



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 05:27 am BST

PDB ID : 1AGN  
Title : X-RAY STRUCTURE OF HUMAN SIGMA ALCOHOL DEHYDROGENASE  
Authors : Hurley, T.D.; Xie, P.  
Deposited on : 1996-06-04  
Resolution : 3.00 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](mailto: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.

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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

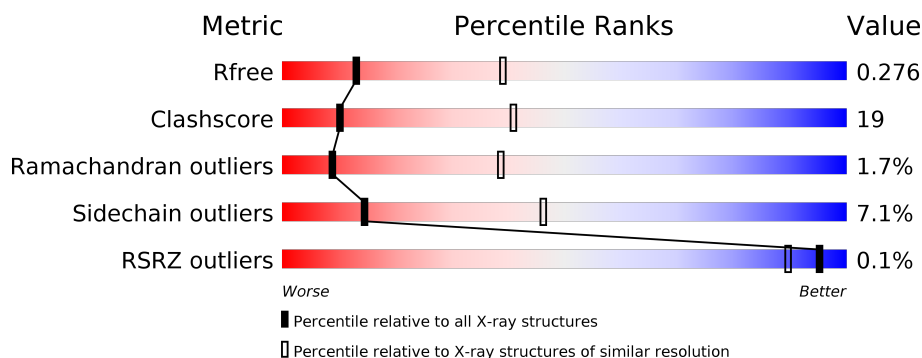
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	373	<div> <div>59%</div> <div>37%</div> <div>.</div> </div>
1	B	373	<div> <div>60%</div> <div>35%</div> <div>5%</div> </div>
1	C	373	<div> <div>59%</div> <div>38%</div> <div>.</div> </div>
1	D	373	<div> <div>62%</div> <div>34%</div> <div>.</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACT	A	502	-	-	X	-
3	ACT	D	378	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11397 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 HUMAN SIGMA ALCOHOL DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	373	Total	C	N	O	S	0	0	0
			2789	1772	468	526	23			
1	B	373	Total	C	N	O	S	0	0	0
			2789	1772	468	526	23			
1	C	373	Total	C	N	O	S	0	0	0
			2789	1772	468	526	23			
1	D	373	Total	C	N	O	S	0	0	0
			2789	1772	468	526	23			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

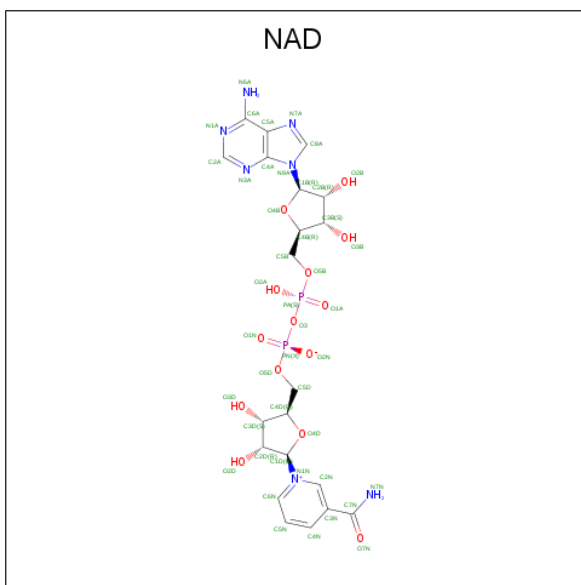
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	5	Total	Zn	0	0
			5	5		
2	A	3	Total	Zn	0	0
			3	3		
2	D	5	Total	Zn	0	0
			5	5		
2	C	3	Total	Zn	0	0
			3	3		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C<sub>21</sub>H<sub>27</sub>N<sub>7</sub>O<sub>14</sub>P<sub>2</sub>).



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

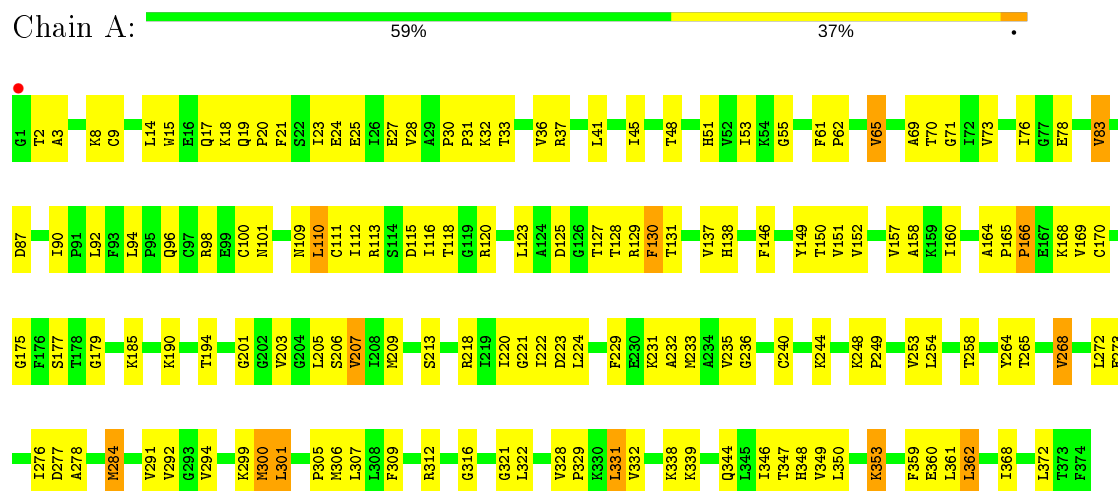
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O 1 1	0	0
5	B	4	Total O 4 4	0	0
5	C	1	Total O 1 1	0	0
5	D	3	Total O 3 3	0	0

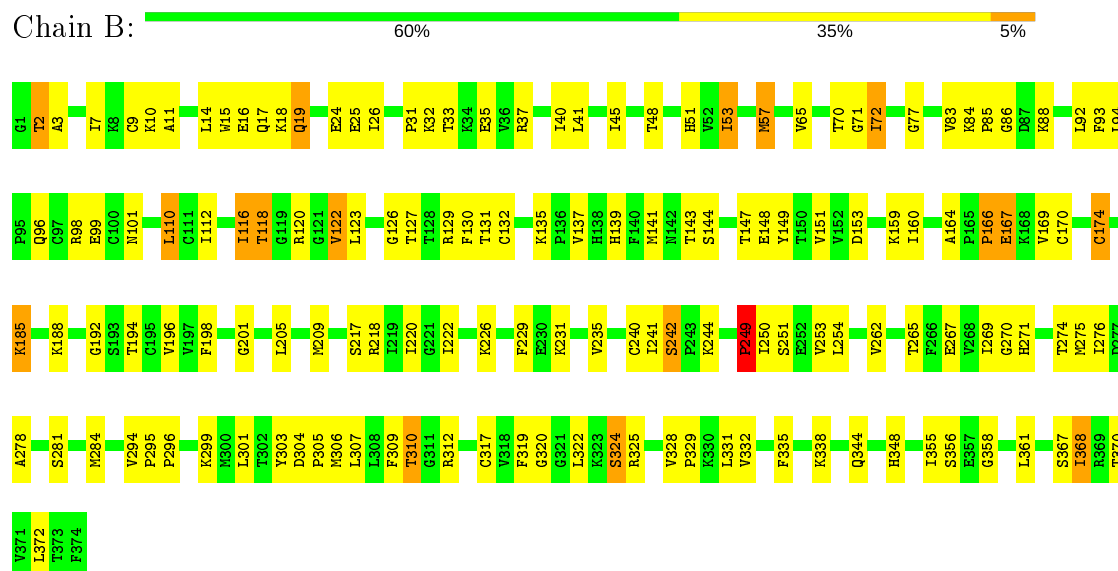
### 3 Residue-property plots

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: HUMAN SIGMA ALCOHOL DEHYDROGENASE

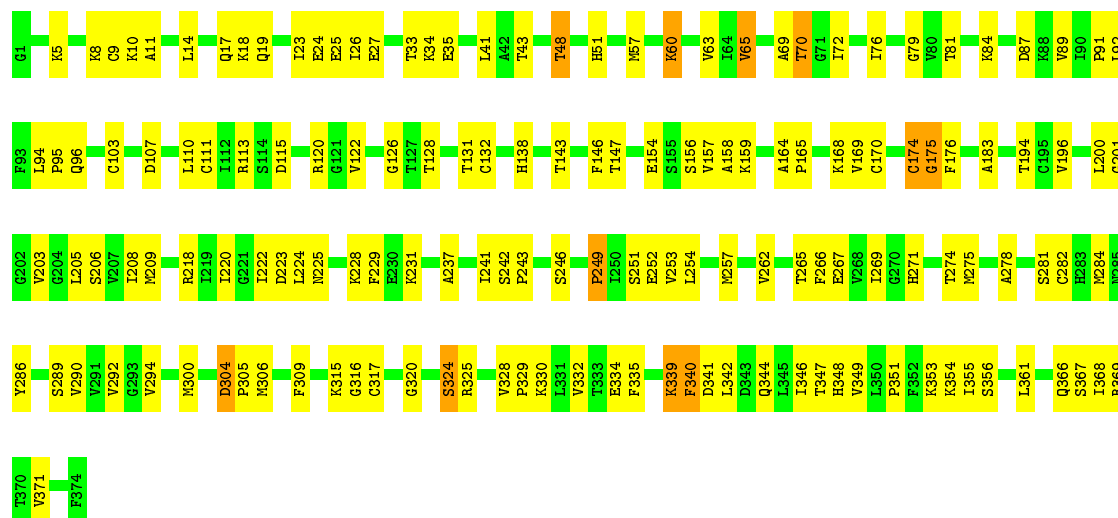


#### • Molecule 1: HUMAN SIGMA ALCOHOL DEHYDROGENASE



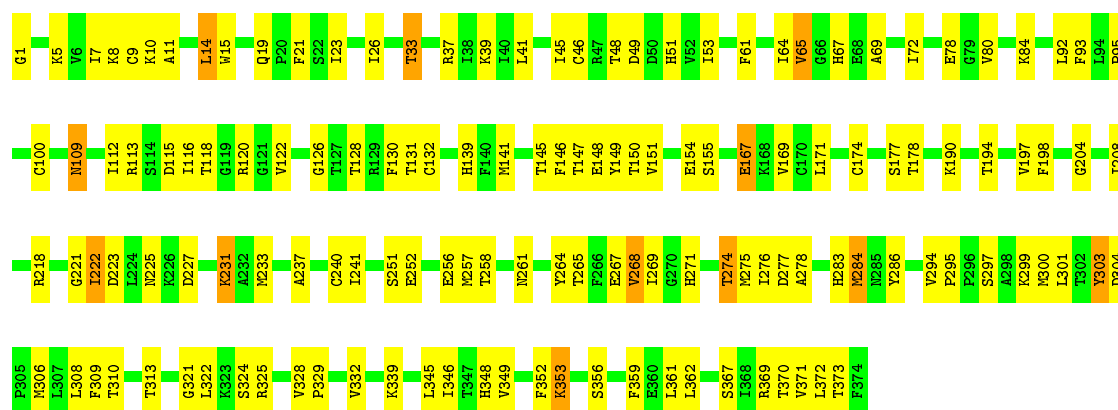
#### • Molecule 1: HUMAN SIGMA ALCOHOL DEHYDROGENASE





• Molecule 1: HUMAN SIGMA ALCOHOL DEHYDROGENASE

Chain D: 62% 34%





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.30 Å 94.65 Å 121.66 Å 90.00° 100.03° 90.00°	Depositor
Resolution (Å)	8.00 – 3.00 41.35 – 3.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-3.00) 89.1 (41.35-3.00)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 3.01 Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.225 , 0.305 0.204 , 0.276	Depositor DCC
$R_{free}$ test set	2410 reflections (6.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.5	Xtriage
Anisotropy	0.490	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 41.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	11397	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: ZN, NAD, 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	0.44	0/2840	0.67	0/3839
1	B	0.47	0/2840	0.69	0/3839
1	C	0.43	0/2840	0.67	0/3839
1	D	0.46	0/2840	0.72	1/3839 (0.0%)
All	All	0.45	0/11360	0.69	1/15356 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	14	LEU	CA-CB-CG	5.31	127.51	115.30

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	2789	0	2858	113	0
1	B	2789	0	2858	107	0
1	C	2789	0	2858	115	0
1	D	2789	0	2858	109	0
2	A	3	0	0	0	0
2	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	3	0	0	0	0
2	D	5	0	0	0	0
3	A	12	0	9	3	0
3	B	16	0	12	0	0
3	C	4	0	3	1	0
3	D	8	0	6	3	0
4	A	44	0	26	2	0
4	B	44	0	26	2	0
4	C	44	0	26	3	0
4	D	44	0	26	9	0
5	A	1	0	0	0	0
5	B	4	0	0	0	0
5	C	1	0	0	0	0
5	D	3	0	0	0	0
All	All	11397	0	11566	431	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 19.

All (431) 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:D:348:HIS:HB2	1:D:370:THR:HG23	1.46	0.96
1:C:304:ASP:HB2	1:D:300:MET:CE	1.96	0.95
1:C:205:LEU:HD11	1:C:368:ILE:HD13	1.46	0.95
1:D:178:THR:HG21	4:D:377:NAD:C4N	1.97	0.93
1:D:46:CYS:HA	1:D:369:ARG:NH1	1.88	0.88
1:C:164:ALA:HB1	1:C:169:VAL:HG11	1.56	0.87
1:C:304:ASP:HB2	1:D:300:MET:HE3	1.57	0.87
1:D:26:ILE:HG22	1:D:132:CYS:HB2	1.55	0.86
1:D:241:ILE:CD1	1:D:257:MET:HE1	2.07	0.85
1:A:70:THR:HG22	1:A:170:CYS:HB3	1.59	0.84
1:D:49:ASP:OD1	1:D:67:HIS:CE1	2.34	0.81
1:D:276:ILE:HD12	1:D:303:TYR:HB2	1.64	0.80
1:C:122:VAL:HG12	1:C:128:THR:HG23	1.63	0.80
1:D:92:LEU:HD13	1:D:324:SER:HB2	1.64	0.80
1:D:14:LEU:HG	1:D:61:PHE:HE1	1.47	0.78
1:C:194:THR:HG22	1:C:218:ARG:HB2	1.65	0.77
1:C:353:LYS:HD2	1:C:353:LYS:H	1.49	0.77
1:C:10:LYS:HD2	1:C:23:ILE:HG22	1.68	0.76
1:A:130:PHE:HB2	1:A:137:VAL:HG23	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:HIS:ND1	1:A:361:LEU:HD13	2.02	0.74
1:B:122:VAL:HG11	1:B:126:GLY:HA2	1.69	0.73
1:C:249:PRO:HB2	1:C:252:GLU:HG3	1.69	0.73
1:D:197:VAL:HG21	1:D:208:ILE:HD13	1.72	0.72
1:A:130:PHE:HB2	1:A:137:VAL:CG2	2.20	0.72
1:B:11:ALA:HB2	1:B:147:THR:HG23	1.73	0.71
1:A:294:VAL:HG22	1:B:309:PHE:CZ	2.26	0.71
1:D:122:VAL:HG12	1:D:128:THR:HG23	1.72	0.70
1:A:164:ALA:HB1	1:A:169:VAL:HG11	1.74	0.69
1:D:194:THR:HG23	1:D:218:ARG:HB3	1.75	0.69
1:B:32:LYS:HD2	1:B:129:ARG:NH2	2.07	0.69
1:D:46:CYS:HA	1:D:369:ARG:HH12	1.55	0.68
1:C:11:ALA:HB3	1:C:26:ILE:HD13	1.75	0.68
1:A:100:CYS:HB2	1:A:112:ILE:HG23	1.74	0.68
1:A:224:LEU:HD21	1:A:244:LYS:HE3	1.75	0.67
1:C:23:ILE:H	1:C:23:ILE:HD12	1.58	0.67
1:D:155:SER:HA	1:D:325:ARG:HH11	1.60	0.67
1:B:276:ILE:HD11	1:B:301:LEU:HD11	1.76	0.67
1:A:231:LYS:HD2	1:A:344:GLN:HG3	1.75	0.67
1:D:252:GLU:O	1:D:256:GLU:HG3	1.95	0.66
1:C:348:HIS:CD2	1:C:361:LEU:HD13	2.30	0.66
1:D:128:THR:HG22	1:D:139:HIS:HD2	1.59	0.66
1:C:231:LYS:HG2	1:C:368:ILE:CD1	2.26	0.66
1:A:231:LYS:HG2	1:A:368:ILE:CD1	2.25	0.66
1:C:76:ILE:HD13	1:C:84:LYS:HA	1.78	0.66
1:D:348:HIS:CB	1:D:370:THR:HG23	2.24	0.66
1:A:94:LEU:HD11	1:A:110:LEU:HA	1.78	0.66
1:D:49:ASP:OD1	1:D:67:HIS:ND1	2.30	0.65
1:C:267:GLU:HG3	1:C:275:MET:HA	1.77	0.65
1:C:218:ARG:HH21	1:C:220:ILE:HD11	1.61	0.65
1:A:19:GLN:HG2	1:A:20:PRO:HD2	1.77	0.65
1:D:155:SER:HA	1:D:325:ARG:NH1	2.11	0.64
1:C:69:ALA:O	1:C:91:PRO:HD2	1.98	0.64
1:B:271:HIS:O	1:B:275:MET:HG3	1.98	0.64
1:A:307:LEU:O	1:A:312:ARG:HD2	1.97	0.64
1:D:100:CYS:HB2	1:D:112:ILE:HG13	1.80	0.63
1:D:223:ASP:OD1	4:D:377:NAD:H1B	1.98	0.63
1:B:304:ASP:OD1	1:B:306:MET:HB2	1.98	0.63
1:A:307:LEU:HD22	1:A:312:ARG:HH12	1.64	0.63
1:A:32:LYS:HD2	1:A:129:ARG:NH2	2.14	0.63
1:A:27:GLU:HB2	1:A:131:THR:HB	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:88:LYS:HG2	1:B:160:ILE:HD11	1.81	0.62
1:D:198:PHE:HD2	1:D:274:THR:HG22	1.65	0.61
1:D:15:TRP:CH2	1:D:132:CYS:SG	2.91	0.61
1:D:39:LYS:HD3	1:D:149:TYR:CZ	2.36	0.61
1:C:353:LYS:HD2	1:C:353:LYS:N	2.13	0.61
1:B:271:HIS:HB2	1:B:274:THR:OG1	2.01	0.61
1:C:341:ASP:O	1:C:344:GLN:HG2	2.00	0.61
1:D:231:LYS:HA	1:D:231:LYS:HE3	1.82	0.61
1:D:11:ALA:HB2	1:D:147:THR:HG23	1.82	0.61
1:D:269:ILE:HD12	1:D:274:THR:HG21	1.82	0.61
1:C:309:PHE:CZ	1:D:294:VAL:HG22	2.35	0.61
1:B:33:THR:O	1:B:35:GLU:HG3	2.01	0.60
1:D:41:LEU:HD11	1:D:72:ILE:HG13	1.82	0.60
1:C:251:SER:HA	1:C:281:SER:HB3	1.83	0.60
1:C:334:GLU:O	1:C:339:LYS:HB2	2.01	0.60
1:A:123:LEU:HD12	1:A:127:THR:O	2.02	0.60
1:A:128:THR:HG21	1:A:138:HIS:HA	1.84	0.60
1:D:128:THR:HG22	1:D:139:HIS:CD2	2.36	0.60
1:C:341:ASP:HB3	1:C:344:GLN:NE2	2.17	0.60
1:A:31:PRO:HD3	1:A:37:ARG:HB2	1.84	0.60
1:A:359:PHE:O	1:A:362:LEU:HB3	2.02	0.59
1:A:17:GLN:OE1	1:A:55:GLY:HA2	2.03	0.59
1:C:65:VAL:HG23	1:C:146:PHE:CD2	2.37	0.59
1:C:94:LEU:HD11	1:C:110:LEU:HD12	1.85	0.59
1:B:262:VAL:HG11	1:B:281:SER:O	2.02	0.59
1:C:165:PRO:HG3	1:C:168:LYS:HD2	1.84	0.59
1:A:272:LEU:HD11	1:A:299:LYS:HB3	1.83	0.59
1:B:129:ARG:HG3	1:B:151:VAL:HB	1.83	0.59
1:C:154:GLU:O	1:C:157:VAL:HG12	2.03	0.59
1:C:317:CYS:SG	1:C:320:GLY:HA2	2.43	0.59
1:B:118:THR:HG23	1:B:120:ARG:HG3	1.83	0.59
1:C:17:GLN:HG2	1:C:18:LYS:HG3	1.85	0.58
1:A:17:GLN:HB2	1:A:61:PHE:HE2	1.67	0.58
1:C:165:PRO:HG2	1:C:168:LYS:HB2	1.86	0.58
1:C:115:ASP:OD1	1:C:120:ARG:HB2	2.04	0.58
1:A:353:LYS:CD	1:A:353:LYS:H	2.17	0.58
1:A:17:GLN:HB2	1:A:61:PHE:CE2	2.38	0.58
1:B:70:THR:HG22	1:B:170:CYS:HB3	1.86	0.58
1:C:96:GLN:HB2	1:C:324:SER:OG	2.04	0.58
1:D:178:THR:HG21	4:D:377:NAD:H4N	1.84	0.58
1:D:190:LYS:HG2	1:D:264:TYR:OH	2.02	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:224:LEU:HD12	1:C:243:PRO:HD2	1.84	0.57
1:D:169:VAL:HG21	1:D:332:VAL:HG13	1.86	0.57
1:D:115:ASP:HA	1:D:120:ARG:NH2	2.20	0.57
1:C:48:THR:HG22	1:C:57:MET:SD	2.45	0.57
1:A:9:CYS:O	1:A:25:GLU:HA	2.03	0.57
1:D:348:HIS:CE1	1:D:367:SER:HB3	2.41	0.56
1:B:31:PRO:HD3	1:B:37:ARG:HB2	1.86	0.56
1:B:41:LEU:HG	1:B:71:GLY:HA2	1.87	0.56
1:C:24:GLU:OE1	1:C:132:CYS:SG	2.61	0.56
1:D:23:ILE:HD12	1:D:352:PHE:CE2	2.40	0.56
1:A:360:GLU:CB	3:A:502:ACT:H3	2.35	0.56
1:B:96:GLN:HE21	1:B:98:ARG:HG2	1.68	0.56
1:A:344:GLN:HA	1:A:344:GLN:OE1	2.05	0.56
1:B:196:VAL:HG12	1:B:220:ILE:HB	1.88	0.56
1:A:301:LEU:HB2	1:B:305:PRO:HG3	1.87	0.56
1:D:122:VAL:HG21	1:D:126:GLY:HA2	1.88	0.56
1:D:65:VAL:HG23	1:D:146:PHE:CD2	2.41	0.56
1:B:348:HIS:CD2	1:B:361:LEU:HD13	2.41	0.55
1:A:185:LYS:HE2	1:A:321:GLY:O	2.06	0.55
1:B:284:MET:HA	1:B:312:ARG:NE	2.22	0.55
1:B:332:VAL:O	1:B:335:PHE:HB3	2.06	0.55
1:C:222:ILE:HD11	1:C:254:LEU:HD11	1.89	0.55
1:A:76:ILE:HG21	1:A:83:VAL:O	2.06	0.55
1:B:15:TRP:HZ2	1:B:132:CYS:HG	1.49	0.55
1:B:147:THR:HG22	1:B:149:TYR:H	1.71	0.55
1:D:241:ILE:HD11	1:D:257:MET:HE1	1.87	0.55
1:C:351:PRO:HD2	1:C:354:LYS:HD2	1.87	0.55
1:D:328:VAL:HB	1:D:329:PRO:HD3	1.87	0.55
1:D:353:LYS:HD3	1:D:353:LYS:H	1.71	0.55
1:A:152:VAL:CG2	1:A:157:VAL:HG23	2.37	0.55
1:B:348:HIS:CE1	1:B:367:SER:HB3	2.42	0.55
1:C:9:CYS:O	1:C:25:GLU:HA	2.07	0.55
1:D:37:ARG:HG3	1:D:151:VAL:HG22	1.89	0.55
1:D:178:THR:CG2	4:D:377:NAD:H4N	2.37	0.55
1:A:265:THR:HG21	1:A:278:ALA:O	2.07	0.54
1:B:164:ALA:HB1	1:B:169:VAL:HG11	1.88	0.54
1:D:48:THR:HA	1:D:51:HIS:CD2	2.43	0.54
1:A:41:LEU:HG	1:A:71:GLY:HA2	1.88	0.54
1:C:200:LEU:HD12	1:C:223:ASP:HB2	1.90	0.54
1:D:276:ILE:HD12	1:D:303:TYR:CB	2.37	0.54
1:A:73:VAL:HG23	1:A:87:ASP:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:21:PHE:CZ	1:D:53:ILE:HD11	2.42	0.54
1:D:274:THR:HA	1:D:277:ASP:HB2	1.90	0.54
3:A:378:ACT:OXT	4:A:377:NAD:C3N	2.56	0.54
1:B:209:MET:HG3	1:B:235:VAL:HG13	1.88	0.54
1:B:122:VAL:CG1	1:B:126:GLY:HA2	2.37	0.54
1:B:14:LEU:HD21	1:B:53:ILE:HG22	1.88	0.54
1:C:347:THR:HG21	1:C:367:SER:CB	2.37	0.54
1:C:347:THR:HG21	1:C:367:SER:HB2	1.90	0.53
1:B:116:ILE:H	1:B:116:ILE:HD13	1.73	0.53
1:B:265:THR:HG21	1:B:278:ALA:O	2.07	0.53
1:B:284:MET:O	1:B:310:THR:HB	2.08	0.53
1:C:92:LEU:O	1:C:156:SER:HB3	2.08	0.53
1:D:348:HIS:ND1	1:D:367:SER:HB3	2.23	0.53
1:C:174:CYS:SG	4:C:377:NAD:H5N	2.48	0.53
4:D:377:NAD:H51N	4:D:377:NAD:H6N	1.90	0.53
1:D:271:HIS:HB2	1:D:274:THR:OG1	2.08	0.53
1:C:292:VAL:O	4:C:377:NAD:H2N	2.08	0.53
1:C:41:LEU:HD11	1:C:72:ILE:HD11	1.91	0.53
1:C:265:THR:HG21	1:C:278:ALA:O	2.09	0.53
1:D:15:TRP:HH2	1:D:132:CYS:SG	2.32	0.53
1:D:297:SER:O	1:D:299:LYS:HG2	2.08	0.53
1:D:9:CYS:HB2	1:D:148:GLU:OE2	2.09	0.53
1:B:222:ILE:HD11	1:B:250:ILE:HD11	1.90	0.53
1:C:290:VAL:HG22	1:C:315:LYS:HG3	1.91	0.53
1:D:100:CYS:CB	1:D:112:ILE:HG13	2.39	0.53
1:C:334:GLU:HB2	1:C:340:PHE:CE1	2.44	0.52
1:D:167:GLU:CD	1:D:167:GLU:H	2.12	0.52
1:D:178:THR:CG2	4:D:377:NAD:C4N	2.79	0.52
1:D:45:ILE:HD11	1:D:372:LEU:HD11	1.91	0.52
1:A:125:ASP:HB3	1:A:127:THR:OG1	2.10	0.52
1:C:334:GLU:HB2	1:C:340:PHE:HE1	1.74	0.52
1:A:21:PHE:CZ	1:A:53:ILE:HD11	2.45	0.52
1:B:201:GLY:O	1:B:205:LEU:HG	2.08	0.52
1:A:349:VAL:O	1:A:350:LEU:HD23	2.09	0.52
1:C:79:GLY:O	1:C:81:THR:HG23	2.09	0.52
1:A:23:ILE:N	1:A:23:ILE:HD12	2.25	0.51
1:D:348:HIS:CE1	1:D:361:LEU:HD13	2.46	0.51
1:A:249:PRO:O	1:A:253:VAL:HG23	2.09	0.51
1:A:300:MET:CE	1:B:304:ASP:HB2	2.40	0.51
3:C:378:ACT:H3	1:D:309:PHE:CZ	2.45	0.51
1:C:349:VAL:HA	1:C:371:VAL:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:296:PRO:HB2	1:B:299:LYS:HD3	1.93	0.51
1:B:174:CYS:SG	4:B:377:NAD:H5N	2.50	0.51
1:B:198:PHE:O	1:B:269:ILE:HG13	2.11	0.51
1:B:222:ILE:CD1	1:B:250:ILE:HD11	2.41	0.51
1:C:304:ASP:HB2	1:D:300:MET:HE1	1.90	0.51
1:C:33:THR:O	1:C:35:GLU:HG3	2.10	0.51
1:C:165:PRO:CG	1:C:168:LYS:HD2	2.41	0.51
1:D:204:GLY:O	1:D:208:ILE:HG12	2.11	0.51
1:B:70:THR:HG21	1:B:166:PRO:HA	1.93	0.51
1:C:332:VAL:O	1:C:335:PHE:HB3	2.11	0.51
1:D:198:PHE:O	1:D:268:VAL:HG23	2.10	0.51
1:C:205:LEU:CD1	1:C:368:ILE:HD13	2.30	0.51
1:C:60:LYS:O	1:C:63:VAL:HB	2.10	0.51
1:D:225:ASN:OD1	1:D:227:ASP:HB2	2.11	0.50
1:A:300:MET:HE1	1:B:304:ASP:HB2	1.92	0.50
1:C:231:LYS:HG2	1:C:368:ILE:HD12	1.92	0.50
1:C:92:LEU:CD1	1:C:325:ARG:HG2	2.41	0.50
1:A:48:THR:O	1:A:51:HIS:HB2	2.12	0.50
1:B:94:LEU:HD11	1:B:110:LEU:HA	1.93	0.50
1:C:94:LEU:HD11	1:C:110:LEU:HA	1.94	0.50
1:C:305:PRO:HG3	1:D:301:LEU:HB2	1.93	0.50
1:C:330:LYS:O	1:C:334:GLU:HG2	2.11	0.50
1:B:122:VAL:HG22	1:B:127:THR:C	2.31	0.50
1:C:95:PRO:HG3	1:C:113:ARG:HB2	1.94	0.50
1:A:305:PRO:HG3	1:B:301:LEU:HB2	1.92	0.50
1:C:89:VAL:HG12	1:C:159:LYS:HA	1.93	0.50
1:B:17:GLN:HG3	1:B:18:LYS:HG2	1.94	0.50
1:D:80:VAL:HG13	1:D:154:GLU:HG3	1.93	0.50
1:C:94:LEU:CD1	1:C:110:LEU:HD12	2.42	0.49
1:A:111:CYS:SG	1:A:112:ILE:N	2.85	0.49
1:A:194:THR:HG21	1:A:258:THR:HG21	1.93	0.49
1:A:231:LYS:HG2	1:A:368:ILE:HD11	1.92	0.49
1:B:167:GLU:H	1:B:167:GLU:CD	2.15	0.49
1:B:209:MET:HG3	1:B:235:VAL:CG1	2.43	0.49
1:C:271:HIS:HB2	1:C:274:THR:OG1	2.12	0.49
1:A:45:ILE:HD11	1:A:372:LEU:HD21	1.94	0.49
1:C:347:THR:HG22	1:C:369:ARG:H	1.77	0.49
1:D:221:GLY:O	1:D:240:CYS:HA	2.13	0.49
1:A:128:THR:CG2	1:A:138:HIS:HA	2.41	0.49
3:D:378:ACT:O	4:D:377:NAD:C3N	2.61	0.49
1:D:241:ILE:HD11	1:D:257:MET:SD	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:GLY:HA2	1:A:203:VAL:HG22	1.95	0.48
1:A:222:ILE:HD11	1:A:254:LEU:HD11	1.95	0.48
1:B:130:PHE:HB2	1:B:137:VAL:HB	1.93	0.48
1:B:269:ILE:HD13	4:B:377:NAD:C4A	2.42	0.48
1:D:178:THR:OG1	4:D:377:NAD:H4N	2.14	0.48
1:B:143:THR:O	1:B:144:SER:HB2	2.12	0.48
1:A:276:ILE:HG12	1:A:301:LEU:HD21	1.94	0.48
1:B:307:LEU:HD22	1:B:312:ARG:NH1	2.29	0.48
1:C:304:ASP:OD1	1:C:306:MET:HB2	2.13	0.48
1:B:26:ILE:HG22	1:B:132:CYS:HB2	1.96	0.48
1:A:201:GLY:O	1:A:205:LEU:HG	2.14	0.48
1:A:306:MET:CE	1:B:295:PRO:HG2	2.44	0.48
1:B:32:LYS:O	1:B:77:GLY:HA3	2.13	0.48
1:C:361:LEU:HB3	1:C:367:SER:OG	2.13	0.48
1:A:33:THR:HG22	1:A:78:GLU:HB2	1.96	0.48
1:D:328:VAL:O	1:D:332:VAL:HG23	2.13	0.48
1:A:284:MET:HA	1:A:312:ARG:NE	2.29	0.48
1:D:241:ILE:CD1	1:D:257:MET:CE	2.88	0.48
1:A:328:VAL:HB	1:A:329:PRO:HD3	1.96	0.47
1:A:164:ALA:O	1:A:166:PRO:HD3	2.14	0.47
1:A:218:ARG:HH21	1:A:220:ILE:HD11	1.79	0.47
1:B:15:TRP:CZ2	1:B:132:CYS:SG	3.02	0.47
1:B:267:GLU:HG3	1:B:275:MET:HA	1.97	0.47
1:A:62:PRO:HG2	1:A:137:VAL:HA	1.97	0.47
1:A:291:VAL:HG13	1:A:316:GLY:HA2	1.97	0.47
1:C:175:GLY:HA2	1:C:203:VAL:HG22	1.97	0.47
1:A:8:LYS:NZ	1:A:25:GLU:HB3	2.30	0.46
1:B:328:VAL:HB	1:B:329:PRO:HD3	1.96	0.46
1:B:355:ILE:HG23	1:B:356:SER:N	2.29	0.46
1:C:335:PHE:CE1	1:C:342:LEU:HG	2.50	0.46
1:C:347:THR:HG21	1:C:368:ILE:H	1.80	0.46
1:D:353:LYS:N	1:D:353:LYS:HD3	2.30	0.46
1:A:62:PRO:CG	1:A:137:VAL:HG12	2.46	0.46
1:D:130:PHE:HZ	1:D:150:THR:OG1	1.98	0.46
1:A:276:ILE:HD11	1:A:301:LEU:HD22	1.97	0.46
1:B:241:ILE:HG22	1:B:242:SER:N	2.31	0.46
1:D:95:PRO:HB2	1:D:113:ARG:HB2	1.98	0.46
1:D:15:TRP:CZ2	1:D:132:CYS:SG	3.00	0.46
1:D:1:GLY:O	1:D:5:LYS:HD2	2.16	0.46
1:C:91:PRO:HB2	1:C:143:THR:HG22	1.97	0.46
1:B:229:PHE:CD1	1:B:229:PHE:N	2.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:CYS:O	1:B:241:ILE:HD13	2.16	0.46
1:B:32:LYS:HD2	1:B:129:ARG:HH22	1.81	0.46
1:D:346:ILE:HG23	1:D:371:VAL:HG23	1.98	0.46
1:B:355:ILE:HG23	1:B:356:SER:H	1.80	0.45
1:D:353:LYS:H	1:D:353:LYS:CD	2.25	0.45
1:A:100:CYS:SG	1:A:111:CYS:HA	2.56	0.45
1:C:201:GLY:O	1:C:205:LEU:HG	2.16	0.45
1:D:7:ILE:HG13	1:D:37:ARG:NH1	2.31	0.45
1:A:30:PRO:HA	1:A:37:ARG:NH1	2.32	0.45
1:B:307:LEU:HD22	1:B:312:ARG:HH12	1.80	0.45
1:C:92:LEU:HD11	1:C:158:ALA:HB2	1.98	0.45
1:A:92:LEU:HD11	1:A:158:ALA:HB2	1.97	0.45
1:C:43:THR:CB	1:C:69:ALA:HB2	2.47	0.45
1:A:112:ILE:HD12	1:A:112:ILE:C	2.37	0.45
1:B:48:THR:O	1:B:51:HIS:HB2	2.17	0.45
1:C:128:THR:HG21	1:C:138:HIS:HA	1.98	0.45
1:B:205:LEU:HD12	1:B:368:ILE:HG21	1.98	0.45
1:B:276:ILE:CD1	1:B:301:LEU:HD11	2.45	0.45
1:C:92:LEU:HD13	1:C:324:SER:HB2	1.98	0.45
1:D:359:PHE:O	1:D:362:LEU:HB3	2.16	0.45
1:C:231:LYS:HD2	1:C:344:GLN:O	2.16	0.45
1:C:208:ILE:HD13	1:C:237:ALA:HB2	1.98	0.45
1:B:93:PHE:HB2	1:B:141:MET:HB3	1.99	0.45
1:B:355:ILE:O	1:B:358:GLY:N	2.49	0.45
1:A:268:VAL:HG13	1:A:292:VAL:HB	1.99	0.45
1:A:205:LEU:HD22	1:A:232:ALA:HA	1.98	0.45
1:C:103:CYS:SG	1:C:111:CYS:HB2	2.57	0.45
1:C:92:LEU:CD2	1:C:328:VAL:HG21	2.47	0.45
1:C:51:HIS:HB3	1:C:57:MET:HB2	1.99	0.45
1:A:78:GLU:N	1:A:78:GLU:OE1	2.50	0.44
1:C:335:PHE:CD1	1:C:342:LEU:HG	2.52	0.44
1:D:33:THR:HG23	1:D:78:GLU:HB2	1.99	0.44
1:B:2:THR:CG2	1:B:7:ILE:HG12	2.47	0.44
1:C:222:ILE:CD1	1:C:254:LEU:HD11	2.47	0.44
1:C:306:MET:HE2	1:D:295:PRO:HD2	2.00	0.44
1:C:316:GLY:HA3	1:D:308:LEU:O	2.18	0.44
1:D:233:MET:HG2	1:D:237:ALA:O	2.18	0.44
1:D:345:LEU:N	1:D:345:LEU:HD12	2.33	0.44
1:B:10:LYS:HA	1:B:24:GLU:O	2.18	0.44
1:B:83:VAL:HG12	1:B:159:LYS:HB2	1.99	0.44
1:B:229:PHE:HD1	1:B:229:PHE:N	2.14	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:ASP:OD1	4:A:377:NAD:H1B	2.17	0.44
1:A:209:MET:HG2	1:A:235:VAL:HG13	2.00	0.44
1:A:221:GLY:O	1:A:240:CYS:HA	2.16	0.44
1:D:283:HIS:CD2	1:D:286:TYR:CZ	3.05	0.44
1:D:177:SER:HB3	1:D:322:LEU:HD12	1.99	0.44
1:A:353:LYS:CD	1:A:353:LYS:N	2.80	0.44
1:C:265:THR:CG2	1:C:289:SER:HA	2.47	0.44
1:C:241:ILE:HG12	1:C:242:SER:N	2.32	0.44
1:A:309:PHE:CZ	1:B:294:VAL:HG22	2.53	0.44
1:B:122:VAL:HG22	1:B:127:THR:O	2.18	0.44
1:B:229:PHE:CD2	1:B:240:CYS:HB2	2.53	0.44
1:A:115:ASP:OD2	1:A:120:ARG:HB3	2.18	0.44
1:C:183:ALA:HA	1:C:266:PHE:CZ	2.52	0.44
1:B:147:THR:HG22	1:B:148:GLU:N	2.33	0.43
1:D:265:THR:HG21	1:D:278:ALA:O	2.18	0.43
1:B:270:GLY:O	1:B:296:PRO:HD3	2.18	0.43
1:C:361:LEU:HD23	1:C:366:GLN:HB2	2.00	0.43
1:D:109:ASN:ND2	1:D:321:GLY:HA2	2.33	0.43
1:A:276:ILE:CG1	1:A:301:LEU:HD21	2.48	0.43
1:A:360:GLU:HB3	3:A:502:ACT:H3	2.00	0.43
1:C:346:ILE:HG23	1:C:371:VAL:HG23	2.00	0.43
3:D:501:ACT:H2	4:D:377:NAD:H62A	1.82	0.43
1:D:294:VAL:HG21	3:D:378:ACT:H3	2.01	0.43
1:A:18:LYS:N	1:A:53:ILE:O	2.48	0.43
1:B:45:ILE:HD11	1:B:372:LEU:HD11	1.99	0.43
1:A:152:VAL:HG23	1:A:157:VAL:HG23	1.99	0.43
1:A:164:ALA:HA	1:A:165:PRO:HD2	1.90	0.43
1:A:328:VAL:O	1:A:332:VAL:HG23	2.18	0.43
1:C:10:LYS:HA	1:C:24:GLU:O	2.19	0.43
1:A:110:LEU:HD11	1:A:116:ILE:CD1	2.48	0.43
1:C:328:VAL:N	1:C:329:PRO:HD2	2.33	0.43
1:A:14:LEU:HD11	1:A:19:GLN:O	2.18	0.43
1:A:347:THR:O	1:A:348:HIS:CD2	2.72	0.43
1:B:185:LYS:O	1:B:188:LYS:HG3	2.19	0.43
1:B:226:LYS:HA	1:B:229:PHE:CE1	2.53	0.43
1:C:253:VAL:O	1:C:257:MET:HG2	2.18	0.43
1:D:7:ILE:HG22	1:D:8:LYS:N	2.33	0.43
1:A:179:GLY:HA2	1:A:207:VAL:HG12	2.01	0.43
1:A:229:PHE:N	1:A:229:PHE:CD1	2.86	0.43
1:A:291:VAL:CG1	1:A:316:GLY:HA2	2.49	0.43
1:B:244:LYS:HD3	1:B:244:LYS:HA	1.64	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:ILE:O	1:A:116:ILE:HG22	2.19	0.43
1:B:317:CYS:SG	1:B:320:GLY:HA2	2.59	0.43
1:D:349:VAL:HA	1:D:371:VAL:O	2.19	0.43
1:B:51:HIS:HB3	1:B:57:MET:HB2	2.01	0.43
1:A:100:CYS:HB2	1:A:112:ILE:CG2	2.44	0.42
1:A:123:LEU:HD11	1:A:129:ARG:HG2	2.00	0.42
1:A:231:LYS:HE2	1:A:344:GLN:OE1	2.19	0.42
1:A:19:GLN:HG2	1:A:20:PRO:CD	2.45	0.42
1:B:231:LYS:O	1:B:235:VAL:HG23	2.20	0.42
1:C:205:LEU:O	1:C:209:MET:HG3	2.20	0.42
1:C:347:THR:CG2	1:C:368:ILE:H	2.32	0.42
1:D:65:VAL:HG23	1:D:146:PHE:HD2	1.85	0.42
1:B:192:GLY:HA2	1:B:217:SER:OG	2.19	0.42
1:C:300:MET:CE	1:D:304:ASP:HB2	2.48	0.42
1:D:171:LEU:HD11	1:D:346:ILE:HG12	2.01	0.42
1:D:361:LEU:HD23	1:D:361:LEU:HA	1.92	0.42
1:B:122:VAL:HG13	1:B:123:LEU:O	2.19	0.42
1:B:348:HIS:HB2	1:B:370:THR:HG23	2.00	0.42
1:C:92:LEU:HD22	1:C:328:VAL:HG21	2.02	0.42
1:B:72:ILE:HG13	1:B:86:GLY:O	2.20	0.42
1:A:36:VAL:O	1:A:151:VAL:HA	2.19	0.42
1:B:122:VAL:HG13	1:B:123:LEU:N	2.35	0.42
1:C:225:ASN:HD22	1:C:228:LYS:HE3	1.83	0.42
1:B:9:CYS:O	1:B:25:GLU:HA	2.18	0.42
1:D:69:ALA:HB3	1:D:145:THR:HG21	2.02	0.42
1:D:198:PHE:HA	1:D:222:ILE:HG13	2.02	0.42
1:A:331:LEU:HD12	1:A:331:LEU:HA	1.85	0.42
1:B:26:ILE:HD11	1:B:147:THR:CG2	2.50	0.42
1:C:43:THR:OG1	1:C:69:ALA:HB2	2.20	0.42
1:D:218:ARG:HH11	1:D:258:THR:HG22	1.83	0.42
1:A:179:GLY:HA3	1:A:206:SER:HB2	2.01	0.41
1:A:353:LYS:HD2	1:A:353:LYS:H	1.82	0.41
1:B:17:GLN:C	1:B:19:GLN:H	2.24	0.41
1:B:307:LEU:CD2	1:B:312:ARG:HH12	2.33	0.41
1:C:347:THR:HG1	1:C:348:HIS:CD2	2.38	0.41
1:A:177:SER:HB3	1:A:322:LEU:HD12	2.02	0.41
1:D:122:VAL:CG2	1:D:126:GLY:HA2	2.50	0.41
1:D:257:MET:HE2	1:D:257:MET:HB2	1.91	0.41
1:A:152:VAL:HG21	1:A:157:VAL:HG23	2.02	0.41
1:A:160:ILE:HD12	1:A:332:VAL:HG11	2.01	0.41
1:A:65:VAL:HG23	1:A:146:PHE:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:LYS:HG2	1:A:264:TYR:OH	2.20	0.41
1:B:84:LYS:HG3	1:B:85:PRO:HD2	2.01	0.41
1:A:224:LEU:CD2	1:A:244:LYS:HE3	2.49	0.41
1:A:15:TRP:HZ2	1:A:24:GLU:OE1	2.04	0.41
1:A:36:VAL:HG22	1:A:76:ILE:HG22	2.02	0.41
1:C:26:ILE:CG2	1:C:27:GLU:N	2.83	0.41
1:A:28:VAL:HG21	1:A:149:TYR:HB2	2.02	0.41
1:B:15:TRP:HZ2	1:B:132:CYS:SG	2.40	0.41
1:A:110:LEU:HD22	1:B:310:THR:HG22	2.02	0.41
1:A:130:PHE:HE1	1:A:150:THR:HA	1.86	0.41
1:B:194:THR:HA	1:B:218:ARG:O	2.21	0.41
1:B:254:LEU:HD23	1:B:254:LEU:HA	1.90	0.41
1:C:306:MET:HE1	1:C:309:PHE:CD2	2.55	0.41
1:D:304:ASP:OD2	1:D:306:MET:HB2	2.21	0.41
1:B:331:LEU:HD23	1:B:331:LEU:HA	1.91	0.41
1:B:231:LYS:NZ	1:B:344:GLN:O	2.49	0.41
1:C:14:LEU:HD11	1:C:19:GLN:O	2.20	0.41
1:C:294:VAL:HG23	4:C:377:NAD:H1D	2.02	0.41
1:B:276:ILE:HD11	1:B:301:LEU:CD1	2.49	0.41
1:A:129:ARG:HG3	1:A:151:VAL:HB	2.02	0.41
1:C:122:VAL:HG21	1:C:126:GLY:HA2	2.02	0.41
1:C:315:LYS:HE2	1:D:313:THR:OG1	2.21	0.41
1:C:355:ILE:HG23	1:C:356:SER:N	2.36	0.41
1:D:241:ILE:HD12	1:D:257:MET:HE1	1.97	0.41
1:C:176:PHE:HD1	1:C:206:SER:OG	2.03	0.41
1:A:69:ALA:O	1:A:90:ILE:HG23	2.21	0.40
1:B:10:LYS:O	1:B:148:GLU:HG3	2.21	0.40
1:B:249:PRO:O	1:B:253:VAL:HG23	2.20	0.40
1:C:8:LYS:HA	1:C:26:ILE:O	2.21	0.40
1:D:222:ILE:HA	1:D:241:ILE:O	2.21	0.40
1:D:241:ILE:HD11	1:D:257:MET:CE	2.50	0.40
1:C:70:THR:OG1	1:C:170:CYS:HB3	2.22	0.40
1:C:241:ILE:CG1	1:C:242:SER:N	2.85	0.40
1:D:64:ILE:HG21	1:D:147:THR:OG1	2.21	0.40
1:B:164:ALA:O	1:B:166:PRO:HD3	2.21	0.40
1:B:92:LEU:HD13	1:B:324:SER:HB3	2.03	0.40
1:C:33:THR:HG22	1:C:34:LYS:HD3	2.02	0.40
1:C:84:LYS:HG2	1:C:87:ASP:OD2	2.21	0.40
1:D:93:PHE:HB2	1:D:141:MET:HB3	2.04	0.40
1:A:168:LYS:HA	1:A:346:ILE:HD11	2.04	0.40
1:B:139:HIS:CD2	1:B:139:HIS:N	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:ASP:OD1	1:D:120:ARG:HB2	2.21	0.40
1:A:353:LYS:HD2	1:A:353:LYS:N	2.37	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	371/373 (100%)	328 (88%)	36 (10%)	7 (2%)	8	36
1	B	371/373 (100%)	332 (90%)	32 (9%)	7 (2%)	8	36
1	C	371/373 (100%)	323 (87%)	41 (11%)	7 (2%)	8	36
1	D	371/373 (100%)	337 (91%)	30 (8%)	4 (1%)	14	50
All	All	1484/1492 (100%)	1320 (89%)	139 (9%)	25 (2%)	9	39

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	VAL
1	B	3	ALA
1	C	324	SER
1	A	3	ALA
1	B	324	SER
1	D	109	ASN
1	B	249	PRO
1	C	175	GLY
1	C	229	PHE
1	C	284	MET
1	A	109	ASN
1	B	110	LEU
1	B	174	CYS

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Mol	Chain	Res	Type
1	D	174	CYS
1	A	110	LEU
1	A	284	MET
1	C	174	CYS
1	D	284	MET
1	B	65	VAL
1	A	166	PRO
1	A	236	GLY
1	C	65	VAL
1	D	65	VAL
1	B	368	ILE
1	C	269	ILE

### 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	312/312 (100%)	290 (93%)	22 (7%)	14	46
1	B	312/312 (100%)	284 (91%)	28 (9%)	9	35
1	C	312/312 (100%)	296 (95%)	16 (5%)	24	60
1	D	312/312 (100%)	289 (93%)	23 (7%)	13	44
All	All	1248/1248 (100%)	1159 (93%)	89 (7%)	14	46

All (89) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	83	VAL
1	A	96	GLN
1	A	98	ARG
1	A	101	ASN
1	A	113	ARG
1	A	118	THR
1	A	130	PHE
1	A	207	VAL

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Mol	Chain	Res	Type
1	A	213	SER
1	A	233	MET
1	A	248	LYS
1	A	268	VAL
1	A	273	GLU
1	A	277	ASP
1	A	300	MET
1	A	301	LEU
1	A	331	LEU
1	A	338	LYS
1	A	339	LYS
1	A	353	LYS
1	A	362	LEU
1	B	2	THR
1	B	16	GLU
1	B	19	GLN
1	B	40	ILE
1	B	53	ILE
1	B	57	MET
1	B	72	ILE
1	B	99	GLU
1	B	101	ASN
1	B	112	ILE
1	B	116	ILE
1	B	118	THR
1	B	122	VAL
1	B	131	THR
1	B	135	LYS
1	B	153	ASP
1	B	166	PRO
1	B	167	GLU
1	B	185	LYS
1	B	242	SER
1	B	249	PRO
1	B	251	SER
1	B	303	TYR
1	B	310	THR
1	B	319	PHE
1	B	322	LEU
1	B	325	ARG
1	B	338	LYS
1	C	5	LYS

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Mol	Chain	Res	Type
1	C	48	THR
1	C	60	LYS
1	C	70	THR
1	C	107	ASP
1	C	131	THR
1	C	147	THR
1	C	196	VAL
1	C	246	SER
1	C	249	PRO
1	C	262	VAL
1	C	282	CYS
1	C	286	TYR
1	C	304	ASP
1	C	339	LYS
1	C	340	PHE
1	D	10	LYS
1	D	19	GLN
1	D	33	THR
1	D	84	LYS
1	D	116	ILE
1	D	118	THR
1	D	131	THR
1	D	167	GLU
1	D	222	ILE
1	D	231	LYS
1	D	251	SER
1	D	261	ASN
1	D	267	GLU
1	D	268	VAL
1	D	274	THR
1	D	275	MET
1	D	284	MET
1	D	303	TYR
1	D	310	THR
1	D	339	LYS
1	D	353	LYS
1	D	356	SER
1	D	373	THR

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

Mol	Chain	Res	Type
1	A	142	ASN
1	A	261	ASN
1	A	283	HIS
1	B	19	GLN
1	B	96	GLN
1	B	101	ASN
1	B	261	ASN
1	B	366	GLN
1	C	142	ASN
1	C	344	GLN
1	D	142	ASN
1	D	261	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 16 are monoatomic - leaving 14 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	$\# Z  > 2$
3	ACT	D	378	-	1,3,3	3.27	1 (100%)	0,3,3	0.00	-
4	NAD	B	377	2	42,48,48	2.48	11 (26%)	50,73,73	2.04	10 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAD	A	377	2	42,48,48	2.02	10 (23%)	50,73,73	1.91	15 (30%)
3	ACT	B	503	2	1,3,3	3.57	1 (100%)	0,3,3	0.00	-
4	NAD	C	377	2	42,48,48	2.67	8 (19%)	50,73,73	1.83	9 (18%)
3	ACT	A	378	-	1,3,3	2.46	1 (100%)	0,3,3	0.00	-
3	ACT	B	502	-	1,3,3	3.36	1 (100%)	0,3,3	0.00	-
4	NAD	D	377	2	42,48,48	2.57	10 (23%)	50,73,73	2.20	13 (26%)
3	ACT	D	501	-	1,3,3	2.64	1 (100%)	0,3,3	0.00	-
3	ACT	A	501	-	1,3,3	2.18	1 (100%)	0,3,3	0.00	-
3	ACT	A	502	-	1,3,3	3.70	1 (100%)	0,3,3	0.00	-
3	ACT	B	501	2	1,3,3	2.43	1 (100%)	0,3,3	0.00	-
3	ACT	C	378	-	1,3,3	2.60	1 (100%)	0,3,3	0.00	-
3	ACT	B	378	2	1,3,3	1.45	0	0,3,3	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAD	B	377	2	-	13/26/62/62	0/5/5/5
4	NAD	A	377	2	-	9/26/62/62	0/5/5/5
4	NAD	D	377	2	-	11/26/62/62	0/5/5/5
4	NAD	C	377	2	-	15/26/62/62	0/5/5/5

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	377	NAD	C3N-C7N	-13.96	1.29	1.50
4	D	377	NAD	C3N-C7N	-12.41	1.31	1.50
4	B	377	NAD	C3N-C7N	-10.90	1.34	1.50
4	A	377	NAD	C3N-C7N	-8.36	1.38	1.50
4	C	377	NAD	C2A-N3A	5.32	1.40	1.32
4	B	377	NAD	C2A-N3A	5.20	1.40	1.32
4	D	377	NAD	O4D-C1D	4.99	1.48	1.41
4	A	377	NAD	C2N-N1N	-4.32	1.29	1.35
4	D	377	NAD	C4N-C3N	-4.10	1.32	1.39
3	A	502	ACT	CH3-C	3.70	1.53	1.48
4	D	377	NAD	C5N-C4N	-3.69	1.31	1.38
4	B	377	NAD	C2A-N1A	3.66	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	377	NAD	C4N-C3N	-3.64	1.33	1.39
4	B	377	NAD	C4N-C3N	-3.64	1.33	1.39
3	B	503	ACT	CH3-C	3.57	1.53	1.48
4	A	377	NAD	C2A-N3A	3.56	1.37	1.32
4	C	377	NAD	C4N-C3N	-3.56	1.33	1.39
4	B	377	NAD	C4A-N3A	3.45	1.40	1.35
4	D	377	NAD	C2A-N3A	3.40	1.37	1.32
3	B	502	ACT	CH3-C	3.36	1.53	1.48
4	B	377	NAD	C5N-C4N	-3.33	1.31	1.38
4	C	377	NAD	C2A-N1A	3.29	1.40	1.33
3	D	378	ACT	CH3-C	3.27	1.52	1.48
4	C	377	NAD	C8A-N7A	3.15	1.40	1.34
4	B	377	NAD	O4B-C1B	3.15	1.45	1.41
4	D	377	NAD	C4A-N3A	3.11	1.39	1.35
4	B	377	NAD	C2N-C3N	-3.09	1.34	1.39
4	D	377	NAD	C2A-N1A	2.88	1.39	1.33
4	D	377	NAD	C2N-C3N	-2.87	1.34	1.39
4	C	377	NAD	C2N-C3N	-2.86	1.34	1.39
4	A	377	NAD	C5N-C4N	-2.85	1.32	1.38
4	A	377	NAD	C8A-N7A	2.79	1.39	1.34
4	D	377	NAD	C2N-N1N	-2.77	1.31	1.35
3	D	501	ACT	CH3-C	2.64	1.52	1.48
4	B	377	NAD	O4D-C1D	-2.61	1.37	1.41
3	C	378	ACT	CH3-C	2.60	1.52	1.48
4	C	377	NAD	C5N-C4N	-2.60	1.33	1.38
4	A	377	NAD	C2A-N1A	2.54	1.38	1.33
4	B	377	NAD	C8A-N7A	2.47	1.39	1.34
3	A	378	ACT	CH3-C	2.46	1.51	1.48
3	B	501	ACT	CH3-C	2.43	1.51	1.48
4	D	377	NAD	C8A-N7A	2.33	1.38	1.34
4	A	377	NAD	C6N-N1N	-2.22	1.30	1.35
3	A	501	ACT	CH3-C	2.18	1.51	1.48
4	A	377	NAD	C4A-N3A	2.14	1.38	1.35
4	A	377	NAD	C2N-C3N	-2.11	1.35	1.39
4	B	377	NAD	C2B-C1B	2.11	1.57	1.53
4	C	377	NAD	C2D-C1D	2.02	1.56	1.53

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	377	NAD	O4D-C1D-C2D	-6.84	96.93	106.93
4	D	377	NAD	O7N-C7N-C3N	-6.65	111.67	119.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	377	NAD	O4D-C1D-C2D	-6.04	98.10	106.93
4	A	377	NAD	O4B-C1B-C2B	-5.59	98.76	106.93
4	D	377	NAD	N3A-C2A-N1A	-5.41	120.23	128.68
4	B	377	NAD	O7N-C7N-N7N	-5.28	115.07	122.58
4	D	377	NAD	C3N-C7N-N7N	4.93	123.67	117.75
4	B	377	NAD	C6N-N1N-C2N	-4.56	117.82	121.97
4	A	377	NAD	C4A-C5A-N7A	4.46	114.04	109.40
4	D	377	NAD	C3B-C2B-C1B	-4.42	94.32	100.98
4	B	377	NAD	C3N-C7N-N7N	4.39	123.02	117.75
4	C	377	NAD	O4B-C1B-C2B	-4.31	100.63	106.93
4	B	377	NAD	O5B-C5B-C4B	-4.28	94.24	108.99
4	C	377	NAD	C6N-N1N-C2N	-4.17	118.17	121.97
4	A	377	NAD	C3D-C2D-C1D	-4.16	94.71	100.98
4	D	377	NAD	C2N-C3N-C4N	4.00	122.79	118.26
4	A	377	NAD	C3N-C7N-N7N	3.96	122.50	117.75
4	B	377	NAD	N3A-C2A-N1A	-3.82	122.70	128.68
4	A	377	NAD	N3A-C2A-N1A	-3.78	122.76	128.68
4	C	377	NAD	C2N-C3N-C4N	3.74	122.50	118.26
4	C	377	NAD	N3A-C2A-N1A	-3.39	123.37	128.68
4	D	377	NAD	C4A-C5A-N7A	3.37	112.91	109.40
4	D	377	NAD	C6N-N1N-C2N	-3.32	118.94	121.97
4	D	377	NAD	O5D-C5D-C4D	3.06	119.53	108.99
4	A	377	NAD	N6A-C6A-N1A	3.05	124.92	118.57
4	D	377	NAD	O2N-PN-O1N	-3.05	97.14	112.24
4	D	377	NAD	N6A-C6A-N1A	3.04	124.89	118.57
4	A	377	NAD	O4D-C1D-C2D	-2.87	102.73	106.93
4	A	377	NAD	O7N-C7N-N7N	-2.82	118.57	122.58
4	A	377	NAD	C5A-C6A-N6A	-2.77	116.15	120.35
4	D	377	NAD	C4N-C3N-C7N	-2.72	113.77	121.04
4	A	377	NAD	O5B-C5B-C4B	-2.71	99.65	108.99
4	C	377	NAD	C2B-C3B-C4B	-2.59	97.60	102.64
4	D	377	NAD	O2N-PN-O5D	2.55	119.58	107.75
4	C	377	NAD	PN-O3-PA	-2.48	124.31	132.83
4	A	377	NAD	C2B-C3B-C4B	-2.47	97.84	102.64
4	B	377	NAD	PN-O3-PA	-2.47	124.35	132.83
4	B	377	NAD	O4B-C4B-C3B	2.39	109.84	105.11
4	C	377	NAD	C2D-C3D-C4D	-2.39	98.00	102.64
4	C	377	NAD	C4N-C3N-C7N	-2.31	114.85	121.04
4	D	377	NAD	C2A-N1A-C6A	2.26	122.62	118.75
4	A	377	NAD	O5D-C5D-C4D	2.25	116.74	108.99
4	A	377	NAD	O5D-PN-O1N	-2.20	100.47	109.07
4	B	377	NAD	O2A-PA-O1A	-2.16	101.56	112.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	377	NAD	C2B-C3B-C4B	-2.08	98.61	102.64
4	A	377	NAD	C2N-N1N-C1D	-2.07	114.53	119.14
4	A	377	NAD	O5B-PA-O1A	-2.06	101.02	109.07

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	377	NAD	O4D-C1D-N1N-C6N
4	A	377	NAD	C2D-C1D-N1N-C2N
4	C	377	NAD	C5B-O5B-PA-O1A
4	C	377	NAD	C5B-O5B-PA-O2A
4	C	377	NAD	C5B-O5B-PA-O3
4	C	377	NAD	C3B-C4B-C5B-O5B
4	C	377	NAD	O4D-C1D-N1N-C2N
4	C	377	NAD	O4D-C1D-N1N-C6N
4	C	377	NAD	C2D-C1D-N1N-C2N
4	C	377	NAD	C2D-C1D-N1N-C6N
4	D	377	NAD	C5B-O5B-PA-O1A
4	D	377	NAD	C5B-O5B-PA-O2A
4	D	377	NAD	PN-O3-PA-O5B
4	D	377	NAD	O4D-C1D-N1N-C2N
4	D	377	NAD	O4D-C1D-N1N-C6N
4	D	377	NAD	C2D-C1D-N1N-C2N
4	B	377	NAD	C5B-O5B-PA-O1A
4	B	377	NAD	C5B-O5B-PA-O2A
4	B	377	NAD	C5B-O5B-PA-O3
4	B	377	NAD	C5D-O5D-PN-O3
4	B	377	NAD	C5D-O5D-PN-O2N
4	A	377	NAD	O4D-C4D-C5D-O5D
4	C	377	NAD	O4D-C4D-C5D-O5D
4	B	377	NAD	O4B-C4B-C5B-O5B
4	B	377	NAD	C3B-C4B-C5B-O5B
4	C	377	NAD	O4B-C4B-C5B-O5B
4	C	377	NAD	C3D-C4D-C5D-O5D
4	A	377	NAD	C3D-C4D-C5D-O5D
4	B	377	NAD	PN-O3-PA-O5B
4	B	377	NAD	PA-O3-PN-O5D
4	D	377	NAD	O4B-C4B-C5B-O5B
4	C	377	NAD	C5D-O5D-PN-O3
4	D	377	NAD	C5B-O5B-PA-O3
4	B	377	NAD	C5D-O5D-PN-O1N

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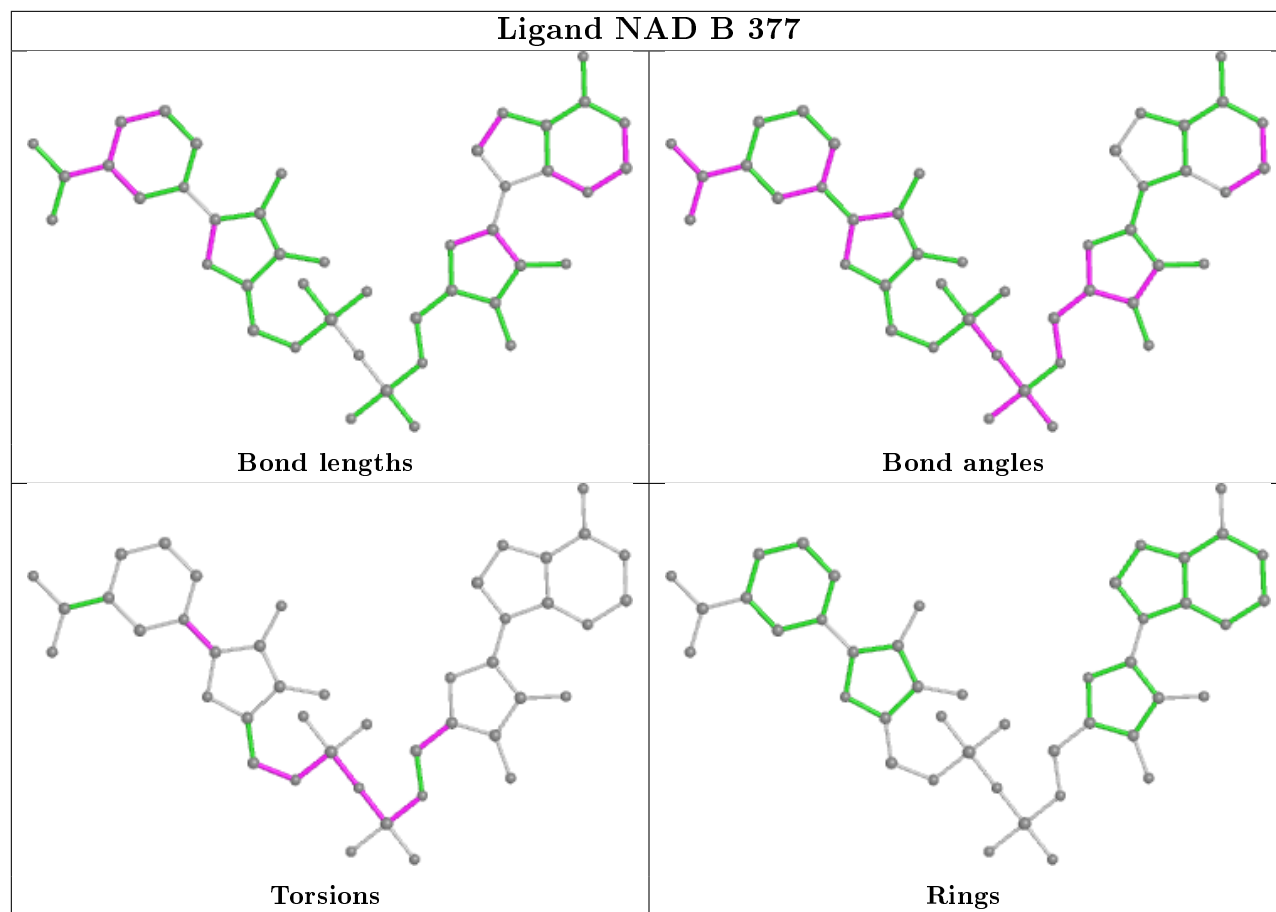
Mol	Chain	Res	Type	Atoms
4	A	377	NAD	O4B-C4B-C5B-O5B
4	D	377	NAD	C3B-C4B-C5B-O5B
4	B	377	NAD	C4D-C5D-O5D-PN
4	A	377	NAD	C3B-C4B-C5B-O5B
4	B	377	NAD	C2D-C1D-N1N-C2N
4	A	377	NAD	PA-O3-PN-O2N
4	C	377	NAD	PA-O3-PN-O1N
4	C	377	NAD	PA-O3-PN-O2N
4	B	377	NAD	PN-O3-PA-O2A
4	A	377	NAD	C5B-O5B-PA-O2A
4	A	377	NAD	C5D-O5D-PN-O2N
4	C	377	NAD	C5D-O5D-PN-O2N
4	D	377	NAD	C5D-O5D-PN-O1N
4	D	377	NAD	O4D-C4D-C5D-O5D

There are no ring outliers.

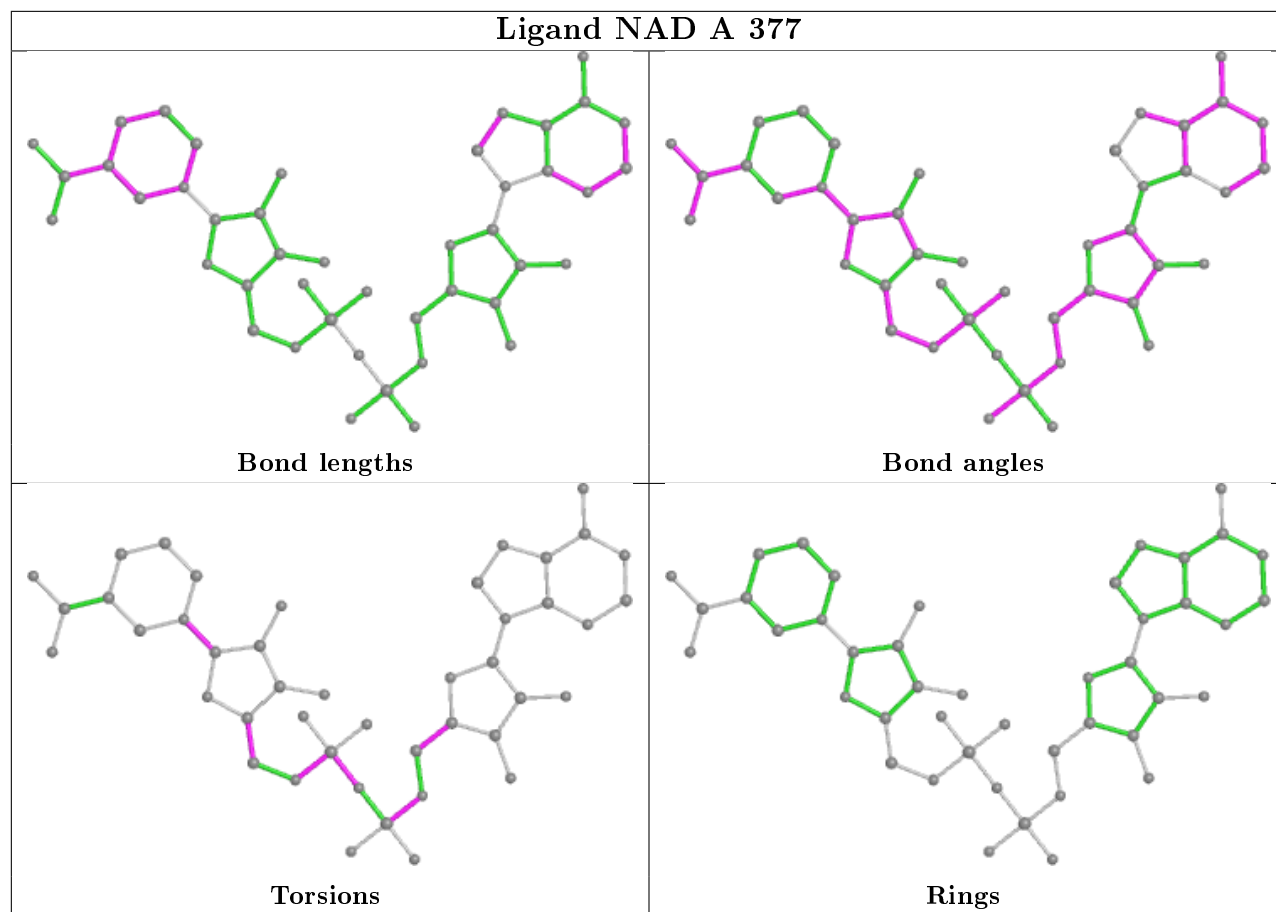
9 monomers are involved in 20 short contacts:

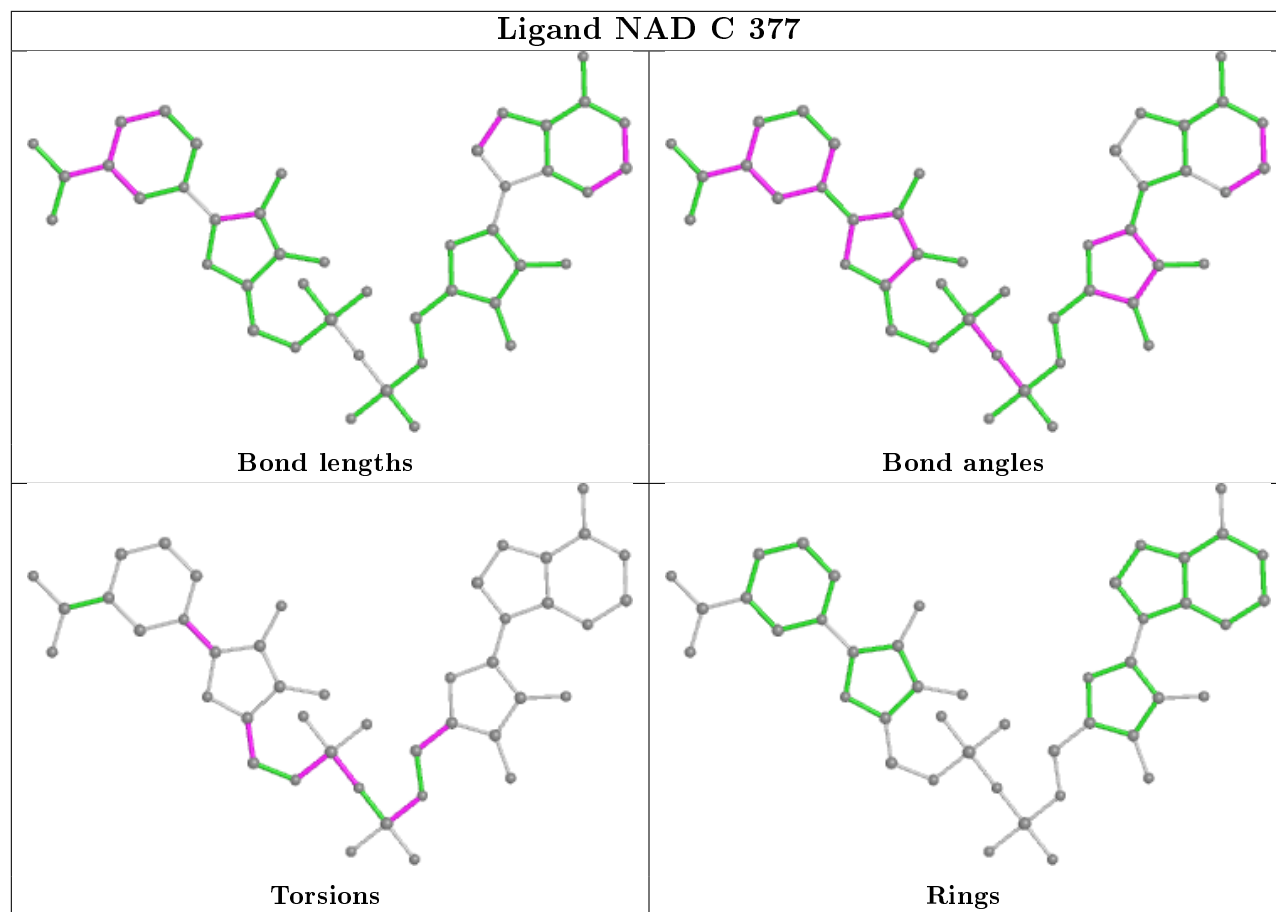
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	378	ACT	2	0
4	B	377	NAD	2	0
4	A	377	NAD	2	0
4	C	377	NAD	3	0
3	A	378	ACT	1	0
4	D	377	NAD	9	0
3	D	501	ACT	1	0
3	A	502	ACT	2	0
3	C	378	ACT	1	0

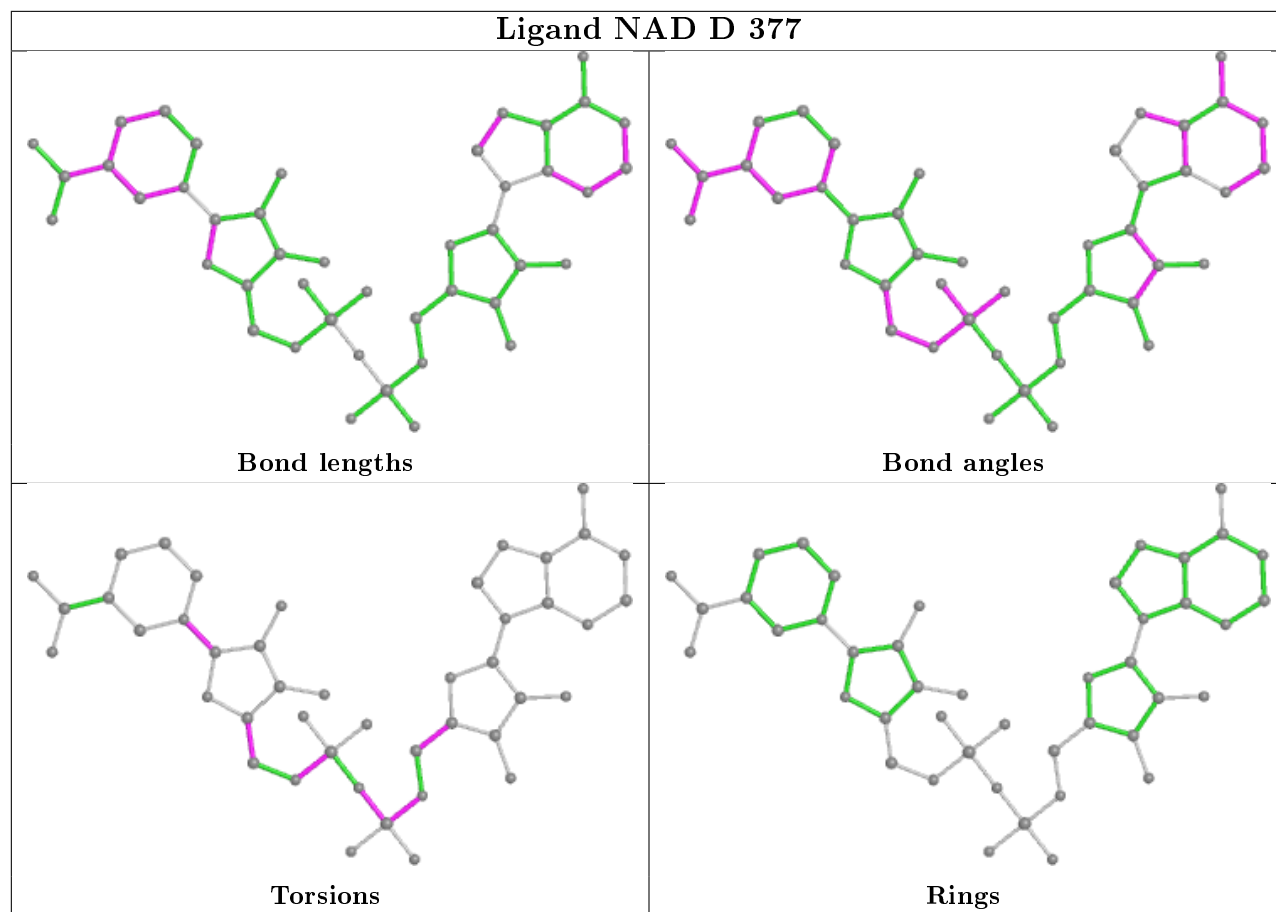
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	373/373 (100%)	-0.52	1 (0%) 94 84	20, 20, 20, 20	0
1	B	373/373 (100%)	-0.66	0 100 100	15, 15, 15, 15	0
1	C	373/373 (100%)	-0.45	0 100 100	26, 26, 26, 26	0
1	D	373/373 (100%)	-0.70	0 100 100	15, 15, 15, 15	0
All	All	1492/1492 (100%)	-0.58	1 (0%) 95 89	15, 15, 26, 26	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	GLY	2.5

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	ACT	A	502	4/4	0.59	0.40	19,19,19,19	0

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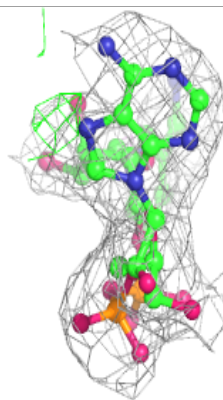
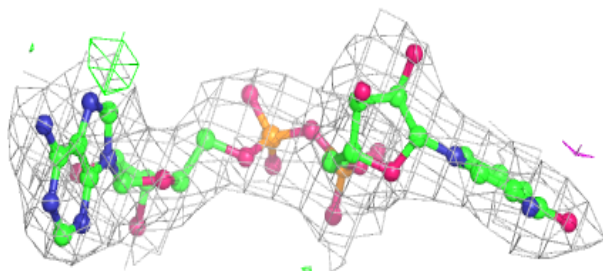
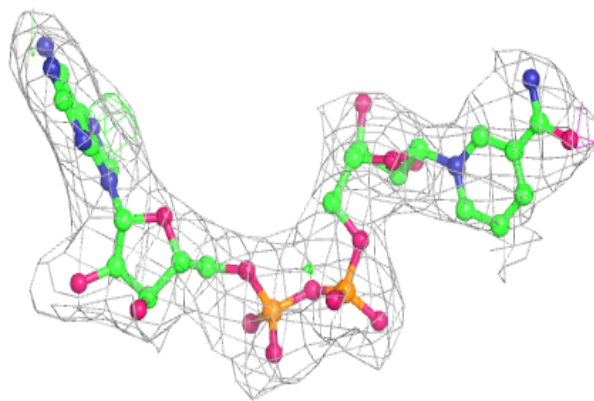
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	C	401	1/1	0.84	0.12	15,15,15,15	1
2	ZN	D	403	1/1	0.86	0.09	17,17,17,17	1
3	ACT	C	378	4/4	0.88	0.48	25,25,25,25	0
3	ACT	A	501	4/4	0.90	0.18	19,19,19,19	0
3	ACT	D	378	4/4	0.93	0.19	14,14,14,14	0
4	NAD	C	377	44/44	0.94	0.14	25,25,25,25	0
3	ACT	B	502	4/4	0.94	0.19	15,15,15,15	0
4	NAD	B	377	44/44	0.95	0.15	15,15,15,15	0
3	ACT	A	378	4/4	0.95	0.17	19,19,19,19	0
3	ACT	D	501	4/4	0.96	0.10	14,14,14,14	0
2	ZN	D	376	1/1	0.96	0.13	14,14,14,14	0
2	ZN	B	401	1/1	0.96	0.04	23,23,23,23	0
2	ZN	D	401	1/1	0.96	0.06	24,24,24,24	0
2	ZN	A	401	1/1	0.96	0.04	15,15,15,15	0
3	ACT	B	503	4/4	0.97	0.23	15,15,15,15	0
4	NAD	A	377	44/44	0.97	0.19	19,19,19,19	0
3	ACT	B	501	4/4	0.97	0.11	15,15,15,15	0
2	ZN	D	375	1/1	0.97	0.08	14,14,14,14	0
2	ZN	D	402	1/1	0.97	0.14	27,27,27,27	0
4	NAD	D	377	44/44	0.97	0.15	14,14,14,14	0
3	ACT	B	378	4/4	0.98	0.18	15,15,15,15	0
2	ZN	A	375	1/1	0.98	0.03	19,19,19,19	0
2	ZN	B	376	1/1	0.98	0.13	15,15,15,15	0
2	ZN	B	403	1/1	0.98	0.10	24,24,24,24	0
2	ZN	B	375	1/1	0.98	0.03	15,15,15,15	0
2	ZN	C	375	1/1	0.99	0.04	25,25,25,25	0
2	ZN	C	376	1/1	0.99	0.12	25,25,25,25	0
2	ZN	B	402	1/1	0.99	0.05	19,19,19,19	0
2	ZN	A	376	1/1	0.99	0.16	19,19,19,19	0

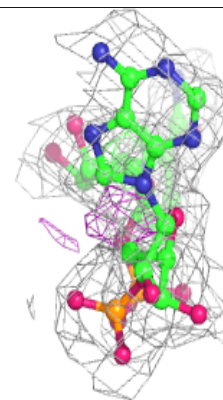
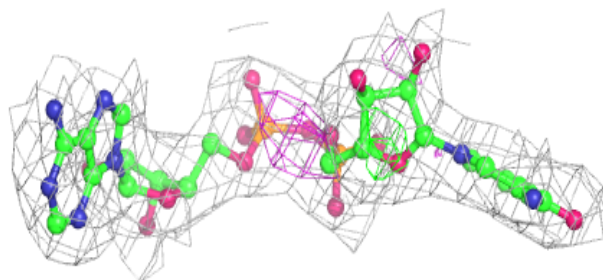
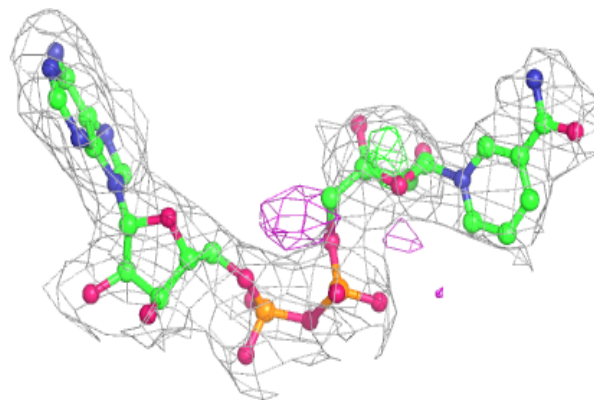
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around NAD C 377:**

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

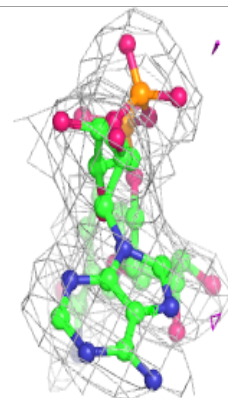
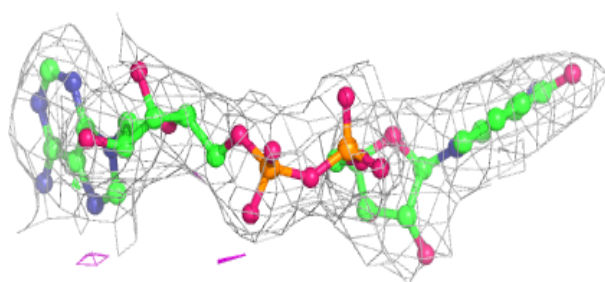
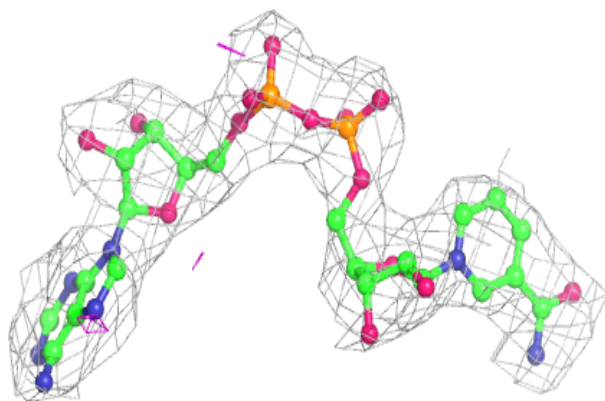
**Electron density around NAD B 377:**

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

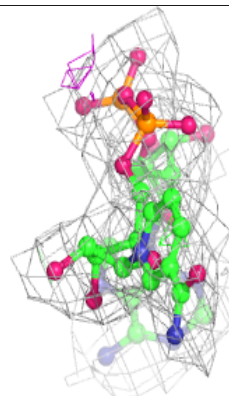
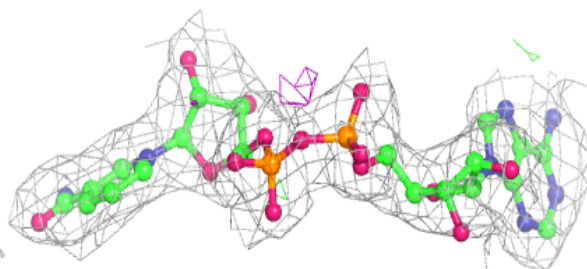
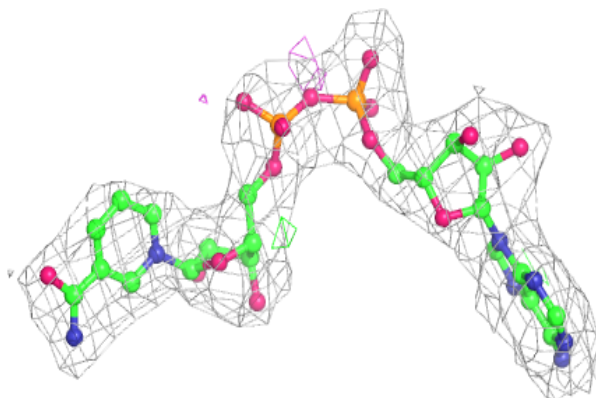


**Electron density around NAD A 377:**

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

**Electron density around NAD D 377:**

$2mF_o-DF_c$  (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.