



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 03:10 am GMT

PDB ID : 4IZA  
Title : Structure of Dually Phosphorylated ERK2 bound to the PEA-15 Death Effector Domain  
Authors : Mace, P.D.; Robinson, H.; Riedl, S.J.  
Deposited on : 2013-01-29  
Resolution : 1.93 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](mailto: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.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

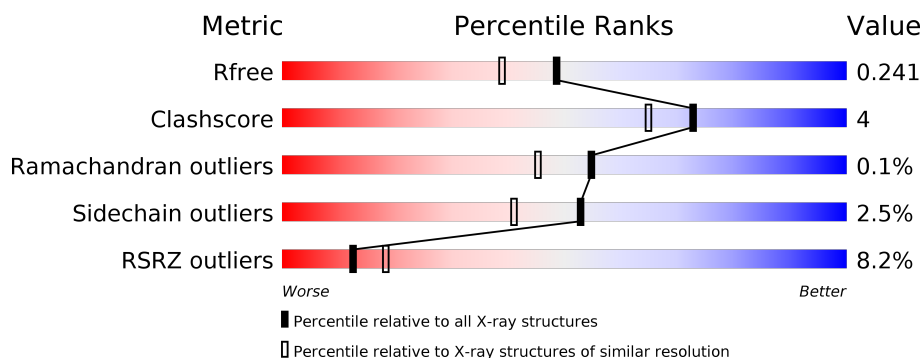
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.93 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))
$R_{free}$	100719	3233 (1.96-1.92)
Clashscore	112137	3430 (1.96-1.92)
Ramachandran outliers	110173	3395 (1.96-1.92)
Sidechain outliers	110143	3395 (1.96-1.92)
RSRZ outliers	101464	3250 (1.96-1.92)

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  $\geq 3$ , 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	356	<div> <div>6%</div> <div>87%</div> <div>10%</div> <div>••</div> </div>
1	C	356	<div> <div>11%</div> <div>82%</div> <div>12%</div> <div>• 6%</div> </div>
2	B	97	<div> <div>3%</div> <div>88%</div> <div>10%</div> <div>•</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6913 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 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	348	Total	C	N	O	P	S	0	5	0
			2852	1829	483	523	2	15			
1	C	335	Total	C	N	O	S		0	5	0
			2675	1726	455	479	15				

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	GLY	-	EXPRESSION TAG	UNP P28482
A	6	PRO	-	EXPRESSION TAG	UNP P28482
A	7	GLY	-	EXPRESSION TAG	UNP P28482
C	5	GLY	-	EXPRESSION TAG	UNP P28482
C	6	PRO	-	EXPRESSION TAG	UNP P28482
C	7	GLY	-	EXPRESSION TAG	UNP P28482

- Molecule 2 is a protein called Astrocytic phosphoprotein PEA-15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	95	Total	C	N	O	S	0	2	0
			753	470	121	159	3			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	EXPRESSION TAG	UNP Q15121

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	385	Total	O	0	0
			385	385		

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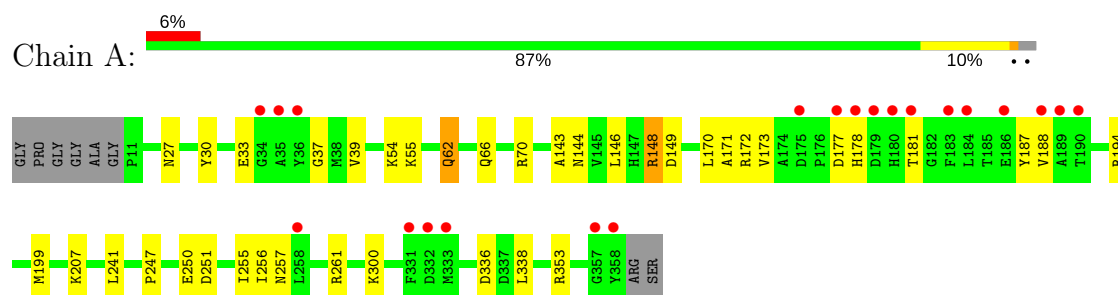
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	179	Total 179	O 179	0	0
3	B	69	Total 69	O 69	0	0

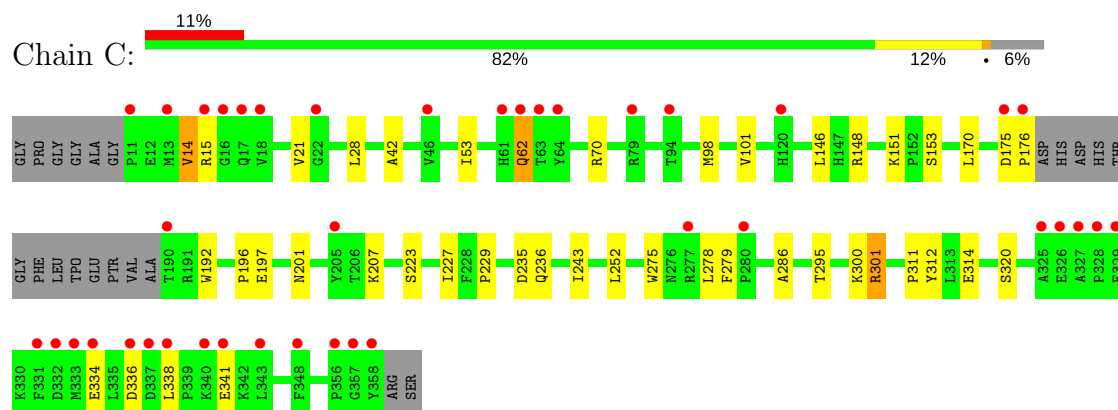
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

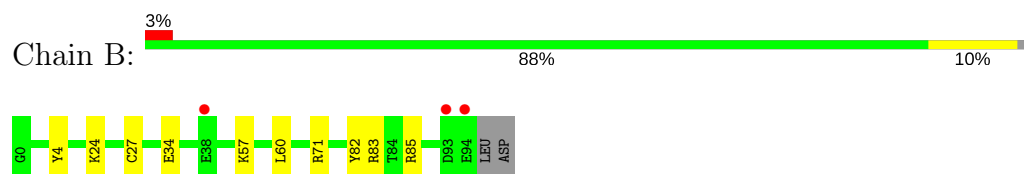
#### • Molecule 1: Mitogen-activated protein kinase 1



#### • Molecule 1: Mitogen-activated protein kinase 1



#### • Molecule 2: Astrocytic phosphoprotein PEA-15



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.76Å 204.02Å 61.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.72 – 1.93 29.72 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.72-1.93) 99.8 (29.72-1.93)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.82 (at 1.93Å)	Xtriage
Refinement program	REFMAC 5.6.0107	Depositor
R, $R_{free}$	0.197 , 0.243 0.196 , 0.241	Depositor DCC
$R_{free}$ test set	3515 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.8	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 53.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6913	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, 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	0.69	0/2911	0.69	3/3946 (0.1%)
1	C	0.55	0/2766	0.64	2/3760 (0.1%)
2	B	0.67	1/774 (0.1%)	0.66	0/1049
All	All	0.63	1/6451 (0.0%)	0.66	5/8755 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	27	CYS	CB-SG	-6.12	1.71	1.82

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	301	ARG	NE-CZ-NH2	-8.71	115.95	120.30
1	C	301	ARG	NE-CZ-NH1	7.66	124.13	120.30
1	A	251	ASP	CB-CG-OD2	7.57	125.11	118.30
1	A	251	ASP	CB-CG-OD1	-6.87	112.12	118.30
1	A	148	ARG	NE-CZ-NH2	-5.03	117.78	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	2852	0	2806	16	1
1	C	2675	0	2624	22	0
2	B	753	0	711	11	0
3	A	385	0	0	0	1
3	B	69	0	0	1	0
3	C	179	0	0	3	0
All	All	6913	0	6141	48	1

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 4.

All (48) 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:98:MET:HE2	1:C:101:VAL:HG22	1.75	0.69
1:A:172[B]:ARG:HG2	1:A:173:VAL:O	1.96	0.64
2:B:60:LEU:HD11	2:B:82:TYR:CE2	2.35	0.62
2:B:85:ARG:HG3	2:B:85:ARG:HH11	1.65	0.62
1:A:188:VAL:HG12	1:A:194:ARG:HH22	1.67	0.58
1:A:241:LEU:HD22	1:A:247:PRO:HD3	1.84	0.58
1:C:146:LEU:HD22	1:C:207:LYS:HA	1.86	0.57
1:A:255:ILE:O	1:A:261:ARG:NH2	2.39	0.56
1:C:243:ILE:HG12	1:C:278:LEU:HD11	1.88	0.54
1:A:37:GLY:HA2	1:A:55:LYS:O	2.08	0.53
1:C:192:TRP:CD1	1:C:229:PRO:HA	2.44	0.52
2:B:60:LEU:HD12	2:B:83:ARG:CG	2.39	0.52
1:A:30:TYR:OH	1:A:33:GLU:HB2	2.10	0.51
1:A:146:LEU:HD22	1:A:207:LYS:HA	1.91	0.51
1:C:98:MET:CE	1:C:101:VAL:HG22	2.40	0.51
2:B:85:ARG:HG3	2:B:85:ARG:NH1	2.26	0.50
1:A:149:ASP:OD2	1:A:187:PTR:O1P	2.30	0.49
2:B:60:LEU:HD11	2:B:82:TYR:HE2	1.78	0.49
2:B:60:LEU:HD12	2:B:83:ARG:HG2	1.95	0.49
1:A:66:GLN:OE1	1:A:70[A]:ARG:NH1	2.40	0.49
2:B:4:TYR:CD1	2:B:57:LYS:HA	2.48	0.48
2:B:83:ARG:NH1	3:B:136:HOH:O	2.46	0.48
1:C:295:THR:O	1:C:301:ARG:HD3	2.13	0.48
1:C:62:GLN:NE2	1:C:338:LEU:O	2.46	0.48
1:C:14:VAL:HG23	1:C:15[B]:ARG:HD3	1.95	0.48
1:C:223:SER:HB3	1:C:279:PHE:HE1	1.79	0.47
1:C:311:PRO:HA	1:C:314:GLU:HG3	1.96	0.47
1:C:28:LEU:HD23	1:C:42:ALA:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:175:ASP:N	1:C:176:PRO:HD3	2.31	0.45
1:C:148:ARG:HD3	1:C:170:LEU:O	2.17	0.44
2:B:60:LEU:HD11	2:B:82:TYR:CD2	2.51	0.44
1:C:236:GLN:NE2	3:C:549:HOH:O	2.29	0.44
1:A:39:VAL:HG22	1:A:54:LYS:HB3	2.00	0.44
2:B:24:LYS:O	2:B:34:GLU:OE1	2.36	0.44
1:C:201[B]:ASN:ND2	3:C:538:HOH:O	2.52	0.43
1:C:286:ALA:HB2	1:C:312:TYR:CE1	2.53	0.43
1:A:143:ALA:O	1:A:144:ASN:HB3	2.19	0.43
1:A:62:GLN:NE2	1:A:338:LEU:O	2.43	0.43
1:A:199:MET:O	2:B:71:ARG:HD2	2.19	0.43
1:C:151:LYS:HE3	1:C:153:SER:OG	2.19	0.43
1:C:227:ILE:HD11	1:C:275:TRP:CZ3	2.54	0.42
1:A:148:ARG:HD3	1:A:170:LEU:O	2.20	0.42
1:A:250:GLU:CD	1:A:300:LYS:HZ1	2.22	0.42
1:A:70[A]:ARG:HD3	1:A:171:ALA:O	2.19	0.41
1:C:197:GLU:OE2	1:C:301:ARG:NH2	2.44	0.41
1:C:223:SER:HB3	1:C:279:PHE:CE1	2.55	0.41
1:C:300:LYS:NZ	3:C:481:HOH:O	2.54	0.41
1:C:21:VAL:HG11	1:C:53:ILE:HG21	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:ASP:OD2	3:A:457:HOH:O[2_655]	2.11	0.09

## 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	349/356 (98%)	338 (97%)	10 (3%)	1 (0%)	44 33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	336/356 (94%)	320 (95%)	16 (5%)	0	100	100
2	B	95/97 (98%)	93 (98%)	2 (2%)	0	100	100
All	All	780/809 (96%)	751 (96%)	28 (4%)	1 (0%)	55	45

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	257	ASN

### 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	309/316 (98%)	302 (98%)	7 (2%)	56	45
1	C	287/316 (91%)	276 (96%)	11 (4%)	38	23
2	B	85/91 (93%)	85 (100%)	0	100	100
All	All	681/723 (94%)	663 (97%)	18 (3%)	53	39

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ASN
1	A	62	GLN
1	A	178	HIS
1	A	181	THR
1	A	256	ILE
1	A	336	ASP
1	A	353	ARG
1	C	14	VAL
1	C	62	GLN
1	C	70	ARG
1	C	196	PRO
1	C	235	ASP
1	C	252	LEU

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Mol	Chain	Res	Type
1	C	320[A]	SER
1	C	320[B]	SER
1	C	334	GLU
1	C	336	ASP
1	C	341	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	ASN
1	A	62	GLN
1	A	97	GLN
1	A	123	ASN
1	C	47	ASN
1	C	62	GLN
1	C	66	GLN
1	C	123	ASN
1	C	238	ASN
1	C	249	GLN
1	C	253	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	TPO	A	185	1	9,10,11	0.80	0	10,14,16	1.43	2 (20%)
1	PTR	A	187	1	15,16,17	2.13	2 (13%)	19,22,24	0.75	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	TPO	A	185	1	-	0/8/11/13	0/0/0/0
1	PTR	A	187	1	-	0/9/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	187	PTR	OH-CZ	-7.70	1.22	1.40
1	A	187	PTR	CA-C	2.45	1.53	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	TPO	O-C-CA	-2.11	120.22	125.15
1	A	185	TPO	C-CA-N	2.62	115.16	109.86

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	187	PTR	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	346/356 (97%)	0.33	21 (6%) 22 29	7, 18, 41, 59	0
1	C	335/356 (94%)	0.62	40 (11%) 5 8	13, 28, 54, 71	0
2	B	95/97 (97%)	0.16	3 (3%) 48 57	14, 21, 42, 54	0
All	All	776/809 (95%)	0.43	64 (8%) 12 18	7, 23, 51, 71	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	181	THR	8.4
1	C	333	MET	7.6
1	C	332	ASP	7.0
1	A	35	ALA	6.6
1	A	36	TYR	6.4
1	A	178	HIS	5.8
1	C	327	ALA	5.8
1	A	183	PHE	5.6
1	A	180[A]	HIS	5.4
1	C	22	GLY	5.3
1	A	184	LEU	5.2
1	A	179	ASP	5.0
1	C	175	ASP	5.0
1	A	188	VAL	5.0
2	B	93	ASP	4.9
1	C	205	TYR	4.8
1	C	356	PRO	4.6
1	A	332	ASP	4.5
1	C	16	GLY	4.5
1	C	357	GLY	3.8
1	A	333	MET	3.7
1	C	176	PRO	3.7
1	A	357	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	190	THR	3.5
1	C	13	MET	3.5
1	A	189	ALA	3.5
1	C	63	THR	3.5
1	C	334	GLU	3.5
1	C	331	PHE	3.4
1	C	343	LEU	3.4
1	A	186	GLU	3.2
1	C	358	TYR	3.1
2	B	38	GLU	3.1
1	C	336	ASP	3.1
1	C	94	THR	3.1
1	A	34	GLY	3.1
1	C	61	HIS	3.0
2	B	94	GLU	2.9
1	A	177	ASP	2.8
1	C	11	PRO	2.7
1	C	338	LEU	2.7
1	C	64	TYR	2.7
1	C	120[A]	HIS	2.7
1	A	331	PHE	2.6
1	C	18	VAL	2.6
1	A	175	ASP	2.6
1	C	15[A]	ARG	2.5
1	C	280	PRO	2.5
1	C	326	GLU	2.4
1	A	258	LEU	2.4
1	C	348	PHE	2.4
1	C	340	LYS	2.4
1	C	325	ALA	2.4
1	C	329	PHE	2.3
1	C	79	ARG	2.2
1	C	17	GLN	2.2
1	A	358	TYR	2.2
1	C	62	GLN	2.2
1	C	341	GLU	2.2
1	C	328	PRO	2.2
1	C	277	ARG	2.2
1	C	46	VAL	2.2
1	C	337	ASP	2.1
1	C	190	THR	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	PTR	A	187	16/17	0.92	0.23	-	37,48,51,52	0
1	TPO	A	185	11/12	0.77	0.27	-	52,54,55,55	0

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.