



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 02:45 am BST

PDB ID : 1T90  
Title : Crystal structure of methylmalonate semialdehyde dehydrogenase from *Bacillus subtilis*  
Authors : Dubourg, H.; Didierjean, C.; Stines-Chaumeil, C.; Talfournier, F.; Branlant, G.; Aubry, A.; Corbier, C.  
Deposited on : 2004-05-14  
Resolution : 2.50 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

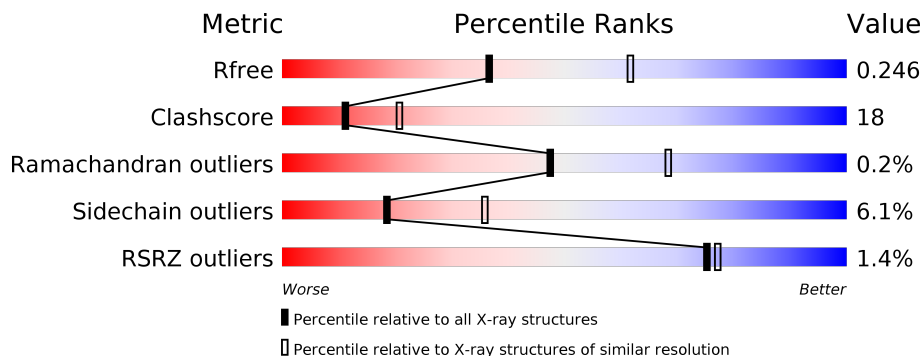
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	486	<p>63% 32%</p>
1	B	486	<p>65% 32%</p>
1	C	486	<p>68% 28%</p>
1	D	486	<p>67% 31%</p>

## 2 Entry composition [i](#)

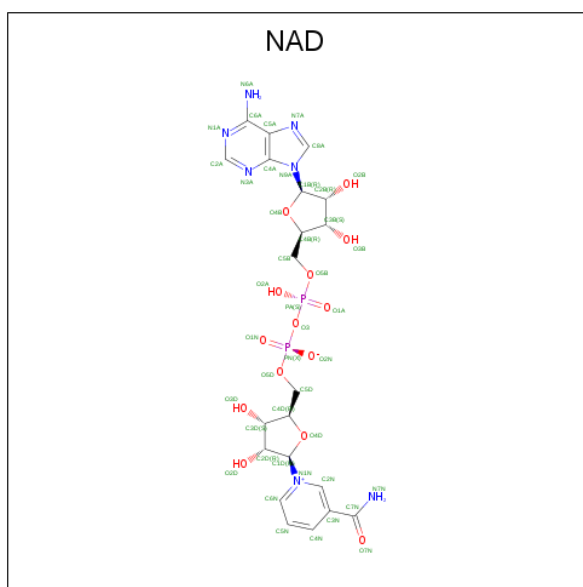
There are 3 unique types of molecules in this entry. The entry contains 16006 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Probable methylmalonate-semialdehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	484	Total 3741	C 2390	N 626	O 708	S 17	0	0	0
1	B	484	Total 3741	C 2390	N 626	O 708	S 17	0	0	0
1	C	484	Total 3741	C 2390	N 626	O 708	S 17	0	0	0
1	D	484	Total 3741	C 2390	N 626	O 708	S 17	0	0	0

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



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

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

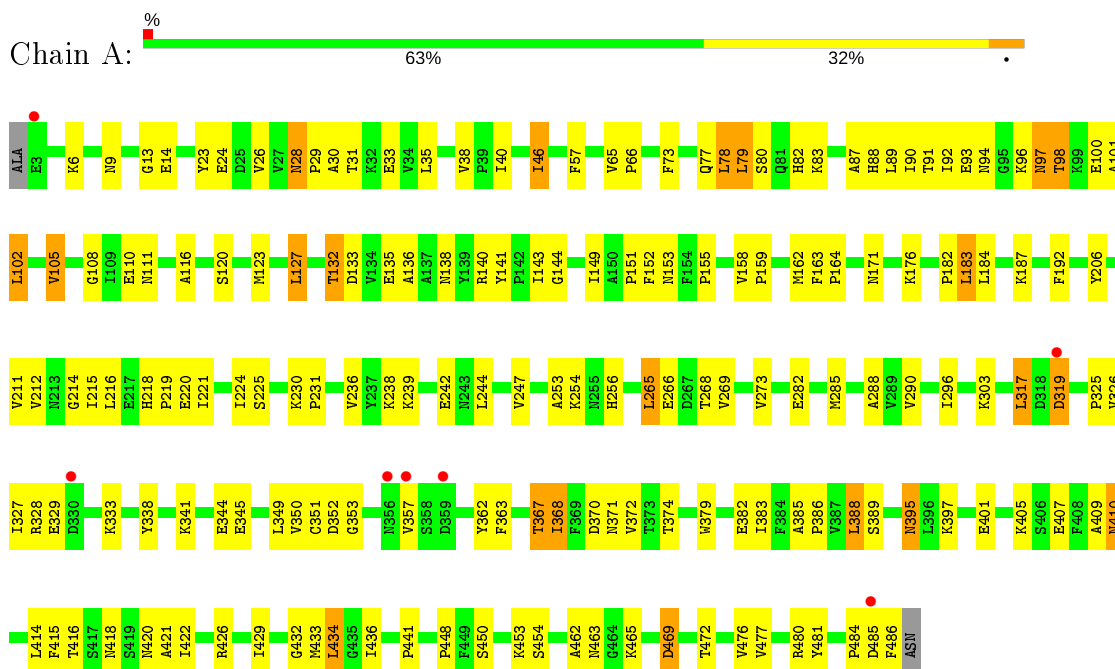
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	202	Total	O	0	0
			202	202		
3	B	229	Total	O	0	0
			229	229		
3	C	246	Total	O	0	0
			246	246		
3	D	189	Total	O	0	0
			189	189		

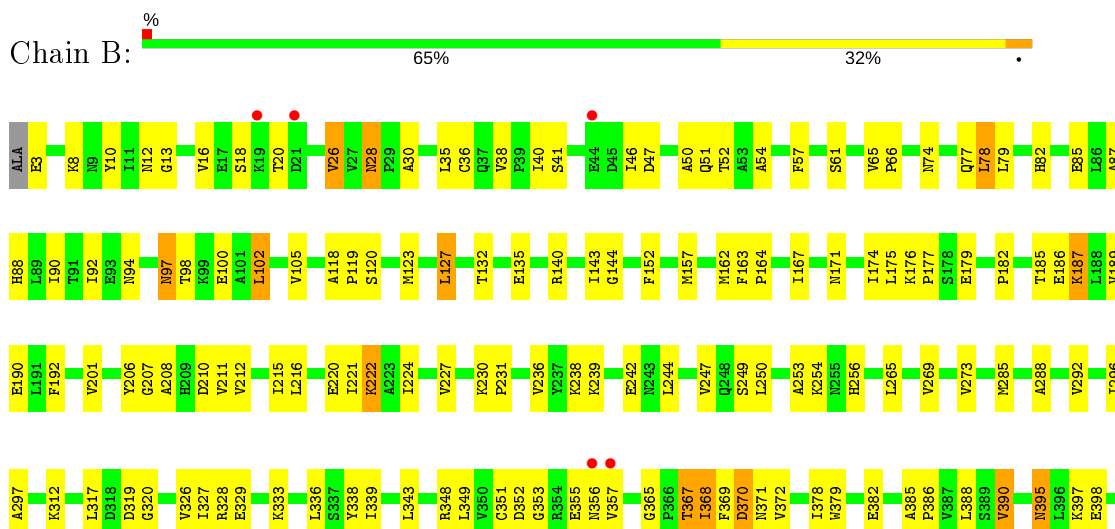
### 3 Residue-property plots [i](#)

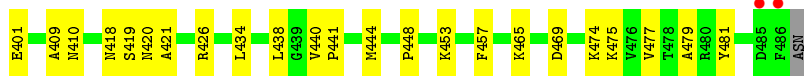
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

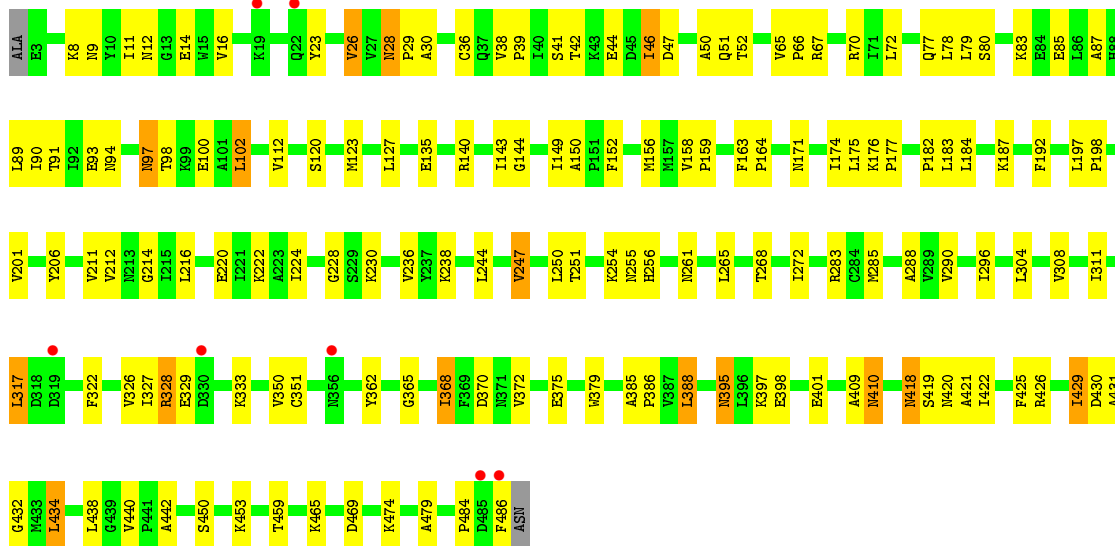


- Molecule 1: Probable methylmalonate-semialdehyde dehydrogenase

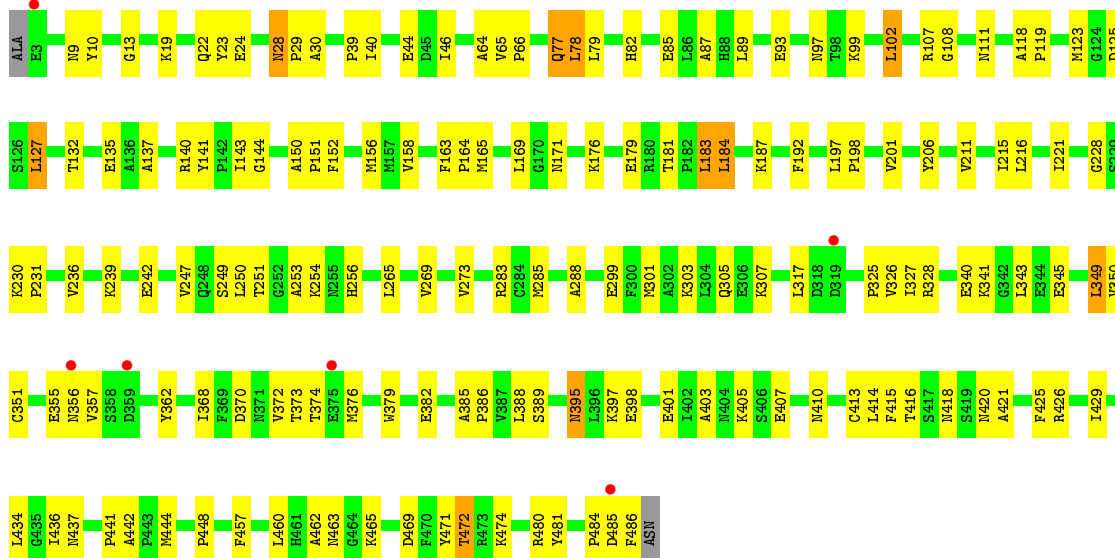




● Molecule 1: Probable methylmalonate-semialdehyde dehydrogenase



● Molecule 1: Probable methylmalonate-semialdehyde dehydrogenase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	195.20Å 192.50Å 83.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 19.77 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.50) 99.6 (19.77-2.50)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.78 (at 2.50Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.211 , 0.250 0.205 , 0.246	Depositor DCC
$R_{free}$ test set	5418 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.0	Xtrriage
Anisotropy	0.431	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 46.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16006	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 52.87 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.5701e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: NAD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.36	0/3818	0.59	0/5171
1	B	0.37	0/3818	0.61	0/5171
1	C	0.36	0/3818	0.60	0/5171
1	D	0.35	0/3818	0.58	0/5171
All	All	0.36	0/15272	0.60	0/20684

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	3741	0	3730	165	0
1	B	3741	0	3730	147	0
1	C	3741	0	3730	141	0
1	D	3741	0	3730	136	0
2	A	44	0	26	0	0
2	B	44	0	26	1	0
2	C	44	0	26	2	0
2	D	44	0	26	1	0
3	A	202	0	0	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	229	0	0	8	0
3	C	246	0	0	9	0
3	D	189	0	0	7	0
All	All	16006	0	15024	540	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 18.

All (540) 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:418:ASN:HD22	1:B:421:ALA:H	1.03	1.00
1:B:77:GLN:HB2	1:D:77:GLN:HE21	1.29	0.96
1:C:143:ILE:H	1:C:171:ASN:HD21	1.14	0.93
1:B:77:GLN:HG2	1:D:77:GLN:HG2	1.55	0.88
1:B:143:ILE:H	1:B:171:ASN:HD21	1.22	0.87
1:C:418:ASN:HD22	1:C:421:ALA:H	1.22	0.87
1:D:143:ILE:H	1:D:171:ASN:HD21	1.23	0.87
1:D:374:THR:HG21	1:D:405:LYS:HD3	1.55	0.87
1:B:77:GLN:HB2	1:D:77:GLN:NE2	1.88	0.86
1:A:374:THR:HG21	1:A:405:LYS:HD3	1.56	0.85
1:B:216:LEU:HD21	1:B:236:VAL:HG13	1.58	0.85
1:B:351:CYS:HB2	1:B:368:ILE:HG23	1.61	0.83
1:A:351:CYS:HB3	1:A:368:ILE:HG23	1.60	0.82
1:B:418:ASN:ND2	1:B:421:ALA:H	1.76	0.82
1:A:265:LEU:HD12	1:A:303:LYS:HD3	1.63	0.81
1:B:351:CYS:HB2	1:B:368:ILE:CG2	2.12	0.80
1:B:397:LYS:O	1:B:401:GLU:HG3	1.81	0.80
1:B:418:ASN:HD21	1:B:420:ASN:HB2	1.49	0.78
1:D:343:LEU:HD21	1:D:349:LEU:HB2	1.66	0.77
1:A:77:GLN:HG3	1:C:77:GLN:CD	2.06	0.76
1:D:93:GLU:OE2	1:D:183:LEU:HB2	1.85	0.76
1:B:167:ILE:HD12	1:B:201:VAL:HG12	1.68	0.76
1:B:97:ASN:ND2	1:B:100:GLU:H	1.83	0.76
1:B:143:ILE:H	1:B:171:ASN:ND2	1.83	0.76
1:A:143:ILE:H	1:A:171:ASN:HD21	1.35	0.74
1:C:143:ILE:H	1:C:171:ASN:ND2	1.86	0.73
1:A:265:LEU:HD23	1:A:296:ILE:HD11	1.71	0.72
1:D:46:ILE:HD11	1:D:211:VAL:HG13	1.71	0.72
1:A:216:LEU:HD21	1:A:236:VAL:HG13	1.71	0.72
1:C:28:ASN:C	1:C:28:ASN:HD22	1.92	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:397:LYS:O	1:D:401:GLU:HG3	1.91	0.71
1:A:123:MET:CE	1:C:465:LYS:HZ1	2.03	0.71
1:A:140:ARG:HH12	1:A:469:ASP:CG	1.94	0.71
1:B:216:LEU:HD13	1:B:239:LYS:HG2	1.71	0.71
1:A:353:GLY:HA3	1:A:367:THR:HG22	1.72	0.71
1:A:123:MET:HE3	1:C:465:LYS:HZ1	1.54	0.71
1:B:97:ASN:HD21	1:B:100:GLU:H	1.38	0.70
1:D:87:ALA:HB2	1:D:102:LEU:HD13	1.74	0.70
1:C:97:ASN:HD21	1:C:100:GLU:HG3	1.57	0.69
1:B:28:ASN:HD22	1:B:28:ASN:C	1.96	0.69
1:C:350:VAL:HB	1:C:368:ILE:HG13	1.73	0.69
1:B:97:ASN:C	1:B:97:ASN:HD22	1.96	0.68
1:C:418:ASN:ND2	1:C:421:ALA:H	1.90	0.68
1:C:28:ASN:ND2	1:C:30:ALA:H	1.91	0.68
1:A:31:THR:OG1	1:A:33:GLU:HG2	1.94	0.67
1:B:26:VAL:HG11	1:B:36:CYS:SG	2.35	0.67
1:B:465:LYS:NZ	1:D:123:MET:HE3	2.10	0.67
3:C:3523:HOH:O	1:D:474:LYS:HE2	1.95	0.66
1:B:329:GLU:HG3	1:B:333:LYS:HE3	1.77	0.66
1:D:216:LEU:HD13	1:D:239:LYS:HD3	1.77	0.66
1:C:350:VAL:CG2	1:C:370:ASP:HB2	2.26	0.66
1:D:301:MET:O	1:D:305:GLN:HG2	1.95	0.66
1:A:350:VAL:HG23	1:A:370:ASP:HB2	1.76	0.66
1:D:305:GLN:HE22	1:D:368:ILE:HD11	1.60	0.66
1:A:144:GLY:H	1:A:171:ASN:HD22	1.43	0.66
1:A:101:ALA:O	1:A:105:VAL:HG12	1.95	0.66
1:D:144:GLY:H	1:D:171:ASN:HD22	1.42	0.66
1:A:97:ASN:ND2	1:A:100:GLU:H	1.94	0.66
1:B:353:GLY:H	1:B:367:THR:HB	1.61	0.65
1:B:87:ALA:HB2	1:B:102:LEU:HD13	1.78	0.65
1:C:418:ASN:HD21	1:C:420:ASN:HB2	1.62	0.65
1:A:77:GLN:HG3	1:C:77:GLN:CG	2.26	0.65
1:D:484:PRO:HG2	1:D:486:PHE:CZ	2.32	0.65
1:B:163:PHE:O	1:B:167:ILE:HG12	1.96	0.65
1:D:327:ILE:O	1:D:328:ARG:HD3	1.96	0.65
1:C:429:ILE:HD13	1:C:430:ASP:N	2.12	0.64
1:A:385:ALA:HB1	1:A:386:PRO:HD2	1.80	0.64
1:A:254:LYS:HE2	1:A:379:TRP:O	1.98	0.64
1:C:350:VAL:HG23	1:C:370:ASP:HB2	1.78	0.64
1:A:94:ASN:HD22	1:A:96:LYS:H	1.44	0.64
1:A:351:CYS:CB	1:A:368:ILE:HG23	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:374:THR:HG21	1:A:405:LYS:CD	2.28	0.63
1:C:26:VAL:HA	3:C:3699:HOH:O	1.99	0.63
1:D:65:VAL:CG1	1:D:66:PRO:HD3	2.29	0.62
1:C:97:ASN:C	1:C:97:ASN:HD22	2.00	0.62
1:C:255:ASN:HB2	3:C:3731:HOH:O	1.99	0.62
1:D:395:ASN:C	1:D:395:ASN:HD22	2.02	0.62
1:B:77:GLN:CB	1:D:77:GLN:HE21	2.09	0.62
1:B:65:VAL:CG1	1:B:66:PRO:HD3	2.30	0.61
1:A:230:LYS:HD2	1:A:454:SER:HB3	1.82	0.61
1:A:28:ASN:HD22	1:A:28:ASN:C	2.02	0.61
1:A:481:TYR:HB3	1:C:420:ASN:HD22	1.65	0.61
1:D:87:ALA:CB	1:D:102:LEU:HD13	2.30	0.61
1:B:338:TYR:O	1:B:378:ILE:HD11	2.00	0.61
1:D:93:GLU:HG2	1:D:181:THR:HG22	1.80	0.61
1:B:465:LYS:HZ1	1:D:123:MET:HE3	1.65	0.61
1:A:132:THR:O	1:A:133:ASP:HB2	2.01	0.61
1:A:97:ASN:HD22	1:A:97:ASN:C	2.04	0.61
1:B:28:ASN:ND2	1:B:30:ALA:H	1.99	0.61
1:C:28:ASN:HD22	1:C:30:ALA:H	1.49	0.61
1:B:256:HIS:HE1	1:B:379:TRP:HE1	1.49	0.60
1:C:85:GLU:O	1:C:89:LEU:HD13	2.01	0.60
1:C:9:ASN:ND2	1:C:206:TYR:H	2.00	0.60
1:B:140:ARG:NH1	1:B:469:ASP:OD1	2.33	0.60
1:B:47:ASP:O	1:B:51:GLN:HG3	2.01	0.60
1:A:397:LYS:O	1:A:401:GLU:HG3	2.01	0.60
1:C:65:VAL:CG1	1:C:66:PRO:HD3	2.31	0.60
1:C:395:ASN:HD22	1:C:395:ASN:C	2.06	0.59
1:A:123:MET:HE3	1:C:465:LYS:NZ	2.16	0.59
1:A:87:ALA:CB	1:A:102:LEU:HD13	2.32	0.59
1:B:216:LEU:HD23	1:B:224:ILE:HD13	1.85	0.59
1:C:216:LEU:HD21	1:C:236:VAL:HG13	1.85	0.59
1:B:249:SER:HB2	1:B:457:PHE:HB2	1.85	0.59
1:B:222:LYS:HE3	3:B:2679:HOH:O	2.03	0.58
1:A:162:MET:HE2	1:A:225:SER:O	2.03	0.58
1:C:97:ASN:ND2	1:C:100:GLU:HG3	2.17	0.58
1:D:374:THR:HG21	1:D:405:LYS:CD	2.32	0.58
1:A:89:LEU:HD13	3:A:1639:HOH:O	2.03	0.58
1:B:418:ASN:HD22	1:B:421:ALA:N	1.87	0.58
1:B:426:ARG:HH22	1:D:135:GLU:CD	2.07	0.58
1:A:469:ASP:HA	1:A:472:THR:HG22	1.85	0.58
1:D:23:TYR:CE1	1:D:39:PRO:HB3	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:VAL:CG2	1:A:370:ASP:HB2	2.34	0.57
1:C:397:LYS:O	1:C:401:GLU:HG3	2.03	0.57
1:A:28:ASN:ND2	1:A:30:ALA:H	2.01	0.57
1:D:385:ALA:HB1	1:D:386:PRO:HD2	1.86	0.57
1:C:150:ALA:HB1	3:C:3513:HOH:O	2.04	0.57
1:C:426:ARG:HD2	1:D:141:TYR:OH	2.05	0.57
1:A:319:ASP:N	1:A:319:ASP:OD2	2.38	0.57
1:B:74:ASN:O	1:B:78:LEU:HD22	2.05	0.57
1:D:143:ILE:N	1:D:171:ASN:HD21	1.97	0.57
1:A:35:LEU:HD11	1:A:92:ILE:HG22	1.87	0.57
1:B:352:ASP:O	1:B:355:GLU:HG2	2.04	0.57
1:D:265:LEU:HD11	1:D:299:GLU:HG2	1.87	0.57
1:A:414:LEU:HG	1:A:416:THR:HG22	1.87	0.57
1:D:97:ASN:ND2	1:D:99:LYS:HB3	2.20	0.57
1:A:230:LYS:N	1:A:231:PRO:HD2	2.20	0.56
1:C:87:ALA:HB2	1:C:102:LEU:HD13	1.86	0.56
1:D:414:LEU:HG	1:D:416:THR:HG22	1.86	0.56
1:C:65:VAL:HG13	1:C:66:PRO:HD3	1.86	0.56
1:A:87:ALA:HB2	1:A:102:LEU:HD13	1.88	0.56
1:A:93:GLU:OE1	1:A:183:LEU:HB2	2.06	0.56
1:A:374:THR:HG23	1:A:379:TRP:CZ3	2.40	0.56
1:B:254:LYS:HE2	1:B:379:TRP:O	2.06	0.56
1:D:9:ASN:ND2	1:D:206:TYR:H	2.03	0.56
1:A:395:ASN:HD22	1:A:395:ASN:C	2.09	0.56
1:A:465:LYS:NZ	1:C:123:MET:HE3	2.21	0.56
1:C:285:MET:HB3	1:C:440:VAL:HG13	1.88	0.56
1:D:305:GLN:NE2	1:D:368:ILE:HD11	2.20	0.56
1:B:216:LEU:HD23	1:B:224:ILE:CD1	2.35	0.55
1:C:12:ASN:HB2	1:C:52:THR:HG21	1.87	0.55
1:A:220:GLU:HA	1:A:220:GLU:OE1	2.07	0.55
1:A:215:ILE:HA	1:A:221:ILE:HD12	1.88	0.55
1:B:35:LEU:HD11	1:B:92:ILE:HG22	1.86	0.55
1:C:350:VAL:HB	1:C:368:ILE:CG1	2.35	0.55
1:A:269:VAL:O	1:A:273:VAL:HG23	2.07	0.55
1:C:143:ILE:N	1:C:171:ASN:HD21	1.94	0.55
1:D:350:VAL:CG2	1:D:370:ASP:HB2	2.36	0.55
1:C:97:ASN:ND2	1:C:100:GLU:H	2.04	0.55
1:C:317:LEU:HD22	3:C:3579:HOH:O	2.06	0.55
1:A:357:VAL:HG11	1:A:363:PHE:O	2.07	0.55
1:C:254:LYS:HD3	1:C:288:ALA:CB	2.37	0.55
1:C:197:LEU:HD12	1:C:198:PRO:HD2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:385:ALA:HB1	1:C:386:PRO:HD2	1.87	0.55
1:B:395:ASN:ND2	1:B:398:GLU:H	2.05	0.54
1:B:182:PRO:HB2	1:B:206:TYR:CE2	2.42	0.54
1:C:438:LEU:HD21	1:D:480:ARG:HB2	1.89	0.54
1:B:46:ILE:HD11	1:B:211:VAL:HG13	1.90	0.54
1:C:459:THR:HB	3:D:4640:HOH:O	2.07	0.54
1:A:28:ASN:HD22	1:A:30:ALA:H	1.56	0.54
1:A:374:THR:HG23	1:A:379:TRP:CH2	2.43	0.54
1:B:208:ALA:O	1:B:212:VAL:HG23	2.07	0.54
1:C:38:VAL:CG2	1:C:182:PRO:HG3	2.38	0.54
1:D:326:VAL:HG22	1:D:362:TYR:O	2.07	0.54
1:B:370:ASP:O	1:B:371:ASN:HB2	2.07	0.54
1:A:13:GLY:O	1:A:14:GLU:HG3	2.08	0.54
1:B:28:ASN:HD22	1:B:30:ALA:H	1.55	0.54
1:B:143:ILE:HG12	1:B:171:ASN:HD21	1.73	0.54
1:C:140:ARG:NH1	1:C:469:ASP:OD1	2.41	0.54
1:A:216:LEU:HD13	1:A:239:LYS:HD3	1.89	0.54
1:C:326:VAL:HG22	1:C:362:TYR:O	2.08	0.54
1:A:135:GLU:CD	1:C:426:ARG:HH22	2.11	0.53
1:A:254:LYS:HD3	1:A:288:ALA:CB	2.38	0.53
1:B:353:GLY:HA3	1:B:367:THR:HG22	1.90	0.53
1:C:91:THR:HG21	1:C:317:LEU:HD13	1.89	0.53
1:B:144:GLY:H	1:B:171:ASN:HD22	1.56	0.53
1:D:29:PRO:HB2	1:D:325:PRO:HG2	1.91	0.53
1:A:9:ASN:ND2	1:A:206:TYR:H	2.05	0.53
1:A:35:LEU:CD1	1:A:92:ILE:HG22	2.38	0.53
1:D:85:GLU:OE1	1:D:187:LYS:HE2	2.08	0.53
1:A:242:GLU:O	1:B:238:LYS:HE2	2.08	0.53
1:A:123:MET:CE	1:C:465:LYS:NZ	2.71	0.53
1:C:87:ALA:CB	1:C:102:LEU:HD13	2.39	0.53
1:D:249:SER:HB2	1:D:457:PHE:HB2	1.89	0.53
1:B:285:MET:SD	1:B:441:PRO:HG2	2.48	0.53
1:A:418:ASN:ND2	1:A:421:ALA:H	2.06	0.53
1:A:65:VAL:CG1	1:A:66:PRO:HD3	2.39	0.53
1:D:269:VAL:O	1:D:273:VAL:HG23	2.09	0.53
1:A:484:PRO:HG2	1:A:486:PHE:CZ	2.44	0.52
1:C:80:SER:O	1:C:83:LYS:HG3	2.09	0.52
1:A:65:VAL:HG12	1:A:66:PRO:HD3	1.91	0.52
1:B:269:VAL:O	1:B:273:VAL:HG23	2.09	0.52
1:C:429:ILE:HD13	1:C:430:ASP:H	1.75	0.52
1:D:253:ALA:O	1:D:382:GLU:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:HIS:O	1:A:92:ILE:HG12	2.10	0.52
1:D:24:GLU:HB2	1:D:40:ILE:HD11	1.91	0.52
1:A:46:ILE:HG21	1:A:214:GLY:HA3	1.91	0.52
1:D:107:ARG:HH12	1:D:444:MET:HA	1.73	0.52
1:A:372:VAL:HG21	1:A:389:SER:HB3	1.91	0.52
1:C:8:LYS:HB3	1:C:16:VAL:O	2.10	0.52
1:C:290:VAL:HG23	1:C:388:LEU:HD21	1.92	0.52
1:D:10:TYR:CZ	1:D:13:GLY:HA2	2.44	0.52
1:D:143:ILE:H	1:D:171:ASN:ND2	2.01	0.52
1:C:409:ALA:HB2	1:C:453:LYS:HE2	1.92	0.52
1:D:156:MET:HB2	1:D:184:LEU:CD1	2.40	0.52
1:C:395:ASN:ND2	1:C:398:GLU:H	2.08	0.52
1:D:179:GLU:CD	1:D:179:GLU:H	2.13	0.52
1:A:329:GLU:OE1	1:A:333:LYS:HE3	2.09	0.52
1:B:319:ASP:OD2	1:B:319:ASP:O	2.28	0.52
1:D:65:VAL:HG13	1:D:66:PRO:HD3	1.92	0.52
1:A:91:THR:HG23	1:A:96:LYS:O	2.09	0.51
1:B:65:VAL:HG13	1:B:66:PRO:HD3	1.92	0.51
1:B:26:VAL:CG1	1:B:36:CYS:SG	2.98	0.51
1:D:216:LEU:HD21	1:D:236:VAL:HG13	1.92	0.51
1:B:123:MET:CE	1:D:465:LYS:NZ	2.74	0.51
1:C:47:ASP:O	1:C:51:GLN:HG3	2.09	0.51
1:A:110:GLU:CG	1:C:70:ARG:HH22	2.24	0.51
1:B:88:HIS:O	1:B:92:ILE:HG12	2.09	0.51
1:B:102:LEU:O	1:B:105:VAL:HG22	2.10	0.51
1:A:429:ILE:HG21	1:A:434:LEU:HD11	1.92	0.51
1:A:98:THR:HB	3:A:1548:HOH:O	2.10	0.51
1:C:479:ALA:CB	1:D:436:ILE:HB	2.40	0.51
1:B:465:LYS:NZ	1:D:123:MET:CE	2.73	0.51
1:C:328:ARG:NH1	3:C:3699:HOH:O	2.43	0.51
1:B:368:ILE:HD11	1:B:390:VAL:CG1	2.41	0.51
1:D:140:ARG:NH1	1:D:469:ASP:OD2	2.44	0.51
1:B:120:SER:O	1:B:123:MET:HE2	2.11	0.51
1:B:395:ASN:C	1:B:395:ASN:HD22	2.15	0.50
1:B:3:GLU:OE1	1:B:3:GLU:HA	2.11	0.50
1:C:90:ILE:O	1:C:94:ASN:HB3	2.11	0.50
1:B:418:ASN:ND2	1:B:421:ALA:N	2.54	0.50
1:C:42:THR:OG1	1:C:44:GLU:HB3	2.12	0.50
1:D:413:CYS:SG	1:D:441:PRO:HD3	2.52	0.50
1:B:175:LEU:HG	1:B:177:PRO:HD3	1.94	0.50
1:B:256:HIS:CE1	1:B:379:TRP:HE1	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:LEU:CD1	1:B:92:ILE:HG22	2.42	0.50
1:D:169:LEU:HD12	1:D:471:TYR:HB2	1.94	0.50
1:A:351:CYS:HB3	1:A:368:ILE:CG2	2.37	0.50
1:D:256:HIS:CE1	1:D:403:ALA:HA	2.46	0.50
1:A:326:VAL:HG22	1:A:362:TYR:O	2.10	0.50
3:B:2676:HOH:O	1:C:67:ARG:HD2	2.12	0.50
1:A:216:LEU:HD23	1:A:224:ILE:CD1	2.42	0.50
1:B:339:ILE:HD11	1:B:367:THR:HG21	1.94	0.50
1:B:92:ILE:HD13	1:B:317:LEU:HD21	1.93	0.50
1:A:426:ARG:HG3	1:B:477:VAL:HG21	1.93	0.50
1:C:304:LEU:O	1:C:308:VAL:HG23	2.11	0.49
1:D:230:LYS:N	1:D:231:PRO:HD2	2.26	0.49
1:B:186:GLU:O	1:B:190:GLU:HG3	2.12	0.49
1:D:156:MET:HB2	1:D:184:LEU:HD11	1.94	0.49
1:A:349:LEU:HD21	1:A:352:ASP:HB2	1.94	0.49
1:B:38:VAL:CG2	1:B:182:PRO:HG3	2.42	0.49
1:B:385:ALA:HB1	1:B:386:PRO:HD2	1.93	0.49
1:A:353:GLY:CA	1:A:367:THR:HG22	2.40	0.49
1:B:123:MET:HE3	1:D:465:LYS:NZ	2.27	0.49
1:D:144:GLY:H	1:D:171:ASN:ND2	2.10	0.49
1:C:216:LEU:HD23	1:C:224:ILE:CD1	2.43	0.49
1:C:28:ASN:ND2	1:C:28:ASN:C	2.64	0.49
1:A:254:LYS:HD3	1:A:288:ALA:HB3	1.94	0.49
1:A:268:THR:HG23	1:A:415:PHE:CG	2.48	0.49
1:A:153:ASN:HB2	1:A:282:GLU:O	2.12	0.49
1:C:368:ILE:HA	1:C:388:LEU:O	2.13	0.49
1:D:107:ARG:NH1	1:D:444:MET:HA	2.28	0.49
1:C:163:PHE:CG	1:C:164:PRO:HD3	2.48	0.49
1:C:198:PRO:HG2	1:C:201:VAL:HG21	1.95	0.49
1:D:469:ASP:HA	1:D:472:THR:HG22	1.94	0.49
1:A:136:ALA:HA	1:A:477:VAL:O	2.13	0.48
1:C:329:GLU:OE1	1:C:333:LYS:HE3	2.12	0.48
1:D:230:LYS:HE3	1:D:407:GLU:OE2	2.13	0.48
1:A:290:VAL:HG23	1:A:388:LEU:HD21	1.94	0.48
1:B:285:MET:HB3	1:B:440:VAL:HG13	1.95	0.48
1:A:110:GLU:HG2	1:C:70:ARG:HH22	1.77	0.48
1:A:327:ILE:HG23	1:A:328:ARG:HG2	1.95	0.48
1:C:184:LEU:O	1:C:184:LEU:HD13	2.13	0.48
1:D:374:THR:HG23	1:D:379:TRP:CZ3	2.49	0.48
1:D:395:ASN:ND2	1:D:398:GLU:H	2.11	0.48
1:A:102:LEU:O	1:A:105:VAL:HG13	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:TYR:OH	1:B:426:ARG:HD2	2.13	0.48
1:A:97:ASN:HD21	1:A:100:GLU:H	1.60	0.48
1:A:94:ASN:ND2	1:A:96:LYS:HE3	2.29	0.48
1:B:92:ILE:CD1	1:B:317:LEU:HD21	2.44	0.48
1:C:93:GLU:OE2	1:C:183:LEU:N	2.43	0.48
1:C:26:VAL:HG11	1:C:36:CYS:SG	2.52	0.48
1:B:135:GLU:CD	1:D:426:ARG:HH22	2.17	0.48
1:D:269:VAL:HG21	1:D:303:LYS:CG	2.43	0.48
1:B:254:LYS:HD3	1:B:288:ALA:CB	2.44	0.48
1:D:65:VAL:HG12	1:D:66:PRO:HD3	1.96	0.48
1:B:163:PHE:CG	1:B:164:PRO:HD3	2.49	0.47
1:B:162:MET:HE3	1:B:227:VAL:HG23	1.95	0.47
1:A:374:THR:O	1:A:374:THR:HG22	2.12	0.47
1:B:50:ALA:HA	1:B:174:ILE:HD11	1.96	0.47
1:B:230:LYS:N	1:B:231:PRO:HD2	2.29	0.47
3:A:1533:HOH:O	1:B:242:GLU:HG3	2.15	0.47
1:B:254:LYS:HD3	1:B:288:ALA:HB3	1.97	0.47
1:A:90:ILE:HG23	1:A:155:PRO:CG	2.44	0.47
1:B:250:LEU:HD12	1:B:250:LEU:N	2.30	0.47
1:D:350:VAL:HG21	1:D:370:ASP:HB2	1.95	0.47
1:A:327:ILE:HG23	1:A:328:ARG:N	2.29	0.47
1:C:429:ILE:CD1	1:C:431:ALA:H	2.27	0.47
1:D:93:GLU:HG2	1:D:181:THR:HA	1.95	0.47
1:D:228:GLY:O	2:D:4490:NAD:H1D	2.15	0.47
1:D:418:ASN:HD21	1:D:420:ASN:HB2	1.80	0.47
1:A:143:ILE:N	1:A:171:ASN:HD21	2.08	0.47
1:B:143:ILE:HG12	1:B:171:ASN:ND2	2.29	0.47
1:C:97:ASN:ND2	1:C:97:ASN:C	2.67	0.47
1:D:28:ASN:HD22	1:D:30:ALA:H	1.61	0.47
1:D:355:GLU:O	1:D:357:VAL:HG23	2.14	0.47
1:A:230:LYS:HE3	1:A:407:GLU:OE2	2.15	0.47
1:B:28:ASN:ND2	1:B:28:ASN:C	2.67	0.47
1:C:228:GLY:O	1:C:251:THR:HA	2.15	0.47
1:C:365:GLY:HA3	3:C:3563:HOH:O	2.15	0.47
1:B:409:ALA:HB2	1:B:453:LYS:HE2	1.96	0.47
1:C:152:PHE:CE1	1:C:327:ILE:HB	2.50	0.47
1:A:78:LEU:O	1:A:82:HIS:HD2	1.98	0.47
1:B:210:ASP:HB2	3:B:2499:HOH:O	2.15	0.47
1:C:143:ILE:N	1:C:171:ASN:ND2	2.57	0.47
1:B:90:ILE:O	1:B:94:ASN:HB3	2.15	0.47
1:B:265:LEU:HG	1:B:296:ILE:HD11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:ALA:CB	1:B:102:LEU:HD13	2.42	0.47
1:D:305:GLN:HE22	1:D:350:VAL:HG12	1.80	0.47
1:A:462:ALA:O	1:A:463:ASN:HB2	2.16	0.46
1:A:127:LEU:HD13	1:D:123:MET:HG2	1.96	0.46
1:D:93:GLU:CG	1:D:181:THR:HA	2.45	0.46
1:B:351:CYS:HB2	1:B:368:ILE:HG22	1.93	0.46
1:B:357:VAL:HG11	1:B:365:GLY:H	1.80	0.46
1:D:198:PRO:HG2	1:D:201:VAL:HG21	1.97	0.46
1:C:184:LEU:C	1:C:184:LEU:HD13	2.36	0.46
1:C:144:GLY:H	1:C:171:ASN:HD22	1.64	0.46
1:A:329:GLU:HB2	1:A:362:TYR:CE2	2.51	0.46
1:D:265:LEU:CD1	1:D:299:GLU:HG2	2.45	0.46
1:A:480:ARG:HB2	1:B:438:LEU:HD21	1.98	0.46
1:B:65:VAL:HG12	1:B:66:PRO:HD3	1.98	0.46
1:D:44:GLU:HG3	3:D:4501:HOH:O	2.15	0.46
1:D:163:PHE:CG	1:D:164:PRO:HD3	2.51	0.46
1:D:28:ASN:HD22	1:D:28:ASN:C	2.18	0.46
1:A:97:ASN:HD21	1:A:100:GLU:HG3	1.80	0.46
1:C:98:THR:O	1:C:102:LEU:HB2	2.16	0.46
1:C:26:VAL:CG1	1:C:36:CYS:SG	3.05	0.45
1:C:26:VAL:HG12	1:C:38:VAL:HG23	1.97	0.45
1:A:152:PHE:C	1:A:152:PHE:CD1	2.89	0.45
1:B:97:ASN:C	1:B:97:ASN:ND2	2.68	0.45
1:C:238:LYS:HE2	1:D:242:GLU:O	2.16	0.45
1:A:238:LYS:HE2	1:B:242:GLU:O	2.16	0.45
1:A:254:LYS:O	1:A:256:HIS:HD2	1.98	0.45
1:A:465:LYS:NZ	1:C:123:MET:CE	2.78	0.45
1:C:38:VAL:HG22	1:C:182:PRO:HG3	1.99	0.45
1:C:176:LYS:HG3	1:C:211:VAL:HG11	1.97	0.45
1:C:484:PRO:HG2	1:C:486:PHE:CZ	2.52	0.45
1:A:163:PHE:CG	1:A:164:PRO:HD3	2.52	0.45
1:B:368:ILE:HD12	1:B:369:PHE:N	2.31	0.45
1:C:120:SER:O	1:C:123:MET:HE2	2.15	0.45
1:A:374:THR:HG21	1:A:405:LYS:CE	2.47	0.45
1:A:410:ASN:HA	1:A:410:ASN:HD22	1.65	0.45
1:A:432:GLY:O	1:B:475:LYS:HA	2.17	0.45
1:B:10:TYR:CZ	1:B:13:GLY:HA2	2.51	0.45
1:B:38:VAL:HG22	1:B:182:PRO:HG3	1.98	0.45
1:A:465:LYS:HZ3	1:C:123:MET:CE	2.30	0.45
1:D:151:PRO:HD2	1:D:158:VAL:HG11	1.99	0.45
1:D:46:ILE:CD1	1:D:211:VAL:HG13	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:462:ALA:O	1:D:463:ASN:HB2	2.16	0.45
1:A:28:ASN:HD22	1:A:29:PRO:N	2.15	0.45
1:A:409:ALA:HB2	1:A:453:LYS:HG3	1.99	0.45
1:A:91:THR:HG21	1:A:317:LEU:HD13	1.99	0.45
1:A:481:TYR:CE2	1:C:419:SER:HB3	2.51	0.45
1:C:72:LEU:HD12	1:C:112:VAL:HG13	1.98	0.45
1:C:285:MET:HG3	1:C:442:ALA:HB2	1.98	0.45
1:A:151:PRO:HD2	1:A:158:VAL:HG11	1.98	0.45
1:D:197:LEU:HD12	1:D:198:PRO:HD2	1.99	0.45
1:C:254:LYS:HD3	1:C:288:ALA:HB3	1.99	0.45
1:C:425:PHE:O	1:C:429:ILE:HB	2.16	0.45
1:D:127:LEU:HA	1:D:127:LEU:HD12	1.85	0.45
1:A:465:LYS:HZ1	1:C:123:MET:HE3	1.80	0.45
1:B:54:ALA:HB2	1:B:220:GLU:CG	2.47	0.45
1:B:77:GLN:CG	1:D:77:GLN:HG2	2.36	0.45
1:B:85:GLU:OE1	1:B:187:LYS:HE2	2.17	0.44
1:A:144:GLY:H	1:A:171:ASN:ND2	2.13	0.44
1:A:73:PHE:CE1	1:A:116:ALA:HB1	2.52	0.44
1:D:250:LEU:HD12	1:D:250:LEU:N	2.33	0.44
1:D:372:VAL:HG21	1:D:389:SER:HB3	1.99	0.44
1:A:90:ILE:O	1:A:94:ASN:HB3	2.18	0.44
1:B:215:ILE:HA	1:B:221:ILE:HD12	1.99	0.44
1:C:250:LEU:N	1:C:250:LEU:HD12	2.33	0.44
1:C:410:ASN:HA	1:C:410:ASN:HD22	1.63	0.44
1:A:418:ASN:HD22	1:A:421:ALA:HB2	1.83	0.44
1:A:285:MET:SD	1:A:441:PRO:HG2	2.58	0.44
1:C:311:ILE:HG23	1:C:322:PHE:HB3	1.99	0.44
1:C:459:THR:HG21	1:D:460:LEU:HD12	1.98	0.44
1:B:54:ALA:HB2	1:B:220:GLU:HG3	1.98	0.44
1:B:465:LYS:HZ3	1:D:123:MET:CE	2.31	0.44
1:A:80:SER:O	1:A:83:LYS:HG3	2.18	0.44
1:C:97:ASN:HD21	1:C:100:GLU:H	1.65	0.44
1:A:472:THR:HG23	3:A:1510:HOH:O	2.16	0.44
1:B:152:PHE:CE1	1:B:327:ILE:HB	2.52	0.44
1:B:395:ASN:HD22	1:B:398:GLU:H	1.65	0.44
1:D:19:LYS:HE3	3:D:4556:HOH:O	2.17	0.44
1:D:28:ASN:ND2	1:D:30:ALA:H	2.15	0.44
1:D:448:PRO:HG2	3:D:4517:HOH:O	2.18	0.44
1:C:149:ILE:HG22	2:C:3490:NAD:H4B	2.00	0.44
1:A:176:LYS:HG3	1:A:211:VAL:HG11	1.99	0.43
1:B:448:PRO:HG2	3:B:2520:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:230:LYS:HA	1:D:251:THR:HB	1.99	0.43
1:D:305:GLN:HE22	1:D:350:VAL:CG1	2.32	0.43
1:B:85:GLU:HG3	3:B:2578:HOH:O	2.17	0.43
1:A:426:ARG:HH22	1:C:135:GLU:CD	2.21	0.43
1:B:444:MET:HE3	3:B:2706:HOH:O	2.18	0.43
1:D:228:GLY:O	1:D:251:THR:HA	2.18	0.43
1:A:296:ILE:O	1:A:296:ILE:HG12	2.18	0.43
1:C:50:ALA:HA	1:C:174:ILE:HD11	2.01	0.43
1:A:140:ARG:NH1	1:A:469:ASP:OD1	2.47	0.43
1:A:436:ILE:HB	1:B:479:ALA:CB	2.48	0.43
1:C:156:MET:O	1:C:159:PRO:HD2	2.17	0.43
1:C:351:CYS:HB3	1:C:368:ILE:HG23	2.00	0.43
1:D:93:GLU:OE2	1:D:183:LEU:N	2.46	0.43
1:A:388:LEU:HD23	1:A:389:SER:H	1.83	0.43
1:A:388:LEU:HD23	1:A:389:SER:N	2.34	0.43
1:C:224:ILE:HB	1:C:247:VAL:HB	2.00	0.43
1:B:177:PRO:HG2	1:B:206:TYR:CD2	2.54	0.43
1:B:419:SER:HB3	1:D:481:TYR:CE2	2.54	0.43
1:B:212:VAL:HG21	2:B:2490:NAD:N3A	2.34	0.43
1:B:312:LYS:HD2	1:B:320:GLY:O	2.19	0.43
1:C:38:VAL:HG21	1:C:182:PRO:HG3	2.00	0.43
1:D:108:GLY:HA2	1:D:111:ASN:HD22	1.83	0.43
1:D:64:ALA:HB1	1:D:66:PRO:HD2	2.00	0.43
1:A:132:THR:HB	3:D:4575:HOH:O	2.19	0.43
1:D:373:THR:N	1:D:376:MET:HE3	2.33	0.43
1:A:149:ILE:HD13	1:A:212:VAL:HG13	2.01	0.42
1:A:448:PRO:HG2	3:A:1530:HOH:O	2.19	0.42
1:B:327:ILE:HG23	1:B:328:ARG:N	2.34	0.42
1:B:57:PHE:CE2	1:B:61:SER:HB3	2.54	0.42
1:C:375:GLU:HG2	3:C:3714:HOH:O	2.18	0.42
1:D:317:LEU:N	1:D:317:LEU:HD22	2.34	0.42
1:D:356:ASN:HD22	1:D:356:ASN:N	2.18	0.42
1:A:253:ALA:O	1:A:382:GLU:HG3	2.19	0.42
1:A:418:ASN:HD21	1:A:420:ASN:HB2	1.85	0.42
1:B:319:ASP:OD2	1:B:319:ASP:C	2.58	0.42
1:B:378:ILE:HD13	1:B:378:ILE:HA	1.80	0.42
1:D:150:ALA:HB1	3:D:4659:HOH:O	2.18	0.42
1:D:350:VAL:HG23	1:D:370:ASP:HB2	2.00	0.42
1:B:8:LYS:HB3	1:B:16:VAL:O	2.18	0.42
1:C:12:ASN:HB2	1:C:52:THR:CG2	2.48	0.42
1:A:344:GLU:O	1:A:344:GLU:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:176:LYS:HG3	1:B:211:VAL:HG11	2.01	0.42
1:D:285:MET:HG3	1:D:442:ALA:HB2	2.01	0.42
1:D:152:PHE:CE1	1:D:327:ILE:HB	2.55	0.42
1:A:57:PHE:CE2	1:A:144:GLY:HA2	2.54	0.42
1:B:292:VAL:HG11	1:B:297:ALA:HA	2.01	0.42
1:C:261:ASN:HA	1:C:296:ILE:HB	2.02	0.42
1:B:127:LEU:HD12	1:B:127:LEU:HA	1.87	0.42
1:C:46:ILE:HA	1:C:46:ILE:HD13	1.92	0.42
1:D:156:MET:HB2	1:D:184:LEU:HG	2.01	0.42
1:B:253:ALA:O	1:B:382:GLU:HG3	2.19	0.42
1:C:212:VAL:HG21	2:C:3490:NAD:N3A	2.35	0.42
1:D:143:ILE:N	1:D:171:ASN:ND2	2.65	0.42
1:D:165:MET:O	1:D:169:LEU:HG	2.20	0.42
1:C:230:LYS:HA	1:C:251:THR:HB	2.01	0.42
1:D:215:ILE:HA	1:D:221:ILE:HD12	2.01	0.42
1:D:140:ARG:HD3	1:D:472:THR:HG21	2.02	0.42
1:A:120:SER:O	1:A:123:MET:HE2	2.19	0.42
1:A:24:GLU:HB2	1:A:40:ILE:HD11	2.01	0.42
1:A:29:PRO:HB2	1:A:325:PRO:HG2	2.02	0.42
1:B:12:ASN:HB2	1:B:52:THR:HG21	2.01	0.42
1:A:26:VAL:HG21	1:A:182:PRO:HG3	2.01	0.41
1:C:350:VAL:HB	1:C:368:ILE:CD1	2.50	0.41
1:D:183:LEU:HD12	1:D:183:LEU:HA	1.88	0.41
1:D:418:ASN:ND2	1:D:420:ASN:HB2	2.35	0.41
1:A:143:ILE:H	1:A:171:ASN:ND2	2.11	0.41
1:A:374:THR:HG21	1:A:405:LYS:NZ	2.35	0.41
1:C:11:ILE:O	1:C:14:GLU:OE1	2.38	0.41
1:C:158:VAL:HB	1:C:159:PRO:HD3	2.01	0.41
1:B:419:SER:OG	1:C:422:ILE:HD12	2.20	0.41
1:D:374:THR:HG22	1:D:374:THR:O	2.19	0.41
1:D:418:ASN:HD22	1:D:421:ALA:H	1.67	0.41
1:B:152:PHE:C	1:B:152:PHE:CD1	2.93	0.41
1:A:218:HIS:HA	1:A:219:PRO:HD2	1.93	0.41
1:A:138:ASN:HA	1:A:476:VAL:HA	2.03	0.41
1:A:97:ASN:ND2	1:A:97:ASN:C	2.73	0.41
1:B:123:MET:HE1	3:B:2492:HOH:O	2.20	0.41
1:C:28:ASN:HD22	1:C:29:PRO:N	2.18	0.41
1:B:40:ILE:HA	1:B:207:GLY:HA2	2.02	0.41
1:C:123:MET:HE1	3:C:3499:HOH:O	2.21	0.41
1:A:158:VAL:HB	1:A:159:PRO:HD3	2.02	0.41
1:A:341:LYS:O	1:A:345:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:157:MET:HB3	1:B:157:MET:HE2	1.90	0.41
1:B:185:THR:O	1:B:189:VAL:HG23	2.21	0.41
1:C:175:LEU:HG	1:C:177:PRO:HD3	2.02	0.41
1:D:415:PHE:CD1	1:D:437:ASN:HA	2.56	0.41
1:A:90:ILE:HG23	1:A:155:PRO:HG3	2.02	0.41
1:A:349:LEU:HD23	1:A:349:LEU:C	2.40	0.41
1:A:433:MET:HG3	1:A:450:SER:O	2.20	0.41
1:A:77:GLN:HG3	1:C:77:GLN:HG2	2.01	0.41
3:A:1540:HOH:O	1:B:474:LYS:HE2	2.20	0.41
1:C:220:GLU:OE2	1:C:220:GLU:HA	2.20	0.41
1:C:254:LYS:O	1:C:256:HIS:HD2	2.04	0.41
1:D:351:CYS:HB3	1:D:368:ILE:HG23	2.03	0.41
1:D:395:ASN:C	1:D:395:ASN:ND2	2.73	0.41
1:A:79:LEU:HA	1:A:79:LEU:HD12	1.93	0.41
1:B:348:ARG:HB2	1:B:370:ASP:OD1	2.20	0.41
1:C:46:ILE:HG21	1:C:214:GLY:HA3	2.03	0.41
1:C:429:ILE:HG21	1:C:434:LEU:HD11	2.02	0.41
1:D:303:LYS:HE3	1:D:307:LYS:HZ2	1.85	0.41
1:D:341:LYS:O	1:D:345:GLU:HG3	2.20	0.41
1:C:268:THR:HG22	1:C:272:ILE:HD12	2.02	0.41
1:D:187:LYS:HD3	1:D:187:LYS:HA	1.84	0.41
1:D:341:LYS:HG3	3:D:4667:HOH:O	2.21	0.41
1:D:78:LEU:O	1:D:82:HIS:HD2	2.03	0.41
1:A:38:VAL:CG1	1:A:182:PRO:HG3	2.52	0.41
1:A:418:ASN:HD22	1:A:421:ALA:H	1.68	0.41
1:B:18:SER:HB3	1:B:20:THR:HG22	2.02	0.41
1:A:422:ILE:HD13	1:B:481:TYR:OH	2.21	0.41
1:C:26:VAL:HG13	1:C:36:CYS:O	2.21	0.41
1:A:123:MET:HE1	1:C:465:LYS:HZ1	1.82	0.41
1:B:123:MET:HE1	1:D:465:LYS:NZ	2.36	0.40
1:B:162:MET:CE	1:B:227:VAL:HG23	2.51	0.40
1:C:140:ARG:NH1	1:C:474:LYS:NZ	2.69	0.40
1:C:14:GLU:N	1:C:14:GLU:OE1	2.53	0.40
1:C:265:LEU:HG	1:C:296:ILE:HD11	2.03	0.40
1:C:89:LEU:O	1:C:93:GLU:HB3	2.21	0.40
1:D:429:ILE:HA	1:D:429:ILE:HD12	1.95	0.40
1:A:266:GLU:OE2	1:A:303:LYS:NZ	2.46	0.40
1:A:77:GLN:HG3	1:C:77:GLN:NE2	2.36	0.40
1:A:83:LYS:HD3	3:A:1569:HOH:O	2.21	0.40
1:B:78:LEU:O	1:B:82:HIS:HD2	2.04	0.40
1:C:432:GLY:HA3	1:C:450:SER:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:125:ASP:O	1:D:137:ALA:HA	2.21	0.40
1:D:176:LYS:HG3	1:D:211:VAL:HG11	2.03	0.40
1:A:338:TYR:CG	1:A:383:ILE:HD12	2.56	0.40
1:B:98:THR:HG21	3:B:2617:HOH:O	2.20	0.40
1:D:414:LEU:HD22	1:D:425:PHE:CB	2.51	0.40
1:A:108:GLY:HA2	1:A:111:ASN:HD22	1.85	0.40
1:A:6:LYS:HE2	1:A:23:TYR:CZ	2.57	0.40
1:A:338:TYR:HA	1:A:341:LYS:HE3	2.04	0.40
1:A:385:ALA:HB1	1:A:386:PRO:CD	2.50	0.40
1:B:343:LEU:HD21	1:B:349:LEU:HG	2.02	0.40
1:C:23:TYR:CE1	1:C:39:PRO:HB3	2.56	0.40
1:C:256:HIS:HE1	1:C:379:TRP:HE1	1.70	0.40
1:D:118:ALA:N	1:D:119:PRO:CD	2.85	0.40
1:A:38:VAL:HG11	1:A:182:PRO:CB	2.51	0.40
1:A:383:ILE:HB	3:A:1595:HOH:O	2.21	0.40
1:A:92:ILE:HD11	1:A:317:LEU:HD21	2.04	0.40
1:B:118:ALA:N	1:B:119:PRO:CD	2.84	0.40
1:D:254:LYS:HD3	1:D:288:ALA:HB3	2.03	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	482/486 (99%)	459 (95%)	22 (5%)	1 (0%)	47	68
1	B	482/486 (99%)	453 (94%)	27 (6%)	2 (0%)	34	54
1	C	482/486 (99%)	463 (96%)	18 (4%)	1 (0%)	47	68
1	D	482/486 (99%)	460 (95%)	22 (5%)	0	100	100
All	All	1928/1944 (99%)	1835 (95%)	89 (5%)	4 (0%)	47	68

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	356	ASN
1	C	41	SER
1	A	371	ASN
1	B	41	SER

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	399/400 (100%)	372 (93%)	27 (7%)	16	30
1	B	399/400 (100%)	374 (94%)	25 (6%)	18	34
1	C	399/400 (100%)	375 (94%)	24 (6%)	19	37
1	D	399/400 (100%)	377 (94%)	22 (6%)	21	41
All	All	1596/1600 (100%)	1498 (94%)	98 (6%)	18	36

All (98) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	46	ILE
1	A	78	LEU
1	A	79	LEU
1	A	97	ASN
1	A	98	THR
1	A	102	LEU
1	A	105	VAL
1	A	127	LEU
1	A	132	THR
1	A	183	LEU
1	A	184	LEU
1	A	187	LYS
1	A	192	PHE
1	A	244	LEU
1	A	247	VAL
1	A	265	LEU
1	A	317	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	319	ASP
1	A	367	THR
1	A	368	ILE
1	A	388	LEU
1	A	395	ASN
1	A	410	ASN
1	A	434	LEU
1	A	469	ASP
1	A	485	ASP
1	B	26	VAL
1	B	28	ASN
1	B	78	LEU
1	B	79	LEU
1	B	97	ASN
1	B	102	LEU
1	B	127	LEU
1	B	132	THR
1	B	179	GLU
1	B	187	LYS
1	B	192	PHE
1	B	222	LYS
1	B	244	LEU
1	B	247	VAL
1	B	326	VAL
1	B	336	LEU
1	B	367	THR
1	B	368	ILE
1	B	370	ASP
1	B	372	VAL
1	B	388	LEU
1	B	390	VAL
1	B	395	ASN
1	B	410	ASN
1	B	434	LEU
1	C	26	VAL
1	C	28	ASN
1	C	46	ILE
1	C	78	LEU
1	C	79	LEU
1	C	97	ASN
1	C	102	LEU
1	C	127	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C	187	LYS
1	C	192	PHE
1	C	222	LYS
1	C	244	LEU
1	C	247	VAL
1	C	283	ARG
1	C	317	LEU
1	C	328	ARG
1	C	368	ILE
1	C	372	VAL
1	C	388	LEU
1	C	395	ASN
1	C	410	ASN
1	C	418	ASN
1	C	429	ILE
1	C	434	LEU
1	D	22	GLN
1	D	28	ASN
1	D	77	GLN
1	D	78	LEU
1	D	79	LEU
1	D	89	LEU
1	D	102	LEU
1	D	127	LEU
1	D	132	THR
1	D	183	LEU
1	D	184	LEU
1	D	192	PHE
1	D	247	VAL
1	D	283	ARG
1	D	340	GLU
1	D	349	LEU
1	D	388	LEU
1	D	395	ASN
1	D	410	ASN
1	D	434	LEU
1	D	472	THR
1	D	485	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (71) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	22	GLN
1	A	28	ASN
1	A	51	GLN
1	A	74	ASN
1	A	77	GLN
1	A	81	GLN
1	A	82	HIS
1	A	94	ASN
1	A	97	ASN
1	A	111	ASN
1	A	171	ASN
1	A	248	GLN
1	A	256	HIS
1	A	356	ASN
1	A	395	ASN
1	A	410	ASN
1	A	418	ASN
1	A	420	ASN
1	A	428	ASN
1	A	463	ASN
1	B	9	ASN
1	B	28	ASN
1	B	51	GLN
1	B	74	ASN
1	B	77	GLN
1	B	81	GLN
1	B	82	HIS
1	B	97	ASN
1	B	171	ASN
1	B	256	HIS
1	B	356	ASN
1	B	395	ASN
1	B	410	ASN
1	B	418	ASN
1	B	420	ASN
1	B	463	ASN
1	C	9	ASN
1	C	28	ASN
1	C	51	GLN
1	C	74	ASN
1	C	81	GLN
1	C	97	ASN

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Mol	Chain	Res	Type
1	C	111	ASN
1	C	171	ASN
1	C	256	HIS
1	C	356	ASN
1	C	371	ASN
1	C	395	ASN
1	C	410	ASN
1	C	418	ASN
1	C	420	ASN
1	C	463	ASN
1	D	9	ASN
1	D	28	ASN
1	D	51	GLN
1	D	74	ASN
1	D	77	GLN
1	D	81	GLN
1	D	82	HIS
1	D	111	ASN
1	D	171	ASN
1	D	256	HIS
1	D	305	GLN
1	D	356	ASN
1	D	395	ASN
1	D	410	ASN
1	D	418	ASN
1	D	420	ASN
1	D	428	ASN
1	D	463	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

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAD	B	2490	-	42,48,48	2.65	10 (23%)	50,73,73	1.62	9 (18%)
2	NAD	D	4490	-	42,48,48	2.65	10 (23%)	50,73,73	1.59	8 (16%)
2	NAD	A	1490	-	42,48,48	2.63	10 (23%)	50,73,73	1.60	8 (16%)
2	NAD	C	3490	-	42,48,48	2.65	10 (23%)	50,73,73	1.58	8 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	B	2490	-	-	1/26/62/62	0/5/5/5
2	NAD	D	4490	-	-	1/26/62/62	0/5/5/5
2	NAD	A	1490	-	-	1/26/62/62	0/5/5/5
2	NAD	C	3490	-	-	1/26/62/62	0/5/5/5

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1490	NAD	C2N-N1N	8.74	1.45	1.35
2	B	2490	NAD	C4N-C3N	8.48	1.53	1.39
2	C	3490	NAD	C4N-C3N	8.42	1.53	1.39
2	D	4490	NAD	C2N-N1N	8.37	1.45	1.35
2	D	4490	NAD	C4N-C3N	8.30	1.53	1.39
2	B	2490	NAD	C2N-N1N	8.17	1.44	1.35
2	A	1490	NAD	C4N-C3N	8.11	1.53	1.39
2	C	3490	NAD	C2N-N1N	7.97	1.44	1.35
2	C	3490	NAD	C5N-C4N	5.71	1.50	1.38
2	B	2490	NAD	C5N-C4N	5.63	1.50	1.38
2	A	1490	NAD	C5N-C4N	5.43	1.50	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	4490	NAD	C5N-C4N	5.37	1.50	1.38
2	D	4490	NAD	C2A-N3A	5.35	1.40	1.32
2	C	3490	NAD	C2A-N3A	5.32	1.40	1.32
2	B	2490	NAD	C2A-N3A	5.22	1.40	1.32
2	A	1490	NAD	C2A-N3A	5.12	1.40	1.32
2	C	3490	NAD	C6N-N1N	4.10	1.45	1.35
2	D	4490	NAD	C4A-N3A	3.91	1.41	1.35
2	A	1490	NAD	C4A-N3A	3.90	1.41	1.35
2	B	2490	NAD	C4A-N3A	3.89	1.41	1.35
2	B	2490	NAD	C6N-N1N	3.88	1.44	1.35
2	C	3490	NAD	C4A-N3A	3.81	1.40	1.35
2	D	4490	NAD	C6N-N1N	3.74	1.44	1.35
2	A	1490	NAD	C6N-N1N	3.56	1.44	1.35
2	D	4490	NAD	O4D-C1D	3.16	1.45	1.41
2	C	3490	NAD	C2N-C3N	-3.13	1.34	1.39
2	A	1490	NAD	O4D-C1D	3.04	1.45	1.41
2	B	2490	NAD	C2N-C3N	-3.03	1.34	1.39
2	D	4490	NAD	C2N-C3N	-2.85	1.34	1.39
2	C	3490	NAD	O4D-C1D	2.83	1.45	1.41
2	A	1490	NAD	C2N-C3N	-2.76	1.34	1.39
2	D	4490	NAD	C2D-C1D	2.62	1.57	1.53
2	B	2490	NAD	O4D-C1D	2.50	1.44	1.41
2	C	3490	NAD	C2D-C1D	2.43	1.57	1.53
2	B	2490	NAD	C2D-C1D	2.35	1.57	1.53
2	A	1490	NAD	C2D-C1D	2.34	1.57	1.53
2	C	3490	NAD	O4D-C4D	2.24	1.50	1.45
2	A	1490	NAD	O4D-C4D	2.18	1.49	1.45
2	D	4490	NAD	O4D-C4D	2.14	1.49	1.45
2	B	2490	NAD	O4B-C1B	2.08	1.44	1.41

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1490	NAD	N3A-C2A-N1A	-4.37	121.84	128.68
2	C	3490	NAD	N3A-C2A-N1A	-4.35	121.88	128.68
2	B	2490	NAD	N3A-C2A-N1A	-4.31	121.95	128.68
2	D	4490	NAD	N3A-C2A-N1A	-4.23	122.07	128.68
2	A	1490	NAD	C2A-N1A-C6A	4.08	125.74	118.75
2	B	2490	NAD	C3B-C2B-C1B	4.07	107.10	100.98
2	B	2490	NAD	C2A-N1A-C6A	4.06	125.70	118.75
2	A	1490	NAD	C3B-C2B-C1B	4.05	107.08	100.98
2	C	3490	NAD	C2A-N1A-C6A	4.00	125.60	118.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	4490	NAD	C2A-N1A-C6A	3.97	125.55	118.75
2	D	4490	NAD	C3B-C2B-C1B	3.97	106.95	100.98
2	C	3490	NAD	C3B-C2B-C1B	3.79	106.69	100.98
2	D	4490	NAD	C2N-C3N-C4N	3.12	121.80	118.26
2	C	3490	NAD	C2N-C3N-C4N	3.06	121.73	118.26
2	C	3490	NAD	C5N-C4N-C3N	-3.01	116.79	120.34
2	D	4490	NAD	C5N-C4N-C3N	-3.00	116.79	120.34
2	B	2490	NAD	C2N-C3N-C4N	2.99	121.65	118.26
2	A	1490	NAD	C2N-C3N-C4N	2.97	121.62	118.26
2	A	1490	NAD	C5N-C4N-C3N	-2.92	116.89	120.34
2	B	2490	NAD	C5N-C4N-C3N	-2.87	116.94	120.34
2	C	3490	NAD	O2A-PA-O1A	2.73	125.75	112.24
2	B	2490	NAD	O2A-PA-O1A	2.72	125.71	112.24
2	D	4490	NAD	O2A-PA-O1A	2.72	125.67	112.24
2	A	1490	NAD	O2A-PA-O1A	2.66	125.38	112.24
2	A	1490	NAD	O4D-C1D-C2D	-2.56	103.19	106.93
2	B	2490	NAD	C5A-C6A-N1A	-2.52	114.65	120.35
2	D	4490	NAD	C5A-C6A-N1A	-2.48	114.73	120.35
2	C	3490	NAD	C5A-C6A-N1A	-2.47	114.74	120.35
2	C	3490	NAD	O4D-C1D-C2D	-2.47	103.31	106.93
2	D	4490	NAD	O4D-C1D-C2D	-2.44	103.36	106.93
2	A	1490	NAD	C5A-C6A-N1A	-2.43	114.84	120.35
2	B	2490	NAD	O4D-C1D-C2D	-2.26	103.63	106.93
2	B	2490	NAD	C6N-N1N-C2N	2.03	123.82	121.97

There are no chirality outliers.

All (4) torsion outliers are listed below:

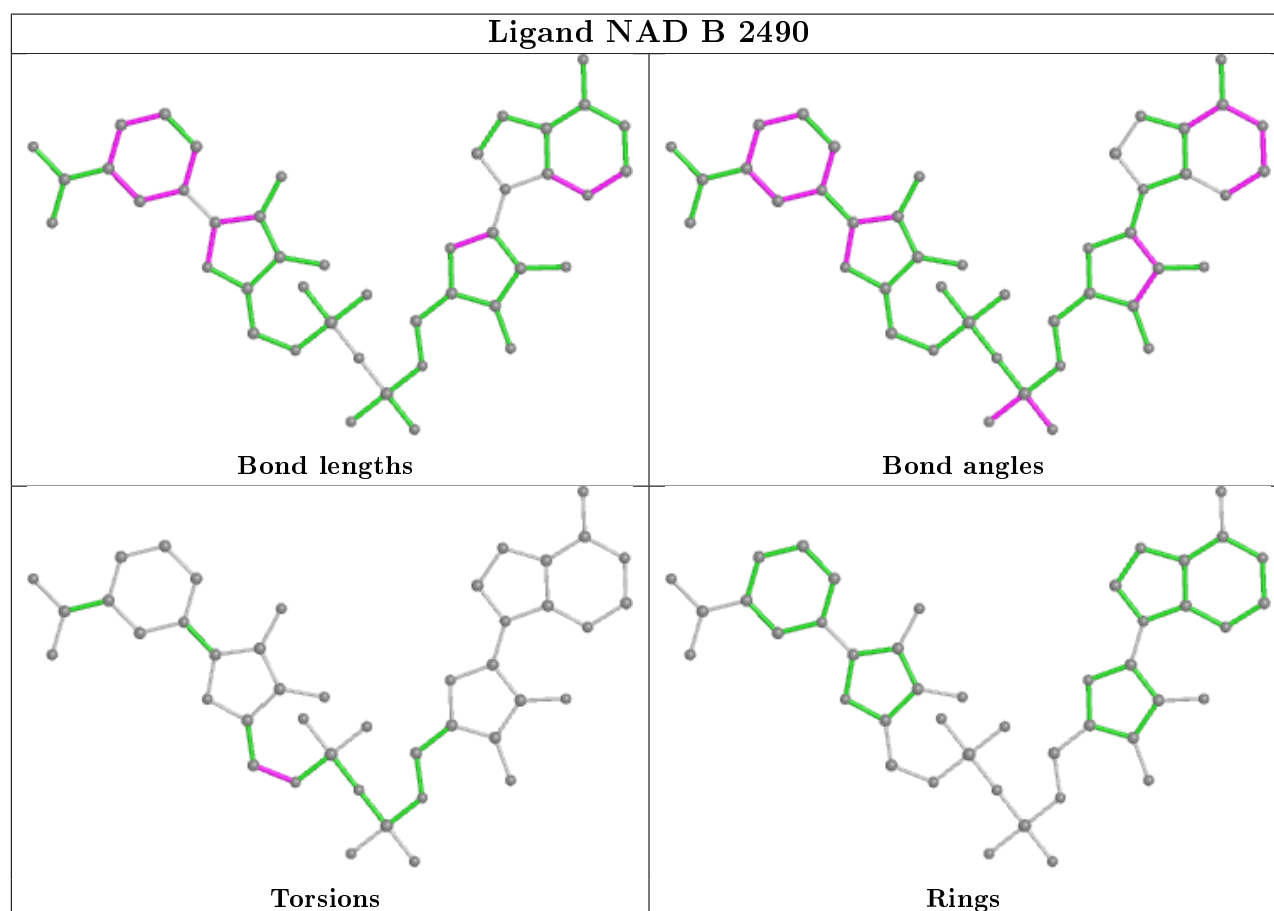
Mol	Chain	Res	Type	Atoms
2	D	4490	NAD	C4D-C5D-O5D-PN
2	A	1490	NAD	C4D-C5D-O5D-PN
2	B	2490	NAD	C4D-C5D-O5D-PN
2	C	3490	NAD	C4D-C5D-O5D-PN

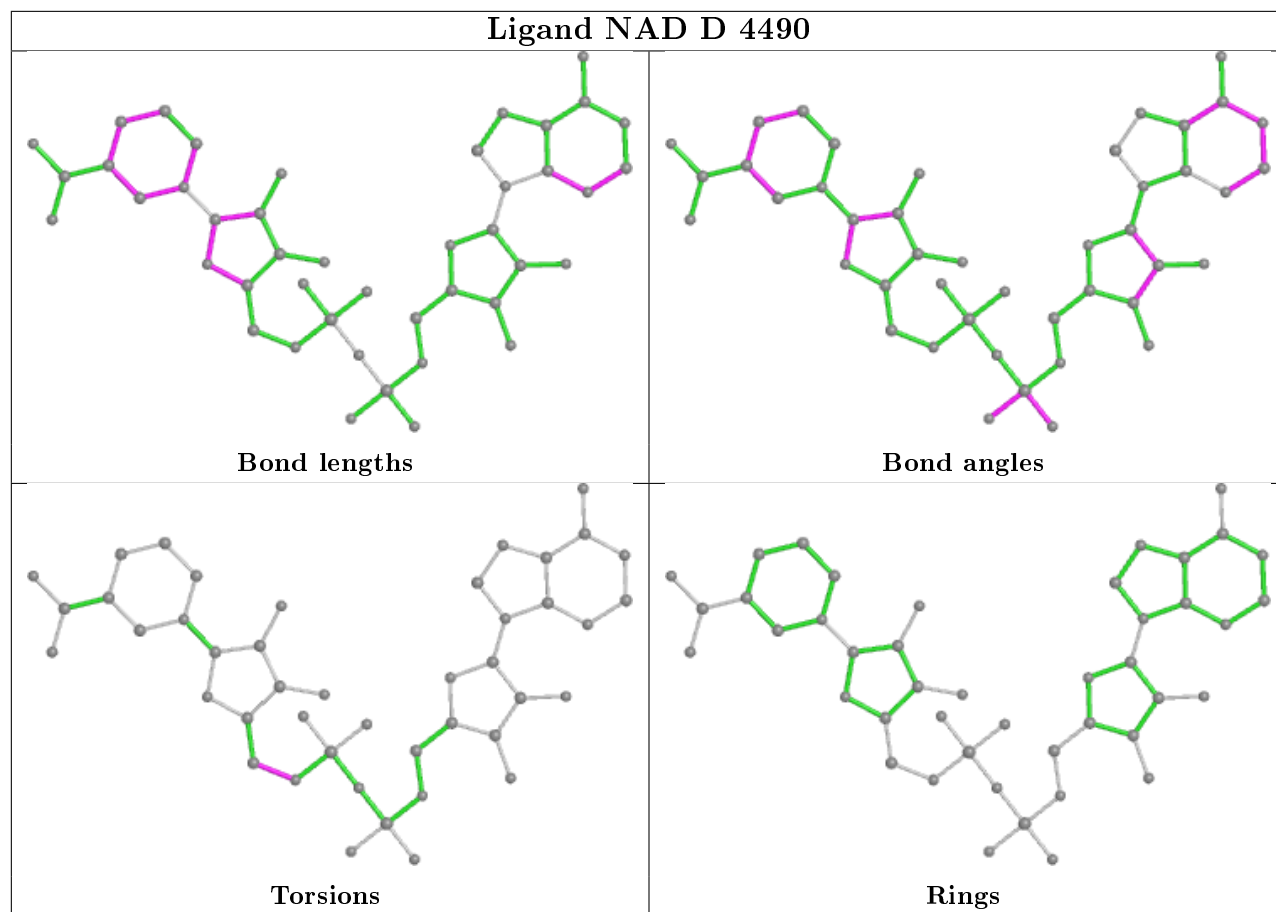
There are no ring outliers.

3 monomers are involved in 4 short contacts:

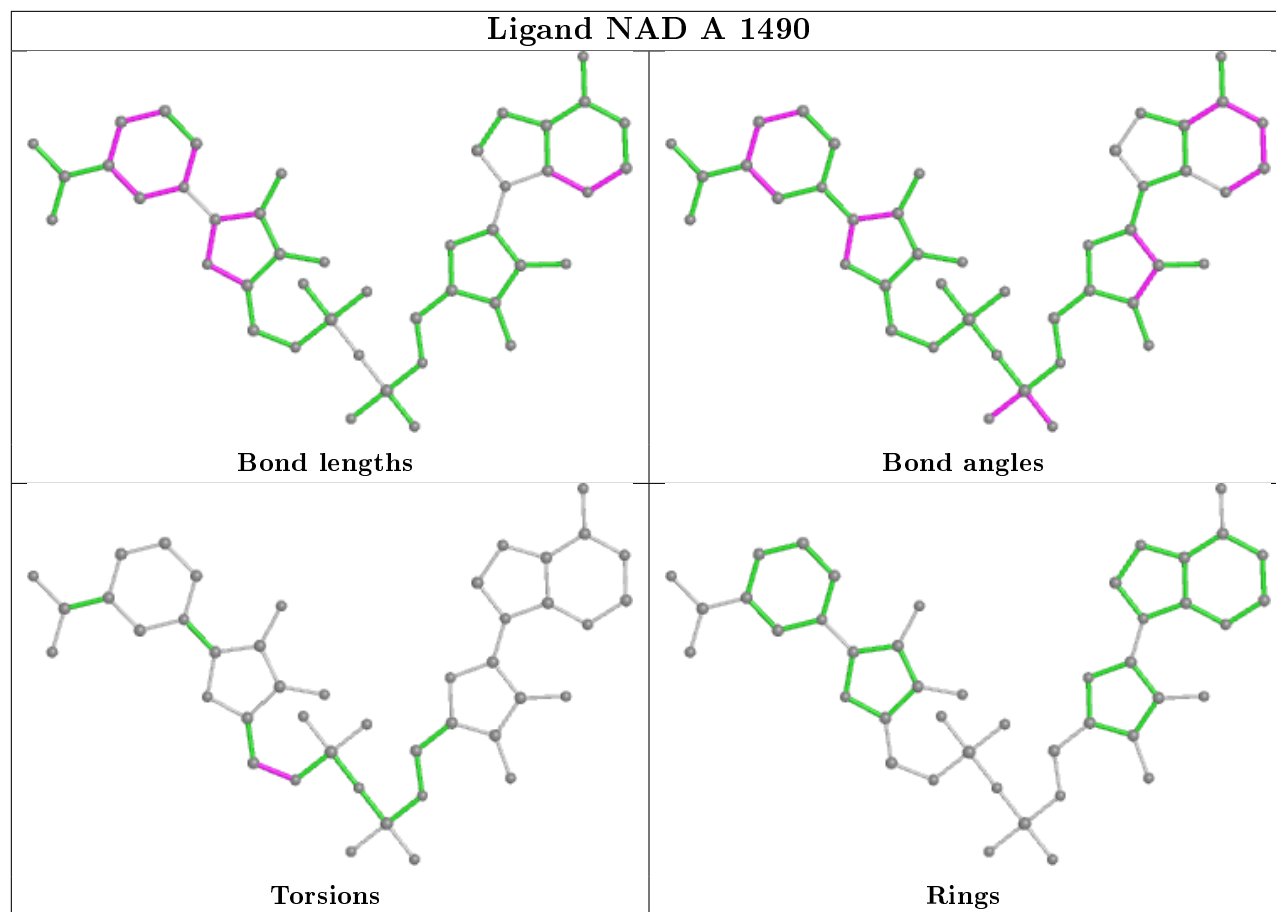
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2490	NAD	1	0
2	D	4490	NAD	1	0
2	C	3490	NAD	2	0

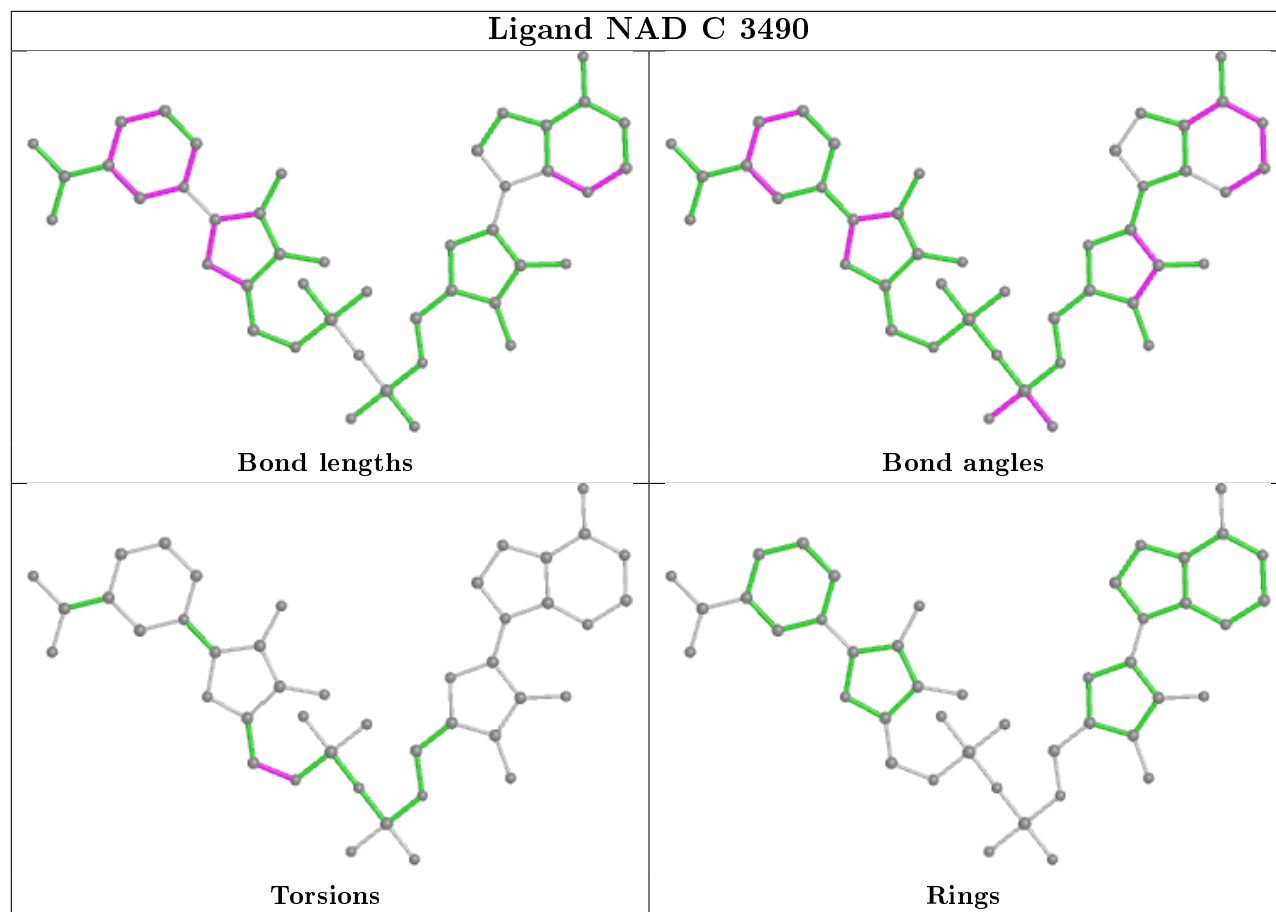
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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, 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	484/486 (99%)	-0.35	7 (1%) 75 77	12, 29, 50, 67	0
1	B	484/486 (99%)	-0.40	7 (1%) 75 77	13, 26, 46, 71	0
1	C	484/486 (99%)	-0.44	7 (1%) 75 77	15, 26, 45, 64	0
1	D	484/486 (99%)	-0.34	6 (1%) 79 80	11, 30, 50, 66	0
All	All	1936/1944 (99%)	-0.39	27 (1%) 75 77	11, 27, 49, 71	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	356	ASN	5.5
1	C	356	ASN	4.1
1	D	356	ASN	3.7
1	B	485	ASP	3.5
1	C	485	ASP	3.4
1	A	356	ASN	3.3
1	C	19	LYS	3.2
1	A	485	ASP	3.1
1	A	359	ASP	3.1
1	A	330	ASP	3.0
1	A	3	GLU	2.9
1	D	485	ASP	2.8
1	A	357	VAL	2.8
1	D	319	ASP	2.8
1	D	359	ASP	2.7
1	B	21	ASP	2.5
1	C	330	ASP	2.5
1	D	375	GLU	2.5
1	B	486	PHE	2.5
1	B	19	LYS	2.4
1	C	319	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	319	ASP	2.4
1	C	22	GLN	2.3
1	C	486	PHE	2.2
1	B	357	VAL	2.2
1	D	3	GLU	2.2
1	B	44	GLU	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](#)

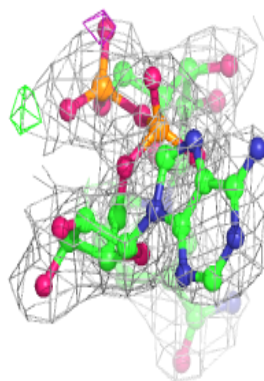
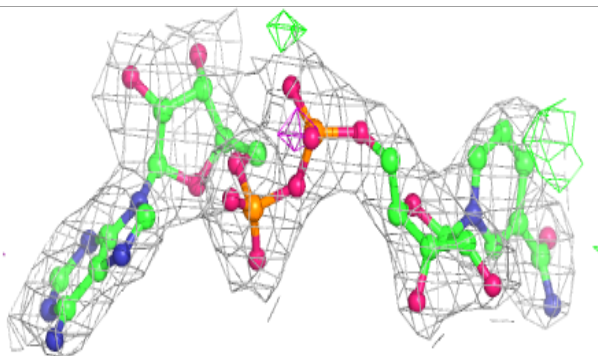
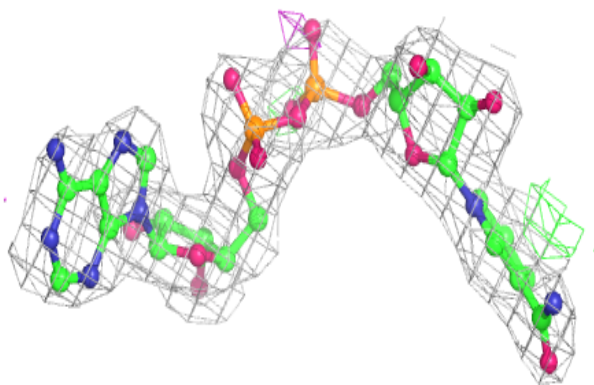
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAD	D	4490	44/44	0.94	0.16	37,42,44,45	0
2	NAD	C	3490	44/44	0.94	0.17	37,40,46,48	0
2	NAD	A	1490	44/44	0.95	0.15	36,40,42,44	0
2	NAD	B	2490	44/44	0.96	0.14	38,41,45,46	0

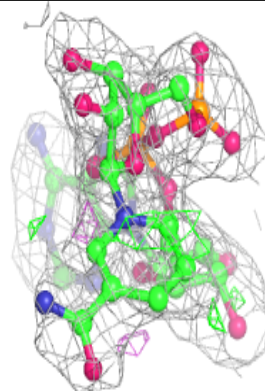
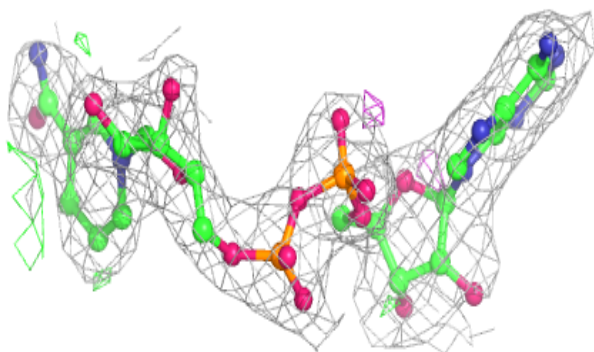
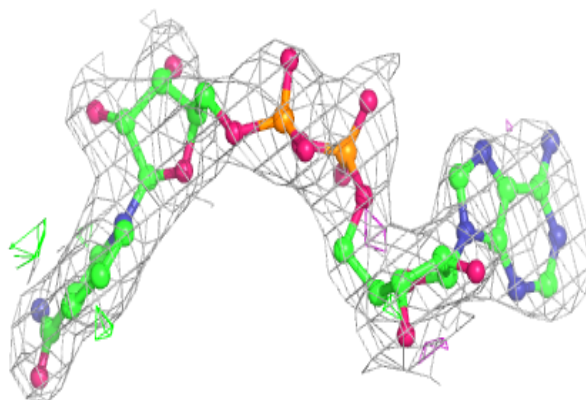
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around NAD D 4490:**

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

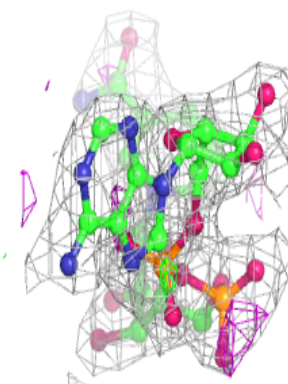
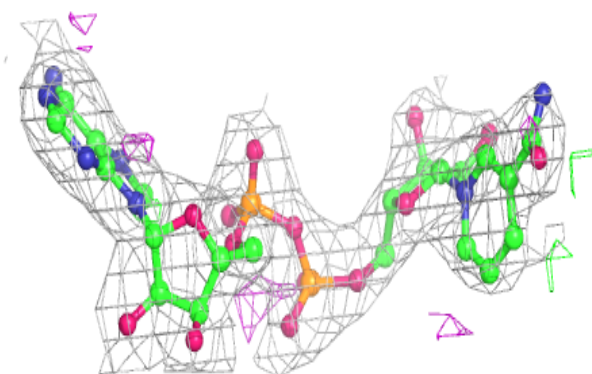
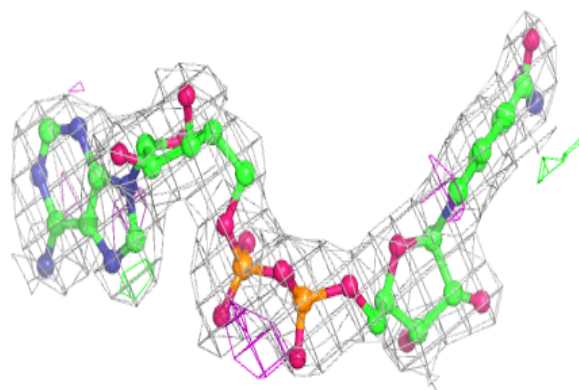
**Electron density around NAD C 3490:**

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

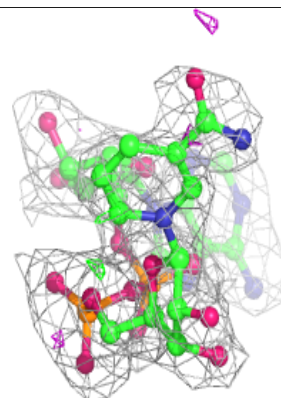
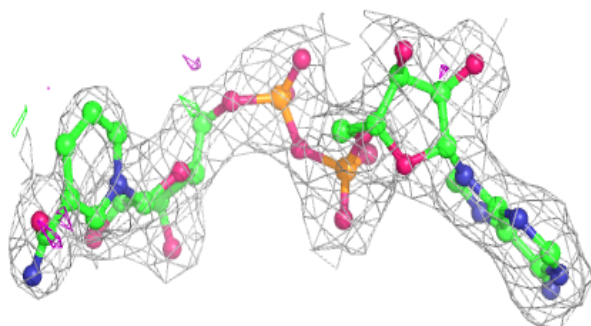
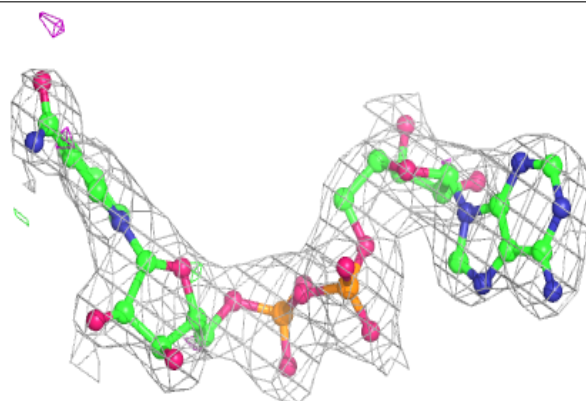


**Electron density around NAD A 1490:**

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

**Electron density around NAD B 2490:**

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



## 6.5 Other polymers

There are no such residues in this entry.