WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Oct 13, 2016 – 11:01 AM EDT

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PDB ID	:	5BT0
Title	:	Switching GFP fluorescence using genetically encoded phenyl azide chemistry through two different non-native post-translational modifications routes at the same position.
Authors	:	Hartley, A.M.; Worthy, H.L.; Reddington, S.C.; Rizkallah, P.J.; Jones, D.D.
Deposited on	:	2015-06-02
Resolution	:	2.03 Å(reported)

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.03 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	Percentile Ranks	Value
Rfree		0.214
Clashscore		5
Ramachandran outliers		0
Sidechain outliers		5.0%
RSRZ outliers		4.1%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
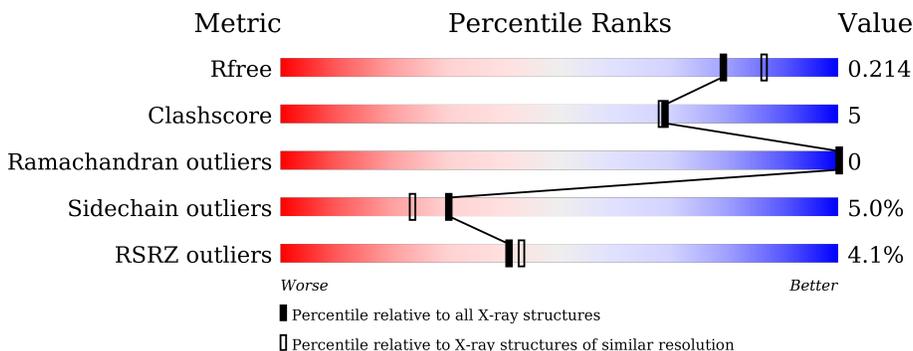
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	7858 (2.04-2.00)
Clashscore	102246	9060 (2.04-2.00)
Ramachandran outliers	100387	8952 (2.04-2.00)
Sidechain outliers	100360	8951 (2.04-2.00)
RSRZ outliers	91569	7873 (2.04-2.00)

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 <=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	231	2% 85% 13% •
1	B	231	6% 86% 11% •

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	SO4	A	301	-	-	-	X
2	SO4	A	303	-	-	-	X
2	SO4	B	301	-	-	-	X
2	SO4	B	303	-	-	-	X

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4079 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 Green fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	231	Total 1856	C 1175	N 319	O 356	S 6	0	2	0
1	B	231	Total 1848	C 1170	N 317	O 355	S 6	0	1	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	SER	-	expression tag	UNP A0A059PIQ0
A	30	ARG	SER	conflict	UNP A0A059PIQ0
A	?	CRO	THR	chromophore	UNP A0A059PIQ0
A	?	CRO	TYR	chromophore	UNP A0A059PIQ0
A	66	CRO	GLY	chromophore	UNP A0A059PIQ0
A	72	SER	ALA	conflict	UNP A0A059PIQ0
A	80	ARG	GLN	conflict	UNP A0A059PIQ0
A	148	HOX	HIS	conflict	UNP A0A059PIQ0
A	206	VAL	ALA	conflict	UNP A0A059PIQ0
B	2	SER	-	expression tag	UNP A0A059PIQ0
B	30	ARG	SER	conflict	UNP A0A059PIQ0
B	?	CRO	THR	chromophore	UNP A0A059PIQ0
B	?	CRO	TYR	chromophore	UNP A0A059PIQ0
B	66	CRO	GLY	chromophore	UNP A0A059PIQ0
B	72	SER	ALA	conflict	UNP A0A059PIQ0
B	80	ARG	GLN	conflict	UNP A0A059PIQ0
B	148	HOX	HIS	conflict	UNP A0A059PIQ0
B	206	VAL	ALA	conflict	UNP A0A059PIQ0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).
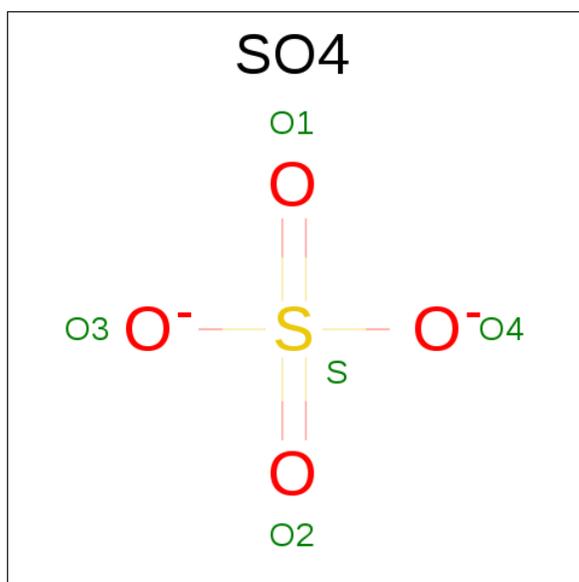
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 5	O 4	S 1	0	0
2	A	1	Total 5	O 4	S 1	0	0
2	A	1	Total 5	O 4	S 1	0	0
2	B	1	Total 5	O 4	S 1	0	0
2	B	1	Total 5	O 4	S 1	0	0
2	B	1	Total 5	O 4	S 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	175	Total 175	O 175	0	0
3	B	170	Total 170	O 170	0	0

3 Residue-property plots ⓘ

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: Green fluorescent protein
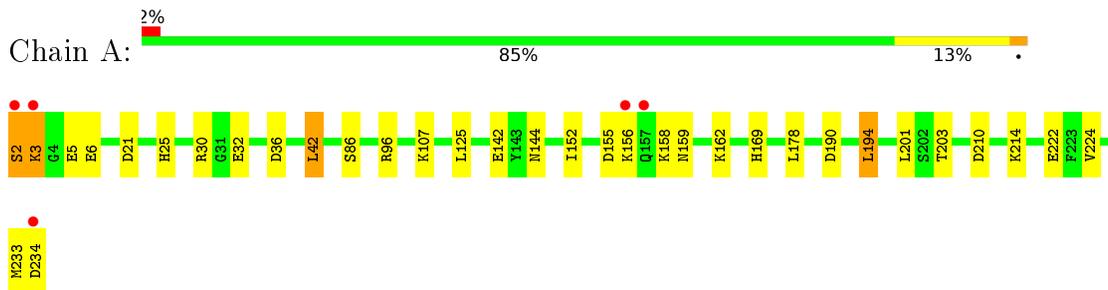
• Molecule 1: Green fluorescent protein
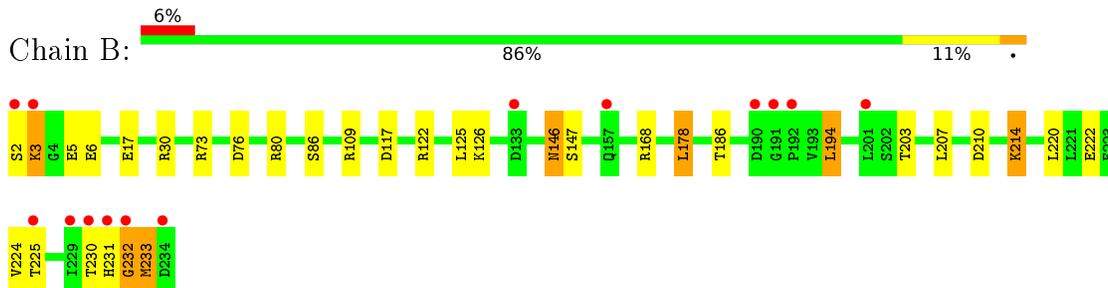
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	135.60Å 135.60Å 69.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.88 – 2.03 42.88 – 2.03	Depositor EDS
% Data completeness (in resolution range)	100.0 (42.88-2.03) 100.0 (42.88-2.03)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	3.73 (at 2.03Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.172 , 0.204 0.181 , 0.214	Depositor DCC
R_{free} test set	2133 reflections (5.33%)	DCC
Wilson B-factor (Å^2)	31.1	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 42.7	EDS
L-test for twinning[2]	$<|L|> = 0.46$, $<L^2> = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4079	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.
[2] Theoretical values of $<|L|>$, $<L^2>$ 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: SO4, HOX, CRO

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	0.92	1/1859 (0.1%)	0.98	6/2508 (0.2%)
1	B	0.93	2/1854 (0.1%)	1.02	7/2502 (0.3%)
All	All	0.93	3/3713 (0.1%)	1.00	13/5010 (0.3%)

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	1
1	B	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	222	GLU	CD-OE1	8.64	1.35	1.25
1	A	222	GLU	CD-OE1	8.14	1.34	1.25
1	B	232	GLY	N-CA	5.51	1.54	1.46

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	210	ASP	CB-CG-OD2	-6.93	112.07	118.30
1	B	73	ARG	NE-CZ-NH1	-6.92	116.84	120.30
1	B	210	ASP	CB-CG-OD1	6.25	123.93	118.30
1	B	178	LEU	CA-CB-CG	6.08	129.29	115.30
1	B	168	ARG	NE-CZ-NH1	-5.90	117.35	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2	SER	Peptide
1	B	232	GLY	Peptide

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	1856	0	1804	16	0
1	B	1848	0	1800	18	0
2	A	15	0	0	0	0
2	B	15	0	0	0	1
3	A	175	0	0	4	0
3	B	170	0	0	4	0
All	All	4079	0	3604	34	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 5.

The worst 5 of 34 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:142:GLU:CB	3:A:559:HOH:O	1.87	1.16
1:B:17:GLU:OE2	1:B:122:ARG:NH1	2.03	0.91
1:B:231:HIS:HB3	1:B:233:MET:SD	2.12	0.88
1:B:146:ASN:HD22	1:B:147:SER:H	1.31	0.76
1:A:42:LEU:HD12	1:A:42:LEU:C	2.12	0.70

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)
2:B:302:SO4:O4	2:B:302:SO4:O4[7_555]	1.73	0.47

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	227/231 (98%)	222 (98%)	5 (2%)	0	100	100
1	B	226/231 (98%)	222 (98%)	4 (2%)	0	100	100
All	All	453/462 (98%)	444 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	201/200 (100%)	191 (95%)	10 (5%)	30	24
1	B	201/200 (100%)	191 (95%)	10 (5%)	30	24
All	All	402/400 (100%)	382 (95%)	20 (5%)	30	24

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	234	ASP
1	B	3	LYS
1	B	194	LEU
1	A	214	LYS
1	A	233	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	177	GLN
1	B	135	ASN
1	B	177	GLN
1	A	169	HIS
1	B	169	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	HOX	A	148	1	10,12,13	0.82	0	13,15,17	0.98	1 (7%)
1	CRO	A	66	1	23,23,24	2.79	7 (30%)	30,32,34	2.31	11 (36%)
1	HOX	B	148	1	10,12,13	0.79	0	13,15,17	1.11	1 (7%)
1	CRO	B	66	1	23,23,24	3.27	5 (21%)	30,32,34	2.78	7 (23%)

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	HOX	A	148	1	-	0/4/6/8	0/1/1/1
1	CRO	A	66	1	-	0/12/31/32	0/2/2/2
1	HOX	B	148	1	-	0/4/6/8	0/1/1/1
1	CRO	B	66	1	-	0/12/31/32	0/2/2/2

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	66	CRO	CA2-C2	-4.44	1.43	1.48
1	A	66	CRO	CA1-C1	-4.11	1.45	1.51
1	A	66	CRO	CA2-C2	-3.34	1.44	1.48
1	A	66	CRO	C2-N3	-3.09	1.32	1.39
1	B	66	CRO	C2-N3	-2.68	1.33	1.39

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	66	CRO	O2-C2-CA2	-8.55	126.06	130.97
1	A	66	CRO	CA2-N2-C1	-5.51	100.91	105.54
1	A	66	CRO	CD1-CE1-CZ	-3.44	115.91	119.86
1	A	66	CRO	C1-CA1-N1	-3.32	102.04	108.99
1	B	66	CRO	CA1-C1-N3	-3.13	121.19	124.98

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)

6 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	SO4	A	301	-	4,4,4	0.62	0	6,6,6	0.60	0
2	SO4	A	302	-	4,4,4	0.56	0	6,6,6	0.30	0
2	SO4	A	303	-	4,4,4	0.57	0	6,6,6	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
2	SO4	B	301	-	4,4,4	0.54	0	6,6,6	0.17	0
2	SO4	B	302	-	4,4,4	0.45	0	6,6,6	0.21	0
2	SO4	B	303	-	4,4,4	0.67	0	6,6,6	0.47	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
2	SO4	A	301	-	-	0/0/0/0	0/0/0/0
2	SO4	A	302	-	-	0/0/0/0	0/0/0/0
2	SO4	A	303	-	-	0/0/0/0	0/0/0/0
2	SO4	B	301	-	-	0/0/0/0	0/0/0/0
2	SO4	B	302	-	-	0/0/0/0	0/0/0/0
2	SO4	B	303	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

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
2	B	302	SO4	0	1

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	229/231 (99%)	-0.03	5 (2%)	65	66	23, 36, 59, 97	0
1	B	229/231 (99%)	0.09	14 (6%)	25	26	25, 37, 64, 94	0
All	All	458/462 (99%)	0.03	19 (4%)	41	43	23, 37, 62, 97	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	ASP	6.7
1	A	2	SER	4.8
1	B	229	ILE	4.2
1	B	232	GLY	3.5
1	B	190	ASP	3.4

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	CRO	A	66	22/23	0.97	0.11	-	22,24,30,35	0
1	CRO	B	66	22/23	0.97	0.12	-	24,26,30,35	0
1	HOX	B	148	12/13	0.98	0.10	-	24,28,33,35	0
1	HOX	A	148	12/13	0.97	0.15	-	22,24,26,26	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	SO4	B	301	5/5	0.88	0.57	13.00	94,97,122,128	0
2	SO4	A	301	5/5	0.82	0.36	6.86	91,93,113,128	0
2	SO4	B	303	5/5	0.55	0.55	4.38	98,114,131,147	0
2	SO4	A	303	5/5	0.83	0.26	4.01	110,115,131,133	0
2	SO4	A	302	5/5	0.82	0.51	-	105,106,119,124	0
2	SO4	B	302	5/5	0.73	0.43	-	97,127,147,169	1

6.5 Other polymers (i)

There are no such residues in this entry.