



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:32 PM GMT

PDB ID : 3U06
Title : Crystal structure of the kinesin-14 NcdG347D
Authors : Liu, H.-L.; Pemble IV, C.W.; Endow, S.A.
Deposited on : 2011-09-28
Resolution : 2.35 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
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

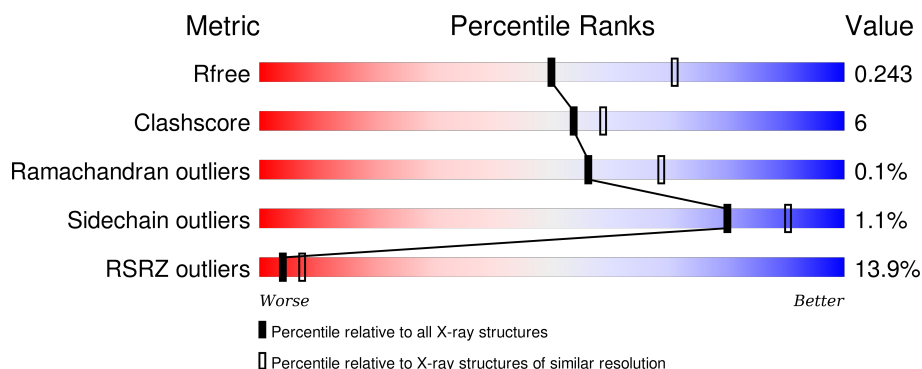
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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	A	412	<div> <div>5%</div> <div>77%</div> <div>9%</div> <div>13%</div> </div>
1	B	412	<div> <div>19%</div> <div>67%</div> <div>17%</div> <div>17%</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
4	GOL	A	2	-	-	-	X
4	GOL	A	4	-	-	-	X
4	GOL	A	702	-	-	-	X
4	GOL	B	5	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11469 atoms, of which 5633 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 Protein claret segregational.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	359	Total	C	H	N	O	S	0	0	0
			5715	1789	2840	506	559	21			
1	B	344	Total	C	H	N	O	S	0	1	0
			5483	1721	2729	480	532	21			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	289	MET	-	EXPRESSION TAG	UNP P20480
A	290	GLY	-	EXPRESSION TAG	UNP P20480
A	291	SER	-	EXPRESSION TAG	UNP P20480
A	292	MET	-	EXPRESSION TAG	UNP P20480
A	347	ASP	GLY	ENGINEERED MUTATION	UNP P20480
B	289	MET	-	EXPRESSION TAG	UNP P20480
B	290	GLY	-	EXPRESSION TAG	UNP P20480
B	291	SER	-	EXPRESSION TAG	UNP P20480
B	292	MET	-	EXPRESSION TAG	UNP P20480
B	347	ASP	GLY	ENGINEERED MUTATION	UNP P20480

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

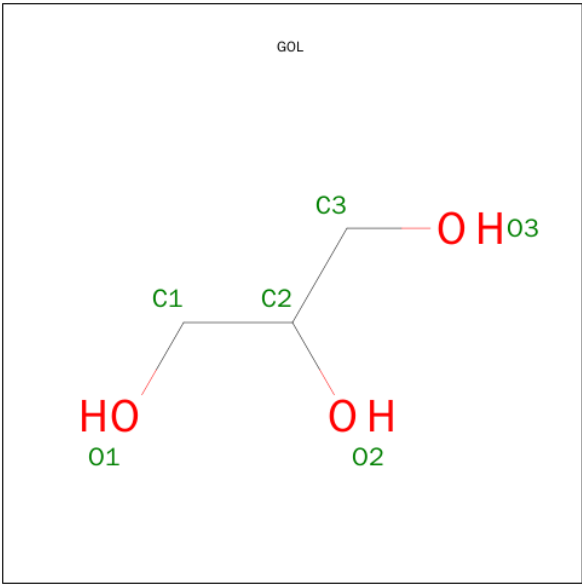


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			39	10	12	5	10	2		
2	B	1	Total	C	H	N	O	P	0	0
			39	10	12	5	10	2		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	A	1	Total	C	H	O	0	0
			14	3	8	3		
4	B	1	Total	C	H	O	0	0
			14	3	8	3		

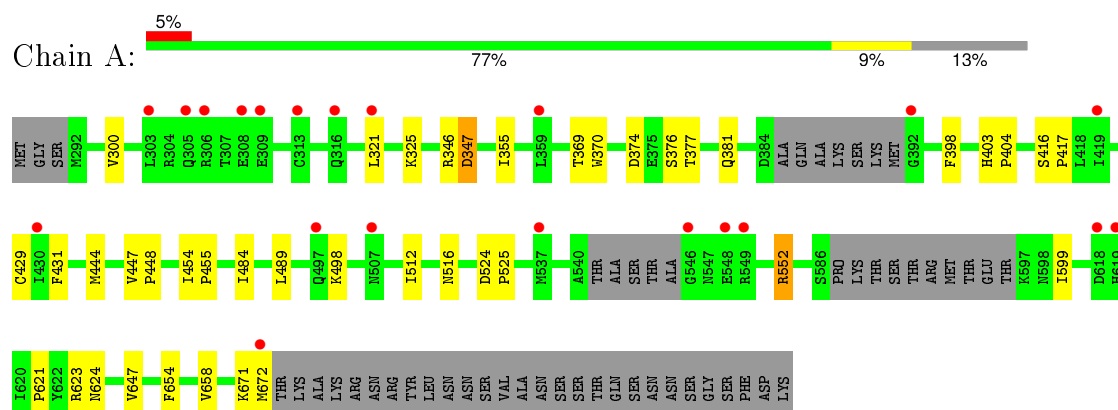
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	88	Total	O	0	0
			88	88		
5	B	34	Total	O	0	0
			34	34		

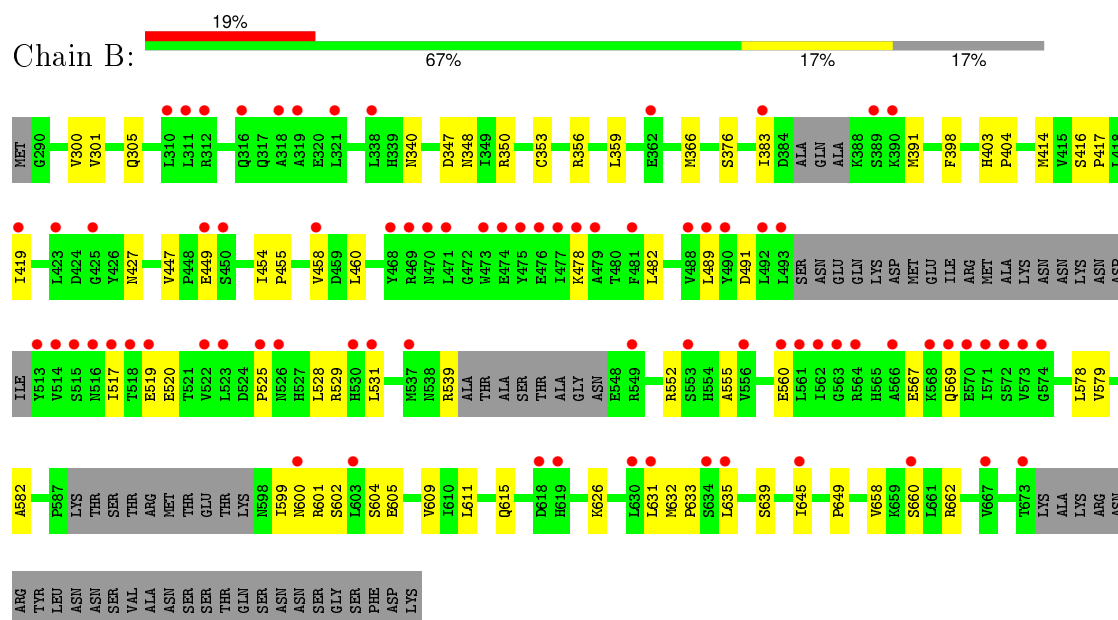
3 Residue-property plots

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: Protein claret segregational



• Molecule 1: Protein claret segregational



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	160.54Å 67.09Å 94.37Å 90.00° 98.91° 90.00°	Depositor
Resolution (Å)	46.62 – 2.35 46.62 – 2.34	Depositor EDS
% Data completeness (in resolution range)	86.1 (46.62-2.35) 86.1 (46.62-2.34)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.34Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_868)	Depositor
R, R_{free}	0.216 , 0.250 0.211 , 0.243	Depositor DCC
R_{free} test set	1806 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	38.8	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 48.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 36360 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11469	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% 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: GOL, MG, ADP

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	0.23	0/2920	0.42	0/3936
1	B	0.23	0/2802	0.43	0/3778
All	All	0.23	0/5722	0.42	0/7714

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2875	2840	2828	30	0
1	B	2754	2729	2718	44	0
2	A	27	12	12	0	0
2	B	27	12	12	1	0
3	A	1	0	0	0	0
4	A	24	32	32	0	0
4	B	6	8	8	0	0
5	A	88	0	0	1	0
5	B	34	0	0	1	0
All	All	5836	5633	5610	73	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 (73) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:567:GLU:N	1:B:567:GLU:OE1	2.29	0.66
1:B:359:LEU:HD21	2:B:1:ADP:H1'	1.81	0.62
1:B:645:ILE:HD11	1:B:660:SER:HB3	1.82	0.62
1:B:458:VAL:HG22	1:B:528:LEU:HD23	1.82	0.62
1:B:301:VAL:O	1:B:305:GLN:HG3	2.02	0.60
1:B:525:PRO:O	1:B:529:ARG:HG3	2.02	0.59
1:A:552:ARG:HD3	1:A:599:ILE:CG2	2.33	0.58
1:A:346:ARG:O	1:A:347:ASP:HB2	2.04	0.58
1:B:631:LEU:O	1:B:635:LEU:N	2.37	0.57
1:A:403:HIS:HB2	1:A:404:PRO:CD	2.34	0.57
1:B:353:CYS:HA	1:B:645:ILE:HG23	1.87	0.57
1:B:454:ILE:HB	1:B:455:PRO:HD3	1.87	0.56
1:A:454:ILE:HB	1:A:455:PRO:HD3	1.87	0.56
1:B:632:MET:HB3	1:B:633:PRO:HD3	1.88	0.55
1:A:403:HIS:HB2	1:A:404:PRO:HD2	1.89	0.55
1:B:599:ILE:N	1:B:599:ILE:HD12	2.22	0.54
1:B:403:HIS:CG	1:B:404:PRO:HD2	2.43	0.54
1:B:601:ARG:O	1:B:604:SER:N	2.41	0.54
1:A:512:ILE:HD12	1:A:512:ILE:C	2.29	0.53
1:B:416:SER:OG	1:B:417:PRO:HD3	2.09	0.53
1:B:489:LEU:HD11	1:B:626:LYS:HD3	1.92	0.51
1:B:519:GLU:O	1:B:520:GLU:HG2	2.10	0.51
1:A:552:ARG:HD3	1:A:599:ILE:HG22	1.91	0.50
1:B:356:ARG:O	1:B:649:PRO:HG3	2.12	0.50
1:B:569:GLN:O	1:B:569:GLN:HG3	2.12	0.50
1:B:366:MET:SD	1:B:383:ILE:HD13	2.52	0.50
1:A:671:LYS:O	1:A:672:MET:CB	2.60	0.49
1:A:346:ARG:O	1:A:347:ASP:CB	2.61	0.49
1:B:520:GLU:HG3	1:B:531:LEU:HD21	1.94	0.49
1:A:552:ARG:HG2	1:A:599:ILE:HG23	1.95	0.49
1:A:374:ASP:OD1	1:A:377:THR:N	2.46	0.49
1:A:621:PRO:HB2	1:A:624:ASN:ND2	2.28	0.49
1:B:454:ILE:HG12	1:B:578:LEU:HD13	1.96	0.47
1:A:671:LYS:O	1:A:672:MET:HB2	2.12	0.47
1:B:605:GLU:O	1:B:609:VAL:HG23	2.14	0.47
1:B:520:GLU:HG3	1:B:531:LEU:CD2	2.45	0.47
1:B:347:ASP:HA	1:B:639:SER:HB3	1.97	0.47
1:B:631:LEU:O	1:B:635:LEU:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:555:ALA:O	1:B:579:VAL:HA	2.14	0.47
1:A:300:VAL:HG23	1:B:300:VAL:CG1	2.46	0.46
1:B:567:GLU:HG2	1:B:567:GLU:O	2.16	0.46
1:B:350:ARG:HD2	1:B:639:SER:O	2.16	0.45
1:A:370:TRP:CH2	1:A:647:VAL:HG11	2.51	0.45
1:A:484:ILE:HG12	1:A:489:LEU:HD23	1.99	0.45
1:A:498:LYS:HD2	1:A:516:ASN:O	2.16	0.45
1:A:654:PHE:O	1:A:658:VAL:HG23	2.17	0.45
1:A:321:LEU:HG	1:A:325:LYS:HE3	1.98	0.44
1:B:552:ARG:HA	1:B:582:ALA:HB1	1.99	0.44
1:B:491:ASP:HB3	1:B:517:ILE:HD12	1.99	0.44
1:B:376:SER:HB2	1:B:398:PHE:O	2.18	0.44
1:B:601:ARG:O	1:B:602:SER:C	2.56	0.44
1:A:355:ILE:HD12	1:A:647:VAL:CG1	2.48	0.44
1:B:611:LEU:O	1:B:615:GLN:HG2	2.18	0.44
1:B:447:VAL:HG23	1:B:449:GLU:HG2	2.00	0.44
1:B:416:SER:N	1:B:417:PRO:CD	2.81	0.43
1:A:524:ASP:HB2	1:A:525:PRO:HD2	2.00	0.43
1:A:429:CYS:HB3	1:A:431:PHE:CE2	2.53	0.43
1:B:539:ARG:CZ	1:B:555:ALA:HB2	2.48	0.43
1:A:623:ARG:NH1	5:A:65:HOH:O	2.51	0.43
1:A:444:MET:HE2	1:A:444:MET:HA	2.01	0.42
1:B:478:LYS:HB2	1:B:560:GLU:HB3	2.01	0.42
1:B:391:MET:O	5:B:57:HOH:O	2.22	0.42
1:A:416:SER:N	1:A:417:PRO:CD	2.82	0.42
1:A:369:THR:HB	1:A:381:GLN:HB2	2.01	0.42
1:B:632:MET:HB3	1:B:633:PRO:CD	2.48	0.42
1:B:403:HIS:CD2	1:B:404:PRO:HD2	2.55	0.42
1:A:621:PRO:HB2	1:A:624:ASN:CG	2.41	0.41
1:B:416:SER:HB2	1:B:460:LEU:HD22	2.02	0.41
1:B:348:ASN:O	1:B:639:SER:HA	2.21	0.41
1:A:376:SER:HB3	1:A:398:PHE:O	2.21	0.40
1:B:658:VAL:O	1:B:662:ARG:HG3	2.22	0.40
1:A:416:SER:OG	1:A:417:PRO:HD3	2.21	0.40
1:A:447:VAL:HB	1:A:448:PRO:HD2	2.04	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	351/412 (85%)	343 (98%)	7 (2%)	1 (0%)	46	55
1	B	335/412 (81%)	319 (95%)	16 (5%)	0	100	100
All	All	686/824 (83%)	662 (96%)	23 (3%)	1 (0%)	56	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	347	ASP

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	328/373 (88%)	327 (100%)	1 (0%)	94	98
1	B	316/373 (85%)	310 (98%)	6 (2%)	65	79
All	All	644/746 (86%)	637 (99%)	7 (1%)	80	90

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	552	ARG
1	B	340	ASN
1	B	414	MET
1	B	419	ILE
1	B	427	ASN

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Mol	Chain	Res	Type
1	B	482	LEU
1	B	600	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	314	ASN
1	B	330	GLN
1	B	598	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](#)

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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$
2	ADP	A	1	3	22,29,29	1.01	1 (4%)	27,45,45	1.99	5 (18%)
4	GOL	A	2	-	5,5,5	0.39	0	5,5,5	0.30	0
4	GOL	A	3	-	5,5,5	0.34	0	5,5,5	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GOL	A	4	-	5,5,5	0.34	0	5,5,5	0.24	0
4	GOL	A	702	-	5,5,5	0.35	0	5,5,5	0.25	0
2	ADP	B	1	-	22,29,29	0.99	1 (4%)	27,45,45	2.00	4 (14%)
4	GOL	B	5	-	5,5,5	0.36	0	5,5,5	0.21	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	ADP	A	1	3	-	0/12/32/32	0/3/3/3
4	GOL	A	2	-	-	0/4/4/4	0/0/0/0
4	GOL	A	3	-	-	0/4/4/4	0/0/0/0
4	GOL	A	4	-	-	0/4/4/4	0/0/0/0
4	GOL	A	702	-	-	0/4/4/4	0/0/0/0
2	ADP	B	1	-	-	0/12/32/32	0/3/3/3
4	GOL	B	5	-	-	0/4/4/4	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	ADP	C5-C4	3.02	1.47	1.40
2	A	1	ADP	C5-C4	3.09	1.47	1.40

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	ADP	N3-C2-N1	-7.92	122.83	128.89
2	B	1	ADP	N3-C2-N1	-7.68	123.01	128.89
2	B	1	ADP	PA-O3A-PB	-3.75	120.08	132.67
2	A	1	ADP	PA-O3A-PB	-3.21	121.91	132.67
2	A	1	ADP	C4-C5-N7	-3.16	106.57	109.48
2	B	1	ADP	C4-C5-N7	-3.01	106.71	109.48
2	B	1	ADP	O3B-PB-O2B	2.01	115.04	107.38
2	A	1	ADP	O3B-PB-O2B	2.02	115.07	107.38
2	A	1	ADP	C2-N1-C6	2.02	122.38	118.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	ADP	1	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, 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	359/412 (87%)	0.81	21 (5%) 26 40	33, 51, 92, 122	0
1	B	344/412 (83%)	1.30	77 (22%) 1 2	34, 70, 120, 140	0
All	All	703/824 (85%)	1.05	98 (13%) 4 7	33, 57, 114, 140	0

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	514	VAL	6.1
1	B	471	LEU	5.2
1	B	549	ARG	5.1
1	B	513	TYR	5.0
1	B	561	LEU	5.0
1	B	311	LEU	4.8
1	B	566	ALA	4.8
1	B	515	SER	4.5
1	B	475	TYR	4.4
1	B	571	ILE	4.4
1	B	630	LEU	4.1
1	B	474	GLU	4.1
1	B	631	LEU	4.1
1	A	618	ASP	3.9
1	B	574	GLY	3.8
1	B	469	ARG	3.8
1	B	481	PHE	3.7
1	A	619	HIS	3.6
1	B	477	ILE	3.6
1	B	450	SER	3.5
1	B	493	LEU	3.5
1	A	306	ARG	3.4
1	B	603	LEU	3.3
1	B	634	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	479	ALA	3.3
1	B	562	ILE	3.2
1	B	488	VAL	3.2
1	B	619	HIS	3.2
1	B	516	ASN	3.2
1	B	563	GLY	3.2
1	B	489	LEU	3.1
1	B	321	LEU	3.1
1	B	531	LEU	3.0
1	A	507	ASN	3.0
1	B	468	TYR	3.0
1	B	569	GLN	3.0
1	B	312	ARG	2.9
1	B	645	ILE	2.8
1	B	673	THR	2.8
1	B	568	LYS	2.8
1	A	316	GLN	2.8
1	B	362	GLU	2.7
1	B	425	GLY	2.7
1	B	573	VAL	2.7
1	B	423	LEU	2.7
1	B	523	LEU	2.7
1	B	389	SER	2.7
1	B	600	ASN	2.7
1	B	419	ILE	2.6
1	B	473	TRP	2.6
1	B	470	ASN	2.6
1	B	556	VAL	2.6
1	A	549	ARG	2.6
1	A	392	GLY	2.5
1	A	672	MET	2.5
1	B	572	SER	2.5
1	B	319	ALA	2.5
1	B	618	ASP	2.5
1	A	546	GLY	2.5
1	B	490	TYR	2.5
1	B	517	ILE	2.5
1	B	519	GLU	2.4
1	B	560	GLU	2.4
1	B	310	LEU	2.4
1	B	338	LEU	2.4
1	B	667	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	309	GLU	2.3
1	B	553	SER	2.3
1	B	458	VAL	2.3
1	A	419	ILE	2.3
1	A	305	GLN	2.3
1	B	449	GLU	2.3
1	B	518	THR	2.3
1	B	390	LYS	2.3
1	B	564	ARG	2.3
1	B	316	GLN	2.2
1	B	478	LYS	2.2
1	B	635	LEU	2.2
1	B	522	VAL	2.2
1	B	318	ALA	2.2
1	A	359	LEU	2.2
1	B	526	ASN	2.2
1	B	383	ILE	2.2
1	A	537	MET	2.2
1	A	548	GLU	2.2
1	B	492	LEU	2.2
1	A	497	GLN	2.1
1	B	525	PRO	2.1
1	A	303	LEU	2.1
1	A	313	CYS	2.1
1	B	530	HIS	2.1
1	B	660	SER	2.1
1	A	430	ILE	2.1
1	B	476	GLU	2.0
1	A	321	LEU	2.0
1	B	537	MET	2.0
1	B	570	GLU	2.0
1	A	308	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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(Å ²)	Q<0.9
4	GOL	A	2	6/6	0.78	0.27	5.08	80,96,98,99	0
4	GOL	B	5	6/6	0.84	0.26	4.55	70,84,87,88	0
4	GOL	A	4	6/6	0.69	0.24	2.78	79,95,96,96	0
4	GOL	A	702	6/6	0.93	0.23	2.52	66,79,80,82	0
2	ADP	B	1	27/27	0.95	0.21	1.39	60,69,84,87	0
2	ADP	A	1	27/27	0.97	0.18	0.77	35,47,62,63	0
4	GOL	A	3	6/6	0.90	0.15	-1.28	44,53,55,56	0
3	MG	A	701	1/1	0.90	0.16	-	50,50,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.