13	1.95	0.48
1:B:1454:LEU:HB2	1:B:1456:ASP:HB3	1.96	0.48
1:D:3431:GLU:OE2	1:D:3452:VAL:HG13	2.13	0.48
1:A:334:GLU:O	1:A:338:GLN:HG3	2.14	0.48
1:D:3370:PRO:HG2	1:D:3384:LEU:HD11	1.96	0.48
1:A:298:ILE:HG22	1:A:300:LYS:CB	2.44	0.48
1:D:3298:ILE:HG21	1:D:3300:LYS:HE3	1.96	0.48
1:A:298:ILE:HG22	1:A:300:LYS:H	1.78	0.47
1:C:2332:LEU:HD12	1:C:2332:LEU:N	2.21	0.47
1:B:1041:THR:O	1:B:1045:ARG:HG3	2.14	0.47
1:D:3194:ARG:HE	1:D:3197:ARG:NE	2.12	0.47
1:A:506:GLU:O	1:A:511:ARG:HB2	2.15	0.47
1:B:1094:LYS:HG3	1:B:1560:SER:O	2.14	0.47
1:B:1075:MSE:HE2	1:B:1080:GLU:OE1	2.14	0.47
1:B:1261:ASN:HA	1:B:1264:ARG:CG	2.45	0.47
1:C:2551:LYS:O	1:C:2555:GLU:HB2	2.15	0.47
1:A:21:ILE:HG22	1:A:23:GLU:H	1.80	0.47
1:A:294:ALA:O	1:A:297:VAL:HG22	2.15	0.47
1:B:1327:MSE:HE3	1:B:1337:ALA:HB1	1.96	0.47
1:B:1110:ILE:N	1:B:1110:ILE:HD12	2.29	0.47
1:D:3261:ASN:ND2	1:D:3264:ARG:HH21	2.12	0.47
1:C:2401:PRO:O	1:C:2405:ARG:HG3	2.15	0.47
1:A:371:GLU:N	1:A:371:GLU:CD	2.68	0.47
1:B:1183:LYS:HE3	1:B:1255:GLU:CD	2.35	0.47
1:B:1332:LEU:CD1	1:B:1332:LEU:H	2.28	0.47
1:C:2061:GLN:HA	1:C:2064:GLN:HE21	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ARG:NH1	1:A:93:GLU:OE1	2.48	0.46
1:B:1306:LYS:HB3	1:B:1386:PRO:HA	1.97	0.46
1:C:2481:CYS:SG	1:C:2531:THR:HG23	2.55	0.46
1:C:2556:ARG:HH11	1:C:2556:ARG:HG3	1.80	0.46
1:B:1289:ALA:CB	1:B:1498:LEU:HD23	2.45	0.46
1:B:1082:TYR:HD2	1:B:1083:ILE:HD12	1.81	0.46
1:B:1302:ILE:HD13	1:B:1305:HIS:CB	2.45	0.46
1:B:1339:LYS:HA	1:B:1367:HIS:CE1	2.50	0.46
1:C:2022:LYS:HZ2	1:C:2022:LYS:HB3	1.80	0.46
1:B:1332:LEU:HD12	1:B:1332:LEU:N	2.30	0.46
1:C:2195:PRO:HG2	6:C:4722:HOH:O	2.16	0.46
1:C:2359:ASP:OD2	1:C:2362:GLN:HG3	2.16	0.46
1:D:3474:VAL:O	1:D:3478:VAL:HG23	2.16	0.46
1:A:33:ARG:HD3	1:A:93:GLU:OE2	2.16	0.46
1:C:2306:LYS:HE3	1:C:2384:LEU:O	2.15	0.46
1:D:3298:ILE:HD11	1:D:3442:LEU:HD11	1.97	0.46
1:D:3300:LYS:HB2	1:D:3300:LYS:HZ2	1.81	0.46
1:A:52:GLY:HA3	1:B:1146:ILE:HG23	1.98	0.45
1:B:1518:ASN:ND2	1:B:1518:ASN:N	2.64	0.45
1:D:3468:VAL:HA	1:D:3471:PHE:CE2	2.51	0.45
1:A:300:LYS:NZ	1:A:387:SER:HB2	2.31	0.45
1:B:1346:LYS:HG2	4:B:1601:NAD:O2B	2.16	0.45
1:C:2538:LYS:N	1:C:2538:LYS:HD2	2.31	0.45
1:D:3302:ILE:HD12	1:D:3305:HIS:CG	2.51	0.45
1:D:3354:ARG:HE	1:D:3358:ILE:CD1	2.29	0.45
1:D:3354:ARG:CZ	1:D:3356:ALA:HB3	2.47	0.45
1:C:2302:ILE:HD13	1:C:2305:HIS:HB2	1.98	0.45
1:D:3058:ILE:HD12	1:D:3058:ILE:N	2.31	0.45
1:B:1298:ILE:O	1:B:1299:SER:HB2	2.17	0.45
1:C:2165:ARG:NE	1:C:2165:ARG:O	2.50	0.45
1:C:2340:LYS:C	1:C:2341:ILE:HD12	2.37	0.45
1:A:332:LEU:HB3	1:A:336:GLU:HG3	1.97	0.45
1:A:363:GLU:HB3	1:A:364:PRO:HD3	1.99	0.45
1:C:2240:LYS:NZ	1:C:2244:ASP:OD2	2.48	0.45
1:C:2314:GLU:HB2	4:C:2601:NAD:O1N	2.17	0.45
1:D:3535:TYR:CE2	1:D:3545:GLU:HG3	2.52	0.45
1:A:23:GLU:HA	1:A:23:GLU:OE1	2.17	0.45
1:A:298:ILE:HG22	1:A:300:LYS:HB3	1.98	0.45
1:A:183:LYS:HE3	1:A:255:GLU:CD	2.37	0.45
1:A:21:ILE:CD1	1:A:565:LEU:HD22	2.47	0.45
1:B:1399:PHE:CG	1:B:1427:GLU:HB3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:LEU:HA	1:A:336:GLU:OE2	2.17	0.45
1:C:2528:ILE:O	1:C:2532:GLU:HG3	2.17	0.45
1:B:1397:ARG:HA	1:B:1427:GLU:O	2.17	0.44
1:C:2083:ILE:HD11	1:C:2126:ILE:HD12	1.99	0.44
6:B:4599:HOH:O	1:D:3024:LYS:HE3	2.17	0.44
1:A:352:LYS:NZ	1:A:367:HIS:HA	2.31	0.44
1:C:2042:LEU:O	1:C:2046:GLN:HG3	2.17	0.44
1:D:3137:ILE:HD13	1:D:3137:ILE:O	2.17	0.44
1:B:1261:ASN:HA	1:B:1264:ARG:HG2	1.98	0.44
1:B:1517:ALA:C	1:B:1518:ASN:HD22	2.20	0.44
1:D:3163:GLY:HA2	1:D:3166:ILE:HD11	1.99	0.44
1:A:314:GLU:HB2	4:A:601:NAD:O1N	2.18	0.44
1:B:1308:LEU:HB3	1:B:1389:ILE:HD12	1.99	0.44
1:C:2085:ILE:HD12	1:C:2085:ILE:C	2.37	0.44
1:C:2085:ILE:HD11	1:C:2111:VAL:CG1	2.47	0.44
1:B:1535:TYR:CE2	1:B:1545:GLU:HG3	2.53	0.44
1:A:46:GLN:HG2	1:A:51:GLN:HG3	2.00	0.44
1:D:3358:ILE:HG23	1:D:3362:GLN:HB2	2.00	0.44
6:A:4359:HOH:O	1:C:2022:LYS:HE2	2.17	0.44
1:C:2075:MSE:HE1	1:C:2084:TYR:CG	2.52	0.44
1:C:2287:ALA:O	1:C:2291:LEU:HD13	2.18	0.44
1:D:3307:ILE:HD12	1:D:3388:THR:HB	2.00	0.44
1:C:2120:CYS:O	1:C:2175:TYR:HB3	2.18	0.44
1:D:3040:PHE:HE2	1:D:3565:LEU:HD12	1.82	0.44
1:D:3332:LEU:H	1:D:3332:LEU:CD1	2.28	0.44
1:A:214:LYS:HE3	6:A:4595:HOH:O	2.18	0.43
1:A:359:ASP:OD2	1:A:362:GLN:HG3	2.17	0.43
1:C:2085:ILE:HG13	1:C:2086:MSE:N	2.33	0.43
1:A:298:ILE:C	1:A:300:LYS:H	2.22	0.43
1:B:1378:GLU:OE1	1:B:1402:ASP:HB3	2.18	0.43
1:D:3023:GLU:CG	1:D:3027:PRO:HB2	2.48	0.43
1:A:165:ARG:NE	1:A:165:ARG:O	2.51	0.43
1:A:381:VAL:HG13	1:A:407:MSE:CE	2.40	0.43
1:B:1507:LEU:H	1:B:1507:LEU:HD12	1.83	0.43
1:C:2177:MSE:O	1:C:2180:PRO:HD2	2.18	0.43
1:D:3021:ILE:HG22	1:D:3023:GLU:H	1.83	0.43
1:B:1374:PRO:HG3	1:B:1383:ILE:HG13	2.00	0.43
1:B:1506:GLU:OE2	1:B:1515:PRO:HD3	2.17	0.43
1:D:3066:LEU:HD22	1:D:3070:ARG:NE	2.32	0.43
1:D:3307:ILE:HD13	1:D:3388:THR:HB	2.00	0.43
1:C:2150:TRP:CE2	1:C:2199:LEU:HD13	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3042:LEU:O	1:D:3046:GLN:HG3	2.18	0.43
1:D:3302:ILE:HG21	1:D:3332:LEU:HD11	2.01	0.43
1:B:1075:MSE:CE	6:B:4694:HOH:O	2.66	0.43
1:B:1208:ASP:OD2	1:B:1227:ARG:NH2	2.45	0.43
1:B:1454:LEU:C	1:B:1456:ASP:H	2.21	0.43
1:C:2135:ILE:HG12	1:C:2146:ILE:HG21	2.00	0.43
1:A:39:ALA:HA	1:A:59:GLU:O	2.19	0.43
1:A:532:GLU:HG2	1:A:549:LYS:CG	2.38	0.43
1:B:1389:ILE:HG23	1:B:1399:PHE:CE1	2.53	0.43
1:C:2454:LEU:O	1:C:2456:ASP:N	2.52	0.43
1:C:2520:GLN:HE21	1:C:2520:GLN:N	2.08	0.43
1:B:1286:VAL:HG13	1:B:1287:ALA:N	2.34	0.43
1:B:1431:GLU:OE2	1:B:1452:VAL:HG13	2.19	0.43
1:B:1057:LYS:HE2	1:B:1059:GLU:HG2	2.01	0.43
1:B:1401:PRO:HA	1:B:1436:LEU:CD2	2.49	0.43
1:A:137:ILE:HD11	1:A:230:GLN:HB3	2.00	0.42
1:A:380:ALA:O	1:A:384:LEU:HB2	2.19	0.42
1:C:2023:GLU:HG3	1:C:2027:PRO:HB2	2.00	0.42
1:C:2454:LEU:C	1:C:2456:ASP:H	2.22	0.42
1:D:3284:ALA:HA	1:D:3319:ILE:HG12	2.01	0.42
1:D:3408:ALA:HB1	1:D:3440:ARG:NH2	2.34	0.42
1:D:3108:MSE:N	1:D:3109:PRO:CD	2.82	0.42
1:D:3194:ARG:NH1	1:D:3194:ARG:HG2	2.34	0.42
1:A:242:ILE:HG22	1:A:243:THR:N	2.34	0.42
1:A:298:ILE:HG21	1:A:300:LYS:HE2	2.02	0.42
1:B:1041:THR:OG1	1:B:1044:GLU:HG3	2.18	0.42
1:B:1381:VAL:O	1:B:1385:LYS:HA	2.20	0.42
1:C:2094:LYS:HG3	1:C:2560:SER:O	2.20	0.42
1:D:3194:ARG:HA	1:D:3195:PRO:HD3	1.93	0.42
1:C:2264:ARG:HG2	1:C:2264:ARG:HH11	1.84	0.42
1:A:572:TRP:CD1	1:D:3138:SER:HB3	2.55	0.42
1:B:1557:THR:O	1:B:1559:ARG:NH1	2.52	0.42
1:C:2079:LEU:O	1:C:2083:ILE:HG12	2.20	0.42
1:D:3184:LEU:HD12	1:D:3200:PRO:CG	2.49	0.42
1:D:3150:TRP:CE2	1:D:3199:LEU:HD13	2.54	0.42
1:D:3295:GLN:HE22	1:D:3305:HIS:CE1	2.37	0.42
1:D:3377:PHE:O	1:D:3381:VAL:HG23	2.20	0.42
1:A:288:LEU:O	1:A:292:LEU:HD13	2.20	0.42
1:B:1509:GLN:NE2	1:B:1511:ARG:HE	2.17	0.42
1:B:1556:ARG:HH11	1:B:1556:ARG:HG3	1.84	0.42
1:C:2069:HIS:HE1	1:C:2102:ASP:OD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3051:GLN:NE2	1:D:3051:GLN:HA	2.34	0.42
1:D:3320:ALA:O	1:D:3324:VAL:HG23	2.20	0.42
1:C:2358:ILE:HD13	1:C:2366:THR:CG2	2.50	0.42
1:C:2383:ILE:HG22	1:C:2384:LEU:HD12	2.02	0.42
1:C:2186:LEU:HD13	1:C:2468:VAL:CG2	2.50	0.42
1:D:3380:ALA:O	1:D:3384:LEU:HB2	2.20	0.42
1:B:1090:GLU:OE1	1:B:1131:LYS:HG2	2.20	0.41
1:A:184:LEU:O	1:A:187:TYR:HB2	2.19	0.41
1:C:2261:ASN:HB3	1:C:2265:PHE:CE1	2.55	0.41
1:C:2556:ARG:HG3	1:C:2556:ARG:NH1	2.35	0.41
1:D:3399:PHE:CG	1:D:3427:GLU:HB3	2.55	0.41
1:A:140:ARG:HH22	1:A:234:LEU:CA	2.32	0.41
1:C:2273:TYR:O	1:C:2485:HIS:HD2	2.03	0.41
1:C:2297:VAL:CG2	1:C:2298:ILE:N	2.82	0.41
1:A:322:LEU:HA	1:A:322:LEU:HD23	1.91	0.41
1:B:1369:ALA:HA	1:B:1370:PRO:HD3	1.94	0.41
1:C:2125:HIS:HE1	1:C:2215:ASP:OD2	2.02	0.41
1:D:3288:LEU:HD22	1:D:3322:LEU:HG	2.03	0.41
1:D:3328:VAL:HA	1:D:3332:LEU:O	2.21	0.41
1:D:3397:ARG:HA	1:D:3427:GLU:O	2.19	0.41
1:B:1401:PRO:HA	1:B:1436:LEU:HD23	2.03	0.41
1:C:2370:PRO:HG2	1:C:2372:SER:O	2.20	0.41
1:D:3298:ILE:CG2	1:D:3300:LYS:HG3	2.49	0.41
1:B:1150:TRP:CE2	1:B:1199:LEU:HD13	2.55	0.41
1:B:1238:PHE:CE1	1:B:1242:ILE:HG13	2.56	0.41
1:C:2165:ARG:HH21	1:C:2167:LEU:N	2.19	0.41
1:A:468:VAL:HA	1:A:471:PHE:CE2	2.56	0.41
1:C:2161:THR:HA	1:C:2257:PHE:CE1	2.56	0.41
1:C:2085:ILE:CD1	1:C:2096:PHE:HE1	2.30	0.41
1:A:131:LYS:O	1:A:177:MSE:HE3	2.21	0.41
1:A:108:MSE:N	1:A:109:PRO:CD	2.84	0.41
1:A:476:LEU:O	1:A:480:LEU:HG	2.20	0.41
1:B:1150:TRP:HA	1:B:1151:PRO:HD3	1.95	0.41
1:B:1294:ALA:HB1	1:B:1442:LEU:HD13	2.02	0.41
1:C:2454:LEU:C	1:C:2456:ASP:N	2.74	0.41
1:D:3066:LEU:CD2	1:D:3070:ARG:NE	2.83	0.41
1:D:3300:LYS:NZ	1:D:3300:LYS:CB	2.83	0.41
1:D:3412:GLU:O	1:D:3413:ARG:HD2	2.21	0.41
1:A:419:LEU:O	4:A:601:NAD:H2N	2.21	0.41
1:B:1033:ARG:HD2	1:B:1196:ASP:HB3	2.03	0.41
1:B:1042:LEU:O	1:B:1046:GLN:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:3324:VAL:O	1:D:3328:VAL:HG23	2.20	0.41
1:B:1068:PHE:CD2	1:B:1099:ILE:CG1	3.02	0.40
1:B:1301:PRO:HD2	1:B:1304:GLU:CD	2.42	0.40
1:D:3242:ILE:HG21	1:D:3252:ILE:HD11	2.02	0.40
1:B:1422:PRO:CD	1:B:1425:GLN:HE21	2.33	0.40
1:D:3471:PHE:CG	1:D:3472:PRO:HD3	2.56	0.40
1:A:343:MSE:HB2	1:A:350:LEU:HG	2.04	0.40
1:A:354:ARG:CZ	1:A:356:ALA:HB3	2.51	0.40
1:A:405:ARG:NH2	6:A:4879:HOH:O	2.52	0.40
1:B:1320:ALA:O	1:B:1324:VAL:HG23	2.21	0.40
1:D:3177:MSE:O	1:D:3180:PRO:HD2	2.22	0.40
1:D:3227:ARG:HG2	1:D:3227:ARG:HH11	1.85	0.40
1:D:3559:ARG:HG3	1:D:3561:GLU:OE1	2.22	0.40
1:A:528:ILE:O	1:A:532:GLU:HG3	2.21	0.40
1:B:1194:ARG:NH1	1:B:1197:ARG:NH2	2.70	0.40
1:B:1140:ARG:HH21	1:B:1230:GLN:HG2	1.85	0.40
1:B:1435:THR:HA	1:B:1454:LEU:HD22	2.03	0.40
1:B:1542:ARG:C	1:B:1542:ARG:HD3	2.42	0.40
1:C:2235:ILE:O	1:C:2239:MSE:HG2	2.21	0.40
1:D:3294:ALA:O	1:D:3298:ILE:HG12	2.21	0.40
1:B:1351:VAL:HA	1:B:1367:HIS:O	2.22	0.40
1:C:2333:SER:OG	1:C:2336:GLU:HG3	2.22	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	551/564 (98%)	531 (96%)	20 (4%)	0	100	100
1	B	551/564 (98%)	528 (96%)	22 (4%)	1 (0%)	47	49
1	C	551/564 (98%)	529 (96%)	20 (4%)	2 (0%)	34	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	551/564 (98%)	527 (96%)	22 (4%)	2 (0%)	34	32
All	All	2204/2256 (98%)	2115 (96%)	84 (4%)	5 (0%)	47	49

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	3397	ARG
1	C	2332	LEU
1	C	2455	THR
1	B	1300	LYS
1	D	3392	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	469/465 (101%)	451 (96%)	18 (4%)	33	34
1	B	469/465 (101%)	455 (97%)	14 (3%)	41	44
1	C	469/465 (101%)	453 (97%)	16 (3%)	37	39
1	D	469/465 (101%)	449 (96%)	20 (4%)	29	29
All	All	1876/1860 (101%)	1808 (96%)	68 (4%)	35	36

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	LEU
1	A	99	ILE
1	A	165	ARG
1	A	169	LEU
1	A	221	LEU
1	A	242	ILE
1	A	251	LEU
1	A	291	LEU
1	A	306	LYS

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Mol	Chain	Res	Type
1	A	322	LEU
1	A	339	LYS
1	A	357	LYS
1	A	384	LEU
1	A	492	LEU
1	A	502	LEU
1	A	505	GLU
1	A	529	LYS
1	A	559	ARG
1	B	1021	ILE
1	B	1043	GLN
1	B	1070	ARG
1	B	1114	PRO
1	B	1123	TYR
1	B	1165	ARG
1	B	1169	LEU
1	B	1251	LEU
1	B	1302	ILE
1	B	1357	LYS
1	B	1371	GLU
1	B	1436	LEU
1	B	1492	LEU
1	B	1502	LEU
1	C	2070	ARG
1	C	2085	ILE
1	C	2094	LYS
1	C	2099	ILE
1	C	2123	TYR
1	C	2165	ARG
1	C	2221	LEU
1	C	2232	ASP
1	C	2251	LEU
1	C	2297	VAL
1	C	2302	ILE
1	C	2436	LEU
1	C	2492	LEU
1	C	2502	LEU
1	C	2520	GLN
1	C	2559	ARG
1	D	3051	GLN
1	D	3066	LEU
1	D	3070	ARG

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Mol	Chain	Res	Type
1	D	3074	LYS
1	D	3085	ILE
1	D	3099	ILE
1	D	3123	TYR
1	D	3133	LEU
1	D	3137	ILE
1	D	3165	ARG
1	D	3221	LEU
1	D	3363	GLU
1	D	3492	LEU
1	D	3502	LEU
1	D	3507	LEU
1	D	3519	ILE
1	D	3520	GLN
1	D	3559	ARG
1	D	3571	GLU
1	D	3572	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (52) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	51	GLN
1	A	64	GLN
1	A	69	HIS
1	A	230	GLN
1	A	261	ASN
1	A	330	ASN
1	A	425	GLN
1	A	482	ASN
1	A	485	HIS
1	A	518	ASN
1	B	1043	GLN
1	B	1064	GLN
1	B	1069	HIS
1	B	1101	GLN
1	B	1125	HIS
1	B	1154	HIS
1	B	1229	GLN
1	B	1230	GLN
1	B	1261	ASN
1	B	1305	HIS

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Mol	Chain	Res	Type
1	B	1330	ASN
1	B	1335	GLN
1	B	1338	GLN
1	B	1425	GLN
1	B	1482	ASN
1	B	1485	HIS
1	B	1509	GLN
1	B	1518	ASN
1	B	1520	GLN
1	C	2043	GLN
1	C	2051	GLN
1	C	2064	GLN
1	C	2069	HIS
1	C	2125	HIS
1	C	2229	GLN
1	C	2230	GLN
1	C	2261	ASN
1	C	2425	GLN
1	C	2482	ASN
1	C	2485	HIS
1	C	2509	GLN
1	C	2518	ASN
1	C	2520	GLN
1	D	3051	GLN
1	D	3064	GLN
1	D	3069	HIS
1	D	3122	GLN
1	D	3230	GLN
1	D	3261	ASN
1	D	3482	ASN
1	D	3520	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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 4 are monoatomic - leaving 16 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	FUM	D	3700	-	1,7,7	1.59	0	2,8,8	0.57	0
4	NAD	B	1601	-	42,48,48	1.96	11 (26%)	50,73,73	1.32	3 (6%)
5	FUM	A	700	-	1,7,7	1.81	0	2,8,8	0.44	0
4	NAD	A	601	-	42,48,48	1.83	11 (26%)	50,73,73	1.30	3 (6%)
3	PYR	B	1603	2	2,5,5	1.69	1 (50%)	2,6,6	0.17	0
5	FUM	B	1700	-	1,7,7	1.73	0	2,8,8	0.45	0
4	NAD	D	3601	-	42,48,48	1.92	10 (23%)	50,73,73	1.31	4 (8%)
3	PYR	A	603	2	2,5,5	1.77	1 (50%)	2,6,6	0.12	0
4	NAD	D	3602	-	42,48,48	2.05	10 (23%)	50,73,73	1.44	6 (12%)
5	FUM	C	2700	-	1,7,7	1.80	0	2,8,8	0.30	0
4	NAD	B	1602	-	42,48,48	2.08	11 (26%)	50,73,73	1.43	5 (10%)
4	NAD	C	2601	-	42,48,48	1.86	11 (26%)	50,73,73	1.30	2 (4%)
3	PYR	C	2603	2	2,5,5	1.66	1 (50%)	2,6,6	0.12	0
4	NAD	C	2602	-	42,48,48	2.01	9 (21%)	50,73,73	1.43	6 (12%)
4	NAD	A	602	-	42,48,48	2.09	10 (23%)	50,73,73	1.50	6 (12%)
3	PYR	D	3603	2	2,5,5	1.67	1 (50%)	2,6,6	0.16	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
5	FUM	D	3700	-	-	0/0/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAD	B	1601	-	-	2/26/62/62	0/5/5/5
5	FUM	A	700	-	-	0/0/5/5	-
4	NAD	A	601	-	-	4/26/62/62	0/5/5/5
3	PYR	B	1603	2	-	0/0/4/4	-
5	FUM	B	1700	-	-	0/0/5/5	-
4	NAD	D	3601	-	-	2/26/62/62	0/5/5/5
3	PYR	A	603	2	-	0/0/4/4	-
4	NAD	D	3602	-	-	9/26/62/62	0/5/5/5
5	FUM	C	2700	-	-	0/0/5/5	-
4	NAD	B	1602	-	-	1/26/62/62	0/5/5/5
4	NAD	C	2601	-	-	5/26/62/62	0/5/5/5
3	PYR	C	2603	2	-	0/0/4/4	-
4	NAD	C	2602	-	-	6/26/62/62	0/5/5/5
4	NAD	A	602	-	-	5/26/62/62	0/5/5/5
3	PYR	D	3603	2	-	0/0/4/4	-

All (87) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1602	NAD	C2N-N1N	8.14	1.44	1.35
4	A	602	NAD	C2N-N1N	7.62	1.44	1.35
4	D	3602	NAD	C2N-N1N	7.24	1.43	1.35
4	C	2602	NAD	C2N-N1N	7.12	1.43	1.35
4	B	1601	NAD	C2N-N1N	6.36	1.42	1.35
4	D	3601	NAD	C2N-N1N	6.29	1.42	1.35
4	A	601	NAD	C2N-N1N	5.96	1.42	1.35
4	C	2601	NAD	C2N-N1N	5.91	1.42	1.35
4	C	2602	NAD	O4D-C1D	4.52	1.47	1.41
4	D	3602	NAD	O4D-C1D	4.51	1.47	1.41
4	A	602	NAD	O4D-C1D	4.47	1.47	1.41
4	B	1602	NAD	O4B-C1B	4.41	1.47	1.41
4	A	602	NAD	O4B-C1B	4.17	1.46	1.41
4	D	3602	NAD	O4B-C1B	4.17	1.46	1.41
4	B	1601	NAD	O4B-C1B	4.00	1.46	1.41
4	A	602	NAD	C6N-N1N	3.87	1.44	1.35
4	B	1602	NAD	O4D-C1D	3.85	1.46	1.41
4	C	2602	NAD	C6N-N1N	3.80	1.44	1.35
4	D	3601	NAD	O4B-C1B	3.78	1.46	1.41
4	D	3602	NAD	C6N-N1N	3.77	1.44	1.35
4	B	1601	NAD	C6N-N1N	3.67	1.44	1.35
4	D	3601	NAD	C2A-N3A	3.66	1.38	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	2601	NAD	C6N-N1N	3.63	1.44	1.35
4	D	3601	NAD	C6N-N1N	3.61	1.44	1.35
4	B	1601	NAD	C2A-N3A	3.60	1.37	1.32
4	C	2602	NAD	O4B-C1B	3.51	1.46	1.41
4	A	601	NAD	C6N-N1N	3.48	1.43	1.35
4	A	601	NAD	C2A-N3A	3.47	1.37	1.32
4	A	602	NAD	C2A-N3A	3.37	1.37	1.32
4	D	3602	NAD	C2A-N3A	3.36	1.37	1.32
4	D	3601	NAD	C3N-C7N	3.33	1.55	1.50
4	A	601	NAD	O4D-C1D	3.31	1.45	1.41
4	D	3601	NAD	O4D-C1D	3.31	1.45	1.41
4	B	1602	NAD	C2A-N3A	3.27	1.37	1.32
4	B	1602	NAD	C6N-N1N	3.24	1.43	1.35
4	C	2601	NAD	C2A-N3A	3.23	1.37	1.32
4	B	1602	NAD	C3N-C7N	3.23	1.55	1.50
4	A	602	NAD	C3N-C7N	3.21	1.55	1.50
4	C	2601	NAD	O4B-C1B	3.20	1.45	1.41
4	C	2602	NAD	C3N-C7N	3.17	1.55	1.50
4	D	3602	NAD	C3N-C7N	3.16	1.55	1.50
4	B	1601	NAD	C3N-C7N	3.12	1.55	1.50
4	C	2602	NAD	C2A-N3A	3.02	1.37	1.32
4	C	2601	NAD	C2B-C1B	-2.98	1.49	1.53
4	C	2601	NAD	C3N-C7N	2.96	1.55	1.50
4	C	2602	NAD	C5A-C4A	-2.83	1.33	1.40
4	A	601	NAD	C2B-C1B	-2.82	1.49	1.53
4	D	3601	NAD	C5A-C4A	-2.80	1.33	1.40
4	A	601	NAD	C3N-C7N	2.78	1.54	1.50
4	B	1601	NAD	O4D-C1D	2.76	1.44	1.41
4	A	601	NAD	C5A-C4A	-2.75	1.33	1.40
4	B	1601	NAD	C5A-C4A	-2.70	1.33	1.40
4	A	602	NAD	C5A-C4A	-2.69	1.33	1.40
4	B	1602	NAD	C5A-C4A	-2.69	1.33	1.40
4	C	2601	NAD	C5A-C4A	-2.65	1.33	1.40
4	B	1601	NAD	C2D-C1D	-2.59	1.49	1.53
4	D	3602	NAD	C5A-C4A	-2.58	1.34	1.40
4	D	3601	NAD	C2D-C1D	-2.55	1.49	1.53
4	A	602	NAD	C2B-C1B	-2.54	1.49	1.53
4	B	1601	NAD	C5A-N7A	-2.52	1.30	1.39
4	C	2601	NAD	O4D-C1D	2.50	1.44	1.41
4	D	3601	NAD	C5A-N7A	-2.44	1.30	1.39
4	A	601	NAD	O4B-C1B	2.40	1.44	1.41
4	C	2601	NAD	C5A-N7A	-2.39	1.31	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	3602	NAD	C5A-N7A	-2.34	1.31	1.39
4	A	601	NAD	C2D-C1D	-2.32	1.50	1.53
4	C	2601	NAD	C2D-C1D	-2.32	1.50	1.53
4	C	2602	NAD	C5A-N7A	-2.30	1.31	1.39
4	A	602	NAD	C5A-N7A	-2.29	1.31	1.39
3	A	603	PYR	O3-C2	2.29	1.29	1.22
3	B	1603	PYR	O3-C2	2.27	1.29	1.22
4	B	1602	NAD	C5A-N7A	-2.24	1.31	1.39
4	B	1601	NAD	C2A-N1A	2.24	1.38	1.33
4	B	1601	NAD	C2B-C1B	-2.23	1.50	1.53
3	D	3603	PYR	O3-C2	2.20	1.29	1.22
4	A	601	NAD	C5A-N7A	-2.18	1.31	1.39
4	D	3602	NAD	C4N-C3N	2.18	1.43	1.39
4	C	2602	NAD	C4N-C3N	2.17	1.43	1.39
3	C	2603	PYR	O3-C2	2.13	1.29	1.22
4	C	2601	NAD	C2A-N1A	2.10	1.37	1.33
4	A	602	NAD	C4N-C3N	2.10	1.42	1.39
4	B	1602	NAD	C4N-C3N	2.10	1.42	1.39
4	D	3602	NAD	C2A-N1A	2.09	1.37	1.33
4	A	601	NAD	C2A-N1A	2.07	1.37	1.33
4	B	1602	NAD	C2B-C1B	-2.03	1.50	1.53
4	B	1602	NAD	C2A-N1A	2.03	1.37	1.33
4	D	3601	NAD	C2B-C1B	-2.03	1.50	1.53

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	601	NAD	N3A-C2A-N1A	-5.25	120.48	128.68
4	A	602	NAD	N3A-C2A-N1A	-5.14	120.64	128.68
4	C	2601	NAD	N3A-C2A-N1A	-5.13	120.65	128.68
4	B	1602	NAD	N3A-C2A-N1A	-5.12	120.67	128.68
4	D	3602	NAD	N3A-C2A-N1A	-5.12	120.67	128.68
4	B	1601	NAD	N3A-C2A-N1A	-5.11	120.69	128.68
4	D	3601	NAD	N3A-C2A-N1A	-5.10	120.71	128.68
4	C	2602	NAD	N3A-C2A-N1A	-5.09	120.73	128.68
4	A	602	NAD	C4A-C5A-N7A	4.24	113.82	109.40
4	B	1602	NAD	C4A-C5A-N7A	4.24	113.81	109.40
4	B	1601	NAD	C4A-C5A-N7A	4.20	113.78	109.40
4	D	3601	NAD	C4A-C5A-N7A	4.17	113.75	109.40
4	D	3602	NAD	C4A-C5A-N7A	4.16	113.73	109.40
4	A	601	NAD	C4A-C5A-N7A	4.15	113.72	109.40
4	A	602	NAD	C3D-C2D-C1D	4.14	107.21	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	2602	NAD	C4A-C5A-N7A	4.12	113.70	109.40
4	C	2601	NAD	C4A-C5A-N7A	4.07	113.64	109.40
4	B	1602	NAD	C3D-C2D-C1D	3.55	106.32	100.98
4	D	3602	NAD	C3D-C2D-C1D	3.54	106.31	100.98
4	C	2602	NAD	C3D-C2D-C1D	3.48	106.22	100.98
4	A	602	NAD	C6N-N1N-C2N	-2.92	119.31	121.97
4	C	2602	NAD	C3B-C2B-C1B	2.82	105.22	100.98
4	B	1602	NAD	C3B-C2B-C1B	2.78	105.16	100.98
4	D	3602	NAD	C6N-N1N-C2N	-2.53	119.66	121.97
4	C	2602	NAD	C6N-N1N-C2N	-2.52	119.68	121.97
4	D	3602	NAD	C3B-C2B-C1B	2.51	104.75	100.98
4	B	1602	NAD	C6N-N1N-C2N	-2.49	119.70	121.97
4	A	602	NAD	C3B-C2B-C1B	2.46	104.68	100.98
4	B	1601	NAD	C3D-C2D-C1D	2.30	104.43	100.98
4	A	602	NAD	C2D-C3D-C4D	2.24	107.00	102.64
4	D	3602	NAD	C2D-C3D-C4D	2.15	106.83	102.64
4	D	3601	NAD	C3D-C2D-C1D	2.13	104.18	100.98
4	C	2602	NAD	C2D-C3D-C4D	2.12	106.75	102.64
4	D	3601	NAD	C3B-C2B-C1B	2.10	104.14	100.98
4	A	601	NAD	C3D-C2D-C1D	2.08	104.11	100.98

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1601	NAD	O4D-C1D-N1N-C6N
4	A	602	NAD	C5D-O5D-PN-O1N
4	A	602	NAD	C5D-O5D-PN-O2N
4	A	601	NAD	O4D-C1D-N1N-C2N
4	A	601	NAD	O4D-C1D-N1N-C6N
4	D	3601	NAD	O4D-C1D-N1N-C6N
4	D	3602	NAD	C5B-O5B-PA-O2A
4	D	3602	NAD	C5B-O5B-PA-O3
4	C	2601	NAD	O4D-C1D-N1N-C2N
4	C	2601	NAD	O4D-C1D-N1N-C6N
4	C	2602	NAD	C5B-O5B-PA-O3
4	C	2602	NAD	C3D-C4D-C5D-O5D
4	D	3602	NAD	C3D-C4D-C5D-O5D
4	C	2602	NAD	O4D-C4D-C5D-O5D
4	D	3602	NAD	O4D-C4D-C5D-O5D
4	C	2602	NAD	C4D-C5D-O5D-PN
4	D	3602	NAD	PA-O3-PN-O5D

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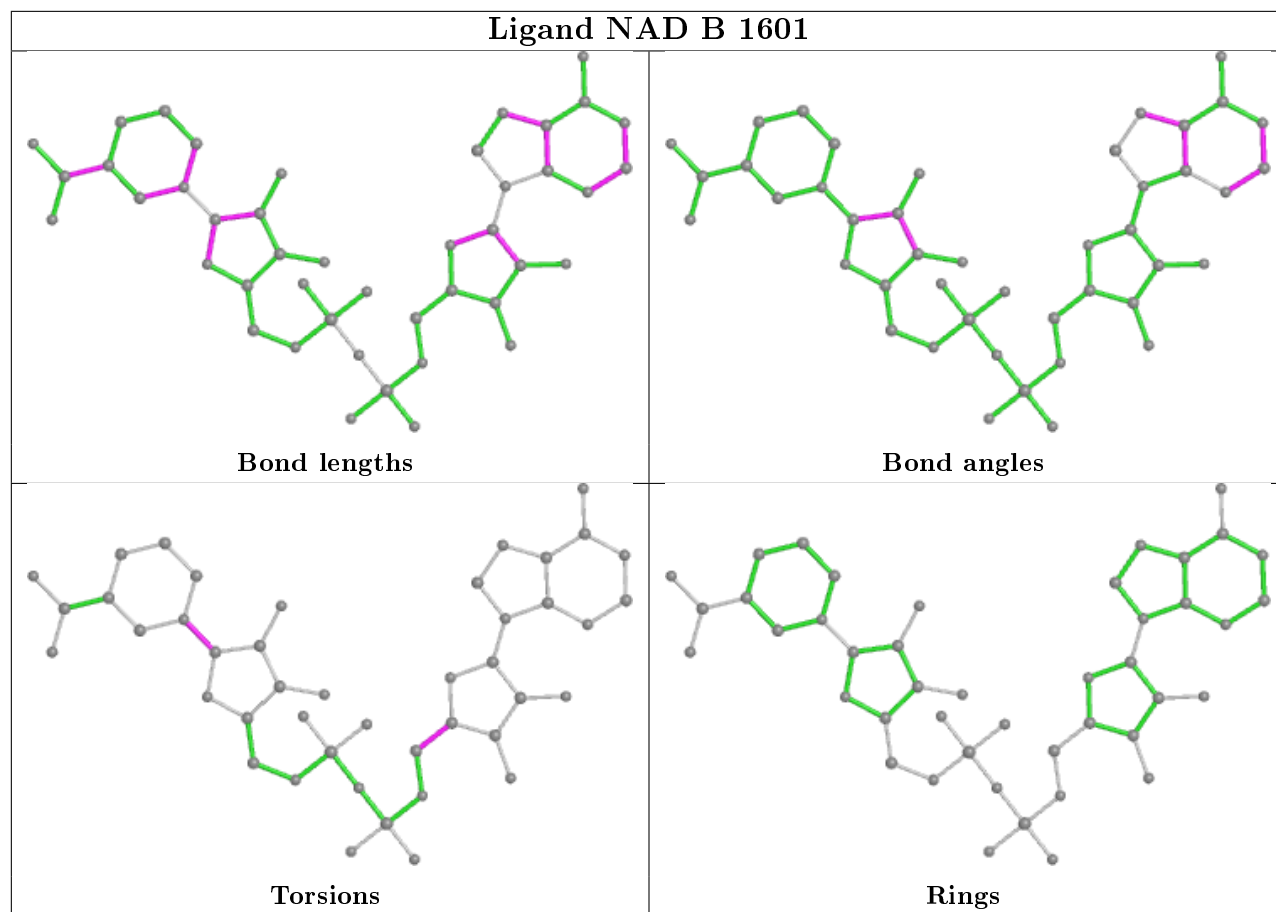
Mol	Chain	Res	Type	Atoms
4	C	2602	NAD	PA-O3-PN-O5D
4	D	3602	NAD	C4D-C5D-O5D-PN
4	A	602	NAD	C5B-O5B-PA-O3
4	A	602	NAD	C5B-O5B-PA-O2A
4	D	3602	NAD	C5D-O5D-PN-O2N
4	C	2602	NAD	C5B-O5B-PA-O2A
4	D	3602	NAD	PA-O3-PN-O1N
4	A	602	NAD	C5D-O5D-PN-O3
4	A	601	NAD	C2D-C1D-N1N-C6N
4	D	3602	NAD	C5D-O5D-PN-O3
4	C	2601	NAD	C2D-C1D-N1N-C2N
4	C	2601	NAD	C2D-C1D-N1N-C6N
4	B	1601	NAD	O4B-C4B-C5B-O5B
4	A	601	NAD	O4B-C4B-C5B-O5B
4	B	1602	NAD	PN-O3-PA-O1A
4	D	3601	NAD	O4B-C4B-C5B-O5B
4	C	2601	NAD	O4B-C4B-C5B-O5B

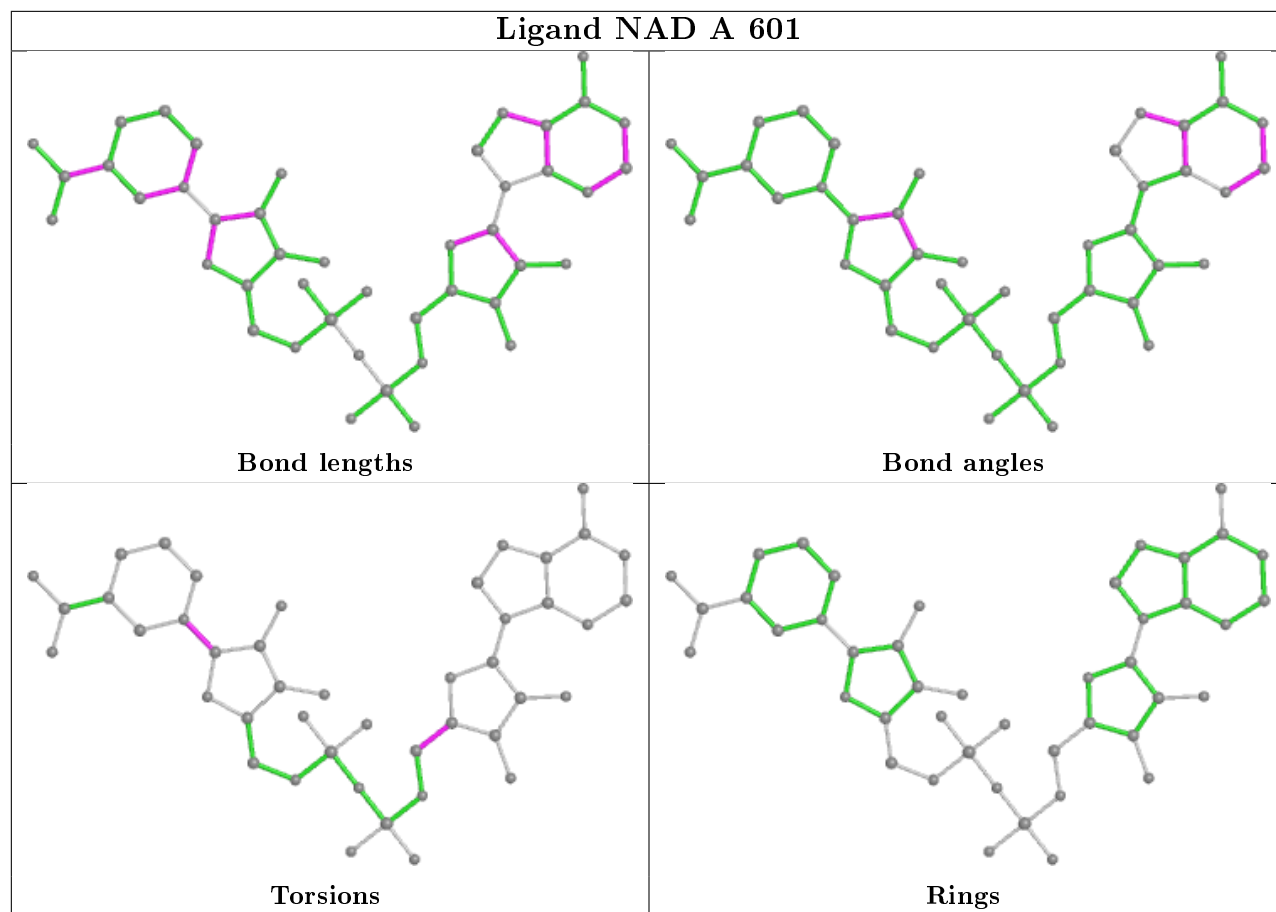
There are no ring outliers.

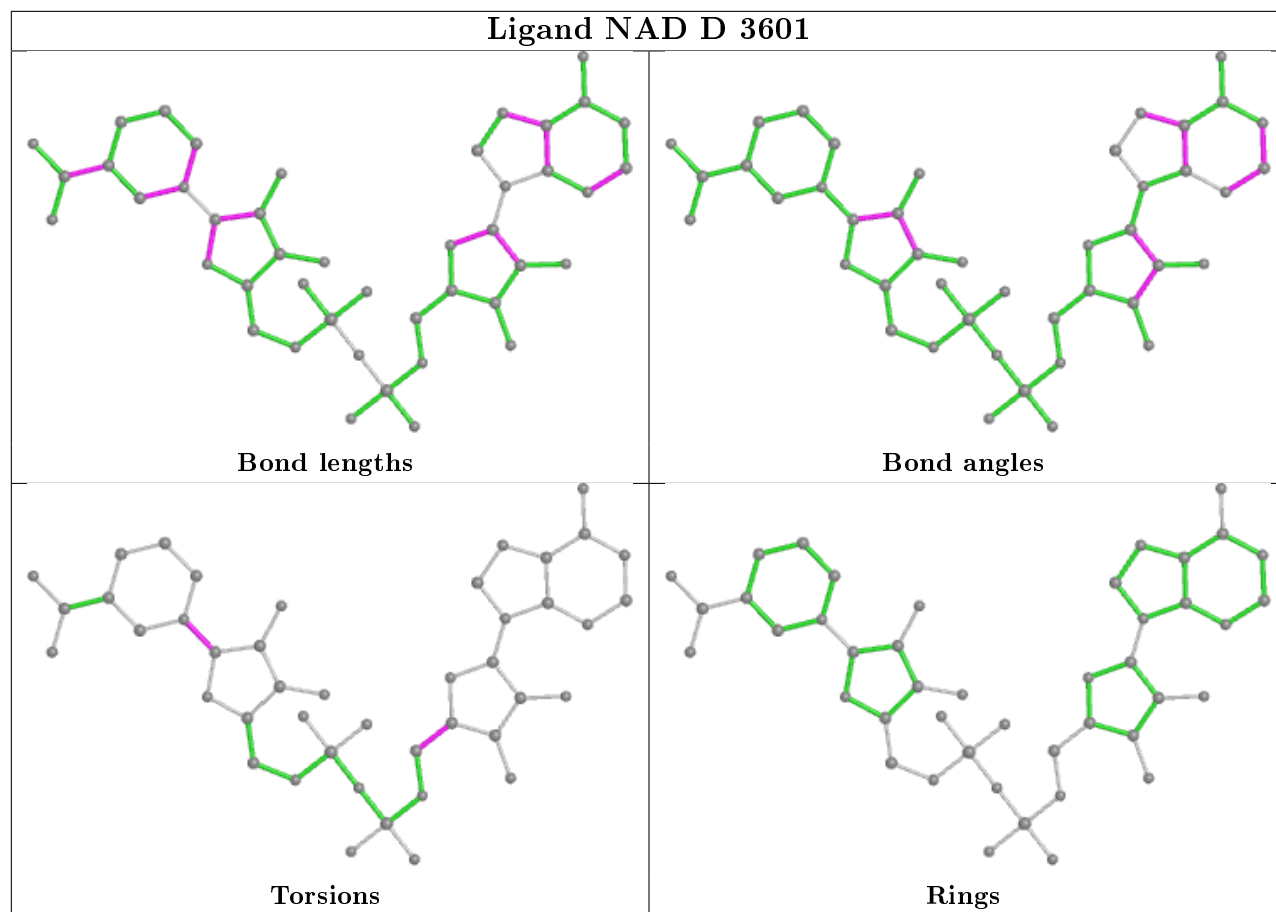
7 monomers are involved in 10 short contacts:

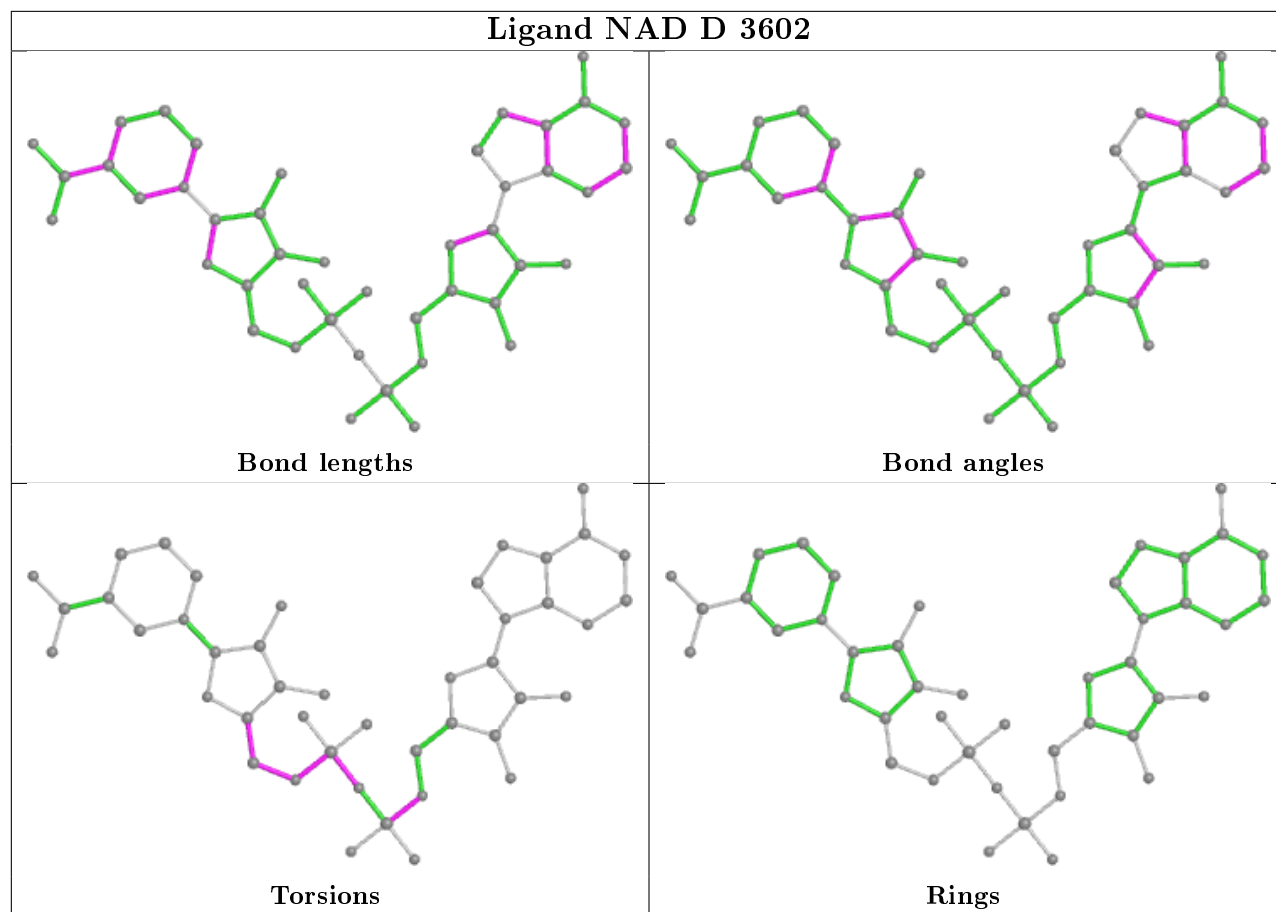
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1601	NAD	1	0
4	A	601	NAD	2	0
3	B	1603	PYR	2	0
4	D	3601	NAD	1	0
3	A	603	PYR	1	0
4	C	2601	NAD	1	0
3	D	3603	PYR	2	0

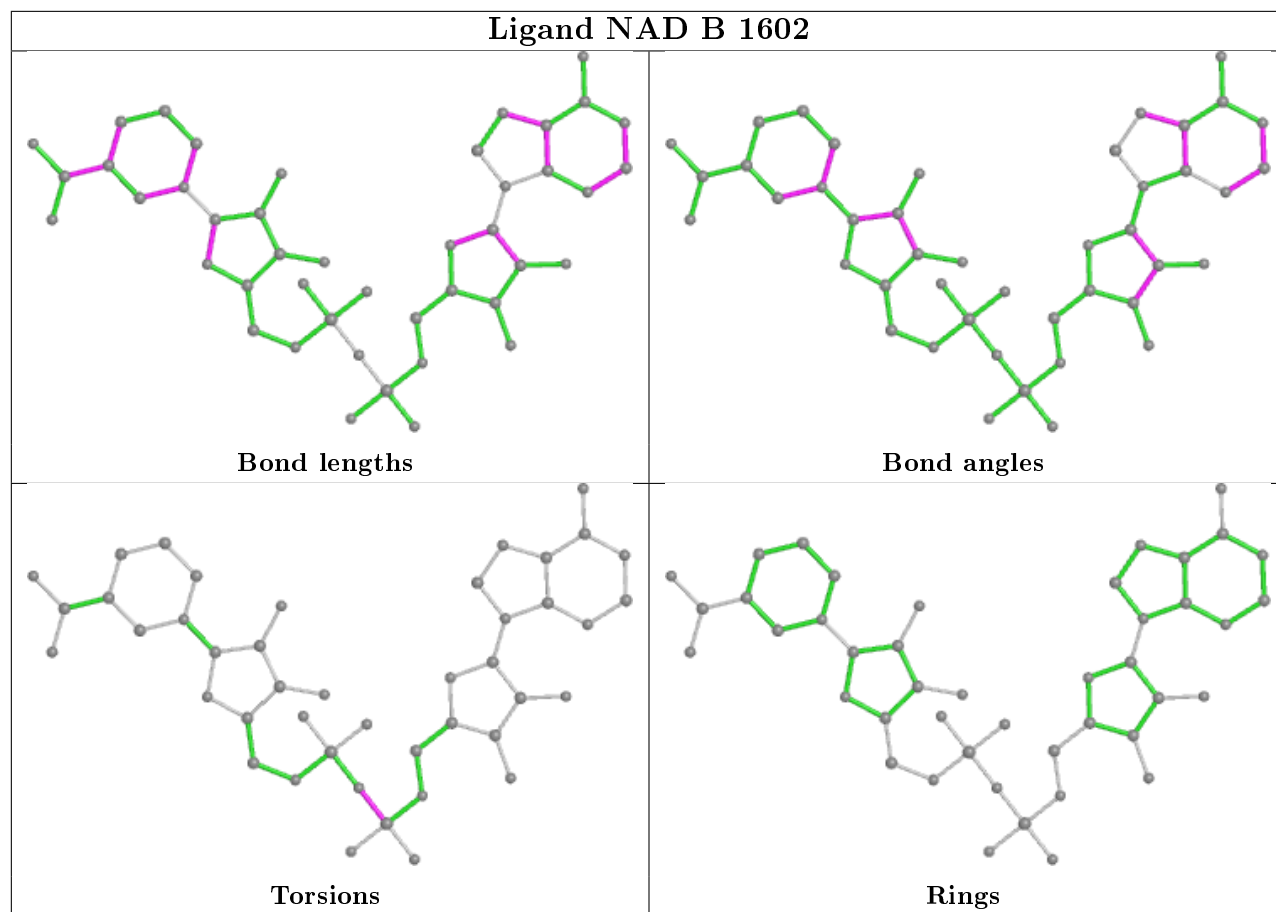
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

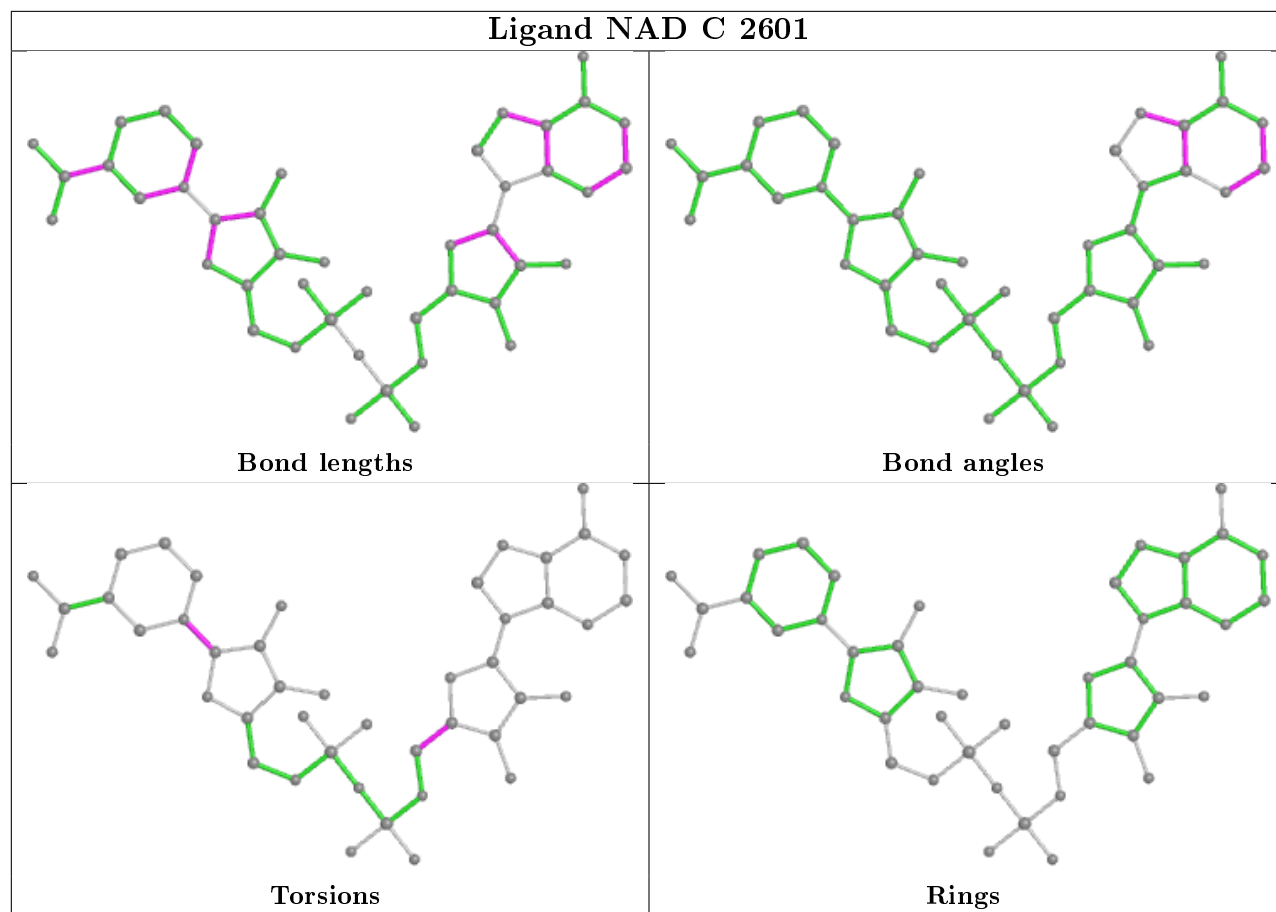


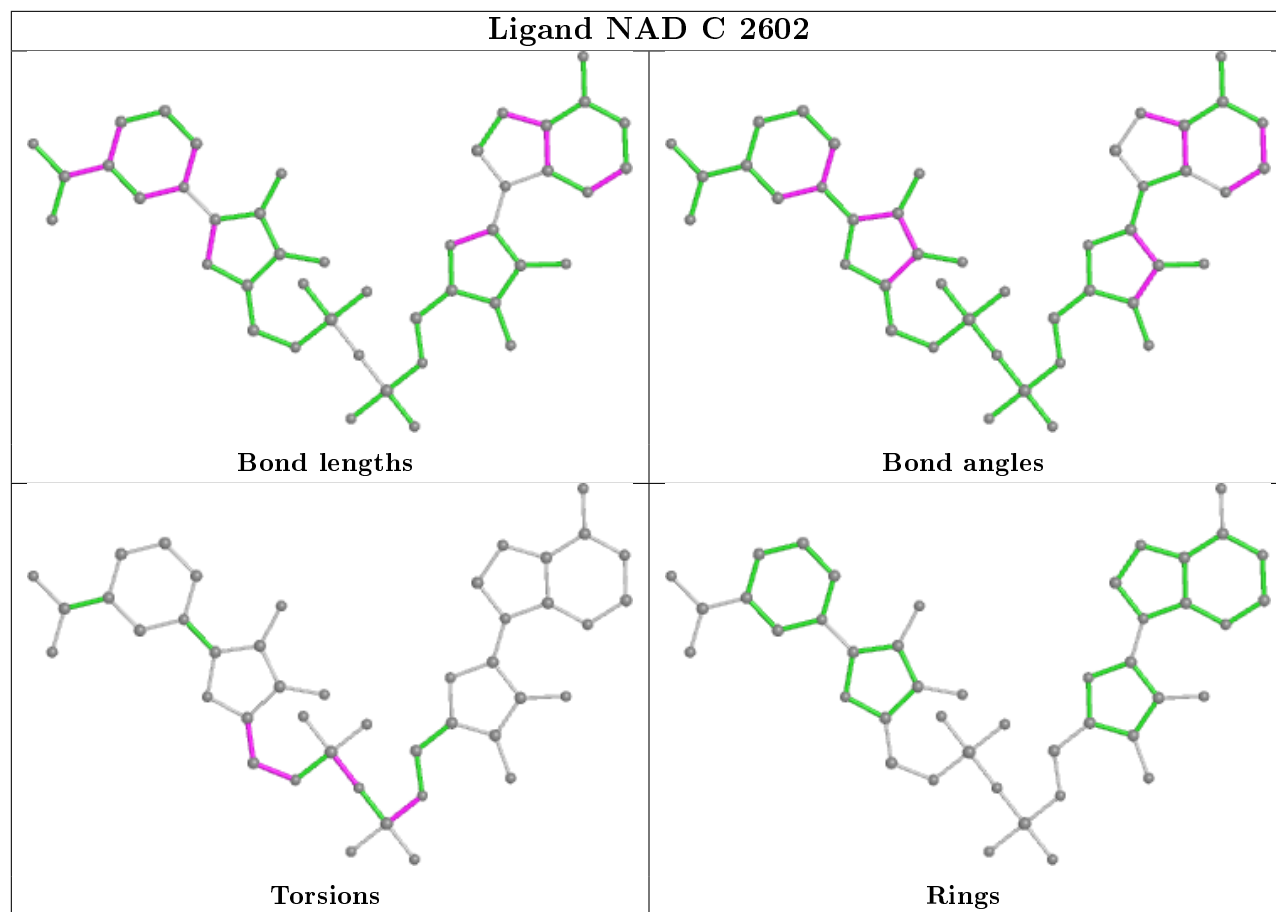


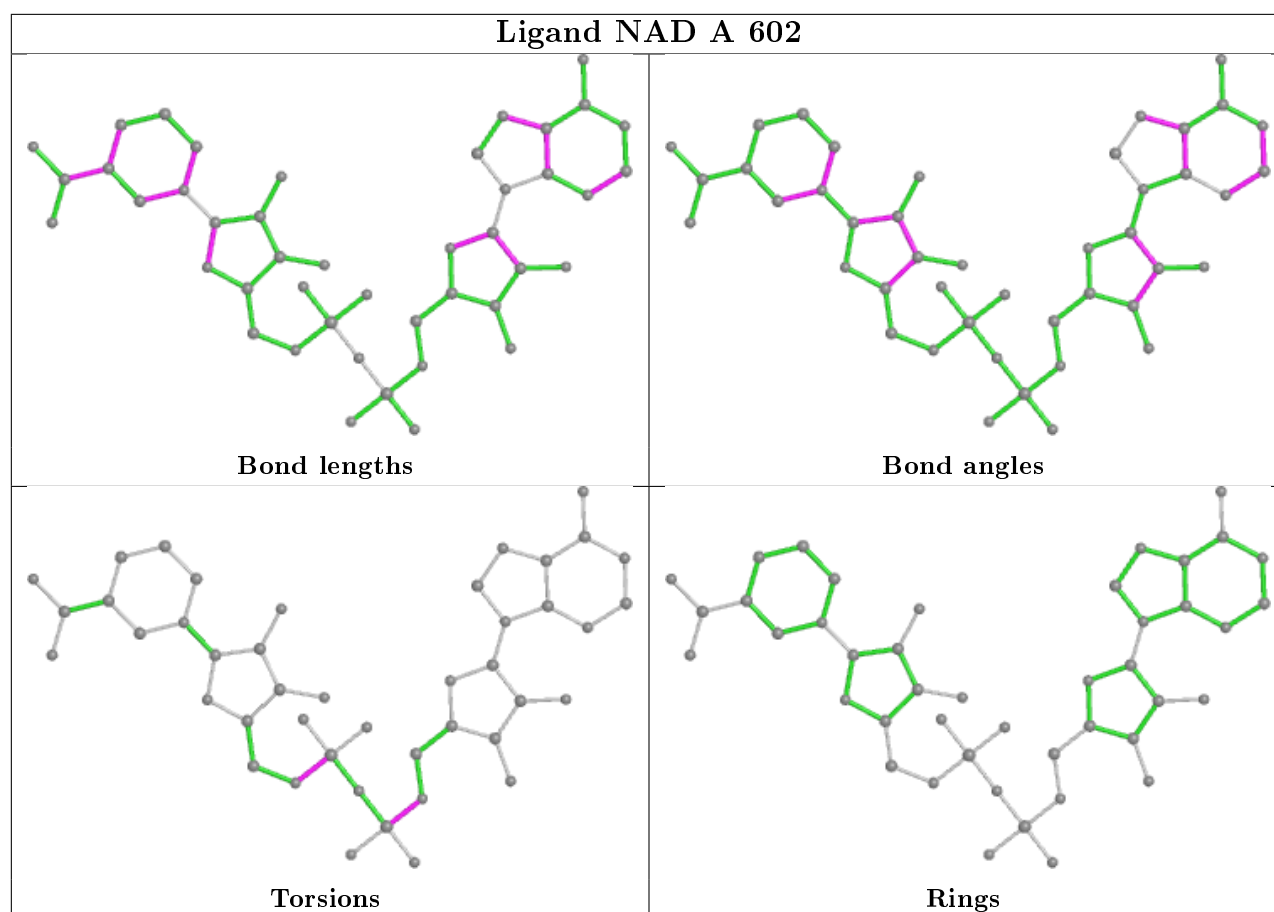












5.7 Other polymers [i](#)

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	539/564 (95%)	-0.02	17 (3%) 47 54	14, 26, 49, 70	0
1	B	539/564 (95%)	0.14	24 (4%) 33 38	16, 29, 56, 76	0
1	C	539/564 (95%)	-0.14	10 (1%) 66 71	15, 24, 45, 67	0
1	D	539/564 (95%)	0.08	24 (4%) 33 38	16, 28, 53, 76	0
All	All	2156/2256 (95%)	0.01	75 (3%) 44 50	14, 27, 51, 76	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1303	SER	10.4
1	B	1301	PRO	8.5
1	B	1304	GLU	6.9
1	A	304	GLU	6.7
1	A	303	SER	5.7
1	A	301	PRO	5.4
1	B	1300	LYS	5.2
1	A	300	LYS	5.1
1	D	3300	LYS	5.0
1	C	2303	SER	4.8
1	D	3303	SER	4.6
1	D	3301	PRO	4.4
1	B	1331	GLY	4.3
1	B	1330	ASN	4.1
1	D	3302	ILE	4.1
1	D	3304	GLU	4.0
1	B	1332	LEU	3.9
1	D	3331	GLY	3.7
1	B	1302	ILE	3.7
1	A	22	LYS	3.6
1	B	1373	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	3299	SER	3.6
1	D	3021	ILE	3.6
1	C	2302	ILE	3.5
1	B	1390	ILE	3.5
1	D	3353	GLY	3.5
1	B	1371	GLU	3.4
1	C	2301	PRO	3.3
1	D	3298	ILE	3.3
1	C	2573	PRO	3.3
1	A	302	ILE	3.1
1	B	1573	PRO	3.1
1	D	3305	HIS	2.9
1	B	1505	GLU	2.9
1	D	3504	ASP	2.9
1	A	509	GLN	2.9
1	A	573	PRO	2.9
1	B	1339	LYS	2.8
1	B	1503	THR	2.8
1	C	2304	GLU	2.8
1	A	21	ILE	2.7
1	B	1022	LYS	2.7
1	C	2022	LYS	2.6
1	A	504	ASP	2.6
1	C	2021	ILE	2.6
1	D	3390	ILE	2.4
1	C	2300	LYS	2.4
1	B	1417	PHE	2.3
1	D	3335	GLN	2.3
1	D	3505	GLU	2.3
1	D	3356	ALA	2.3
1	A	505	GLU	2.3
1	D	3329	GLU	2.3
1	B	1328	VAL	2.3
1	C	2457	GLY	2.3
1	D	3355	LYS	2.2
1	A	76	THR	2.2
1	D	3455	THR	2.2
1	A	214	LYS	2.2
1	A	260	HIS	2.2
1	D	3022	LYS	2.2
1	B	1509	GLN	2.1
1	B	1370	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	3573	PRO	2.1
1	B	1507	LEU	2.1
1	C	2260	HIS	2.1
1	B	1458	ARG	2.1
1	A	571	GLU	2.1
1	D	3214	LYS	2.1
1	D	3330	ASN	2.1
1	B	1547	GLU	2.1
1	A	298	ILE	2.0
1	D	3415	VAL	2.0
1	A	547	GLU	2.0
1	B	1510	GLY	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 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. 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(\AA^2)	Q<0.9
4	NAD	D	3602	44/44	0.86	0.17	20,45,70,70	9
4	NAD	C	2602	44/44	0.87	0.16	18,46,71,71	9
4	NAD	B	1602	44/44	0.89	0.14	27,51,73,73	9
4	NAD	A	602	44/44	0.89	0.15	22,46,72,72	9
3	PYR	C	2603	6/6	0.92	0.15	16,23,24,30	0
4	NAD	B	1601	44/44	0.93	0.12	22,27,32,34	0
3	PYR	A	603	6/6	0.94	0.13	14,17,19,26	0
4	NAD	D	3601	44/44	0.95	0.10	22,26,29,30	0
3	PYR	B	1603	6/6	0.95	0.14	16,23,27,29	0
5	FUM	C	2700	8/8	0.96	0.11	25,27,28,28	0
4	NAD	A	601	44/44	0.96	0.09	12,20,21,23	0

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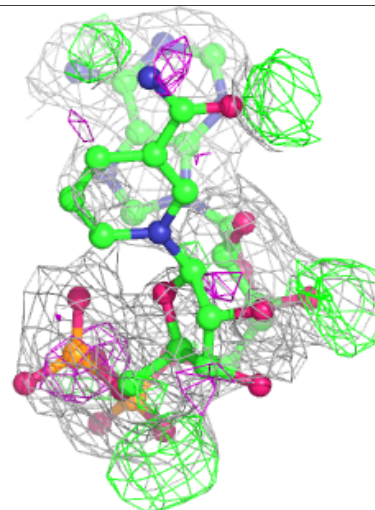
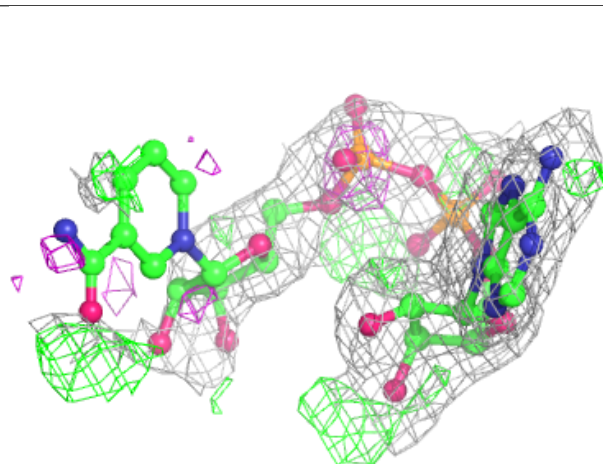
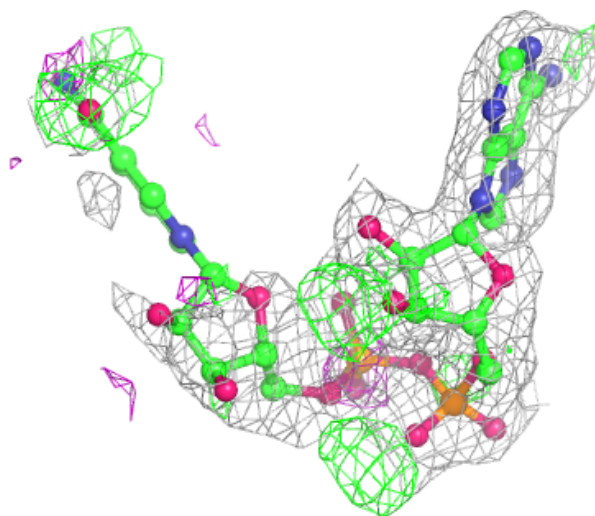
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	FUM	B	1700	8/8	0.97	0.11	24,27,29,29	0
4	NAD	C	2601	44/44	0.97	0.10	18,22,25,26	0
5	FUM	D	3700	8/8	0.97	0.12	21,24,28,31	0
3	PYR	D	3603	6/6	0.97	0.13	19,23,24,27	0
5	FUM	A	700	8/8	0.98	0.10	24,26,29,30	0
2	MN	D	3604	1/1	0.99	0.09	24,24,24,24	0
2	MN	B	1604	1/1	0.99	0.13	26,26,26,26	0
2	MN	A	604	1/1	1.00	0.08	20,20,20,20	0
2	MN	C	2604	1/1	1.00	0.11	20,20,20,20	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.

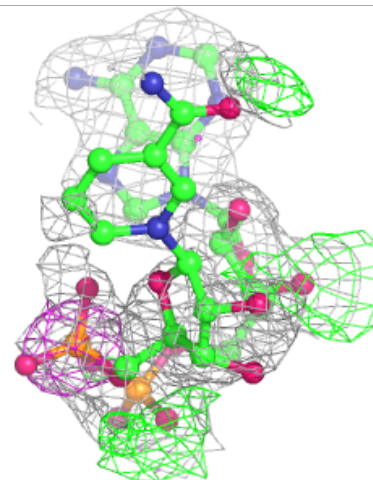
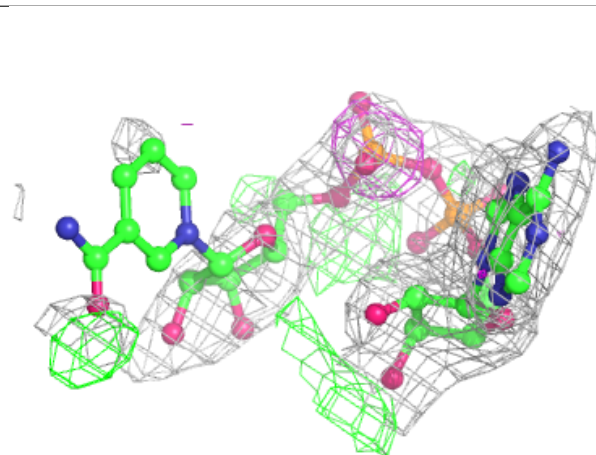
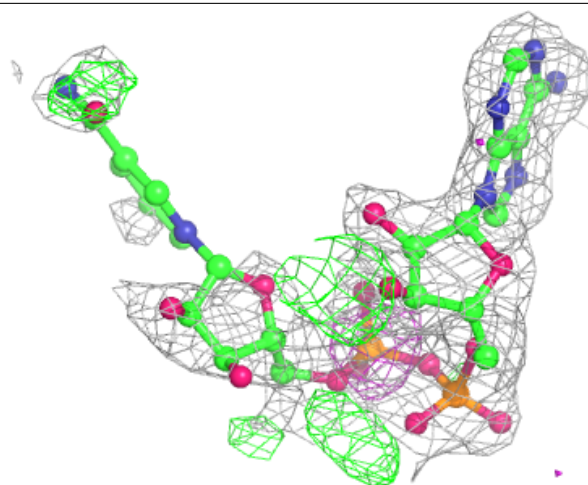
Electron density around NAD D 3602:

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



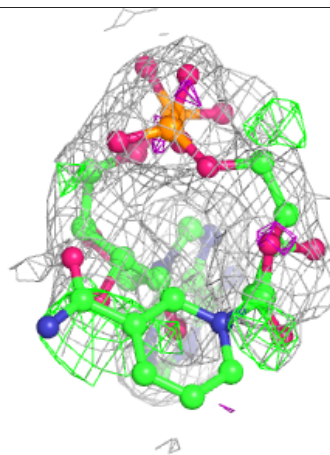
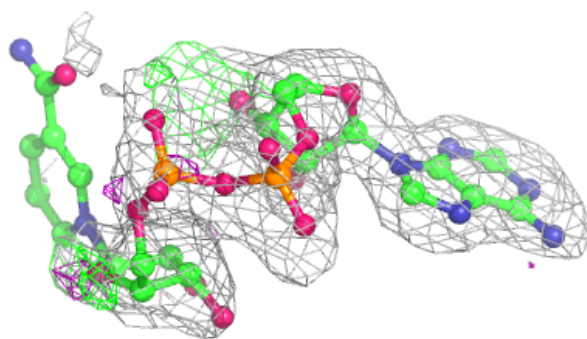
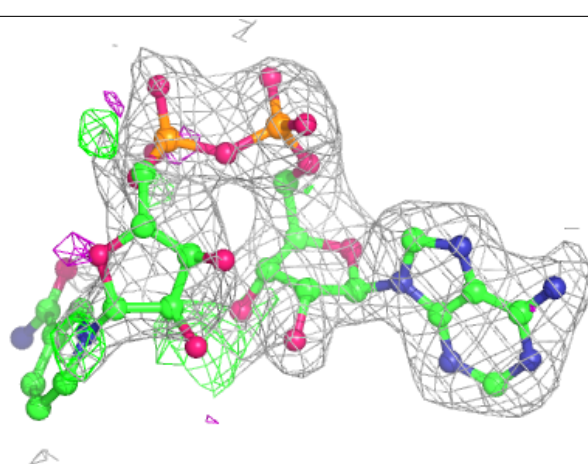
Electron density around NAD C 2602:

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



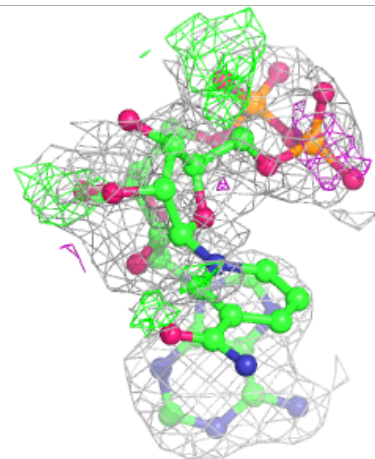
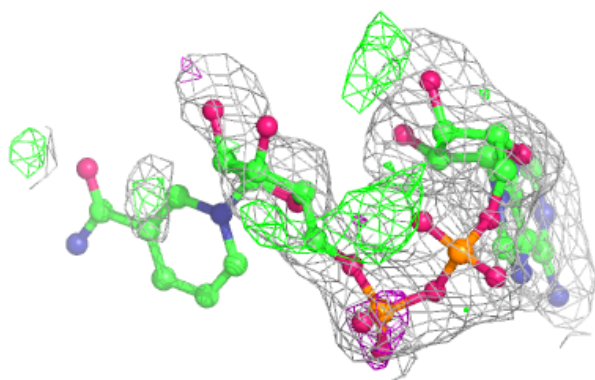
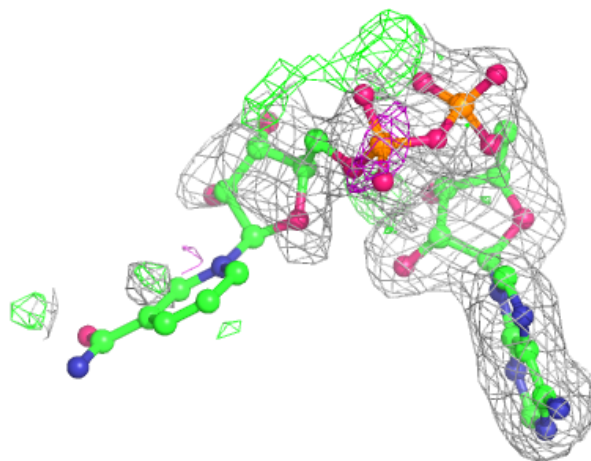
Electron density around NAD B 1602:

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



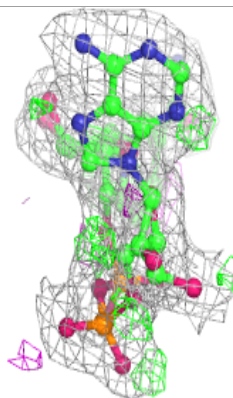
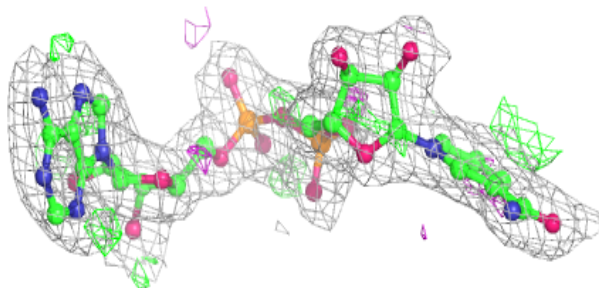
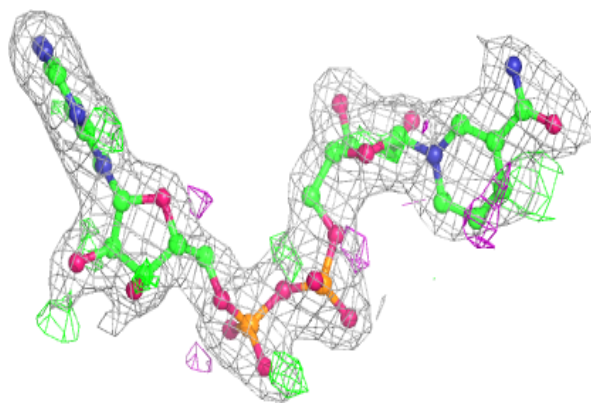
Electron density around NAD A 602:

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

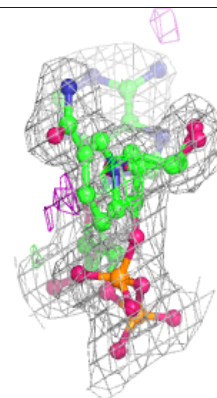
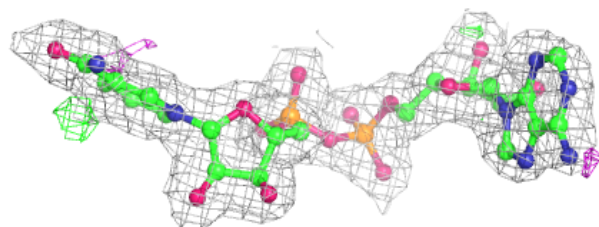
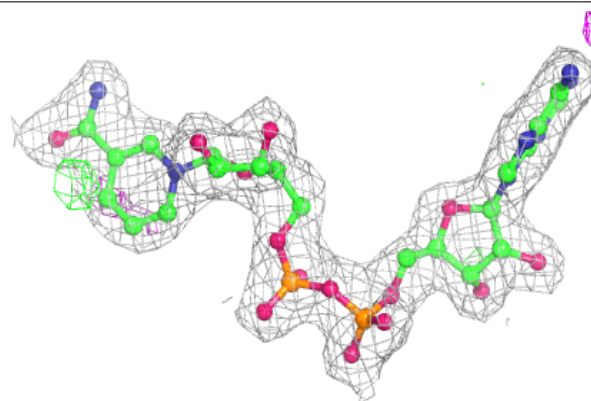


Electron density around NAD B 1601:

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

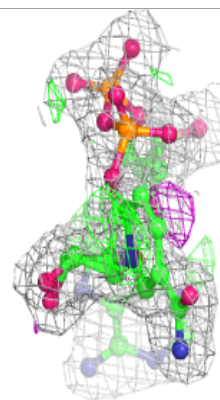
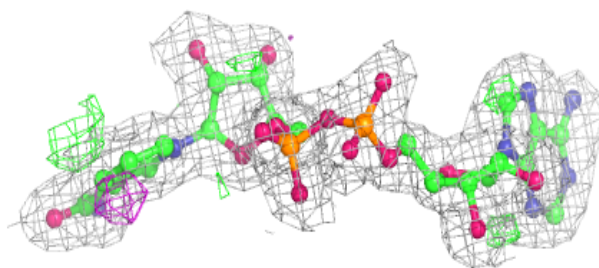
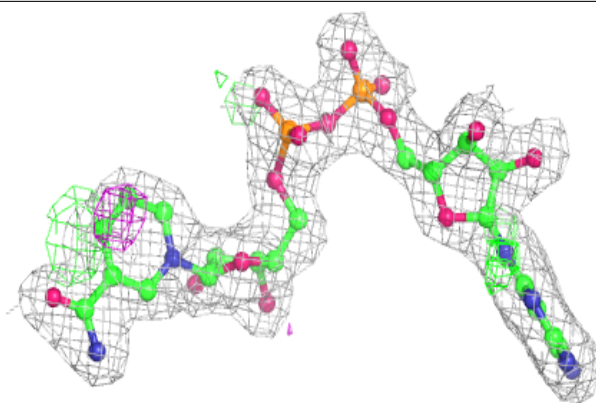
**Electron density around NAD D 3601:**

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

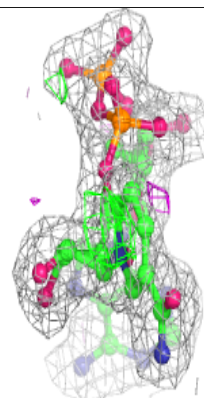
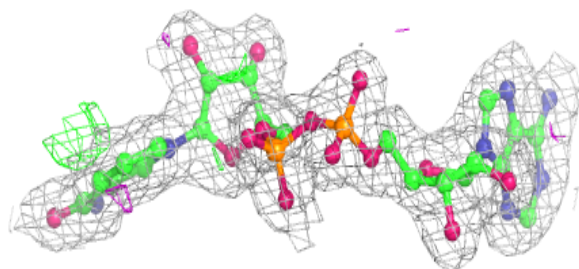
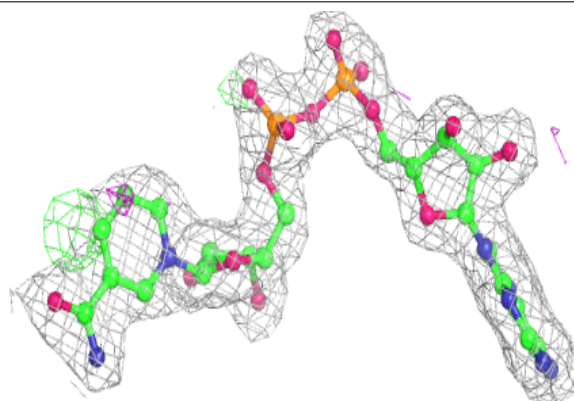


Electron density around NAD A 601:

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

**Electron density around NAD C 2601:**

$2mF_o-DF_c$ (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.