Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:09 AM GMT

PDB ID	:	1ZY5
Title	:	Crystal Structure of eIF2alpha Protein Kinase GCN2: R794G Hyperactivating Mutant Complexed with AMPPNP.
Authors	:	Padyana, A.K.; Qiu, H.; Roll-Mecak, A.; Hinnebusch, A.G.; Burley, S.K.
Deposited on	:	2005-06-09
Resolution	:	2.00 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 ①) were used in the production of this report:

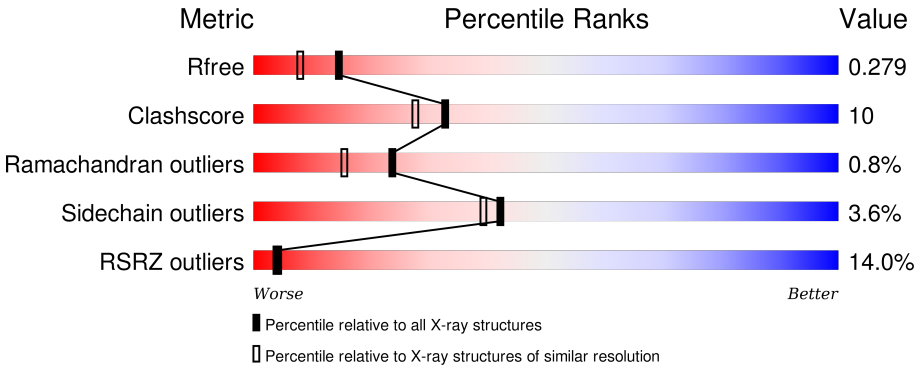
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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 >=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 <=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	303	9% 75% 13% • 11%
1	B	303	15% 62% 18% • 18%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4590 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 Serine/threonine-protein kinase GCN2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	S	9	0	0
			2236	1434	390	403	9			
1	B	249	Total	C	N	O	S	0	0	0
			2059	1326	354	370	9			

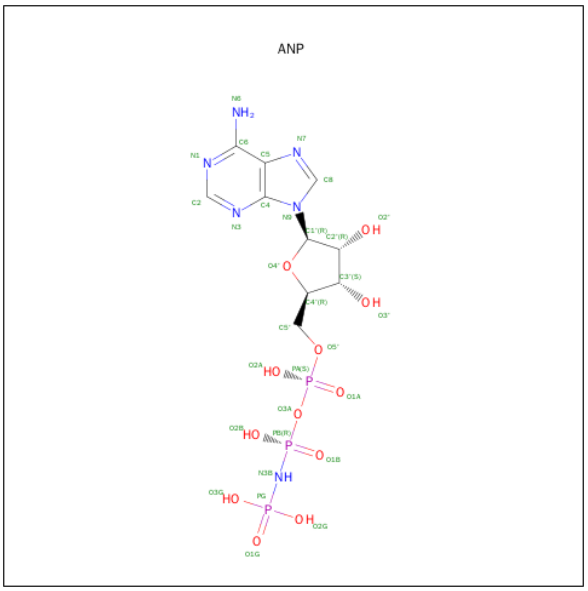
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	592	SER	-	CLONING ARTIFACT	UNP P15442
A	593	LEU	-	CLONING ARTIFACT	UNP P15442
A	794	GLY	ARG	ENGINEERED	UNP P15442
B	592	SER	-	CLONING ARTIFACT	UNP P15442
B	593	LEU	-	CLONING ARTIFACT	UNP P15442
B	794	GLY	ARG	ENGINEERED	UNP P15442

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
3	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 4 is water.

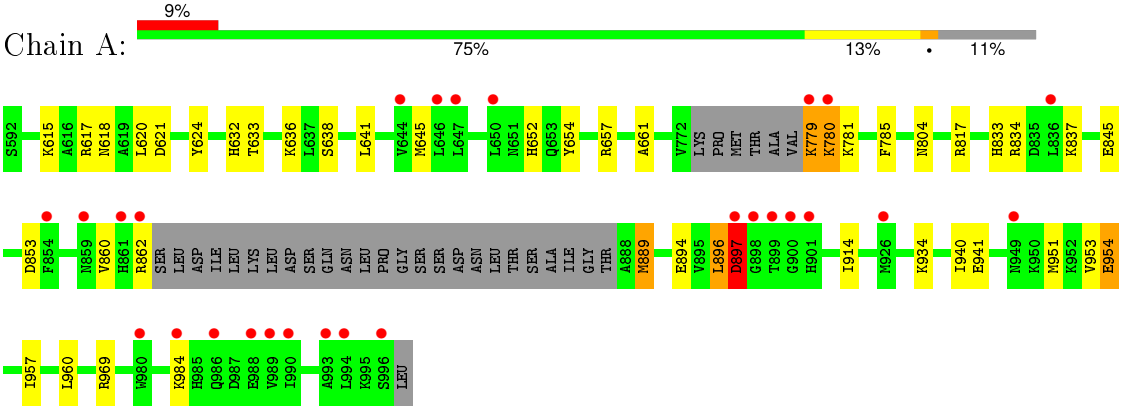
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	156	Total	O	0	0
			156	156		
4	B	75	Total	O	0	0
			75	75		

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.

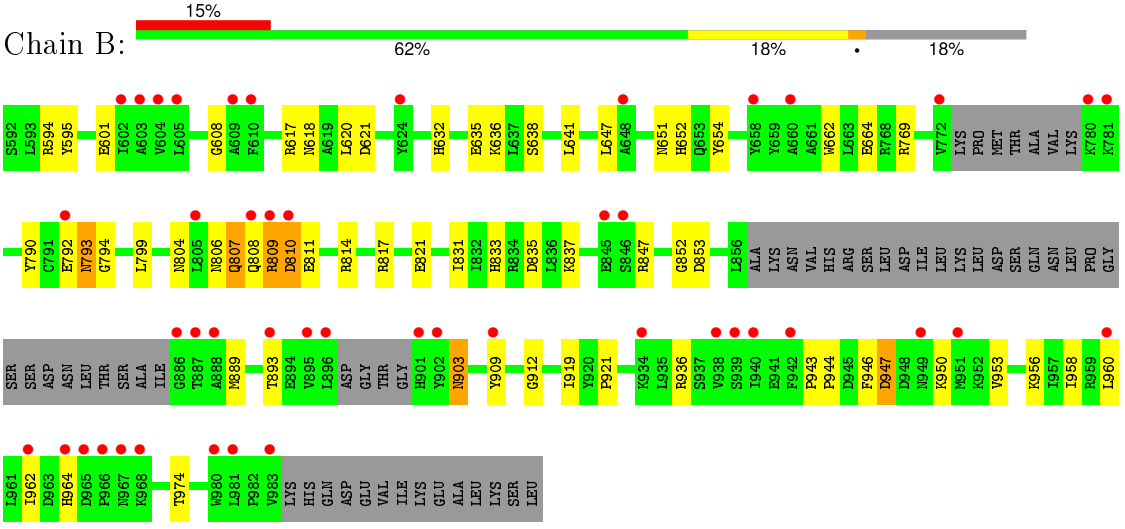
- Molecule 1: Serine/threonine-protein kinase GCN2

Chain A:



- Molecule 1: Serine/threonine-protein kinase GCN2

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	52.61Å 78.92Å 146.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.58 – 2.00 36.57 – 2.00	Depositor EDS
% Data completeness (in resolution range)	94.3 (36.58-2.00) 94.4 (36.57-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.04 (at 2.00Å)	Xtriage
Refinement program	CNX 2000.1, REFMAC	Depositor
R, R_{free}	0.235 , 0.279 0.230 , 0.279	Depositor DCC
R_{free} test set	1222 reflections (3.19%)	DCC
Wilson B-factor (Å^2)	37.0	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 61.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 39491 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4590	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, ANP

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	0.38	0/2281	0.65	0/3068
1	B	0.34	0/2101	0.65	3/2828 (0.1%)
All	All	0.37	0/4382	0.65	3/5896 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	809	ARG	N-CA-C	6.43	128.36	111.00
1	B	810	ASP	N-CA-C	-6.07	94.62	111.00
1	B	808	GLN	N-CA-C	5.97	127.12	111.00

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	2236	0	2253	36	0
1	B	2059	0	2068	54	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	31	0	13	0	0
3	B	31	0	13	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	156	0	0	10	0
4	B	75	0	0	11	1
All	All	4590	0	4347	90	1

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 10.

All (90) 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:821:GLU:HB2	4:B:157:HOH:O	1.38	1.23
1:B:809:ARG:HB3	1:B:811:GLU:HB2	1.45	0.98
1:B:809:ARG:CB	1:B:811:GLU:HB2	2.02	0.90
1:A:953:VAL:HG12	4:A:35:HOH:O	1.70	0.90
1:B:654:TYR:HD1	4:B:157:HOH:O	1.59	0.85
1:B:809:ARG:HB3	1:B:811:GLU:H	1.41	0.85
1:B:790:TYR:CE2	1:B:792:GLU:HB3	2.13	0.82
1:B:809:ARG:HG2	1:B:811:GLU:HB2	1.64	0.78
1:A:853:ASP:OD2	4:A:90:HOH:O	2.03	0.76
1:B:809:ARG:CG	1:B:811:GLU:HB2	2.16	0.75
1:B:833:HIS:HD2	1:B:835:ASP:H	1.33	0.75
1:B:809:ARG:HB3	1:B:811:GLU:CB	2.16	0.74
1:A:652:HIS:HD2	1:A:654:TYR:H	1.38	0.72
1:B:654:TYR:CD1	4:B:157:HOH:O	2.36	0.71
1:B:809:ARG:HB3	1:B:811:GLU:N	2.04	0.71
1:B:608:GLY:HA3	4:B:201:HOH:O	1.91	0.70
1:B:632:HIS:CE1	1:B:636:LYS:HD2	2.28	0.69
1:A:957:ILE:HG13	4:A:152:HOH:O	1.94	0.68
1:A:652:HIS:CD2	1:A:654:TYR:H	2.12	0.68
1:B:790:TYR:HE2	1:B:792:GLU:HB3	1.57	0.67
1:B:804:ASN:O	1:B:807:GLN:HB2	1.95	0.66
1:B:953:VAL:HG12	4:B:184:HOH:O	1.95	0.65
1:A:845:GLU:HG2	4:A:51:HOH:O	1.97	0.65
1:B:793:ASN:HB3	4:B:177:HOH:O	1.95	0.65
1:A:618:ASN:HD21	1:A:620:LEU:HB2	1.63	0.64
1:B:793:ASN:HB2	4:B:117:HOH:O	1.97	0.63
1:B:618:ASN:HD22	1:B:621:ASP:H	1.47	0.63
1:A:633:THR:HG21	1:A:779:LYS:HB2	1.82	0.62
1:B:799:LEU:HD11	1:B:847:ARG:HH21	1.64	0.61
1:A:618:ASN:ND2	1:A:620:LEU:H	1.99	0.60
1:B:944:PRO:HD3	4:B:143:HOH:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:617:ARG:HG2	1:A:624:TYR:CE2	2.38	0.59
1:B:853:ASP:OD2	3:B:304:ANP:H5'2	2.02	0.59
1:A:951:MET:HB3	1:A:954:GLU:HG2	1.86	0.58
1:B:833:HIS:HE1	1:B:852:GLY:O	1.85	0.58
1:B:811:GLU:CD	1:B:847:ARG:HH12	2.06	0.58
1:A:618:ASN:HD22	1:A:621:ASP:H	1.53	0.57
1:B:806:ASN:CB	1:B:921:PRO:HD3	2.34	0.57
1:B:595:TYR:OH	1:B:601:GLU:HB3	2.05	0.57
1:B:618:ASN:HD21	1:B:620:LEU:HB2	1.70	0.56
1:B:853:ASP:OD2	3:B:304:ANP:H8	2.05	0.56
1:B:903:ASN:HD22	1:B:903:ASN:H	1.54	0.55
1:A:633:THR:CG2	1:A:779:LYS:HB2	2.36	0.55
1:B:889:MET:CE	1:B:936:ARG:HD3	2.37	0.54
1:B:652:HIS:CD2	1:B:654:TYR:H	2.26	0.54
1:B:809:ARG:CB	1:B:811:GLU:H	2.19	0.52
1:B:618:ASN:HB3	1:B:621:ASP:OD2	2.10	0.52
1:B:664:GLU:HB3	1:B:769:ARG:HH12	1.75	0.52
1:A:617:ARG:HG2	1:A:624:TYR:CD2	2.45	0.52
1:B:652:HIS:HD2	1:B:654:TYR:H	1.57	0.52
1:A:845:GLU:CG	4:A:51:HOH:O	2.56	0.51
1:A:984:LYS:NZ	4:A:174:HOH:O	2.41	0.51
1:B:809:ARG:HB3	1:B:811:GLU:CA	2.41	0.50
1:B:944:PRO:HG2	4:B:81:HOH:O	2.11	0.50
1:B:638:SER:HA	1:B:641:LEU:HG	1.93	0.50
1:B:833:HIS:CE1	1:B:852:GLY:O	2.65	0.49
1:B:958:ILE:O	1:B:962:ILE:HG12	2.11	0.49
1:B:647:LEU:HD23	1:B:831:ILE:HD13	1.94	0.49
1:B:806:ASN:HA	1:B:919:ILE:HA	1.94	0.49
1:A:853:ASP:OD2	4:A:205:HOH:O	2.18	0.48
1:A:837:LYS:HA	1:A:914:ILE:HD11	1.95	0.48
1:A:934:LYS:HB3	1:A:941:GLU:HB2	1.96	0.47
1:A:953:VAL:HG23	4:A:152:HOH:O	2.13	0.47
1:A:889:MET:HE2	1:A:889:MET:HA	1.97	0.47
1:B:810:ASP:O	1:B:814:ARG:HB2	2.14	0.46
1:A:940:ILE:O	1:A:940:ILE:HG22	2.16	0.46
1:A:632:HIS:CE1	1:A:636:LYS:HG3	2.50	0.46
1:A:641:LEU:O	1:A:645:MET:HG2	2.16	0.45
1:A:657:ARG:HD3	4:A:107:HOH:O	2.15	0.45
1:B:889:MET:HE2	1:B:936:ARG:HD3	1.99	0.45
1:B:893:THR:HG21	1:B:964:HIS:CD2	2.51	0.45
1:A:817:ARG:HD3	4:A:99:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:780:LYS:HE2	1:A:781:LYS:N	2.32	0.45
1:B:594:ARG:HD3	1:B:662:TRP:CD2	2.53	0.44
1:B:793:ASN:CB	4:B:117:HOH:O	2.58	0.44
1:B:794:GLY:HA2	4:B:178:HOH:O	2.18	0.44
1:B:809:ARG:C	1:B:811:GLU:N	2.66	0.44
1:A:951:MET:HB3	1:A:954:GLU:CG	2.47	0.44
1:B:943:PRO:HG2	1:B:946:PHE:HB2	2.01	0.43
1:A:661:ALA:HA	1:A:785:PHE:O	2.18	0.42
1:A:638:SER:HA	1:A:641:LEU:HG	2.00	0.42
1:B:889:MET:HE3	1:B:936:ARG:HD3	2.02	0.41
1:A:860:VAL:C	1:A:862:ARG:H	2.22	0.41
1:B:909:TYR:O	1:B:912:GLY:N	2.54	0.41
1:A:960:LEU:O	1:A:969:ARG:HG3	2.21	0.41
1:A:833:HIS:O	1:A:834:ARG:HB2	2.21	0.41
1:A:896:LEU:HB2	1:A:897:ASP:H	1.66	0.40
1:B:617:ARG:HG3	1:B:617:ARG:HH11	1.85	0.40
1:A:615:LYS:HE2	1:A:624:TYR:CD2	2.57	0.40
1:A:894:GLU:OE2	1:A:969:ARG:NH2	2.51	0.40

All (1) 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:B:601:GLU:OE1	4:B:218:HOH:O[3_545]	2.16	0.04

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	265/303 (88%)	253 (96%)	10 (4%)	2 (1%)	24 15
1	B	241/303 (80%)	224 (93%)	15 (6%)	2 (1%)	24 15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	506/606 (84%)	477 (94%)	25 (5%)	4 (1%)	24 15

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	897	ASP
1	B	807	GLN
1	B	947	ASP
1	A	896	LEU

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	243/271 (90%)	237 (98%)	6 (2%)	55 55
1	B	224/271 (83%)	213 (95%)	11 (5%)	31 25
All	All	467/542 (86%)	450 (96%)	17 (4%)	42 39

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	779	LYS
1	A	780	LYS
1	A	804	ASN
1	A	889	MET
1	A	897	ASP
1	A	954	GLU
1	B	635	GLU
1	B	651	ASN
1	B	793	ASN
1	B	817	ARG
1	B	837	LYS
1	B	903	ASN
1	B	947	ASP
1	B	950	LYS

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Mol	Chain	Res	Type
1	B	956	LYS
1	B	960	LEU
1	B	974	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	618	ASN
1	A	652	HIS
1	A	787	GLN
1	A	807	GLN
1	A	840	ASN
1	A	930	ASN
1	A	964	HIS
1	A	977	ASN
1	B	612	GLN
1	B	618	ASN
1	B	652	HIS
1	B	787	GLN
1	B	793	ASN
1	B	833	HIS
1	B	840	ASN
1	B	903	ASN
1	B	964	HIS
1	B	977	ASN

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 (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
3	ANP	A	303	2	27,33,33	1.51	5 (18%)	30,52,52	2.74	5 (16%)
3	ANP	B	304	2	27,33,33	1.47	3 (11%)	30,52,52	2.80	5 (16%)

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
3	ANP	A	303	2	-	0/12/38/38	0/3/3/3
3	ANP	B	304	2	-	0/12/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	303	ANP	PA-O1A	-2.13	1.43	1.51
3	B	304	ANP	PG-O1G	2.44	1.48	1.46
3	A	303	ANP	PB-O1B	2.66	1.49	1.46
3	A	303	ANP	PG-O1G	2.79	1.49	1.46
3	A	303	ANP	C2-N1	3.49	1.40	1.33
3	B	304	ANP	C2-N1	3.72	1.41	1.33
3	A	303	ANP	C2-N3	4.34	1.39	1.32
3	B	304	ANP	C2-N3	4.50	1.40	1.32

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	303	ANP	N3-C2-N1	-13.11	118.86	128.89
3	B	304	ANP	N3-C2-N1	-12.93	119.00	128.89
3	B	304	ANP	C2'-C1'-N9	-4.80	106.95	114.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	303	ANP	C2'-C1'-N9	-4.04	108.13	114.29
3	A	303	ANP	PA-O3A-PB	-2.15	125.46	132.67
3	B	304	ANP	O2G-PG-O1G	-2.08	107.95	113.49
3	B	304	ANP	O1G-PG-N3B	-2.08	108.71	111.90
3	A	303	ANP	C1'-N9-C4	-2.06	123.83	126.94
3	A	303	ANP	O4'-C1'-N9	2.29	112.90	108.10
3	B	304	ANP	O4'-C1'-N9	3.01	114.40	108.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	304	ANP	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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	271/303 (89%)	0.51	27 (9%)	9	10	23, 42, 75, 101	2 (0%)
1	B	249/303 (82%)	1.04	46 (18%)	2	2	27, 59, 92, 104	0
All	All	520/606 (85%)	0.76	73 (14%)	4	4	23, 51, 90, 104	2 (0%)

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	896	LEU	12.2
1	A	899	THR	7.4
1	B	983	VAL	6.9
1	B	886	GLY	6.9
1	B	808	GLN	5.9
1	B	609	ALA	5.5
1	B	610	PHE	5.3
1	A	779	LYS	5.1
1	B	901	HIS	5.1
1	B	602	ILE	5.0
1	B	938	VAL	4.7
1	B	605	LEU	4.7
1	B	893	THR	4.6
1	B	887	THR	4.6
1	B	980	TRP	4.5
1	A	994	LEU	4.5
1	B	902	TYR	4.3
1	A	901	HIS	3.9
1	A	990	ILE	3.9
1	A	898	GLY	3.9
1	A	780	LYS	3.8
1	A	861	HIS	3.8
1	B	895	VAL	3.8
1	B	942	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	809	ARG	3.5
1	B	962	ILE	3.5
1	B	940	ILE	3.5
1	B	967	ASN	3.4
1	A	862	ARG	3.3
1	B	805	LEU	3.3
1	A	897	ASP	3.2
1	A	926	MET	3.2
1	B	960	LEU	3.2
1	A	986	GLN	3.2
1	B	939	SER	3.1
1	A	650	LEU	3.0
1	A	647	LEU	3.0
1	A	836	LEU	2.9
1	B	966	PRO	2.9
1	A	859	ASN	2.9
1	B	780	LYS	2.9
1	A	949	ASN	2.9
1	A	989	VAL	2.8
1	B	603	ALA	2.8
1	B	810	ASP	2.6
1	B	934	LYS	2.6
1	B	772	VAL	2.6
1	B	968	LYS	2.6
1	B	845	GLU	2.5
1	B	846	SER	2.5
1	A	900	GLY	2.5
1	B	781	LYS	2.4
1	B	951	MET	2.4
1	A	993	ALA	2.3
1	A	644	VAL	2.3
1	B	792	GLU	2.3
1	B	964	HIS	2.3
1	B	660	ALA	2.3
1	B	604	VAL	2.2
1	A	984	LYS	2.2
1	A	996	SER	2.2
1	A	646	LEU	2.2
1	B	624	TYR	2.2
1	B	888	ALA	2.2
1	B	949	ASN	2.1
1	B	981	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	965	ASP	2.1
1	B	648	ALA	2.1
1	B	909	TYR	2.1
1	A	980	TRP	2.1
1	A	988	GLU	2.1
1	B	658	TYR	2.1
1	A	854	PHE	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^{th} 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
3	ANP	A	303	31/31	0.93	0.11	-0.45	22,52,92,97	0
3	ANP	B	304	31/31	0.90	0.13	-0.49	42,74,110,115	0
2	MG	A	305	1/1	0.52	0.21	-	98,98,98,98	0
2	MG	B	306	1/1	0.88	0.12	-	94,94,94,94	0

6.5 Other polymers (i)

There are no such residues in this entry.