



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:39 AM GMT

PDB ID : 2BAL
Title : p38alpha MAP kinase bound to pyrazoloamine
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Deposited on : 2005-10-14
Resolution : 2.10 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

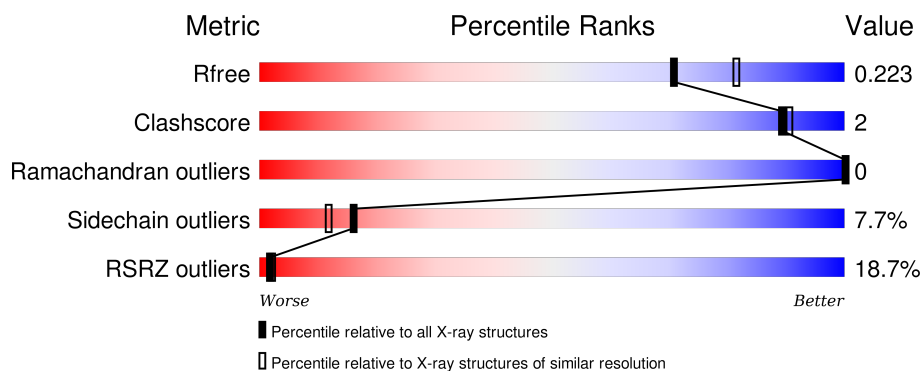
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	365	<div> <div>17%</div> <div> <div></div> <div>81%</div> <div>10%</div> <div>7%</div> </div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2843 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.

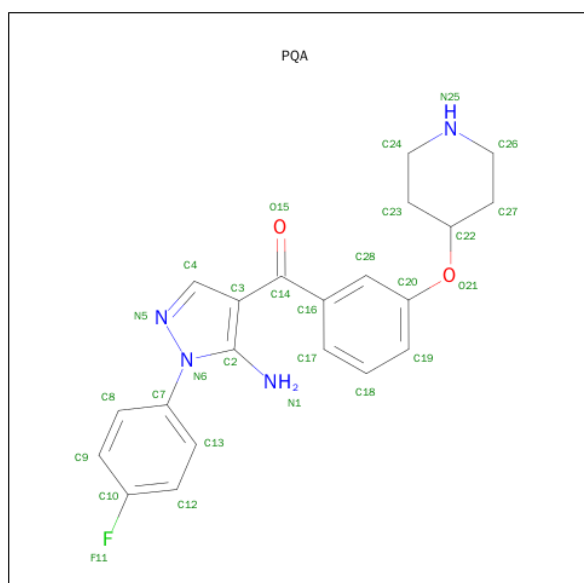
- Molecule 1 is a protein called Mitogen-activated protein kinase 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	338	2726	1750	465	498	13	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	HIS	-	EXPRESSION TAG	UNP Q16539
A	-3	HIS	-	EXPRESSION TAG	UNP Q16539
A	-2	HIS	-	EXPRESSION TAG	UNP Q16539
A	-1	HIS	-	EXPRESSION TAG	UNP Q16539
A	0	HIS	-	EXPRESSION TAG	UNP Q16539
A	1	HIS	-	EXPRESSION TAG	UNP Q16539
A	162	CSS	CYS	MODIFIED RESIDUE	UNP Q16539

- Molecule 2 is [5-AMINO-1-(4-FLUOROPHENYL)-1H-PYRAZOL-4-YL][3-(PIPERIDIN-4-YLOXY)PHENYL]METHANONE (three-letter code: PQA) (formula: C₂₁H₂₁FN₄O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			28	21	1	4	2		

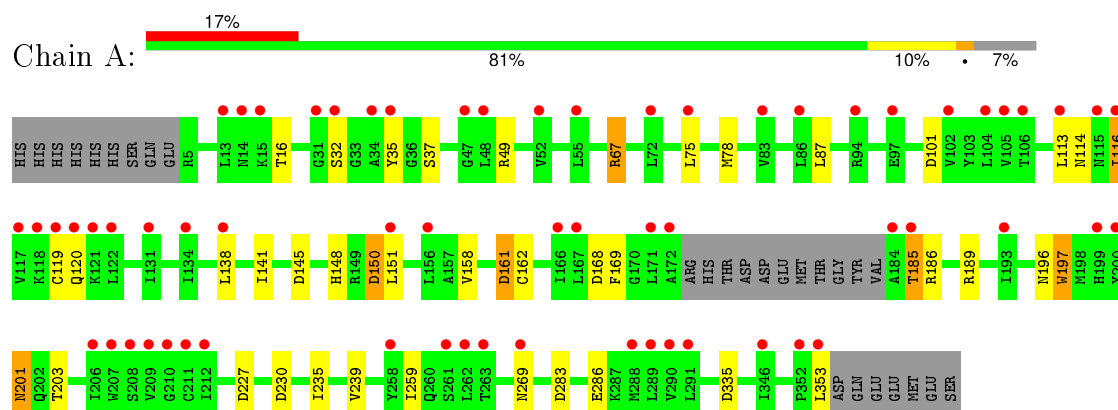
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	89	Total	O	0	0
			89	89		

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: Mitogen-activated protein kinase 14



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.19Å 75.16Å 77.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.54 – 2.10 24.51 – 2.10	Depositor EDS
% Data completeness (in resolution range)	89.1 (24.54-2.10) 89.1 (24.51-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.15 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.217 , 0.265 0.234 , 0.223	Depositor DCC
R_{free} test set	1067 reflections (5.50%)	DCC
Wilson B-factor (Å ²)	37.4	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.0	EDS
Estimated twinning fraction	0.027 for -h,l,k	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 21402 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2843	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.94% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.44	0/2781	0.73	8/3774 (0.2%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	230	ASP	CB-CG-OD2	5.94	123.64	118.30
1	A	283	ASP	CB-CG-OD2	5.64	123.37	118.30
1	A	150	ASP	CB-CG-OD2	5.47	123.22	118.30
1	A	227	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	101	ASP	CB-CG-OD2	5.25	123.02	118.30
1	A	145	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	335	ASP	CB-CG-OD2	5.19	122.97	118.30
1	A	168	ASP	CB-CG-OD2	5.03	122.83	118.30

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	2726	0	2731	13	0
2	A	28	0	21	0	0
3	A	89	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	2843	0	2752	13	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 (13) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:HIS:CD2	1:A:169:PHE:HA	2.17	0.80
1:A:148:HIS:CD2	1:A:169:PHE:CA	2.85	0.60
1:A:35:TYR:CE1	1:A:67:ARG:HG3	2.41	0.55
1:A:78:MET:HG3	1:A:169:PHE:CZ	2.43	0.54
1:A:116:ILE:HG21	1:A:158:VAL:CG2	2.39	0.53
1:A:148:HIS:HD2	1:A:169:PHE:HB3	1.75	0.50
1:A:150:ASP:OD1	1:A:185:THR:OG1	2.27	0.50
1:A:138:LEU:HD23	1:A:141:ILE:HD11	1.94	0.50
1:A:201:ASN:ND2	1:A:203:THR:OG1	2.44	0.48
1:A:161:ASP:O	1:A:162:CSS:HB3	2.14	0.48
1:A:235:ILE:O	1:A:239:VAL:HG22	2.18	0.43
1:A:197:TRP:CZ3	1:A:259:ILE:HD11	2.54	0.41
1:A:116:ILE:HG21	1:A:158:VAL:HG21	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	333/365 (91%)	324 (97%)	9 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	298 / 324 (92%)	275 (92%)	23 (8%)	16	12

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	THR
1	A	32	SER
1	A	37	SER
1	A	49	ARG
1	A	67	ARG
1	A	75	LEU
1	A	87	LEU
1	A	113	LEU
1	A	114	ASN
1	A	116	ILE
1	A	119	CYS
1	A	120	GLN
1	A	151	LEU
1	A	161	ASP
1	A	185	THR
1	A	186	ARG
1	A	189	ARG
1	A	196	ASN
1	A	197	TRP
1	A	201	ASN
1	A	269	ASN
1	A	286	GLU
1	A	353	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	HIS
1	A	114	ASN

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Mol	Chain	Res	Type
1	A	196	ASN
1	A	201	ASN
1	A	272	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	CSS	A	162	1	4,6,7	0.58	0	3,6,8	1.66	1 (33%)

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	CSS	A	162	1	-	0/1/5/7	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	CSS	O-C-CA	-2.80	118.19	125.49

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	A	162	CSS	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	PQA	A	401	-	28,31,31	0.93	2 (7%)	31,43,43	1.77	7 (22%)

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	PQA	A	401	-	-	0/12/24/24	1/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	PQA	C3-C14	-2.30	1.45	1.50
2	A	401	PQA	C13-C7	2.03	1.41	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	401	PQA	C13-C7-N6	-4.14	113.80	119.50
2	A	401	PQA	C20-O21-C22	-3.07	114.14	119.06
2	A	401	PQA	C8-C9-C10	2.09	120.60	118.35
2	A	401	PQA	C23-C24-N25	2.23	114.24	110.46
2	A	401	PQA	C24-C23-C22	2.45	112.77	110.19
2	A	401	PQA	C26-C27-C22	3.84	114.24	110.19
2	A	401	PQA	C8-C7-N6	5.08	126.48	119.50

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	PQA	C22-C23-C24-C26-C27-N25

No monomer is involved in short contacts.

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	337/365 (92%)	1.07	63 (18%) 2 2	18, 26, 44, 56	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	119	CYS	8.8
1	A	120	GLN	6.7
1	A	14	ASN	5.6
1	A	48	LEU	5.6
1	A	104	LEU	5.5
1	A	353	LEU	5.4
1	A	121	LYS	5.3
1	A	118	LYS	5.3
1	A	184	ALA	5.2
1	A	134	ILE	4.9
1	A	185	THR	4.9
1	A	131	ILE	4.6
1	A	209	VAL	4.5
1	A	166	ILE	4.2
1	A	263	THR	4.1
1	A	94	ARG	4.0
1	A	34	ALA	3.9
1	A	211	CYS	3.8
1	A	352	PRO	3.7
1	A	207	TRP	3.6
1	A	52	VAL	3.6
1	A	171	LEU	3.5
1	A	200	TYR	3.4
1	A	117	VAL	3.4
1	A	138	LEU	3.3
1	A	102	VAL	3.3
1	A	289	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	172	ALA	3.2
1	A	206	ILE	3.1
1	A	105	VAL	3.0
1	A	13	LEU	3.0
1	A	55	LEU	3.0
1	A	193	ILE	2.9
1	A	35	TYR	2.9
1	A	210	GLY	2.9
1	A	15	LYS	2.9
1	A	116	ILE	2.8
1	A	97	GLU	2.5
1	A	269	ASN	2.5
1	A	261	SER	2.5
1	A	208	SER	2.4
1	A	290	VAL	2.4
1	A	75	LEU	2.4
1	A	151	LEU	2.4
1	A	258	TYR	2.4
1	A	346	ILE	2.3
1	A	115	ASN	2.3
1	A	72	LEU	2.3
1	A	31	GLY	2.3
1	A	262	LEU	2.3
1	A	156	LEU	2.2
1	A	106	THR	2.2
1	A	122	LEU	2.2
1	A	291	LEU	2.2
1	A	212	ILE	2.1
1	A	86	LEU	2.1
1	A	113	LEU	2.1
1	A	288	MET	2.1
1	A	199	HIS	2.1
1	A	47	GLY	2.1
1	A	32	SER	2.1
1	A	83	VAL	2.0
1	A	167	LEU	2.0

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	CSS	A	162	7/8	0.91	0.12	-	24,25,25,27	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(Å ²)	Q<0.9
2	PQA	A	401	28/28	0.85	0.17	-0.40	20,26,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.