



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:30 PM GMT

PDB ID : 4F3X  
Title : Crystal structure of putative aldehyde dehydrogenase from *Sinorhizobium meliloti* 1021 complexed with NAD  
Authors : Malashkevich, V.N.; Bhosle, R.; Toro, R.; Hillerich, B.; Gizzi, A.; Garforth, S.; Kar, A.; Chan, M.K.; Laffuer, J.; Patel, H.; Matikainen, B.; Chamala, S.; Lim, S.; Celikgil, A.; Villegas, G.; Evans, B.; Zenchek, W.; Love, J.; Fiser, A.; Khafizov, K.; Seidel, R.; Bonanno, J.B.; Almo, S.C.; New York Structural Genomics Research Consortium (NYSGRG)  
Deposited on : 2012-05-09  
Resolution : 2.01 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

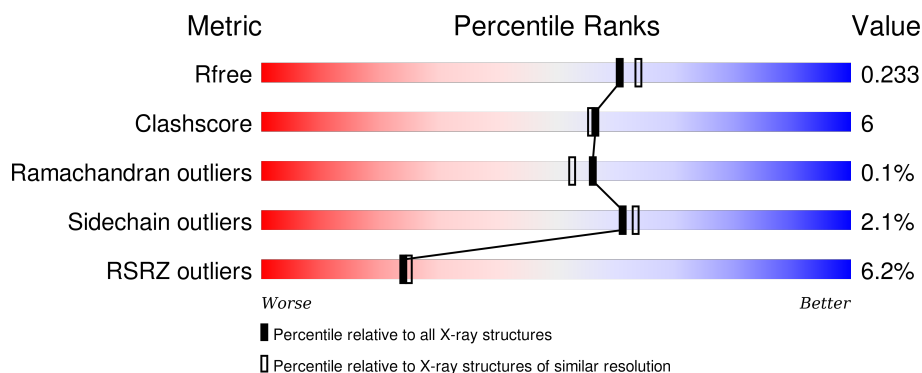
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.01 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))
$R_{free}$	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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. 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	498	<div> <div>3%</div> <div>83%</div> <div>13%</div> <div>.</div> </div>
1	B	498	<div> <div>3%</div> <div>83%</div> <div>13%</div> <div>.</div> </div>
1	C	498	<div> <div>4%</div> <div>82%</div> <div>13%</div> <div>.</div> </div>
1	D	498	<div> <div>14%</div> <div>82%</div> <div>13%</div> <div>5%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	B	501	-	-	-	X
3	GOL	C	501	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15314 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 Putative aldehyde dehydrogenase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	Se	0	2	0
			3621	2276	636	692	5	12			
1	B	476	Total	C	N	O	S	Se	0	4	0
			3628	2281	636	693	5	13			
1	C	476	Total	C	N	O	S	Se	0	2	0
			3618	2274	633	694	5	12			
1	D	475	Total	C	N	O	S	Se	0	0	0
			3599	2262	632	689	5	11			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	MSE	-	EXPRESSION TAG	UNP Q92ND9
A	-21	HIS	-	EXPRESSION TAG	UNP Q92ND9
A	-20	HIS	-	EXPRESSION TAG	UNP Q92ND9
A	-19	HIS	-	EXPRESSION TAG	UNP Q92ND9
A	-18	HIS	-	EXPRESSION TAG	UNP Q92ND9
A	-17	HIS	-	EXPRESSION TAG	UNP Q92ND9
A	-16	HIS	-	EXPRESSION TAG	UNP Q92ND9
A	-15	SER	-	EXPRESSION TAG	UNP Q92ND9
A	-14	SER	-	EXPRESSION TAG	UNP Q92ND9
A	-13	GLY	-	EXPRESSION TAG	UNP Q92ND9
A	-12	VAL	-	EXPRESSION TAG	UNP Q92ND9
A	-11	ASP	-	EXPRESSION TAG	UNP Q92ND9
A	-10	LEU	-	EXPRESSION TAG	UNP Q92ND9
A	-9	GLY	-	EXPRESSION TAG	UNP Q92ND9
A	-8	THR	-	EXPRESSION TAG	UNP Q92ND9
A	-7	GLU	-	EXPRESSION TAG	UNP Q92ND9
A	-6	ASN	-	EXPRESSION TAG	UNP Q92ND9
A	-5	LEU	-	EXPRESSION TAG	UNP Q92ND9
A	-4	TYR	-	EXPRESSION TAG	UNP Q92ND9
A	-3	PHE	-	EXPRESSION TAG	UNP Q92ND9
A	-2	GLN	-	EXPRESSION TAG	UNP Q92ND9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	EXPRESSION TAG	UNP Q92ND9
A	0	MSE	-	EXPRESSION TAG	UNP Q92ND9
B	-22	MSE	-	EXPRESSION TAG	UNP Q92ND9
B	-21	HIS	-	EXPRESSION TAG	UNP Q92ND9
B	-20	HIS	-	EXPRESSION TAG	UNP Q92ND9
B	-19	HIS	-	EXPRESSION TAG	UNP Q92ND9
B	-18	HIS	-	EXPRESSION TAG	UNP Q92ND9
B	-17	HIS	-	EXPRESSION TAG	UNP Q92ND9
B	-16	HIS	-	EXPRESSION TAG	UNP Q92ND9
B	-15	SER	-	EXPRESSION TAG	UNP Q92ND9
B	-14	SER	-	EXPRESSION TAG	UNP Q92ND9
B	-13	GLY	-	EXPRESSION TAG	UNP Q92ND9
B	-12	VAL	-	EXPRESSION TAG	UNP Q92ND9
B	-11	ASP	-	EXPRESSION TAG	UNP Q92ND9
B	-10	LEU	-	EXPRESSION TAG	UNP Q92ND9
B	-9	GLY	-	EXPRESSION TAG	UNP Q92ND9
B	-8	THR	-	EXPRESSION TAG	UNP Q92ND9
B	-7	GLU	-	EXPRESSION TAG	UNP Q92ND9
B	-6	ASN	-	EXPRESSION TAG	UNP Q92ND9
B	-5	LEU	-	EXPRESSION TAG	UNP Q92ND9
B	-4	TYR	-	EXPRESSION TAG	UNP Q92ND9
B	-3	PHE	-	EXPRESSION TAG	UNP Q92ND9
B	-2	GLN	-	EXPRESSION TAG	UNP Q92ND9
B	-1	SER	-	EXPRESSION TAG	UNP Q92ND9
B	0	MSE	-	EXPRESSION TAG	UNP Q92ND9
C	-22	MSE	-	EXPRESSION TAG	UNP Q92ND9
C	-21	HIS	-	EXPRESSION TAG	UNP Q92ND9
C	-20	HIS	-	EXPRESSION TAG	UNP Q92ND9
C	-19	HIS	-	EXPRESSION TAG	UNP Q92ND9
C	-18	HIS	-	EXPRESSION TAG	UNP Q92ND9
C	-17	HIS	-	EXPRESSION TAG	UNP Q92ND9
C	-16	HIS	-	EXPRESSION TAG	UNP Q92ND9
C	-15	SER	-	EXPRESSION TAG	UNP Q92ND9
C	-14	SER	-	EXPRESSION TAG	UNP Q92ND9
C	-13	GLY	-	EXPRESSION TAG	UNP Q92ND9
C	-12	VAL	-	EXPRESSION TAG	UNP Q92ND9
C	-11	ASP	-	EXPRESSION TAG	UNP Q92ND9
C	-10	LEU	-	EXPRESSION TAG	UNP Q92ND9
C	-9	GLY	-	EXPRESSION TAG	UNP Q92ND9
C	-8	THR	-	EXPRESSION TAG	UNP Q92ND9
C	-7	GLU	-	EXPRESSION TAG	UNP Q92ND9
C	-6	ASN	-	EXPRESSION TAG	UNP Q92ND9

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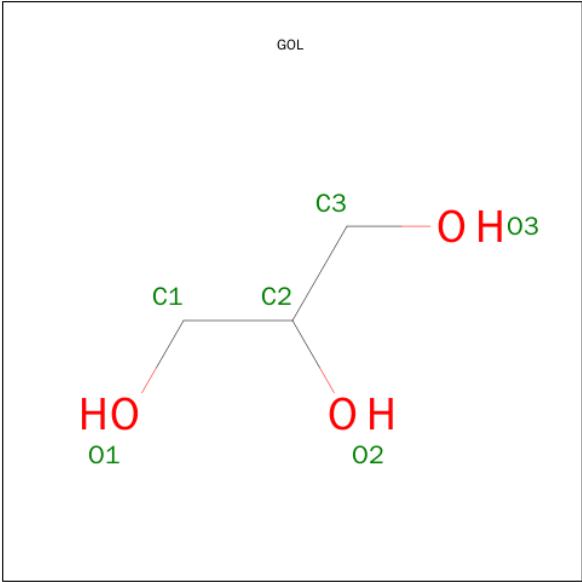
Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	LEU	-	EXPRESSION TAG	UNP Q92ND9
C	-4	TYR	-	EXPRESSION TAG	UNP Q92ND9
C	-3	PHE	-	EXPRESSION TAG	UNP Q92ND9
C	-2	GLN	-	EXPRESSION TAG	UNP Q92ND9
C	-1	SER	-	EXPRESSION TAG	UNP Q92ND9
C	0	MSE	-	EXPRESSION TAG	UNP Q92ND9
D	-22	MSE	-	EXPRESSION TAG	UNP Q92ND9
D	-21	HIS	-	EXPRESSION TAG	UNP Q92ND9
D	-20	HIS	-	EXPRESSION TAG	UNP Q92ND9
D	-19	HIS	-	EXPRESSION TAG	UNP Q92ND9
D	-18	HIS	-	EXPRESSION TAG	UNP Q92ND9
D	-17	HIS	-	EXPRESSION TAG	UNP Q92ND9
D	-16	HIS	-	EXPRESSION TAG	UNP Q92ND9
D	-15	SER	-	EXPRESSION TAG	UNP Q92ND9
D	-14	SER	-	EXPRESSION TAG	UNP Q92ND9
D	-13	GLY	-	EXPRESSION TAG	UNP Q92ND9
D	-12	VAL	-	EXPRESSION TAG	UNP Q92ND9
D	-11	ASP	-	EXPRESSION TAG	UNP Q92ND9
D	-10	LEU	-	EXPRESSION TAG	UNP Q92ND9
D	-9	GLY	-	EXPRESSION TAG	UNP Q92ND9
D	-8	THR	-	EXPRESSION TAG	UNP Q92ND9
D	-7	GLU	-	EXPRESSION TAG	UNP Q92ND9
D	-6	ASN	-	EXPRESSION TAG	UNP Q92ND9
D	-5	LEU	-	EXPRESSION TAG	UNP Q92ND9
D	-4	TYR	-	EXPRESSION TAG	UNP Q92ND9
D	-3	PHE	-	EXPRESSION TAG	UNP Q92ND9
D	-2	GLN	-	EXPRESSION TAG	UNP Q92ND9
D	-1	SER	-	EXPRESSION TAG	UNP Q92ND9
D	0	MSE	-	EXPRESSION TAG	UNP Q92ND9

- Molecule 2 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
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
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 GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

- Molecule 4 is water.

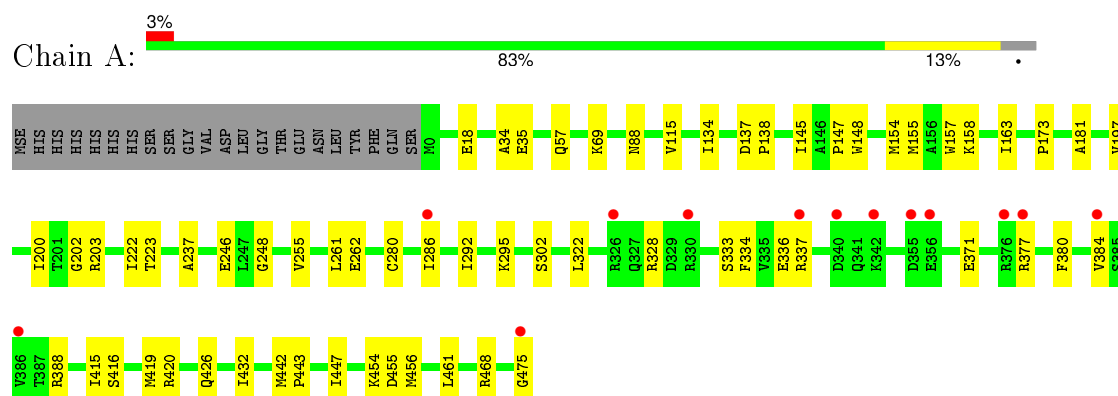
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	187	Total	O	0	0
			187	187		
4	B	170	Total	O	0	0
			170	170		
4	C	165	Total	O	0	0
			165	165		
4	D	120	Total	O	0	0
			120	120		



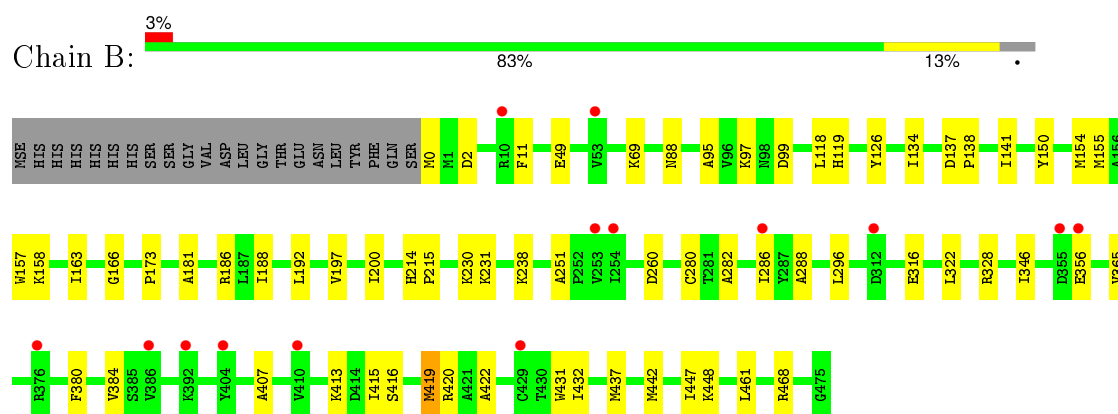
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

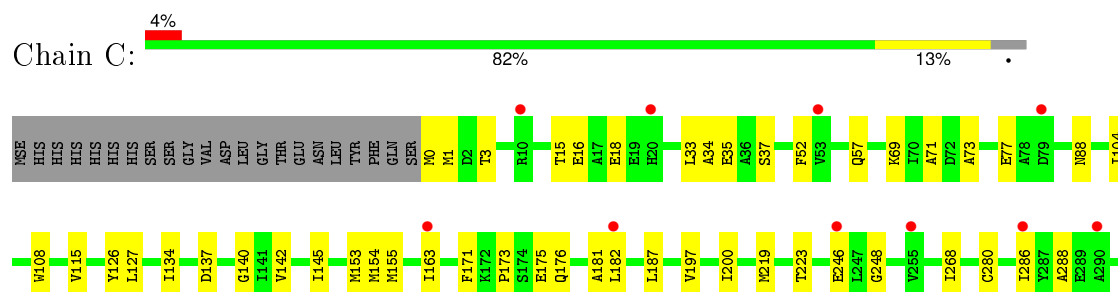
#### • Molecule 1: Putative aldehyde dehydrogenase



#### • Molecule 1: Putative aldehyde dehydrogenase

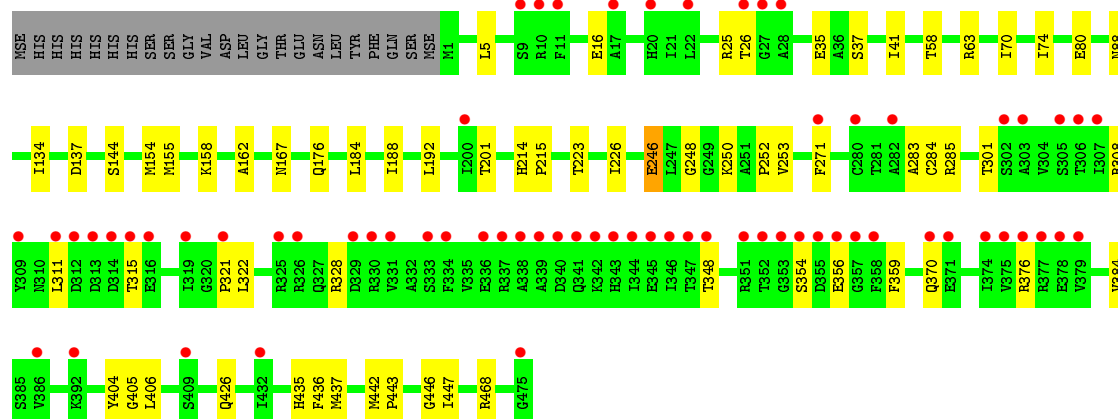
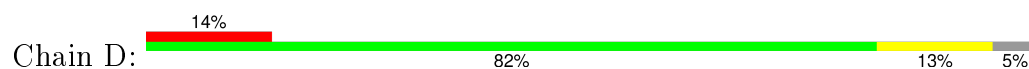


#### • Molecule 1: Putative aldehyde dehydrogenase





● Molecule 1: Putative aldehyde dehydrogenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.44Å 96.91Å 121.81Å 90.00° 89.98° 90.00°	Depositor
Resolution (Å)	19.91 – 2.01 19.87 – 2.01	Depositor EDS
% Data completeness (in resolution range)	95.5 (19.91-2.01) 95.7 (19.87-2.01)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.49 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.7.0025	Depositor
R, $R_{free}$	0.180 , 0.233 0.179 , 0.233	Depositor DCC
$R_{free}$ test set	6376 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	39.8	Xtriage
Anisotropy	0.166	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 57.2	EDS
Estimated twinning fraction	0.018 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	2 of 126673 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	15314	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, 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	0.48	0/3686	0.65	0/4987
1	B	0.46	0/3698	0.66	1/5001 (0.0%)
1	C	0.45	0/3683	0.64	0/4984
1	D	0.44	0/3659	0.61	0/4954
All	All	0.46	0/14726	0.64	1/19926 (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	B	419	MSE	CG-SE-CE	6.73	113.70	98.90

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	3621	0	3589	47	0
1	B	3628	0	3601	47	0
1	C	3618	0	3580	48	0
1	D	3599	0	3561	39	0
2	A	44	0	26	6	0
2	B	44	0	26	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	44	0	26	7	0
2	D	44	0	26	2	0
3	A	6	0	8	1	0
3	B	12	0	16	2	0
3	C	6	0	8	2	0
3	D	6	0	8	0	0
4	A	187	0	0	4	0
4	B	170	0	0	2	0
4	C	165	0	0	1	0
4	D	120	0	0	3	0
All	All	15314	0	14475	177	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 6.

All (177) 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:C:378:GLU:OE1	2:C:500:NAD:H5N	1.79	0.83
1:A:261:LEU:HD11	1:A:292:ILE:HD12	1.63	0.80
1:C:280:CYS:HB2	4:C:703:HOH:O	1.81	0.80
1:A:442:MSE:SE	1:B:134:ILE:HD11	2.33	0.79
1:B:286:ILE:HD12	1:B:384:VAL:HG13	1.65	0.78
1:D:248:GLY:HA3	2:D:500:NAD:H5N	1.65	0.78
1:C:442:MSE:SE	1:D:134:ILE:HD11	2.34	0.78
1:B:163:ILE:HD11	1:B:197:VAL:CG2	2.14	0.78
1:D:26:THR:O	1:D:356:GLU:HG3	1.85	0.76
1:A:69:LYS:HE3	3:A:501:GOL:H2	1.68	0.75
1:C:339:ALA:HB2	1:C:346:ILE:HD11	1.70	0.73
1:B:118:LEU:HD21	1:B:461:LEU:HD23	1.68	0.73
1:A:443:PRO:HB2	1:A:454:LYS:HD2	1.71	0.72
1:C:322:LEU:HD12	1:C:328:ARG:HA	1.71	0.72
1:C:69:LYS:NZ	3:C:501:GOL:H11	2.07	0.69
1:C:268:ILE:HD13	1:C:286:ILE:HD13	1.73	0.69
1:B:119:HIS:HE1	4:B:627:HOH:O	1.75	0.68
1:B:286:ILE:HD12	1:B:384:VAL:CG1	2.24	0.68
1:C:333:SER:OG	1:C:337:ARG:NH1	2.27	0.67
1:C:248:GLY:HA2	1:C:280:CYS:SG	2.34	0.67
1:C:137:ASP:OD2	1:C:468:ARG:HD3	1.97	0.65
1:A:35:GLU:OE2	1:A:203[B]:ARG:HG3	1.97	0.65
1:D:376:ARG:HG3	4:D:713:HOH:O	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:280:CYS:HB2	4:B:719:HOH:O	1.97	0.64
1:A:442:MSE:HE3	1:B:126:TYR:CE1	2.32	0.64
1:C:163:ILE:HD11	1:C:197:VAL:HG22	1.81	0.62
2:C:500:NAD:O2A	2:C:500:NAD:H51N	2.00	0.62
1:A:137:ASP:OD2	1:A:468:ARG:HD3	1.98	0.62
1:C:286:ILE:HD11	1:C:384:VAL:HG11	1.83	0.61
1:C:15:THR:HB	1:C:37:SER:HB3	1.84	0.60
1:A:280:CYS:HB2	4:A:743:HOH:O	2.02	0.60
1:A:334:PHE:HZ	1:A:377:ARG:HG2	1.66	0.60
1:A:255:VAL:HG12	1:A:292:ILE:HD11	1.84	0.59
1:D:58:THR:O	1:D:63:ARG:NH2	2.36	0.58
1:C:154:MSE:HE1	1:C:223:THR:OG1	2.03	0.58
1:A:475:GLY:HA2	4:A:734:HOH:O	2.03	0.58
1:C:339:ALA:HB2	1:C:346:ILE:CD1	2.34	0.58
1:B:163:ILE:HD11	1:B:197:VAL:HG21	1.85	0.57
1:C:69:LYS:HZ3	3:C:501:GOL:H11	1.69	0.57
1:A:280:CYS:SG	2:A:500:NAD:H4N	2.46	0.56
1:D:370:GLN:HB2	4:D:690:HOH:O	2.04	0.56
1:B:437:MSE:HA	1:B:437:MSE:HE2	1.86	0.56
1:B:69:LYS:HE3	3:B:503:GOL:H31	1.86	0.55
1:C:104:ILE:HG12	1:C:153:MSE:HA	1.88	0.55
1:D:223:THR:HG23	1:D:246:GLU:HB3	1.88	0.55
1:A:57:GLN:HG3	4:A:757:HOH:O	2.05	0.55
1:B:155:MSE:SE	1:B:181:ALA:HA	2.57	0.55
1:A:154:MSE:HE1	1:A:157:TRP:CZ3	2.41	0.54
1:A:419:MSE:HE1	1:A:432:ILE:HG13	1.88	0.54
1:C:322:LEU:CD1	1:C:328:ARG:HA	2.37	0.54
1:A:322:LEU:CD1	1:A:328:ARG:HA	2.37	0.54
1:A:163:ILE:HD11	1:A:197:VAL:HG21	1.89	0.54
1:D:284:CYS:HB3	4:D:694:HOH:O	2.07	0.53
1:A:248:GLY:HA2	1:A:280:CYS:SG	2.48	0.53
1:B:419:MSE:CE	1:B:432:ILE:HD13	2.38	0.53
1:A:415:ILE:HG13	1:C:415:ILE:HD12	1.90	0.53
1:C:142:VAL:HG22	1:C:219:MSE:HB3	1.91	0.53
1:B:286:ILE:CD1	1:B:384:VAL:CG1	2.87	0.53
1:C:422:ALA:HB2	1:C:432:ILE:HD11	1.91	0.53
1:D:284:CYS:HA	1:D:384:VAL:HG22	1.91	0.53
1:B:322:LEU:HD13	1:B:328[B]:ARG:HA	1.91	0.52
1:B:322:LEU:HD13	1:B:328[A]:ARG:HA	1.92	0.52
1:A:147:PRO:HG3	1:A:223:THR:HG22	1.91	0.52
1:B:416:SER:HB3	1:B:420:ARG:HH22	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:ASP:HB2	1:B:413:LYS:HE3	1.92	0.51
1:A:416:SER:HB3	1:A:420:ARG:HH22	1.75	0.51
1:A:134:ILE:HD11	1:B:442:MSE:SE	2.61	0.51
1:A:154:MSE:HE1	1:A:157:TRP:CE3	2.45	0.51
1:A:416:SER:HB3	1:A:420:ARG:NH2	2.26	0.50
1:B:419:MSE:CE	1:B:432:ILE:CD1	2.89	0.50
1:A:163:ILE:HD11	1:A:197:VAL:CG2	2.42	0.50
1:A:155:MSE:SE	1:A:181:ALA:HA	2.62	0.50
1:A:35:GLU:HG2	1:A:202:GLY:HA2	1.93	0.50
1:B:286:ILE:CD1	1:B:384:VAL:HG13	2.39	0.50
1:A:145:ILE:HB	1:A:222:ILE:HD12	1.94	0.49
1:D:37:SER:O	1:D:41:ILE:HG13	2.11	0.49
1:B:415:ILE:O	1:B:419:MSE:HG2	2.11	0.49
1:D:188:ILE:CG2	1:D:192:LEU:HD12	2.41	0.49
2:A:500:NAD:H2N	2:A:500:NAD:O1N	2.12	0.49
1:B:447:ILE:HG22	1:B:448:LYS:N	2.28	0.49
1:A:334:PHE:CZ	1:A:377:ARG:HG2	2.47	0.48
1:B:416:SER:HB3	1:B:420:ARG:NH2	2.27	0.48
1:C:378:GLU:OE1	2:C:500:NAD:C5N	2.57	0.48
1:B:280:CYS:SG	2:B:502:NAD:H4N	2.54	0.48
1:D:435:HIS:O	1:D:436:PHE:CB	2.62	0.48
1:A:286:ILE:HD11	1:A:384:VAL:HG11	1.95	0.48
1:C:293:TYR:O	1:C:297:VAL:HG23	2.14	0.48
1:C:126:TYR:CE1	1:D:442:MSE:HE3	2.49	0.48
1:B:419:MSE:HE2	1:B:432:ILE:CD1	2.43	0.48
1:D:80:GLU:H	1:D:80:GLU:CD	2.15	0.48
1:A:248:GLY:HA3	2:A:500:NAD:H5N	1.94	0.47
1:D:155:MSE:SE	1:D:184:LEU:HD23	2.64	0.47
1:A:322:LEU:HD13	1:A:328:ARG:HA	1.95	0.47
1:B:173:PRO:HD2	1:B:200:ILE:O	2.15	0.47
1:C:163:ILE:HD11	1:C:197:VAL:CG2	2.44	0.47
1:B:288:ALA:HB2	1:B:296:LEU:HD23	1.96	0.47
1:B:154[A]:MSE:HE1	1:B:157:TRP:CZ3	2.50	0.47
1:B:11:PHE:CZ	1:B:186:ARG:HA	2.50	0.47
1:D:271:PHE:HB3	1:D:436:PHE:HB2	1.98	0.46
1:C:52:PHE:CE1	1:C:140:GLY:HA2	2.50	0.46
1:B:188:ILE:HG23	1:B:192:LEU:HD12	1.97	0.46
1:B:0:MSE:HE2	1:B:2:ASP:HA	1.98	0.46
1:A:148:TRP:HE1	2:A:500:NAD:C5D	2.29	0.46
1:C:155:MSE:HG3	1:C:171:PHE:CZ	2.50	0.46
2:C:500:NAD:N7N	2:C:500:NAD:O1N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:5:LEU:HD21	1:D:201:THR:OG1	2.16	0.46
2:C:500:NAD:H2N	2:C:500:NAD:O1N	2.16	0.45
1:C:33:LEU:HD21	1:C:182:LEU:HD11	1.98	0.45
1:D:437:MSE:HA	1:D:437:MSE:HE2	1.98	0.45
1:A:237:ALA:O	1:B:230:LYS:HG2	2.15	0.45
1:C:16:GLU:HG2	1:C:37:SER:HA	1.97	0.45
1:B:137:ASP:OD2	1:B:468:ARG:HD3	2.16	0.45
1:B:95:ALA:O	1:B:99:ASP:HB2	2.17	0.45
1:D:226:ILE:HD11	1:D:404:TYR:CE1	2.52	0.45
1:A:115:VAL:HA	1:A:461:LEU:HD21	1.98	0.45
1:D:322:LEU:HD13	1:D:328:ARG:HA	1.99	0.44
1:B:251:ALA:HB3	1:B:282:ALA:O	2.17	0.44
1:D:308:ARG:HB3	1:D:311:LEU:HD12	2.00	0.44
1:D:271:PHE:CE1	1:D:437:MSE:HE3	2.53	0.44
1:D:253:VAL:HG21	1:D:283:ALA:HB1	2.00	0.43
1:C:175:GLU:HG2	1:C:176:GLN:NE2	2.33	0.43
1:C:268:ILE:HG21	1:C:286:ILE:HD11	2.01	0.43
1:A:173:PRO:HD2	1:A:200:ILE:O	2.18	0.43
1:A:147:PRO:HD3	1:A:223:THR:HB	1.99	0.43
1:C:73:ALA:HB1	1:C:187:LEU:HD13	2.00	0.43
1:A:455:ASP:O	1:A:456:MSE:HB2	2.18	0.43
1:C:77:GLU:OE2	1:C:187:LEU:HD11	2.19	0.43
1:A:333:SER:OG	1:A:337:ARG:NH1	2.46	0.43
1:D:154:MSE:O	1:D:158:LYS:HG2	2.19	0.43
1:D:248:GLY:HA3	2:D:500:NAD:C5N	2.44	0.43
1:D:426:GLN:HB3	1:D:447:ILE:HD11	2.00	0.43
1:B:150:TYR:O	1:B:154[B]:MSE:HG2	2.18	0.42
1:B:346:ILE:HD12	1:B:365:VAL:HG22	2.01	0.42
1:C:268:ILE:HD13	1:C:286:ILE:CD1	2.46	0.42
1:C:154:MSE:HE1	1:C:223:THR:CB	2.49	0.42
2:A:500:NAD:N7N	2:A:500:NAD:O1N	2.52	0.42
1:D:301:THR:HG23	1:D:348:THR:HB	2.02	0.42
1:D:70:ILE:O	1:D:74:ILE:HG13	2.19	0.42
1:C:16:GLU:HB2	1:C:35:GLU:HB2	2.00	0.42
1:B:11:PHE:HZ	1:B:186:ARG:HA	1.84	0.42
1:A:426:GLN:HB3	1:A:447:ILE:HD11	2.01	0.42
1:D:137:ASP:OD2	1:D:468:ARG:HD3	2.19	0.42
1:B:138:PRO:HG3	1:B:166:GLY:HA3	2.00	0.42
1:B:407:ALA:HB1	1:B:431:TRP:CZ3	2.54	0.42
1:B:422:ALA:HB2	1:B:432:ILE:HD11	2.02	0.42
1:C:115:VAL:HA	1:C:461:LEU:HD21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:25:ARG:HG2	1:D:321:PRO:HG3	2.01	0.42
1:D:16:GLU:HB2	1:D:35:GLU:HG3	2.01	0.42
1:C:71:ALA:HB2	1:C:108:TRP:HB2	2.01	0.42
1:A:145:ILE:HG21	2:A:500:NAD:H1B	2.02	0.41
1:D:435:HIS:O	1:D:436:PHE:HB3	2.19	0.41
1:D:354:SER:OG	1:D:359:PHE:HB2	2.19	0.41
1:A:137:ASP:HB3	1:A:138:PRO:CD	2.50	0.41
1:C:145:ILE:HG21	2:C:500:NAD:H1B	2.03	0.41
1:B:214:HIS:HA	1:B:215:PRO:HD3	1.92	0.41
1:A:18:GLU:HA	1:A:34:ALA:HA	2.02	0.41
1:C:18:GLU:HA	1:C:34:ALA:HA	2.03	0.41
1:B:49:GLU:HA	1:B:141:ILE:HD11	2.02	0.41
1:D:406:LEU:HA	1:D:446:GLY:HA2	2.01	0.41
1:A:286:ILE:CD1	1:A:384:VAL:CG1	2.98	0.41
1:A:158:LYS:HD3	1:A:158:LYS:HA	1.92	0.41
1:D:162:ALA:O	1:D:167:ASN:HB2	2.20	0.41
1:D:188:ILE:HG23	1:D:192:LEU:HD12	2.03	0.41
1:C:155:MSE:SE	1:C:181:ALA:HA	2.70	0.41
1:B:419:MSE:HE2	1:B:432:ILE:HD13	2.01	0.41
1:D:252:PRO:HD3	1:D:285:ARG:NH2	2.36	0.41
1:A:442:MSE:HE3	1:B:126:TYR:CZ	2.55	0.40
1:C:286:ILE:CD1	1:C:384:VAL:CG1	2.99	0.40
1:C:134:ILE:HD11	1:D:443:PRO:HD2	2.03	0.40
1:C:173:PRO:HD2	1:C:200:ILE:O	2.21	0.40
1:C:154:MSE:HB3	1:C:154:MSE:HE3	1.78	0.40
1:B:69:LYS:HE3	3:B:503:GOL:H12	2.03	0.40
1:C:280:CYS:SG	2:C:500:NAD:H4N	2.62	0.40
1:C:288:ALA:HB2	1:C:296:LEU:HD23	2.02	0.40
1:C:286:ILE:HD11	1:C:384:VAL:CG1	2.51	0.40
1:D:214:HIS:HA	1:D:215:PRO:HD3	1.91	0.40
1:A:388:ARG:HD2	4:A:678:HOH:O	2.22	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	476/498 (96%)	463 (97%)	13 (3%)	0	100	100
1	B	478/498 (96%)	463 (97%)	15 (3%)	0	100	100
1	C	476/498 (96%)	461 (97%)	15 (3%)	0	100	100
1	D	473/498 (95%)	458 (97%)	14 (3%)	1 (0%)	52	48
All	All	1903/1992 (96%)	1845 (97%)	57 (3%)	1 (0%)	56	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	405	GLY

### 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	372/377 (99%)	363 (98%)	9 (2%)	57	58
1	B	374/377 (99%)	366 (98%)	8 (2%)	61	63
1	C	372/377 (99%)	362 (97%)	10 (3%)	52	52
1	D	369/377 (98%)	363 (98%)	6 (2%)	70	73
All	All	1487/1508 (99%)	1454 (98%)	33 (2%)	61	62

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	ASN
1	A	246[A]	GLU
1	A	246[B]	GLU
1	A	262	GLU
1	A	295	LYS
1	A	302	SER
1	A	336	GLU

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Mol	Chain	Res	Type
1	A	371	GLU
1	A	380	PHE
1	B	88	ASN
1	B	97	LYS
1	B	158	LYS
1	B	231	LYS
1	B	238	LYS
1	B	316	GLU
1	B	356	GLU
1	B	380	PHE
1	C	0	MSE
1	C	1	MSE
1	C	3	THR
1	C	57	GLN
1	C	88	ASN
1	C	127	LEU
1	C	246[A]	GLU
1	C	246[B]	GLU
1	C	326	ARG
1	C	380	PHE
1	D	88	ASN
1	D	144	SER
1	D	176	GLN
1	D	246	GLU
1	D	250	LYS
1	D	315	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	HIS
1	C	341	GLN
1	D	94	ASN
1	D	444	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

9 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	A	500	-	38,48,48	0.88	2 (5%)	47,73,73	1.51	6 (12%)
3	GOL	A	501	-	5,5,5	0.24	0	5,5,5	0.69	0
3	GOL	B	501	-	5,5,5	0.20	0	5,5,5	0.32	0
2	NAD	B	502	-	38,48,48	1.02	3 (7%)	47,73,73	1.62	7 (14%)
3	GOL	B	503	-	5,5,5	0.21	0	5,5,5	0.12	0
2	NAD	C	500	-	38,48,48	0.96	3 (7%)	47,73,73	1.50	4 (8%)
3	GOL	C	501	-	5,5,5	0.32	0	5,5,5	0.43	0
2	NAD	D	500	-	38,48,48	0.90	3 (7%)	47,73,73	1.70	5 (10%)
3	GOL	D	501	-	5,5,5	0.28	0	5,5,5	0.35	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	A	500	-	-	0/22/62/62	0/5/5/5
3	GOL	A	501	-	-	0/4/4/4	0/0/0/0
3	GOL	B	501	-	-	0/4/4/4	0/0/0/0
2	NAD	B	502	-	-	0/22/62/62	0/5/5/5
3	GOL	B	503	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	C	500	-	-	0/22/62/62	0/5/5/5
3	GOL	C	501	-	-	0/4/4/4	0/0/0/0
2	NAD	D	500	-	-	0/22/62/62	0/5/5/5
3	GOL	D	501	-	-	0/4/4/4	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	NAD	O4B-C1B	2.16	1.43	1.41
2	B	502	NAD	O4D-C1D	2.22	1.44	1.41
2	C	500	NAD	O4D-C1D	2.27	1.44	1.41
2	C	500	NAD	O4B-C1B	2.34	1.44	1.41
2	D	500	NAD	O4D-C1D	2.41	1.44	1.41
2	A	500	NAD	O4D-C1D	2.47	1.44	1.41
2	A	500	NAD	C5A-C4A	2.78	1.46	1.40
2	D	500	NAD	C5A-C4A	2.78	1.46	1.40
2	B	502	NAD	C5A-C4A	3.08	1.47	1.40
2	C	500	NAD	C5A-C4A	3.14	1.47	1.40
2	B	502	NAD	O4B-C1B	3.45	1.45	1.41

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	NAD	N3A-C2A-N1A	-7.53	123.13	128.89
2	B	502	NAD	N3A-C2A-N1A	-6.57	123.86	128.89
2	C	500	NAD	N3A-C2A-N1A	-6.35	124.03	128.89
2	A	500	NAD	N3A-C2A-N1A	-6.05	124.26	128.89
2	D	500	NAD	PN-O3-PA	-4.15	121.07	132.73
2	D	500	NAD	C4A-C5A-N7A	-3.65	106.12	109.48
2	A	500	NAD	PN-O3-PA	-3.35	123.32	132.73
2	B	502	NAD	C2B-C1B-N9A	-3.02	109.67	114.29
2	B	502	NAD	PN-O3-PA	-3.00	124.29	132.73
2	A	500	NAD	C4A-C5A-N7A	-2.99	106.73	109.48
2	B	502	NAD	C4A-C5A-N7A	-2.96	106.75	109.48
2	C	500	NAD	C4A-C5A-N7A	-2.91	106.80	109.48
2	A	500	NAD	O3-PN-O5D	-2.49	96.33	102.94
2	D	500	NAD	C1B-N9A-C4A	-2.37	123.36	126.94
2	C	500	NAD	PN-O3-PA	-2.33	126.19	132.73
2	B	502	NAD	C1B-N9A-C4A	-2.23	123.58	126.94
2	A	500	NAD	C2B-C1B-N9A	-2.08	111.12	114.29
2	B	502	NAD	O4B-C1B-N9A	2.43	113.19	108.10
2	B	502	NAD	O4D-C1D-N1N	2.68	111.07	108.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	NAD	O4D-C1D-N1N	3.14	111.58	108.13
2	C	500	NAD	O4D-C1D-N1N	3.55	112.03	108.13
2	D	500	NAD	O4D-C1D-N1N	3.93	112.45	108.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	NAD	6	0
3	A	501	GOL	1	0
2	B	502	NAD	1	0
3	B	503	GOL	2	0
2	C	500	NAD	7	0
3	C	501	GOL	2	0
2	D	500	NAD	2	0

## 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	464/498 (93%)	0.01	13 (2%) 56 57	27, 44, 69, 95	0
1	B	464/498 (93%)	-0.06	14 (3%) 54 55	28, 45, 65, 83	0
1	C	464/498 (93%)	-0.01	20 (4%) 39 40	31, 47, 66, 86	0
1	D	464/498 (93%)	0.63	68 (14%) 3 4	31, 50, 104, 122	0
All	All	1856/1992 (93%)	0.14	115 (6%) 24 25	27, 47, 81, 122	0

All (115) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	355	ASP	7.3
1	D	271	PHE	7.3
1	D	315	THR	7.3
1	D	340	ASP	7.0
1	D	377	ARG	6.0
1	D	313	ASP	6.0
1	D	311	LEU	6.0
1	D	342	LYS	5.9
1	D	339	ALA	5.8
1	D	326	ARG	5.7
1	D	20	HIS	5.6
1	D	312	ASP	5.4
1	D	316	GLU	5.4
1	D	282	ALA	5.2
1	D	351	ARG	5.1
1	D	371	GLU	5.1
1	D	343	HIS	5.0
1	D	17	ALA	4.8
1	D	475	GLY	4.8
1	D	305	SER	4.7
1	D	341	GLN	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	355	ASP	4.5
1	C	475	GLY	4.5
1	D	354	SER	4.5
1	D	376	ARG	4.4
1	D	378	GLU	4.3
1	D	374	ILE	4.2
1	D	309	TYR	4.2
1	D	325	ARG	4.0
1	C	10	ARG	3.9
1	D	353	GLY	3.8
1	C	20	HIS	3.8
1	D	329	ASP	3.8
1	D	280	CYS	3.8
1	D	314	ASP	3.7
1	D	379	VAL	3.7
1	A	376	ARG	3.7
1	D	307	ILE	3.5
1	D	338	ALA	3.5
1	D	348	THR	3.5
1	D	356	GLU	3.4
1	D	337	ARG	3.4
1	D	345	GLU	3.4
1	D	27	GLY	3.4
1	D	303	ALA	3.4
1	D	9	SER	3.3
1	B	312	ASP	3.3
1	A	475	GLY	3.3
1	B	404	TYR	3.3
1	A	286	ILE	3.3
1	D	346	ILE	3.3
1	D	375	VAL	3.3
1	D	319	ILE	3.3
1	D	302	SER	3.2
1	D	336	GLU	3.2
1	C	392	LYS	3.1
1	B	10	ARG	3.1
1	D	10	ARG	3.0
1	B	286	ILE	3.0
1	C	286	ILE	3.0
1	A	337	ARG	3.0
1	D	28	ALA	3.0
1	C	340	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	315	THR	2.9
1	D	370	GLN	2.8
1	B	376	ARG	2.8
1	A	340	ASP	2.8
1	D	333	SER	2.8
1	A	356	GLU	2.8
1	A	326	ARG	2.8
1	D	330	ARG	2.7
1	D	26	THR	2.7
1	D	331	VAL	2.7
1	B	410	VAL	2.7
1	D	347	THR	2.7
1	D	200	ILE	2.6
1	A	384	VAL	2.6
1	B	53	VAL	2.5
1	C	391	GLY	2.5
1	D	357	GLY	2.5
1	D	432	ILE	2.5
1	A	377	ARG	2.4
1	B	392	LYS	2.4
1	B	254	ILE	2.4
1	A	330	ARG	2.4
1	B	355	ASP	2.4
1	C	290	ALA	2.3
1	B	253	VAL	2.3
1	D	386	VAL	2.3
1	D	321	PRO	2.3
1	C	355	ASP	2.3
1	D	306	THR	2.3
1	A	342	LYS	2.3
1	C	316	GLU	2.3
1	D	334	PHE	2.3
1	C	432	ILE	2.3
1	C	79	ASP	2.2
1	C	255	VAL	2.2
1	D	392	LYS	2.2
1	D	11	PHE	2.2
1	D	358	PHE	2.2
1	B	429	CYS	2.1
1	C	53	VAL	2.1
1	A	386	VAL	2.1
1	C	182	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	22	LEU	2.1
1	B	386	VAL	2.1
1	D	352	THR	2.1
1	D	344	ILE	2.1
1	B	356	GLU	2.1
1	C	377	ARG	2.1
1	C	246[A]	GLU	2.0
1	C	342	LYS	2.0
1	D	409	SER	2.0
1	C	163	ILE	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	GOL	B	501	6/6	0.94	0.13	3.94	56,63,73,76	0
3	GOL	C	501	6/6	0.89	0.16	3.35	55,57,61,70	0
3	GOL	B	503	6/6	0.83	0.16	1.89	59,68,69,73	0
3	GOL	A	501	6/6	0.94	0.12	0.46	53,61,62,79	0
2	NAD	B	502	44/44	0.95	0.14	0.38	37,52,99,104	0
3	GOL	D	501	6/6	0.92	0.16	0.10	59,62,66,67	0
2	NAD	A	500	44/44	0.96	0.13	0.03	35,49,114,121	0
2	NAD	D	500	44/44	0.94	0.14	-0.07	43,58,119,121	0
2	NAD	C	500	44/44	0.95	0.12	-0.23	45,60,111,124	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.