



# Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 07:40 pm BST

PDB ID : 1HYG  
Title : Crystal structure of MJ0490 gene product, the family of lactate/malate dehydrogenase  
Authors : Lee, B.I.; Chang, C.; Cho, S.-J.; Suh, S.W.  
Deposited on : 2001-01-19  
Resolution : 2.80 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

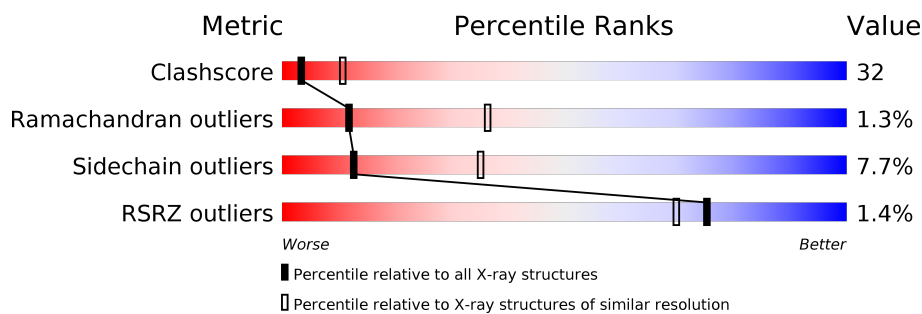
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	313	 2% 52% 44%
1	B	313	 2% 54% 41% 5%

## 2 Entry composition [i](#)

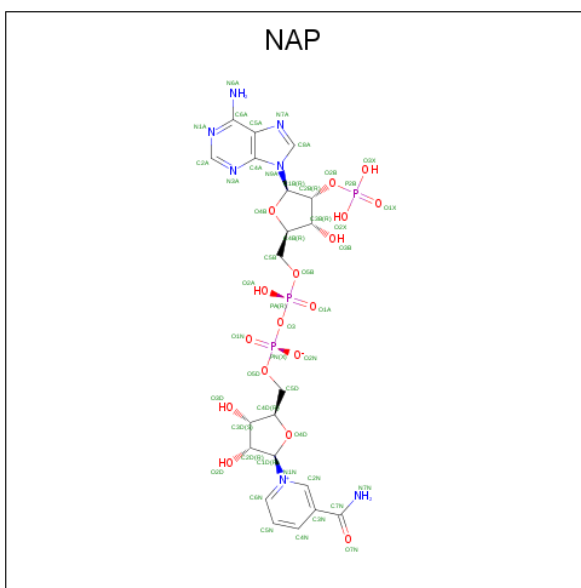
There are 3 unique types of molecules in this entry. The entry contains 5094 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called L-LACTATE/MALATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	313	Total 2429	1544	415	460	10	0	0	0
1	B	313	Total 2429	1544	415	460	10	0	0	0

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 48	21	7	17	3	0	0
2	B	1	Total 48	21	7	17	3	0	0

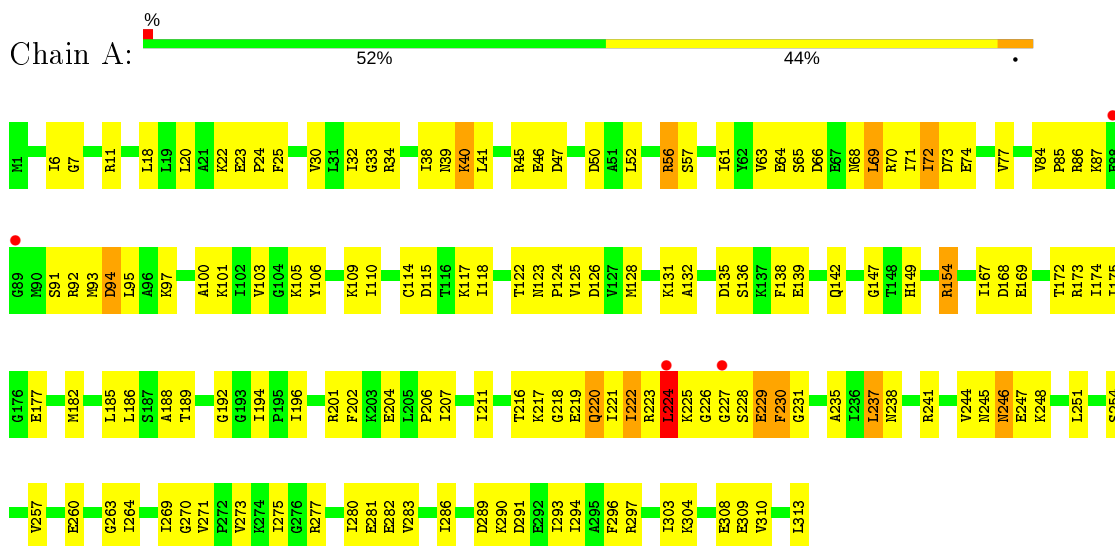
- Molecule 3 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	A	75	Total 75	O 75	0	0
3	B	65	Total 65	O 65	0	0

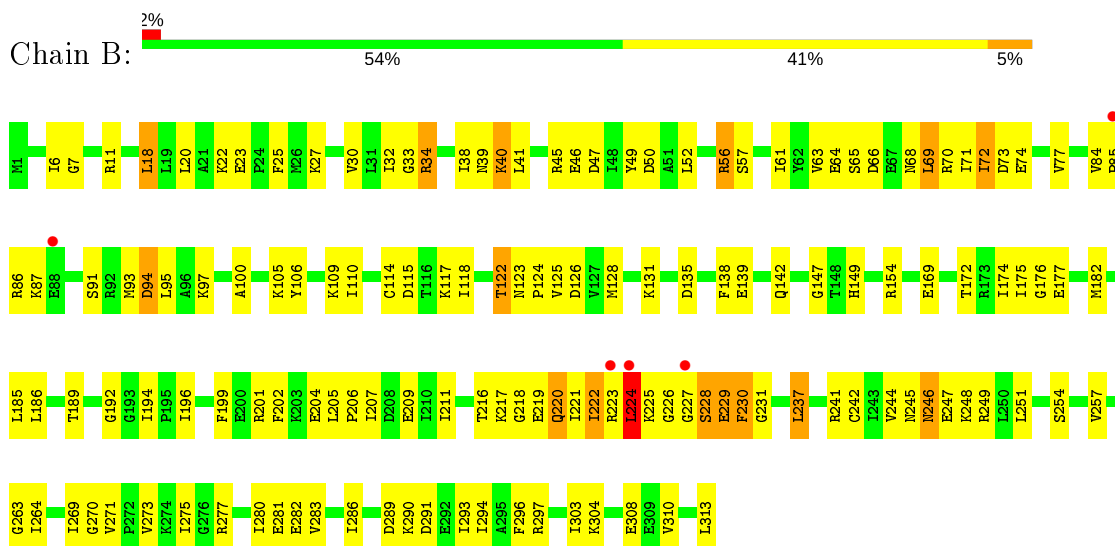
### 3 Residue-property plots [i](#)

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: L-LACTATE/MALATE DEHYDROGENASE



- Molecule 1: L-LACTATE/MALATE DEHYDROGENASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	98.21Å 98.21Å 167.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.51 – 2.80 19.68 – 2.80	Depositor EDS
% Data completeness (in resolution range)	86.4 (19.51-2.80) 94.6 (19.68-2.80)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.53 (at 2.79Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.216 , 0.282 0.236 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.0	Xtrriage
Anisotropy	0.276	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 55.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5094	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	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 46.15 % 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 1.1926e-04. 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: NAP

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	0.39	0/2458	0.62	0/3306
1	B	0.41	1/2458 (0.0%)	0.62	0/3306
All	All	0.40	1/4916 (0.0%)	0.62	0/6612

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	242	CYS	CB-SG	-5.80	1.72	1.81

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	2429	0	2531	180	0
1	B	2429	0	2531	168	0
2	A	48	0	25	2	0
2	B	48	0	25	6	0
3	A	75	0	0	14	0
3	B	65	0	0	7	0
All	All	5094	0	5112	327	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 32.

All (327) 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:A:6:ILE:HA	3:A:806:HOH:O	1.66	0.94
1:A:100:ALA:HA	1:A:128:MET:HE1	1.50	0.91
1:B:100:ALA:HA	1:B:128:MET:HE1	1.53	0.90
1:A:246:ASN:ND2	1:A:277:ARG:H	1.72	0.87
1:B:7:GLY:HA2	2:B:901:NAP:O3B	1.76	0.86
1:B:246:ASN:ND2	1:B:277:ARG:H	1.75	0.84
1:B:11:ARG:HE	1:B:226:GLY:HA3	1.42	0.83
1:A:11:ARG:NE	1:A:226:GLY:HA3	1.94	0.83
1:B:11:ARG:NE	1:B:226:GLY:HA3	1.93	0.83
1:A:221:ILE:HD12	1:A:221:ILE:H	1.44	0.83
1:A:185:LEU:HB2	3:A:825:HOH:O	1.79	0.82
1:B:221:ILE:H	1:B:221:ILE:HD12	1.45	0.82
1:A:11:ARG:HE	1:A:226:GLY:HA3	1.44	0.82
1:A:175:ILE:HD13	1:A:185:LEU:HD11	1.63	0.81
1:A:131:LYS:HD3	1:A:310:VAL:HG12	1.62	0.81
1:B:105:LYS:O	1:B:109:LYS:HG2	1.81	0.80
1:A:139:GLU:HB2	1:A:142:GLN:HE21	1.45	0.80
1:B:139:GLU:HB2	1:B:142:GLN:HE21	1.45	0.80
1:A:105:LYS:O	1:A:109:LYS:HG2	1.83	0.79
1:A:123:ASN:HD22	1:A:125:VAL:H	1.30	0.78
1:A:229:GLU:HB2	1:B:47:ASP:OD1	1.84	0.77
1:B:123:ASN:HD22	1:B:125:VAL:H	1.32	0.76
1:B:131:LYS:HD3	1:B:310:VAL:HG12	1.67	0.76
1:A:139:GLU:H	1:A:142:GLN:NE2	1.85	0.74
1:B:257:VAL:HG21	1:B:271:VAL:HG11	1.69	0.74
1:B:139:GLU:H	1:B:142:GLN:NE2	1.86	0.74
1:B:175:ILE:HD13	1:B:185:LEU:HD11	1.69	0.74
1:A:86:ARG:HD2	3:A:812:HOH:O	1.85	0.74
1:A:47:ASP:OD1	1:B:229:GLU:HB2	1.89	0.73
1:A:173:ARG:HG2	3:A:825:HOH:O	1.89	0.72
1:B:106:TYR:O	1:B:110:ILE:HG13	1.89	0.72
1:A:92:ARG:HD2	3:A:815:HOH:O	1.90	0.72
1:A:33:GLY:O	1:A:65:SER:HA	1.89	0.71
1:A:32:ILE:HB	3:A:806:HOH:O	1.91	0.70
1:B:70:ARG:NH1	3:B:704:HOH:O	2.24	0.70
1:A:106:TYR:O	1:A:110:ILE:HG13	1.92	0.70
1:B:33:GLY:O	1:B:65:SER:HA	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ALA:HB1	1:A:310:VAL:HG13	1.73	0.69
1:A:257:VAL:HG21	1:A:271:VAL:HG11	1.74	0.69
1:B:100:ALA:HB1	1:B:310:VAL:HG13	1.74	0.69
1:A:139:GLU:CB	1:A:142:GLN:HE21	2.06	0.69
1:B:275:ILE:HD12	1:B:275:ILE:N	2.08	0.68
1:B:131:LYS:HE3	1:B:135:ASP:OD2	1.93	0.68
1:B:139:GLU:CB	1:B:142:GLN:HE21	2.06	0.68
1:B:219:GLU:O	1:B:223:ARG:HB2	1.93	0.68
1:A:219:GLU:HA	1:A:222:ILE:HG23	1.76	0.68
1:B:220:GLN:HE21	1:B:220:GLN:N	1.92	0.68
1:A:220:GLN:N	1:A:220:GLN:HE21	1.90	0.67
1:A:275:ILE:HD12	1:A:275:ILE:N	2.10	0.67
1:A:263:GLY:HA3	1:A:297:ARG:HE	1.60	0.67
1:A:297:ARG:HG3	1:A:297:ARG:HH21	1.61	0.66
1:A:7:GLY:HA2	2:A:900:NAP:O3B	1.95	0.66
1:B:269:ILE:HG23	1:B:271:VAL:HG13	1.78	0.66
1:B:297:ARG:HH21	1:B:297:ARG:HG3	1.60	0.66
1:B:219:GLU:HA	1:B:222:ILE:HG23	1.77	0.66
1:B:201:ARG:HG3	1:B:201:ARG:HH21	1.61	0.66
1:A:201:ARG:HH21	1:A:201:ARG:HG3	1.60	0.66
1:A:219:GLU:O	1:A:223:ARG:HB2	1.95	0.65
1:B:263:GLY:HA3	1:B:297:ARG:HE	1.61	0.65
1:A:124:PRO:O	1:A:128:MET:HG2	1.97	0.65
1:A:224:LEU:HD22	1:B:40:LYS:HZ2	1.62	0.65
1:B:186:LEU:HD23	1:B:202:PHE:HE1	1.62	0.65
1:A:131:LYS:HE3	1:A:135:ASP:OD2	1.96	0.64
1:A:293:ILE:O	1:A:297:ARG:HG2	1.96	0.64
1:B:221:ILE:N	1:B:221:ILE:HD12	2.12	0.64
1:A:221:ILE:HD12	1:A:221:ILE:N	2.10	0.64
1:B:91:SER:OG	1:B:94:ASP:HB2	1.97	0.64
1:A:186:LEU:HD23	1:A:202:PHE:HE1	1.62	0.63
1:A:269:ILE:HG23	1:A:271:VAL:HG13	1.79	0.63
1:A:246:ASN:HD22	1:A:277:ARG:H	1.45	0.63
1:B:221:ILE:H	1:B:221:ILE:CD1	2.12	0.62
1:A:221:ILE:CD1	1:A:221:ILE:H	2.11	0.62
1:B:64:GLU:HG3	1:B:71:ILE:HG21	1.81	0.62
1:A:263:GLY:HA3	1:A:297:ARG:NE	2.15	0.62
1:B:293:ILE:O	1:B:297:ARG:HG2	1.99	0.61
1:B:249:ARG:NH2	3:B:763:HOH:O	2.33	0.61
1:A:244:VAL:HG13	1:A:245:ASN:ND2	2.16	0.60
1:A:64:GLU:HG3	1:A:71:ILE:HG21	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:ASN:HA	1:B:125:VAL:N	2.17	0.60
1:A:273:VAL:HG23	1:A:275:ILE:CD1	2.32	0.60
1:B:273:VAL:HG23	1:B:275:ILE:CD1	2.32	0.60
1:B:56:ARG:HD2	1:B:57:SER:N	2.15	0.60
1:A:123:ASN:HA	1:A:125:VAL:N	2.15	0.60
1:B:186:LEU:HD23	1:B:202:PHE:CE1	2.36	0.60
1:A:217:LYS:C	1:A:219:GLU:H	2.05	0.60
1:A:56:ARG:HD2	1:A:57:SER:N	2.16	0.59
1:B:124:PRO:O	1:B:128:MET:HG2	2.03	0.59
1:B:263:GLY:HA3	1:B:297:ARG:NE	2.17	0.59
1:A:271:VAL:HG12	1:A:296:PHE:HZ	1.68	0.59
1:A:186:LEU:HD23	1:A:202:PHE:CE1	2.37	0.59
1:A:224:LEU:HB3	1:B:40:LYS:CA	2.33	0.59
1:B:219:GLU:HA	1:B:222:ILE:CG2	2.34	0.58
1:B:273:VAL:HG23	1:B:275:ILE:HD11	1.85	0.58
1:B:217:LYS:C	1:B:219:GLU:H	2.04	0.58
1:B:244:VAL:HG13	1:B:245:ASN:ND2	2.18	0.58
1:A:91:SER:OG	1:A:94:ASP:HB2	2.04	0.57
1:B:271:VAL:HG12	1:B:296:PHE:HZ	1.70	0.57
1:B:297:ARG:NH2	1:B:297:ARG:HG3	2.20	0.57
1:A:219:GLU:HA	1:A:222:ILE:CG2	2.35	0.57
1:B:209:GLU:HG2	3:B:846:HOH:O	2.04	0.57
1:A:273:VAL:HG23	1:A:275:ILE:HD11	1.86	0.56
1:B:290:LYS:O	1:B:294:ILE:HG13	2.05	0.56
1:A:7:GLY:CA	2:A:900:NAP:O3B	2.53	0.56
1:B:246:ASN:HD22	1:B:277:ARG:H	1.50	0.56
1:A:297:ARG:HG3	1:A:297:ARG:NH2	2.20	0.56
1:B:32:ILE:HD13	1:B:64:GLU:HB2	1.87	0.56
1:B:275:ILE:H	1:B:275:ILE:HD12	1.70	0.56
1:A:273:VAL:HG21	1:A:280:ILE:HD12	1.87	0.56
1:A:290:LYS:O	1:A:294:ILE:HG13	2.06	0.56
1:A:188:ALA:HB3	3:A:825:HOH:O	2.04	0.56
1:B:86:ARG:O	1:B:87:LYS:HB2	2.06	0.56
1:A:169:GLU:OE1	1:A:192:GLY:HA2	2.06	0.55
1:A:194:ILE:HD12	1:A:194:ILE:N	2.21	0.55
1:B:169:GLU:OE1	1:B:192:GLY:HA2	2.06	0.55
1:A:11:ARG:CZ	1:A:226:GLY:HA3	2.37	0.55
1:A:72:ILE:O	1:A:72:ILE:HG13	2.06	0.55
1:B:220:GLN:O	1:B:225:LYS:HB2	2.06	0.55
1:B:41:LEU:HD12	1:B:63:VAL:HG13	1.89	0.55
1:A:32:ILE:HD13	1:A:64:GLU:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:247:GLU:O	1:A:248:LYS:HB2	2.07	0.55
1:B:11:ARG:CZ	1:B:226:GLY:HA3	2.36	0.55
1:B:304:LYS:HZ3	1:B:308:GLU:HG2	1.72	0.55
1:B:216:THR:O	1:B:219:GLU:HG2	2.07	0.54
1:A:220:GLN:HE21	1:A:220:GLN:H	1.55	0.54
1:B:273:VAL:HG21	1:B:280:ILE:HD12	1.89	0.54
1:A:220:GLN:O	1:A:225:LYS:HB2	2.07	0.54
1:B:247:GLU:O	1:B:248:LYS:HB2	2.07	0.54
1:A:100:ALA:HB1	1:A:310:VAL:CG1	2.36	0.53
1:A:275:ILE:HD12	1:A:275:ILE:H	1.73	0.53
1:A:217:LYS:HE3	1:B:46:GLU:OE1	2.07	0.53
1:B:100:ALA:HB1	1:B:310:VAL:CG1	2.39	0.53
1:A:194:ILE:H	1:A:194:ILE:HD12	1.74	0.53
1:A:177:GLU:HA	1:A:303:ILE:HD11	1.91	0.53
1:B:304:LYS:NZ	1:B:308:GLU:CG	2.72	0.53
1:A:216:THR:O	1:A:219:GLU:HG2	2.09	0.53
1:A:86:ARG:O	1:A:87:LYS:HB2	2.07	0.53
1:A:271:VAL:HG12	1:A:296:PHE:CZ	2.43	0.52
1:B:201:ARG:HG3	1:B:201:ARG:NH2	2.24	0.52
1:B:69:LEU:O	1:B:72:ILE:HG23	2.08	0.52
1:B:7:GLY:CA	2:B:901:NAP:O3B	2.52	0.52
1:A:304:LYS:NZ	1:A:308:GLU:CG	2.73	0.52
1:A:41:LEU:HD12	1:A:63:VAL:HG13	1.92	0.52
1:B:177:GLU:HA	1:B:303:ILE:HD11	1.91	0.52
1:A:69:LEU:O	1:A:72:ILE:HG23	2.09	0.52
1:A:40:LYS:HZ2	1:B:224:LEU:HD22	1.74	0.52
1:A:264:ILE:HD12	1:A:297:ARG:HD3	1.92	0.52
1:A:304:LYS:HZ3	1:A:308:GLU:HG2	1.75	0.52
1:B:220:GLN:HE21	1:B:220:GLN:H	1.57	0.52
1:A:40:LYS:CA	1:B:224:LEU:HB3	2.40	0.51
1:B:271:VAL:HG12	1:B:296:PHE:CZ	2.45	0.51
1:A:30:VAL:HG12	1:A:32:ILE:HG12	1.92	0.51
1:A:221:ILE:HG13	1:A:227:GLY:HA2	1.93	0.51
1:B:72:ILE:HG13	1:B:72:ILE:O	2.09	0.51
1:A:63:VAL:O	1:A:64:GLU:HG2	2.10	0.51
1:A:216:THR:C	1:A:218:GLY:H	2.14	0.51
1:B:216:THR:C	1:B:218:GLY:H	2.13	0.51
1:A:20:LEU:HD23	1:A:237:LEU:HD23	1.93	0.50
1:A:224:LEU:HB2	1:B:39:ASN:CB	2.41	0.50
1:B:73:ASP:OD1	1:B:74:GLU:HG3	2.11	0.50
1:B:221:ILE:HG13	1:B:227:GLY:HA2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:LYS:HE3	3:B:759:HOH:O	2.11	0.50
1:B:40:LYS:HB2	1:B:40:LYS:HZ2	1.76	0.50
1:B:34:ARG:HB2	2:B:901:NAP:O2X	2.11	0.50
1:A:224:LEU:O	1:B:40:LYS:HA	2.11	0.49
1:A:73:ASP:OD1	1:A:74:GLU:HG3	2.12	0.49
1:B:30:VAL:HG12	1:B:32:ILE:HG12	1.94	0.49
1:A:40:LYS:HB2	1:A:40:LYS:HZ2	1.77	0.49
1:B:194:ILE:HD12	1:B:194:ILE:N	2.27	0.49
1:A:224:LEU:HB3	1:B:40:LYS:N	2.28	0.49
1:A:177:GLU:CB	1:A:303:ILE:HD11	2.43	0.49
1:B:63:VAL:O	1:B:64:GLU:HG2	2.13	0.49
1:A:105:LYS:HD2	3:A:807:HOH:O	2.12	0.48
1:A:201:ARG:HG3	1:A:201:ARG:NH2	2.24	0.48
1:B:257:VAL:HG22	1:B:283:VAL:HG11	1.96	0.48
1:A:281:GLU:O	1:A:282:GLU:HB2	2.14	0.48
1:A:39:ASN:CB	1:B:224:LEU:HB2	2.44	0.47
1:A:304:LYS:NZ	1:A:308:GLU:HG2	2.29	0.47
1:B:207:ILE:O	1:B:211:ILE:HG12	2.14	0.47
1:B:289:ASP:O	1:B:293:ILE:HG22	2.15	0.47
1:A:125:VAL:HG21	1:A:147:GLY:H	1.79	0.47
1:A:177:GLU:CA	1:A:303:ILE:HD11	2.43	0.47
1:A:32:ILE:CB	3:A:806:HOH:O	2.57	0.47
1:B:264:ILE:HD12	1:B:297:ARG:HD3	1.97	0.47
1:A:257:VAL:CG2	1:A:271:VAL:HG21	2.44	0.47
1:B:123:ASN:HA	1:B:124:PRO:C	2.35	0.47
1:B:105:LYS:O	1:B:109:LYS:HE2	2.15	0.47
1:B:304:LYS:NZ	1:B:308:GLU:HG2	2.29	0.47
1:B:217:LYS:HA	1:B:219:GLU:HG2	1.97	0.47
1:A:132:ALA:O	1:A:136:SER:OG	2.28	0.46
1:B:11:ARG:HG2	1:B:11:ARG:HH11	1.80	0.46
1:A:66:ASP:HB2	1:A:106:TYR:HE2	1.80	0.46
1:A:177:GLU:HB2	1:A:303:ILE:HD11	1.97	0.46
1:A:40:LYS:HA	1:B:224:LEU:O	2.15	0.46
1:A:45:ARG:HG3	1:A:61:ILE:HB	1.96	0.46
1:A:68:ASN:C	1:A:70:ARG:H	2.19	0.46
1:B:125:VAL:HG21	1:B:147:GLY:H	1.80	0.46
1:A:289:ASP:O	1:A:293:ILE:HG22	2.15	0.46
1:A:207:ILE:O	1:A:211:ILE:HG12	2.16	0.46
1:A:217:LYS:HA	1:A:219:GLU:HG2	1.98	0.46
1:A:223:ARG:O	1:A:225:LYS:N	2.49	0.46
1:B:257:VAL:CG2	1:B:271:VAL:HG21	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:269:ILE:HG12	1:B:270:GLY:N	2.31	0.45
1:B:139:GLU:H	1:B:142:GLN:HE21	1.59	0.45
1:A:237:LEU:O	1:A:237:LEU:HD22	2.16	0.45
1:B:186:LEU:HD12	1:B:186:LEU:N	2.31	0.45
1:A:224:LEU:O	1:B:40:LYS:HD3	2.16	0.45
1:A:263:GLY:C	1:A:264:ILE:HD12	2.37	0.45
1:B:20:LEU:HD23	1:B:237:LEU:HD23	1.97	0.45
1:B:269:ILE:HG13	1:B:303:ILE:HD12	1.98	0.45
1:B:68:ASN:C	1:B:70:ARG:H	2.19	0.45
1:A:294:ILE:O	1:A:297:ARG:HB2	2.17	0.45
1:B:194:ILE:HD12	1:B:194:ILE:H	1.80	0.45
1:B:45:ARG:HG3	1:B:61:ILE:HB	1.97	0.45
1:A:93:MET:CE	1:A:309:GLU:HG3	2.46	0.45
1:B:217:LYS:C	1:B:219:GLU:N	2.70	0.45
1:A:91:SER:H	1:A:94:ASP:CB	2.30	0.45
1:A:105:LYS:O	1:A:109:LYS:HE2	2.16	0.45
1:A:204:GLU:O	1:A:206:PRO:HD3	2.17	0.45
1:A:23:GLU:HG3	1:A:25:PHE:CZ	2.51	0.45
1:A:230:PHE:O	1:A:231:GLY:C	2.55	0.44
1:B:177:GLU:CA	1:B:303:ILE:HD11	2.46	0.44
1:B:219:GLU:OE1	3:B:798:HOH:O	2.21	0.44
1:A:309:GLU:OE2	3:A:788:HOH:O	2.21	0.44
1:B:23:GLU:HG3	1:B:25:PHE:CZ	2.52	0.44
1:B:275:ILE:CD1	1:B:275:ILE:N	2.80	0.44
1:A:264:ILE:CD1	1:A:297:ARG:HD3	2.48	0.44
1:A:39:ASN:HB3	1:B:224:LEU:HB2	1.99	0.44
1:A:123:ASN:HA	1:A:124:PRO:C	2.35	0.44
1:A:271:VAL:CG1	1:A:296:PHE:HZ	2.31	0.44
1:B:196:ILE:HG12	1:B:202:PHE:CD1	2.52	0.44
1:A:154:ARG:HH21	1:B:50:ASP:CG	2.20	0.44
1:A:11:ARG:HG2	1:A:11:ARG:HH11	1.82	0.44
1:A:269:ILE:HG13	1:A:303:ILE:HD12	1.98	0.44
1:A:38:ILE:HD11	1:A:65:SER:HA	2.00	0.44
1:A:86:ARG:CD	3:A:812:HOH:O	2.54	0.44
1:A:46:GLU:OE1	1:B:217:LYS:HE3	2.17	0.44
1:B:223:ARG:O	1:B:225:LYS:N	2.51	0.44
1:B:263:GLY:C	1:B:264:ILE:HD12	2.37	0.44
1:B:66:ASP:HB2	1:B:106:TYR:HE2	1.82	0.44
1:A:186:LEU:N	1:A:186:LEU:HD12	2.33	0.44
1:B:237:LEU:O	1:B:237:LEU:HD22	2.18	0.44
1:A:172:THR:HB	1:A:189:THR:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:LYS:NZ	1:A:313:LEU:H	2.16	0.43
1:A:50:ASP:CG	1:B:154:ARG:HH21	2.22	0.43
1:B:176:GLY:HA2	1:B:269:ILE:HD11	2.00	0.43
1:A:118:ILE:HD11	1:A:138:PHE:CE2	2.53	0.43
1:B:177:GLU:CB	1:B:303:ILE:HD11	2.49	0.43
1:A:264:ILE:O	1:A:264:ILE:HG22	2.18	0.43
1:A:196:ILE:HG12	1:A:202:PHE:CD1	2.53	0.43
1:B:125:VAL:HG13	1:B:126:ASP:N	2.33	0.43
1:B:230:PHE:O	1:B:231:GLY:C	2.57	0.43
1:B:205:LEU:O	1:B:207:ILE:N	2.46	0.43
1:A:125:VAL:HG13	1:A:126:ASP:N	2.34	0.43
1:B:174:ILE:CG2	1:B:182:MET:HB2	2.49	0.43
1:B:11:ARG:HB2	2:B:901:NAP:O1N	2.18	0.43
1:A:91:SER:H	1:A:94:ASP:HB2	1.84	0.43
1:B:172:THR:HB	1:B:189:THR:HG23	2.00	0.43
1:B:38:ILE:HD11	1:B:65:SER:HA	2.01	0.43
1:A:40:LYS:N	1:B:224:LEU:HB3	2.34	0.43
1:B:273:VAL:CG2	1:B:275:ILE:HD11	2.49	0.42
1:B:91:SER:H	1:B:94:ASP:CB	2.32	0.42
1:A:246:ASN:HD22	1:A:277:ARG:N	2.12	0.42
1:A:22:LYS:HD3	3:A:766:HOH:O	2.18	0.42
1:A:126:ASP:HA	1:A:254:SER:OG	2.19	0.42
1:B:281:GLU:O	1:B:282:GLU:HB2	2.19	0.42
1:B:93:MET:HG3	1:B:97:LYS:HD2	2.00	0.42
1:A:103:VAL:HB	1:A:128:MET:CE	2.50	0.42
1:B:248:LYS:HE3	1:B:281:GLU:OE2	2.20	0.42
1:A:123:ASN:HD22	1:A:125:VAL:N	2.07	0.42
1:A:217:LYS:C	1:A:219:GLU:N	2.71	0.42
1:A:257:VAL:HG22	1:A:283:VAL:HG11	2.01	0.42
1:A:221:ILE:HA	1:A:227:GLY:HA2	2.01	0.42
1:A:248:LYS:HE3	1:A:281:GLU:OE2	2.20	0.42
1:B:246:ASN:HD22	1:B:277:ARG:N	2.16	0.42
1:A:11:ARG:NH2	1:A:226:GLY:HA3	2.35	0.42
1:A:269:ILE:HG12	1:A:270:GLY:N	2.34	0.42
1:B:86:ARG:HA	1:B:95:LEU:HD13	2.02	0.42
1:A:101:LYS:O	1:A:105:LYS:HB2	2.20	0.42
1:B:237:LEU:HD11	1:B:241:ARG:NH1	2.35	0.42
1:B:149:HIS:CE1	1:B:251:LEU:HD22	2.55	0.42
1:B:294:ILE:O	1:B:297:ARG:HB2	2.20	0.42
1:A:185:LEU:HD12	3:A:825:HOH:O	2.20	0.42
1:A:273:VAL:HB	1:A:280:ILE:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:VAL:C	1:A:86:ARG:H	2.24	0.42
1:B:6:ILE:CD1	1:B:110:ILE:HD11	2.50	0.42
1:A:207:ILE:HD12	1:A:207:ILE:O	2.20	0.41
1:A:237:LEU:HD11	1:A:241:ARG:NH1	2.36	0.41
1:A:293:ILE:O	1:A:297:ARG:CG	2.66	0.41
1:B:223:ARG:O	1:B:224:LEU:C	2.58	0.41
1:B:293:ILE:O	1:B:297:ARG:CG	2.68	0.41
1:A:167:ILE:HG23	1:A:168:ASP:N	2.35	0.41
1:A:174:ILE:CG2	1:A:182:MET:HB2	2.50	0.41
1:A:235:ALA:O	1:A:238:ASN:HB2	2.20	0.41
1:A:100:ALA:CB	1:A:310:VAL:HG13	2.46	0.41
1:A:224:LEU:HB2	1:B:39:ASN:HB3	2.00	0.41
1:A:40:LYS:HD3	1:B:224:LEU:O	2.20	0.41
1:A:86:ARG:HA	1:A:95:LEU:HD13	2.02	0.41
1:A:93:MET:HG3	1:A:97:LYS:HD2	2.01	0.41
1:A:260:GLU:HG2	1:A:283:VAL:HB	2.03	0.41
1:B:131:LYS:NZ	1:B:313:LEU:H	2.19	0.41
1:B:84:VAL:C	1:B:86:ARG:H	2.23	0.41
1:A:23:GLU:HA	1:A:24:PRO:HD3	1.88	0.41
1:A:73:ASP:OD2	1:A:114:CYS:HB3	2.19	0.41
1:A:224:LEU:HB3	1:B:40:LYS:HA	2.01	0.41
1:B:45:ARG:HG2	1:B:49:TYR:CE2	2.55	0.41
1:A:126:ASP:HB2	3:A:818:HOH:O	2.20	0.41
1:B:118:ILE:HD11	1:B:138:PHE:CE2	2.55	0.41
1:B:126:ASP:HA	1:B:254:SER:OG	2.20	0.41
1:B:11:ARG:NH2	1:B:226:GLY:HA3	2.34	0.41
1:B:227:GLY:O	1:B:228:SER:CB	2.69	0.41
1:B:27:LYS:HD2	1:B:27:LYS:HA	1.94	0.41
1:A:149:HIS:CE1	1:A:251:LEU:HD22	2.56	0.41
1:A:223:ARG:O	1:A:224:LEU:C	2.59	0.41
1:B:32:ILE:CD1	1:B:64:GLU:HB2	2.49	0.41
1:B:199:PHE:HB3	3:B:850:HOH:O	2.21	0.41
1:B:97:LYS:O	1:B:100:ALA:HB3	2.20	0.41
1:A:304:LYS:HZ1	1:A:308:GLU:HG3	1.86	0.40
1:A:32:ILE:CD1	1:A:64:GLU:HB2	2.50	0.40
1:B:204:GLU:O	1:B:206:PRO:HD3	2.20	0.40
1:A:139:GLU:H	1:A:142:GLN:HE21	1.61	0.40
1:B:221:ILE:HA	1:B:227:GLY:HA2	2.02	0.40
1:A:273:VAL:CG2	1:A:275:ILE:HD11	2.48	0.40
1:B:11:ARG:N	2:B:901:NAP:O1N	2.53	0.40
1:B:122:THR:HA	2:B:901:NAP:O2D	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:LEU:CD1	3:B:759:HOH:O	2.69	0.40
1:B:304:LYS:HZ1	1:B:308:GLU:HG3	1.87	0.40
1:B:73:ASP:OD2	1:B:114:CYS:HB3	2.21	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	311/313 (99%)	267 (86%)	40 (13%)	4 (1%)	12	36
1	B	311/313 (99%)	268 (86%)	39 (12%)	4 (1%)	12	36
All	All	622/626 (99%)	535 (86%)	79 (13%)	8 (1%)	12	36

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	LEU
1	B	224	LEU
1	A	228	SER
1	B	228	SER
1	A	69	LEU
1	B	69	LEU
1	A	85	PRO
1	B	85	PRO

### 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	267/267 (100%)	246 (92%)	21 (8%)	12	34
1	B	267/267 (100%)	247 (92%)	20 (8%)	13	37
All	All	534/534 (100%)	493 (92%)	41 (8%)	13	35

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	LEU
1	A	34	ARG
1	A	40	LYS
1	A	52	LEU
1	A	56	ARG
1	A	72	ILE
1	A	77	VAL
1	A	94	ASP
1	A	115	ASP
1	A	117	LYS
1	A	122	THR
1	A	154	ARG
1	A	220	GLN
1	A	222	ILE
1	A	224	LEU
1	A	229	GLU
1	A	230	PHE
1	A	237	LEU
1	A	246	ASN
1	A	286	ILE
1	A	291	ASP
1	B	18	LEU
1	B	34	ARG
1	B	40	LYS
1	B	52	LEU
1	B	56	ARG
1	B	72	ILE
1	B	77	VAL
1	B	94	ASP
1	B	115	ASP
1	B	117	LYS
1	B	122	THR
1	B	220	GLN

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Mol	Chain	Res	Type
1	B	222	ILE
1	B	224	LEU
1	B	229	GLU
1	B	230	PHE
1	B	237	LEU
1	B	246	ASN
1	B	286	ILE
1	B	291	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	123	ASN
1	A	141	ASN
1	A	142	GLN
1	A	220	GLN
1	A	238	ASN
1	A	245	ASN
1	A	246	ASN
1	B	60	ASN
1	B	68	ASN
1	B	123	ASN
1	B	141	ASN
1	B	142	GLN
1	B	220	GLN
1	B	238	ASN
1	B	245	ASN
1	B	246	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](#)

2 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	NAP	B	901	-	45,52,52	1.39	6 (13%)	56,80,80	1.54	9 (16%)
2	NAP	A	900	-	45,52,52	1.75	9 (20%)	56,80,80	1.30	7 (12%)

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	NAP	B	901	-	-	9/31/67/67	0/5/5/5
2	NAP	A	900	-	-	7/31/67/67	0/5/5/5

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	900	NAP	C2N-N1N	6.35	1.42	1.35
2	A	900	NAP	C2N-C3N	3.99	1.45	1.39
2	B	901	NAP	C2N-C3N	3.67	1.44	1.39
2	A	900	NAP	C2D-C1D	3.28	1.58	1.53
2	B	901	NAP	C6N-N1N	3.08	1.42	1.35
2	A	900	NAP	C6N-N1N	3.08	1.42	1.35
2	B	901	NAP	C4A-N3A	2.93	1.39	1.35
2	A	900	NAP	C4A-N3A	2.92	1.39	1.35
2	B	901	NAP	C3N-C7N	-2.48	1.46	1.50
2	A	900	NAP	O4D-C1D	2.30	1.44	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	NAP	O4B-C1B	2.25	1.44	1.41
2	B	901	NAP	C2A-N3A	2.11	1.35	1.32
2	A	900	NAP	C3N-C7N	-2.04	1.47	1.50
2	A	900	NAP	C3B-C4B	-2.01	1.47	1.53
2	A	900	NAP	PA-O2A	-2.01	1.45	1.55

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	NAP	C3N-C2N-N1N	-5.01	115.53	120.43
2	B	901	NAP	O7N-C7N-N7N	-4.16	116.66	122.58
2	A	900	NAP	O7N-C7N-N7N	-4.00	116.90	122.58
2	B	901	NAP	C6N-N1N-C2N	3.94	125.57	121.97
2	A	900	NAP	C3N-C2N-N1N	-2.96	117.53	120.43
2	B	901	NAP	C3N-C7N-N7N	2.85	121.17	117.75
2	B	901	NAP	C5N-C4N-C3N	2.73	123.58	120.34
2	A	900	NAP	C5N-C4N-C3N	2.62	123.44	120.34
2	A	900	NAP	O7N-C7N-C3N	2.40	122.50	119.63
2	A	900	NAP	C3N-C7N-N7N	2.38	120.60	117.75
2	A	900	NAP	N3A-C2A-N1A	-2.32	125.06	128.68
2	B	901	NAP	C2N-N1N-C1D	-2.31	113.99	119.14
2	B	901	NAP	O4B-C1B-C2B	-2.31	102.58	106.59
2	B	901	NAP	O7N-C7N-C3N	2.12	122.16	119.63
2	A	900	NAP	C2N-N1N-C1D	-2.08	114.51	119.14
2	B	901	NAP	N3A-C2A-N1A	-2.02	125.51	128.68

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	901	NAP	O4D-C1D-N1N-C2N
2	B	901	NAP	O4D-C1D-N1N-C6N
2	A	900	NAP	O4D-C1D-N1N-C2N
2	A	900	NAP	O4D-C1D-N1N-C6N
2	A	900	NAP	C2D-C1D-N1N-C2N
2	A	900	NAP	C2D-C1D-N1N-C6N
2	B	901	NAP	PA-O3-PN-O5D
2	A	900	NAP	PA-O3-PN-O5D
2	B	901	NAP	C5D-O5D-PN-O2N
2	A	900	NAP	O4D-C4D-C5D-O5D
2	B	901	NAP	C4D-C5D-O5D-PN
2	B	901	NAP	O4D-C4D-C5D-O5D

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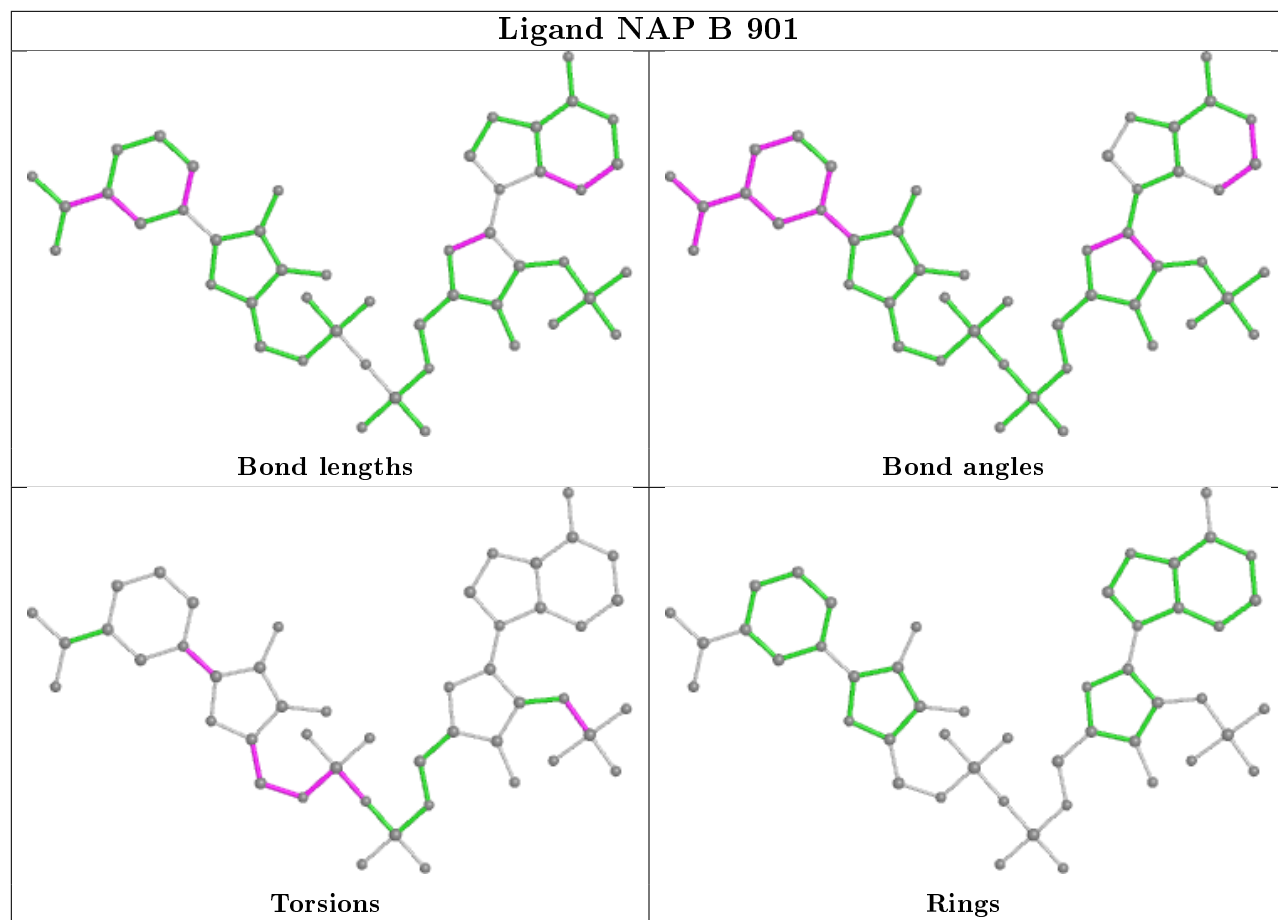
Mol	Chain	Res	Type	Atoms
2	B	901	NAP	C2B-O2B-P2B-O3X
2	B	901	NAP	C5D-O5D-PN-O3
2	B	901	NAP	C2D-C1D-N1N-C6N
2	A	900	NAP	PA-O3-PN-O2N

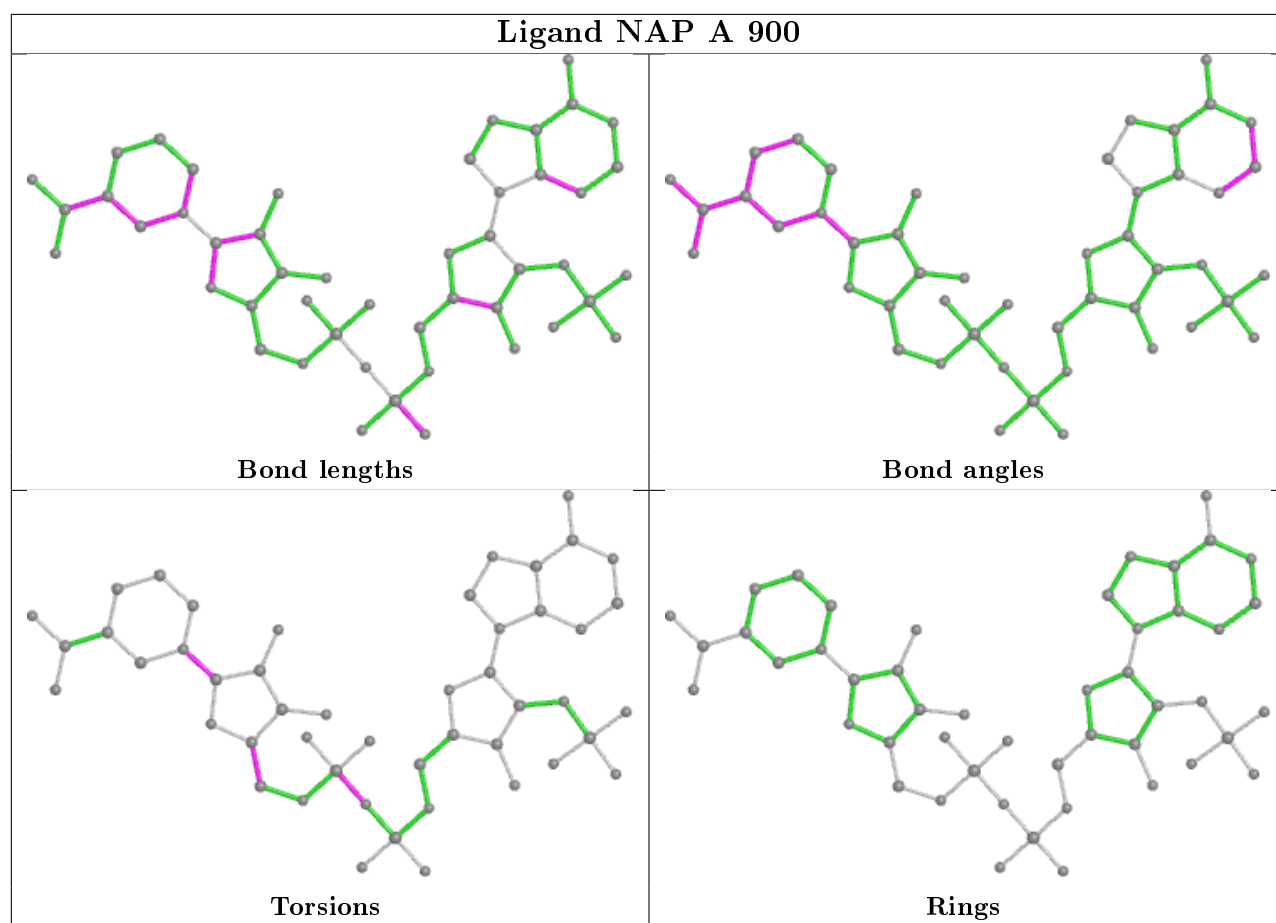
There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	901	NAP	6	0
2	A	900	NAP	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 [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	313/313 (100%)	-0.46	4 (1%) 77 72	11, 31, 62, 98	0
1	B	313/313 (100%)	-0.55	5 (1%) 72 66	8, 28, 60, 96	0
All	All	626/626 (100%)	-0.50	9 (1%) 75 70	8, 30, 62, 98	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	227	GLY	3.9
1	A	224	LEU	3.7
1	B	224	LEU	3.2
1	B	227	GLY	2.7
1	A	88	GLU	2.7
1	B	85	PRO	2.3
1	A	89	GLY	2.2
1	B	88	GLU	2.1
1	B	223	ARG	2.1

### 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](#)

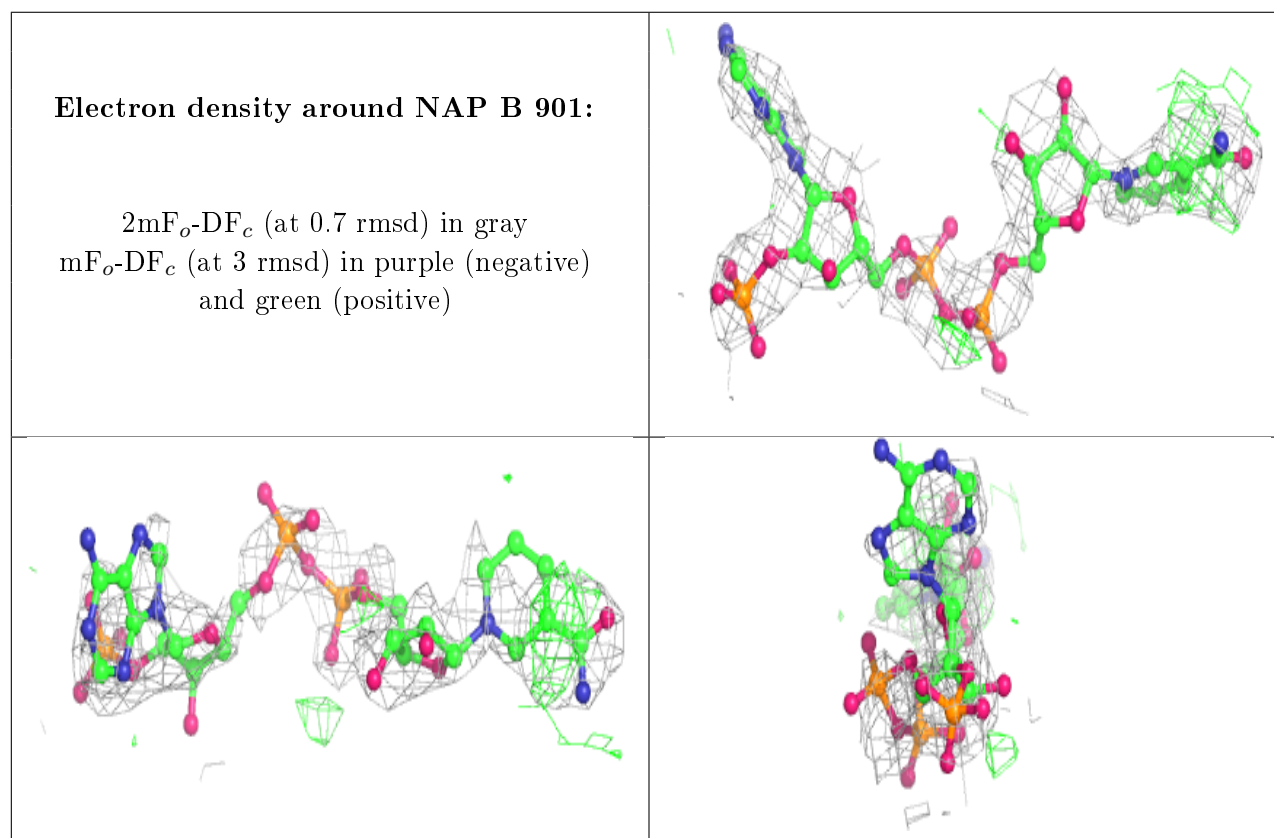
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

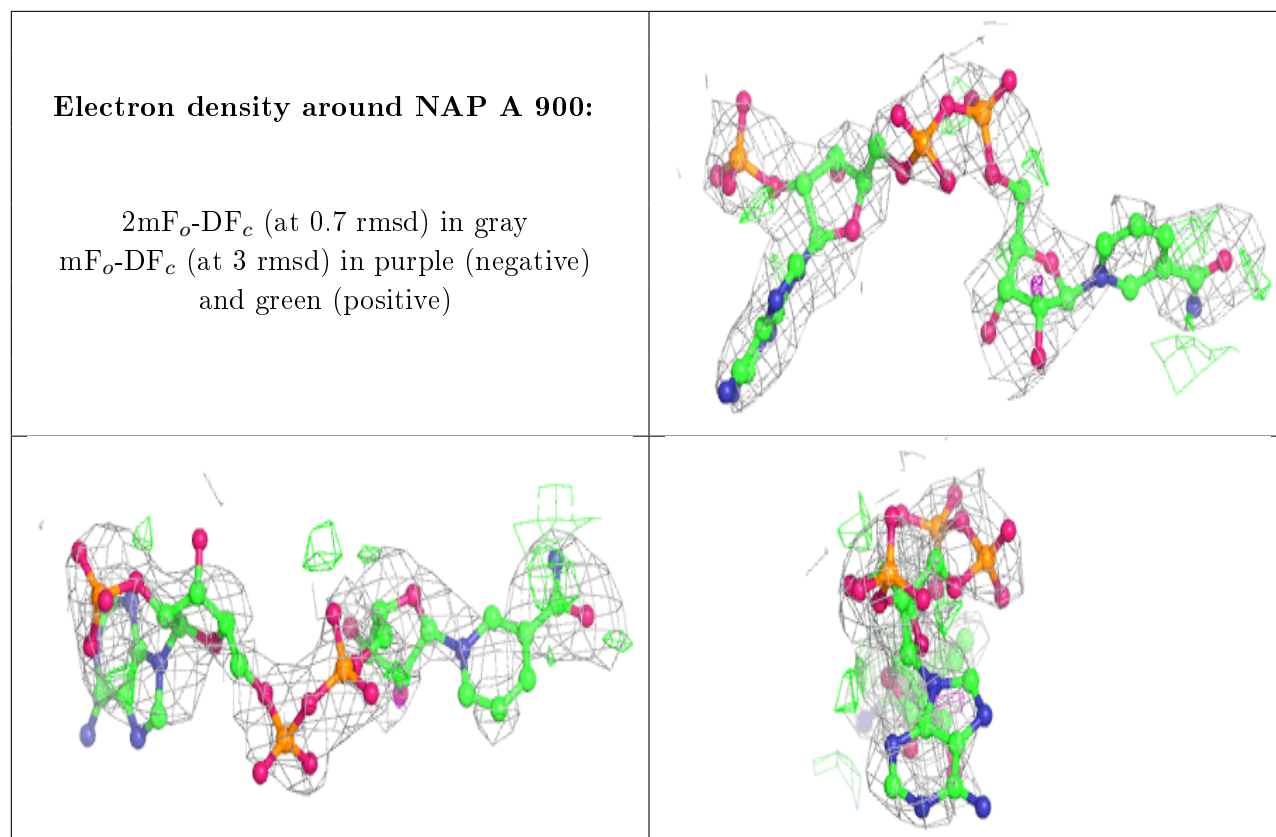


median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAP	B	901	48/48	0.77	0.34	12,34,58,63	48
2	NAP	A	900	48/48	0.78	0.30	10,31,55,60	48

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.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.