



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:12 PM GMT

PDB ID : 1NXD
Title : Crystal structure of MnMn Concanavalin A
Authors : Lopez-Jaramillo, F.J.; Gonzalez-Ramirez, L.A.; Albert, A.; Santoyo-Gonzalez, F.; Vargas-Berenguel, A.; Otalora, F.
Deposited on : 2003-02-10
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at 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.

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

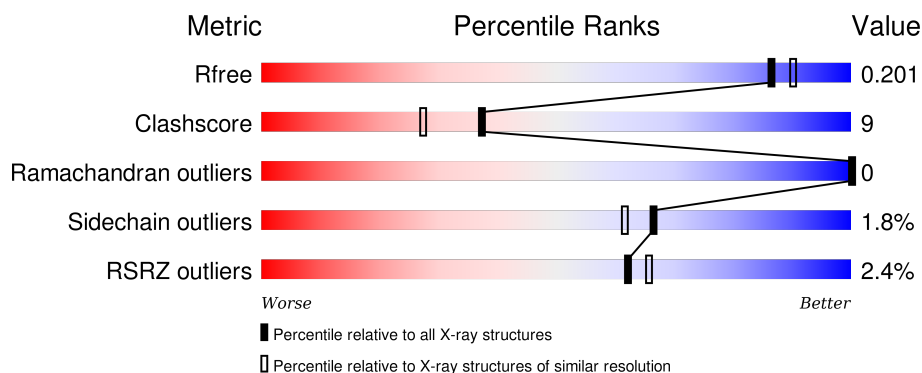
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	1	237	<div> <div>3%</div> <div>87%</div> <div>12%</div> </div>
1	2	237	<div> <div>3%</div> <div>81%</div> <div>18%</div> </div>
1	3	237	<div> <div>2%</div> <div>80%</div> <div>19%</div> </div>
1	4	237	<div> <div>2%</div> <div>84%</div> <div>14%</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
2	AZI	1	907	-	-	-	X
2	AZI	1	910	-	-	-	X
2	AZI	1	912	-	-	-	X
2	AZI	2	905	-	-	-	X
2	AZI	2	913	-	-	X	X
2	AZI	2	915	-	-	X	X
2	AZI	3	901	-	-	X	X
2	AZI	3	909	-	-	-	X
2	AZI	4	903	-	-	X	-
2	AZI	4	906	-	-	-	X
2	AZI	4	911	-	-	-	X
4	NA	3	1011	-	-	-	X
5	GOL	1	804	-	X	-	X
5	GOL	1	806	-	X	-	X
5	GOL	1	807	-	X	-	X
5	GOL	1	812	-	X	-	X
5	GOL	1	821	-	X	-	X
5	GOL	1	822	-	X	-	-
5	GOL	1	823	-	X	X	X
5	GOL	1	824	-	X	-	X
5	GOL	2	809	-	X	-	X
5	GOL	2	811	-	X	X	X
5	GOL	2	814	-	X	-	X
5	GOL	2	815	-	X	-	X
5	GOL	2	818	-	X	-	-
5	GOL	2	820	-	X	-	X
5	GOL	3	802	-	X	-	X
5	GOL	3	803	-	X	-	-
5	GOL	3	808	-	X	-	X
5	GOL	3	816	-	X	-	X
5	GOL	3	825	-	X	-	X
5	GOL	4	801	-	X	-	X
5	GOL	4	805	-	X	-	X
5	GOL	4	810	-	X	-	X
5	GOL	4	813	-	X	-	X
5	GOL	4	817	-	X	-	X
5	GOL	4	819	-	X	X	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8210 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.

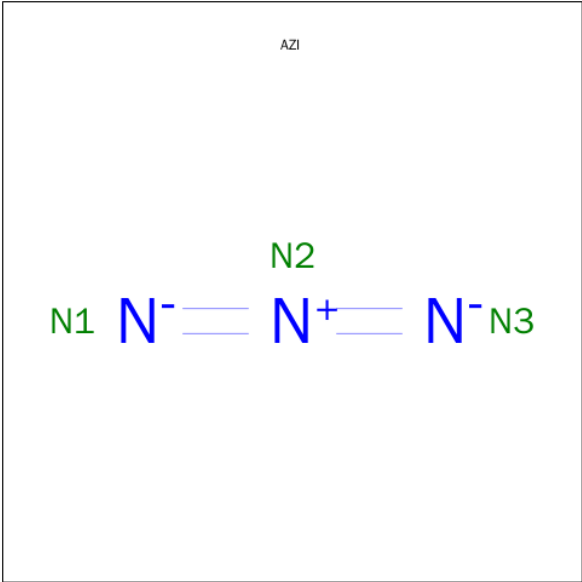
- Molecule 1 is a protein called concanavalin A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	237	Total	C	N	O	S	0	0	0
			1809	1141	302	364	2			
1	2	237	Total	C	N	O	S	0	0	0
			1809	1141	302	364	2			
1	3	237	Total	C	N	O	S	0	0	0
			1809	1141	302	364	2			
1	4	237	Total	C	N	O	S	0	0	0
			1809	1141	302	364	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	151	ASP	GLU	CONFLICT	UNP P02866
1	155	GLU	ARG	CONFLICT	UNP P02866
2	151	ASP	GLU	CONFLICT	UNP P02866
2	155	GLU	ARG	CONFLICT	UNP P02866
3	151	ASP	GLU	CONFLICT	UNP P02866
3	155	GLU	ARG	CONFLICT	UNP P02866
4	151	ASP	GLU	CONFLICT	UNP P02866
4	155	GLU	ARG	CONFLICT	UNP P02866

- Molecule 2 is AZIDE ION (three-letter code: AZI) (formula: N₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	3	1	Total N 3 3	0	0
2	2	1	Total N 3 3	0	0
2	4	1	Total N 3 3	0	0
2	3	1	Total N 3 3	0	0
2	2	1	Total N 3 3	0	0
2	4	1	Total N 3 3	0	0
2	1	1	Total N 3 3	0	0
2	2	1	Total N 3 3	0	0
2	3	1	Total N 3 3	0	0
2	1	1	Total N 3 3	0	0
2	4	1	Total N 3 3	0	0
2	1	1	Total N 3 3	0	0
2	2	1	Total N 3 3	0	0
2	3	1	Total N 3 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	2	1	Total 3	N 3	0	0
2	4	1	Total 3	N 3	0	0

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	2	2	Total 2	Mn 2	0	0
3	1	2	Total 2	Mn 2	0	0
3	4	2	Total 2	Mn 2	0	0
3	3	2	Total 2	Mn 2	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	2	1	Total 1	Na 1	0	0
4	1	1	Total 1	Na 1	0	0
4	4	1	Total 1	Na 1	0	0
4	3	1	Total 1	Na 1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	4	1	Total	C	O	0	0
			6	3	3		
5	3	1	Total	C	O	0	0
			6	3	3		
5	3	1	Total	C	O	0	0
			6	3	3		
5	1	1	Total	C	O	0	0
			6	3	3		
5	4	1	Total	C	O	0	0
			6	3	3		
5	1	1	Total	C	O	0	0
			6	3	3		
5	1	1	Total	C	O	0	0
			6	3	3		
5	3	1	Total	C	O	0	0
			6	3	3		
5	2	1	Total	C	O	0	0
			6	3	3		
5	4	1	Total	C	O	0	0
			6	3	3		
5	2	1	Total	C	O	0	0
			6	3	3		
5	1	1	Total	C	O	0	0
			6	3	3		
5	4	1	Total	C	O	0	0
			6	3	3		
5	2	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	2	1	Total	C	O	0	0
			6	3	3		
5	3	1	Total	C	O	0	0
			6	3	3		
5	4	1	Total	C	O	0	0
			6	3	3		
5	2	1	Total	C	O	0	0
			6	3	3		
5	4	1	Total	C	O	0	0
			6	3	3		
5	2	1	Total	C	O	0	0
			6	3	3		
5	1	1	Total	C	O	0	0
			6	3	3		
5	1	1	Total	C	O	0	0
			6	3	3		
5	1	1	Total	C	O	0	0
			6	3	3		
5	1	1	Total	C	O	0	0
			6	3	3		
5	3	1	Total	C	O	0	0
			6	3	3		

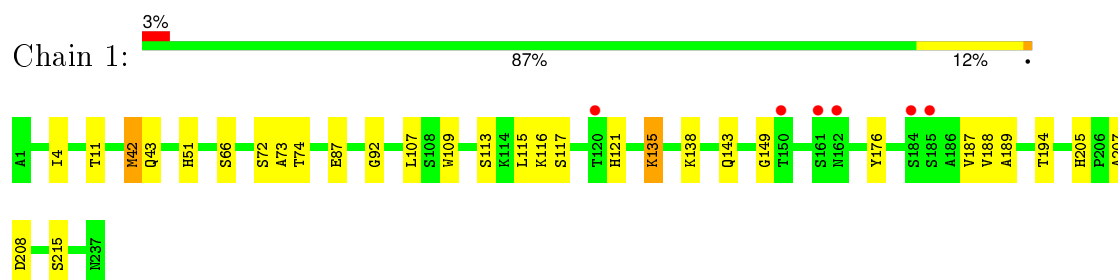
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	1	214	Total	O	0	0
			214	214		
6	2	183	Total	O	0	0
			183	183		
6	3	165	Total	O	0	0
			165	165		
6	4	202	Total	O	0	0
			202	202		

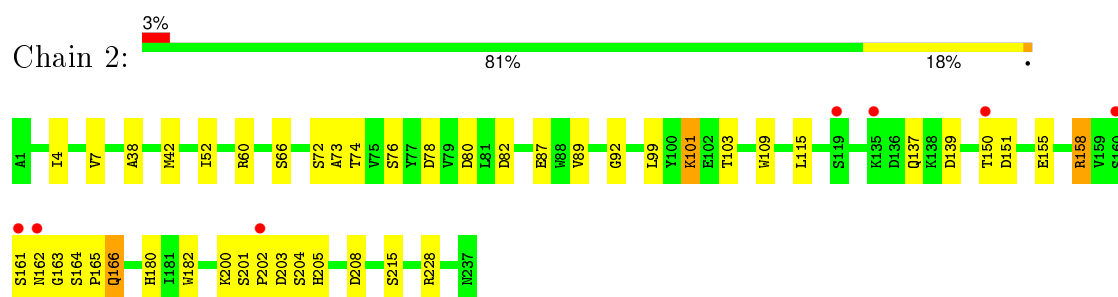
3 Residue-property plots [i](#)

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.

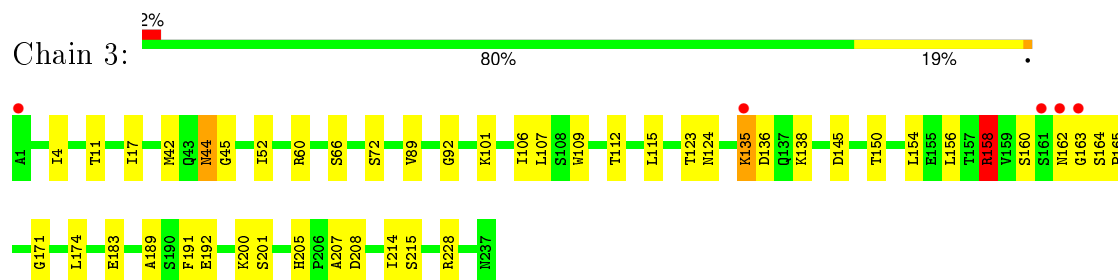
- Molecule 1: concanavalin A



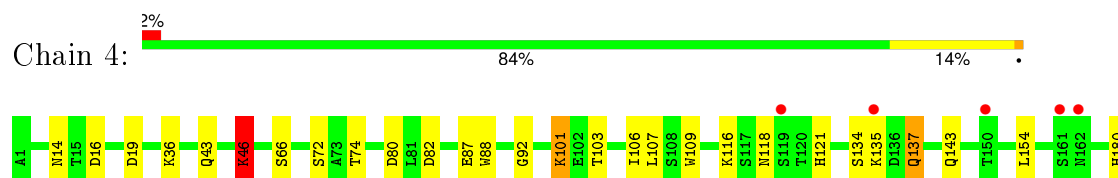
- Molecule 1: concanavalin A



- Molecule 1: concanavalin A



- Molecule 1: concanavalin A



I181	W182	V187	V188	K200	S204	I217	D218	S219	S220	P234	I237
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4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	101.30Å 118.00Å 249.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.00 – 1.90 19.61 – 1.84	Depositor EDS
% Data completeness (in resolution range)	95.0 (19.00-1.90) 94.2 (19.61-1.84)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.02	Depositor
$\langle I/\sigma(I) \rangle$ ¹	10.52 (at 1.85Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.184 , 0.201 0.184 , 0.201	Depositor DCC
R_{free} test set	11146 reflections (10.01%)	DCC
Wilson B-factor (Å ²)	15.0	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 53.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 120758 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8210	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AZI, GOL, MN, NA

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	1	0.34	0/1851	0.70	0/2522
1	2	0.44	0/1851	0.83	4/2522 (0.2%)
1	3	0.46	2/1851 (0.1%)	0.79	3/2522 (0.1%)
1	4	0.43	0/1851	0.80	6/2522 (0.2%)
All	All	0.42	2/7404 (0.0%)	0.78	13/10088 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	2	0	2
1	3	0	2
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	3	164	SER	CB-OG	-6.23	1.34	1.42
1	3	158	ARG	C-O	-6.18	1.11	1.23

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	3	158	ARG	CD-NE-CZ	11.34	139.48	123.60
1	2	201	SER	C-N-CD	10.76	151.00	128.40
1	2	202	PRO	CA-N-CD	-6.78	102.00	111.50
1	4	46	LYS	CB-CA-C	-6.61	97.18	110.40
1	4	118	ASN	CB-CA-C	-6.36	97.67	110.40

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2	163	GLY	Mainchain
1	2	203	ASP	Mainchain
1	3	160	SER	Mainchain
1	3	162	ASN	Mainchain

5.2 Too-close contacts

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	1	1809	0	1755	30	0
1	2	1809	0	1755	35	0
1	3	1809	0	1755	31	1
1	4	1809	0	1755	31	0
2	1	9	0	0	1	0
2	2	15	0	0	4	0
2	3	12	0	0	2	0
2	4	12	0	0	2	0
3	1	2	0	0	0	0
3	2	2	0	0	0	0
3	3	2	0	0	0	0
3	4	2	0	0	0	0
4	1	1	0	0	0	0
4	2	1	0	0	0	0
4	3	1	0	0	0	0
4	4	1	0	0	0	0
5	1	48	0	32	10	0
5	2	36	0	24	13	0
5	3	30	0	20	2	1
5	4	36	0	24	8	1
6	1	214	0	0	2	0
6	2	183	0	0	9	0
6	3	165	0	0	6	1
6	4	202	0	0	2	1
All	All	8210	0	7120	134	3

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 9.

The worst 5 of 134 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)
5:2:809:GOL:O2	6:2:1192:HOH:O	1.67	1.10
1:2:158:ARG:HB3	1:2:166:GLN:HG2	1.46	0.97
1:1:135:LYS:H	1:1:135:LYS:HZ1	1.07	0.94
1:1:135:LYS:H	1:1:135:LYS:NZ	1.73	0.85
1:2:180:HIS:H	5:2:811:GOL:H12	1.46	0.80

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:60:ARG:NH2	1:3:60:ARG:NH2[4_565]	1.68	0.52
5:3:802:GOL:O2	6:4:1149:HOH:O[5_555]	2.17	0.03
5:4:813:GOL:C1	6:3:1147:HOH:O[5_445]	2.18	0.02

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	1	235/237 (99%)	224 (95%)	11 (5%)	0	100	100
1	2	235/237 (99%)	225 (96%)	10 (4%)	0	100	100
1	3	235/237 (99%)	225 (96%)	10 (4%)	0	100	100
1	4	235/237 (99%)	220 (94%)	15 (6%)	0	100	100
All	All	940/948 (99%)	894 (95%)	46 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	1	203/203 (100%)	201 (99%)	2 (1%)	82	81
1	2	203/203 (100%)	196 (97%)	7 (3%)	44	33
1	3	203/203 (100%)	200 (98%)	3 (2%)	72	69
1	4	203/203 (100%)	200 (98%)	3 (2%)	72	69
All	All	812/812 (100%)	797 (98%)	15 (2%)	66	61

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	2	162	ASN
1	2	166	GLN
1	4	46	LYS
1	2	161	SER
1	3	158	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	2	237	ASN
1	3	44	ASN
1	4	83	ASN
1	2	118	ASN
1	2	205	HIS

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 53 ligands modelled in this entry, 12 are monoatomic - leaving 41 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	GOL	1	804	-	5,5,5	4.80	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	1	806	-	5,5,5	4.80	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	1	807	-	5,5,5	4.79	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	1	812	-	5,5,5	4.80	5 (100%)	5,5,5	5.70	3 (60%)
5	GOL	1	821	-	5,5,5	4.80	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	1	822	-	5,5,5	4.80	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	1	823	-	5,5,5	4.81	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	1	824	-	5,5,5	4.80	5 (100%)	5,5,5	5.70	3 (60%)
2	AZI	1	907	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	1	910	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	1	912	-	0,2,2	0.00	-	0,1,1	0.00	-
5	GOL	2	809	-	5,5,5	4.81	5 (100%)	5,5,5	5.70	3 (60%)
5	GOL	2	811	-	5,5,5	4.79	5 (100%)	5,5,5	5.68	3 (60%)
5	GOL	2	814	-	5,5,5	4.80	5 (100%)	5,5,5	3.62	3 (60%)
5	GOL	2	815	-	5,5,5	4.79	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	2	818	-	5,5,5	4.81	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	2	820	-	5,5,5	4.80	5 (100%)	5,5,5	5.69	3 (60%)
2	AZI	2	902	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	2	905	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	2	908	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	2	913	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	2	915	-	0,2,2	0.00	-	0,1,1	0.00	-
5	GOL	3	802	-	5,5,5	4.81	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	3	803	-	5,5,5	4.80	5 (100%)	5,5,5	5.69	3 (60%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	GOL	3	808	-	5,5,5	4.81	5 (100%)	5,5,5	5.68	3 (60%)
5	GOL	3	816	-	5,5,5	4.80	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	3	825	-	5,5,5	4.80	5 (100%)	5,5,5	5.69	3 (60%)
2	AZI	3	901	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	3	904	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	3	909	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	3	914	-	0,2,2	0.00	-	0,1,1	0.00	-
5	GOL	4	801	-	5,5,5	4.81	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	4	805	-	5,5,5	4.80	5 (100%)	5,5,5	5.68	3 (60%)
5	GOL	4	810	-	5,5,5	4.79	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	4	813	1	5,5,5	4.80	5 (100%)	5,5,5	5.70	3 (60%)
5	GOL	4	817	-	5,5,5	4.81	5 (100%)	5,5,5	5.69	3 (60%)
5	GOL	4	819	-	5,5,5	4.81	5 (100%)	5,5,5	5.69	3 (60%)
2	AZI	4	903	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	4	906	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	4	911	-	0,2,2	0.00	-	0,1,1	0.00	-
2	AZI	4	916	-	0,2,2	0.00	-	0,1,1	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	1	804	-	-	0/4/4/4	0/0/0/0
5	GOL	1	806	-	-	0/4/4/4	0/0/0/0
5	GOL	1	807	-	-	0/4/4/4	0/0/0/0
5	GOL	1	812	-	-	0/4/4/4	0/0/0/0
5	GOL	1	821	-	-	0/4/4/4	0/0/0/0
5	GOL	1	822	-	-	0/4/4/4	0/0/0/0
5	GOL	1	823	-	-	0/4/4/4	0/0/0/0
5	GOL	1	824	-	-	0/4/4/4	0/0/0/0
2	AZI	1	907	-	-	0/0/0/0	0/0/0/0
2	AZI	1	910	-	-	0/0/0/0	0/0/0/0
2	AZI	1	912	-	-	0/0/0/0	0/0/0/0
5	GOL	2	809	-	-	0/4/4/4	0/0/0/0
5	GOL	2	811	-	-	0/4/4/4	0/0/0/0
5	GOL	2	814	-	-	0/4/4/4	0/0/0/0
5	GOL	2	815	-	-	0/4/4/4	0/0/0/0
5	GOL	2	818	-	-	0/4/4/4	0/0/0/0
5	GOL	2	820	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AZI	2	902	-	-	0/0/0/0	0/0/0/0
2	AZI	2	905	-	-	0/0/0/0	0/0/0/0
2	AZI	2	908	-	-	0/0/0/0	0/0/0/0
2	AZI	2	913	-	-	0/0/0/0	0/0/0/0
2	AZI	2	915	-	-	0/0/0/0	0/0/0/0
5	GOL	3	802	-	-	0/4/4/4	0/0/0/0
5	GOL	3	803	-	-	0/4/4/4	0/0/0/0
5	GOL	3	808	-	-	0/4/4/4	0/0/0/0
5	GOL	3	816	-	-	0/4/4/4	0/0/0/0
5	GOL	3	825	-	-	0/4/4/4	0/0/0/0
2	AZI	3	901	-	-	0/0/0/0	0/0/0/0
2	AZI	3	904	-	-	0/0/0/0	0/0/0/0
2	AZI	3	909	-	-	0/0/0/0	0/0/0/0
2	AZI	3	914	-	-	0/0/0/0	0/0/0/0
5	GOL	4	801	-	-	0/4/4/4	0/0/0/0
5	GOL	4	805	-	-	0/4/4/4	0/0/0/0
5	GOL	4	810	-	-	0/4/4/4	0/0/0/0
5	GOL	4	813	1	-	0/4/4/4	0/0/0/0
5	GOL	4	817	-	-	0/4/4/4	0/0/0/0
5	GOL	4	819	-	-	0/4/4/4	0/0/0/0
2	AZI	4	903	-	-	0/0/0/0	0/0/0/0
2	AZI	4	906	-	-	0/0/0/0	0/0/0/0
2	AZI	4	911	-	-	0/0/0/0	0/0/0/0
2	AZI	4	916	-	-	0/0/0/0	0/0/0/0

The worst 5 of 125 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	2	818	GOL	C3-C2	-8.16	1.21	1.52
5	4	817	GOL	C3-C2	-8.15	1.21	1.52
5	1	823	GOL	C3-C2	-8.15	1.21	1.52
5	3	802	GOL	C3-C2	-8.15	1.21	1.52
5	1	804	GOL	C3-C2	-8.15	1.21	1.52

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	4	810	GOL	O1-C1-C2	3.19	125.67	110.18
5	1	804	GOL	O1-C1-C2	3.19	125.67	110.18
5	3	802	GOL	O1-C1-C2	3.19	125.68	110.18
5	2	809	GOL	O1-C1-C2	3.20	125.68	110.18
5	1	806	GOL	O1-C1-C2	3.20	125.68	110.18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

21 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	1	807	GOL	1	0
5	1	812	GOL	2	0
5	1	822	GOL	1	0
5	1	823	GOL	4	0
5	1	824	GOL	2	0
2	1	912	AZI	1	0
5	2	809	GOL	3	0
5	2	811	GOL	5	0
5	2	814	GOL	3	0
5	2	815	GOL	2	0
5	2	820	GOL	1	0
2	2	913	AZI	2	0
2	2	915	AZI	2	0
5	3	802	GOL	0	1
5	3	825	GOL	2	0
2	3	901	AZI	2	0
5	4	801	GOL	2	0
5	4	810	GOL	1	0
5	4	813	GOL	0	1
5	4	819	GOL	5	0
2	4	903	AZI	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 [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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	1	237/237 (100%)	-0.24	6 (2%) 61 64	7, 13, 31, 45	0
1	2	237/237 (100%)	-0.16	7 (2%) 54 57	9, 16, 32, 50	0
1	3	237/237 (100%)	-0.13	5 (2%) 67 70	10, 18, 31, 49	0
1	4	237/237 (100%)	-0.29	5 (2%) 67 70	8, 14, 29, 47	0
All	All	948/948 (100%)	-0.20	23 (2%) 62 66	7, 15, 31, 50	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	2	161	SER	4.3
1	2	162	ASN	4.1
1	4	162	ASN	3.6
1	1	161	SER	3.4
1	3	162	ASN	3.4

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, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	GOL	4	819	6/6	0.70	0.31	22.54	22,27,28,29	0
5	GOL	2	814	6/6	0.70	0.30	20.42	29,31,33,34	0
5	GOL	4	817	6/6	0.79	0.24	19.12	43,44,45,45	0
5	GOL	2	815	6/6	0.79	0.31	17.70	42,42,43,43	0
5	GOL	1	823	6/6	0.65	0.35	14.87	36,38,40,40	0
2	AZI	3	901	3/3	0.87	0.33	13.87	38,38,39,41	0
2	AZI	1	912	3/3	0.44	0.32	13.39	37,37,40,41	0
5	GOL	2	809	6/6	0.76	0.32	12.51	29,34,35,37	0
5	GOL	4	810	6/6	0.74	0.21	12.05	33,37,39,40	0
5	GOL	2	811	6/6	0.66	0.32	11.86	34,36,37,38	0
5	GOL	2	820	6/6	0.69	0.32	11.69	38,39,39,39	0
5	GOL	3	808	6/6	0.78	0.37	10.30	35,39,40,41	0
5	GOL	1	806	6/6	0.86	0.31	9.66	30,32,33,33	0
5	GOL	3	825	6/6	0.70	0.41	9.48	45,46,46,46	0
5	GOL	4	813	6/6	0.81	0.29	9.31	34,37,40,41	0
5	GOL	1	804	6/6	0.84	0.20	8.35	34,34,35,35	0
2	AZI	3	909	3/3	0.06	0.44	8.16	56,56,57,58	0
2	AZI	4	906	3/3	0.68	0.25	7.20	36,36,36,39	0
2	AZI	4	911	3/3	0.85	0.26	7.00	31,31,34,34	0
2	AZI	2	905	3/3	0.87	0.21	6.93	35,35,37,38	0
5	GOL	1	824	6/6	0.85	0.33	6.17	40,42,43,43	0
5	GOL	1	807	6/6	0.84	0.19	6.05	16,19,23,28	0
2	AZI	2	915	3/3	0.71	0.30	5.79	33,33,34,36	0
5	GOL	4	805	6/6	0.86	0.17	5.79	16,19,21,21	0
5	GOL	4	801	6/6	0.77	0.28	5.60	29,35,36,37	0
5	GOL	1	812	6/6	0.80	0.23	4.81	29,32,34,37	0
5	GOL	3	802	6/6	0.74	0.22	4.67	30,31,34,34	0
5	GOL	1	821	6/6	0.86	0.26	3.79	33,36,36,36	0
2	AZI	2	913	3/3	0.66	0.27	3.59	35,35,37,38	0
2	AZI	1	907	3/3	0.82	0.20	2.87	31,31,34,35	0
5	GOL	3	816	6/6	0.75	0.22	2.74	37,39,39,42	0
2	AZI	1	910	3/3	0.88	0.18	2.59	33,33,35,36	0
4	NA	3	1011	1/1	0.52	0.22	2.37	35,35,35,35	0
4	NA	4	1010	1/1	0.63	0.17	1.38	34,34,34,34	0
4	NA	2	1009	1/1	0.69	0.18	1.32	38,38,38,38	0
5	GOL	3	803	6/6	0.87	0.13	1.21	28,28,30,30	0
3	MN	3	1005	1/1	0.92	0.11	0.95	24,24,24,24	0
4	NA	1	1012	1/1	0.91	0.17	0.75	30,30,30,30	0
3	MN	4	1007	1/1	0.98	0.07	0.71	18,18,18,18	0
3	MN	1	1002	1/1	0.99	0.05	-1.63	10,10,10,10	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	MN	2	1004	1/1	0.99	0.05	-1.73	12,12,12,12	0
3	MN	4	1008	1/1	1.00	0.04	-2.04	11,11,11,11	0
3	MN	3	1006	1/1	0.99	0.05	-3.28	15,15,15,15	0
3	MN	1	1001	1/1	1.00	0.02	-3.38	16,16,16,16	0
3	MN	2	1003	1/1	1.00	0.03	-3.78	18,18,18,18	0
2	AZI	2	902	3/3	0.60	0.26	-	45,45,46,47	0
2	AZI	4	903	3/3	0.52	0.25	-	29,29,35,35	0
2	AZI	3	914	3/3	0.32	0.34	-	45,45,45,47	0
2	AZI	3	904	3/3	0.78	0.24	-	43,43,44,44	0
5	GOL	1	822	6/6	0.78	0.31	-	15,28,30,33	0
2	AZI	4	916	3/3	0.52	0.31	-	42,42,43,45	0
5	GOL	2	818	6/6	0.69	0.36	-	28,31,33,33	0
2	AZI	2	908	3/3	0.78	0.28	-	34,34,34,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.