



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 21, 2017 – 01:27 PM EDT

PDB ID : 1UV5
Title : GLYCOGEN SYNTHASE KINASE 3 BETA COMPLEXED WITH 6-BROM
OINDIRUBIN-3'-OXIME
Authors : Dajani, R.; Pearl, L.H.; Roe, S.M.
Deposited on : 2004-01-14
Resolution : 2.80 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029077
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20029077

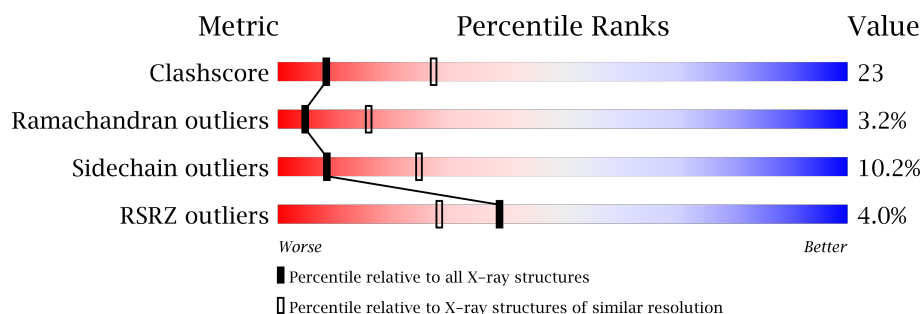
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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 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	350	

2 Entry composition [i](#)

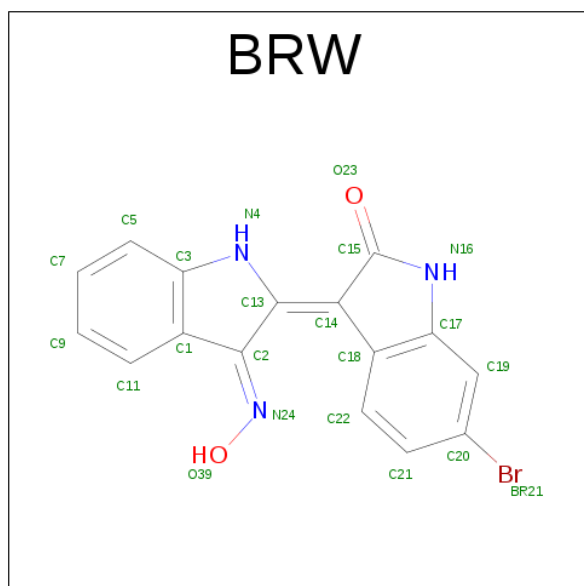
There are 6 unique types of molecules in this entry. The entry contains 2906 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GLYCOGEN SYNTHASE KINASE-3 BETA.

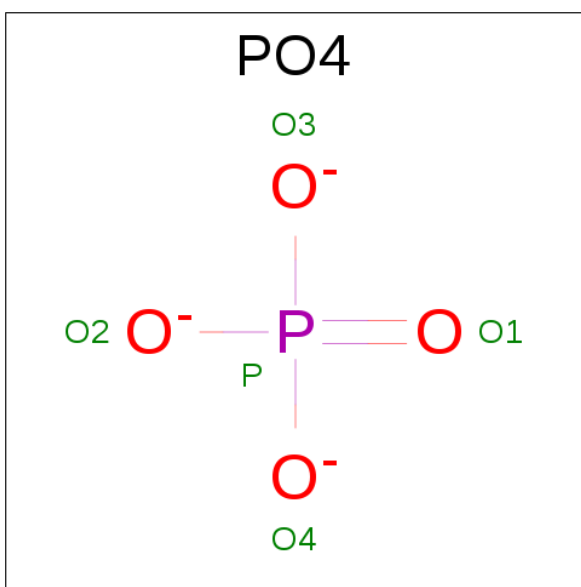
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	1
			2760	1776	471	502	11			

- Molecule 2 is 6-BROMOINDIRUBIN-3'-OXIME (three-letter code: BRW) (formula: $C_{16}H_{10}BrN_3O_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	Br	C	N	O	0	0
			22	1	16	3	2		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Co	0	0
			1	1		

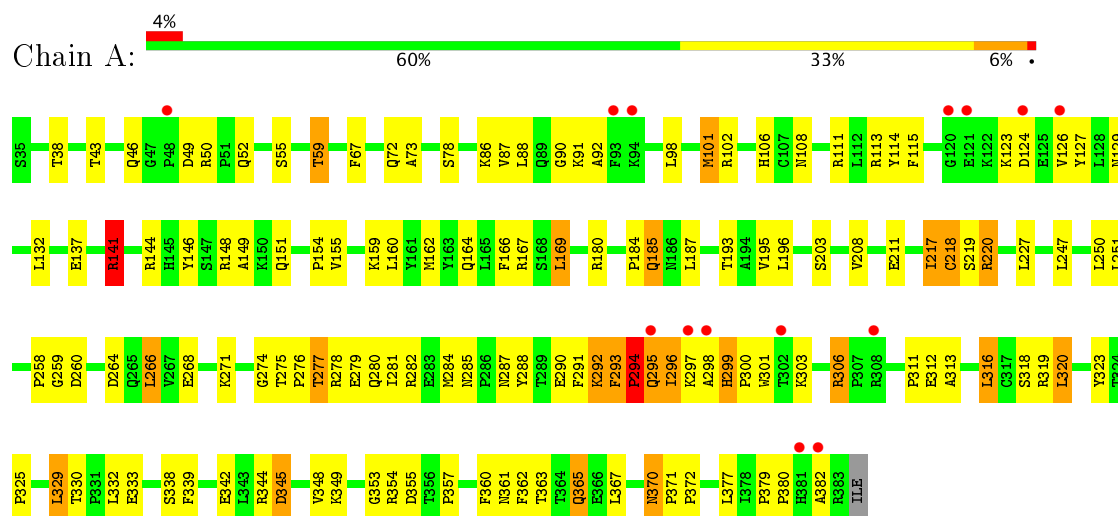
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	112	Total	O	0	0
			112	112		

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 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: GLYCOGEN SYNTHASE KINASE-3 BETA



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	98.33Å 98.33Å 198.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.46 – 2.80 47.87 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (24.46-2.80) 99.5 (47.87-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 2.81Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.193 , 0.226 0.194 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	66.7	Xtriage
Anisotropy	0.702	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 61.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2906	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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: BRW, PO4, CO, CL

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	0.96	1/2831 (0.0%)	0.93	1/3858 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	166	PHE	CE2-CZ	5.04	1.47	1.37

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	141	ARG	NE-CZ-NH2	-6.20	117.20	120.30

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	2760	0	2763	127	0
2	A	22	0	10	1	0
3	A	10	0	0	0	0
4	A	1	0	0	0	0
5	A	1	0	0	0	0
6	A	112	0	0	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2906	0	2773	128	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 23.

All (128) 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:A:275:THR:H	1:A:297:LYS:HG3	1.29	0.96
1:A:106:HIS:HD2	1:A:108:ASN:H	1.22	0.85
1:A:67:PHE:HB2	6:A:2018:HOH:O	1.74	0.85
1:A:300:PRO:HB2	1:A:303:LYS:HB3	1.59	0.85
1:A:293:PHE:CB	1:A:294:PRO:CD	2.57	0.83
1:A:293:PHE:CB	1:A:294:PRO:HD3	2.10	0.81
1:A:293:PHE:HB2	1:A:294:PRO:HD3	1.63	0.79
1:A:275:THR:HB	1:A:297:LYS:HE2	1.65	0.77
1:A:193:THR:O	1:A:357:PRO:HG3	1.87	0.75
1:A:300:PRO:HB2	1:A:303:LYS:CB	2.17	0.74
1:A:292:LYS:O	1:A:293:PHE:HB2	1.88	0.72
1:A:296:ILE:CG2	1:A:299:HIS:CE1	2.74	0.70
1:A:277:THR:O	1:A:281:ILE:HD12	1.93	0.69
1:A:219:SER:HB2	6:A:2053:HOH:O	1.93	0.69
1:A:312:GLU:OE2	1:A:338:SER:HB2	1.92	0.69
1:A:164:GLN:HG2	6:A:2022:HOH:O	1.91	0.68
1:A:195:VAL:HG22	1:A:357:PRO:HB3	1.74	0.68
1:A:208:VAL:HB	1:A:211:GLU:OE1	1.94	0.67
1:A:344:ARG:HG2	1:A:379:PRO:HG3	1.76	0.67
1:A:137:GLU:OE2	1:A:137:GLU:HA	1.95	0.67
1:A:167:ARG:HD3	6:A:2046:HOH:O	1.95	0.67
1:A:306:ARG:HH11	1:A:306:ARG:HB3	1.60	0.67
1:A:316:LEU:HD22	1:A:320:LEU:HD22	1.76	0.67
1:A:185:GLN:H	1:A:185:GLN:NE2	1.93	0.67
1:A:106:HIS:CD2	1:A:108:ASN:H	2.10	0.66
1:A:293:PHE:HB2	1:A:294:PRO:CD	2.22	0.66
1:A:184:PRO:HD2	1:A:185:GLN:HE22	1.61	0.66
1:A:380:PRO:HD2	6:A:2103:HOH:O	1.97	0.64
1:A:296:ILE:HG23	1:A:299:HIS:CE1	2.32	0.64
1:A:260:ASP:HB2	6:A:2084:HOH:O	1.99	0.63
1:A:90:GLY:C	1:A:92:ALA:H	2.03	0.62
1:A:50:ARG:O	6:A:2006:HOH:O	2.16	0.61
1:A:160:LEU:O	1:A:164:GLN:HG3	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:ARG:HB2	6:A:2085:HOH:O	2.00	0.60
1:A:264:ASP:O	1:A:268:GLU:HG2	2.01	0.60
1:A:371:PRO:HB2	1:A:372:PRO:HD3	1.83	0.59
1:A:258:PRO:O	1:A:268:GLU:HG3	2.03	0.58
1:A:292:LYS:O	1:A:294:PRO:HD2	2.04	0.56
1:A:349:LYS:HE2	1:A:355:ASP:OD1	2.05	0.56
1:A:251:LEU:HD11	1:A:313:ALA:HB1	1.87	0.56
1:A:72:GLN:HG2	1:A:73:ALA:N	2.20	0.56
1:A:217:ILE:H	1:A:217:ILE:HD13	1.71	0.56
1:A:295:GLN:HA	1:A:295:GLN:NE2	2.21	0.55
1:A:279:GLU:OE1	1:A:282:ARG:NH1	2.39	0.55
1:A:220:ARG:NH2	6:A:2067:HOH:O	2.39	0.55
2:A:1383:BRW:H22	2:A:1383:BRW:N24	2.21	0.55
1:A:354:ARG:HG2	1:A:355:ASP:N	2.22	0.54
1:A:180:ARG:HB3	1:A:217:ILE:HG13	1.88	0.54
1:A:106:HIS:HD2	1:A:108:ASN:N	1.97	0.54
1:A:293:PHE:HB3	1:A:294:PRO:HD3	1.89	0.54
1:A:259:GLY:N	6:A:2082:HOH:O	2.10	0.54
1:A:319:ARG:HB3	1:A:329:LEU:HD22	1.89	0.54
1:A:88:LEU:HD13	1:A:127:TYR:CE2	2.42	0.54
1:A:296:ILE:HG23	1:A:299:HIS:HE1	1.71	0.53
1:A:49:ASP:O	1:A:49:ASP:OD1	2.26	0.53
1:A:274:GLY:CA	1:A:298:ALA:H	2.22	0.53
1:A:370:ASN:HD22	1:A:372:PRO:HD2	1.73	0.53
1:A:184:PRO:HD2	1:A:185:GLN:NE2	2.24	0.53
1:A:293:PHE:HB3	1:A:294:PRO:CD	2.39	0.52
1:A:98:LEU:O	1:A:102:ARG:HG3	2.10	0.52
1:A:319:ARG:HA	1:A:319:ARG:NE	2.24	0.52
1:A:155:VAL:O	1:A:159:LYS:HG3	2.08	0.52
1:A:195:VAL:CG2	1:A:357:PRO:HB3	2.39	0.52
1:A:88:LEU:HD13	1:A:127:TYR:CZ	2.45	0.51
1:A:271:LYS:O	1:A:299:HIS:HB2	2.10	0.51
1:A:146:TYR:CE2	1:A:154:PRO:HD3	2.45	0.51
1:A:370:ASN:N	1:A:371:PRO:HD3	2.26	0.51
1:A:59:THR:HG22	1:A:59:THR:O	2.10	0.51
1:A:113:ARG:HD3	6:A:2025:HOH:O	2.09	0.51
1:A:149:ALA:HB1	1:A:151:GLN:NE2	2.26	0.50
1:A:217:ILE:O	1:A:218:CYS:CB	2.59	0.50
1:A:164:GLN:CG	6:A:2022:HOH:O	2.54	0.50
1:A:361:ASN:OD1	1:A:361:ASN:N	2.44	0.50
1:A:159:LYS:HD3	1:A:339:PHE:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:GLU:OE2	1:A:338:SER:CB	2.58	0.49
1:A:330:THR:OG1	1:A:333:GLU:HG3	2.12	0.48
1:A:276:PRO:HG3	1:A:323:TYR:CZ	2.47	0.48
1:A:319:ARG:HH11	1:A:319:ARG:HG3	1.79	0.48
1:A:312:GLU:HA	1:A:312:GLU:OE1	2.13	0.48
1:A:296:ILE:HG21	1:A:299:HIS:CE1	2.49	0.48
1:A:266:LEU:HA	1:A:266:LEU:HD12	1.78	0.47
1:A:332:LEU:HB2	6:A:2094:HOH:O	2.14	0.47
1:A:247:LEU:HD22	1:A:316:LEU:HD13	1.96	0.47
1:A:295:GLN:O	1:A:296:ILE:HB	2.15	0.47
1:A:316:LEU:HD22	1:A:320:LEU:CD2	2.43	0.47
1:A:137:GLU:OE2	1:A:141:ARG:HD3	2.14	0.47
1:A:144:ARG:HD2	1:A:148:ARG:NH2	2.30	0.46
1:A:296:ILE:O	1:A:297:LYS:HB2	2.15	0.46
1:A:303:LYS:HG2	1:A:303:LYS:O	2.16	0.46
1:A:319:ARG:HH12	1:A:329:LEU:HD13	1.79	0.46
1:A:185:GLN:N	1:A:185:GLN:NE2	2.62	0.46
1:A:115:PHE:HA	1:A:129:ASN:O	2.16	0.46
1:A:377:LEU:HD23	1:A:377:LEU:HA	1.71	0.46
1:A:50:ARG:HB2	6:A:2006:HOH:O	2.16	0.46
1:A:86:LYS:HE3	1:A:127:TYR:CG	2.51	0.45
1:A:187:LEU:HB3	1:A:196:LEU:HD11	1.97	0.45
1:A:38:THR:O	1:A:55:SER:HA	2.16	0.45
1:A:295:GLN:HA	1:A:295:GLN:HE21	1.81	0.45
1:A:342:GLU:O	1:A:345:ASP:HB2	2.16	0.45
1:A:279:GLU:O	1:A:282:ARG:HB3	2.16	0.45
1:A:300:PRO:HB2	1:A:303:LYS:HB2	1.98	0.45
1:A:294:PRO:O	1:A:295:GLN:HB2	2.18	0.44
1:A:90:GLY:O	1:A:92:ALA:N	2.50	0.43
1:A:332:LEU:HD12	1:A:332:LEU:HA	1.84	0.43
1:A:319:ARG:NH1	1:A:329:LEU:HD13	2.33	0.43
1:A:360:PHE:O	1:A:362:PHE:N	2.49	0.43
1:A:169:LEU:HA	1:A:169:LEU:HD12	1.93	0.43
1:A:274:GLY:HA3	1:A:298:ALA:H	1.84	0.43
1:A:162:MET:HG3	1:A:247:LEU:HD13	2.00	0.42
1:A:285:ASN:O	1:A:288:TYR:HB3	2.19	0.42
1:A:319:ARG:CG	1:A:319:ARG:HH11	2.31	0.42
1:A:323:TYR:O	1:A:325:PRO:HD3	2.20	0.42
1:A:196:LEU:HD23	1:A:196:LEU:C	2.40	0.42
1:A:274:GLY:HA2	1:A:298:ALA:H	1.83	0.42
1:A:101:MET:CE	1:A:101:MET:HA	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:PRO:O	1:A:295:GLN:CB	2.67	0.42
1:A:126:VAL:HG12	1:A:127:TYR:N	2.35	0.42
1:A:111:ARG:NH1	6:A:2024:HOH:O	2.52	0.41
1:A:367:LEU:CD2	1:A:377:LEU:HD12	2.50	0.41
1:A:258:PRO:CA	6:A:2082:HOH:O	2.68	0.41
1:A:319:ARG:CG	1:A:319:ARG:NH1	2.83	0.41
1:A:365:GLN:H	1:A:365:GLN:HG3	1.52	0.41
1:A:275:THR:HA	1:A:276:PRO:HD3	1.88	0.41
1:A:123:LYS:O	1:A:124:ASP:C	2.58	0.41
1:A:280:GLN:O	1:A:284:MET:HG3	2.21	0.41
1:A:43:THR:O	1:A:114:TYR:HA	2.22	0.40
1:A:88:LEU:HD12	1:A:126:VAL:O	2.20	0.40
1:A:291:PHE:O	1:A:292:LYS:O	2.40	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	347/350 (99%)	304 (88%)	32 (9%)	11 (3%)	5 16

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	292	LYS
1	A	293	PHE
1	A	294	PRO
1	A	295	GLN
1	A	296	ILE
1	A	348	VAL
1	A	382	ALA
1	A	220	ARG

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Mol	Chain	Res	Type
1	A	91	LYS
1	A	218	CYS
1	A	353	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	304/310 (98%)	273 (90%)	31 (10%)	8	25

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	52	GLN
1	A	59	THR
1	A	78	SER
1	A	87	VAL
1	A	101	MET
1	A	132	LEU
1	A	141	ARG
1	A	169	LEU
1	A	185	GLN
1	A	203	SER
1	A	217	ILE
1	A	227	LEU
1	A	250	LEU
1	A	266	LEU
1	A	277	THR
1	A	287	ASN
1	A	290	GLU
1	A	294	PRO
1	A	299	HIS
1	A	301	TRP
1	A	306	ARG
1	A	311	PRO

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Mol	Chain	Res	Type
1	A	316	LEU
1	A	318	SER
1	A	320	LEU
1	A	329	LEU
1	A	345	ASP
1	A	363	THR
1	A	365	GLN
1	A	370	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	GLN
1	A	106	HIS
1	A	108	ASN
1	A	185	GLN
1	A	295	GLN
1	A	299	HIS
1	A	370	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 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	BRW	A	1383	-	25,25,25	3.19	13 (52%)	34,37,37	2.35	7 (20%)
3	PO4	A	1384	-	4,4,4	1.41	1 (25%)	6,6,6	0.81	0
3	PO4	A	1387	-	4,4,4	2.20	1 (25%)	6,6,6	0.51	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	BRW	A	1383	-	-	0/5/30/30	0/4/4/4
3	PO4	A	1384	-	-	0/0/0/0	0/0/0/0
3	PO4	A	1387	-	-	0/0/0/0	0/0/0/0

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1383	BRW	C14-C13	-3.22	1.32	1.40
2	A	1383	BRW	O39-N24	-3.01	1.32	1.40
2	A	1383	BRW	C18-C17	-2.82	1.37	1.41
2	A	1383	BRW	C5-C3	-2.11	1.36	1.39
2	A	1383	BRW	C22-C21	-2.05	1.35	1.38
3	A	1384	PO4	P-O1	2.53	1.55	1.50
2	A	1383	BRW	C13-N4	3.30	1.42	1.38
3	A	1387	PO4	P-O1	3.94	1.59	1.50
2	A	1383	BRW	C21-C20	4.14	1.47	1.38
2	A	1383	BRW	C22-C18	4.51	1.47	1.39
2	A	1383	BRW	C1-C3	4.74	1.47	1.41
2	A	1383	BRW	C19-C17	5.57	1.48	1.39
2	A	1383	BRW	C9-C11	5.72	1.49	1.38
2	A	1383	BRW	C7-C5	5.76	1.49	1.38
2	A	1383	BRW	C15-N16	6.59	1.42	1.36

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1383	BRW	C17-N16-C15	-7.88	106.68	111.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1383	BRW	C18-C14-C15	-3.02	103.21	105.27
2	A	1383	BRW	C19-C17-N16	-2.17	125.89	130.60
2	A	1383	BRW	C17-C18-C14	2.75	108.74	106.48
2	A	1383	BRW	C18-C17-N16	3.19	111.98	108.26
2	A	1383	BRW	C14-C15-N16	3.77	109.28	106.84
2	A	1383	BRW	O39-N24-C2	7.18	131.69	113.82

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	A	1383	BRW	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 [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	349/350 (99%)	0.04	14 (4%) 39 28	46, 68, 109, 126	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	124	ASP	4.3
1	A	298	ALA	4.3
1	A	120	GLY	4.0
1	A	121	GLU	3.7
1	A	381	HIS	3.5
1	A	297	LYS	3.4
1	A	295	GLN	3.2
1	A	308	ARG	3.1
1	A	48	PRO	2.6
1	A	93	PHE	2.6
1	A	126	VAL	2.3
1	A	302	THR	2.2
1	A	94	LYS	2.1
1	A	382	ALA	2.1

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
2	BRW	A	1383	22/22	0.97	0.21	1.94	59,66,75,82	1
3	PO4	A	1384	5/5	0.99	0.17	0.10	70,71,71,74	0
3	PO4	A	1387	5/5	0.95	0.17	-0.31	90,94,96,96	0
5	CO	A	1386	1/1	0.99	0.17	-1.66	93,93,93,93	0
4	CL	A	1385	1/1	0.83	0.15	-	87,87,87,87	0

6.5 Other polymers [i](#)

There are no such residues in this entry.