



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:07 PM GMT

PDB ID : 5AIK
Title : Human DYRK1A in complex with LDN-211898
Authors : Elkins, J.M.; Soundararajan, M.; Muniz, J.R.C.; Cuny, G.; Higgins, J.; Edwards, A.; Bountra, C.; Knapp, S.
Deposited on : 2015-02-15
Resolution : 2.70 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

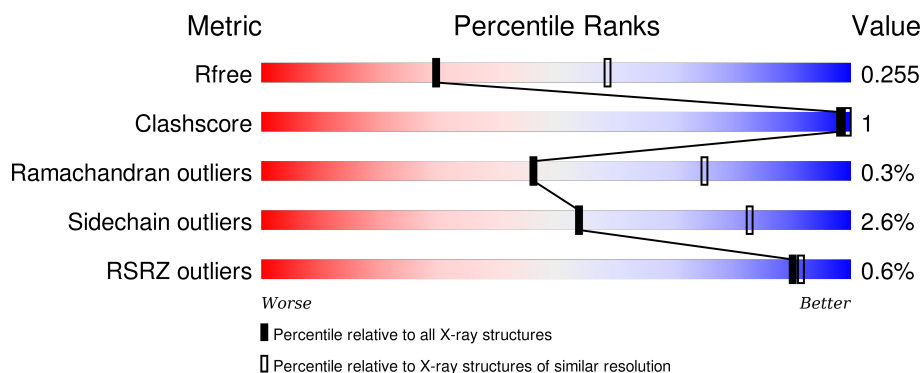
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	382	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>10%</div> </div> </div>
1	B	382	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>10%</div> </div> </div>
1	C	382	<div> <div></div> <div> <div></div> <div>86%</div> <div>10%</div> </div> </div>
1	D	382	<div> <div></div> <div> <div></div> <div>85%</div> <div>10%</div> </div> </div>

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	AWR	D	900	-	-	-	X
3	PO4	D	1482	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11321 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 DYRK1A DUAL-SPECIFICITY TYROSINE-PHOSPHORYLATION REGULATED KINASE 1A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	P	S	0	0	0
			2794	1799	473	504	1	17			
1	B	343	Total	C	N	O	P	S	0	0	0
			2770	1786	469	497	1	17			
1	C	343	Total	C	N	O	P	S	0	0	0
			2777	1789	468	502	1	17			
1	D	343	Total	C	N	O	P	S	0	0	0
			2770	1789	464	499	1	17			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	104	MET	-	EXPRESSION TAG	UNP Q13627
A	105	HIS	-	EXPRESSION TAG	UNP Q13627
A	106	HIS	-	EXPRESSION TAG	UNP Q13627
A	107	HIS	-	EXPRESSION TAG	UNP Q13627
A	108	HIS	-	EXPRESSION TAG	UNP Q13627
A	109	HIS	-	EXPRESSION TAG	UNP Q13627
A	110	HIS	-	EXPRESSION TAG	UNP Q13627
A	111	SER	-	EXPRESSION TAG	UNP Q13627
A	112	SER	-	EXPRESSION TAG	UNP Q13627
A	113	GLY	-	EXPRESSION TAG	UNP Q13627
A	114	VAL	-	EXPRESSION TAG	UNP Q13627
A	115	ASP	-	EXPRESSION TAG	UNP Q13627
A	116	LEU	-	EXPRESSION TAG	UNP Q13627
A	117	GLY	-	EXPRESSION TAG	UNP Q13627
A	118	THR	-	EXPRESSION TAG	UNP Q13627
A	119	GLU	-	EXPRESSION TAG	UNP Q13627
A	120	ASN	-	EXPRESSION TAG	UNP Q13627
A	121	LEU	-	EXPRESSION TAG	UNP Q13627
A	122	TYR	-	EXPRESSION TAG	UNP Q13627
A	123	PHE	-	EXPRESSION TAG	UNP Q13627

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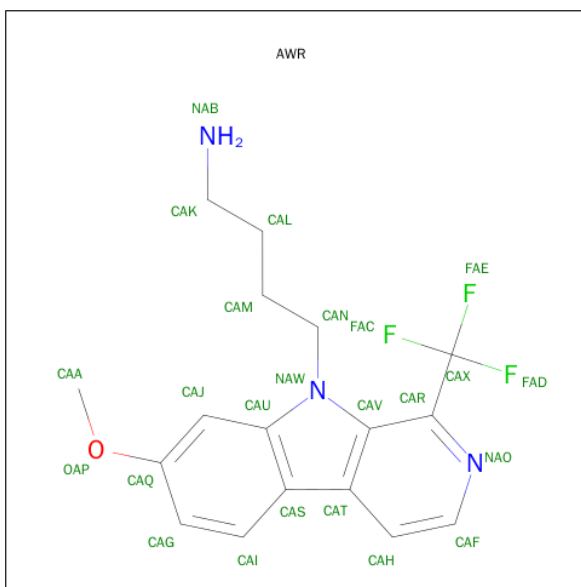
Chain	Residue	Modelled	Actual	Comment	Reference
A	124	GLN	-	EXPRESSION TAG	UNP Q13627
A	125	SER	-	EXPRESSION TAG	UNP Q13627
A	126	MET	-	EXPRESSION TAG	UNP Q13627
A	127	SER	-	EXPRESSION TAG	UNP Q13627
B	104	MET	-	EXPRESSION TAG	UNP Q13627
B	105	HIS	-	EXPRESSION TAG	UNP Q13627
B	106	HIS	-	EXPRESSION TAG	UNP Q13627
B	107	HIS	-	EXPRESSION TAG	UNP Q13627
B	108	HIS	-	EXPRESSION TAG	UNP Q13627
B	109	HIS	-	EXPRESSION TAG	UNP Q13627
B	110	HIS	-	EXPRESSION TAG	UNP Q13627
B	111	SER	-	EXPRESSION TAG	UNP Q13627
B	112	SER	-	EXPRESSION TAG	UNP Q13627
B	113	GLY	-	EXPRESSION TAG	UNP Q13627
B	114	VAL	-	EXPRESSION TAG	UNP Q13627
B	115	ASP	-	EXPRESSION TAG	UNP Q13627
B	116	LEU	-	EXPRESSION TAG	UNP Q13627
B	117	GLY	-	EXPRESSION TAG	UNP Q13627
B	118	THR	-	EXPRESSION TAG	UNP Q13627
B	119	GLU	-	EXPRESSION TAG	UNP Q13627
B	120	ASN	-	EXPRESSION TAG	UNP Q13627
B	121	LEU	-	EXPRESSION TAG	UNP Q13627
B	122	TYR	-	EXPRESSION TAG	UNP Q13627
B	123	PHE	-	EXPRESSION TAG	UNP Q13627
B	124	GLN	-	EXPRESSION TAG	UNP Q13627
B	125	SER	-	EXPRESSION TAG	UNP Q13627
B	126	MET	-	EXPRESSION TAG	UNP Q13627
B	127	SER	-	EXPRESSION TAG	UNP Q13627
C	104	MET	-	EXPRESSION TAG	UNP Q13627
C	105	HIS	-	EXPRESSION TAG	UNP Q13627
C	106	HIS	-	EXPRESSION TAG	UNP Q13627
C	107	HIS	-	EXPRESSION TAG	UNP Q13627
C	108	HIS	-	EXPRESSION TAG	UNP Q13627
C	109	HIS	-	EXPRESSION TAG	UNP Q13627
C	110	HIS	-	EXPRESSION TAG	UNP Q13627
C	111	SER	-	EXPRESSION TAG	UNP Q13627
C	112	SER	-	EXPRESSION TAG	UNP Q13627
C	113	GLY	-	EXPRESSION TAG	UNP Q13627
C	114	VAL	-	EXPRESSION TAG	UNP Q13627
C	115	ASP	-	EXPRESSION TAG	UNP Q13627
C	116	LEU	-	EXPRESSION TAG	UNP Q13627
C	117	GLY	-	EXPRESSION TAG	UNP Q13627

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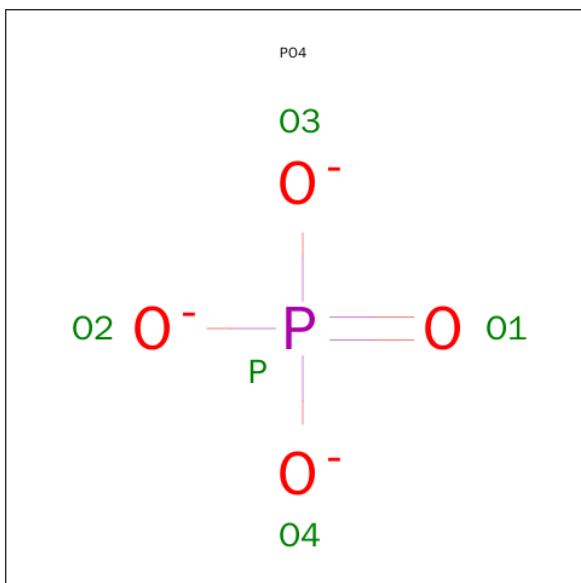
Chain	Residue	Modelled	Actual	Comment	Reference
C	118	THR	-	EXPRESSION TAG	UNP Q13627
C	119	GLU	-	EXPRESSION TAG	UNP Q13627
C	120	ASN	-	EXPRESSION TAG	UNP Q13627
C	121	LEU	-	EXPRESSION TAG	UNP Q13627
C	122	TYR	-	EXPRESSION TAG	UNP Q13627
C	123	PHE	-	EXPRESSION TAG	UNP Q13627
C	124	GLN	-	EXPRESSION TAG	UNP Q13627
C	125	SER	-	EXPRESSION TAG	UNP Q13627
C	126	MET	-	EXPRESSION TAG	UNP Q13627
C	127	SER	-	EXPRESSION TAG	UNP Q13627
D	104	MET	-	EXPRESSION TAG	UNP Q13627
D	105	HIS	-	EXPRESSION TAG	UNP Q13627
D	106	HIS	-	EXPRESSION TAG	UNP Q13627
D	107	HIS	-	EXPRESSION TAG	UNP Q13627
D	108	HIS	-	EXPRESSION TAG	UNP Q13627
D	109	HIS	-	EXPRESSION TAG	UNP Q13627
D	110	HIS	-	EXPRESSION TAG	UNP Q13627
D	111	SER	-	EXPRESSION TAG	UNP Q13627
D	112	SER	-	EXPRESSION TAG	UNP Q13627
D	113	GLY	-	EXPRESSION TAG	UNP Q13627
D	114	VAL	-	EXPRESSION TAG	UNP Q13627
D	115	ASP	-	EXPRESSION TAG	UNP Q13627
D	116	LEU	-	EXPRESSION TAG	UNP Q13627
D	117	GLY	-	EXPRESSION TAG	UNP Q13627
D	118	THR	-	EXPRESSION TAG	UNP Q13627
D	119	GLU	-	EXPRESSION TAG	UNP Q13627
D	120	ASN	-	EXPRESSION TAG	UNP Q13627
D	121	LEU	-	EXPRESSION TAG	UNP Q13627
D	122	TYR	-	EXPRESSION TAG	UNP Q13627
D	123	PHE	-	EXPRESSION TAG	UNP Q13627
D	124	GLN	-	EXPRESSION TAG	UNP Q13627
D	125	SER	-	EXPRESSION TAG	UNP Q13627
D	126	MET	-	EXPRESSION TAG	UNP Q13627
D	127	SER	-	EXPRESSION TAG	UNP Q13627

- Molecule 2 is 4-(7-METHOXY-1-(TRIFLUOROMETHYL)-9H-PYRIDO[3,4-B]INDOL-9-YL)BUTAN-1-AMINE (three-letter code: AWR) (formula: C₁₇H₁₈F₃N₃O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			24	17	3	3	1		
2	B	1	Total	C	F	N	O	0	0
			24	17	3	3	1		
2	C	1	Total	C	F	N	O	0	0
			24	17	3	3	1		
2	D	1	Total	C	F	N	O	0	0
			24	17	3	3	1		

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



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

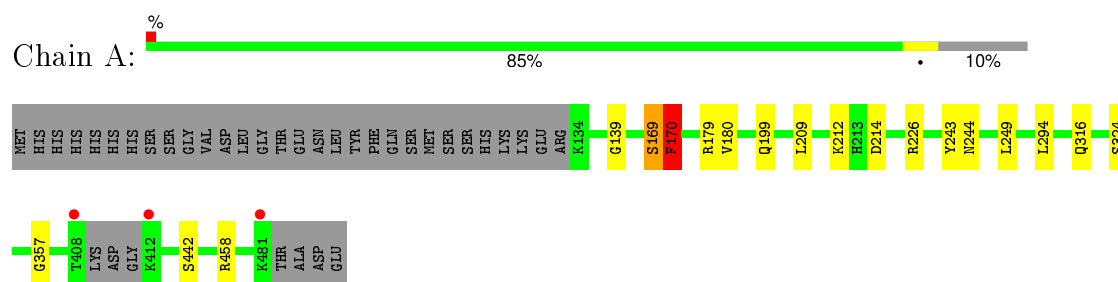
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	20	Total O 20 20	0	0
4	B	23	Total O 23 23	0	0
4	C	13	Total O 13 13	0	0
4	D	8	Total O 8 8	0	0

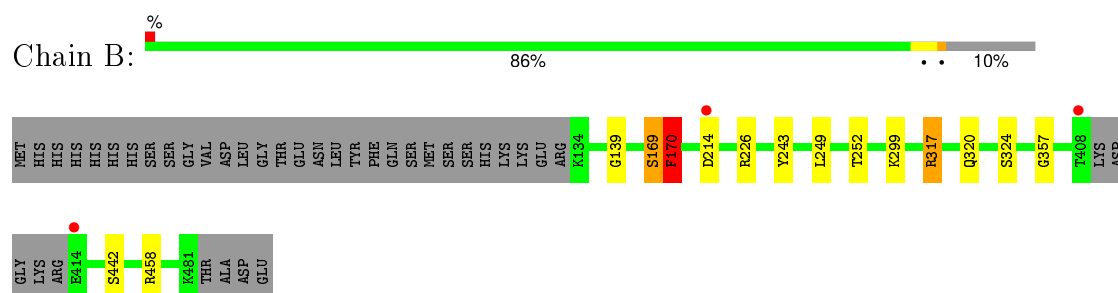
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

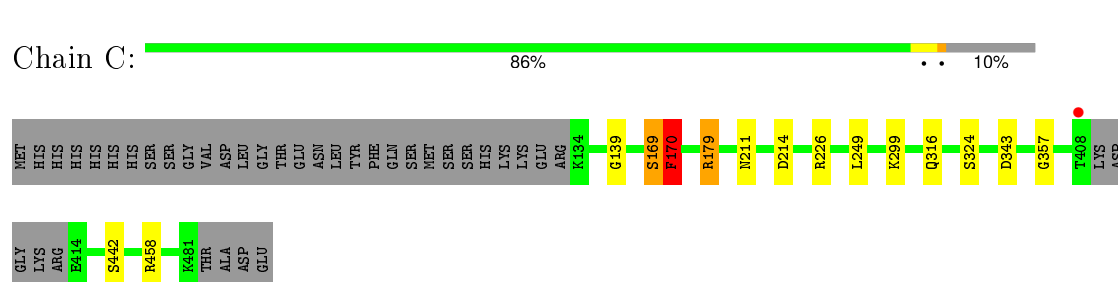
- Molecule 1: DYRK1A DUAL-SPECIFICITY TYROSINE-PHOSPHORYLATION REGULATED KINASE 1A



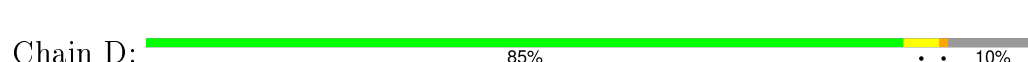
- Molecule 1: DYRK1A DUAL-SPECIFICITY TYROSINE-PHOSPHORYLATION REGULATED KINASE 1A

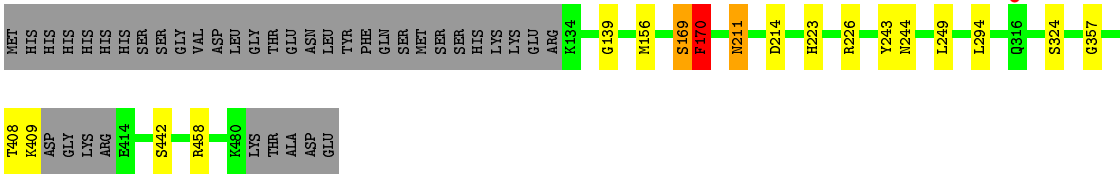


- Molecule 1: DYRK1A DUAL-SPECIFICITY TYROSINE-PHOSPHORYLATION REGULATED KINASE 1A



- Molecule 1: DYRK1A 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	89.95Å 90.89Å 232.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	116.23 – 2.70 35.76 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.4 (116.23-2.70) 98.4 (35.76-2.70)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.227 , 0.252 0.230 , 0.255	Depositor DCC
R_{free} test set	2665 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	38.3	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 0.4	EDS
Estimated twinning fraction	0.068 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	1 of 52364 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	11321	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, AWR, PTR

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	0.59	0/2842	0.76	3/3838 (0.1%)
1	B	0.54	0/2818	0.76	4/3808 (0.1%)
1	C	0.55	0/2825	0.76	5/3816 (0.1%)
1	D	0.52	0/2818	0.74	5/3806 (0.1%)
All	All	0.55	0/11303	0.76	17/15268 (0.1%)

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	2
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	179	ARG	NE-CZ-NH1	6.80	123.70	120.30
1	A	458	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	B	317	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	D	458	ARG	NE-CZ-NH1	6.08	123.34	120.30
1	B	169	SER	C-N-CA	5.89	136.44	121.70
1	A	169	SER	C-N-CA	5.73	136.02	121.70
1	C	169	SER	C-N-CA	5.68	135.90	121.70
1	D	169	SER	C-N-CA	5.63	135.77	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	170	PHE	CB-CA-C	5.50	121.40	110.40
1	B	170	PHE	CB-CA-C	5.45	121.29	110.40
1	D	170	PHE	CB-CA-C	5.44	121.28	110.40
1	B	458	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	C	170	PHE	CB-CA-C	5.28	120.95	110.40
1	C	458	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	C	343	ASP	CB-CG-OD1	5.16	122.94	118.30
1	D	156	MET	CG-SD-CE	5.12	108.39	100.20
1	D	169	SER	CA-C-N	5.04	128.28	117.20

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	139	GLY	Peptide
1	A	169	SER	Peptide
1	B	139	GLY	Peptide
1	B	169	SER	Peptide
1	C	139	GLY	Peptide
1	C	169	SER	Peptide
1	D	139	GLY	Peptide
1	D	169	SER	Peptide

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	2794	0	2752	6	0
1	B	2770	0	2717	5	0
1	C	2777	0	2735	3	0
1	D	2770	0	2728	8	0
2	A	24	0	18	1	0
2	B	24	0	18	0	0
2	C	24	0	18	0	0
2	D	24	0	18	3	0
3	A	10	0	0	0	0
3	B	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	10	0	0	0	0
3	D	15	0	0	0	0
4	A	20	0	0	0	0
4	B	23	0	0	0	0
4	C	13	0	0	0	0
4	D	8	0	0	0	0
All	All	11321	0	11004	23	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 1.

All (23) 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:D:408:THR:HB	1:D:409:LYS:HA	1.57	0.86
2:D:900:AWR:FAD	2:D:900:AWR:HAN2	1.74	0.78
1:A:180:VAL:HG11	1:B:252:THR:HG22	1.69	0.72
1:A:180:VAL:CG1	1:B:252:THR:HG22	2.26	0.66
1:D:408:THR:HB	1:D:409:LYS:CA	2.31	0.57
1:D:408:THR:CB	1:D:409:LYS:HA	2.33	0.54
1:C:170:PHE:C	1:C:170:PHE:CD1	2.80	0.53
1:B:170:PHE:C	1:B:170:PHE:CD1	2.82	0.52
1:B:317:ARG:HD3	1:B:320:GLN:HG3	1.94	0.50
1:D:170:PHE:C	1:D:170:PHE:CD1	2.84	0.50
1:A:209:LEU:HD12	1:A:212:LYS:HE3	1.93	0.49
2:D:900:AWR:HAN2	2:D:900:AWR:CAX	2.41	0.49
1:A:170:PHE:CD1	1:A:170:PHE:C	2.86	0.49
1:B:249:LEU:HD22	1:B:357:GLY:HA2	1.96	0.48
1:D:211:ASN:HD21	1:D:223:HIS:CE1	2.33	0.46
1:D:249:LEU:HD22	1:D:357:GLY:HA2	1.97	0.46
1:C:249:LEU:HD22	1:C:357:GLY:HA2	1.97	0.45
1:A:249:LEU:HD22	1:A:357:GLY:HA2	1.97	0.45
1:D:294:LEU:HD23	2:D:900:AWR:HAA3	2.00	0.44
1:C:211:ASN:HD22	1:C:211:ASN:HA	1.68	0.41
1:D:244:ASN:HA	1:D:294:LEU:HA	2.03	0.41
1:A:244:ASN:HA	1:A:294:LEU:HA	2.03	0.41
2:A:900:AWR:FAD	2:A:900:AWR:HAN2	2.11	0.41

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	340/382 (89%)	327 (96%)	12 (4%)	1 (0%)	46	75
1	B	338/382 (88%)	326 (96%)	11 (3%)	1 (0%)	46	75
1	C	338/382 (88%)	326 (96%)	11 (3%)	1 (0%)	46	75
1	D	338/382 (88%)	325 (96%)	12 (4%)	1 (0%)	46	75
All	All	1354/1528 (89%)	1304 (96%)	46 (3%)	4 (0%)	46	75

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	170	PHE
1	B	170	PHE
1	C	170	PHE
1	D	170	PHE

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	296/339 (87%)	287 (97%)	9 (3%)	48	79
1	B	290/339 (86%)	283 (98%)	7 (2%)	57	85
1	C	295/339 (87%)	287 (97%)	8 (3%)	52	82
1	D	292/339 (86%)	285 (98%)	7 (2%)	57	85
All	All	1173/1356 (86%)	1142 (97%)	31 (3%)	54	83

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

Mol	Chain	Res	Type
1	A	170	PHE
1	A	179	ARG
1	A	199	GLN
1	A	214	ASP
1	A	226	ARG
1	A	243	TYR
1	A	316	GLN
1	A	324	SER
1	A	442	SER
1	B	170	PHE
1	B	214	ASP
1	B	226	ARG
1	B	243	TYR
1	B	299	LYS
1	B	324	SER
1	B	442	SER
1	C	170	PHE
1	C	179	ARG
1	C	214	ASP
1	C	226	ARG
1	C	299	LYS
1	C	316	GLN
1	C	324	SER
1	C	442	SER
1	D	170	PHE
1	D	211	ASN
1	D	214	ASP
1	D	226	ARG
1	D	243	TYR
1	D	324	SER
1	D	442	SER

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

Mol	Chain	Res	Type
1	A	198	ASN
1	A	199	GLN
1	A	201	GLN
1	A	316	GLN
1	B	198	ASN
1	B	201	GLN

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Mol	Chain	Res	Type
1	C	198	ASN
1	C	201	GLN
1	C	211	ASN
1	C	313	GLN
1	D	198	ASN
1	D	201	GLN
1	D	211	ASN
1	D	223	HIS

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	A	321	1	14,16,17	0.76	0	18,22,24	1.14	1 (5%)
1	PTR	B	321	1	14,16,17	0.79	0	18,22,24	0.97	0
1	PTR	C	321	1	14,16,17	0.88	0	18,22,24	1.08	2 (11%)
1	PTR	D	321	1	14,16,17	0.71	0	18,22,24	0.96	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
1	PTR	A	321	1	-	0/9/11/13	0/1/1/1
1	PTR	B	321	1	-	0/9/11/13	0/1/1/1
1	PTR	C	321	1	-	0/9/11/13	0/1/1/1
1	PTR	D	321	1	-	0/9/11/13	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	O-C-CA	-2.05	120.14	125.49
1	C	321	PTR	O2P-P-O1P	2.71	119.31	110.58
1	A	321	PTR	O2P-P-O1P	2.75	119.43	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

14 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	$\# Z > 2$
3	PO4	A	1483	-	4,4,4	0.36	0	6,6,6	0.28	0
3	PO4	A	1484	-	4,4,4	0.46	0	6,6,6	0.28	0
2	AWR	A	900	-	25,26,26	0.81	1 (4%)	29,38,38	1.89	2 (6%)
3	PO4	B	1483	-	4,4,4	0.48	0	6,6,6	0.27	0
3	PO4	B	1484	-	4,4,4	0.36	0	6,6,6	0.27	0
3	PO4	B	1485	-	4,4,4	0.41	0	6,6,6	0.31	0
2	AWR	B	900	-	25,26,26	0.76	1 (4%)	29,38,38	1.29	2 (6%)
3	PO4	C	1483	-	4,4,4	0.41	0	6,6,6	0.28	0
3	PO4	C	1484	-	4,4,4	0.44	0	6,6,6	0.28	0
2	AWR	C	900	-	25,26,26	0.80	2 (8%)	29,38,38	2.17	3 (10%)
3	PO4	D	1482	-	4,4,4	0.40	0	6,6,6	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PO4	D	1483	-	4,4,4	0.47	0	6,6,6	0.27	0
3	PO4	D	1484	-	4,4,4	0.44	0	6,6,6	0.27	0
2	AWR	D	900	-	25,26,26	0.94	3 (12%)	29,38,38	1.55	3 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PO4	A	1483	-	-	0/0/0/0	0/0/0/0
3	PO4	A	1484	-	-	0/0/0/0	0/0/0/0
2	AWR	A	900	-	-	0/13/13/13	0/3/3/3
3	PO4	B	1483	-	-	0/0/0/0	0/0/0/0
3	PO4	B	1484	-	-	0/0/0/0	0/0/0/0
3	PO4	B	1485	-	-	0/0/0/0	0/0/0/0
2	AWR	B	900	-	-	0/13/13/13	0/3/3/3
3	PO4	C	1483	-	-	0/0/0/0	0/0/0/0
3	PO4	C	1484	-	-	0/0/0/0	0/0/0/0
2	AWR	C	900	-	-	0/13/13/13	0/3/3/3
3	PO4	D	1482	-	-	0/0/0/0	0/0/0/0
3	PO4	D	1483	-	-	0/0/0/0	0/0/0/0
3	PO4	D	1484	-	-	0/0/0/0	0/0/0/0
2	AWR	D	900	-	-	0/13/13/13	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	900	AWR	CAJ-CAQ	2.03	1.40	1.37
2	C	900	AWR	CAJ-CAQ	2.04	1.40	1.37
2	B	900	AWR	CAH-CAF	2.09	1.39	1.36
2	C	900	AWR	CAH-CAF	2.11	1.39	1.36
2	A	900	AWR	CAH-CAF	2.21	1.39	1.36
2	D	900	AWR	CAR-CAV	2.32	1.46	1.42
2	D	900	AWR	CAH-CAF	2.58	1.39	1.36

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	900	AWR	CAF-CAH-CAT	-2.31	117.54	119.71
2	C	900	AWR	CAF-CAH-CAT	-2.30	117.55	119.71
2	B	900	AWR	CAF-CAH-CAT	-2.29	117.56	119.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	AWR	CAF-CAH-CAT	-2.29	117.56	119.71
2	C	900	AWR	CAM-CAN-NAW	3.31	115.09	112.29
2	D	900	AWR	CAM-CAN-NAW	3.60	115.33	112.29
2	B	900	AWR	CAX-CAR-CAV	5.04	122.75	119.58
2	D	900	AWR	CAX-CAR-CAV	6.16	123.46	119.58
2	A	900	AWR	CAX-CAR-CAV	9.30	125.44	119.58
2	C	900	AWR	CAX-CAR-CAV	10.50	126.19	119.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	AWR	1	0
2	D	900	AWR	3	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	344/382 (90%)	-0.47	3 (0%) 85 86	17, 32, 54, 82	0
1	B	342/382 (89%)	-0.45	3 (0%) 85 86	22, 35, 64, 93	0
1	C	342/382 (89%)	-0.36	1 (0%) 94 95	18, 41, 71, 86	0
1	D	342/382 (89%)	-0.27	1 (0%) 94 95	25, 49, 82, 109	0
All	All	1370/1528 (89%)	-0.39	8 (0%) 90 91	17, 39, 71, 109	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	408	THR	4.0
1	B	214	ASP	2.6
1	A	412	LYS	2.5
1	A	408	THR	2.4
1	D	316	GLN	2.3
1	B	414	GLU	2.2
1	C	408	THR	2.2
1	A	481	LYS	2.1

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. 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
1	PTR	C	321	16/17	0.97	0.14	-	34,36,37,38	0
1	PTR	B	321	16/17	0.99	0.11	-	31,35,36,36	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	PTR	D	321	16/17	0.96	0.14	-	46,48,50,53	0
1	PTR	A	321	16/17	0.98	0.11	-	21,23,24,25	0

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(\AA^2)	Q<0.9
2	AWR	D	900	24/24	0.95	0.20	3.33	36,40,56,57	0
3	PO4	D	1482	5/5	0.89	0.22	2.52	65,66,69,69	0
2	AWR	B	900	24/24	0.95	0.18	1.72	35,37,51,56	0
2	AWR	C	900	24/24	0.95	0.16	1.31	26,27,38,39	0
2	AWR	A	900	24/24	0.96	0.14	0.09	32,36,52,60	0
3	PO4	B	1485	5/5	0.96	0.14	-0.34	41,44,44,47	0
3	PO4	A	1483	5/5	0.96	0.09	-2.43	66,68,71,72	0
3	PO4	B	1483	5/5	0.96	0.10	-	53,55,55,55	0
3	PO4	A	1484	5/5	0.99	0.08	-	34,36,37,37	0
3	PO4	D	1484	5/5	0.97	0.10	-	62,62,64,66	0
3	PO4	B	1484	5/5	0.96	0.15	-	50,51,53,56	0
3	PO4	C	1483	5/5	0.98	0.06	-	58,59,63,63	0
3	PO4	D	1483	5/5	0.97	0.10	-	59,60,61,62	0
3	PO4	C	1484	5/5	0.97	0.16	-	58,59,62,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.