



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 23, 2023 – 01:29 AM EDT

PDB ID : 3E2Z
Title : Crystal structure of mouse kynurenine aminotransferase III in complex with kynurenine
Authors : Han, Q.; Robinson, R.; Cai, T.; Tagle, D.A.; Li, J.
Deposited on : 2008-08-06
Resolution : 2.81 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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 : 2.35
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) : 2.35

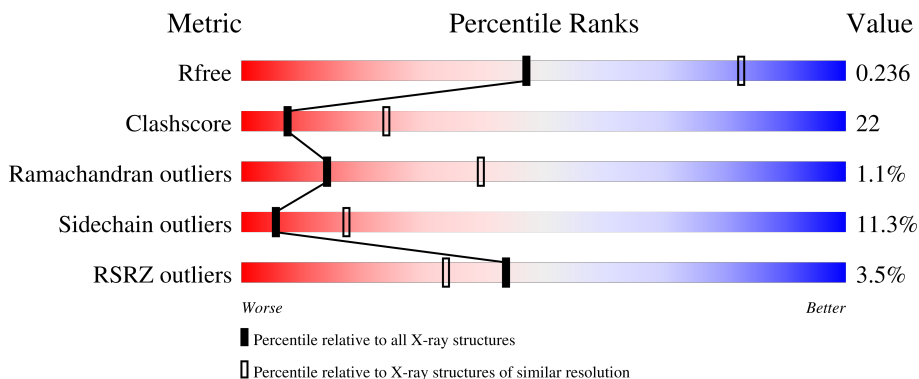
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	410	
2	B	410	

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
1	LLP	A	281	-	X	-	-
3	KYN	A	456	-	-	X	-
3	KYN	B	457	-	-	X	-
4	GOL	B	459	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6674 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.

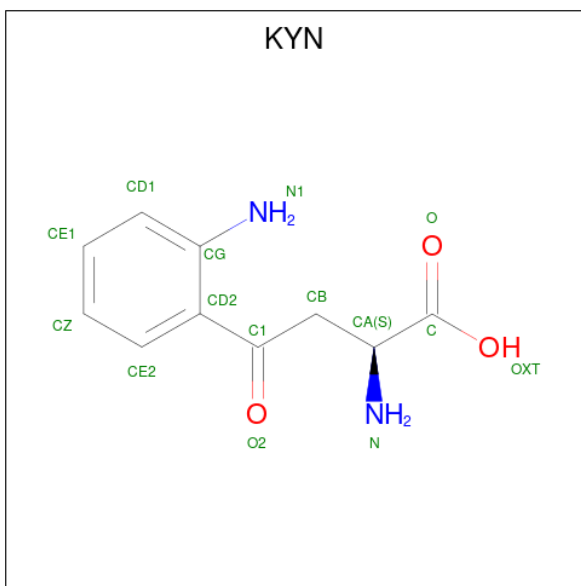
- Molecule 1 is a protein called Kynurenine-oxoglutarate transaminase 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	410	3268	2108	537	604	1	18	0	0	0

- Molecule 2 is a protein called Kynurenine-oxoglutarate transaminase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	410	3253	2100	536	599	18	0	0	0

- Molecule 3 is (2S)-2-amino-4-(2-aminophenyl)-4-oxobutanoic acid (three-letter code: KYN) (formula: C₁₀H₁₂N₂O₃).



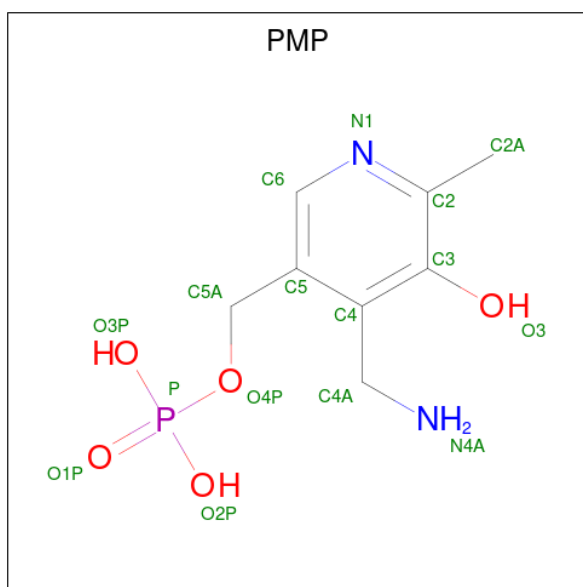
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	15	10	2	3	0	0
3	B	1	15	10	2	3	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is 4'-DEOXY-4'-AMINOPYRIDOXAL-5'-PHOSPHATE (three-letter code: PMP) (formula: $C_8H_{13}N_2O_5P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	B	1	16	8	2	5	1	0	0

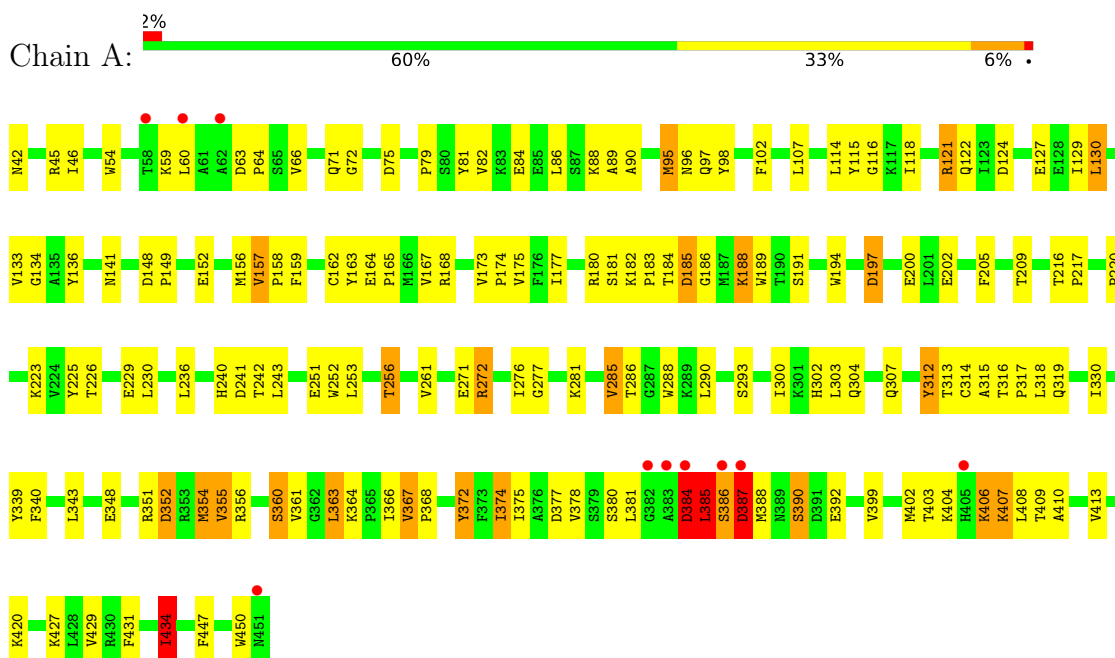
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	46	Total	O	0	0
			46	46		
6	B	37	Total	O	0	0
			37	37		

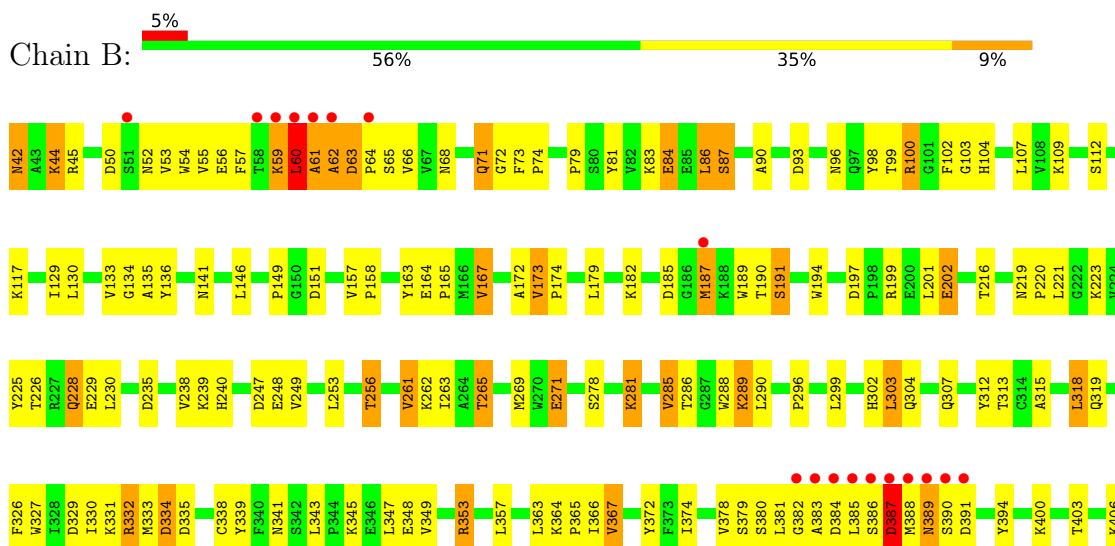
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Kynurenine-oxoglutarate transaminase 3



- Molecule 2: Kynurenine-oxoglutarate transaminase 3





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	91.49Å 91.49Å 233.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.64 – 2.81 29.64 – 2.81	Depositor EDS
% Data completeness (in resolution range)	95.6 (29.64-2.81) 95.6 (29.64-2.81)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.80Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.192 , 0.237 0.193 , 0.236	Depositor DCC
R_{free} test set	1227 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtrriage
Anisotropy	0.305	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 45.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6674	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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, 0.333 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: PMP, KYN, GOL, LLP

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	1.18	6/3331 (0.2%)	1.06	11/4525 (0.2%)
2	B	1.10	4/3341 (0.1%)	1.03	11/4539 (0.2%)
All	All	1.14	10/6672 (0.1%)	1.04	22/9064 (0.2%)

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	A	1	3
2	B	0	7
All	All	1	10

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	256	THR	CB-OG1	6.12	1.55	1.43
1	A	136	TYR	CE1-CZ	5.86	1.46	1.38
1	A	355	VAL	CB-CG1	5.59	1.64	1.52
2	B	45	ARG	CG-CD	5.38	1.65	1.51
2	B	407	LYS	CD-CE	5.29	1.64	1.51

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	60	LEU	CB-CA-C	8.47	126.29	110.20
2	B	61	ALA	N-CA-CB	6.43	119.11	110.10
2	B	387	ASP	CB-CA-C	6.28	122.97	110.40
2	B	60	LEU	N-CA-C	-5.81	95.31	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	61	ALA	N-CA-C	-5.74	95.51	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	434	ILE	CB

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	384	ASP	Peptide
1	A	385	LEU	Peptide
1	A	387	ASP	Peptide
2	B	219	ASN	Peptide
2	B	60	LEU	Peptide

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	3268	0	3235	152	0
2	B	3253	0	3231	149	0
3	A	15	0	11	7	0
3	B	15	0	11	9	0
4	A	12	0	16	3	0
4	B	12	0	16	8	0
5	B	16	0	11	3	0
6	A	46	0	0	2	0
6	B	37	0	0	0	0
All	All	6674	0	6531	289	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 22.

The worst 5 of 289 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)
2:B:262:LYS:O	2:B:265:THR:HG23	1.39	1.22
3:A:456:KYN:CB	3:A:456:KYN:HN1A	1.62	1.10
1:A:79:PRO:HB3	1:A:81:TYR:CE2	1.87	1.09
3:A:456:KYN:HN1A	3:A:456:KYN:HBA	0.99	1.08
2:B:448:ARG:HG3	2:B:448:ARG:HH11	0.91	1.03

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	407/410 (99%)	368 (90%)	35 (9%)	4 (1%)	15	42
2	B	408/410 (100%)	360 (88%)	43 (10%)	5 (1%)	13	37
All	All	815/820 (99%)	728 (89%)	78 (10%)	9 (1%)	14	39

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	434	ILE
2	B	191	SER
1	A	312	TYR
1	A	251	GLU
2	B	64	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	357/357 (100%)	323 (90%)	34 (10%)	8	24
2	B	358/358 (100%)	311 (87%)	47 (13%)	4	12
All	All	715/715 (100%)	634 (89%)	81 (11%)	6	17

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	281	LYS
2	B	387	ASP
2	B	289	LYS
2	B	345	LYS
2	B	408	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	71	GLN
2	B	307	GLN
2	B	96	ASN
2	B	405	HIS
2	B	228	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	LLP	A	281	1	23,24,25	3.02	11 (47%)	25,32,34	2.85	13 (52%)

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
1	LLP	A	281	1	-	6/16/17/19	0/1/1/1

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	281	LLP	CE-NZ	7.84	1.63	1.46
1	A	281	LLP	O3-C3	-5.37	1.24	1.37
1	A	281	LLP	C4'-NZ	4.93	1.43	1.27
1	A	281	LLP	C2-N1	4.58	1.42	1.33
1	A	281	LLP	C3-C2	3.70	1.44	1.40

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	281	LLP	CD-CE-NZ	7.83	130.12	110.93
1	A	281	LLP	C2'-C2-C3	4.81	126.83	120.89
1	A	281	LLP	OP3-P-OP4	-4.17	95.63	106.73
1	A	281	LLP	C5-C6-N1	-3.74	117.59	123.82
1	A	281	LLP	OP4-C5'-C5	3.55	116.11	109.35

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	281	LLP	C4-C4'-NZ-CE
1	A	281	LLP	C3-C4-C4'-NZ
1	A	281	LLP	CG-CD-CE-NZ
1	A	281	LLP	C5-C4-C4'-NZ
1	A	281	LLP	CD-CE-NZ-C4'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry

7 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
4	GOL	A	458	-	5,5,5	0.57	0	5,5,5	0.89	0
4	GOL	B	459	-	5,5,5	0.68	0	5,5,5	0.34	0
4	GOL	A	457	-	5,5,5	0.85	0	5,5,5	1.55	0
4	GOL	B	458	-	5,5,5	0.51	0	5,5,5	0.92	0
3	KYN	A	456	-	13,15,15	1.30	2 (15%)	17,20,20	1.46	4 (23%)
5	PMP	B	456	-	16,16,16	1.50	3 (18%)	21,23,23	1.83	3 (14%)
3	KYN	B	457	-	13,15,15	1.11	2 (15%)	17,20,20	1.49	5 (29%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	458	-	-	2/4/4/4	-
4	GOL	B	459	-	-	2/4/4/4	-
4	GOL	A	457	-	-	2/4/4/4	-
4	GOL	B	458	-	-	0/4/4/4	-
3	KYN	A	456	-	-	4/12/12/12	0/1/1/1
5	PMP	B	456	-	-	5/8/8/8	0/1/1/1
3	KYN	B	457	-	-	6/12/12/12	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	456	KYN	CD2-CG	-3.46	1.37	1.41
5	B	456	PMP	C3-C2	3.16	1.44	1.40
5	B	456	PMP	C2-N1	2.97	1.39	1.33
5	B	456	PMP	C5-C4	2.83	1.44	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	456	KYN	OXT-C	-2.64	1.21	1.30

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	456	PMP	O4P-C5A-C5	4.32	117.59	109.35
5	B	456	PMP	C5A-C5-C6	-4.02	112.76	119.37
5	B	456	PMP	C2A-C2-C3	3.31	124.97	120.89
3	A	456	KYN	CD2-CG-N1	-3.24	118.39	122.67
3	B	457	KYN	OXT-C-CA	2.68	122.50	113.38

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	456	KYN	O2-C1-CD2-CG
3	A	456	KYN	CB-C1-CD2-CG
3	B	457	KYN	O2-C1-CD2-CG
3	B	457	KYN	CB-C1-CD2-CG
4	A	457	GOL	C1-C2-C3-O3

There are no ring outliers.

6 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	459	GOL	6	0
4	A	457	GOL	3	0
4	B	458	GOL	2	0
3	A	456	KYN	7	0
5	B	456	PMP	3	0
3	B	457	KYN	9	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	A	409/410 (99%)	-0.35	10 (2%) 59 49	6, 18, 44, 64	0
2	B	410/410 (100%)	-0.27	19 (4%) 32 22	9, 20, 49, 76	0
All	All	819/820 (99%)	-0.31	29 (3%) 44 34	6, 19, 48, 76	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	387	ASP	5.7
2	B	386	SER	5.2
2	B	58	THR	4.3
2	B	60	LEU	4.2
2	B	62	ALA	4.1

6.2 Non-standard residues in protein, DNA, RNA chains [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, 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	B-factors(Å ²)	Q<0.9
1	LLP	A	281	24/25	0.97	0.17	12,18,22,26	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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, 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	B-factors(Å ²)	Q<0.9
3	KYN	A	456	15/15	0.78	0.35	10,23,32,36	0
3	KYN	B	457	15/15	0.78	0.31	10,23,32,36	0
4	GOL	B	459	6/6	0.79	0.22	14,35,36,38	0
4	GOL	B	458	6/6	0.87	0.18	43,45,46,46	0
4	GOL	A	457	6/6	0.89	0.14	22,38,42,47	0
4	GOL	A	458	6/6	0.94	0.13	24,30,31,37	0
5	PMP	B	456	16/16	0.99	0.15	14,27,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.