



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 21, 2016 – 01:25 PM EST

PDB ID : 5A54
Title : DYRK1A IN COMPLEX WITH NITRO BENZOTHAZOLE FRAGMENT
Authors : Rothweiler, U.
Deposited on : 2015-06-16
Resolution : 2.63 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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.

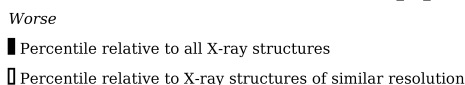
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
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) : rb-20028442

i





X-RAY DIFFRACTION

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	3377 (2.68-2.60)
Clashscore	102246	3781 (2.68-2.60)
Ramachandran outliers	100387	3722 (2.68-2.60)
Sidechain outliers	100360	3722 (2.68-2.60)
RSRZ outliers	91569	3388 (2.68-2.60)

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 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	368	 <div>89% 7%</div>
1	B	368	 <div>88% 8%</div>
1	C	368	 <div>87% 10%</div>
1	D	368	 <div>85% 6% 9%</div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11063 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.

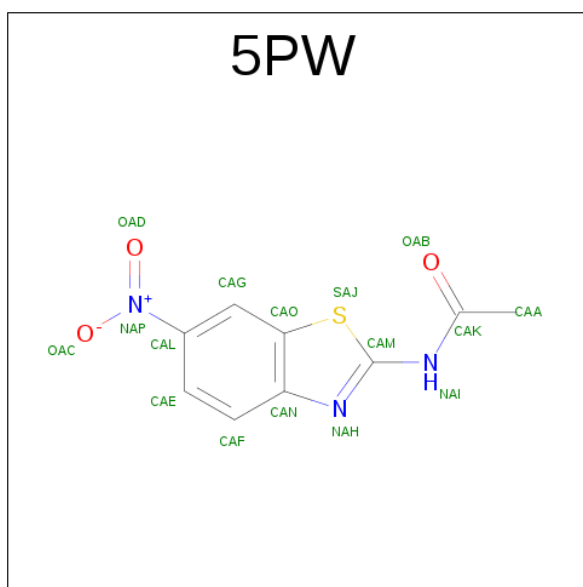
- Molecule 1 is a protein called DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION-REGULATED KINASE 1A.

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
			2726	1760	457	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-(6-NITRO-1,3-BENZOTHAZOL-2-YL)ETHANAMIDE (three-letter code: 5PW) (formula: C₉H₇N₃O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			16	9	3	3	1		
2	B	1	Total	C	N	O	S	0	0
			16	9	3	3	1		
2	C	1	Total	C	N	O	S	0	0
			16	9	3	3	1		
2	D	1	Total	C	N	O	S	0	0
			16	9	3	3	1		


- Molecule 3 is water.

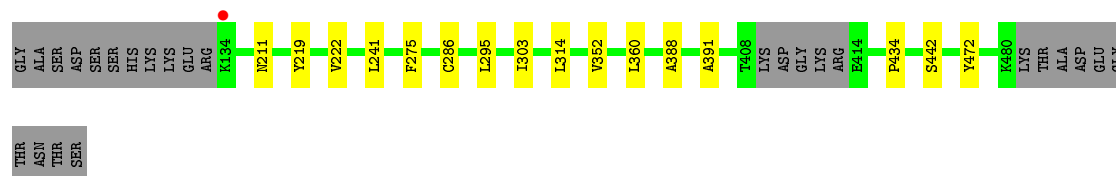
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	18	Total	O	0	0
			18	18		
3	B	4	Total	O	0	0
			4	4		
3	C	11	Total	O	0	0
			11	11		
3	D	11	Total	O	0	0
			11	11		

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.

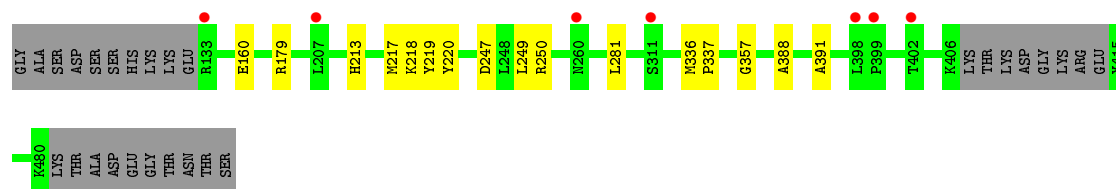
- Molecule 1: DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION-REGULATED KINASE 1A

Chain A: 




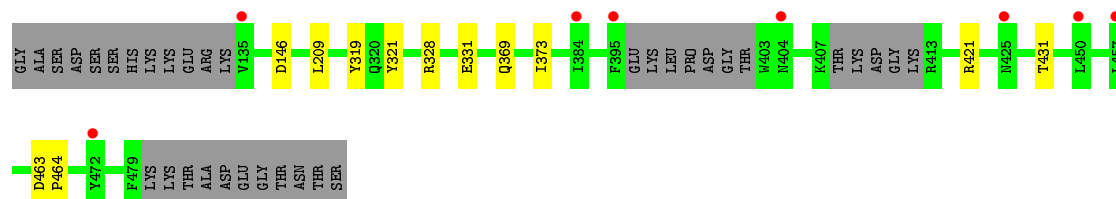
- Molecule 1: DUAL SPECIFICITY TYROSINE-PHOSPHORYLATION-REGULATED KINASE 1A

Chain B: 




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

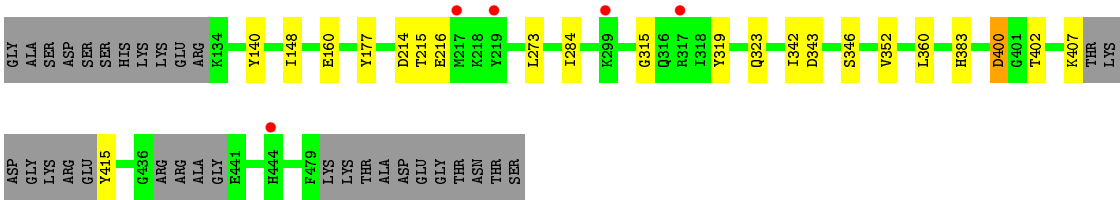
Chain C: 



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

Chain D: 





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.82Å 88.02Å 228.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.19 – 2.63 48.19 – 2.63	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.19-2.63) 95.3 (48.19-2.63)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.222 , 0.255 0.199 , 0.227	Depositor DCC
R_{free} test set	2000 reflections (4.05%)	DCC
Wilson B-factor (Å ²)	50.4	Xtriage
Anisotropy	0.674	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 21.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.278 for k,h,-l	Xtriage
Reported twinning fraction	0.726 for H, K, L 0.274 for K, H, -L	Depositor
Outliers	0 of 53493 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11063	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% 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: 5PW, 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	0.30	0/2838	0.49	0/3829
1	B	0.29	0/2808	0.48	0/3789
1	C	0.29	0/2724	0.48	0/3686
1	D	0.30	0/2773	0.48	0/3743
All	All	0.30	0/11143	0.48	0/15047

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	8	0
1	B	2761	0	2745	7	0
1	C	2678	0	2599	3	0
1	D	2726	0	2704	10	0
2	A	16	0	0	1	0
2	B	16	0	0	1	0
2	C	16	0	0	1	0
2	D	16	0	0	1	0
3	A	18	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	4	0	0	0	0
3	C	11	0	0	0	0
3	D	11	0	0	0	0
All	All	11063	0	10824	30	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.

The worst 5 of 30 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:B:1482:5PW:CAA	2:B:1482:5PW:SAJ	2.79	0.70
1:A:472:TYR:OH	1:D:383:HIS:HA	1.96	0.65
2:A:1482:5PW:CAA	2:A:1482:5PW:SAJ	2.85	0.65
2:D:1481:5PW:CAA	2:D:1481:5PW:SAJ	2.84	0.65
1:B:249:LEU:HD22	1:B:357:GLY:HA2	1.82	0.60

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	337/368 (92%)	316 (94%)	20 (6%)	1 (0%)	46	70
1	B	335/368 (91%)	311 (93%)	22 (7%)	2 (1%)	30	53
1	C	326/368 (89%)	305 (94%)	19 (6%)	2 (1%)	30	53
1	D	328/368 (89%)	309 (94%)	17 (5%)	2 (1%)	30	53
All	All	1326/1472 (90%)	1241 (94%)	78 (6%)	7 (0%)	34	57

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	216	GLU
1	C	421	ARG
1	D	215	THR
1	B	219	TYR
1	C	331	GLU

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%)	298 (99%)	2 (1%)	88	96
1	B	296/324 (91%)	296 (100%)	0	100	100
1	C	282/324 (87%)	278 (99%)	4 (1%)	74	90
1	D	294/324 (91%)	291 (99%)	3 (1%)	82	93
All	All	1172/1296 (90%)	1163 (99%)	9 (1%)	86	95

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	319	TYR
1	D	400	ASP
1	D	214	ASP
1	C	146	ASP
1	C	431	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	320	GLN
1	B	213	HIS
1	D	201	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	A	321	1	13,16,17	0.68	0	19,22,24	0.84	0
1	PTR	B	321	1	13,16,17	0.67	0	19,22,24	0.86	0
1	PTR	C	321	1	13,16,17	0.67	0	19,22,24	0.92	1 (5%)
1	PTR	D	321	1	13,16,17	0.73	0	19,22,24	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 (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	321	PTR	O3P-P-O2P	2.58	116.91	107.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

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

5.5 Carbohydrates ⓘ

There are no carbohydrates 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	5PW	A	1482	-	12,17,17	3.57	4 (33%)	12,24,24	2.08	7 (58%)
2	5PW	B	1482	-	12,17,17	3.67	4 (33%)	12,24,24	2.31	4 (33%)
2	5PW	C	1481	-	12,17,17	2.43	4 (33%)	12,24,24	1.82	5 (41%)
2	5PW	D	1481	-	12,17,17	3.62	4 (33%)	12,24,24	1.94	3 (25%)

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	5PW	A	1482	-	-	0/6/8/8	0/2/2/2
2	5PW	B	1482	-	-	0/6/8/8	0/2/2/2
2	5PW	C	1481	-	-	0/6/8/8	0/2/2/2
2	5PW	D	1481	-	-	0/6/8/8	0/2/2/2

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1482	5PW	CAF-CAN	-4.32	1.34	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1481	5PW	CAF-CAN	-4.28	1.34	1.41
2	C	1481	5PW	CAF-CAN	-4.25	1.34	1.41
2	B	1482	5PW	CAF-CAN	-4.06	1.34	1.41
2	B	1482	5PW	CAG-CAO	-2.29	1.33	1.37

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1482	5PW	OAB-CAK-CAA	-2.22	117.99	122.07
2	B	1482	5PW	OAB-CAK-CAA	-2.20	118.02	122.07
2	C	1481	5PW	CAE-CAL-CAG	-2.18	117.28	120.68
2	B	1482	5PW	CAE-CAL-CAG	-2.18	117.28	120.68
2	A	1482	5PW	CAE-CAL-CAG	-2.04	117.50	120.68

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1482	5PW	1	0
2	B	1482	5PW	1	0
2	C	1481	5PW	1	0
2	D	1481	5PW	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%)	-0.00	1 (0%) 94 94	32, 48, 70, 89	0
1	B	339/368 (92%)	0.23	7 (2%) 67 61	36, 61, 88, 111	0
1	C	332/368 (90%)	0.26	8 (2%) 62 56	37, 67, 99, 108	0
1	D	334/368 (90%)	0.11	5 (1%) 76 71	37, 60, 88, 104	0
All	All	1346/1472 (91%)	0.15	21 (1%) 74 70	32, 59, 92, 111	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	217	MET	4.4
1	B	399	PRO	3.9
1	B	133	ARG	3.8
1	C	450	LEU	3.8
1	C	135	VAL	3.5

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

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	D	321	16/17	0.94	0.16	-	49,51,56,57	0
1	PTR	B	321	16/17	0.96	0.17	-	58,66,68,68	0
1	PTR	C	321	16/17	0.89	0.19	-	61,65,67,67	0
1	PTR	A	321	16/17	0.96	0.16	-	40,42,45,46	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	5PW	D	1481	16/16	0.90	0.20	0.84	49,52,58,58	0
2	5PW	B	1482	16/16	0.94	0.19	0.07	51,54,58,61	0
2	5PW	C	1481	16/16	0.93	0.18	-0.03	51,54,57,57	0
2	5PW	A	1482	16/16	0.94	0.17	-0.05	45,47,49,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.