



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 05:53 PM BST

PDB ID : 5A4Q
Title : DYRK1A IN COMPLEX WITH CHLORO BENZOTHAZOLE FRAGMENT
Authors : Rothweiler, U.
Deposited on : 2015-06-11
Resolution : 2.37 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

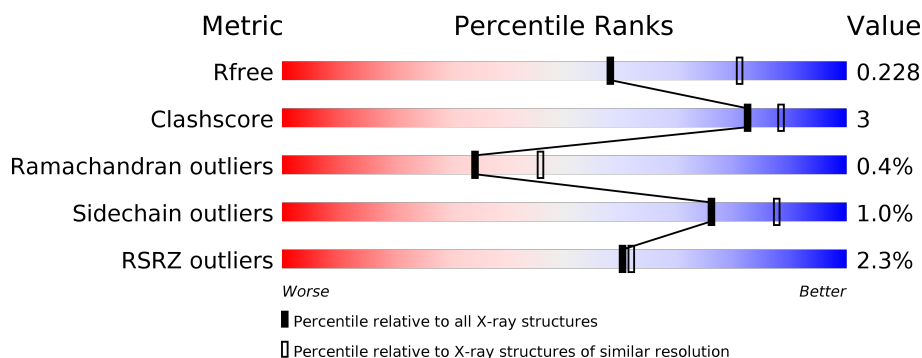
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.37 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}	130704	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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 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	<div> <div style="width: 2%; background-color: red;"></div> <div style="width: 89%; background-color: green;"></div> <div style="width: 7%; background-color: yellow;"></div> <div style="width: 4%; background-color: grey;"></div> <div style="position: absolute; left: 0; top: -10px;">%</div> <div style="position: absolute; left: 44.5%; top: -10px;">89%</div> <div style="position: absolute; left: 93.5%; top: -10px;">7%</div> </div>
1	B	368	<div> <div style="width: 2%; background-color: red;"></div> <div style="width: 84%; background-color: green;"></div> <div style="width: 7%; background-color: yellow;"></div> <div style="width: 9%; background-color: grey;"></div> <div style="position: absolute; left: 0; top: -10px;">%</div> <div style="position: absolute; left: 43%; top: -10px;">84%</div> <div style="position: absolute; left: 85.5%; top: -10px;">7%</div> <div style="position: absolute; left: 94.5%; top: -10px;">9%</div> </div>
1	C	368	<div> <div style="width: 5%; background-color: red;"></div> <div style="width: 79%; background-color: green;"></div> <div style="width: 11%; background-color: yellow;"></div> <div style="width: 10%; background-color: grey;"></div> <div style="position: absolute; left: 0; top: -10px;">5%</div> <div style="position: absolute; left: 42%; top: -10px;">79%</div> <div style="position: absolute; left: 86.5%; top: -10px;">11%</div> <div style="position: absolute; left: 96.5%; top: -10px;">10%</div> </div>
1	D	368	<div> <div style="width: 2%; background-color: red;"></div> <div style="width: 85%; background-color: green;"></div> <div style="width: 6%; background-color: yellow;"></div> <div style="width: 9%; background-color: grey;"></div> <div style="position: absolute; left: 0; top: -10px;">2%</div> <div style="position: absolute; left: 43.5%; top: -10px;">85%</div> <div style="position: absolute; left: 91.5%; top: -10px;">6%</div> <div style="position: absolute; left: 95.5%; top: -10px;">9%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11318 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.

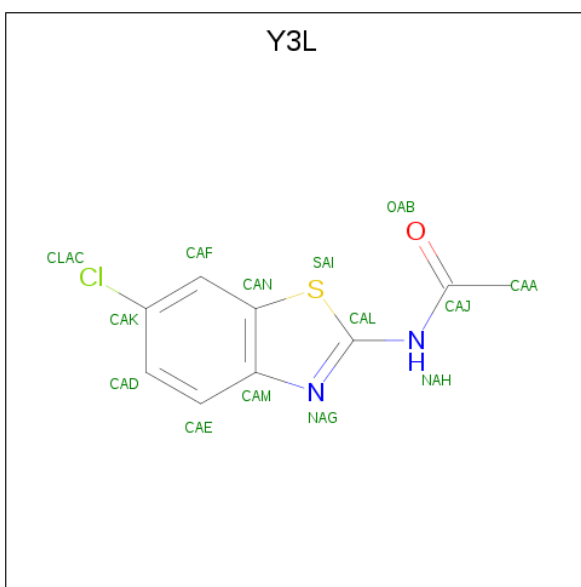
- Molecule 1 is a protein called DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION-REGULATED KINASE 1A.

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	336	Total	C	N	O	P	S	0	0	0
			2727	1756	467	487	1	16			
1	C	333	Total	C	N	O	P	S	0	0	0
			2668	1718	448	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-CHLORANYL-1,3-BENZOTHAZOL-2-YL)ETHANAMIDE (three-letter code: Y3L) (formula: C₉H₇ClN₂OS).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 14	C 9	Cl 1	N 2	O 1	S 1	0	0
2	B	1	Total 14	C 9	Cl 1	N 2	O 1	S 1	0	0
2	C	1	Total 14	C 9	Cl 1	N 2	O 1	S 1	0	0
2	D	1	Total 14	C 9	Cl 1	N 2	O 1	S 1	0	0

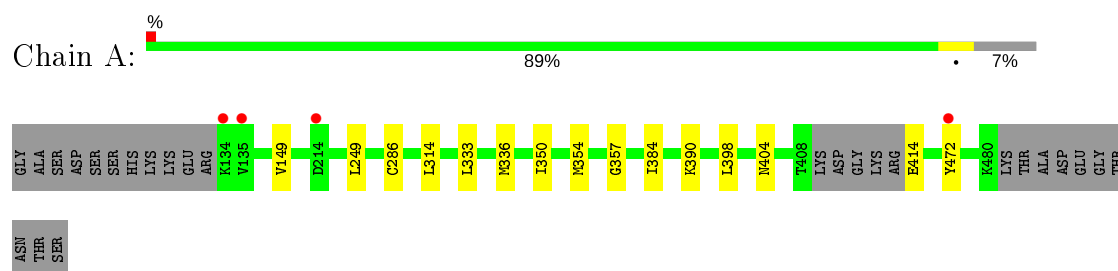
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	127	Total	O	0	0
			127	127		
3	B	71	Total	O	0	0
			71	71		
3	C	60	Total	O	0	0
			60	60		
3	D	87	Total	O	0	0
			87	87		

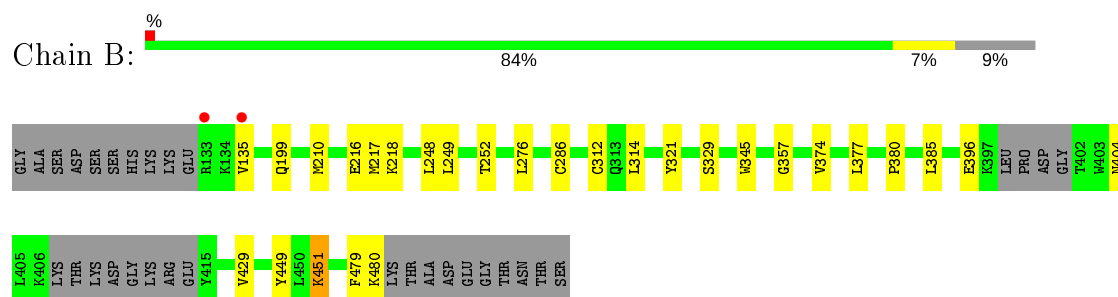
3 Residue-property plots [i](#)

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.

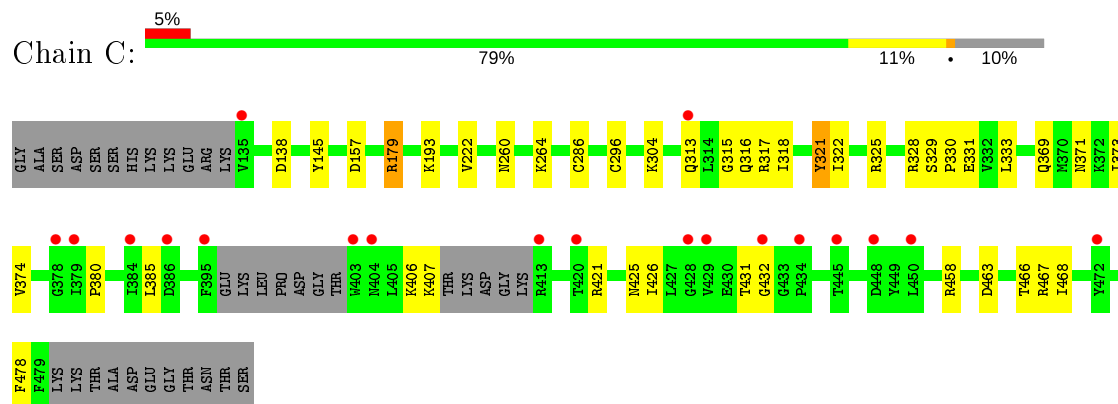
- Molecule 1: DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION-REGULATED KINASE 1A



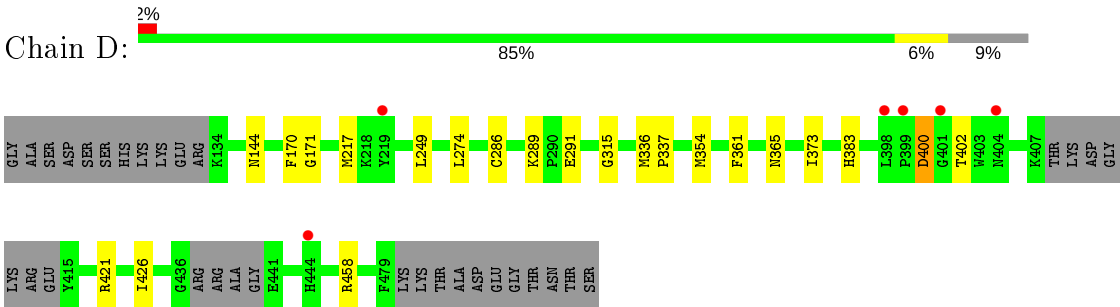
- Molecule 1: DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION-REGULATED KINASE 1A



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.04Å 88.94Å 229.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.45 – 2.37 48.45 – 2.37	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.45-2.37) 99.3 (48.45-2.37)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.37Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.207 , 0.243 0.198 , 0.228	Depositor DCC
R_{free} test set	2101 reflections (2.86%)	wwPDB-VP
Wilson B-factor (Å ²)	45.2	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 31.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.046 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11318	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 3.40% 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, Y3L

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	0.56	0/2838	0.69	0/3829
1	B	0.49	0/2772	0.65	0/3739
1	C	0.49	0/2714	0.68	1/3675 (0.0%)
1	D	0.52	0/2779	0.66	1/3750 (0.0%)
All	All	0.51	0/11103	0.67	2/14993 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	179	ARG	NE-CZ-NH1	5.11	122.85	120.30
1	D	458	ARG	NE-CZ-NH2	-5.08	117.76	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	2790	0	2776	7	0
1	B	2727	0	2708	13	0
1	C	2668	0	2577	21	0
1	D	2732	0	2715	14	0
2	A	14	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	14	0	0	1	0
2	C	14	0	0	1	0
2	D	14	0	0	1	0
3	A	127	0	0	1	0
3	B	71	0	0	0	0
3	C	60	0	0	1	0
3	D	87	0	0	1	0
All	All	11318	0	10776	55	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 3.

All (55) 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:C:296:CYS:SG	3:C:2028:HOH:O	2.47	0.73
2:A:1482:Y3L:CAA	2:A:1482:Y3L:SAI	2.81	0.68
1:A:314:LEU:O	1:D:315:GLY:HA2	1.96	0.64
2:C:1481:Y3L:CAA	2:C:1481:Y3L:SAI	2.88	0.62
2:B:1482:Y3L:CAA	2:B:1482:Y3L:SAI	2.91	0.59
3:A:2022:HOH:O	1:B:199:GLN:NE2	2.35	0.58
1:B:216:GLU:O	1:B:218:LYS:N	2.37	0.58
1:D:400:ASP:N	1:D:400:ASP:OD1	2.37	0.58
1:C:321:PTR:O2P	1:C:325:ARG:NH1	2.38	0.56
1:C:431:THR:HG22	1:C:432:GLY:H	1.71	0.56
1:C:331:GLU:OE2	1:C:467:ARG:NH1	2.40	0.55
1:C:425:ASN:O	1:C:426:ILE:HB	2.08	0.54
1:C:380:PRO:HB2	1:C:385:LEU:HD11	1.92	0.51
1:B:248:LEU:O	1:B:252:THR:HG23	2.12	0.50
1:C:316:GLN:O	1:C:318:ILE:N	2.46	0.49
1:B:479:PHE:O	1:B:480:LYS:HB2	2.13	0.49
1:C:145:TYR:CZ	1:C:193:LYS:HE3	2.47	0.49
2:D:1481:Y3L:SAI	2:D:1481:Y3L:CAA	3.02	0.48
1:C:458:ARG:HG3	1:C:468:ILE:HB	1.95	0.48
1:C:371:ASN:HA	1:C:374:VAL:HG22	1.95	0.48
1:D:421:ARG:HG2	1:D:426:ILE:HD11	1.96	0.48
1:C:260:ASN:O	1:C:264:LYS:HG3	2.14	0.47
1:C:369:GLN:O	1:C:373:ILE:HD12	2.15	0.47
1:D:289:LYS:HE3	1:D:291:GLU:HG2	1.98	0.46
1:C:431:THR:HG22	1:C:432:GLY:N	2.31	0.46
1:C:330:PRO:HA	1:C:333:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:380:PRO:HB2	1:B:385:LEU:HD13	1.99	0.44
1:A:333:LEU:O	1:A:390:LYS:HE3	2.18	0.44
1:B:314:LEU:O	1:C:315:GLY:HA2	2.17	0.43
1:C:138:ASP:OD1	1:D:365:ASN:HB2	2.17	0.43
1:A:350:ILE:O	1:A:354:MET:HG2	2.17	0.43
1:D:336:MET:HB3	1:D:337:PRO:HD2	2.00	0.43
1:B:329:SER:HA	1:B:345:TRP:CD1	2.54	0.43
1:B:210:MET:CE	1:B:276:LEU:HD22	2.49	0.43
1:D:217:MET:SD	1:D:274:LEU:HD23	2.59	0.43
1:D:144:ASN:ND2	3:D:2002:HOH:O	2.51	0.42
1:A:472:TYR:OH	1:D:383:HIS:HB2	2.18	0.42
1:C:222:VAL:HA	1:C:304:LYS:HD3	2.01	0.42
1:C:322:ILE:O	1:C:328:ARG:NH1	2.51	0.42
1:D:249:LEU:HD11	1:D:354:MET:HE2	2.00	0.42
1:D:289:LYS:HG3	1:D:291:GLU:HG2	2.02	0.42
1:D:289:LYS:HE3	1:D:291:GLU:CG	2.49	0.42
1:B:249:LEU:HD22	1:B:357:GLY:HA2	2.00	0.42
1:C:406:LYS:O	1:C:407:LYS:C	2.59	0.41
1:C:157:ASP:O	1:C:179:ARG:NH2	2.53	0.41
1:B:429:VAL:HG22	1:B:449:TYR:HB3	2.03	0.41
1:C:463:ASP:HB3	1:C:466:THR:OG1	2.21	0.41
1:B:396:GLU:N	1:B:404:ASN:O	2.48	0.41
1:D:361:PHE:CE1	1:D:373:ILE:HA	2.56	0.41
1:B:451:LYS:N	1:B:451:LYS:HD3	2.35	0.41
1:D:170:PHE:CD1	1:D:171:GLY:N	2.89	0.41
1:A:336:MET:HE1	1:A:384:ILE:HG23	2.04	0.40
1:A:398:LEU:HD11	1:A:404:ASN:OD1	2.22	0.40
1:A:249:LEU:HD22	1:A:357:GLY:HA2	2.02	0.40
1:B:374:VAL:O	1:B:377:LEU:O	2.40	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%)	323 (96%)	14 (4%)	0	100	100
1	B	329/368 (89%)	317 (96%)	11 (3%)	1 (0%)	41	53
1	C	326/368 (89%)	302 (93%)	20 (6%)	4 (1%)	13	17
1	D	328/368 (89%)	312 (95%)	16 (5%)	0	100	100
All	All	1320/1472 (90%)	1254 (95%)	61 (5%)	5 (0%)	34	46

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	217	MET
1	C	478	PHE
1	C	421	ARG
1	C	313	GLN
1	C	317	ARG

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%)	76	87
1	B	291/324 (90%)	287 (99%)	4 (1%)	67	81
1	C	280/324 (86%)	278 (99%)	2 (1%)	84	92
1	D	295/324 (91%)	292 (99%)	3 (1%)	76	87
All	All	1166/1296 (90%)	1154 (99%)	12 (1%)	76	87

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	149	VAL
1	A	286	CYS
1	A	414	GLU
1	B	135	VAL
1	B	286	CYS
1	B	312	CYS

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Mol	Chain	Res	Type
1	B	451	LYS
1	C	286	CYS
1	C	329	SER
1	D	286	CYS
1	D	400	ASP
1	D	402	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	404	ASN

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	B	321	1	15,16,17	0.83	0	19,22,24	1.09	2 (10%)
1	PTR	A	321	1	15,16,17	0.98	0	19,22,24	0.87	0
1	PTR	D	321	1	15,16,17	0.82	0	19,22,24	1.01	0
1	PTR	C	321	1	15,16,17	0.93	1 (6%)	19,22,24	0.90	1 (5%)

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	B	321	1	-	1/10/11/13	0/1/1/1
1	PTR	A	321	1	-	0/10/11/13	0/1/1/1
1	PTR	D	321	1	-	1/10/11/13	0/1/1/1
1	PTR	C	321	1	-	0/10/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	321	PTR	P-OH	2.06	1.62	1.59

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	321	PTR	O3P-P-O2P	3.05	119.28	107.64
1	C	321	PTR	O3P-P-O2P	2.53	117.32	107.64
1	B	321	PTR	O2P-P-OH	-2.49	97.45	105.24

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	321	PTR	CZ-OH-P-O1P
1	D	321	PTR	CZ-OH-P-O2P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	321	PTR	1	0

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

4 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	Y3L	A	1482	-	12,15,15	1.81	4 (33%)	14,21,21	2.27	4 (28%)
2	Y3L	C	1481	-	12,15,15	1.94	1 (8%)	14,21,21	1.88	4 (28%)
2	Y3L	B	1482	-	12,15,15	1.91	2 (16%)	14,21,21	2.17	4 (28%)
2	Y3L	D	1481	-	12,15,15	2.08	2 (16%)	14,21,21	2.09	5 (35%)

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	Y3L	A	1482	-	-	2/2/4/4	0/2/2/2
2	Y3L	C	1481	-	-	2/2/4/4	0/2/2/2
2	Y3L	B	1482	-	-	2/2/4/4	0/2/2/2
2	Y3L	D	1481	-	-	2/2/4/4	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1481	Y3L	CAE-CAM	-5.02	1.33	1.41
2	D	1481	Y3L	CAE-CAM	-4.48	1.34	1.41
2	A	1482	Y3L	CAE-CAM	-4.17	1.34	1.41
2	B	1482	Y3L	CAE-CAM	-3.92	1.35	1.41
2	D	1481	Y3L	CAK-CLAC	3.53	1.82	1.74
2	B	1482	Y3L	CAK-CLAC	3.06	1.81	1.74
2	A	1482	Y3L	CAL-NAH	-2.41	1.32	1.36
2	A	1482	Y3L	CAM-CAN	-2.12	1.35	1.42
2	A	1482	Y3L	CAF-CAN	-2.02	1.33	1.38

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1482	Y3L	CAA-CAJ-NAH	5.32	122.78	114.98
2	B	1482	Y3L	CAA-CAJ-NAH	4.52	121.62	114.98
2	D	1481	Y3L	CAA-CAJ-NAH	4.23	121.19	114.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1481	Y3L	CAA-CAJ-NAH	3.81	120.58	114.98
2	D	1481	Y3L	CAD-CAK-CAF	-3.57	117.77	121.99
2	B	1482	Y3L	CAD-CAK-CAF	-3.29	118.09	121.99
2	C	1481	Y3L	CAD-CAK-CAF	-3.12	118.30	121.99
2	B	1482	Y3L	CAD-CAK-CLAC	3.07	124.16	119.35
2	A	1482	Y3L	CAD-CAK-CAF	-2.96	118.48	121.99
2	A	1482	Y3L	OAB-CAJ-CAA	-2.92	116.62	122.06
2	D	1481	Y3L	CAN-CAM-NAG	2.59	114.07	108.04
2	B	1482	Y3L	OAB-CAJ-NAH	-2.54	119.71	123.04
2	C	1481	Y3L	CAM-CAN-SAI	-2.28	108.83	111.85
2	A	1482	Y3L	CAN-CAM-NAG	2.27	113.32	108.04
2	C	1481	Y3L	CAN-CAM-NAG	2.25	113.27	108.04
2	D	1481	Y3L	CAM-CAN-SAI	-2.14	109.01	111.85
2	D	1481	Y3L	OAB-CAJ-NAH	-2.13	120.23	123.04

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1482	Y3L	CAA-CAJ-NAH-CAL
2	B	1482	Y3L	CAA-CAJ-NAH-CAL
2	A	1482	Y3L	OAB-CAJ-NAH-CAL
2	B	1482	Y3L	OAB-CAJ-NAH-CAL
2	D	1481	Y3L	CAA-CAJ-NAH-CAL
2	C	1481	Y3L	OAB-CAJ-NAH-CAL
2	C	1481	Y3L	CAA-CAJ-NAH-CAL
2	D	1481	Y3L	OAB-CAJ-NAH-CAL

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1482	Y3L	1	0
2	C	1481	Y3L	1	0
2	B	1482	Y3L	1	0
2	D	1481	Y3L	1	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, 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%)	-0.23	4 (1%) 79 80	23, 35, 58, 94	0
1	B	335/368 (91%)	-0.14	2 (0%) 89 89	29, 47, 83, 112	0
1	C	332/368 (90%)	0.17	19 (5%) 23 26	27, 56, 90, 112	0
1	D	334/368 (90%)	0.04	6 (1%) 68 70	27, 47, 79, 105	0
All	All	1342/1472 (91%)	-0.04	31 (2%) 60 62	23, 46, 84, 112	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	135	VAL	6.5
1	B	133	ARG	6.4
1	D	398	LEU	4.4
1	C	472	TYR	3.9
1	C	450	LEU	3.9
1	C	395	PHE	3.7
1	C	403	TRP	3.6
1	D	219	TYR	3.4
1	C	404	ASN	3.4
1	D	399	PRO	3.4
1	A	134	LYS	3.3
1	C	428	GLY	3.1
1	A	472	TYR	3.1
1	B	135	VAL	3.0
1	C	413	ARG	2.9
1	A	214	ASP	2.8
1	C	384	ILE	2.8
1	D	404	ASN	2.7
1	C	378	GLY	2.5
1	C	386	ASP	2.5
1	C	432	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	444	HIS	2.3
1	A	135	VAL	2.3
1	C	434	PRO	2.3
1	D	401	GLY	2.2
1	C	420	THR	2.2
1	C	429	VAL	2.1
1	C	448	ASP	2.1
1	C	445	THR	2.0
1	C	313	GLN	2.0
1	C	379	ILE	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	C	321	16/17	0.95	0.12	48,51,54,56	0
1	PTR	D	321	16/17	0.96	0.12	33,41,46,46	0
1	PTR	B	321	16/17	0.97	0.11	45,49,50,52	0
1	PTR	A	321	16/17	0.97	0.13	31,32,35,35	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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	Y3L	A	1482	14/14	0.96	0.11	31,34,37,41	0
2	Y3L	C	1481	14/14	0.96	0.10	34,38,41,41	0
2	Y3L	B	1482	14/14	0.97	0.11	37,41,50,54	0
2	Y3L	D	1481	14/14	0.97	0.10	43,48,65,68	0

6.5 Other polymers [i](#)

There are no such residues in this entry.