



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:56 PM UTC

PDB ID : 2XGO / pdb_00002xgo
Title : XcOGT in complex with UDP-S-GlcNAc
Authors : Dorfmueller, H.C.; Borodkin, V.S.; Blair, D.E.; Pathak, S.; Navratilova, I.;
van Aalten, D.M.
Deposited on : 2010-06-07
Resolution : 2.60 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

<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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

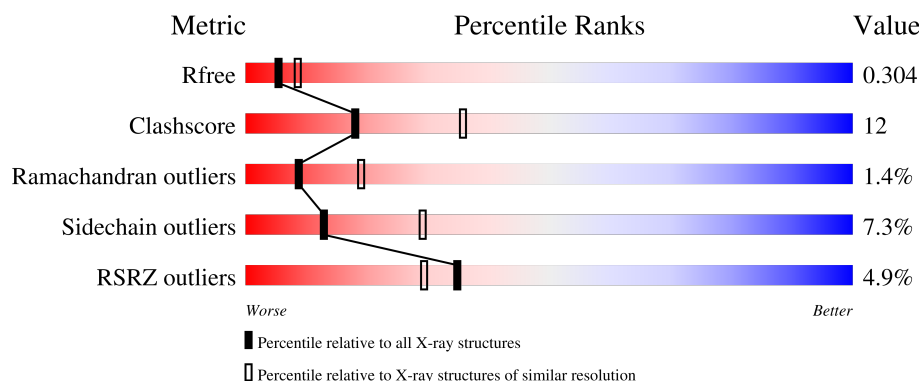
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	568	5% 70% 22% 5% • •
1	B	568	4% 71% 20% • • 5%

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	ZKD	A	1569	X	-	-	-

2 Entry composition [i](#)

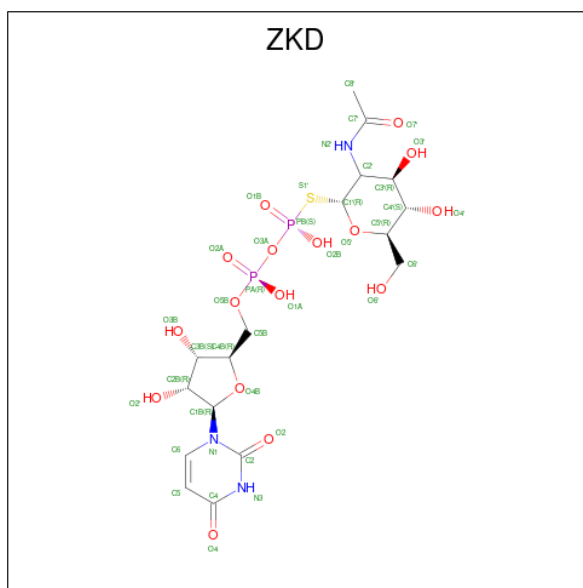
There are 3 unique types of molecules in this entry. The entry contains 8353 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 XCOGT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	548	Total	C	N	O	S	0	0	0
			4171	2635	771	749	16			
1	B	541	Total	C	N	O	S	0	0	0
			4104	2589	760	739	16			

- Molecule 2 is URIDINE-DIPHOSPHATE-1-DEOXY-1-THIO-N-ACETYLGLUCOSAMINE (CCD ID: ZKD) (formula: $C_{17}H_{27}N_3O_{16}P_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P S	0	0
			39	17	3	16	2 1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	23	Total	O	0	0
			23	23		

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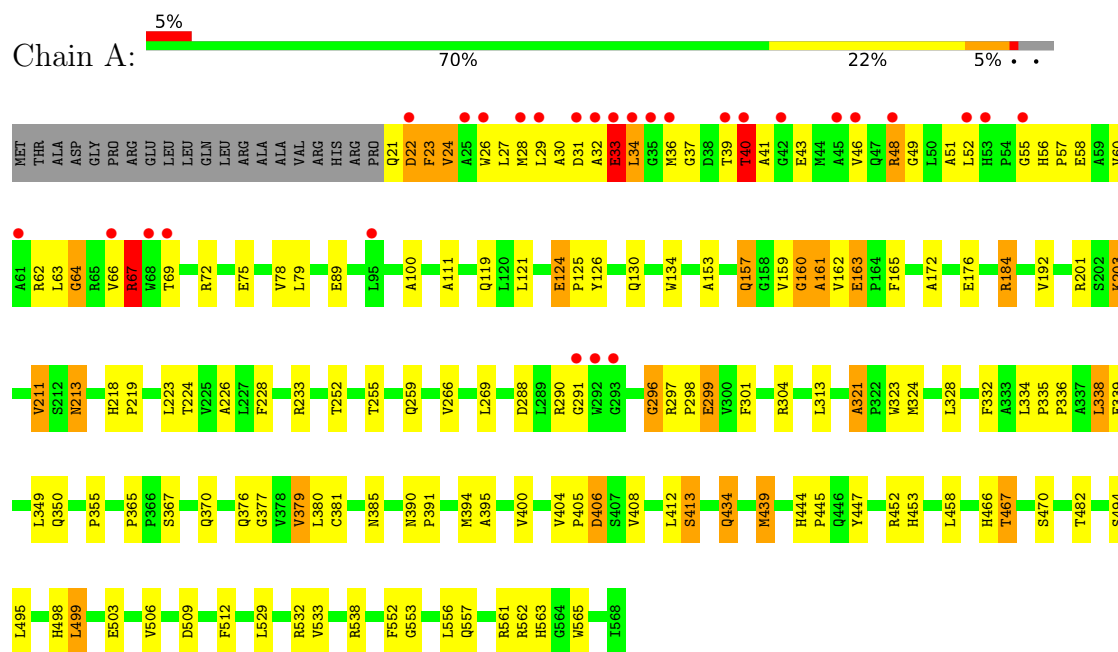
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	16	Total	O	0	0
			16	16		

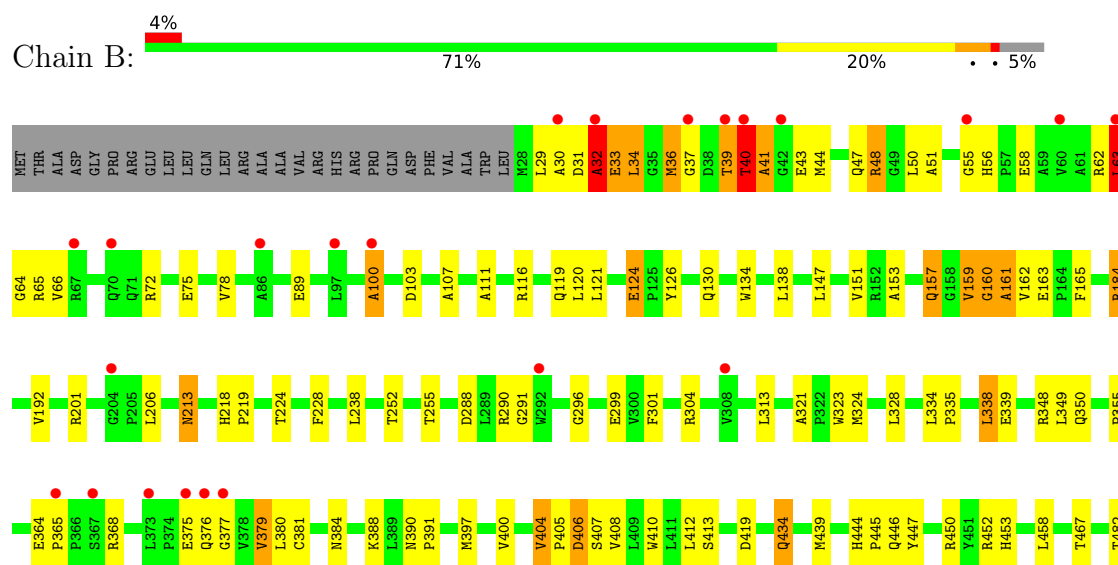
3 Residue-property plots

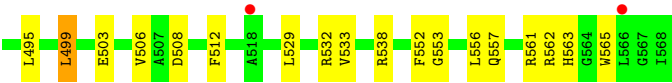
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: XCOGT



• Molecule 1: XCOGT





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.66Å 100.02Å 155.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.84 – 2.60 19.84 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.84-2.60) 91.2 (19.84-2.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 2.59Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.259 , 0.309 0.258 , 0.304	Depositor DCC
R_{free} test set	759 reflections (2.04%)	wwPDB-VP
Wilson B-factor (Å ²)	69.6	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 23.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	8353	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZKD

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	0.88	0/4280	1.07	11/5840 (0.2%)
1	B	0.78	1/4209 (0.0%)	1.11	16/5742 (0.3%)
All	All	0.83	1/8489 (0.0%)	1.09	27/11582 (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	0	5
1	B	0	6
All	All	0	11

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	40	THR	CA-CB	6.07	1.63	1.53

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	33	GLU	N-CA-C	14.05	126.59	111.28
1	B	407	SER	N-CA-C	-9.56	94.74	109.85
1	B	32	ALA	CA-C-N	8.80	132.08	120.28
1	B	32	ALA	C-N-CA	8.80	132.08	120.28
1	B	63	LEU	N-CA-C	6.86	118.45	110.97
1	B	36	MET	CA-C-N	6.74	133.84	121.70
1	B	36	MET	C-N-CA	6.74	133.84	121.70
1	B	321	ALA	CA-C-N	6.45	126.16	119.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	321	ALA	C-N-CA	6.45	126.16	119.64
1	B	192	VAL	N-CA-C	6.34	116.96	108.27
1	B	64	GLY	N-CA-C	-6.20	98.49	113.18
1	A	33	GLU	N-CA-C	-6.11	105.85	113.55
1	A	192	VAL	N-CA-C	6.11	116.64	108.27
1	A	159	VAL	CB-CA-C	-6.05	101.37	111.29
1	B	562	ARG	NE-CZ-NH2	5.78	124.40	119.20
1	B	32	ALA	N-CA-C	-5.77	98.51	110.80
1	B	404	VAL	N-CA-C	5.60	112.65	107.56
1	A	321	ALA	CA-C-N	5.53	125.22	119.64
1	A	321	ALA	C-N-CA	5.53	125.22	119.64
1	B	562	ARG	NE-CZ-NH1	-5.45	116.05	121.50
1	A	163	GLU	CA-C-N	5.26	125.32	119.32
1	A	163	GLU	C-N-CA	5.26	125.32	119.32
1	B	508	ASP	N-CA-C	5.17	114.65	107.73
1	A	439	MET	CA-C-N	-5.14	115.48	120.98
1	A	439	MET	C-N-CA	-5.14	115.48	120.98
1	A	226	ALA	N-CA-C	-5.08	105.83	112.23
1	A	381	CYS	N-CA-C	5.02	116.70	109.07

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	160	GLY	Peptide
1	A	32	ALA	Peptide
1	A	40	THR	Peptide
1	A	406	ASP	Peptide
1	A	63	LEU	Peptide
1	B	160	GLY	Peptide
1	B	32	ALA	Peptide
1	B	39	THR	Peptide
1	B	40	THR	Peptide
1	B	406	ASP	Peptide
1	B	63	LEU	Peptide

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	4171	0	4093	108	0
1	B	4104	0	4032	87	0
2	A	39	0	24	14	0
3	A	23	0	0	5	0
3	B	16	0	0	3	0
All	All	8353	0	8149	200	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 12.

All (200) 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:67:ARG:NH2	3:A:2003:HOH:O	1.98	0.95
1:A:213:ASN:HD22	1:A:213:ASN:H	1.12	0.92
1:A:48:ARG:HH11	1:A:48:ARG:HG3	1.36	0.90
1:B:213:ASN:HD22	1:B:213:ASN:H	1.21	0.84
1:B:377:GLY:O	3:B:2015:HOH:O	1.96	0.83
1:A:467:THR:HG21	2:A:1569:ZKD:H3B	1.61	0.83
1:B:153:ALA:O	1:B:157:GLN:HG2	1.80	0.81
1:B:48:ARG:HG3	1:B:48:ARG:HH11	1.45	0.79
1:A:160:GLY:C	1:A:162:VAL:H	1.91	0.78
2:A:1569:ZKD:H1'	2:A:1569:ZKD:C8'	2.14	0.77
1:B:72:ARG:HB3	1:B:75:GLU:OE1	1.84	0.77
1:A:434:GLN:HE21	1:A:434:GLN:HA	1.50	0.77
1:A:31:ASP:OD1	1:A:62:ARG:HD3	1.86	0.74
2:A:1569:ZKD:H6'	3:A:2021:HOH:O	1.89	0.72
1:A:72:ARG:HB3	1:A:75:GLU:OE1	1.89	0.71
1:A:213:ASN:HD22	1:A:213:ASN:N	1.84	0.70
1:B:159:VAL:HG22	1:B:159:VAL:O	1.93	0.69
1:A:126:TYR:HA	1:A:161:ALA:HB1	1.75	0.69
1:B:288:ASP:HB2	1:B:301:PHE:CZ	2.27	0.68
1:B:368:ARG:NH1	3:B:2015:HOH:O	2.27	0.67
1:B:365:PRO:HD3	1:B:452:ARG:HD2	1.76	0.67
1:B:384:ASN:HB3	1:B:388:LYS:HD2	1.77	0.66
1:A:201:ARG:O	1:A:565:TRP:HD1	1.79	0.66
1:A:160:GLY:C	1:A:162:VAL:N	2.52	0.65
1:B:434:GLN:HE21	1:B:434:GLN:HA	1.59	0.65
1:A:290:ARG:HE	1:A:296:GLY:C	2.04	0.65
1:B:224:THR:HB	1:B:228:PHE:CE2	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:ALA:O	1:A:157:GLN:HG2	1.99	0.63
1:B:290:ARG:HE	1:B:296:GLY:C	2.07	0.62
1:B:379:VAL:HG11	1:B:453:HIS:O	1.98	0.62
1:A:23:PHE:O	1:A:26:TRP:HB2	2.00	0.62
1:B:290:ARG:HB2	1:B:291:GLY:HA2	1.83	0.61
1:B:130:GLN:HA	1:B:130:GLN:OE1	2.01	0.60
2:A:1569:ZKD:H1'	2:A:1569:ZKD:H8'B	1.83	0.60
1:A:130:GLN:HA	1:A:130:GLN:OE1	2.03	0.59
1:B:552:PHE:CE2	1:B:556:LEU:HD11	2.36	0.59
1:B:39:THR:O	1:B:39:THR:OG1	2.15	0.59
1:A:296:GLY:O	1:A:297:ARG:HB2	2.03	0.58
1:A:288:ASP:HB2	1:A:301:PHE:CZ	2.38	0.58
1:A:288:ASP:CG	1:A:290:ARG:HH21	2.12	0.58
1:B:553:GLY:O	1:B:557:GLN:HG3	2.03	0.58
1:B:328:LEU:HD11	1:B:349:LEU:HG	1.85	0.57
1:B:439:MET:HE1	1:B:447:TYR:HD1	1.69	0.57
1:A:48:ARG:HH11	1:A:48:ARG:CG	2.13	0.57
1:B:163:GLU:HG2	1:B:184:ARG:HH21	1.68	0.57
1:B:163:GLU:HG2	1:B:184:ARG:NH2	2.20	0.57
1:B:444:HIS:HB3	1:B:445:PRO:HD3	1.85	0.57
1:A:466:HIS:HB3	3:A:2014:HOH:O	2.06	0.56
1:B:288:ASP:CG	1:B:290:ARG:HH21	2.14	0.56
1:A:467:THR:HB	2:A:1569:ZKD:O2A	2.06	0.56
1:A:224:THR:HB	1:A:228:PHE:CE2	2.41	0.56
1:B:446:GLN:O	1:B:450:ARG:NH2	2.39	0.56
1:B:538:ARG:HB3	1:B:538:ARG:NH2	2.21	0.55
1:B:30:ALA:O	1:B:34:LEU:HB2	2.07	0.55
1:B:153:ALA:O	1:B:157:GLN:CG	2.53	0.55
1:A:33:GLU:CD	1:A:41:ALA:HB1	2.32	0.55
1:A:529:LEU:O	1:A:533:VAL:HG23	2.06	0.54
1:B:213:ASN:HD22	1:B:213:ASN:N	1.95	0.54
1:A:553:GLY:O	1:A:557:GLN:HG3	2.07	0.54
1:A:40:THR:HA	1:A:43:GLU:H	1.73	0.54
1:B:529:LEU:O	1:B:533:VAL:HG23	2.07	0.54
1:A:252:THR:HG21	1:B:255:THR:OG1	2.07	0.54
1:A:379:VAL:HG11	1:A:453:HIS:O	2.08	0.54
1:A:467:THR:CG2	2:A:1569:ZKD:H3B	2.36	0.54
1:B:124:GLU:OE1	1:B:126:TYR:HB3	2.08	0.53
1:A:298:PRO:HD2	1:A:299:GLU:OE1	2.09	0.53
1:A:365:PRO:HD3	1:A:452:ARG:HD2	1.90	0.53
2:A:1569:ZKD:H1'	2:A:1569:ZKD:H8'A	1.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:ARG:O	1:A:51:ALA:HB3	2.08	0.53
1:B:48:ARG:O	1:B:51:ALA:HB3	2.09	0.52
1:B:160:GLY:C	1:B:162:VAL:H	2.17	0.52
1:A:111:ALA:HB2	1:A:134:TRP:HD1	1.75	0.52
1:A:385:ASN:ND2	2:A:1569:ZKD:H8'B	2.25	0.52
1:B:503:GLU:OE2	1:B:532:ARG:NH1	2.37	0.52
1:A:290:ARG:HB2	1:A:291:GLY:HA2	1.90	0.51
1:B:31:ASP:OD1	1:B:62:ARG:HD3	2.09	0.51
1:A:444:HIS:HB3	1:A:445:PRO:HD3	1.92	0.51
1:A:30:ALA:O	1:A:34:LEU:HB2	2.10	0.51
1:A:64:GLY:H	1:A:79:LEU:HD13	1.74	0.51
1:B:377:GLY:HA2	1:B:406:ASP:HB3	1.90	0.51
1:A:163:GLU:HG2	1:A:184:ARG:NH2	2.26	0.51
1:A:385:ASN:HD21	2:A:1569:ZKD:C1'	2.24	0.51
1:B:34:LEU:HD11	1:B:66:VAL:HG22	1.93	0.51
1:A:434:GLN:HA	1:A:434:GLN:NE2	2.22	0.51
1:A:56:HIS:HD2	1:A:58:GLU:H	1.58	0.51
1:A:213:ASN:H	1:A:213:ASN:ND2	1.94	0.51
1:B:48:ARG:HG3	1:B:48:ARG:NH1	2.22	0.50
1:A:288:ASP:OD1	1:A:290:ARG:HB2	2.12	0.50
1:B:147:LEU:O	1:B:151:VAL:HG23	2.11	0.50
1:B:335:PRO:HD2	1:B:338:LEU:HB2	1.93	0.50
1:A:552:PHE:CE2	1:A:556:LEU:HD11	2.45	0.50
1:A:121:LEU:HB3	1:A:124:GLU:HB2	1.93	0.50
1:A:33:GLU:OE2	1:A:41:ALA:HB1	2.12	0.50
1:A:412:LEU:HD11	2:A:1569:ZKD:H5	1.93	0.50
1:A:439:MET:HE1	1:A:447:TYR:HD1	1.75	0.50
1:A:482:THR:HG22	1:A:506:VAL:HG23	1.93	0.50
1:B:379:VAL:CG1	1:B:453:HIS:O	2.59	0.50
1:B:288:ASP:OD1	1:B:290:ARG:HB2	2.12	0.49
1:A:56:HIS:CD2	1:A:58:GLU:H	2.30	0.49
1:B:290:ARG:NE	1:B:296:GLY:O	2.39	0.48
1:A:394:MET:O	1:A:395:ALA:C	2.54	0.48
1:B:201:ARG:O	1:B:565:TRP:HD1	1.96	0.48
1:A:163:GLU:OE1	1:A:165:PHE:HB3	2.13	0.48
1:A:390:ASN:HB2	1:A:391:PRO:HD2	1.96	0.48
1:B:40:THR:HA	1:B:43:GLU:H	1.79	0.47
1:B:34:LEU:O	1:B:37:GLY:HA2	2.14	0.47
1:A:328:LEU:HD11	1:A:349:LEU:HG	1.96	0.47
1:B:381:CYS:HB2	1:B:410:TRP:HB3	1.97	0.47
1:B:412:LEU:CD2	1:B:439:MET:HE2	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1569:ZKD:C6'	3:A:2021:HOH:O	2.54	0.47
1:A:23:PHE:HB2	1:A:52:LEU:HD13	1.96	0.47
1:A:367:SER:H	1:A:370:GLN:NE2	2.12	0.47
1:B:107:ALA:HB1	1:B:138:LEU:HD21	1.97	0.47
1:B:218:HIS:O	1:B:219:PRO:C	2.58	0.47
1:A:203:LYS:HD3	1:A:203:LYS:HA	1.60	0.47
1:A:211:VAL:HG13	1:A:301:PHE:CZ	2.50	0.47
1:B:412:LEU:HD23	1:B:439:MET:HE2	1.96	0.47
1:A:218:HIS:O	1:A:219:PRO:C	2.55	0.46
1:A:223:LEU:O	1:A:355:PRO:HG2	2.16	0.46
2:A:1569:ZKD:S1'	2:A:1569:ZKD:O5B	2.73	0.46
1:B:213:ASN:H	1:B:213:ASN:ND2	2.02	0.46
1:A:323:TRP:CD1	1:A:324:MET:HE2	2.50	0.46
1:B:206:LEU:HB3	1:B:238:LEU:CD2	2.46	0.46
1:A:66:VAL:O	1:A:67:ARG:C	2.57	0.46
1:B:375:GLU:HG2	3:B:2014:HOH:O	2.15	0.46
2:A:1569:ZKD:H4'	3:A:2022:HOH:O	2.15	0.46
1:A:385:ASN:HD21	2:A:1569:ZKD:H1'	1.81	0.46
1:A:259:GLN:HE21	1:A:259:GLN:HB2	1.52	0.45
1:A:538:ARG:HB3	1:A:538:ARG:NH2	2.31	0.45
1:A:39:THR:O	1:A:39:THR:OG1	2.31	0.45
1:B:313:LEU:CD1	1:B:355:PRO:HD2	2.47	0.45
1:B:160:GLY:CA	1:B:162:VAL:H	2.29	0.45
1:A:266:VAL:O	1:A:269:LEU:HB2	2.16	0.45
1:B:111:ALA:HB2	1:B:134:TRP:HD1	1.82	0.45
1:B:159:VAL:O	1:B:159:VAL:CG2	2.63	0.45
1:A:153:ALA:O	1:A:157:GLN:CG	2.65	0.45
1:A:172:ALA:HB1	1:A:176:GLU:HB2	1.98	0.45
1:A:380:LEU:HD22	1:A:458:LEU:HD11	1.98	0.45
1:A:233:ARG:HH11	1:A:233:ARG:HG2	1.82	0.44
1:A:213:ASN:N	1:A:213:ASN:ND2	2.56	0.44
1:B:160:GLY:C	1:B:162:VAL:N	2.76	0.44
1:B:482:THR:HG22	1:B:506:VAL:HG23	1.99	0.44
1:B:364:GLU:OE2	1:B:365:PRO:HD2	2.18	0.44
1:A:23:PHE:CD1	1:A:23:PHE:C	2.93	0.44
1:A:37:GLY:O	1:A:39:THR:HG23	2.18	0.44
1:A:124:GLU:OE1	1:A:126:TYR:HB3	2.18	0.44
1:B:323:TRP:CD1	1:B:324:MET:HE2	2.52	0.44
1:A:290:ARG:NE	1:A:296:GLY:O	2.41	0.44
1:B:495:LEU:O	1:B:499:LEU:HB2	2.18	0.43
1:A:377:GLY:HA2	1:A:406:ASP:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:LEU:O	1:A:499:LEU:HB2	2.18	0.43
1:A:24:VAL:O	1:A:28:MET:HB2	2.18	0.43
1:A:494:SER:O	1:A:498:HIS:ND1	2.46	0.43
1:A:255:THR:OG1	1:B:252:THR:HG21	2.19	0.43
1:A:313:LEU:CD1	1:A:355:PRO:HD2	2.49	0.43
1:B:121:LEU:HB3	1:B:124:GLU:HB2	2.00	0.43
1:A:48:ARG:HG3	1:A:48:ARG:NH1	2.15	0.43
1:A:56:HIS:O	1:A:57:PRO:C	2.62	0.43
1:B:100:ALA:O	1:B:103:ASP:N	2.51	0.43
1:B:506:VAL:HG21	1:B:512:PHE:HA	2.01	0.43
1:A:64:GLY:N	1:A:79:LEU:HD13	2.33	0.42
1:A:163:GLU:HG2	1:A:184:ARG:HH21	1.83	0.42
1:B:48:ARG:HH11	1:B:48:ARG:CG	2.22	0.42
1:B:56:HIS:HD2	1:B:58:GLU:H	1.65	0.42
1:B:62:ARG:C	1:B:65:ARG:H	2.26	0.42
1:B:397:MET:HE2	1:B:458:LEU:O	2.19	0.42
1:B:116:ARG:O	1:B:120:LEU:HG	2.19	0.42
1:B:288:ASP:CG	1:B:290:ARG:NH2	2.77	0.42
1:A:404:VAL:HA	1:A:405:PRO:HD3	1.93	0.42
1:B:44:MET:HE3	1:B:48:ARG:HH12	1.83	0.42
1:A:503:GLU:OE2	1:A:532:ARG:NH1	2.45	0.42
1:A:509:ASP:O	1:A:512:PHE:HB3	2.20	0.42
1:B:160:GLY:HA2	1:B:161:ALA:HB3	2.02	0.42
1:A:34:LEU:HD11	1:A:66:VAL:HG22	2.01	0.42
1:B:390:ASN:HB2	1:B:391:PRO:HD2	2.01	0.42
1:B:434:GLN:HA	1:B:434:GLN:NE2	2.32	0.42
1:A:332:PHE:CD2	1:A:332:PHE:C	2.97	0.42
1:A:367:SER:N	1:A:370:GLN:HE21	2.18	0.42
1:A:335:PRO:HD2	1:A:338:LEU:HB2	2.01	0.42
1:A:413:SER:HB2	1:A:439:MET:O	2.20	0.42
1:A:561:ARG:C	1:A:563:HIS:N	2.77	0.42
1:B:339:GLU:CG	1:B:348:ARG:HH22	2.32	0.41
1:B:561:ARG:C	1:B:563:HIS:N	2.78	0.41
1:A:126:TYR:CA	1:A:161:ALA:HB1	2.47	0.41
1:A:336:PRO:HA	1:A:339:GLU:HG3	2.01	0.41
1:B:50:LEU:HD11	1:B:63:LEU:HD22	2.03	0.41
1:A:46:VAL:O	1:A:49:GLY:N	2.54	0.41
1:B:36:MET:H	1:B:37:GLY:HA2	1.85	0.41
1:B:163:GLU:OE1	1:B:165:PHE:HB3	2.20	0.41
1:A:124:GLU:HA	1:A:125:PRO:HD3	1.86	0.41
1:A:34:LEU:C	1:A:36:MET:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:33:GLU:CD	1:B:41:ALA:HB1	2.46	0.41
1:A:379:VAL:CG1	1:A:453:HIS:O	2.69	0.41
1:B:419:ASP:OD1	1:B:419:ASP:N	2.54	0.41
1:A:27:LEU:H	1:A:27:LEU:HD12	1.87	0.40
1:A:321:ALA:HB1	1:A:323:TRP:CE2	2.57	0.40
1:A:367:SER:H	1:A:370:GLN:HE21	1.69	0.40
1:B:404:VAL:HA	1:B:405:PRO:HD3	1.95	0.40
1:A:48:ARG:CG	1:A:48:ARG:NH1	2.76	0.40
1:A:467:THR:O	1:A:470:SER:HB3	2.21	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	546/568 (96%)	501 (92%)	36 (7%)	9 (2%)	7	16
1	B	539/568 (95%)	495 (92%)	38 (7%)	6 (1%)	11	25
All	All	1085/1136 (96%)	996 (92%)	74 (7%)	15 (1%)	9	19

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	161	ALA
1	B	40	THR
1	B	41	ALA
1	B	161	ALA
1	A	40	THR
1	A	64	GLY
1	B	32	ALA
1	A	55	GLY
1	A	67	ARG

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Mol	Chain	Res	Type
1	B	55	GLY
1	B	100	ALA
1	A	22	ASP
1	A	100	ALA
1	A	296	GLY
1	A	60	VAL

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	413/429 (96%)	380 (92%)	33 (8%)	11	25
1	B	406/429 (95%)	379 (93%)	27 (7%)	15	33
All	All	819/858 (96%)	759 (93%)	60 (7%)	13	29

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	22	ASP
1	A	23	PHE
1	A	24	VAL
1	A	29	LEU
1	A	33	GLU
1	A	34	LEU
1	A	48	ARG
1	A	67	ARG
1	A	69	THR
1	A	78	VAL
1	A	89	GLU
1	A	119	GLN
1	A	124	GLU
1	A	157	GLN
1	A	184	ARG
1	A	203	LYS

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Mol	Chain	Res	Type
1	A	211	VAL
1	A	213	ASN
1	A	299	GLU
1	A	304	ARG
1	A	334	LEU
1	A	338	LEU
1	A	350	GLN
1	A	376	GLN
1	A	379	VAL
1	A	400	VAL
1	A	408	VAL
1	A	413	SER
1	A	434	GLN
1	A	467	THR
1	A	499	LEU
1	A	562	ARG
1	B	29	LEU
1	B	34	LEU
1	B	40	THR
1	B	47	GLN
1	B	48	ARG
1	B	78	VAL
1	B	89	GLU
1	B	119	GLN
1	B	124	GLU
1	B	157	GLN
1	B	159	VAL
1	B	184	ARG
1	B	213	ASN
1	B	299	GLU
1	B	304	ARG
1	B	334	LEU
1	B	338	LEU
1	B	350	GLN
1	B	376	GLN
1	B	379	VAL
1	B	380	LEU
1	B	400	VAL
1	B	408	VAL
1	B	413	SER
1	B	434	GLN
1	B	467	THR

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Mol	Chain	Res	Type
1	B	499	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	47	GLN
1	A	56	HIS
1	A	81	GLN
1	A	99	HIS
1	A	150	GLN
1	A	177	GLN
1	A	213	ASN
1	A	259	GLN
1	A	345	HIS
1	A	370	GLN
1	A	385	ASN
1	A	392	GLN
1	A	429	GLN
1	A	434	GLN
1	B	47	GLN
1	B	56	HIS
1	B	81	GLN
1	B	118	HIS
1	B	150	GLN
1	B	177	GLN
1	B	213	ASN
1	B	239	GLN
1	B	259	GLN
1	B	277	HIS
1	B	280	HIS
1	B	345	HIS
1	B	370	GLN
1	B	392	GLN
1	B	429	GLN
1	B	434	GLN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand 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
2	ZKD	A	1569	-	37,41,41	1.69	7 (18%)	52,62,62	2.52	17 (32%)

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	ZKD	A	1569	-	1/1/12/13	9/21/63/63	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1569	ZKD	C2'-N2'	-5.33	1.37	1.45
2	A	1569	ZKD	C2-N1	3.18	1.43	1.38
2	A	1569	ZKD	C2-N3	3.05	1.43	1.38
2	A	1569	ZKD	PB-O2B	-2.80	1.49	1.56
2	A	1569	ZKD	O5'-C1'	2.76	1.46	1.42
2	A	1569	ZKD	C6-C5	2.75	1.41	1.35
2	A	1569	ZKD	PA-O3A	2.63	1.62	1.59

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1569	ZKD	C1'-C2'-N2'	7.99	125.60	111.07
2	A	1569	ZKD	C3'-C2'-N2'	7.38	124.22	110.62
2	A	1569	ZKD	C4-N3-C2	-5.31	120.03	126.61
2	A	1569	ZKD	C4'-C3'-C2'	-4.60	103.70	110.40
2	A	1569	ZKD	C2B-C1B-N1	4.29	125.18	113.25
2	A	1569	ZKD	O2B-PB-O1B	4.24	119.96	109.86
2	A	1569	ZKD	N3-C2-N1	3.94	120.02	114.89
2	A	1569	ZKD	C2'-N2'-C7'	3.67	131.70	123.11
2	A	1569	ZKD	C5-C4-N3	3.25	119.35	114.80
2	A	1569	ZKD	C5B-C4B-C3B	-3.23	103.59	115.21
2	A	1569	ZKD	O4-C4-C5	-2.62	120.65	125.16
2	A	1569	ZKD	O7'-C7'-C8'	-2.60	117.43	122.05
2	A	1569	ZKD	O5'-C1'-S1'	-2.49	103.59	108.88
2	A	1569	ZKD	C3B-C2B-C1B	-2.43	96.86	101.46
2	A	1569	ZKD	C8'-C7'-N2'	2.35	120.02	116.12
2	A	1569	ZKD	O2-C2-N1	-2.20	119.93	122.80
2	A	1569	ZKD	O2'-C2B-C3B	-2.17	104.86	111.82

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1569	ZKD	C2'

All (9) torsion outliers are listed below:

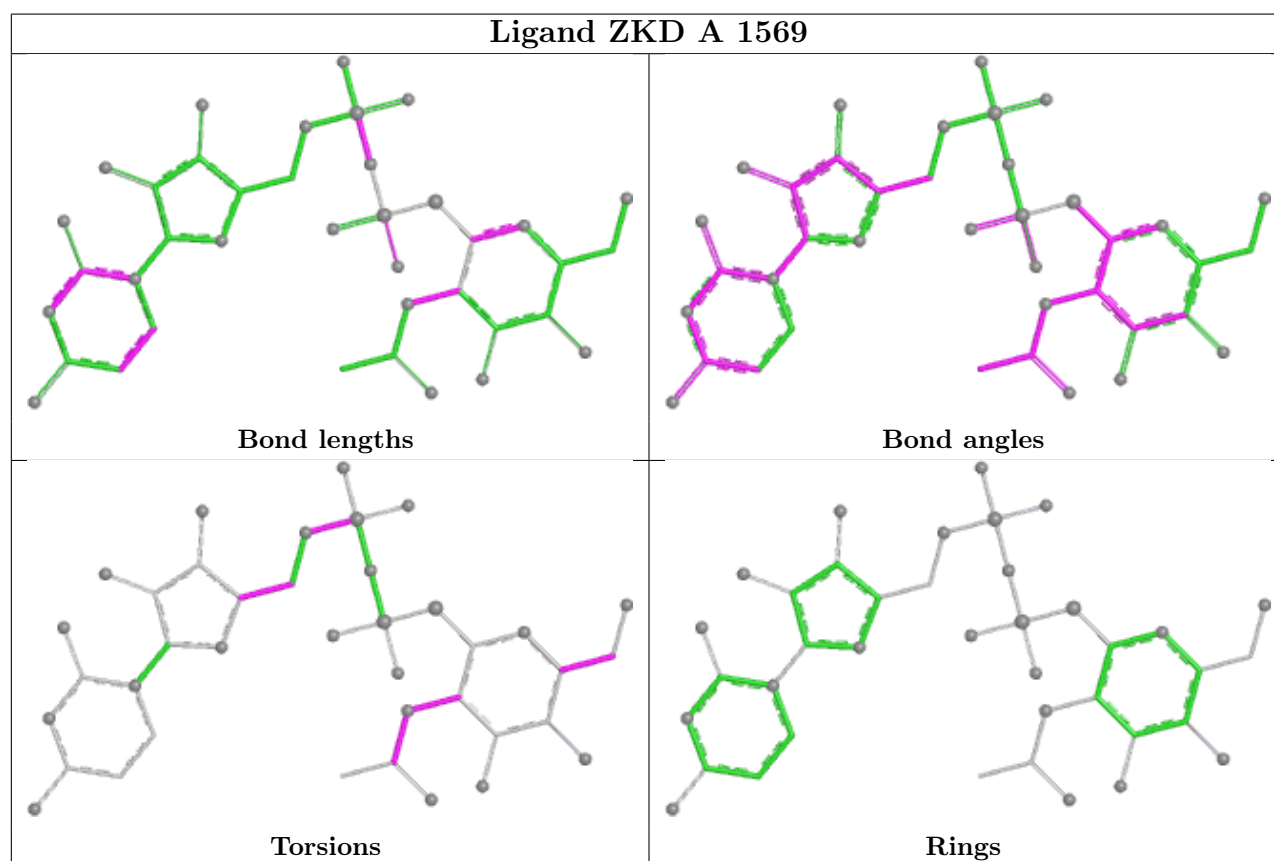
Mol	Chain	Res	Type	Atoms
2	A	1569	ZKD	C5B-O5B-PA-O2A
2	A	1569	ZKD	C5B-O5B-PA-O3A
2	A	1569	ZKD	C1'-C2'-N2'-C7'
2	A	1569	ZKD	O7'-C7'-N2'-C2'
2	A	1569	ZKD	C8'-C7'-N2'-C2'
2	A	1569	ZKD	O4B-C4B-C5B-O5B
2	A	1569	ZKD	C3'-C2'-N2'-C7'
2	A	1569	ZKD	C3B-C4B-C5B-O5B
2	A	1569	ZKD	O5'-C5'-C6'-O6'

There are no ring outliers.

1 monomer is involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1569	ZKD	14	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	548/568 (96%)	0.44	28 (5%) 33 28	44, 49, 54, 65	0
1	B	541/568 (95%)	0.49	25 (4%) 37 32	44, 49, 53, 65	0
All	All	1089/1136 (95%)	0.47	53 (4%) 35 29	44, 49, 54, 65	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	30	ALA	5.9
1	A	32	ALA	4.7
1	A	35	GLY	4.6
1	A	31	ASP	4.3
1	A	293	GLY	4.2
1	A	55	GLY	4.1
1	A	36	MET	3.9
1	A	52	LEU	3.9
1	B	97	LEU	3.8
1	A	42	GLY	3.8
1	B	39	THR	3.6
1	A	61	ALA	3.5
1	A	33	GLU	3.4
1	A	26	TRP	3.2
1	B	63	LEU	3.0
1	B	60	VAL	3.0
1	A	25	ALA	3.0
1	A	22	ASP	3.0
1	B	377	GLY	3.0
1	A	40	THR	2.9
1	B	375	GLU	2.9
1	B	42	GLY	2.8
1	A	69	THR	2.8
1	B	308	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	292	TRP	2.7
1	A	34	LEU	2.6
1	A	66	VAL	2.6
1	A	29	LEU	2.5
1	B	365	PRO	2.5
1	A	28	MET	2.5
1	B	32	ALA	2.5
1	B	40	THR	2.5
1	B	55	GLY	2.4
1	A	45	ALA	2.4
1	B	37	GLY	2.3
1	B	100	ALA	2.3
1	A	39	THR	2.3
1	B	376	GLN	2.3
1	B	70	GLN	2.2
1	B	367	SER	2.2
1	B	292	TRP	2.2
1	B	86	ALA	2.1
1	B	518	ALA	2.1
1	B	67	ARG	2.1
1	A	46	VAL	2.1
1	A	95	LEU	2.1
1	A	68	TRP	2.1
1	B	566	LEU	2.1
1	A	291	GLY	2.1
1	B	204	GLY	2.1
1	A	48	ARG	2.0
1	B	373	LEU	2.0
1	A	53	HIS	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](#)

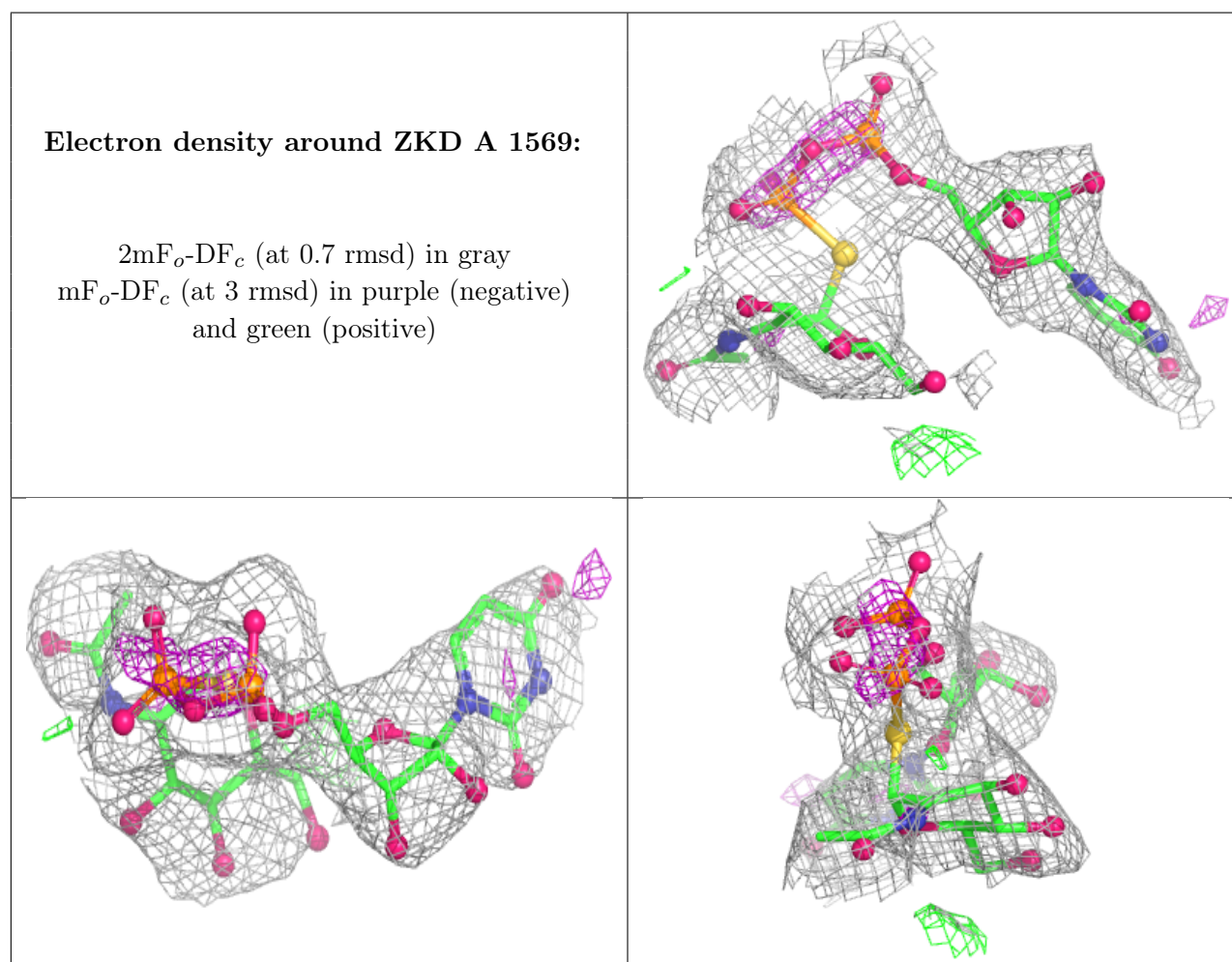
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
2	ZKD	A	1569	39/39	0.82	0.10	34,48,57,61	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.