



Full wwPDB X-ray Structure Validation Report ⓘ

May 7, 2026 – 09:53 AM EDT

PDB ID : 5A4L / pdb_00005a4l
Title : DYRK1A IN COMPLEX WITH FLUORO BENZOTHAZOLE FRAGMENT
Authors : Rothweiler, U.
Deposited on : 2015-06-10
Resolution : 2.73 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
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

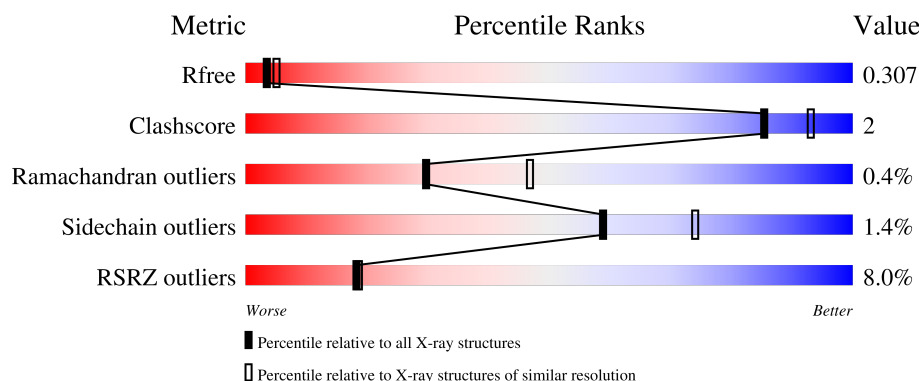
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

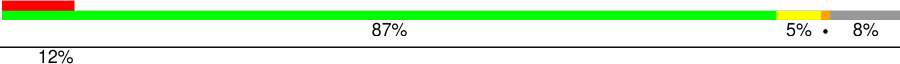
The reported resolution of this entry is 2.73 Å.

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	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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	368	
1	B	368	
1	C	368	
1	D	368	

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	ZC3	A	1481[A]	-	X	-	-
2	ZC3	A	1481[B]	-	X	-	-
2	ZC3	B	1481	-	X	-	-
2	ZC3	D	1480	-	X	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11309 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.

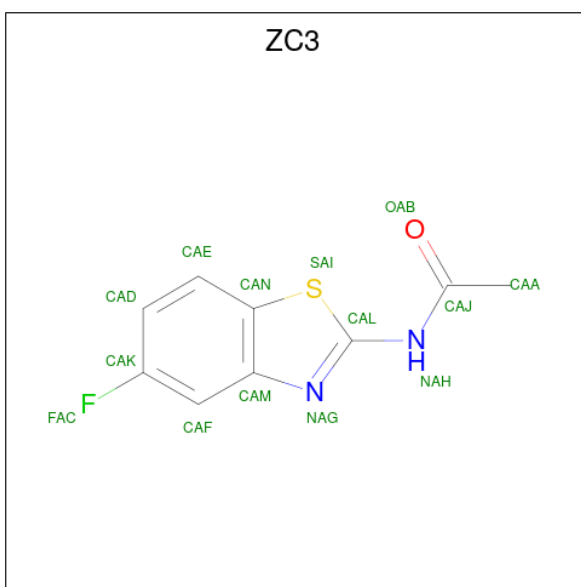
- Molecule 1 is a protein called DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION-REGULATED KINASE 1A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	P	S	0	0	0
			2790	1795	476	501	1	17			
1	B	340	Total	C	N	O	P	S	0	0	0
			2761	1777	471	495	1	17			
1	C	333	Total	C	N	O	P	S	0	0	0
			2678	1724	452	484	1	17			
1	D	335	Total	C	N	O	P	S	0	0	0
			2732	1763	460	491	1	17			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	123	GLY	-	expression tag	UNP Q13627
A	124	ALA	-	expression tag	UNP Q13627
A	125	SER	-	expression tag	UNP Q13627
B	123	GLY	-	expression tag	UNP Q13627
B	124	ALA	-	expression tag	UNP Q13627
B	125	SER	-	expression tag	UNP Q13627
C	123	GLY	-	expression tag	UNP Q13627
C	124	ALA	-	expression tag	UNP Q13627
C	125	SER	-	expression tag	UNP Q13627
D	123	GLY	-	expression tag	UNP Q13627
D	124	ALA	-	expression tag	UNP Q13627
D	125	SER	-	expression tag	UNP Q13627

- Molecule 2 is N-(5-FLUORANYL-1,3-BENZOTHAZOL-2-YL)ETHANAMIDE (CCD ID: ZC3) (formula: C₉H₇FN₂OS).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	1
			28	18	2	4	2	2		
2	B	1	Total	C	F	N	O	S	0	0
			14	9	1	2	1	1		
2	C	1	Total	C	F	N	O	S	0	0
			14	9	1	2	1	1		
2	D	1	Total	C	F	N	O	S	0	0
			14	9	1	2	1	1		

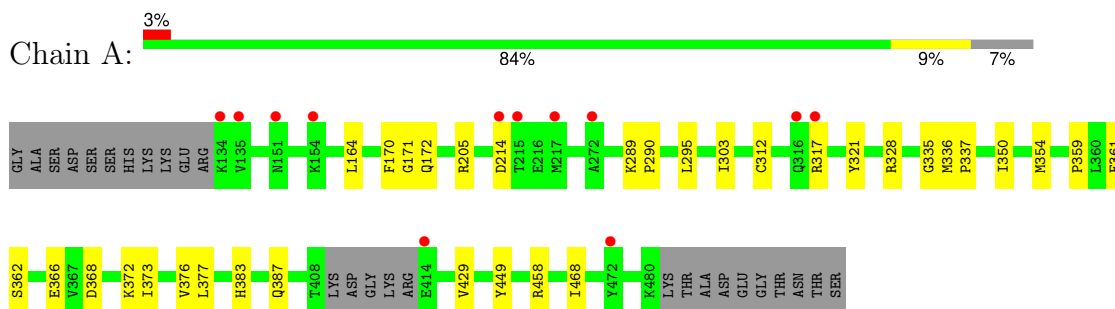
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	68	Total	O	0	0
			68	68		
3	B	64	Total	O	0	0
			64	64		
3	C	75	Total	O	0	0
			75	75		
3	D	71	Total	O	0	0
			71	71		

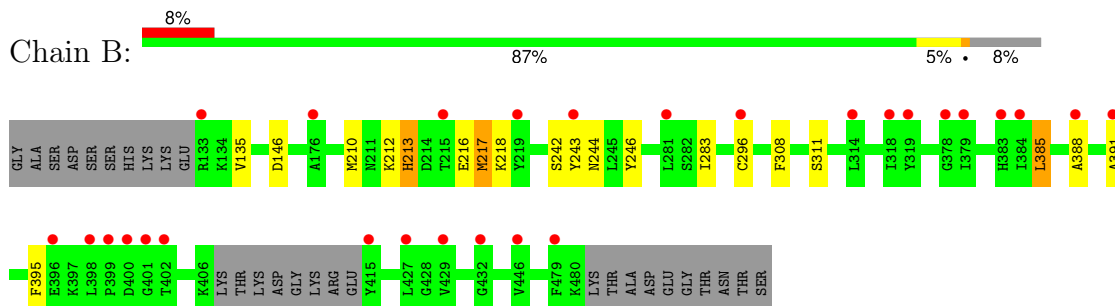
3 Residue-property plots [i](#)

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.

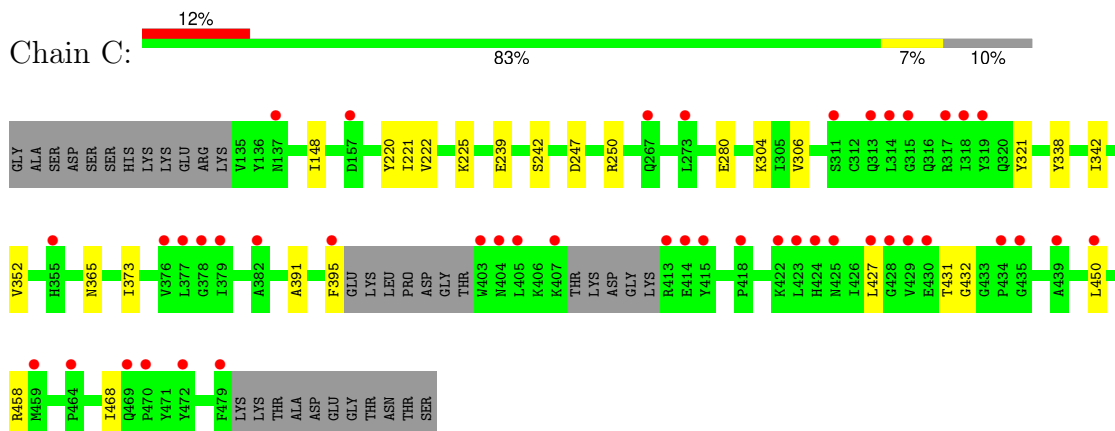
- Molecule 1: DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION- REGULATED KINASE 1A



- Molecule 1: DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION- REGULATED KINASE 1A

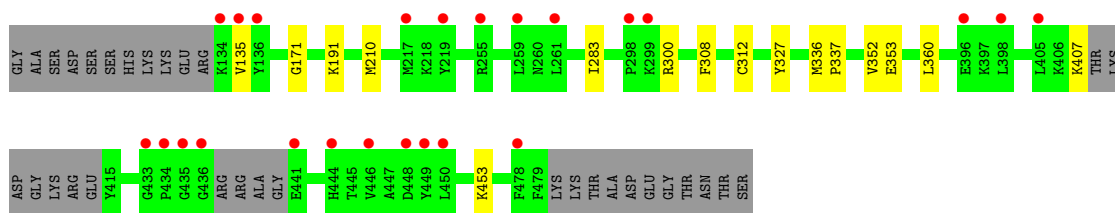


- Molecule 1: DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION- REGULATED KINASE 1A



● Molecule 1: DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION- REGULATED KINASE 1A

Chain D:  7% 87% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.99Å 87.47Å 228.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.08 – 2.73 48.08 – 2.73	Depositor EDS
% Data completeness (in resolution range)	98.4 (48.08-2.73) 99.1 (48.08-2.73)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.221 , 0.267 0.281 , 0.307	Depositor DCC
R_{free} test set	2379 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	48.4	Xtriage
Anisotropy	0.723	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 11.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.029 for k,h,-l	Xtriage
Reported twinning fraction	0.753 for H, K, L 0.247 for K, H, -L	Depositor
Outliers	0 of 47004 reflections	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	11309	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% 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: PTR, ZC3

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	0.49	0/2838	0.74	0/3829
1	B	0.44	0/2808	0.72	0/3789
1	C	0.43	0/2724	0.68	0/3686
1	D	0.43	0/2779	0.68	0/3750
All	All	0.45	0/11149	0.71	0/15054

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 [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	2790	0	2776	16	0
1	B	2761	0	2745	10	0
1	C	2678	0	2599	10	0
1	D	2732	0	2715	7	0
2	A	28	0	0	2	0
2	B	14	0	0	0	0
2	C	14	0	0	1	0
2	D	14	0	0	1	0
3	A	68	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	64	0	0	0	0
3	C	75	0	0	1	0
3	D	71	0	0	1	0
All	All	11309	0	10835	47	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 2.

All (47) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1481[B]:ZC3:CAA	2:A:1481[B]:ZC3:NAG	2.12	1.10
2:A:1481[A]:ZC3:CAA	2:A:1481[A]:ZC3:NAG	2.29	0.94
1:B:210:MET:HE3	1:B:283:ILE:HD13	1.85	0.58
1:B:210:MET:HE1	1:B:308:PHE:CE2	2.42	0.54
1:A:361:PHE:CE1	1:A:373:ILE:HA	2.44	0.52
1:C:365:ASN:ND2	3:C:2057:HOH:O	2.42	0.52
1:C:222:VAL:HA	1:C:304:LYS:HD3	1.92	0.52
1:A:336:MET:HB3	1:A:337:PRO:HD2	1.92	0.51
2:D:1480:ZC3:CAA	2:D:1480:ZC3:NAG	2.74	0.51
1:C:458:ARG:HG3	1:C:468:ILE:HB	1.93	0.50
1:B:212:LYS:O	1:B:213:HIS:HB2	2.13	0.49
1:A:328:ARG:NH1	1:A:366:GLU:OE2	2.39	0.49
1:C:225:LYS:HE3	1:C:239:GLU:HA	1.96	0.48
2:C:1480:ZC3:CAA	2:C:1480:ZC3:NAG	2.76	0.48
1:D:453:LYS:NZ	3:D:2062:HOH:O	2.47	0.47
1:A:317:ARG:NH1	1:A:335:GLY:O	2.48	0.47
1:A:170:PHE:CD1	1:A:171:GLY:N	2.83	0.46
1:B:388:ALA:HB3	1:B:391:ALA:HB2	1.96	0.46
1:D:327:TYR:OH	1:D:353:GLU:OE1	2.21	0.46
1:B:242:SER:OG	1:B:243:TYR:N	2.48	0.46
1:B:212:LYS:O	1:B:213:HIS:CB	2.64	0.45
1:C:220:TYR:C	1:C:221:ILE:HD12	2.41	0.45
1:D:352:VAL:HG11	1:D:360:LEU:HD13	1.98	0.45
1:B:210:MET:HE3	1:B:283:ILE:CD1	2.47	0.45
1:B:385:LEU:HD21	1:B:395:PHE:CD2	2.52	0.44
1:C:338:TYR:HB2	1:C:342:ILE:HG21	2.00	0.44
1:A:350:ILE:O	1:A:354:MET:HG2	2.18	0.43
1:D:171:GLY:HA2	1:D:191:LYS:HG3	2.00	0.43
1:A:295:LEU:HD23	1:A:303:ILE:HG22	2.00	0.43
1:A:368:ASP:O	1:A:372:LYS:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:210:MET:HE2	1:D:283:ILE:HD13	2.00	0.43
1:D:210:MET:HE1	1:D:308:PHE:CE2	2.54	0.42
1:A:376:VAL:HG12	1:A:377:LEU:HD23	2.00	0.42
1:B:244:ASN:OD1	1:B:246:TYR:N	2.53	0.42
1:C:391:ALA:O	1:C:395:PHE:N	2.52	0.42
1:A:164:LEU:HD11	1:A:172:GLN:HB3	2.00	0.42
1:D:336:MET:HB3	1:D:337:PRO:HD2	2.01	0.42
1:A:359:PRO:HB2	1:A:362:SER:HB3	2.01	0.42
1:C:247:ASP:OD1	1:C:250:ARG:NH2	2.52	0.41
1:A:429:VAL:HG22	1:A:449:TYR:HB3	2.02	0.41
1:A:289:LYS:HA	1:A:350:ILE:HD11	2.03	0.41
1:A:383:HIS:O	1:A:387:GLN:HG2	2.21	0.41
1:B:216:GLU:O	1:B:218:LYS:N	2.53	0.41
1:C:431:THR:HG22	1:C:432:GLY:H	1.85	0.41
1:C:352:VAL:HG13	1:C:427:LEU:HD21	2.04	0.40
1:A:290:PRO:HD3	1:A:350:ILE:HG12	2.04	0.40
1:A:458:ARG:HB3	1:A:468:ILE:HB	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	337/368 (92%)	314 (93%)	23 (7%)	0	100	100
1	B	335/368 (91%)	309 (92%)	23 (7%)	3 (1%)	14	26
1	C	326/368 (89%)	301 (92%)	24 (7%)	1 (0%)	36	54
1	D	328/368 (89%)	304 (93%)	23 (7%)	1 (0%)	36	54
All	All	1326/1472 (90%)	1228 (93%)	93 (7%)	5 (0%)	30	47

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	217	MET
1	B	213	HIS
1	C	242	SER
1	D	300	ARG
1	B	311	SER

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	300/324 (93%)	297 (99%)	3 (1%)	68	80
1	B	296/324 (91%)	291 (98%)	5 (2%)	53	71
1	C	282/324 (87%)	277 (98%)	5 (2%)	51	69
1	D	295/324 (91%)	292 (99%)	3 (1%)	68	80
All	All	1173/1296 (90%)	1157 (99%)	16 (1%)	59	74

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	205	ARG
1	A	214	ASP
1	A	312	CYS
1	B	135	VAL
1	B	146	ASP
1	B	217	MET
1	B	296	CYS
1	B	385	LEU
1	C	148	ILE
1	C	280	GLU
1	C	306	VAL
1	C	373	ILE
1	C	450	LEU
1	D	135	VAL
1	D	312	CYS
1	D	407	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	GLN
1	A	425	ASN
1	B	213	HIS
1	B	285	HIS
1	B	469	GLN
1	C	232	ASN
1	C	297	ASN
1	C	365	ASN
1	C	387	GLN
1	D	201	GLN
1	D	251	ASN
1	D	260	ASN
1	D	316	GLN
1	D	469	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	PTR	D	321	1	15,16,17	0.71	0	17,22,24	0.74	0
1	PTR	B	321	1	15,16,17	0.69	0	17,22,24	0.82	0
1	PTR	C	321	1	15,16,17	0.74	0	17,22,24	0.90	1 (5%)
1	PTR	A	321	1	15,16,17	0.74	0	17,22,24	0.91	2 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PTR	D	321	1	-	1/10/11/13	0/1/1/1
1	PTR	B	321	1	-	0/10/11/13	0/1/1/1
1	PTR	C	321	1	-	0/10/11/13	0/1/1/1
1	PTR	A	321	1	-	0/10/11/13	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	321	PTR	O3P-P-O2P	2.07	115.58	107.80
1	A	321	PTR	O3P-P-O2P	2.04	115.44	107.80
1	A	321	PTR	OH-P-O1P	-2.03	102.69	109.48

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	321	PTR	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ZC3	D	1480	-	15,15,15	3.67	8 (53%)	21,21,21	3.40	7 (33%)
2	ZC3	A	1481[B]	-	15,15,15	3.38	7 (46%)	21,21,21	3.09	9 (42%)
2	ZC3	B	1481	-	15,15,15	4.13	8 (53%)	21,21,21	2.94	6 (28%)
2	ZC3	C	1480	-	15,15,15	3.66	6 (40%)	21,21,21	3.22	6 (28%)
2	ZC3	A	1481[A]	-	15,15,15	4.14	7 (46%)	21,21,21	2.90	6 (28%)

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	ZC3	D	1480	-	-	4/4/4/4	0/2/2/2
2	ZC3	A	1481[B]	-	-	4/4/4/4	0/2/2/2
2	ZC3	B	1481	-	-	4/4/4/4	0/2/2/2
2	ZC3	C	1480	-	-	4/4/4/4	0/2/2/2
2	ZC3	A	1481[A]	-	-	4/4/4/4	0/2/2/2

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1481	ZC3	CAL-SAI	-13.23	1.59	1.75
2	A	1481[A]	ZC3	CAL-SAI	-12.90	1.59	1.75
2	C	1480	ZC3	CAL-SAI	-10.03	1.63	1.75
2	A	1481[B]	ZC3	CAL-SAI	-9.96	1.63	1.75
2	D	1480	ZC3	CAL-SAI	-9.89	1.63	1.75
2	C	1480	ZC3	CAN-SAI	-6.70	1.61	1.74
2	D	1480	ZC3	CAN-SAI	-6.60	1.61	1.74
2	A	1481[A]	ZC3	CAN-SAI	-4.97	1.64	1.74
2	B	1481	ZC3	CAN-SAI	-4.10	1.66	1.74
2	A	1481[A]	ZC3	CAE-CAN	-3.96	1.33	1.39
2	A	1481[B]	ZC3	CAF-CAM	-3.92	1.34	1.40
2	A	1481[A]	ZC3	CAF-CAM	-3.89	1.34	1.40
2	D	1480	ZC3	CAE-CAN	-3.82	1.33	1.39
2	D	1480	ZC3	CAF-CAM	-3.82	1.34	1.40
2	B	1481	ZC3	CAF-CAM	-3.77	1.34	1.40
2	A	1481[B]	ZC3	CAE-CAN	-3.71	1.33	1.39
2	A	1481[B]	ZC3	CAN-SAI	-3.69	1.67	1.74
2	B	1481	ZC3	CAE-CAN	-3.67	1.33	1.39
2	C	1480	ZC3	CAE-CAN	-3.60	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1480	ZC3	CAF-CAM	-3.58	1.34	1.40
2	A	1481[B]	ZC3	CAM-CAN	-3.18	1.35	1.40
2	B	1481	ZC3	CAM-CAN	-3.18	1.35	1.40
2	A	1481[A]	ZC3	CAM-CAN	-3.16	1.35	1.40
2	A	1481[A]	ZC3	CAL-NAH	-3.12	1.33	1.38
2	D	1480	ZC3	CAM-CAN	-3.11	1.35	1.40
2	B	1481	ZC3	CAL-NAH	-2.89	1.33	1.38
2	A	1481[B]	ZC3	CAL-NAH	-2.71	1.34	1.38
2	C	1480	ZC3	CAM-CAN	-2.63	1.36	1.40
2	B	1481	ZC3	CAM-NAG	-2.39	1.35	1.39
2	C	1480	ZC3	CAL-NAH	-2.37	1.34	1.38
2	D	1480	ZC3	FAC-CAK	2.12	1.41	1.36
2	A	1481[B]	ZC3	CAM-NAG	-2.10	1.35	1.39
2	A	1481[A]	ZC3	CAM-NAG	-2.10	1.35	1.39
2	D	1480	ZC3	CAL-NAH	-2.10	1.35	1.38
2	D	1480	ZC3	CAM-NAG	-2.07	1.35	1.39
2	B	1481	ZC3	FAC-CAK	-2.01	1.31	1.36

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1480	ZC3	CAN-SAI-CAL	9.96	97.54	88.33
2	C	1480	ZC3	CAN-SAI-CAL	9.45	97.08	88.33
2	B	1481	ZC3	CAN-SAI-CAL	8.79	96.46	88.33
2	A	1481[A]	ZC3	CAN-SAI-CAL	8.62	96.31	88.33
2	D	1480	ZC3	SAI-CAL-NAG	-8.37	107.01	117.06
2	A	1481[B]	ZC3	CAN-SAI-CAL	8.03	95.77	88.33
2	C	1480	ZC3	SAI-CAL-NAG	-7.59	107.94	117.06
2	A	1481[B]	ZC3	SAI-CAL-NAG	-7.22	108.38	117.06
2	B	1481	ZC3	SAI-CAL-NAG	-6.86	108.81	117.06
2	A	1481[A]	ZC3	SAI-CAL-NAG	-6.46	109.30	117.06
2	C	1480	ZC3	NAH-CAL-NAG	5.62	130.47	120.87
2	D	1480	ZC3	NAH-CAL-NAG	5.27	129.88	120.87
2	A	1481[B]	ZC3	CAJ-NAH-CAL	-5.23	115.44	124.05
2	A	1481[A]	ZC3	CAJ-NAH-CAL	-3.85	117.72	124.05
2	D	1480	ZC3	CAD-CAK-CAF	-3.57	118.51	123.23
2	A	1481[B]	ZC3	CAD-CAK-CAF	-3.55	118.54	123.23
2	A	1481[A]	ZC3	CAD-CAK-CAF	-3.51	118.60	123.23
2	B	1481	ZC3	CAD-CAK-CAF	-3.39	118.75	123.23
2	B	1481	ZC3	NAH-CAL-NAG	3.39	126.66	120.87
2	A	1481[A]	ZC3	NAH-CAL-NAG	3.25	126.43	120.87
2	C	1480	ZC3	CAD-CAK-CAF	-3.10	119.14	123.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1481[B]	ZC3	SAI-CAL-NAH	2.82	126.81	121.87
2	C	1480	ZC3	CAA-CAJ-NAH	2.80	119.78	115.27
2	A	1481[B]	ZC3	CAM-NAG-CAL	2.70	115.05	108.66
2	D	1480	ZC3	CAA-CAJ-NAH	2.68	119.60	115.27
2	B	1481	ZC3	CAM-NAG-CAL	2.62	114.86	108.66
2	D	1480	ZC3	CAM-NAG-CAL	2.47	114.52	108.66
2	B	1481	ZC3	CAA-CAJ-NAH	2.31	119.00	115.27
2	A	1481[B]	ZC3	NAH-CAL-NAG	2.30	124.80	120.87
2	A	1481[A]	ZC3	CAM-NAG-CAL	2.22	113.93	108.66
2	A	1481[B]	ZC3	CAM-CAF-CAK	2.21	121.49	118.14
2	D	1480	ZC3	CAM-CAF-CAK	2.20	121.47	118.14
2	C	1480	ZC3	CAM-NAG-CAL	2.16	113.78	108.66
2	A	1481[B]	ZC3	OAB-CAJ-NAH	2.02	125.07	121.90

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1481[A]	ZC3	NAG-CAL-NAH-CAJ
2	A	1481[A]	ZC3	SAI-CAL-NAH-CAJ
2	A	1481[A]	ZC3	OAB-CAJ-NAH-CAL
2	A	1481[A]	ZC3	CAA-CAJ-NAH-CAL
2	A	1481[B]	ZC3	NAG-CAL-NAH-CAJ
2	A	1481[B]	ZC3	SAI-CAL-NAH-CAJ
2	A	1481[B]	ZC3	OAB-CAJ-NAH-CAL
2	A	1481[B]	ZC3	CAA-CAJ-NAH-CAL
2	B	1481	ZC3	NAG-CAL-NAH-CAJ
2	B	1481	ZC3	SAI-CAL-NAH-CAJ
2	B	1481	ZC3	OAB-CAJ-NAH-CAL
2	B	1481	ZC3	CAA-CAJ-NAH-CAL
2	C	1480	ZC3	NAG-CAL-NAH-CAJ
2	C	1480	ZC3	SAI-CAL-NAH-CAJ
2	C	1480	ZC3	OAB-CAJ-NAH-CAL
2	C	1480	ZC3	CAA-CAJ-NAH-CAL
2	D	1480	ZC3	NAG-CAL-NAH-CAJ
2	D	1480	ZC3	SAI-CAL-NAH-CAJ
2	D	1480	ZC3	OAB-CAJ-NAH-CAL
2	D	1480	ZC3	CAA-CAJ-NAH-CAL

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1480	ZC3	1	0
2	A	1481[B]	ZC3	1	0
2	C	1480	ZC3	1	0
2	A	1481[A]	ZC3	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	341/368 (92%)	0.32	12 (3%) 47 45	2, 7, 22, 46	0
1	B	339/368 (92%)	0.82	28 (8%) 17 17	9, 25, 47, 55	0
1	C	332/368 (90%)	0.97	44 (13%) 7 7	10, 26, 54, 63	0
1	D	334/368 (90%)	0.67	24 (7%) 21 21	7, 19, 36, 43	0
All	All	1346/1472 (91%)	0.69	108 (8%) 18 19	2, 21, 47, 63	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	436	GLY	4.1
1	C	314	LEU	4.1
1	C	413	ARG	3.8
1	C	407	LYS	3.7
1	A	215	THR	3.6
1	C	414	GLU	3.5
1	D	435	GLY	3.5
1	C	435	GLY	3.4
1	A	472	TYR	3.3
1	C	313	GLN	3.3
1	C	423	LEU	3.2
1	C	418	PRO	3.2
1	B	388	ALA	3.2
1	B	219	TYR	3.1
1	D	298	PRO	3.1
1	C	429	VAL	3.1
1	B	384	ILE	3.0
1	B	432	GLY	3.0
1	D	434	PRO	2.9
1	C	472	TYR	2.9
1	C	315	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	415	TYR	2.9
1	D	450	LEU	2.9
1	C	395	PHE	2.9
1	B	318	ILE	2.8
1	D	398	LEU	2.8
1	A	151	ASN	2.8
1	B	398	LEU	2.7
1	A	214	ASP	2.7
1	C	377	LEU	2.7
1	C	311	SER	2.7
1	D	217	MET	2.7
1	C	428	GLY	2.7
1	C	424	HIS	2.6
1	C	464	PRO	2.6
1	D	255	ARG	2.6
1	D	405	LEU	2.6
1	C	405	LEU	2.6
1	A	134	LYS	2.5
1	B	133	ARG	2.5
1	C	434	PRO	2.5
1	B	402	THR	2.5
1	D	134	LYS	2.5
1	C	427	LEU	2.5
1	C	319	TYR	2.5
1	B	399	PRO	2.5
1	A	316	GLN	2.5
1	C	404	ASN	2.5
1	B	446	VAL	2.5
1	C	318	ILE	2.4
1	C	157	ASP	2.4
1	B	243	TYR	2.4
1	B	479	PHE	2.4
1	A	317	ARG	2.4
1	C	379	ILE	2.4
1	B	401	GLY	2.4
1	D	219	TYR	2.4
1	B	391	ALA	2.4
1	B	281	LEU	2.4
1	A	154	LYS	2.3
1	B	400	ASP	2.3
1	C	317	ARG	2.3
1	D	261	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	136	TYR	2.3
1	A	217	MET	2.3
1	A	135	VAL	2.3
1	C	450	LEU	2.3
1	D	448	ASP	2.3
1	C	403	TRP	2.3
1	D	446	VAL	2.3
1	B	314	LEU	2.2
1	D	259	LEU	2.2
1	C	415	TYR	2.2
1	D	433	GLY	2.2
1	C	376	VAL	2.2
1	D	299	LYS	2.2
1	B	379	ILE	2.2
1	B	383	HIS	2.2
1	C	439	ALA	2.2
1	C	355	HIS	2.2
1	A	414	GLU	2.2
1	D	396	GLU	2.2
1	D	441	GLU	2.2
1	C	267	GLN	2.2
1	C	459	MET	2.2
1	C	382	ALA	2.1
1	B	296	CYS	2.1
1	C	469	GLN	2.1
1	B	427	LEU	2.1
1	D	135	VAL	2.1
1	A	272	ALA	2.1
1	C	470	PRO	2.1
1	C	137	ASN	2.1
1	B	319	TYR	2.1
1	D	478	PHE	2.1
1	C	425	ASN	2.1
1	C	479	PHE	2.1
1	B	176	ALA	2.0
1	B	396	GLU	2.0
1	C	422	LYS	2.0
1	B	215	THR	2.0
1	C	273	LEU	2.0
1	D	444	HIS	2.0
1	C	430	GLU	2.0
1	B	378	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	378	GLY	2.0
1	B	429	VAL	2.0
1	D	449	TYR	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	PTR	B	321	16/17	0.90	0.10	24,25,26,26	0
1	PTR	C	321	16/17	0.90	0.12	21,21,22,22	0
1	PTR	D	321	16/17	0.92	0.09	11,13,14,14	0
1	PTR	A	321	16/17	0.93	0.11	3,3,3,4	0

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(Å ²)	Q<0.9
2	ZC3	A	1481[A]	14/14	0.53	0.21	9,9,9,9	14
2	ZC3	A	1481[B]	14/14	0.53	0.21	10,10,10,10	14
2	ZC3	B	1481	14/14	0.79	0.15	29,29,30,31	0
2	ZC3	D	1480	14/14	0.85	0.12	16,16,16,17	0
2	ZC3	C	1480	14/14	0.89	0.11	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.